Table S2. ***H. polygyrus*** **RNA-seq assembly automated annotation.**

		BLASTX							
Seq. Name	**Seq. Length**	**#Hits Blastx (Max 20)**	**Closest Blastx Hit eValue**	**Accession Number**	**Similarity**	**Score**	**Alignment length**	**Positives**	**Blastx Hit description**
Locus_1_Transcript_1/1_Conf_1.000	487	0							
Locus_10_Transcript_1/3_Conf_0.714	1415	0							
Locus_10_Transcript_2/3_Conf_0.714	1412	0							
Locus_10_Transcript_3/3_Conf_0.714	1412	0							
Locus_100_Transcript_1/1_Conf_1.000	670	20	1.95E-64	P51535.1	97	135.961	70	68	Myoglobin
Locus_1000_Transcript_1/1_Conf_1.000	1191	20	9.94E-145	XP_002641637.1	93	517.694	308	289	Hypothetical protein CBG09959
Locus_10000_Transcript_1/1_Conf_1.000	296	2	3.67E-04	XP_001893253.1	53	48.1358	89	48	hypothetical protein Bm1_08910
Locus_10001_Transcript_1/1_Conf_1.000	1203	20	2.20E-99	EFO22809.1	70	367.081	374	262	hypothetical protein LOAG_05677
Locus_10002_Transcript_1/1_Conf_1.000	1304	20	1.62E-159	CAB59919.1	83	567	386	324	hypothetical protein
Locus_10003_Transcript_1/1_Conf_1.000	517	20	3.87E-47	XP_002630442.1	73	191.045	156	114	Hypothetical protein CBG11175
Locus_10004_Transcript_1/1_Conf_1.000	2212	0							
Locus_10005_Transcript_1/1_Conf_1.000	226	0							
Locus_10006_Transcript_1/1_Conf_1.000	254	0							
Locus_10007_Transcript_1/1_Conf_1.000	140	17	1.84E-16	AAA69729.1	100	88.9669	43	43	immunoglobulin heavy chain
Locus_10008_Transcript_1/1_Conf_1.000	575	0							
Locus_10009_Transcript_1/1_Conf_1.000	1649	20	1.54E-168	NP_510624.1	76	597.43	509	391	hypothetical protein B0395.3

Locus_1001_Transcript_1/1_Conf_1.000	2115	20	0	XP_001892620.1	83	790.801	592	496	Vinculin family protein
Locus_10010_Transcript_1/1_Conf_1.000	416	0							
Locus_10011_Transcript_1/1_Conf_1.000	508	0							
Locus_10012_Transcript_1/1_Conf_1.000	401	3	4.34E-05	YP_002722239.1	39	51.2174	98	39	hypothetical protein BHWA1_02076
Locus_10013_Transcript_1/1_Conf_1.000	1561	20	1.93E-165	ACY40006.1	83	587.03	444	372	K+/cl- cotransporter protein 2, isoform a
Locus_10014_Transcript_1/1_Conf_1.000	543	20	3.06E-27	EFO17297.1	75	125.176	100	75	abhydrolase domain-containing protein 2
Locus_10015_Transcript_1/1_Conf_1.000	260	0							
Locus_10016_Transcript_1/1_Conf_1.000	2578	20	0	XP_002641770.1	77	798.89	844	650	C. briggsae CBR-EMB-9 protein
Locus_10017_Transcript_1/1_Conf_1.000	562	20	7.35E-75	XP_002631736.1	91	283.493	184	168	C. briggsae CBR-RAS-1 protein
Locus_10018_Transcript_1/1_Conf_1.000	179	0							
Locus_10019_Transcript_1/1_Conf_1.000	427	0							
Locus_1002_Transcript_1/1_Conf_1.000	306	2	4.72E-04	AAO63578.1	47	47.7506	69	33	secreted protein 6 precursor
Locus_10020_Transcript_1/1_Conf_1.000	561	4	3.36E-11	NP_001122450.1	41	72.0182	179	74	hypothetical protein F10G8.8
Locus_10021_Transcript_1/1_Conf_1.000	166	20	1.09E-24	XP_002923590.1	100	116.316	55	55	PREDICTED: DAZ-associated protein 1-like
Locus_10022_Transcript_1/1_Conf_1.000	484	4	9.71E-05	XP_002645151.1	56	50.0618	87	49	C. briggsae CBR-TNT-3 protein

Locus_10023_Transcript_1/1_Conf_1.000	914	20	3.68E-63	ACI49197.1	71	246.128	304	217	hypothetical protein Csp3_JD03.006
Locus_10024_Transcript_1/1_Conf_1.000	148	20	7.00E-11	NP_495256.1	86	70.4774	46	40	hypothetical protein F13H8.2
Locus_10025_Transcript_1/1_Conf_1.000	270	0							
Locus_10026_Transcript_1/1_Conf_1.000	604	20	2.55E-37	EFO24023.1	74	159.073	164	122	hypothetical protein LOAG_04465
Locus_10027_Transcript_1/1_Conf_1.000	139	0							
Locus_10028_Transcript_1/1_Conf_1.000	384	20	3.83E-46	XP_002630180.1	90	187.578	121	109	Hypothetical protein CBG00585
Locus_10029_Transcript_1/1_Conf_1.000	1272	20	1.43E-128	NP_493169.2	76	464.151	379	290	hypothetical protein T27F6.6
Locus_1003_Transcript_1/1_Conf_1.000	173	0							
Locus_10030_Transcript_1/2_Conf_1.000	820	20	1.05E-55	XP_002632396.1	97	221.09	114	111	C. briggsae CBR-UAF-2 protein
Locus_10030_Transcript_2/2_Conf_1.000	814	20	7.05E-97	XP_002632396.1	93	357.836	191	179	C. briggsae CBR-UAF-2 protein

Locus_10031_Transcript_1/1_Conf_1.000	805	5	2.46E-17	NP_741607.1	66	93.5893	145	97	hypothetical protein T07C12.12
Locus_10032_Transcript_1/1_Conf_1.000	867	20	1.39E-24	EFO23381.1	57	117.857	180	103	hypothetical protein LOAG_05102
Locus_10033_Transcript_1/1_Conf_1.000	997	20	3.89E-141	EFO24933.1	93	505.368	294	275	AGC/PKN protein kinase
Locus_10034_Transcript_1/1_Conf_1.000	1208	20	4.99E-59	NP_496704.1	80	233.032	183	147	Regulator of G protein Signaling family member (rgs-4)
Locus_10035_Transcript_1/1_Conf_1.000	512	20	1.61E-26	XP_001895780.1	78	122.479	97	76	transcription elongation factor B polypeptide 1
Locus_10036_Transcript_1/1_Conf_1.000	1041	20	5.84E-119	ACI49224.1	76	431.795	347	266	hypothetical protein Csp3_JD05.009
Locus_10037_Transcript_1/1_Conf_1.000	564	0							
Locus_10038_Transcript_1/1_Conf_1.000	674	0							
Locus_10039_Transcript_1/1_Conf_1.000	384	14	2.34E-11	XP_002827014.1	97	72.0182	73	71	PREDICTED: macrosialin-like isoform 3
Locus_1004_Transcript_1/1_Conf_1.000	855	20	3.92E-48	CBK19457.1	73	196.052	176	130	C. elegans protein K01A6.2e, partially confirmed by transcript evidence
Locus_10040_Transcript_1/2_Conf_1.000	419	20	1.21E-47	AAK62032.1	76	192.586	139	106	metalloprotease 1 precursor
Locus_10040_Transcript_2/2_Conf_1.000	419	20	1.21E-47	AAK62032.1	76	192.586	139	106	metalloprotease 1 precursor
Locus_10041_Transcript_1/1_Conf_1.000	543	20	4.13E-32	NP_492142.1	72	141.354	153	111	hypothetical protein T23G11.4
Locus_10042_Transcript_1/1_Conf_1.000	378	0							
Locus_10043_Transcript_1/1_Conf_1.000	326	0							
Locus_10044_Transcript_1/1_Conf_1.000	385	20	1.23E-36	NP_740947.2	73	155.992	126	92	hypothetical protein Y105E8A.19

Locus_10045_Transcript_1/1_Conf_1.000	1082	20	1.57E-138	AAC47238.1	83	496.893	360	301	non-muscle myosin heavy chain II
Locus_10046_Transcript_1/1_Conf_1.000	809	2	3.35E-06	EFO28415.1	40	56.6102	206	84	hypothetical protein LOAG_00061
Locus_10047_Transcript_1/1_Conf_1.000	456	20	2.94E-22	XP_001901176.1	76	108.227	95	73	Sec63 domain containing protein
Locus_10048_Transcript_1/1_Conf_1.000	1603	20	6.27E-135	XP_002649084.1	72	485.723	441	320	Hypothetical protein CBG22670
Locus_10049_Transcript_1/1_Conf_1.000	950	0							
Locus_1005_Transcript_1/1_Conf_1.000	2715	20	5.29E-58	NP_496514.1	56	231.106	401	228	yeast PAT1(protein associated with topo II) Related family member (patr-1)
Locus_10050_Transcript_1/1_Conf_1.000	527	0							
Locus_10051_Transcript_1/2_Conf_1.000	1023	20	7.32E-74	XP_002641487.1	63	281.952	341	217	Hypothetical protein CBG09778
Locus_10051_Transcript_2/2_Conf_1.000	1023	20	7.32E-74	XP_002641487.1	63	281.952	341	217	Hypothetical protein CBG09778
Locus_10052_Transcript_1/1_Conf_1.000	447	20	5.76E-50	NP_001009108.2	100	200.29	91	91	ribonuclease pancreatic precursor
Locus_10053_Transcript_1/1_Conf_1.000	1360	20	5.34E-60	AAK84590.1	71	236.498	180	129	AC084153_8Hypothetical protein Y22D7AL.16

Locus_10054_Transcript_1/1_Conf_1.000	1183	20	3.37E-36	EFO25544.1	76	157.147	119	91	hypothetical protein LOAG_02944
Locus_10055_Transcript_1/1_Conf_1.000	630	20	1.88E-65	XP_002633222.1	84	252.677	200	169	Hypothetical protein CBG05941
Locus_10056_Transcript_1/1_Conf_1.000	351	10	5.26E-19	P34288.4	58	97.4413	112	66	GTPase-activating protein pac-1
Locus_10057_Transcript_1/1_Conf_1.000	176	0							
Locus_10058_Transcript_1/1_Conf_1.000	236	0							
Locus_10059_Transcript_1/1_Conf_1.000	470	0							
Locus_1006_Transcript_1/3_Conf_0.583	142	0							
Locus_1006_Transcript_3/3_Conf_0.667	200	0							
Locus_10060_Transcript_1/1_Conf_1.000	997	20	1.61E-78	XP_002642022.1	80	297.36	215	174	Hypothetical protein CBG17958
Locus_10061_Transcript_1/1_Conf_1.000	769	20	1.13E-77	EFO22550.1	74	293.893	256	191	TATA binding protein associated factor
Locus_10062_Transcript_1/1_Conf_1.000	1124	20	1.05E-23	XP_001895613.1	54	115.546	183	100	Zinc finger, C2H2 type family protein

Locus_10063_Transcript_1/1_Conf_1.000	980	20	7.43E-105	XP_002638488.1	94	384.8	209	197	C. briggsae CBR-SEC-23 protein
Locus_10064_Transcript_1/1_Conf_1.000	170	20	2.35E-11	EFO21941.1	75	72.0182	52	39	hypothetical protein LOAG_06543
Locus_10065_Transcript_1/1_Conf_1.000	561	5	9.13E-17	EFO26231.1	70	90.5077	80	56	hypothetical protein LOAG_02257
Locus_10066_Transcript_1/1_Conf_1.000	1224	20	8.66E-75	XP_002637804.1	75	285.419	224	170	Hypothetical protein CBG04590
Locus_10067_Transcript_1/1_Conf_1.000	632	20	7.91E-64	NP_502658.1	95	247.284	134	128	hypothetical protein Y45F10D.4
Locus_10068_Transcript_1/1_Conf_1.000	195	0							
Locus_10069_Transcript_1/1_Conf_1.000	533	0							
Locus_1007_Transcript_1/1_Conf_1.000	192	0							
Locus_10070_Transcript_1/1_Conf_1.000	735	0							
Locus_10071_Transcript_1/1_Conf_1.000	910	20	1.44E-59	EFO15252.1	63	234.187	267	169	hypothetical protein LOAG_13260

Locus_10072_Transcript_1/1_Conf_1.000	951	8	7.01E-20	EFO20947.1	50	102.449	293	147	hypothetical protein LOAG_07543
Locus_10073_Transcript_1/1_Conf_1.000	718	7	7.32E-57	NP_492628.1	76	224.557	204	156	hypothetical protein Y106G6A.5
Locus_10074_Transcript_1/1_Conf_1.000	523	0							
Locus_10075_Transcript_1/1_Conf_1.000	285	19	3.35E-13	NP_510156.2	73	78.1814	56	41	hypothetical protein F11C1.4
Locus_10076_Transcript_1/1_Conf_1.000	521	3	1.97E-30	NP_504395.2	60	135.576	178	107	hypothetical protein Y47A7.1
Locus_10077_Transcript_1/1_Conf_1.000	130	0							
Locus_10078_Transcript_1/1_Conf_1.000	690	0							
Locus_10079_Transcript_1/1_Conf_1.000	743	3	1.27E-14	NP_001024476.1	50	84.3445	212	108	hypothetical protein C46H3.2
Locus_1008_Transcript_1/1_Conf_1.000	1080	20	1.98E-149	XP_002641166.1	90	533.102	347	313	C. briggsae CBR-EFT-1 protein

Locus_10080_Transcript_1/1_Conf_1.000	261	20	1.17E-42	BAG36500.1	100	176.022	87	87	unnamed protein product
Locus_10081_Transcript_1/1_Conf_1.000	596	20	1.03E-27	EFO26895.1	59	127.102	187	112	organic solute transporter alpha-like protein
Locus_10082_Transcript_1/1_Conf_1.000	816	20	1.38E-108	NP_510580.1	86	396.741	253	219	hypothetical protein F59D12.1
Locus_10083_Transcript_1/1_Conf_1.000	379	0							
Locus_10084_Transcript_1/2_Conf_1.000	589	20	3.54E-41	NP_503101.1	70	171.785	151	107	hypothetical protein C30H6.8
Locus_10084_Transcript_2/2_Conf_1.000	589	20	3.54E-41	NP_503101.1	70	171.785	151	107	hypothetical protein C30H6.8
Locus_10085_Transcript_1/1_Conf_1.000	133	6	7.54E-10	XP_002639323.1	81	67.0106	43	35	C. briggsae CBR-HUM-7 protein
Locus_10086_Transcript_1/1_Conf_1.000	249	2	1.84E-08	XP_002632297.1	57	62.3882	75	43	C. briggsae CBR-NOL-6 protein
Locus_10087_Transcript_1/1_Conf_1.000	405	2	2.60E-10	XP_001898097.1	47	68.5514	135	64	Asparaginase family protein
Locus_10088_Transcript_1/1_Conf_1.000	884	20	5.34E-64	NP_497461.1	63	248.825	238	151	PDGF/VEGF growth factor related family member (pvf-1)
Locus_10089_Transcript_1/1_Conf_1.000	366	3	1.56E-07	XP_001892279.1	63	59.3066	66	42	GrpE protein homolog, mitochondrial precursor
Locus_1009_Transcript_1/1_Conf_1.000	823	0							
Locus_10090_Transcript_1/2_Conf_1.000	1358	20	7.89E-88	NP_001040656.2	76	328.946	363	276	hypothetical protein F27D4.4

Locus_10090_Transcript_2/2_Conf_1.000	1358	20	7.88E-88	NP_001040656.2	76	328.946	363	276	hypothetical protein F27D4.4
Locus_10091_Transcript_1/1_Conf_1.000	431	20	7.76E-39	NP_001022773.1	85	163.31	122	104	Myc and Mondo-Like family member (mml-1)
Locus_10092_Transcript_1/1_Conf_1.000	508	20	5.34E-54	XP_001900544.1	84	213.772	149	126	Type III restriction enzyme, res subunit family protein
Locus_10093_Transcript_1/1_Conf_1.000	827	0							
Locus_10094_Transcript_1/1_Conf_1.000	804	20	2.88E-42	XP_002632817.1	82	176.407	111	92	C. briggsae CBR-CKA-1 protein
Locus_10095_Transcript_1/3_Conf_0.667	639	20	2.62E-86	NP_499324.1	86	322.013	200	173	4-HydroxyPhenylpyruvate Dioxygenase (HPD) family member (hpd-1)
Locus_10095_Transcript_2/3_Conf_0.667	639	20	9.97E-86	NP_499324.1	86	320.087	200	173	4-HydroxyPhenylpyruvate Dioxygenase (HPD) family member (hpd-1)
Locus_10095_Transcript_3/3_Conf_0.667	639	20	9.97E-86	NP_499324.1	86	320.087	200	173	4-HydroxyPhenylpyruvate Dioxygenase (HPD) family member (hpd-1)
Locus_10096_Transcript_1/1_Conf_1.000	957	2	5.27E-07	EFO20717.1	55	59.6918	145	81	hypothetical protein LOAG_07773

Locus_10097_Transcript_1/1_Conf_1.000	568	0							
Locus_10098_Transcript_1/1_Conf_1.000	712	3	4.12E-12	XP_002639131.1	44	75.8702	219	98	Hypothetical protein CBG14951
Locus_10099_Transcript_1/1_Conf_1.000	318	0							
Locus_101_Transcript_1/1_Conf_1.000	334	0							
Locus_1010_Transcript_1/1_Conf_1.000	901	20	1.01E-49	XP_002639673.1	83	201.445	139	116	Hypothetical protein CBG12391
Locus_10100_Transcript_1/1_Conf_1.000	767	20	3.99E-59	EFO23920.1	67	232.261	252	171	hypothetical protein LOAG_04569
Locus_10101_Transcript_1/1_Conf_1.000	672	16	6.14E-68	XP_002647278.1	72	261.151	224	163	C. briggsae CBR-KETN-1 protein
Locus_10102_Transcript_1/1_Conf_1.000	973	20	4.66E-67	XP_002646453.1	80	259.225	184	149	C. briggsae CBR-SMD-1 protein
Locus_10103_Transcript_1/1_Conf_1.000	330	0							
Locus_10104_Transcript_1/1_Conf_1.000	452	20	2.10E-60	XP_002630896.1	89	234.958	134	120	Hypothetical protein CBG02618
Locus_10105_Transcript_1/1_Conf_1.000	302	13	1.42E-16	NP_502242.2	64	89.3521	92	59	hypothetical protein F38H4.6
Locus_10106_Transcript_1/1_Conf_1.000	290	4	7.68E-10	XP_002639822.1	60	67.0106	87	53	C. briggsae CBR-APH-2 protein
Locus_10107_Transcript_1/1_Conf_1.000	128	0							
Locus_10108_Transcript_1/1_Conf_1.000	946	0							
Locus_10109_Transcript_1/1_Conf_1.000	1428	20	0	XP_002637424.1	80	646.351	471	381	Hypothetical protein CBG19133
Locus_1011_Transcript_1/1_Conf_1.000	1290	5	4.22E-35		48	153.68	406	197	DNA topoisomerase II
Locus_10110_Transcript_1/1_Conf_1.000	455	0							
Locus_10111_Transcript_1/1_Conf_1.000	184	0							

Locus_10112_Transcript_1/2_Conf_1.000	2126	20	1.47E-20	XP_002420141.1	48	106.301	458	221	ER to Golgi vesicle transport protein, putative; intracellular protein transport protein, putative
Locus_10112_Transcript_2/2_Conf_1.000	2099	20	1.45E-20	XP_002420141.1	48	106.301	458	221	ER to Golgi vesicle transport protein, putative; intracellular protein transport protein, putative
Locus_10113_Transcript_1/1_Conf_1.000	250	2	9.14E-08	ADG63133.1	75	60.077	57	43	calcium-dependent apyrase
Locus_10114_Transcript_1/1_Conf_1.000	371	0							
Locus_10115_Transcript_1/1_Conf_1.000	177	2	1.12E-05	EFO13974.1	65	53.1434	58	38	hypothetical protein LOAG_14552
Locus_10116_Transcript_1/1_Conf_1.000	642	6	3.92E-05	EEC79812.1	42	52.373	145	62	hypothetical protein OsI_21251
Locus_10117_Transcript_1/3_Conf_0.714	956	20	3.52E-112	XP_002634865.1	78	409.068	314	247	C. briggsae CBR-PLX-1 protein
Locus_10117_Transcript_2/3_Conf_0.714	956	20	7.10E-113	XP_002634865.1	78	411.379	314	248	C. briggsae CBR-PLX-1 protein
Locus_10117_Transcript_3/3_Conf_0.714	956	20	7.10E-113	XP_002634865.1	78	411.379	314	248	C. briggsae CBR-PLX-1 protein
Locus_10118_Transcript_1/1_Conf_1.000	515	20	3.30E-51	NP_741193.1	91	204.527	122	112	hypothetical protein C16A3.10
Locus_10119_Transcript_1/1_Conf_1.000	716	0							

Locus_1012_Transcript_1/1_Conf_1.000	609	20	5.29E-38	EFO28242.1	88	161.384	107	95	hypothetical protein LOAG_00237
Locus_10120_Transcript_1/1_Conf_1.000	502	20	1.54E-42	EFO18902.1	71	175.637	150	107	glycosyl hydrolase family 85 protein
Locus_10121_Transcript_1/1_Conf_1.000	567	20	2.24E-34	AAC47238.1	77	149.058	163	127	non-muscle myosin heavy chain II
Locus_10122_Transcript_1/1_Conf_1.000	596	20	1.93E-42	EFO22910.1	85	176.022	127	109	hypothetical protein LOAG_05577

Locus_10123_Transcript_1/1_Conf_1.000	1861	20	0	NP_001022671.1	90	808.135	478	433	hypothetical protein K08E3.5
Locus_10124_Transcript_1/1_Conf_1.000	201	0							
Locus_10125_Transcript_1/1_Conf_1.000	136	20	1.51E-18	1WZV	100	95.9005	44	44	CrystalStructure Of Ubch8
Locus_10126_Transcript_1/1_Conf_1.000	867	0							
Locus_10127_Transcript_1/1_Conf_1.000	821	0							
Locus_10128_Transcript_1/1_Conf_1.000	150	19	2.02E-18	XP_002344856.1	91	95.5153	48	44	PREDICTED: similar to hCG2042717
Locus_10129_Transcript_1/1_Conf_1.000	1173	20	4.94E-56	NP_504952.1	75	223.016	258	195	hypothetical protein F19F10.9
Locus_1013_Transcript_1/1_Conf_1.000	1634	20	3.28E-155	CAA84656.2	73	553.132	525	384	C. elegans protein F10F2.2, confirmed by transcript evidence
Locus_10130_Transcript_1/1_Conf_1.000	217	0							
Locus_10131_Transcript_1/1_Conf_1.000	1770	0							
Locus_10132_Transcript_1/1_Conf_1.000	219	0							
Locus_10133_Transcript_1/1_Conf_1.000	515	20	3.63E-74	XP_001897106.1	86	280.796	169	147	hypothetical protein
Locus_10134_Transcript_1/1_Conf_1.000	300	3	2.86E-25	NP_495991.1	72	118.242	100	72	hypothetical protein F42A8.1

Locus_10135_Transcript_1/1_Conf_1.000	553	20	3.09E-78	XP_002640158.1	82	294.664	183	151	C. briggsae CBR-TRE-1 protein
Locus_10136_Transcript_1/1_Conf_1.000	563	20	3.07E-89	NP_491857.1	95	331.257	180	172	RAB family member (rab-10)
Locus_10137_Transcript_1/1_Conf_1.000	1208	20	7.94E-65	ACZ54690.1	59	252.292	357	214	Uncoordinated protein 82, isoform h
Locus_10138_Transcript_1/1_Conf_1.000	445	20	8.91E-59	NP_503352.1	80	229.565	147	118	Flavin-containing MonoOxygenase family member (fmo-5)
Locus_10139_Transcript_1/1_Conf_1.000	620	20	2.03E-24	Q9NA80.3	51	116.316	225	115	Stress-activated map kinase-interacting protein 1 homolog
Locus_1014_Transcript_1/2_Conf_1.000	838	20	3.04E-90	CAR63714.1	88	335.88	226	201	hypothetical protein
Locus_1014_Transcript_2/2_Conf_1.000	869	20	4.25E-90	CAR63714.1	88	335.495	229	203	hypothetical protein
Locus_10140_Transcript_1/1_Conf_1.000	341	20	9.11E-16	EFO21559.1	58	86.6557	113	66	hypothetical protein LOAG_06930
Locus_10141_Transcript_1/3_Conf_0.400	422	0							
Locus_10141_Transcript_2/3_Conf_0.400	233	0							
Locus_10141_Transcript_3/3_Conf_0.400	433	0							
Locus_10142_Transcript_1/1_Conf_1.000	348	0							

Locus_10143_Transcript_1/1_Conf_1.000	598	20	1.58E-92	XP_002834351.1	100	342.428	164	164	PREDICTED: hypothetical protein LOC100438152
Locus_10144_Transcript_1/1_Conf_1.000	256	7	3.58E-07	NP_499886.1	50	58.151	76	38	hypothetical protein R02D3.7
Locus_10145_Transcript_1/1_Conf_1.000	851	20	1.94E-124	A8WVU9.2	92	449.514	274	254	Rho-associated protein kinase let-502
Locus_10146_Transcript_1/1_Conf_1.000	394	0							
Locus_10147_Transcript_1/1_Conf_1.000	294	0							
Locus_10148_Transcript_1/1_Conf_1.000	141	0							

Locus_10149_Transcript_1/1_Conf_1.000	1208	15	3.60E-33	XP_002638550.1	50	147.132	253	129	Hypothetical protein CBG05586
Locus_1015_Transcript_1/3_Conf_0.714	795	0							
Locus_1015_Transcript_2/3_Conf_0.429	535	0							
Locus_1015_Transcript_3/3_Conf_0.714	976	0							
Locus_10150_Transcript_1/1_Conf_1.000	385	0							
Locus_10151_Transcript_1/2_Conf_1.000	619	20	5.34E-33	XP_001900984.1	89	144.821	91	81	HMG box family protein
Locus_10151_Transcript_2/2_Conf_1.000	610	20	5.13E-33	XP_001900984.1	89	144.821	91	81	HMG box family protein
Locus_10152_Transcript_1/2_Conf_1.000	971	20	1.01E-37	EFO16052.1	60	161.77	178	108	hypothetical protein LOAG_12456
Locus_10152_Transcript_2/2_Conf_1.000	911	20	8.21E-39	XP_002633000.1	65	165.236	203	132	C. briggsae CBR-ICL-1 protein
Locus_10153_Transcript_1/2_Conf_1.000	1095	20	3.43E-48	CBB15981.1	74	196.823	169	126	C. elegans protein B0285.1c, partially confirmed by transcript evidence

Locus_10153_Transcript_2/2_Conf_1.000	1199	20	3.91E-48	CBB15981.1	74	196.823	169	126	C. elegans protein B0285.1c, partially confirmed by transcript evidence
Locus_10154_Transcript_1/1_Conf_1.000	752	6	6.13E-89	NP_501400.1	81	331.257	246	200	hypothetical protein F35H10.10
Locus_10155_Transcript_1/1_Conf_1.000	226	18	5.13E-22	NP_001021991.1	75	107.457	74	56	hypothetical protein C26D10.6
Locus_10156_Transcript_1/1_Conf_1.000	254	0							
Locus_10157_Transcript_1/1_Conf_1.000	421	20	1.44E-32	NP_497814.3	64	142.51	154	100	UNCoordinated family member (unc-79)
Locus_10158_Transcript_1/1_Conf_1.000	1123	20	2.83E-45	NP_494847.2	94	187.193	141	133	hypothetical protein F41C3.4
Locus_10159_Transcript_1/1_Conf_1.000	414	0							
Locus_1016_Transcript_1/1_Conf_1.000	706	20	1.75E-23	XP_001896558.1	61	113.62	126	78	Ser/Thr protein phosphatase family protein
Locus_10160_Transcript_1/1_Conf_1.000	164	20	2.07E-15	XP_001899041.1	87	85.5001	54	47	Transcription initiation factor IID, 18kD subunit family protein
Locus_10161_Transcript_1/2_Conf_1.000	360	0							
Locus_10161_Transcript_2/2_Conf_1.000	366	0							
Locus_10162_Transcript_1/1_Conf_1.000	562	0							
Locus_10163_Transcript_1/1_Conf_1.000	159	0							
Locus_10164_Transcript_1/1_Conf_1.000	385	0							
Locus_10165_Transcript_1/1_Conf_1.000	373	20	2.45E-24	NP_491935.1	96	115.161	62	60	G Protein, Gamma subunit family member (gpc-2)
Locus_10166_Transcript_1/1_Conf_1.000	482	20	1.49E-58	CAR63593.1	89	228.794	155	139	putative PQ loop repeat family protein
Locus_10167_Transcript_1/1_Conf_1.000	168	0							

Locus_10168_Transcript_1/1_Conf_1.000	1250	9	1.88E-40	CAA10033.1	49	171.4	430	212	DYS-1 protein
Locus_10169_Transcript_1/1_Conf_1.000	374	4	1.00E-09	CAA91482.3	71	66.6254	59	42	C. elegans protein T04F8.6, partially confirmed by transcript evidence
Locus_1017_Transcript_1/1_Conf_1.000	186	20	1.04E-14	XP_002631360.1	81	83.1889	61	50	Hypothetical protein CBG03195
Locus_10170_Transcript_1/1_Conf_1.000	398	20	1.48E-53	XP_002641446.1	92	212.231	127	118	Hypothetical protein CBG13315
Locus_10171_Transcript_1/1_Conf_1.000	369	0							
Locus_10172_Transcript_1/1_Conf_1.000	359	3	4.15E-08	XP_002634119.1	84	61.2326	57	48	Hypothetical protein CBG01673
Locus_10173_Transcript_1/1_Conf_1.000	700	20	4.63E-101	XP_002630114.1	96	371.318	233	224	C. briggsae CBR-PYR-1 protein
Locus_10174_Transcript_1/1_Conf_1.000	270	20	2.04E-39	EFO25642.1	98	165.236	89	88	hypothetical protein LOAG_02841
Locus_10175_Transcript_1/1_Conf_1.000	1220	20	3.40E-164	XP_001899489.1	81	582.408	411	337	Trehalose 6-phosphate synthase protein 1
Locus_10176_Transcript_1/1_Conf_1.000	226	0							
Locus_10177_Transcript_1/1_Conf_1.000	227	0							
Locus_10178_Transcript_1/1_Conf_1.000	765	20	3.80E-118	XP_002638375.1	86	428.328	254	219	Hypothetical protein CBG18580

Locus_10179_Transcript_1/1_Conf_1.000	541	20	1.26E-41	XP_002642775.1	75	172.94	148	112	C. briggsae CBR-NEX-1 protein
Locus_1018_Transcript_1/2_Conf_1.000	548	0							
Locus_1018_Transcript_2/2_Conf_1.000	599	0							
Locus_10180_Transcript_1/1_Conf_1.000	671	20	3.97E-43	NP_504518.3	69	178.718	202	141	Nuclear Hormone Receptor family member (nhr-142)
Locus_10181_Transcript_1/1_Conf_1.000	354	0							
Locus_10182_Transcript_1/1_Conf_1.000	183	0							
Locus_10183_Transcript_1/1_Conf_1.000	293	0							
Locus_10184_Transcript_1/1_Conf_1.000	276	20	6.99E-32	CBA11613.1	77	140.198	88	68	C. elegans protein F54F3.1c, partially confirmed by transcript evidence
Locus_10185_Transcript_1/1_Conf_1.000	314	5	3.96E-14	XP_002639081.1	67	81.2629	91	61	Hypothetical protein CBG14899
Locus_10186_Transcript_1/1_Conf_1.000	193	0							
Locus_10187_Transcript_1/1_Conf_1.000	491	0							
Locus_10188_Transcript_1/1_Conf_1.000	534	5	5.64E-23	NP_506872.1	72	110.923	102	74	hypothetical protein F28F8.5
Locus_10189_Transcript_1/1_Conf_1.000	670	20	1.55E-63	EFO27261.1	78	246.514	185	146	APB-1 protein
Locus_1019_Transcript_1/2_Conf_1.000	1234	20	4.97E-70	AAK84571.2	76	269.626	190	146	AC006685_2Hypothetical protein T13G4.2
Locus_1019_Transcript_2/2_Conf_1.000	1183	17	1.96E-60	AAK84571.2	82	237.654	151	124	AC006685_2Hypothetical protein T13G4.2
Locus_10190_Transcript_1/1_Conf_1.000	328	0							
Locus_10191_Transcript_1/1_Conf_1.000	591	20	1.11E-50	NP_506089.1	74	203.371	162	120	hypothetical protein R04F11.5
Locus_10192_Transcript_1/1_Conf_1.000	1275	2	1.25E-23	XP_002647382.1	47	115.546	425	201	Hypothetical protein CBG06447
Locus_10193_Transcript_1/1_Conf_1.000	338	20	2.40E-24	NP_001021246.1	88	115.161	71	63	Kinesin-Associated Protein family member (kap-1)
Locus_10194_Transcript_1/1_Conf_1.000	249	0							

Locus_10195_Transcript_1/1_Conf_1.000	1026	20	1.43E-77	XP_002636449.1	65	294.278	301	196	Hypothetical protein CBG23110
Locus_10196_Transcript_1/1_Conf_1.000	779	20	2.51E-48	XP_002630873.1	74	196.438	167	124	Hypothetical protein CBG02590
Locus_10197_Transcript_1/1_Conf_1.000	360	5	2.83E-41	NP_506424.2	84	171.4	119	100	Nose Resistant to Fluoxetine family member (nrf-5)
Locus_10198_Transcript_1/1_Conf_1.000	326	20	1.02E-30	XP_002639478.1	76	136.346	110	84	C. briggsae CBR-CYP-36A1 protein
Locus_10199_Transcript_1/1_Conf_1.000	1546	2	2.87E-12	XP_002638680.1	43	78.1814	314	138	Hypothetical protein CBG11872
Locus_102_Transcript_1/2_Conf_1.000	2142	20	0	XP_002636957.1	95	1261.13	713	683	C. briggsae CBR-EAT-6 protein
Locus_102_Transcript_2/2_Conf_1.000	1125	20	0	NP_506269.1	97	671.774	374	366	EATing: abnormal pharyngeal pumping family member (eat-6)

Locus_1020_Transcript_1/1_Conf_1.000	436	20	1.19E-31	XP_002636877.1	84	139.428	84	71	Hypothetical protein CBG09336
Locus_10200_Transcript_1/2_Conf_1.000	2648	20	0	NP_495537.1	77	899.042	731	568	HAlF transporter (PGP related) family member (haf-2)
Locus_10200_Transcript_2/2_Conf_1.000	635	4	1.34E-10	NP_495537.1	54	70.4774	113	62	HAlF transporter (PGP related) family member (haf-2)
Locus_10201_Transcript_1/1_Conf_1.000	238	0							
Locus_10202_Transcript_1/1_Conf_1.000	402	5	8.37E-25	NP_001022999.1	63	116.701	132	84	hypothetical protein ZK418.2
Locus_10203_Transcript_1/2_Conf_1.000	638	0							
Locus_10203_Transcript_2/2_Conf_1.000	641	0							
Locus_10204_Transcript_1/1_Conf_1.000	510	20	3.92E-65	NP_500247.2	89	250.751	144	129	hypothetical protein Y94H6A.8
Locus_10205_Transcript_1/1_Conf_1.000	362	20	3.59E-36	NP_493616.1	76	154.451	121	92	hypothetical protein F33H2.5
Locus_10206_Transcript_1/1_Conf_1.000	446	20	6.59E-62	XP_002642996.1	89	239.965	148	133	C. briggsae CBR-UNC-45 protein
Locus_10207_Transcript_1/2_Conf_1.000	360	9	3.47E-31	XP_002644619.1	91	137.887	90	82	C. briggsae CBR-LFI-1 protein
Locus_10207_Transcript_2/2_Conf_1.000	473	14	1.42E-32	NP_001024981.1	55	142.51	216	119	Lin-5 (Five) Interacting protein family member (lfi-1)
Locus_10208_Transcript_1/1_Conf_1.000	1004	20	3.23E-18	AAM98045.2	57	97.0561	106	61	Hypothetical protein C34H4.5
Locus_10209_Transcript_1/1_Conf_1.000	1087	20	8.04E-58	NP_491700.2	57	228.794	384	219	hypothetical protein F33D11.9

Locus_1021_Transcript_1/1_Conf_1.000	1285	20	1.70E-153	XP_002631561.1	80	546.969	364	293	C. briggsae CBR-GLN-2 protein
Locus_10210_Transcript_1/1_Conf_1.000	194	2	3.81E-09	EFO17919.1	73	64.6994	64	47	hypothetical protein LOAG_10578
Locus_10211_Transcript_1/3_Conf_0.667	576	4	2.00E-09	XP_002638722.1	71	66.2402	66	47	C. briggsae CBR-RLBP-1 protein
Locus_10211_Transcript_2/3_Conf_0.667	731	4	3.46E-09	XP_002638722.1	71	66.2402	66	47	C. briggsae CBR-RLBP-1 protein
Locus_10211_Transcript_3/3_Conf_0.667	731	4	3.46E-09	XP_002638722.1	71	66.2402	66	47	C. briggsae CBR-RLBP-1 protein
Locus_10212_Transcript_1/1_Conf_1.000	678	20	1.65E-68	XP_002763858.1	100	263.077	128	128	PREDICTED: ADP/ATP translocase 3-like, partial
Locus_10213_Transcript_1/1_Conf_1.000	256	0							
Locus_10214_Transcript_1/1_Conf_1.000	412	20	3.70E-33	NP_491412.1	92	144.436	85	79	Acyl-Coenzyme A Binding Protein family member (acbp-1)
Locus_10215_Transcript_1/1_Conf_1.000	400	20	7.83E-39	XP_002630251.1	78	163.31	123	96	Hypothetical protein CBG00670
Locus_10216_Transcript_1/2_Conf_1.000	1174	20	2.46E-47	NP_504203.1	56	194.126	296	168	hypothetical protein F32D1.9
Locus_10216_Transcript_2/2_Conf_1.000	1174	20	2.46E-47	NP_504203.1	56	194.126	296	168	hypothetical protein F32D1.9
Locus_10217_Transcript_1/1_Conf_1.000	262	0							
Locus_10218_Transcript_1/1_Conf_1.000	273	0							
Locus_10219_Transcript_1/1_Conf_1.000	283	20	5.18E-14	NP_001024551.1	60	80.8777	93	56	Nuclear Hormone Receptor family member (nhr-25)
Locus_1022_Transcript_1/1_Conf_1.000	499	0							
Locus_10220_Transcript_1/1_Conf_1.000	446	0							
Locus_10221_Transcript_1/1_Conf_1.000	766	0							
Locus_10222_Transcript_1/1_Conf_1.000	1189	20	1.65E-115	ACS36091.1	78	420.624	343	268	cysteine proteinase
Locus_10223_Transcript_1/1_Conf_1.000	389	0							
Locus_10224_Transcript_1/1_Conf_1.000	407	20	3.40E-10	EFO23403.1	56	68.1662	101	57	hypothetical protein LOAG_05077
Locus_10225_Transcript_1/1_Conf_1.000	144	20	1.67E-12	XP_002642817.1	79	75.8702	48	38	C. briggsae CBR-NAS-1 protein
Locus_10226_Transcript_1/1_Conf_1.000	1967	20	8.40E-124	XP_001901370.1	70	449.129	459	324	Lateral signaling target protein 2

Locus_10227_Transcript_1/1_Conf_1.000	270	20	1.12E-45	NP_001021871.1	100	186.037	90	90	UNCoordinated family member (unc-13)
Locus_10228_Transcript_1/1_Conf_1.000	307	18	5.21E-11	XP_002634644.1	60	70.8626	98	59	Hypothetical protein CBG03497
Locus_10229_Transcript_1/1_Conf_1.000	204	20	1.38E-11	NP_501554.2	72	72.7886	68	49	hypothetical protein D1046.5
Locus_1023_Transcript_1/1_Conf_1.000	844	20	2.37E-74	NP_508168.1	80	283.108	192	154	hypothetical protein F56F10.3
Locus_10230_Transcript_1/1_Conf_1.000	159	0							
Locus_10231_Transcript_1/1_Conf_1.000	325	0							
Locus_10232_Transcript_1/1_Conf_1.000	346	20	2.54E-21	NP_492549.2	62	105.145	117	73	hypothetical protein K07A1.9
Locus_10233_Transcript_1/1_Conf_1.000	532	20	7.38E-31	XP_002631098.1	63	137.117	158	100	Hypothetical protein CBG02872
Locus_10234_Transcript_1/1_Conf_1.000	149	0							
Locus_10235_Transcript_1/1_Conf_1.000	658	0							
Locus_10236_Transcript_1/1_Conf_1.000	353	20	7.83E-31	XP_001896501.1	78	136.732	99	78	Hypothetical subtilase-type proteinase F21H12.6 in chromosome II

Locus_10237_Transcript_1/1_Conf_1.000	176	20	1.46E-21	XP_002640668.1	94	105.916	58	55	C. briggsae CBR-UNC-54 protein
Locus_10238_Transcript_1/1_Conf_1.000	588	19	7.59E-52	XP_002640213.1	74	207.223	195	145	Hypothetical protein CBG12724
Locus_10239_Transcript_1/1_Conf_1.000	428	20	8.12E-12	AAO63577.1	53	73.559	145	77	secreted protein 5 precursor
Locus_1024_Transcript_1/1_Conf_1.000	1081	20	1.14E-88	XP_002633118.1	84	331.257	206	175	C. briggsae CBR-CAP-1 protein

Locus_10240_Transcript_1/1_Conf_1.000	926	20	1.80E-73	XP_002647138.1	91	280.411	164	150	Hypothetical protein CBG16436
Locus_10241_Transcript_1/1_Conf_1.000	289	0							
Locus_10242_Transcript_1/1_Conf_1.000	668	0							
Locus_10243_Transcript_1/1_Conf_1.000	283	20	3.12E-35	NP_509361.1	89	151.369	93	83	hypothetical protein K07E3.4
Locus_10244_Transcript_1/1_Conf_1.000	407	0							
Locus_10245_Transcript_1/1_Conf_1.000	972	20	1.41E-47	NP_493972.3	67	194.512	207	140	NucleOLar protein family member (nol-6)
Locus_10246_Transcript_1/1_Conf_1.000	768	6	3.68E-20	XP_002647225.1	47	102.834	255	122	Hypothetical protein CBG23815
Locus_10247_Transcript_1/1_Conf_1.000	592	20	4.23E-50	NP_497138.1	77	201.445	187	145	hypothetical protein F54C4.1
Locus_10248_Transcript_1/1_Conf_1.000	221	0							
Locus_10249_Transcript_1/1_Conf_1.000	538	20	3.27E-18	XP_001892089.1	57	95.1301	127	73	S-antigen protein precursor
Locus_1025_Transcript_1/1_Conf_1.000	796	3	1.42E-102	NP_501020.2	83	376.711	265	222	hypothetical protein C01B10.3
Locus_10250_Transcript_1/1_Conf_1.000	901	20	1.11E-88	NP_501399.1	66	330.872	321	215	Vacuolar H ATPase family member (vha-5)
Locus_10251_Transcript_1/1_Conf_1.000	312	20	1.55E-34	NP_501176.1	81	149.058	105	86	hypothetical protein T12B3.3
Locus_10252_Transcript_1/1_Conf_1.000	673	20	3.40E-34	XP_640893.1	57	149.058	221	126	hypothetical protein DDB_G0281219
Locus_10253_Transcript_1/1_Conf_1.000	307	0							
Locus_10254_Transcript_1/1_Conf_1.000	571	0							

Locus_10255_Transcript_1/1_Conf_1.000	213	20	2.74E-28	XP_002640693.1	94	128.257	69	65	Hypothetical protein CBG19758
Locus_10256_Transcript_1/1_Conf_1.000	493	0							
Locus_10257_Transcript_1/1_Conf_1.000	926	20	1.13E-75	XP_002641397.1	79	287.73	239	190	Hypothetical protein CBG13259
Locus_10258_Transcript_1/1_Conf_1.000	274	2	2.68E-07	ACZ64269.1	68	58.5362	83	57	astacin metalloprotease b
Locus_10259_Transcript_1/1_Conf_1.000	1718	20	1.54E-126	XP_002631305.1	62	457.988	576	361	C. briggsae CBR-DNA-2 protein
Locus_1026_Transcript_1/1_Conf_1.000	256	20	1.35E-38	BAC01681.1	96	162.54	85	82	immunoglobulin kappa light chain VLJ region
Locus_10260_Transcript_1/2_Conf_1.000	672	20	1.59E-15	XP_002637557.1	52	87.0409	185	97	Hypothetical protein CBG19289
Locus_10260_Transcript_2/2_Conf_1.000	284	0							
Locus_10261_Transcript_1/1_Conf_1.000	538	20	2.81E-70	AAG44663.1	100	268.085	131	131	AF260332_1DC33
Locus_10262_Transcript_1/1_Conf_1.000	616	20	2.88E-39	EFO21094.1	66	165.622	176	117	cyclophilin
Locus_10263_Transcript_1/1_Conf_1.000	1100	20	3.72E-18	NP_495696.2	61	97.0561	109	67	hypothetical protein K02C4.3
Locus_10264_Transcript_1/1_Conf_1.000	511	20	2.62E-77	XP_002630855.1	90	291.197	169	153	Hypothetical protein CBG02570

Locus_10265_Transcript_1/1_Conf_1.000	276	2	7.76E-15	NP_740947.2	65	83.5741	90	59	hypothetical protein Y105E8A.19
Locus_10266_Transcript_1/1_Conf_1.000	347	20	3.65E-44	NP_001022207.1	96	181.03	89	86	hypothetical protein F56D1.3
Locus_10267_Transcript_1/1_Conf_1.000	739	20	2.68E-57	NP_497019.1	67	226.098	250	168	hypothetical protein F57C2.5
Locus_10268_Transcript_1/1_Conf_1.000	198	0							
Locus_10269_Transcript_1/1_Conf_1.000	376	0							
Locus_1027_Transcript_1/1_Conf_1.000	488	2	6.05E-07	XP_002637168.1	65	57.3806	46	30	Hypothetical protein CBG09680
Locus_10270_Transcript_1/1_Conf_1.000	907	20	9.88E-69	XP_001898880.1	67	264.618	302	204	RhoGAP domain containing protein
Locus_10271_Transcript_1/1_Conf_1.000	197	0							
Locus_10272_Transcript_1/1_Conf_1.000	586	20	5.31E-37	XP_002646234.1	63	157.918	187	118	Hypothetical protein CBG11927
Locus_10273_Transcript_1/1_Conf_1.000	872	11	2.02E-23	AAM12418.1	53	114.005	226	121	spliced leader 30 kDa protein
Locus_10274_Transcript_1/1_Conf_1.000	329	0							
Locus_10275_Transcript_1/1_Conf_1.000	153	4	9.06E-19	EFO26119.1	97	96.6709	49	48	myotactin form A
Locus_10276_Transcript_1/1_Conf_1.000	424	11	1.29E-33	XP_001900740.1	73	145.976	131	96	BTB/POZ domain containing protein
Locus_10277_Transcript_1/1_Conf_1.000	542	20	2.01E-31	EFO18735.1	67	139.043	137	92	amidase
Locus_10278_Transcript_1/1_Conf_1.000	1362	20	1.52E-155	XP_002631669.1	82	553.903	455	374	C. briggsae CBR-MOG-4 protein
Locus_10279_Transcript_1/1_Conf_1.000	795	0							
Locus_1028_Transcript_1/1_Conf_1.000	779	20	2.12E-47	XP_002633078.1	66	193.356	224	149	Hypothetical protein CBG05761
Locus_10280_Transcript_1/1_Conf_1.000	535	0							
Locus_10281_Transcript_1/1_Conf_1.000	997	20	1.23E-86	EFO23979.1	70	324.324	334	234	metallopeptidase family M24 containing protein
Locus_10282_Transcript_1/1_Conf_1.000	435	4	2.50E-05	XP_843162.1	53	51.9878	91	49	proteophosphoglycan ppg4

Locus_10283_Transcript_1/1_Conf_1.000	508	20	1.52E-16	NP_491203.1	50	89.3521	171	87	human HUS1 related family member (hus-1)
Locus_10284_Transcript_1/1_Conf_1.000	1041	20	9.13E-72	XP_002633355.1	62	275.018	329	206	Hypothetical protein CBG06099
Locus_10285_Transcript_1/1_Conf_1.000	240	0							
Locus_10286_Transcript_1/1_Conf_1.000	327	20	4.56E-39	AAK31527.3	84	164.081	110	93	Neuronal symmetry protein 1, partially confirmed by transcript evidence
Locus_10287_Transcript_1/1_Conf_1.000	462	20	1.98E-74	XP_002643587.1	96	281.567	154	148	Hypothetical protein CBG16309
Locus_10288_Transcript_1/1_Conf_1.000	303	2	2.43E-08	NP_507813.1	58	62.003	73	43	hypothetical protein Y43F8C.13
Locus_10289_Transcript_1/1_Conf_1.000	215	0							
Locus_1029_Transcript_1/1_Conf_1.000	1027	20	2.13E-97	ACO15780.1	78	360.147	286	224	Lethal protein 767, isoform b, confirmed by transcript evidence
Locus_10290_Transcript_1/1_Conf_1.000	299	0							
Locus_10291_Transcript_1/1_Conf_1.000	141	0							
Locus_10292_Transcript_1/1_Conf_1.000	943	20	4.02E-76	XP_002644619.1	84	289.271	275	231	C. briggsae CBR-LFI-1 protein
Locus_10293_Transcript_1/2_Conf_1.000	2047	20	0	NP_001023608.1	88	915.99	564	498	CCR (yeast CCR4/NOT complex component) homolog family member (ccr-4)

Locus_10293_Transcript_2/2_Conf_1.000	2030	20	0	NP_001023608.1	88	915.99	564	498	CCR (yeast CCR4/NOT complex component) homolog family member (ccr-4)
Locus_10294_Transcript_1/1_Conf_1.000	364	14	3.26E-05	XP_002076888.1	59	51.6026	92	55	GD24585
Locus_10295_Transcript_1/1_Conf_1.000	806	20	7.06E-57	NP_507527.2	75	224.942	193	146	hypothetical protein Y59A8B.8
Locus_10296_Transcript_1/1_Conf_1.000	360	20	3.68E-57	NP_492775.2	86	224.172	119	103	LAMinin related. See also lmb- family member (lam-3)
Locus_10297_Transcript_1/1_Conf_1.000	198	0							
Locus_10298_Transcript_1/1_Conf_1.000	916	5	3.52E-05	XP_002029777.1	42	53.5286	213	91	GM25090
Locus_10299_Transcript_1/1_Conf_1.000	349	2	2.81E-12	NP_510633.1	69	75.0998	83	58	hypothetical protein ZK1073.2
Locus_103_Transcript_1/1_Conf_1.000	867	0							
Locus_1030_Transcript_1/2_Conf_1.000	1305	20	1.25E-18	XP_001894934.1	60	98.9821	128	77	chromobox protein homolog 3
Locus_1030_Transcript_2/2_Conf_1.000	1305	20	1.25E-18	XP_001894934.1	60	98.9821	128	77	chromobox protein homolog 3
Locus_10300_Transcript_1/2_Conf_1.000	308	0							
Locus_10300_Transcript_2/2_Conf_1.000	308	0							
Locus_10301_Transcript_1/1_Conf_1.000	464	0							
Locus_10302_Transcript_1/1_Conf_1.000	254	2	3.59E-07	NP_491456.2	71	58.151	56	40	hypothetical protein F57C9.6
Locus_10303_Transcript_1/1_Conf_1.000	167	2	2.44E-08	NP_500298.3	83	62.003	36	30	hypothetical protein Y67D8B.4
Locus_10304_Transcript_1/1_Conf_1.000	785	0							

Locus_10305_Transcript_1/1_Conf_1.000	456	0							
Locus_10306_Transcript_1/1_Conf_1.000	1038	0							
Locus_10307_Transcript_1/1_Conf_1.000	130	3	1.63E-04	NP_505377.2	77	49.2914	44	34	hypothetical protein B0222.9
Locus_10308_Transcript_1/2_Conf_1.000	1079	0							
Locus_10308_Transcript_2/2_Conf_1.000	1025	0							
Locus_10309_Transcript_1/1_Conf_1.000	398	4	7.16E-16	NP_501455.1	73	87.0409	71	52	Temporarily Assigned Gene name family member (tag-77)
Locus_1031_Transcript_1/1_Conf_1.000	650	20	1.13E-15	NP_499437.2	70	87.4261	92	65	hypothetical protein Y47D3A.29
Locus_10310_Transcript_1/1_Conf_1.000	1034	20	4.39E-50	EFO24890.1	60	202.986	242	146	RING finger protein 170
Locus_10311_Transcript_1/1_Conf_1.000	620	0							
Locus_10312_Transcript_1/1_Conf_1.000	314	20	6.74E-22	EFO15797.1	70	107.071	98	69	hypothetical protein LOAG_12712
Locus_10313_Transcript_1/1_Conf_1.000	315	20	1.27E-20	CAR63649.1	94	102.834	53	50	hypothetical protein
Locus_10314_Transcript_1/1_Conf_1.000	335	19	1.37E-19	ADI61822.1	64	99.3673	111	72	endonuclease-reverse transcriptase
Locus_10315_Transcript_1/1_Conf_1.000	313	0							
Locus_10316_Transcript_1/1_Conf_1.000	163	3	1.94E-05	XP_002634631.1	64	52.373	53	34	Hypothetical protein CBG18490
Locus_10317_Transcript_1/1_Conf_1.000	1241	0							

Locus_10318_Transcript_1/1_Conf_1.000	438	2	1.23E-04	NP_001023357.2	56	49.6766	73	41	hypothetical protein T04C4.1
Locus_10319_Transcript_1/1_Conf_1.000	281	0							
Locus_1032_Transcript_1/1_Conf_1.000	1008	20	4.63E-73	NP_506393.1	76	279.256	259	197	hypothetical protein T01D3.5
Locus_10320_Transcript_1/1_Conf_1.000	203	20	4.90E-25	XP_002648832.1	95	117.472	67	64	Hypothetical protein CBG16947
Locus_10321_Transcript_1/1_Conf_1.000	566	20	9.18E-57	2ON7	77	223.402	187	145	Structure Of Nagst-1
Locus_10322_Transcript_1/1_Conf_1.000	128	0							
Locus_10323_Transcript_1/1_Conf_1.000	131	20	1.29E-17	XP_002631390.1	97	92.8189	43	42	Hypothetical protein CBG03232
Locus_10324_Transcript_1/1_Conf_1.000	159	0							
Locus_10325_Transcript_1/1_Conf_1.000	1205	20	8.95E-101	NP_001024679.1	71	371.703	337	242	DiacylGlycerol Kinase family member (dgk-2)
Locus_10326_Transcript_1/1_Conf_1.000	862	20	3.09E-109	XP_002633235.1	87	399.053	273	240	Hypothetical protein CBG05956
Locus_10327_Transcript_1/1_Conf_1.000	398	20	1.58E-47	NP_492590.1	89	192.2	114	102	hypothetical protein K02A11.3
Locus_10328_Transcript_1/1_Conf_1.000	256	5	2.32E-06	XP_002645945.1	57	55.4546	84	48	C. briggsae CBR-GOB-1 protein

Locus_10329_Transcript_1/1_Conf_1.000	805	20	1.63E-53	NP_491160.1	75	213.772	179	135	SEParase family member (sep-1)
Locus_1033_Transcript_1/1_Conf_1.000	482	0							
Locus_10330_Transcript_1/1_Conf_1.000	129	0							
Locus_10331_Transcript_1/1_Conf_1.000	591	20	1.62E-25	NP_001024529.1	68	119.783	132	90	SLOwpoke potassium channel family member (slo-2)
Locus_10332_Transcript_1/1_Conf_1.000	304	0							
Locus_10333_Transcript_1/3_Conf_0.714	2944	20	3.56E-116	XP_694117.3	50	424.476	949	483	PREDICTED: KIAA1033-like
Locus_10333_Transcript_2/3_Conf_0.714	2944	20	6.08E-116	XP_694117.3	50	423.705	949	483	PREDICTED: KIAA1033-like
Locus_10333_Transcript_3/3_Conf_0.714	2944	20	6.08E-116	XP_694117.3	50	423.705	949	483	PREDICTED: KIAA1033-like
Locus_10334_Transcript_1/1_Conf_1.000	200	0							
Locus_10335_Transcript_1/1_Conf_1.000	404								
Locus_10336_Transcript_1/1_Conf_1.000	264	20	1.25E-20	XP_002636692.1	79	102.834	73	58	Hypothetical protein CBG23406
Locus_10337_Transcript_1/1_Conf_1.000	438	0							
Locus_10338_Transcript_1/1_Conf_1.000	998	4	7.36E-15	ACI49256.1	38	85.8853	372	145	hypothetical protein Csp3_JD07.006
Locus_10339_Transcript_1/1_Conf_1.000	610	6	2.31E-25	EFO24329.1	60	119.398	145	87	hypothetical protein LOAG_04162
Locus_1034_Transcript_1/1_Conf_1.000	1330	20	4.75E-122	CAA96571.1	66	442.58	427	282	parasite pepsinogen
Locus_10340_Transcript_1/1_Conf_1.000	175	20	1.73E-06	XP_002813545.1	72	55.8398	48	35	PREDICTED: histone-lysine N-methyltransferase SETMAR-like

Locus_10341_Transcript_1/2_Conf_1.000	765	20	1.05E-59	CBL43465.1	63	234.187	242	154	C. elegans protein Y55D9A.1d, confirmed by transcript evidence
Locus_10341_Transcript_2/2_Conf_1.000	765	20	2.76E-60	CBL43465.1	64	236.113	242	155	C. elegans protein Y55D9A.1d, confirmed by transcript evidence
Locus_10342_Transcript_1/1_Conf_1.000	777	3	4.48E-05	XP_787339.1	70	52.7582	54	38	PREDICTED: similar to replication factor C p37 subunit
Locus_10343_Transcript_1/2_Conf_1.000	526	20	3.25E-68	XP_002641367.1	84	261.151	193	163	C. briggsae CBR-GBF-1 protein
Locus_10343_Transcript_2/2_Conf_1.000	511	20	1.22E-66	XP_002641367.1	84	255.758	189	159	C. briggsae CBR-GBF-1 protein
Locus_10344_Transcript_1/1_Conf_1.000	727	20	9.02E-10	XP_001493987.1	57	68.1662	94	54	PREDICTED: similar to C-type lectin domain family 9, member A

Locus_10345_Transcript_1/1_Conf_1.000	459								
Locus_10346_Transcript_1/1_Conf_1.000	232	0							
Locus_10347_Transcript_1/1_Conf_1.000	213	0							
Locus_10348_Transcript_1/1_Conf_1.000	188	0							
Locus_10349_Transcript_1/1_Conf_1.000	1012	4	1.09E-05	CAP09614.1	39	55.4546	297	116	novel protein containing multiple sushi domains (SCR repeat)
Locus_1035_Transcript_1/4_Conf_0.400	669	20	4.49E-79	NP_502255.1	81	298.13	203	165	FATty acid desaturase family member (fat-6)
Locus_1035_Transcript_2/4_Conf_0.400	669	20	2.91E-78	NP_502255.1	81	295.434	201	164	FATty acid desaturase family member (fat-6)
Locus_1035_Transcript_3/4_Conf_0.400	1246	20	4.62E-140	NP_502255.1	81	502.286	339	277	FATty acid desaturase family member (fat-6)
Locus_1035_Transcript_4/4_Conf_0.400	1204	20	4.39E-140	NP_502255.1	81	502.286	339	277	FATty acid desaturase family member (fat-6)
Locus_10350_Transcript_1/1_Conf_1.000	2138	20	6.01E-147	NP_501725.2	61	526.168	683	421	hypothetical protein ZK1251.9
Locus_10351_Transcript_1/1_Conf_1.000	287	20	9.36E-32	NP_496465.1	86	139.813	92	80	hypothetical protein F54D5.12
Locus_10352_Transcript_1/1_Conf_1.000	334	0							
Locus_10353_Transcript_1/1_Conf_1.000	366	20	6.47E-46	XP_002640448.1	88	186.808	117	104	Hypothetical protein CBG08504
Locus_10354_Transcript_1/1_Conf_1.000	604	20	1.04E-22	XP_001902019.1	64	110.538	96	62	PRPF39 protein

Locus_10355_Transcript_1/1_Conf_1.000	153	20	4.34E-21	NP_497235.2	98	104.375	50	49	G-protein-coupled Receptor Kinase family member (grk-2)
Locus_10356_Transcript_1/1_Conf_1.000	137	0							
Locus_10357_Transcript_1/1_Conf_1.000	247	0							
Locus_10358_Transcript_1/1_Conf_1.000	301	20	3.86E-30	O61570.1	100	134.42	70	70	60S ribosomal protein L38
Locus_10359_Transcript_1/1_Conf_1.000	581	20	2.98E-77	NP_492474.2	82	291.582	193	160	hypothetical protein F14B4.1
Locus_1036_Transcript_1/1_Conf_1.000	1476	20	1.17E-39	XP_002646159.1	47	169.088	510	241	Hypothetical protein CBG08044
Locus_10360_Transcript_1/1_Conf_1.000	196	0							
Locus_10361_Transcript_1/1_Conf_1.000	1040	20	6.95E-72	NP_001129806.1	69	275.404	266	184	hypothetical protein C08H9.16
Locus_10362_Transcript_1/1_Conf_1.000	737	20	4.68E-62	XP_002639998.1	87	241.891	177	154	Hypothetical protein CBG10828
Locus_10363_Transcript_1/1_Conf_1.000	993	20	1.54E-89	EFO18920.1	78	333.954	283	222	hypothetical protein LOAG_09572
Locus_10364_Transcript_1/1_Conf_1.000	1147	20	9.17E-100	XP_002631224.1	67	368.237	385	260	Hypothetical protein CBG03022
Locus_10365_Transcript_1/1_Conf_1.000	196	0							

Locus_10366_Transcript_1/1_Conf_1.000	1067	20	1.32E-119	EAX03629.1	100	398.282	189	189	major histocompatibility complex, class II, DR alpha, isoform CRA_a
Locus_10367_Transcript_1/1_Conf_1.000	360	0							
Locus_10368_Transcript_1/3_Conf_0.333	518	3	4.61E-16	XP_001894994.1	53	87.8113	123	66	hypothetical protein Bm1_17685
Locus_10368_Transcript_2/3_Conf_0.333	857	2	7.46E-15	EFO17899.1	54	85.5001	182	100	hypothetical protein LOAG_10600
Locus_10368_Transcript_3/3_Conf_0.667	1374	3	1.82E-39	EFO17899.1	51	168.318	390	200	hypothetical protein LOAG_10600
Locus_10369_Transcript_1/1_Conf_1.000	333	20	2.42E-08	XP_002076646.1	66	62.003	71	47	GD15089
Locus_1037_Transcript_1/1_Conf_1.000	1779	20	1.87E-42	EFO25902.1	47	178.718	312	147	hypothetical protein LOAG_02587
Locus_10370_Transcript_1/1_Conf_1.000	509	20	6.55E-44	XP_002640526.1	72	180.259	170	123	Hypothetical protein CBG18688
Locus_10371_Transcript_1/1_Conf_1.000	261	2	2.63E-10	NP_741595.1	80	68.5514	36	29	hypothetical protein K06A4.7
Locus_10372_Transcript_1/1_Conf_1.000	288	20	4.64E-23	XP_002645469.1	77	110.923	93	72	C. briggsae CBR-CDD-1 protein
Locus_10373_Transcript_1/2_Conf_1.000	1858	20	2.07E-116	NP_499770.1	66	424.476	439	293	hypothetical protein F45G2.3
Locus_10373_Transcript_2/2_Conf_1.000	1786	20	5.73E-116	NP_499770.1	63	422.935	471	301	hypothetical protein F45G2.3
Locus_10374_Transcript_1/1_Conf_1.000	337	0							
Locus_10375_Transcript_1/1_Conf_1.000	848	20	5.54E-47	AAC46544.4	56	192.2	278	158	Hypothetical protein F48E8.4
Locus_10376_Transcript_1/1_Conf_1.000	476	20	8.04E-20	EFO24692.1	63	100.138	117	74	protein-tyrosine phosphatase
Locus_10377_Transcript_1/3_Conf_0.667	1121	20	1.97E-123	NP_001041037.1	83	446.817	268	223	GLYcosylation related family member (gly-10)

Locus_10377_Transcript_2/3_Conf_0.667	1097	20	2.66E-117	NP_001041037.1	82	426.402	260	215	GLYcosylation related family member (gly-10)
Locus_10377_Transcript_3/3_Conf_0.667	1121	20	1.51E-123	NP_001041037.1	83	447.203	268	223	GLYcosylation related family member (gly-10)
Locus_10378_Transcript_1/1_Conf_1.000	340	0							
Locus_10379_Transcript_1/2_Conf_1.000	404	20	9.80E-58	XP_002642327.1	95	226.098	120	114	C. briggsae CBR-TAT-3 protein
Locus_10379_Transcript_2/2_Conf_1.000	416	20	2.99E-67	XP_002642327.1	94	257.684	137	129	C. briggsae CBR-TAT-3 protein
Locus_1038_Transcript_1/2_Conf_1.000	511	2	3.85E-12	NP_505787.1	65	74.7146	98	64	hypothetical protein F58B4.4
Locus_1038_Transcript_2/2_Conf_1.000	523	2	4.22E-12	NP_505787.1	65	74.7146	98	64	hypothetical protein F58B4.4
Locus_10380_Transcript_1/1_Conf_1.000	429	20	5.03E-38	XP_002640436.1	70	160.614	140	99	Hypothetical protein CBG08488
Locus_10381_Transcript_1/2_Conf_1.000	260	0							
Locus_10381_Transcript_2/2_Conf_1.000	455	0							
Locus_10382_Transcript_1/1_Conf_1.000	526	20	8.34E-40	NP_872133.1	69	166.777	176	122	hypothetical protein F32D8.13
Locus_10383_Transcript_1/1_Conf_1.000	1145	20	8.89E-79	NP_001023510.1	62	298.516	325	202	hypothetical protein Y55F3AM.6
Locus_10384_Transcript_1/1_Conf_1.000	939	4	2.30E-23	XP_002639960.1	52	114.005	224	118	Hypothetical protein CBG10780
Locus_10385_Transcript_1/1_Conf_1.000	192	0							
Locus_10386_Transcript_1/2_Conf_1.000	676	6	2.08E-47	NP_496952.1	65	192.971	227	148	hypothetical protein K09E4.1

Locus_10386_Transcript_2/2_Conf_1.000	676	6	2.08E-47	NP_496952.1	65	192.971	227	148	hypothetical protein K09E4.1
Locus_10387_Transcript_1/1_Conf_1.000	720	20	1.18E-54	XP_002112403.1	70	217.238	188	133	hypothetical protein TRIADDRAFT_25844
Locus_10388_Transcript_1/1_Conf_1.000	935	20	3.03E-68	NP_497589.3	66	263.077	252	167	hypothetical protein Y71H2B.5
Locus_10389_Transcript_1/1_Conf_1.000	375	0							
Locus_1039_Transcript_1/1_Conf_1.000	260	0							
Locus_10390_Transcript_1/1_Conf_1.000	331	20	1.20E-39	ACJ65168.1	84	166.007	110	93	Uncoordinated protein 68, isoform b, partially confirmed by transcript evidence
Locus_10391_Transcript_1/1_Conf_1.000	239	0							
Locus_10392_Transcript_1/1_Conf_1.000	475	0							
Locus_10393_Transcript_1/1_Conf_1.000	371	20	7.37E-45	XP_002633716.1	81	183.341	119	97	C. briggsae CBR-GTA-1 protein
Locus_10394_Transcript_1/1_Conf_1.000	383	0							
Locus_10395_Transcript_1/1_Conf_1.000	985	20	6.24E-51	NP_505460.1	75	205.682	178	135	hypothetical protein C50F4.12
Locus_10396_Transcript_1/1_Conf_1.000	726	0							

Locus_10397_Transcript_1/3_Conf_0.714	1981	20	0	NP_001040912.1	78	675.241	508	398	hypothetical protein C08F8.2
Locus_10397_Transcript_2/3_Conf_0.714	1981	20	0	NP_001040912.1	78	675.241	508	398	hypothetical protein C08F8.2
Locus_10397_Transcript_3/3_Conf_0.714	1981	20	0	NP_001040912.1	78	675.241	508	398	hypothetical protein C08F8.2
Locus_10398_Transcript_1/1_Conf_1.000	1271	20	1.19E-66	NP_001021632.1	59	258.455	392	234	RaB GAP related family member (rbg-2)
Locus_10399_Transcript_1/1_Conf_1.000	143	0							
Locus_104_Transcript_1/1_Conf_1.000	885	20	5.71E-82	NP_497701.1	81	308.531	238	195	Conserved Regulator of Innate immunity family member (cri-3)
Locus_1040_Transcript_1/1_Conf_1.000	2567	20	0	XP_002647804.1	78	1044.65	860	678	Hypothetical protein CBG23578
Locus_10400_Transcript_1/1_Conf_1.000	628	2	6.29E-05	XP_002645190.1	45	51.6026	148	68	C. briggsae CBR-PPK-3 protein

Locus_10401_Transcript_1/1_Conf_1.000	1318	20	1.77E-145	NP_493982.1	82	520.39	399	328	hypothetical protein H17B01.1
Locus_10402_Transcript_1/1_Conf_1.000	355	20	5.24E-19	XP_001891914.1	66	97.4413	112	74	ThiF family protein
Locus_10403_Transcript_1/1_Conf_1.000	1042	20	5.60E-146	XP_002638849.1	84	521.546	347	293	Hypothetical protein CBG22061
Locus_10404_Transcript_1/1_Conf_1.000	404	20	1.29E-17	XP_001898675.1	61	92.8189	121	74	MGC82625 protein
Locus_10405_Transcript_1/1_Conf_1.000	598	20	1.18E-63	EFO20819.1	74	246.514	198	148	CK1/TTBKL protein kinase
Locus_10406_Transcript_1/1_Conf_1.000	1276	20	1.46E-72	NP_492469.1	71	278.1	256	183	Anterior PHarynx defective family member (aph-1)
Locus_10407_Transcript_1/1_Conf_1.000	185	20	3.46E-26	XP_001894250.1	88	121.324	61	54	Low-density lipoprotein receptor-related protein
Locus_10408_Transcript_1/1_Conf_1.000	822	20	4.74E-48	XP_001894112.1	68	195.667	235	162	RING finger domain containing protein
Locus_10409_Transcript_1/1_Conf_1.000	844	20	1.35E-53	XP_002642327.1	74	214.157	183	137	C. briggsae CBR-TAT-3 protein
Locus_1041_Transcript_1/2_Conf_1.000	668	20	1.48E-58	NP_496281.1	70	229.95	200	140	hypothetical protein C14A4.14
Locus_1041_Transcript_2/2_Conf_1.000	668	20	3.30E-58	NP_496281.1	69	228.794	200	139	hypothetical protein C14A4.14

Locus_10410_Transcript_1/1_Conf_1.000	354	11	4.31E-05	XP_647112.1	55	51.2174	78	43	N-terminal kinase-like protein
Locus_10411_Transcript_1/1_Conf_1.000	355	0							
Locus_10412_Transcript_1/1_Conf_1.000	533	20	1.70E-27	NP_494840.1	57	125.946	175	100	Temporarily Assigned Gene name family member (tag-151)
Locus_10413_Transcript_1/1_Conf_1.000	282	20	7.69E-34	CBW44372.1	90	146.747	94	85	C. elegans protein F21A10.2e, partially confirmed by transcript evidence
Locus_10414_Transcript_1/1_Conf_1.000	308	0							
Locus_10415_Transcript_1/1_Conf_1.000	975	0							
Locus_10416_Transcript_1/1_Conf_1.000	254	0							
Locus_10417_Transcript_1/1_Conf_1.000	836	20	2.25E-61	XP_002635871.1	66	239.965	271	180	Hypothetical protein CBG01087
Locus_10418_Transcript_1/1_Conf_1.000	275	0							
Locus_10419_Transcript_1/1_Conf_1.000	479	0							
Locus_1042_Transcript_1/1_Conf_1.000	1305	20	8.61E-52	NP_001024476.1	78	209.149	148	116	hypothetical protein C46H3.2
Locus_10420_Transcript_1/1_Conf_1.000	345	20	6.07E-15	AAD51334.1	79	83.9593	54	43	Kunitz type serine protease inhibitor
Locus_10421_Transcript_1/1_Conf_1.000	620	0							
Locus_10422_Transcript_1/1_Conf_1.000	475	0							
Locus_10423_Transcript_1/1_Conf_1.000	631	20	1.15E-46	XP_002645686.1	74	190.274	208	154	C. briggsae CBR-SYN-2 protein
Locus_10424_Transcript_1/1_Conf_1.000	294	0							
Locus_10425_Transcript_1/1_Conf_1.000	579	20	4.04E-66	AAK73885.2	79	254.603	192	153	AF003142_2Hypothetical protein F57C9.1b
Locus_10426_Transcript_1/1_Conf_1.000	613	0							
Locus_10427_Transcript_1/1_Conf_1.000	1274	20	2.53E-117	XP_002633543.1	72	426.787	383	276	Hypothetical protein CBG05410
Locus_10428_Transcript_1/1_Conf_1.000	816	20	4.40E-139	AAA72418.1	96	498.049	269	259	unnamed protein product
Locus_10429_Transcript_1/1_Conf_1.000	868	2	1.60E-04	XP_001897166.1	48	51.2174	125	60	hypothetical protein Bm1_28590
Locus_1043_Transcript_1/1_Conf_1.000	994	20	1.27E-75	XP_001897099.1	67	287.73	333	226	amidase
Locus_10430_Transcript_1/1_Conf_1.000	183	0							

Locus_10431_Transcript_1/1_Conf_1.000	505	0							
Locus_10432_Transcript_1/1_Conf_1.000	401	4	1.44E-08	XP_002634229.1	76	62.7734	55	42	C. briggsae CBR-UNC-26 protein
Locus_10433_Transcript_1/1_Conf_1.000	1434	5	9.23E-26	XP_001902031.1	49	122.865	248	122	hypothetical protein
Locus_10434_Transcript_1/2_Conf_1.000	1040	0							
Locus_10434_Transcript_2/2_Conf_1.000	1040	0							
Locus_10435_Transcript_1/1_Conf_1.000	618	4	2.17E-26	NP_502212.1	54	122.865	200	108	hypothetical protein ZK792.5
Locus_10436_Transcript_1/1_Conf_1.000	809								
Locus_10437_Transcript_1/1_Conf_1.000	287	0							
Locus_10438_Transcript_1/1_Conf_1.000	210	3	2.19E-09	ACI49256.1	73	65.4698	53	39	hypothetical protein Csp3_JD07.006
Locus_10439_Transcript_1/1_Conf_1.000	580	6	1.84E-10	XP_001902168.1	70	69.707	64	45	myotactin form B
Locus_1044_Transcript_1/1_Conf_1.000	684	4	5.28E-46	A8X3A7.2	65	188.348	241	157	Integrin alpha pat-2
Locus_10440_Transcript_1/1_Conf_1.000	391	0							
Locus_10441_Transcript_1/1_Conf_1.000	340	0							
Locus_10442_Transcript_1/4_Conf_0.167	403	13	8.62E-33	ZP_03149866.1	67	126.716	118	80	hypothetical protein G11MC16DRAFT_3625
Locus_10442_Transcript_2/4_Conf_0.167	763	20	1.04E-67	ACR38454.1	78	260.766	199	156	unknown
Locus_10442_Transcript_3/4_Conf_0.500	322	20	2.21E-33	ABO20854.1	92	145.206	78	72	hypothetical protein
Locus_10442_Transcript_4/4_Conf_0.722	757	19	6.26E-33	ABO20854.1	92	145.206	78	72	hypothetical protein
Locus_10443_Transcript_1/1_Conf_1.000	387	20	4.80E-57	EFO27005.1	94	223.787	128	121	intermediate filament protein
Locus_10444_Transcript_1/1_Conf_1.000	264	0							
Locus_10445_Transcript_1/1_Conf_1.000	267	6	1.48E-05	XP_002640597.1	67	52.7582	59	40	C. briggsae CBR-DLK-1 protein
Locus_10446_Transcript_1/1_Conf_1.000	317	0							
Locus_10447_Transcript_1/1_Conf_1.000	246	0							

Locus_10448_Transcript_1/1_Conf_1.000	835	20	1.40E-95	XP_002635350.1	81	353.599	249	204	Hypothetical protein CBG01521
Locus_10449_Transcript_1/1_Conf_1.000	403	0							
Locus_1045_Transcript_1/2_Conf_1.000	1283	20	2.37E-147	EFO18658.1	80	526.554	368	297	F-box domain-containing protein
Locus_1045_Transcript_2/2_Conf_1.000	1176	20	4.41E-121	EFO18658.1	81	439.113	303	247	F-box domain-containing protein
Locus_10450_Transcript_1/1_Conf_1.000	135	0							
Locus_10451_Transcript_1/1_Conf_1.000	401	7	2.36E-35	NP_495958.1	69	151.754	139	97	yeast SEC homolog family member (sec-5)
Locus_10452_Transcript_1/1_Conf_1.000	225	0							
Locus_10453_Transcript_1/1_Conf_1.000	228	0							
Locus_10454_Transcript_1/1_Conf_1.000	716	0							
Locus_10455_Transcript_1/1_Conf_1.000	795	20	1.48E-67	NP_495540.1	77	260.381	187	145	hypothetical protein F43E2.5
Locus_10456_Transcript_1/1_Conf_1.000	190	0							
Locus_10457_Transcript_1/1_Conf_1.000	194	0							
Locus_10458_Transcript_1/1_Conf_1.000	443	0							
Locus_10459_Transcript_1/2_Conf_1.000	849	20	5.89E-89	XP_002640838.1	88	331.643	200	176	C. briggsae CBR-UBC-20 protein
Locus_10459_Transcript_2/2_Conf_1.000	848	20	5.85E-89	XP_002640838.1	88	331.643	200	176	C. briggsae CBR-UBC-20 protein
Locus_1046_Transcript_1/1_Conf_1.000	1631	20	6.30E-82	EFO27811.1	56	309.686	501	281	3'-5' exonuclease

Locus_10460_Transcript_1/1_Conf_1.000	790	20	3.99E-49	NP_741083.1	85	199.134	132	113	ALdehyde deHydrogenase family member (alh-11)
Locus_10461_Transcript_1/1_Conf_1.000	279	20	1.78E-11	XP_002632331.1	67	72.4034	64	43	C. briggsae CBR-ROM-4 protein
Locus_10462_Transcript_1/2_Conf_1.000	798	20	1.40E-65	NP_496560.1	78	253.832	206	161	hypothetical protein Y17G7B.12
Locus_10462_Transcript_2/2_Conf_1.000	798	20	1.40E-65	NP_496560.1	78	253.832	206	161	hypothetical protein Y17G7B.12
Locus_10463_Transcript_1/1_Conf_1.000	608	20	1.06E-22	EFO18313.1	66	110.538	130	87	nuclear DNA-binding protein C1D
Locus_10464_Transcript_1/2_Conf_1.000	424	0							
Locus_10464_Transcript_2/2_Conf_1.000	424	0							
Locus_10465_Transcript_1/1_Conf_1.000	287	0							
Locus_10466_Transcript_1/1_Conf_1.000	366	0							
Locus_10467_Transcript_1/1_Conf_1.000	854	20	1.13E-63	NP_507692.1	63	247.669	282	178	hypothetical protein Y80D3A.9
Locus_10468_Transcript_1/1_Conf_1.000	659	20	1.15E-79	XP_002639222.1	78	300.056	233	184	Hypothetical protein CBG03773
Locus_10469_Transcript_1/1_Conf_1.000	238	20	4.29E-13	ZP_02737110.1	69	77.7962	69	48	Pyridoxal-5'-phosphate-dependent enzyme, beta subunit
Locus_1047_Transcript_1/1_Conf_1.000	2165	20	1.05E-90	EFO26769.1	53	339.347	744	399	hypothetical protein LOAG_01716
Locus_10470_Transcript_1/1_Conf_1.000	394	20	1.03E-46	XP_002630612.1	80	189.504	130	104	Hypothetical protein CBG02276
Locus_10471_Transcript_1/1_Conf_1.000	371	0							
Locus_10472_Transcript_1/1_Conf_1.000	280	2	4.54E-07	XP_002641621.1	64	57.7658	75	48	Hypothetical protein CBG09941

Locus_10473_Transcript_1/1_Conf_1.000	431	5	5.04E-30	XP_002810887.1	68	134.035	116	79	PREDICTED: cofilin-1-like
Locus_10474_Transcript_1/1_Conf_1.000	406	0							
Locus_10475_Transcript_1/1_Conf_1.000	179	0							
Locus_10476_Transcript_1/1_Conf_1.000	1826	20	1.27E-126	NP_499625.2	67	458.373	473	318	hypothetical protein Y49E10.20
Locus_10477_Transcript_1/1_Conf_1.000	254	0							
Locus_10478_Transcript_1/1_Conf_1.000	231	20	1.49E-13	EFO25902.1	68	79.337	72	49	hypothetical protein LOAG_02587
Locus_10479_Transcript_1/1_Conf_1.000	585	5	2.02E-36	CAG28316.1	71	155.992	162	116	spindle assembly abnormal protein 5, SAS-5
Locus_1048_Transcript_1/1_Conf_1.000	301	20	3.88E-14	EFO22751.1	88	81.2629	50	44	hypothetical protein LOAG_05734
Locus_10480_Transcript_1/1_Conf_1.000	408	20	2.11E-36	XP_002642327.1	68	155.221	151	103	C. briggsae CBR-TAT-3 protein
Locus_10481_Transcript_1/1_Conf_1.000	311	0							
Locus_10482_Transcript_1/1_Conf_1.000	344	20	1.88E-40	XP_001892739.1	89	168.703	103	92	Zinc finger, C2H2 type family protein
Locus_10483_Transcript_1/1_Conf_1.000	1178	5	8.58E-08	XP_002632964.1	37	62.7734	266	101	Hypothetical protein CBG21722
Locus_10484_Transcript_1/1_Conf_1.000	913	20	1.12E-11	XP_001899507.1	47	75.0998	242	114	hypothetical protein
Locus_10485_Transcript_1/1_Conf_1.000	487	2	6.61E-46	XP_002634524.1	78	186.808	146	115	Hypothetical protein CBG08318
Locus_10486_Transcript_1/1_Conf_1.000	336	1	9.80E-10	XP_002645528.1	72	66.6254	59	43	C. briggsae CBR-FLP-5 protein
Locus_10487_Transcript_1/1_Conf_1.000	225	0							
Locus_10488_Transcript_1/1_Conf_1.000	196	0							
Locus_10489_Transcript_1/1_Conf_1.000	447	1	3.66E-04	NP_495162.1	55	48.1358	79	44	hypothetical protein ZK1248.15

Locus_1049_Transcript_1/1_Conf_1.000	1318	20	3.34E-136	XP_002640719.1	91	489.574	284	259	C. briggsae CBR-EXC-4 protein
Locus_10490_Transcript_1/1_Conf_1.000	201	0							
Locus_10491_Transcript_1/1_Conf_1.000	368	20	3.23E-21	XP_002802296.1	100	104.76	50	50	PREDICTED: SH3 domain-binding glutamic acid-rich-like protein 3-like
Locus_10492_Transcript_1/1_Conf_1.000	189	0							
Locus_10493_Transcript_1/1_Conf_1.000	1062	20	7.25E-173	NP_498740.2	88	610.912	352	310	CaLPain family member (clp-1)
Locus_10494_Transcript_1/1_Conf_1.000	921	20	1.68E-63	NP_493578.1	92	247.284	139	129	Ubiquitin E2 (conjugating enzyme) variant family member (uev-1)
Locus_10495_Transcript_1/1_Conf_1.000	729	0							
Locus_10496_Transcript_1/1_Conf_1.000	357	0							
Locus_10497_Transcript_1/1_Conf_1.000	973	4	6.79E-34	EFO25502.1	53	149.058	252	134	F/Y-rich family protein
Locus_10498_Transcript_1/1_Conf_1.000	503	0							
Locus_10499_Transcript_1/1_Conf_1.000	767	20	9.76E-82	XP_002633444.1	85	307.375	188	160	Hypothetical protein CBG06212
Locus_105_Transcript_1/1_Conf_1.000	621	8	8.50E-23	NP_500399.2	66	110.923	120	80	hypothetical protein Y37E11AL.2

Locus_1050_Transcript_1/1_Conf_1.000	967	20	4.93E-61	XP_002630909.1	98	239.195	119	117	C. briggsae CBR-LGG-1 protein
Locus_10500_Transcript_1/1_Conf_1.000	279	20	5.67E-50	P00736.2	100	200.29	92	92	Complement C1r subcomponent
Locus_10501_Transcript_1/1_Conf_1.000	215	20	1.78E-19	XP_002639413.1	79	98.9821	68	54	C. briggsae CBR-CPS-6 protein
Locus_10502_Transcript_1/1_Conf_1.000	251	7	3.45E-31		92	137.887	76	70	hypothetical protein F09E10.7
Locus_10503_Transcript_1/1_Conf_1.000	709	20	1.51E-99	NP_496447.1	93	366.311	221	206	hypothetical protein W02B12.9
Locus_10504_Transcript_1/1_Conf_1.000	291	7	1.03E-14	NP_001041154.2	71	83.1889	77	55	hypothetical protein R31.2
Locus_10505_Transcript_1/1_Conf_1.000	789	20	6.41E-31	NP_498099.1	54	138.658	185	101	Caffeine Induced Death (S. pombe Cid) homolog family member (cid-1)
Locus_10506_Transcript_1/1_Conf_1.000	337	0							
Locus_10507_Transcript_1/1_Conf_1.000	549	0							

Locus_10508_Transcript_1/1_Conf_1.000	1312	20	1.22E-130	XP_002636654.1	82	471.085	357	294	C. briggsae CBR-CLH-6 protein
Locus_10509_Transcript_1/1_Conf_1.000	1024	20	6.82E-88	XP_001899663.1	68	328.561	335	231	Pyridine nucleotide-disulphide oxidoreductase family protein
Locus_1051_Transcript_1/1_Conf_1.000	258	20	1.39E-43	XP_002753304.1	100	179.104	85	85	PREDICTED: 60S ribosomal protein L4-like
Locus_10510_Transcript_1/1_Conf_1.000	145	0							
Locus_10511_Transcript_1/4_Conf_0.667	589	0							
Locus_10511_Transcript_2/4_Conf_0.667	604	0							
Locus_10511_Transcript_3/4_Conf_0.556	422	0							
Locus_10511_Transcript_4/4_Conf_0.667	605	0							
Locus_10512_Transcript_1/1_Conf_1.000	511	0							
Locus_10513_Transcript_1/2_Conf_1.000	756	20	2.87E-70	XP_001894547.1	73	269.24	234	171	Cyclin C
Locus_10513_Transcript_2/2_Conf_1.000	756	20	2.87E-70	XP_001894547.1	73	269.24	234	171	Cyclin C
Locus_10514_Transcript_1/1_Conf_1.000	444	0							
Locus_10515_Transcript_1/1_Conf_1.000	510	20	9.45E-27	AAC24231.1	64	123.25	135	87	cytoplasmic signalling transducer
Locus_10516_Transcript_1/1_Conf_1.000	433	4	5.01E-38	XP_002636981.1	83	160.614	124	103	C. briggsae CBR-LIN-33 protein
Locus_10517_Transcript_1/1_Conf_1.000	447	20	4.03E-19	XP_002635349.1	57	97.8265	140	81	Hypothetical protein CBG01520
Locus_10518_Transcript_1/1_Conf_1.000	1026	20	2.18E-126	XP_002639452.1	86	456.447	312	271	Hypothetical protein CBG04047
Locus_10519_Transcript_1/3_Conf_0.500	407	20	1.13E-55	NP_498300.2	97	208.764	96	94	MLP/CRP family (Muscle LIM Protein/Cysteine-rich Protein) family member (mlp-1)

Locus_10519_Transcript_2/3_Conf_0.500	495	20	4.98E-54	XP_002641170.1	97	213.772	97	95	C. briggsae CBR-MLP-1 protein
Locus_10519_Transcript_3/3_Conf_0.667	489	20	1.56E-63	NP_498300.2	98	245.358	113	111	MLP/CRP family (Muscle LIM Protein/Cysteine-rich Protein) family member (mlp-1)
Locus_1052_Transcript_1/1_Conf_1.000	715	20	3.95E-79	XP_002646318.1	91	298.516	193	176	C. briggsae CBR-RAB-8 protein
Locus_10520_Transcript_1/1_Conf_1.000	536	20	2.22E-11	XP_001942770.1	69	72.4034	85	59	PREDICTED: similar to CG32795 CG32795-PB
Locus_10521_Transcript_1/1_Conf_1.000	383	0							
Locus_10522_Transcript_1/1_Conf_1.000	523	0							
Locus_10523_Transcript_1/1_Conf_1.000	366	0							
Locus_10524_Transcript_1/1_Conf_1.000	387	0							
Locus_10525_Transcript_1/1_Conf_1.000	520	20	2.26E-18	XP_002432666.1	79	95.5153	67	53	5'-nucleotidase domain-containing protein, putative
Locus_10526_Transcript_1/1_Conf_1.000	579	20	2.08E-46	EFO16762.1	72	189.119	152	110	zinc knuckle family protein
Locus_10527_Transcript_1/1_Conf_1.000	264	0							
Locus_10528_Transcript_1/2_Conf_1.000	287	0							
Locus_10528_Transcript_2/2_Conf_1.000	811	20	6.60E-71	XP_002633717.1	84	271.552	189	159	Hypothetical protein CBG03401
Locus_10529_Transcript_1/1_Conf_1.000	484	0							
Locus_1053_Transcript_1/1_Conf_1.000	1542	20	7.52E-21	EFN82558.1	52	106.686	211	110	Choline transporter-like protein 1
Locus_10530_Transcript_1/1_Conf_1.000	308	20	3.58E-36	NP_509947.1	85	154.451	102	87	hypothetical protein T04F8.2
Locus_10531_Transcript_1/1_Conf_1.000	400	20	9.93E-26	XP_001901258.1	98	119.783	75	74	polyprotein

Locus_10532_Transcript_1/1_Conf_1.000	593	4	1.91E-34	EFO21187.1	72	149.443	204	147	hypothetical protein LOAG_07303
Locus_10533_Transcript_1/1_Conf_1.000	1129	2	1.32E-50	NP_500393.2	53	204.912	321	173	hypothetical protein Y37E11AL.5
Locus_10534_Transcript_1/1_Conf_1.000	371	0							
Locus_10535_Transcript_1/1_Conf_1.000	178	0							
Locus_10536_Transcript_1/1_Conf_1.000	168	20	5.07E-06	XP_001487335.1	65	54.299	52	34	hypothetical protein PGUG_00712
Locus_10537_Transcript_1/2_Conf_1.000	1172	20	2.15E-43	EFO24463.1	51	181.03	324	166	hypothetical protein LOAG_04022
Locus_10537_Transcript_2/2_Conf_1.000	1298	20	3.13E-54	EFO24463.1	50	217.238	407	207	hypothetical protein LOAG_04022
Locus_10538_Transcript_1/1_Conf_1.000	1087	0							
Locus_10539_Transcript_1/1_Conf_1.000	983	0							
Locus_1054_Transcript_1/1_Conf_1.000	395	20	2.91E-33	NP_001040743.1	71	144.821	126	90	hypothetical protein C17C3.1
Locus_10540_Transcript_1/1_Conf_1.000	741	20	3.17E-90	NP_502165.2	79	335.495	247	196	hypothetical protein C10C6.6
Locus_10541_Transcript_1/1_Conf_1.000	214	0							
Locus_10542_Transcript_1/1_Conf_1.000	520	0							

Locus_10543_Transcript_1/1_Conf_1.000	191	20	1.22E-23	XP_001893730.1	93	112.849	63	59	hypothetical protein
Locus_10544_Transcript_1/1_Conf_1.000	1113	20	1.19E-96	AAR86713.1	72	357.836	309	223	LIN-45 isoform 3
Locus_10545_Transcript_1/1_Conf_1.000	484	20	1.21E-63	CBJ25054.1	83	245.743	161	135	C. elegans protein C10C6.1b, confirmed by transcript evidence
Locus_10546_Transcript_1/1_Conf_1.000	644	20	5.76E-65	XP_002642138.1	73	251.136	230	169	C. briggsae CBR-HSE-5 protein
Locus_10547_Transcript_1/1_Conf_1.000	219	0							
Locus_10548_Transcript_1/2_Conf_1.000	593	20	2.56E-55	NP_001022992.1	76	218.779	198	151	CYtoKinesis defect family member (cyk-3)
Locus_10548_Transcript_2/2_Conf_1.000	593	20	4.22E-58	NP_001022992.1	75	228.024	198	150	CYtoKinesis defect family member (cyk-3)
Locus_10549_Transcript_1/1_Conf_1.000	853	0							
Locus_1055_Transcript_1/2_Conf_1.000	1953	20	1.42E-139	NP_495443.1	67	501.516	621	420	hypothetical protein ZK1127.9
Locus_1055_Transcript_2/2_Conf_1.000	1953	20	1.41E-139	NP_495443.1	67	501.516	621	420	hypothetical protein ZK1127.9

Locus_10550_Transcript_1/1_Conf_1.000	351	0							
Locus_10551_Transcript_1/1_Conf_1.000	138	0							
Locus_10552_Transcript_1/1_Conf_1.000	740	20	1.17E-36	NP_507534.1	59	157.532	206	122	hypothetical protein Y37H2A.1
Locus_10553_Transcript_1/1_Conf_1.000	769	20	2.77E-76	ADF56010.1	90	289.271	193	175	nicotinic acetylcholine receptor alpha subunit 63a
Locus_10554_Transcript_1/1_Conf_1.000	682	5	3.37E-61	NP_498608.1	76	238.81	192	146	hypothetical protein B0361.9
Locus_10555_Transcript_1/2_Conf_1.000	593	20	5.86E-76	XP_002634704.1	90	287.345	159	144	Hypothetical protein CBG19690
Locus_10555_Transcript_2/2_Conf_1.000	441	20	1.58E-47	XP_002634704.1	93	192.2	102	95	Hypothetical protein CBG19690
Locus_10556_Transcript_1/1_Conf_1.000	427	13	1.38E-19	NP_505729.1	67	99.3673	107	72	hypothetical protein F29F11.3
Locus_10557_Transcript_1/1_Conf_1.000	658	20	5.59E-26	XP_001893620.1	57	121.709	168	97	TAP C-terminal domain containing protein
Locus_10558_Transcript_1/1_Conf_1.000	599	20	3.70E-41	NP_491404.2	80	171.785	135	108	hypothetical protein D1007.16
Locus_10559_Transcript_1/1_Conf_1.000	475	20	2.33E-27	AAN10061.1	48	125.176	172	84	Kunitz-like protease inhibitor precursor
Locus_1056_Transcript_1/2_Conf_1.000	1610	3	1.16E-96	NP_495676.1	64	358.607	400	259	hypothetical protein DH11.2
Locus_1056_Transcript_2/2_Conf_1.000	383	0							
Locus_10560_Transcript_1/1_Conf_1.000	138	0							
Locus_10561_Transcript_1/1_Conf_1.000	389	20	1.95E-66	XP_002632356.1	94	254.988	128	121	Hypothetical protein CBG00370
Locus_10562_Transcript_1/1_Conf_1.000	421	20	4.59E-55	XP_002636678.1	87	217.238	138	121	C. briggsae CBR-CHE-11 protein
Locus_10563_Transcript_1/1_Conf_1.000	923	1	6.50E-07	XP_002647226.1	55	59.3066	68	38	Hypothetical protein CBG23816

Locus_10564_Transcript_1/1_Conf_1.000	693	20	1.07E-17	CAR63567.1	73	94.3597	64	47	putative COLlagen
Locus_10565_Transcript_1/1_Conf_1.000	436	20	1.27E-33	NP_497617.1	68	145.976	142	97	hypothetical protein Y71H2AM.20
Locus_10566_Transcript_1/1_Conf_1.000	393	14	8.21E-20	NP_496207.1	62	100.138	124	77	hypothetical protein T01E8.4
Locus_10567_Transcript_1/1_Conf_1.000	1264	19	1.32E-25	NP_001020993.1	41	122.094	452	187	Suppressor of PResenilin defect family member (spr-4)
Locus_10568_Transcript_1/1_Conf_1.000	894	5	1.73E-09	XP_002645552.1	42	67.781	182	78	Hypothetical protein CBG05235
Locus_10569_Transcript_1/1_Conf_1.000	587	20	2.71E-57	P34578.3	75	225.328	195	147	Rap guanine nucleotide exchange factor 1
Locus_1057_Transcript_1/1_Conf_1.000	637	20	3.22E-28	XP_001901523.1	95	129.028	66	63	U6 snRNA-associated Sm-like protein LSm5
Locus_10570_Transcript_1/2_Conf_1.000	359	1	3.51E-07	NP_502367.2	81	58.151	60	49	hypothetical protein F28D1.9
Locus_10570_Transcript_2/2_Conf_1.000	359	1	9.24E-08	NP_502367.2	81	60.077	60	49	hypothetical protein F28D1.9
Locus_10571_Transcript_1/1_Conf_1.000	199	2	1.22E-07	NP_505304.1	78	59.6918	42	33	TransThyretin-Related family domain family member (ttr-47)
Locus_10572_Transcript_1/1_Conf_1.000	226	20	7.16E-24	EFO24987.1	89	113.62	74	66	hypothetical protein LOAG_03502
Locus_10573_Transcript_1/1_Conf_1.000	461	20	1.89E-37	NP_500964.1	92	158.688	96	89	LSM Sm-like protein family member (lsm-8)
Locus_10574_Transcript_1/1_Conf_1.000	265	0							

Locus_10575_Transcript_1/1_Conf_1.000	215	20	2.83E-25	NP_491658.2	92	118.242	71	66	PaTched Related family member (ptr-10)
Locus_10576_Transcript_1/1_Conf_1.000	293	0							
Locus_10577_Transcript_1/1_Conf_1.000	434	3	2.12E-04	NP_001021684.1	66	48.9062	65	43	hypothetical protein Y105E8A.24
Locus_10578_Transcript_1/1_Conf_1.000	444	20	1.33E-46	NP_494807.1	75	189.119	160	120	Variable ABnormal morphology family member (vab-1)
Locus_10579_Transcript_1/1_Conf_1.000	804	20	9.79E-83	NP_509268.1	76	310.842	263	202	hypothetical protein F48E3.3
Locus_1058_Transcript_1/1_Conf_1.000	944	0							
Locus_10580_Transcript_1/1_Conf_1.000	466	20	6.02E-31	CAA75875.1	98	137.117	90	89	COL1A1 and PDGFB fusion transcript

Locus_10581_Transcript_1/2_Conf_1.000	538	0							
Locus_10581_Transcript_2/2_Conf_1.000	1550	20	5.99E-135	NP_001129871.1	90	485.723	302	272	related to yeast Vacuolar Protein Sorting factor family member (vps-26)
Locus_10582_Transcript_1/1_Conf_1.000	205	0							
Locus_10583_Transcript_1/1_Conf_1.000	374	20	1.34E-46	2WS2	84	189.119	124	105	The 2 AngstromStructure Of A Nu-Class Gst From Haemonchus Contortus
Locus_10584_Transcript_1/1_Conf_1.000	868	20	6.23E-33	NP_510225.2	61	145.591	187	115	hypothetical protein C49F8.2
Locus_10585_Transcript_1/1_Conf_1.000	350	0							
Locus_10586_Transcript_1/1_Conf_1.000	302	0							
Locus_10587_Transcript_1/1_Conf_1.000	701	20	2.69E-24	XP_002639987.1	73	116.316	96	71	C. briggsae CBR-AAP-1 protein
Locus_10588_Transcript_1/1_Conf_1.000	1545	1	3.76E-04	NP_496209.1	42	51.2174	224	95	hypothetical protein T01E8.5
Locus_10589_Transcript_1/1_Conf_1.000	171	0							
Locus_1059_Transcript_1/1_Conf_1.000	1512	20	1.62E-76	EFO22174.1	52	291.582	561	293	hypothetical protein LOAG_06316
Locus_10590_Transcript_1/1_Conf_1.000	167	0							
Locus_10591_Transcript_1/1_Conf_1.000	348	20	7.32E-45	XP_002641854.1	85	183.341	114	97	Hypothetical protein CBG16528
Locus_10592_Transcript_1/1_Conf_1.000	344	2	2.03E-10	NP_506363.1	64	68.9366	70	45	hypothetical protein C50B8.4
Locus_10593_Transcript_1/1_Conf_1.000	204	20	1.05E-27	XP_001900447.1	95	126.331	67	64	cyclin fold protein 1 variant b
Locus_10594_Transcript_1/1_Conf_1.000	676	20	3.31E-53	NP_491872.1	62	212.231	229	142	hypothetical protein C55B7.3
Locus_10595_Transcript_1/1_Conf_1.000	532	20	9.25E-58	XP_002631571.1	86	226.483	137	118	C. briggsae CBR-HOT-3 protein
Locus_10596_Transcript_1/1_Conf_1.000	908	0							
Locus_10597_Transcript_1/3_Conf_0.667	1299	20	5.39E-30	NP_498099.1	51	136.732	283	145	Caffeine Induced Death (S. pombe Cid) homolog family member (cid-1)
Locus_10597_Transcript_2/3_Conf_0.667	1140	20	8.12E-32	NP_498099.1	48	142.51	347	168	Caffeine Induced Death (S. pombe Cid) homolog family member (cid-1)
Locus_10597_Transcript_3/3_Conf_0.667	1281	20	9.63E-32	NP_498099.1	48	142.51	347	168	Caffeine Induced Death (S. pombe Cid) homolog family member (cid-1)
Locus_10598_Transcript_1/1_Conf_1.000	517	20	7.01E-65	NP_497837.1	89	249.98	169	151	Leucyl tRNA Synthetase family member (lrs-1)

Locus_10599_Transcript_1/1_Conf_1.000	921	20	4.31E-43	EFO17749.1	67	179.489	190	129	hypothetical protein LOAG_10750
Locus_106_Transcript_1/1_Conf_1.000	1858	20	0	ABC86956.1	98	882.863	493	484	protein disulfide isomerase
Locus_1060_Transcript_1/6_Conf_0.462	757	0							
Locus_1060_Transcript_2/6_Conf_0.154	387	0							
Locus_1060_Transcript_3/6_Conf_0.231	760	0							
Locus_1060_Transcript_4/6_Conf_0.385	760	0							
Locus_1060_Transcript_5/6_Conf_0.308	760	0							
Locus_1060_Transcript_6/6_Conf_0.615	778	0							
Locus_10600_Transcript_1/1_Conf_1.000	309	0							
Locus_10601_Transcript_1/1_Conf_1.000	361	20	5.54E-29	EFO20355.1	70	130.568	120	85	aminotransferase
Locus_10602_Transcript_1/1_Conf_1.000	668								
Locus_10603_Transcript_1/1_Conf_1.000	184	1	8.01E-07	NP_509241.1	63	56.9954	61	39	AuTophaGy (yeast Atg homolog) family member (atg-11)
Locus_10604_Transcript_1/1_Conf_1.000	728	0							
Locus_10605_Transcript_1/1_Conf_1.000	649	4	1.37E-29	XP_002639894.1	61	133.65	214	131	C. briggsae CBR-CDC-48.3 protein
Locus_10606_Transcript_1/1_Conf_1.000	557	11	8.65E-44	CAR63705.1	88	180.259	139	123	putative CREB Homolog family member
Locus_10607_Transcript_1/1_Conf_1.000	311	20	8.24E-25	XP_002642057.1	76	116.701	103	79	C. briggsae CBR-COL-89 protein
Locus_10608_Transcript_1/1_Conf_1.000	134	0							
Locus_10609_Transcript_1/1_Conf_1.000	424	0							
Locus_1061_Transcript_1/1_Conf_1.000	143	0							
Locus_10610_Transcript_1/1_Conf_1.000	673	20	1.72E-78	NP_497896.1	72	296.204	228	165	PDCD (mammalian ProgrammeD Cell Death protein) homolog family member (pdcd-2)
Locus_10611_Transcript_1/1_Conf_1.000	568	3	1.08E-12	NP_740803.1	46	77.0258	195	90	Nuclear Pore complex Protein family member (npp-13)
Locus_10612_Transcript_1/1_Conf_1.000	1135	20	5.05E-175	XP_002632772.1	87	618.231	383	334	C. briggsae CBR-TAT-2 protein

Locus_10613_Transcript_1/1_Conf_1.000	331	5	5.42E-08	XP_001637135.1	60	60.8474	74	45	predicted protein
Locus_10614_Transcript_1/1_Conf_1.000	155	0							
Locus_10615_Transcript_1/1_Conf_1.000	513	20	3.44E-24	EFO25156.1	76	114.775	96	73	hypothetical protein LOAG_03329
Locus_10616_Transcript_1/1_Conf_1.000	942	20	2.46E-41	NP_493396.1	54	173.711	303	164	hypothetical protein W04A4.5
Locus_10617_Transcript_1/1_Conf_1.000	986	20	1.53E-73	AAK62032.1	66	280.796	299	199	metalloprotease 1 precursor
Locus_10618_Transcript_1/1_Conf_1.000	654	16	4.64E-49	NP_741081.1	69	198.364	227	158	GEX Interacting protein family member (gei-16)
Locus_10619_Transcript_1/2_Conf_1.000	1872	20	1.26E-44	EFO20169.1	46	186.037	505	233	hypothetical protein LOAG_08321
Locus_10619_Transcript_2/2_Conf_1.000	212	0							
Locus_1062_Transcript_1/1_Conf_1.000	500	20	9.02E-64	NP_497837.1	87	246.128	166	146	Leucyl tRNA Synthetase family member (lrs-1)
Locus_10620_Transcript_1/1_Conf_1.000	515	20	1.58E-53	XP_002637051.1	80	212.231	144	116	C. briggsae CBR-TAG-315 protein
Locus_10621_Transcript_1/1_Conf_1.000	449	20	1.97E-66	NP_494777.1	87	254.988	149	130	MoLTing defective family member (mlt-7)
Locus_10622_Transcript_1/2_Conf_1.000	376	0							
Locus_10622_Transcript_2/2_Conf_1.000	376	0							
Locus_10623_Transcript_1/1_Conf_1.000	134	0							
Locus_10624_Transcript_1/1_Conf_1.000	134	2	1.13E-05	XP_002644763.1	79	53.1434	39	31	Hypothetical protein CBG14774
Locus_10625_Transcript_1/1_Conf_1.000	237	0							
Locus_10626_Transcript_1/1_Conf_1.000	243	2	2.51E-05	NP_507767.2	72	51.9878	55	40	hypothetical protein C14B4.2
Locus_10627_Transcript_1/1_Conf_1.000	493	0							
Locus_10628_Transcript_1/1_Conf_1.000	298	0							

Locus_10629_Transcript_1/1_Conf_1.000	299	20	3.50E-39	XP_002640690.1	88	164.466	99	88	Hypothetical protein CBG19753
Locus_1063_Transcript_1/2_Conf_1.000	392	20	7.20E-29	CAC51087.1	87	130.183	80	70	ES protein
Locus_1063_Transcript_2/2_Conf_1.000	794	20	1.70E-39	CAC51087.1	74	167.162	150	111	ES protein
Locus_10630_Transcript_1/1_Conf_1.000	375	20	2.78E-36	EFO20071.1	79	154.836	114	91	hypothetical protein LOAG_08420
Locus_10631_Transcript_1/1_Conf_1.000	710	20	4.53E-112	Q61YG1.2	88	407.912	236	209	Leishmanolysin-like peptidase
Locus_10632_Transcript_1/1_Conf_1.000	209	0							

Locus_10633_Transcript_1/1_Conf_1.000	231	20	3.43E-10	XP_001950127.1	77	68.1662	53	41	PREDICTED: similar to neuralized
Locus_10634_Transcript_1/1_Conf_1.000	151	0							
Locus_10635_Transcript_1/1_Conf_1.000	341	3	3.83E-14	XP_002631596.1	61	81.2629	107	66	Hypothetical protein CBG20777
Locus_10636_Transcript_1/1_Conf_1.000	2072	20	2.07E-128	ACI49231.1	62	464.537	636	395	hypothetical protein Csp3_JD05.016
Locus_10637_Transcript_1/1_Conf_1.000	776	20	1.23E-47	NP_504560.1	78	194.126	173	135	hypothetical protein F29G9.2
Locus_10638_Transcript_1/1_Conf_1.000	145	0							
Locus_10639_Transcript_1/1_Conf_1.000	354	0							
Locus_1064_Transcript_1/1_Conf_1.000	249	0							
Locus_10640_Transcript_1/1_Conf_1.000	675	20	1.27E-12	NP_001022292.1	72	77.411	81	59	hypothetical protein T01B7.5
Locus_10641_Transcript_1/5_Conf_0.167	440	0							
Locus_10641_Transcript_2/5_Conf_0.667	1651	20	5.81E-75	EFO23614.1	60	286.574	370	223	hypothetical protein LOAG_04870

Locus_10641_Transcript_3/5_Conf_0.667	1651	20	5.81E-75	EFO23614.1	60	286.574	370	223	hypothetical protein LOAG_04870
Locus_10641_Transcript_4/5_Conf_0.667	1651	20	5.81E-75	EFO23614.1	60	286.574	370	223	hypothetical protein LOAG_04870
Locus_10641_Transcript_5/5_Conf_0.667	1651	20	5.82E-75	EFO23614.1	60	286.574	370	223	hypothetical protein LOAG_04870
Locus_10642_Transcript_1/1_Conf_1.000	178	20	6.98E-24	XP_002632085.1	98	113.62	57	56	Hypothetical protein CBG17053
Locus_10643_Transcript_1/1_Conf_1.000	182	1	4.88E-04	NP_501925.2	68	47.7506	48	33	hypothetical protein F13B12.2
Locus_10644_Transcript_1/1_Conf_1.000	380	0							
Locus_10645_Transcript_1/1_Conf_1.000	182	0							
Locus_10646_Transcript_1/1_Conf_1.000	591	20	8.84E-40	NP_501552.1	77	167.162	150	116	hypothetical protein D1046.3
Locus_10647_Transcript_1/3_Conf_0.500	239	0							
Locus_10647_Transcript_2/3_Conf_0.333	1328	20	7.09E-110	XP_002646340.1	69	402.134	383	266	C. briggsae CBR-INX-15 protein
Locus_10647_Transcript_3/3_Conf_0.500	337	15	3.48E-07	NP_001021592.1	72	58.151	44	32	INneXin family member (inx-17)
Locus_10648_Transcript_1/1_Conf_1.000	988	19	1.32E-08	XP_001892028.1	50	65.0846	196	99	hypothetical protein Bm1_02630
Locus_10649_Transcript_1/1_Conf_1.000	145	0							
Locus_1065_Transcript_1/2_Conf_1.000	1061	20	1.57E-34	NP_505463.1	96	151.369	103	99	HIStone family member (his-35)

Locus_1065_Transcript_2/2_Conf_1.000	1061	20	8.30E-36	NP_505463.1	96	155.606	104	100	HIStone family member (his-35)
Locus_10650_Transcript_1/1_Conf_1.000	211	20	1.73E-14	XP_002428738.1	72	82.4185	70	51	Sex-determining protein fem-1, putative
Locus_10651_Transcript_1/1_Conf_1.000	577	18	1.69E-16	XP_002630479.1	60	89.7373	193	116	Hypothetical protein CBG11215
Locus_10652_Transcript_1/2_Conf_1.000	297	0							
Locus_10652_Transcript_2/2_Conf_1.000	286	0							
Locus_10653_Transcript_1/2_Conf_1.000	426	20	2.85E-57	NP_496822.2	85	224.557	141	121	hypothetical protein Y48C3A.14
Locus_10653_Transcript_2/2_Conf_1.000	397	20	6.20E-52	NP_496822.2	84	206.838	132	112	hypothetical protein Y48C3A.14
Locus_10654_Transcript_1/1_Conf_1.000	347	20	3.56E-15	XP_002429463.1	55	84.7297	106	59	set domain protein, putative

Locus_10655_Transcript_1/1_Conf_1.000	436	20	4.68E-28	AAC47238.1	73	127.487	114	84	non-muscle myosin heavy chain II
Locus_10656_Transcript_1/1_Conf_1.000	145	0							
Locus_10657_Transcript_1/1_Conf_1.000	153	0							
Locus_10658_Transcript_1/1_Conf_1.000	566	20	3.16E-49	XP_001901789.1	70	198.364	185	130	protein F41H10.5
Locus_1066_Transcript_1/1_Conf_1.000	781	20	2.95E-97	XP_002639719.1	91	358.992	199	182	Hypothetical protein CBG12445
Locus_10660_Transcript_1/1_Conf_1.000	353	20	1.33E-38	NP_496500.1	82	162.54	117	96	hypothetical protein VF13D12L.3
Locus_10661_Transcript_1/1_Conf_1.000	451	9	6.40E-17	XP_002632202.1	54	90.5077	121	66	Hypothetical protein CBG07069
Locus_10662_Transcript_1/1_Conf_1.000	607	20	2.58E-53	XP_002639587.1	75	212.231	183	138	Hypothetical protein CBG04225

Locus_10663_Transcript_1/1_Conf_1.000	242	20	4.58E-07	Q90WA0.1	63	57.7658	57	36	Textilinin-2
Locus_10664_Transcript_1/1_Conf_1.000	484	20	5.68E-13	NP_500023.1	64	77.411	94	61	hypothetical protein Y55F3AM.9
Locus_10665_Transcript_1/1_Conf_1.000	435	20	2.32E-27	NP_871792.1	90	125.176	81	73	hypothetical protein F08A10.1
Locus_10666_Transcript_1/1_Conf_1.000	468	20	8.99E-11	XP_001604140.1	63	70.0922	82	52	PREDICTED: similar to GM05135p
Locus_10667_Transcript_1/1_Conf_1.000	686	2	8.79E-17	NP_505881.3	63	91.2781	82	52	hypothetical protein T02E9.5
Locus_10668_Transcript_1/1_Conf_1.000	380	3	2.53E-05	AAK93849.3	49	51.9878	69	34	U12964_12Hypothetical protein F26F4.9a
Locus_10669_Transcript_1/1_Conf_1.000	514	20	4.20E-30	XP_001899440.1	62	134.42	159	99	CPSF A subunit region family protein
Locus_1067_Transcript_1/1_Conf_1.000	503	20	1.18E-42	NP_496168.1	78	176.022	140	110	hypothetical protein F52H3.5
Locus_10670_Transcript_1/1_Conf_1.000	660	1	7.82E-04	ZP_05807298.1	50	48.1358	81	41	glycosyl transferase family 51
Locus_10671_Transcript_1/1_Conf_1.000	370	0							
Locus_10672_Transcript_1/2_Conf_1.000	1034	0							
Locus_10672_Transcript_2/2_Conf_1.000	1034	0							
Locus_10673_Transcript_1/1_Conf_1.000	662	1	2.69E-04	YP_031621.1	50	49.6766	51	26	hypothetical protein FV3gorf43R
Locus_10674_Transcript_1/1_Conf_1.000	140	0							
Locus_10675_Transcript_1/1_Conf_1.000	698	2	1.79E-12	NP_497036.1	46	77.0258	150	70	hypothetical protein F19H8.2
Locus_10676_Transcript_1/1_Conf_1.000	903	20	1.21E-159	AAD39095.1	100	566.614	278	278	AF105337_1galectin GAL-1
Locus_10677_Transcript_1/1_Conf_1.000	243	0							
Locus_10678_Transcript_1/1_Conf_1.000	242	0							

Locus_10679_Transcript_1/1_Conf_1.000	149	20	4.23E-16	NP_502747.1	85	87.8113	48	41	hypothetical protein F55B11.1
Locus_1068_Transcript_1/1_Conf_1.000	1134	20	4.40E-78	NP_492519.2	74	296.204	315	236	hypothetical protein F30A10.3
Locus_10680_Transcript_1/1_Conf_1.000	783	20	7.66E-53	XP_002631256.1	66	211.46	245	164	C. briggsae CBR-CRN-3 protein
Locus_10681_Transcript_1/1_Conf_1.000	411	0							
Locus_10682_Transcript_1/1_Conf_1.000	1489	4	2.57E-10	NP_492568.1	46	71.633	179	83	Nuclear Pore complex Protein family member (npp-14)
Locus_10683_Transcript_1/1_Conf_1.000	483	0							
Locus_10684_Transcript_1/1_Conf_1.000	1015	3	3.53E-12	NP_499551.1	55	77.0258	177	99	Nuclear Pore complex Protein family member (npp-16)
Locus_10685_Transcript_1/1_Conf_1.000	262	0							
Locus_10686_Transcript_1/1_Conf_1.000	769	20	9.71E-13	NP_493412.2	55	78.1814	114	63	hypothetical protein Y37H9A.3
Locus_10687_Transcript_1/1_Conf_1.000	481	6	7.46E-18	XP_001899819.1	56	93.5893	141	79	protein ZK524.3
Locus_10688_Transcript_1/1_Conf_1.000	152	0							
Locus_10689_Transcript_1/1_Conf_1.000	886	7	1.72E-70	XP_002646401.1	69	270.396	321	223	C. briggsae CBR-DYS-1 protein

Locus_1069_Transcript_1/1_Conf_1.000	984	20	9.76E-121	XP_002637163.1	88	437.573	296	262	C. briggsae CBR-SQV-4 protein
Locus_10690_Transcript_1/1_Conf_1.000	409	20	5.97E-15	NP_508961.2	70	83.9593	74	52	CYtochrome P450 family member (cyp-43A1)
Locus_10691_Transcript_1/1_Conf_1.000	596	20	3.74E-70	NP_001021801.1	85	268.085	187	159	hypothetical protein Y6B3B.5
Locus_10692_Transcript_1/1_Conf_1.000	314	20	5.17E-14	ABO70952.1	96	80.8777	89	86	NADH dehydrogenase subunit 3
Locus_10693_Transcript_1/2_Conf_0.500	650	20	9.14E-50	AAK94765.1	64	200.675	208	135	GLY-2
Locus_10693_Transcript_2/2_Conf_0.500	650	20	9.14E-50	AAK94765.1	64	200.675	208	135	GLY-2
Locus_10694_Transcript_1/1_Conf_1.000	236	0							
Locus_10695_Transcript_1/1_Conf_1.000	401	7	1.59E-07	XP_002630536.1	56	59.3066	96	54	Hypothetical protein CBG12976

Locus_10696_Transcript_1/2_Conf_1.000	371	20	6.91E-35	NP_508412.1	92	150.214	84	78	Vacuolar H ATPase family member (vha-15)
Locus_10696_Transcript_2/2_Conf_1.000	238	17	1.17E-10	NP_508412.1	90	69.707	40	36	Vacuolar H ATPase family member (vha-15)
Locus_10697_Transcript_1/1_Conf_1.000	693	20	1.93E-67	NP_001122528.1	74	259.61	233	173	Cation transporting ATPase family member (catp-1)
Locus_10698_Transcript_1/1_Conf_1.000	429	0							
Locus_10699_Transcript_1/1_Conf_1.000	178	10	2.93E-22	ABD62754.1	91	108.227	58	53	Hc38
Locus_107_Transcript_1/2_Conf_1.000	4141	20	0	XP_002631199.1	79	1784.62	1356	1082	C. briggsae CBR-PTP-3 protein
Locus_107_Transcript_2/2_Conf_1.000	1751	20	0	XP_002631199.1	77	707.212	532	414	C. briggsae CBR-PTP-3 protein
Locus_1070_Transcript_1/1_Conf_1.000	271	0							

Locus_10700_Transcript_1/1_Conf_1.000	737	20	1.27E-67	XP_001099416.2	100	260.381	141	141	PREDICTED: profilin-1 isoform 1
Locus_10701_Transcript_1/1_Conf_1.000	935	0							
Locus_10702_Transcript_1/1_Conf_1.000	601	20	1.05E-75	NP_001023382.1	84	286.574	200	169	Amino Acid Transporter family member (aat-4)
Locus_10703_Transcript_1/1_Conf_1.000	663	20	2.26E-59	NP_498961.2	87	232.646	142	124	hypothetical protein ZK637.2
Locus_10704_Transcript_1/2_Conf_1.000	770	20	2.68E-87	NP_502782.2	88	325.865	212	188	hypothetical protein Y57G11C.34
Locus_10704_Transcript_2/2_Conf_1.000	770	20	2.67E-87	NP_502782.2	88	325.865	212	188	hypothetical protein Y57G11C.34
Locus_10705_Transcript_1/1_Conf_1.000	265	0							
Locus_10706_Transcript_1/1_Conf_1.000	1172	20	7.09E-63	XP_002630790.1	57	245.743	383	222	Hypothetical protein CBG02487
Locus_10707_Transcript_1/1_Conf_1.000	299	0							
Locus_10708_Transcript_1/3_Conf_0.714	971	20	1.86E-108	XP_002641258.1	79	396.741	323	256	Hypothetical protein CBG05169
Locus_10708_Transcript_2/3_Conf_0.714	969	20	7.81E-107	XP_002641258.1	78	391.349	322	254	Hypothetical protein CBG05169
Locus_10708_Transcript_3/3_Conf_0.714	971	20	1.86E-108	XP_002641258.1	79	396.741	323	257	Hypothetical protein CBG05169

Locus_10709_Transcript_1/1_Conf_1.000	132	20	4.71E-20	XP_002818641.1	100	100.908	43	43	PREDICTED: LOW QUALITY PROTEIN: zyxin-like
Locus_1071_Transcript_1/1_Conf_1.000	643	20	3.61E-59	XP_002637505.1	70	231.876	195	138	C. briggsae CBR-ASP-2 protein
Locus_10710_Transcript_1/1_Conf_1.000	966	20	2.85E-109	XP_002636903.1	91	399.438	241	220	C. briggsae CBR-PAS-6 protein
Locus_10711_Transcript_1/1_Conf_1.000	183	20	3.14E-19	CAR63581.1	100	98.2117	49	49	putative COLlagen
Locus_10712_Transcript_1/1_Conf_1.000	259	2	6.06E-23	NP_499479.2	97	110.538	70	68	hypothetical protein Y66D12A.24
Locus_10713_Transcript_1/1_Conf_1.000	148	0							
Locus_10714_Transcript_1/1_Conf_1.000	728	3	1.13E-36	XP_002630207.1	87	157.532	125	109	Hypothetical protein CBG00617
Locus_10715_Transcript_1/3_Conf_0.400	195	0							
Locus_10715_Transcript_2/3_Conf_0.400	392	2	8.84E-11	NP_495177.2	87	70.0922	48	42	hypothetical protein F59G1.4
Locus_10715_Transcript_3/3_Conf_0.600	433	2	8.90E-11	NP_495177.2	87	70.0922	48	42	hypothetical protein F59G1.4
Locus_10716_Transcript_1/1_Conf_1.000	186	0							
Locus_10717_Transcript_1/1_Conf_1.000	272	0							
Locus_10718_Transcript_1/1_Conf_1.000	341	7	3.95E-19	NP_500997.1	65	97.8265	110	72	hypothetical protein C01G5.8
Locus_10719_Transcript_1/1_Conf_1.000	945	10	4.83E-37	XP_002640248.1	59	159.458	300	179	Hypothetical protein CBG12766
Locus_1072_Transcript_1/2_Conf_1.000	2564	3	1.89E-33	NP_498678.3	48	149.443	305	148	abnormal cell LINeage family member (lin-13)

Locus_1072_Transcript_2/2_Conf_1.000	1280	20	4.40E-69	XP_002635275.1	73	266.544	234	171	Hypothetical protein CBG11519
Locus_10720_Transcript_1/1_Conf_1.000	251	1	1.61E-04	XP_002639641.1	76	49.2914	76	58	C. briggsae CBR-PRP-4 protein
Locus_10721_Transcript_1/1_Conf_1.000	458	20	1.56E-31	ACS36089.1	69	139.043	140	97	cysteine proteinase
Locus_10722_Transcript_1/1_Conf_1.000	321	3	2.54E-05	NP_506163.1	63	51.9878	60	38	CCCH-type zinc finger transcription factor family member (ccch-3)
Locus_10723_Transcript_1/1_Conf_1.000	352	20	2.20E-33	EFN83153.1	100	145.206	74	74	Histone H3.3
Locus_10724_Transcript_1/1_Conf_1.000	371	20	7.87E-47	EFO19031.1	86	189.889	123	107	hypothetical protein LOAG_09464
Locus_10725_Transcript_1/1_Conf_1.000	358	0							
Locus_10726_Transcript_1/1_Conf_1.000	676	20	3.26E-101	XP_002823818.1	100	371.703	218	218	PREDICTED: 60S ribosomal protein L6-like isoform 1
Locus_10727_Transcript_1/1_Conf_1.000	408	20	1.01E-54	CAA10033.1	87	216.083	136	119	DYS-1 protein
Locus_10728_Transcript_1/1_Conf_1.000	254	0							
Locus_10729_Transcript_1/1_Conf_1.000	301	20	2.88E-09	EFN62060.1	76	65.0846	47	36	tRNA (cytosine-5-)-methyltransferase

Locus_1073_Transcript_1/3_Conf_0.571	293	20	7.17E-08	XP_002639373.1	66	60.4622	51	34	C. briggsae CBR-CEJ-1 protein
Locus_1073_Transcript_2/3_Conf_0.571	306	20	4.12E-08	XP_002639373.1	57	61.2326	70	40	C. briggsae CBR-CEJ-1 protein
Locus_1073_Transcript_3/3_Conf_0.714	321	20	4.19E-08	XP_002639373.1	57	61.2326	70	40	C. briggsae CBR-CEJ-1 protein
Locus_10730_Transcript_1/1_Conf_1.000	129	2	1.25E-04	XP_002646625.1	66	49.6766	42	28	Hypothetical protein CBG11055
Locus_10731_Transcript_1/1_Conf_1.000	172	0							
Locus_10732_Transcript_1/1_Conf_1.000	653								
Locus_10733_Transcript_1/2_Conf_1.000	1085	20	5.61E-136	XP_002630855.1	92	488.419	284	263	Hypothetical protein CBG02570
Locus_10733_Transcript_2/2_Conf_1.000	1087	20	2.80E-135	XP_002630855.1	92	486.108	284	262	Hypothetical protein CBG02570
Locus_10734_Transcript_1/1_Conf_1.000	409	0							
Locus_10735_Transcript_1/1_Conf_1.000	311	20	6.10E-28	NP_505267.1	81	127.102	88	72	Regulator of Presynaptic Morphology family member (rpm-1)
Locus_10736_Transcript_1/1_Conf_1.000	927	4	1.67E-10	NP_505473.1	62	71.2478	110	69	hypothetical protein F25B3.6
Locus_10737_Transcript_1/1_Conf_1.000	902	20	1.16E-61	EFO21137.1	71	241.121	261	186	hypothetical protein LOAG_07352
Locus_10738_Transcript_1/1_Conf_1.000	137	0							
Locus_10739_Transcript_1/1_Conf_1.000	253	3	6.53E-17	NP_001076639.1	67	90.5077	89	60	TWiK family of potassium channels family member (twk-39)
Locus_1074_Transcript_1/2_Conf_1.000	1338	20	3.59E-85	EFO26413.1	69	320.087	289	202	F-box only protein 11

Locus_1074_Transcript_2/2_Conf_1.000	1332	20	3.57E-85	EFO26413.1	69	320.087	289	202	F-box only protein 11
Locus_10740_Transcript_1/1_Conf_1.000	843	20	2.53E-84	NP_508198.1	88	316.235	214	189	hypothetical protein F55A4.1
Locus_10741_Transcript_3/7_Conf_0.346	106	0							
Locus_10741_Transcript_4/7_Conf_0.346	107	0							
Locus_10741_Transcript_6/7_Conf_0.308	111	0							
Locus_10742_Transcript_1/1_Conf_1.000	314	20	3.01E-38	XP_002753447.1	98	161.384	91	90	PREDICTED: 40S ribosomal protein S27-like
Locus_10743_Transcript_1/1_Conf_1.000	1003	20	7.20E-10	XP_001849742.1	41	69.3218	294	122	conserved hypothetical protein
Locus_10744_Transcript_1/2_Conf_1.000	1228	20	1.39E-56	XP_002640319.1	68	224.942	241	166	C. briggsae CBR-DHS-1 protein
Locus_10744_Transcript_2/2_Conf_1.000	1228	20	8.17E-57	XP_002640319.1	69	225.713	241	167	C. briggsae CBR-DHS-1 protein
Locus_10745_Transcript_1/1_Conf_1.000	393	15	4.67E-07	XP_002639228.1	57	57.7658	105	60	Hypothetical protein CBG03783
Locus_10746_Transcript_1/1_Conf_1.000	685	20	1.73E-89	XP_002634879.1	85	332.798	218	186	Hypothetical protein CBG10547
Locus_10747_Transcript_1/1_Conf_1.000	476	0							
Locus_10748_Transcript_1/1_Conf_1.000	501	0							
Locus_10749_Transcript_1/1_Conf_1.000	357	3	1.02E-06	ABH10655.1	71	56.6102	52	37	FMRFamide-related peptide FLP-32 precursor
Locus_1075_Transcript_1/2_Conf_1.000	2643	20	3.43E-54	XP_001898464.1	50	218.394	385	196	Innexin inx-3
Locus_1075_Transcript_2/2_Conf_1.000	2484	20	3.19E-54	XP_001898464.1	50	218.394	385	196	Innexin inx-3
Locus_10750_Transcript_1/1_Conf_1.000	786	0							

Locus_10751_Transcript_1/1_Conf_1.000	241	0							
Locus_10752_Transcript_1/1_Conf_1.000	202	0							
Locus_10753_Transcript_1/1_Conf_1.000	257	0							
Locus_10754_Transcript_1/1_Conf_1.000	275	5	4.71E-20	XP_002642379.1	69	100.908	91	63	Hypothetical protein CBG18383
Locus_10755_Transcript_1/1_Conf_1.000	1057	20	5.08E-102	NP_496236.1	88	375.555	229	202	hypothetical protein T09F3.2
Locus_10756_Transcript_1/1_Conf_1.000	714	20	3.87E-34	NP_494539.1	57	149.058	231	132	hypothetical protein C16C8.18
Locus_10757_Transcript_1/1_Conf_1.000	437	0							
Locus_10758_Transcript_1/1_Conf_1.000	154	0							
Locus_10759_Transcript_1/1_Conf_1.000	194	20	1.39E-19	NP_509702.3	90	99.3673	52	47	UNCoordinated family member (unc-115)
Locus_1076_Transcript_1/1_Conf_1.000	462	20	1.39E-27	ABF69516.1	100	125.946	63	63	acidic ribosomal protein P1
Locus_10760_Transcript_1/1_Conf_1.000	325	0							
Locus_10761_Transcript_1/1_Conf_1.000	582	18	1.41E-58	XP_002633595.1	79	229.565	154	123	Hypothetical protein CBG05472
Locus_10762_Transcript_1/2_Conf_1.000	541	20	6.44E-46	NP_001041131.1	79	187.193	144	115	ADDucin family member (add-2)
Locus_10762_Transcript_2/2_Conf_1.000	521	20	5.71E-46	NP_001041131.1	79	187.193	144	115	ADDucin family member (add-2)
Locus_10763_Transcript_1/1_Conf_1.000	457	3	5.57E-05	NP_741332.1	81	50.8322	38	31	hypothetical protein F52C12.2
Locus_10764_Transcript_1/1_Conf_1.000	319	0							
Locus_10765_Transcript_1/1_Conf_1.000	309	3	1.46E-13	NP_493616.1	57	79.337	106	61	hypothetical protein F33H2.5
Locus_10766_Transcript_1/1_Conf_1.000	171	0							

Locus_10767_Transcript_1/1_Conf_1.000	346	20	2.00E-42	XP_002636771.1	90	175.252	102	92	C. briggsae CBR-ATN-1 protein
Locus_10768_Transcript_1/1_Conf_1.000	153	0							
Locus_10769_Transcript_1/1_Conf_1.000	914	20	1.59E-82	NP_493618.1	66	310.457	316	211	Deletions Of G-rich DNA family member (dog-1)
Locus_1077_Transcript_1/1_Conf_1.000	1873	20	2.01E-34	XP_001898097.1	47	152.14	461	218	Asparaginase family protein
Locus_10770_Transcript_1/2_Conf_1.000	464	1	8.23E-04	NP_502410.2	43	46.9802	150	65	hypothetical protein K08E7.6
Locus_10770_Transcript_2/2_Conf_1.000	416	0							
Locus_10771_Transcript_1/1_Conf_1.000	440	20	1.60E-28	XP_002631177.1	90	129.028	82	74	C. briggsae CBR-LSM-1 protein
Locus_10772_Transcript_1/1_Conf_1.000	352	0							
Locus_10773_Transcript_1/1_Conf_1.000	384	20	2.27E-14	EFO23261.1	58	82.0333	85	50	hypothetical protein LOAG_05224
Locus_10774_Transcript_1/1_Conf_1.000	582	20	1.33E-48	NP_506007.1	73	196.438	163	120	CYclin L family member (cyl-1)
Locus_10775_Transcript_1/1_Conf_1.000	235	0							
Locus_10776_Transcript_1/1_Conf_1.000	212	0							

Locus_10777_Transcript_1/2_Conf_1.000	454	20	5.36E-40	NP_509572.1	86	167.162	149	129	AdaPtin, Alpha chain (clathrin associated complex) family member (apa-2)
Locus_10777_Transcript_2/2_Conf_1.000	454	20	5.36E-40	NP_509572.1	86	167.162	149	129	AdaPtin, Alpha chain (clathrin associated complex) family member (apa-2)
Locus_10778_Transcript_1/1_Conf_1.000	967	20	8.19E-40	XP_002631527.1	71	168.703	145	104	Hypothetical protein CBG20693
Locus_10779_Transcript_1/1_Conf_1.000	815	0							
Locus_1078_Transcript_1/1_Conf_1.000	3058	20	1.14E-72	XP_002634123.1	50	280.026	638	324	Hypothetical protein CBG01680
Locus_10780_Transcript_1/2_Conf_1.000	280	0							
Locus_10780_Transcript_2/2_Conf_1.000	234	0							
Locus_10781_Transcript_1/2_Conf_1.000	572	20	2.19E-45	EFO27189.1	70	185.652	190	133	hypothetical protein LOAG_01295
Locus_10781_Transcript_2/2_Conf_1.000	566	20	6.59E-47	EFO27189.1	70	190.66	188	133	hypothetical protein LOAG_01295
Locus_10782_Transcript_1/1_Conf_1.000	376	20	2.62E-18	NP_001032980.2	64	95.1301	103	66	hypothetical protein T23H2.3
Locus_10783_Transcript_1/1_Conf_1.000	150	0							

Locus_10784_Transcript_1/1_Conf_1.000	196	20	8.68E-30	XP_002758725.1	100	133.265	65	65	PREDICTED: dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1-like isoform 2
Locus_10785_Transcript_1/1_Conf_1.000	430	0							
Locus_10786_Transcript_1/1_Conf_1.000	691	3	5.45E-14	XP_002631728.1	47	82.0333	223	107	Hypothetical protein CBG20930
Locus_10787_Transcript_1/1_Conf_1.000	185	0							
Locus_10788_Transcript_1/1_Conf_1.000	781	20	5.13E-25	NP_503033.1	68	119.013	115	79	Splicing FActor family member (sfa-1)
Locus_10789_Transcript_1/1_Conf_1.000	174	5	2.19E-09	XP_002634414.1	70	65.4698	57	40	C. briggsae CBR-EPI-1 protein
Locus_1079_Transcript_1/1_Conf_1.000	838	20	1.05E-66	XP_001896264.1	83	257.684	181	152	cyclophilin-type peptidyl-prolyl cis-trans isomerase-15, Bmcyp-5
Locus_10790_Transcript_1/1_Conf_1.000	241	3	3.63E-04	AAQ06435.1	70	48.1358	44	31	ABC6 protein
Locus_10791_Transcript_1/1_Conf_1.000	732	0							
Locus_10792_Transcript_1/1_Conf_1.000	139	0							

Locus_10793_Transcript_1/1_Conf_1.000	281	7	9.16E-08	NP_510369.2	55	60.077	79	44	CYtochrome P450 family member (cyp-13B2)
Locus_10794_Transcript_1/1_Conf_1.000	315	20	2.16E-20	XP_002633256.1	70	102.064	100	70	Hypothetical protein CBG05981
Locus_10795_Transcript_1/2_Conf_1.000	519	20	2.49E-33	XP_002636807.1	76	145.206	113	87	Hypothetical protein CBG09249
Locus_10795_Transcript_2/2_Conf_1.000	816	20	3.00E-79	XP_002636807.1	78	299.286	230	181	Hypothetical protein CBG09249
Locus_10796_Transcript_1/1_Conf_1.000	187	3	6.33E-04	NP_001122796.1	68	47.3654	50	34	Kinesin-Like Protein family member (klp-12)
Locus_10797_Transcript_1/1_Conf_1.000	275	13	2.68E-07	XP_001989288.1	61	58.5362	59	36	GH11645
Locus_10798_Transcript_1/1_Conf_1.000	215	20	3.69E-33	NP_001123995.1	100	144.436	71	71	cold shock domain-containing protein E1 isoform 3
Locus_10799_Transcript_1/1_Conf_1.000	496	5	1.92E-13	XP_001900701.1	55	78.9518	136	76	hypothetical protein Bm1_46195
Locus_108_Transcript_1/6_Conf_0.333	475	0							
Locus_108_Transcript_2/6_Conf_0.333	475	0							
Locus_108_Transcript_3/6_Conf_0.333	342	2	2.32E-06	XP_002648823.1	50	55.4546	60	30	Hypothetical protein CBG16936
Locus_108_Transcript_4/6_Conf_0.333	342	2	2.32E-06	XP_002648823.1	50	55.4546	60	30	Hypothetical protein CBG16936
Locus_108_Transcript_5/6_Conf_0.333	291	0							
Locus_108_Transcript_6/6_Conf_0.333	333	1	1.24E-04	XP_002648823.1	46	49.6766	60	28	Hypothetical protein CBG16936
Locus_1080_Transcript_1/1_Conf_1.000	1309	7	2.24E-108	NP_492018.1	66	397.127	474	313	UNCoordinated family member (unc-14)
Locus_10800_Transcript_1/1_Conf_1.000	502	20	7.67E-18	XP_002645115.1	73	93.5893	84	62	Hypothetical protein CBG16808
Locus_10801_Transcript_1/1_Conf_1.000	531	20	2.46E-18	XP_002634401.1	74	95.5153	82	61	C. briggsae CBR-PQN-55 protein

Locus_10802_Transcript_1/1_Conf_1.000	744	20	8.72E-80	NP_508573.1	82	300.827	195	160	Discoidin Domain Receptor family member (ddr-2)
Locus_10803_Transcript_1/1_Conf_1.000	216	0							
Locus_10804_Transcript_1/1_Conf_1.000	1267	20	1.57E-127	XP_002642404.1	75	460.685	398	299	Hypothetical protein CBG06798
Locus_10805_Transcript_1/1_Conf_1.000	295	20	1.74E-38	XP_002640025.1	89	162.155	97	87	Hypothetical protein CBG12497
Locus_10806_Transcript_1/1_Conf_1.000	257	20	5.90E-10	ACI49231.1	67	67.3958	80	54	hypothetical protein Csp3_JD05.016
Locus_10807_Transcript_1/1_Conf_1.000	144	0							
Locus_10808_Transcript_1/1_Conf_1.000	842	20	2.77E-91	NP_741746.1	80	339.347	255	204	Kinesin-Like Protein family member (klp-4)
Locus_10809_Transcript_1/1_Conf_1.000	138	9	1.20E-07	NP_499580.1	82	59.6918	45	37	hypothetical protein Y75B8A.7

Locus_1081_Transcript_1/2_Conf_1.000	268	14	5.81E-10	Q94637.1	63	67.3958	87	55	Vitellogenin-6
Locus_1081_Transcript_2/2_Conf_1.000	159	0							
Locus_10810_Transcript_1/1_Conf_1.000	713	0							
Locus_10811_Transcript_1/2_Conf_1.000	501	0							
Locus_10811_Transcript_2/2_Conf_1.000	501	0							
Locus_10812_Transcript_1/1_Conf_1.000	606	3	2.70E-10	EFO20116.1	59	69.3218	98	58	hypothetical protein LOAG_08374
Locus_10813_Transcript_1/1_Conf_1.000	365	0							
Locus_10814_Transcript_1/1_Conf_1.000	287	2	5.00E-09	NP_495751.1	94	64.3142	34	32	hypothetical protein F14F11.2
Locus_10815_Transcript_1/1_Conf_1.000	510	20	1.23E-50	NP_500615.1	87	202.601	125	109	hypothetical protein T22B11.2
Locus_10816_Transcript_1/1_Conf_1.000	319	2	3.56E-15	XP_001894519.1	67	84.7297	101	68	hypothetical protein Bm1_15295
Locus_10817_Transcript_1/1_Conf_1.000	659	20	7.27E-42	XP_002631454.1	74	174.481	154	115	Hypothetical protein CBG25152
Locus_10818_Transcript_1/1_Conf_1.000	842	12	1.39E-42	NP_499555.1	79	177.563	181	143	hypothetical protein Y56A3A.22
Locus_10819_Transcript_1/1_Conf_1.000	939	20	1.34E-55	XP_002644604.1	95	221.09	124	118	C. briggsae CBR-TSP-14 protein
Locus_1082_Transcript_1/1_Conf_1.000	577	3	4.92E-24	XP_002633740.1	60	114.775	179	109	Hypothetical protein CBG03425
Locus_10820_Transcript_1/1_Conf_1.000	548	4	7.64E-50	XP_002641200.1	80	200.29	170	137	Hypothetical protein CBG09061
Locus_10821_Transcript_1/1_Conf_1.000	283	20	6.52E-25	XP_001900378.1	75	117.087	94	71	DNA gyrase/topoisomerase IV, A subunit family protein
Locus_10822_Transcript_1/1_Conf_1.000	435	20	2.31E-51	NP_505697.2	84	204.912	143	121	hypothetical protein C35A5.7

Locus_10823_Transcript_1/1_Conf_1.000	756	20	1.69E-54	NP_872058.1	70	216.853	226	160	hypothetical protein 2RSSE.1
Locus_10824_Transcript_1/1_Conf_1.000	776	2	2.52E-08	NP_498032.1	47	63.5438	191	90	hypothetical protein F26F4.2
Locus_10825_Transcript_1/1_Conf_1.000	220	0							
Locus_10826_Transcript_1/1_Conf_1.000	833	20	8.78E-66	XP_001894435.1	71	254.603	238	170	Ser/Thr protein phosphatase family protein
Locus_10827_Transcript_1/1_Conf_1.000	451	20	7.54E-26	EFO21349.1	82	120.168	102	84	hypothetical protein LOAG_07141
Locus_10828_Transcript_1/4_Conf_0.625	958	0							
Locus_10828_Transcript_2/4_Conf_0.625	958	0							
Locus_10828_Transcript_3/4_Conf_0.625	621	0							
Locus_10828_Transcript_4/4_Conf_0.625	958	0							
Locus_10829_Transcript_1/2_Conf_1.000	717	20	4.77E-40	EFO15133.1	64	168.703	179	115	hypothetical protein LOAG_13378
Locus_10829_Transcript_2/2_Conf_1.000	719	20	4.77E-40	EFO15133.1	64	168.703	179	115	hypothetical protein LOAG_13378
Locus_1083_Transcript_1/1_Conf_1.000	151	0							
Locus_10830_Transcript_1/1_Conf_1.000	453	0							
Locus_10831_Transcript_1/2_Conf_1.000	194	3	1.54E-18	CAR63588.1	83	95.9005	65	54	hypothetical protein
Locus_10831_Transcript_2/2_Conf_1.000	513	10	2.29E-52	CAR63588.1	83	208.379	136	113	hypothetical protein
Locus_10832_Transcript_1/1_Conf_1.000	448	6	9.61E-13	EFO28040.1	69	76.6406	71	49	sema domain-containing protein
Locus_10833_Transcript_1/1_Conf_1.000	202	0							
Locus_10834_Transcript_1/1_Conf_1.000	561	20	2.43E-86	P29190.1	92	321.627	173	160	Phosphoenolpyruvate carboxylase
Locus_10835_Transcript_1/1_Conf_1.000	738	20	2.43E-50	NP_509589.1	79	202.986	147	117	hypothetical protein ZK899.2
Locus_10836_Transcript_1/1_Conf_1.000	848	0							
Locus_10837_Transcript_1/1_Conf_1.000	414	20	5.87E-39	AAS99337.1	94	163.696	97	92	putative calmodulin isoform a
Locus_10838_Transcript_1/1_Conf_1.000	688	0							
Locus_10839_Transcript_1/1_Conf_1.000	226	2	2.31E-06	NP_871818.1	81	55.4546	38	31	FMRF-Like Peptide family member (flp-33)
Locus_1084_Transcript_1/1_Conf_1.000	415	0							
Locus_10840_Transcript_1/1_Conf_1.000	311	5	1.77E-27	NP_872143.2	92	125.561	76	70	TropoMoDulin family member (tmd-2)
Locus_10841_Transcript_1/1_Conf_1.000	534	2	7.90E-09	XP_001893258.1	58	63.929	103	60	hypothetical protein Bm1_08935

Locus_10842_Transcript_1/2_Conf_1.000	1371	20	8.86E-87	NP_510462.2	59	325.479	465	278	EGR (Early Growth factor Response factor) Homolog family member (egrh-1)
Locus_10842_Transcript_2/2_Conf_1.000	1493	20	1.38E-88	NP_510462.2	59	331.643	471	282	EGR (Early Growth factor Response factor) Homolog family member (egrh-1)
Locus_10843_Transcript_1/1_Conf_1.000	342	3	1.26E-36	NP_495991.1	75	155.992	109	82	hypothetical protein F42A8.1
Locus_10844_Transcript_1/2_Conf_1.000	330	20	8.28E-41	NP_499203.1	82	169.859	108	89	TransThyretin-Related family domain family member (ttr-2)
Locus_10844_Transcript_2/2_Conf_1.000	330	20	8.28E-41	NP_499203.1	82	169.859	108	89	TransThyretin-Related family domain family member (ttr-2)
Locus_10845_Transcript_1/2_Conf_1.000	1363	2	1.33E-26	EFO27879.1	46	125.561	471	219	hypothetical protein LOAG_00601
Locus_10845_Transcript_2/2_Conf_1.000	1312	2	1.18E-24	EFO27879.1	46	119.013	452	208	hypothetical protein LOAG_00601
Locus_10846_Transcript_1/1_Conf_1.000	182	20	9.16E-19	XP_001898349.1	86	96.6709	60	52	calpain D
Locus_10847_Transcript_1/1_Conf_1.000	1188	20	1.44E-127	XP_001899692.1	81	460.685	382	310	WW domain containing protein

Locus_10848_Transcript_1/1_Conf_1.000	818	20	2.78E-109	NP_491881.2	90	399.053	232	209	NADH Ubiquinone Oxidoreductase family member (nuo-2)
Locus_10849_Transcript_1/1_Conf_1.000	319	20	8.74E-22	EFO20229.1	71	106.686	106	76	hypothetical protein LOAG_08261
Locus_1085_Transcript_1/4_Conf_0.667	1807	20	0	NP_502997.1	85	669.078	431	367	Methionine AminoPeptidase family member (map-2)
Locus_1085_Transcript_2/4_Conf_0.667	1807	20	0	NP_502997.1	85	669.078	431	367	Methionine AminoPeptidase family member (map-2)
Locus_1085_Transcript_3/4_Conf_0.667	1561	20	0	NP_502997.1	85	669.078	431	367	Methionine AminoPeptidase family member (map-2)

Locus_1085_Transcript_4/4_Conf_0.667	1807	20	0	NP_502997.1	85	669.078	431	367	Methionine AminoPeptidase family member (map-2)
Locus_10850_Transcript_1/1_Conf_1.000	321	0							
Locus_10851_Transcript_1/1_Conf_1.000	907	20	1.01E-113	NP_497751.1	78	414.075	304	239	hypothetical protein C14B1.10
Locus_10852_Transcript_1/1_Conf_1.000	371	0							
Locus_10853_Transcript_1/1_Conf_1.000	434	1	1.63E-04	XP_002642900.1	60	49.2914	78	47	Hypothetical protein CBG15174
Locus_10854_Transcript_1/1_Conf_1.000	177	0							
Locus_10855_Transcript_1/1_Conf_1.000	805	8	1.69E-34	NP_497963.1	57	150.599	241	139	Suppressor/Enhancer of Lin-12 family member (sel-13)
Locus_10856_Transcript_1/1_Conf_1.000	267	7	8.93E-27	AAL77521.1	87	123.25	71	62	L80003_1guanylyl cyclase
Locus_10857_Transcript_1/1_Conf_1.000	145	0							
Locus_10858_Transcript_1/1_Conf_1.000	1455	0							
Locus_10859_Transcript_1/1_Conf_1.000	329	20	3.27E-37	XP_002636129.1	84	157.918	108	91	C. briggsae CBR-ATGR-9 protein
Locus_1086_Transcript_1/1_Conf_1.000	1090	4	2.38E-09	EFO19781.1	47	67.781	224	107	hypothetical protein LOAG_08708
Locus_10860_Transcript_1/1_Conf_1.000	329	20	5.56E-45	XP_002637938.1	88	183.726	109	96	Hypothetical protein CBG04750
Locus_10861_Transcript_1/2_Conf_1.000	451	0							
Locus_10861_Transcript_2/2_Conf_1.000	460	0							

Locus_10862_Transcript_1/1_Conf_1.000	554	20	2.63E-53	AAP36737.1	100	211.846	105	105	Homo sapiens S100 calcium binding protein A11 (calgizzarin)
Locus_10863_Transcript_1/1_Conf_1.000	219	0							
Locus_10864_Transcript_1/1_Conf_1.000	401	0							
Locus_10865_Transcript_1/2_Conf_1.000	458	2	6.16E-04	XP_001592033.1	54	47.3654	104	57	hypothetical protein SS1G_07480
Locus_10865_Transcript_2/2_Conf_1.000	485	2	6.29E-04	XP_001592033.1	54	47.3654	104	57	hypothetical protein SS1G_07480
Locus_10866_Transcript_1/1_Conf_1.000	915	2	2.79E-10	XP_002631368.1	59	70.4774	147	88	Hypothetical protein CBG03210
Locus_10867_Transcript_1/1_Conf_1.000	873	20	1.53E-87	NP_001023891.2	75	327.02	291	219	HIF (hypoxia inducible factor) homolog family member (hif-1)
Locus_10868_Transcript_1/1_Conf_1.000	248	0							
Locus_10869_Transcript_1/1_Conf_1.000	264	20	8.11E-28	XP_002632407.1	82	126.716	88	73	Hypothetical protein CBG00431
Locus_1087_Transcript_1/1_Conf_1.000	375	20	3.50E-55	NP_502165.2	93	217.624	125	117	hypothetical protein C10C6.6
Locus_10870_Transcript_1/1_Conf_1.000	438	10	3.52E-76	NP_509848.2	97	287.345	143	139	hypothetical protein C09F12.2
Locus_10871_Transcript_1/1_Conf_1.000	409	7	2.57E-42	ABM91438.1	80	174.866	120	97	defective mitochondrial respiration family member protein 1

Locus_10872_Transcript_1/1_Conf_1.000	481	20	4.49E-39	NP_491212.1	67	164.081	154	104	INneXin family member (inx-13)
Locus_10873_Transcript_1/1_Conf_1.000	623	0							
Locus_10874_Transcript_1/1_Conf_1.000	960	20	5.97E-59	XP_001894229.1	61	232.261	326	199	Variant SH3 domain containing protein
Locus_10875_Transcript_1/1_Conf_1.000	587	20	3.20E-58	AAV28323.2	72	228.409	187	136	Hypothetical protein T15B7.1
Locus_10876_Transcript_1/1_Conf_1.000	228	0							
Locus_10877_Transcript_1/2_Conf_1.000	791	5	1.87E-22	XP_002639505.1	67	110.538	167	112	Hypothetical protein CBG04107
Locus_10877_Transcript_2/2_Conf_1.000	789	5	1.87E-22	XP_002639505.1	67	110.538	167	112	Hypothetical protein CBG04107
Locus_10878_Transcript_1/1_Conf_1.000	500	13	4.06E-56	XP_002632942.1	69	220.705	166	116	Hypothetical protein CBG21698
Locus_10879_Transcript_1/1_Conf_1.000	157	0							
Locus_1088_Transcript_1/1_Conf_1.000	140	0							
Locus_10880_Transcript_1/1_Conf_1.000	145	0							
Locus_10881_Transcript_1/5_Conf_0.636	1386	20	6.09E-51	CBG22751.1	63	206.453	206	130	C. elegans protein Y59A8B.13b, partially confirmed by transcript evidence
Locus_10881_Transcript_2/5_Conf_0.636	1213	20	8.59E-51	EFO25339.1	54	205.682	293	161	zinc finger protein
Locus_10881_Transcript_3/5_Conf_0.636	1358	20	1.01E-50	EFO25339.1	54	205.682	293	161	zinc finger protein
Locus_10881_Transcript_4/5_Conf_0.636	1386	20	7.96E-51	EFO25339.1	55	206.068	293	162	zinc finger protein
Locus_10881_Transcript_5/5_Conf_0.636	1386	20	1.04E-50	EFO25339.1	54	205.682	293	161	zinc finger protein
Locus_10882_Transcript_1/1_Conf_1.000	434	0							
Locus_10883_Transcript_1/1_Conf_1.000	175	0							
Locus_10884_Transcript_1/1_Conf_1.000	333	0							
Locus_10885_Transcript_1/1_Conf_1.000	444	20	4.29E-45	NP_499344.2	77	184.111	147	114	hypothetical protein Y39A1A.9
Locus_10886_Transcript_1/1_Conf_1.000	331	0							
Locus_10887_Transcript_1/1_Conf_1.000	284	2	2.18E-04	XP_002642364.1	70	48.9062	47	33	Hypothetical protein CBG18362

Locus_10888_Transcript_1/1_Conf_1.000	203	20	1.38E-27	EDM06125.1	100	125.946	62	62	rCG35185, isoform CRA_c
Locus_10889_Transcript_1/1_Conf_1.000	371	20	1.82E-27	XP_002637830.1	81	125.561	88	72	C. briggsae CBR-DHS-22 protein
Locus_1089_Transcript_1/1_Conf_1.000	1208	20	1.64E-86	XP_002648569.1	68	324.324	330	227	Hypothetical protein CBG24890
Locus_10890_Transcript_1/1_Conf_1.000	272	0							
Locus_10891_Transcript_1/1_Conf_1.000	621	4	3.81E-31	XP_002640017.1	54	138.658	217	119	Hypothetical protein CBG12487
Locus_10892_Transcript_1/2_Conf_1.000	1303	20	3.27E-43	XP_002633896.1	63	180.644	346	221	Hypothetical protein CBG19958
Locus_10892_Transcript_2/2_Conf_1.000	1303	20	2.50E-43	XP_002633896.1	63	181.03	346	221	Hypothetical protein CBG19958
Locus_10893_Transcript_1/1_Conf_1.000	295	20	5.83E-18	XP_002646426.1	78	93.9745	74	58	C. briggsae CBR-EYA-1 protein
Locus_10894_Transcript_1/2_Conf_1.000	271	20	8.09E-12	XP_002598195.1	62	73.559	83	52	hypothetical protein BRAFLDRAFT_261117
Locus_10894_Transcript_2/2_Conf_1.000	260	20	8.20E-12	ZP_01160100.1	64	73.559	76	49	Alkaline phosphatase
Locus_10895_Transcript_1/1_Conf_1.000	312	20	1.11E-24	XP_002647071.1	86	116.316	82	71	C. briggsae CBR-NIT-1 protein
Locus_10896_Transcript_1/1_Conf_1.000	921	20	1.19E-101	NP_496800.1	76	374.015	306	234	hypothetical protein W09H1.5
Locus_10897_Transcript_1/1_Conf_1.000	295	0							
Locus_10898_Transcript_1/1_Conf_1.000	548	20	6.74E-22	CAD21647.3	60	107.457	153	93	C. elegans protein T03F6.6, confirmed by transcript evidence
Locus_10899_Transcript_1/1_Conf_1.000	396	20	3.53E-39	XP_002647861.1	84	164.466	107	90	Hypothetical protein CBG23659
Locus_109_Transcript_1/8_Conf_0.100	106	7	1.16E-05	NP_501859.1	89	53.1434	37	33	RACK1 (mammalian Receptor of Activated C Kinase) homolog family member (rack-1)

Locus_109_Transcript_2/8_Conf_0.100	148	20	3.04E-06	NP_501859.1	85	55.0694	41	35	RACK1 (mammalian Receptor of Activated C Kinase) homolog family member (rack-1)
Locus_109_Transcript_3/8_Conf_0.450	837	20	1.85E-71	XP_002633718.1	97	273.478	134	131	C. briggsae CBR-RACK-1 protein
Locus_109_Transcript_4/8_Conf_0.450	837	20	6.37E-72	XP_002633718.1	95	275.018	138	132	C. briggsae CBR-RACK-1 protein
Locus_109_Transcript_5/8_Conf_0.100	283	20	1.78E-14	NP_501859.1	92	82.4185	54	50	RACK1 (mammalian Receptor of Activated C Kinase) homolog family member (rack-1)

Locus_109_Transcript_6/8_Conf_0.100	283	20	1.78E-14	NP_501859.1	92	82.4185	54	50	RACK1 (mammalian Receptor of Activated C Kinase) homolog family member (rack-1)
Locus_109_Transcript_7/8_Conf_0.300	842	20	4.35E-145	XP_002633718.1	93	518.079	280	263	C. briggsae CBR-RACK-1 protein
Locus_109_Transcript_8/8_Conf_0.350	948	20	1.85E-145	XP_002633718.1	92	519.62	284	264	C. briggsae CBR-RACK-1 protein
Locus_1090_Transcript_1/1_Conf_1.000	824	20	7.76E-75	CAM84573.1	65	284.648	302	198	intestinal prolyl carboxypeptidase 1
Locus_10900_Transcript_1/3_Conf_0.714	447	4	3.09E-11	NP_505417.1	60	71.633	121	73	hypothetical protein K07B1.6
Locus_10900_Transcript_2/3_Conf_0.429	322	0							
Locus_10900_Transcript_3/3_Conf_0.714	322	0							
Locus_10901_Transcript_1/1_Conf_1.000	224	0							
Locus_10902_Transcript_1/1_Conf_1.000	995	20	1.49E-100	XP_002636180.1	75	370.548	326	245	Hypothetical protein CBG01437
Locus_10903_Transcript_1/1_Conf_1.000	150	20	3.69E-20	XP_002914026.1	100	101.293	49	49	PREDICTED: polyadenylate-binding protein 1-like
Locus_10904_Transcript_1/1_Conf_1.000	1255	20	6.83E-67	XP_002640612.1	68	259.225	314	214	Hypothetical protein CBG08723

Locus_10905_Transcript_1/1_Conf_1.000	482	0							
Locus_10906_Transcript_1/1_Conf_1.000	1876	20	6.50E-134	XP_002645956.1	72	482.641	431	311	C. briggsae CBR-ENT-2 protein
Locus_10907_Transcript_1/1_Conf_1.000	423	3	1.88E-08	NP_495495.1	59	62.3882	83	49	hypothetical protein E04F6.6
Locus_10908_Transcript_1/1_Conf_1.000	1041	0							
Locus_10909_Transcript_1/1_Conf_1.000	1410	20	2.96E-69	CAA10033.1	65	267.314	369	240	DYS-1 protein
Locus_1091_Transcript_1/1_Conf_1.000	410	20	1.99E-10	EFO19957.1	60	68.9366	115	69	hypothetical protein LOAG_08536
Locus_10910_Transcript_1/1_Conf_1.000	730	20	9.18E-95	XP_002638788.1	88	350.517	205	181	Hypothetical protein CBG05143
Locus_10911_Transcript_1/1_Conf_1.000	706	20	3.86E-55	NP_491763.1	66	218.779	235	156	hypothetical protein T27A3.6
Locus_10912_Transcript_1/1_Conf_1.000	731	0							
Locus_10913_Transcript_1/1_Conf_1.000	691	0							
Locus_10914_Transcript_1/1_Conf_1.000	996	20	2.80E-14	XP_001463473.1	50	83.9593	106	53	hypothetical protein
Locus_10915_Transcript_1/1_Conf_1.000	417	0							
Locus_10916_Transcript_1/1_Conf_1.000	316	20	4.66E-15	EFO23801.1	62	84.3445	105	66	replication factor C
Locus_10917_Transcript_1/1_Conf_1.000	568	20	7.38E-62	NP_872022.1	76	240.35	188	143	CysTiNoSin (lysosomal protein) homolog family member (ctns-1)
Locus_10918_Transcript_1/1_Conf_1.000	559	2	2.35E-25	NP_498100.1	65	119.013	124	81	Poly(U) Polymerase family member (pup-2)
Locus_10919_Transcript_1/1_Conf_1.000	813	0							
Locus_1092_Transcript_1/1_Conf_1.000	2516	20	0	NP_001022033.1	86	1185.24	715	620	Threonyl tRNA Synthetase family member (trs-1)
Locus_10920_Transcript_1/1_Conf_1.000	156	0							
Locus_10921_Transcript_1/1_Conf_1.000	752	20	5.25E-48	ACI48997.1	67	195.282	233	157	hypothetical protein Cbre_JD01.004
Locus_10922_Transcript_1/1_Conf_1.000	1450	20	1.88E-151	NP_502613.2	73	540.421	489	359	QUInine non-avoider family member (qui-1)
Locus_10923_Transcript_1/1_Conf_1.000	638	3	1.55E-22	XP_002634007.1	72	110.153	92	67	Hypothetical protein CBG01539

Locus_10924_Transcript_1/1_Conf_1.000	603	20	1.31E-49	NP_501913.1	72	199.904	159	115	hypothetical protein R11A8.5
Locus_10925_Transcript_1/1_Conf_1.000	543	20	6.12E-60	XP_002639515.1	77	233.802	179	138	Hypothetical protein CBG04121
Locus_10926_Transcript_1/1_Conf_1.000	447	0							
Locus_10927_Transcript_1/1_Conf_1.000	278	3	2.12E-04	NP_490888.1	73	48.9062	41	30	Mitochondrial Processing Peptidase Alpha family member (mppa-1)
Locus_10928_Transcript_1/1_Conf_1.000	929	20	2.56E-43	NP_491522.1	56	180.259	308	174	phosphoinositide kinase AdAPter subunit family member (aap-1)
Locus_10929_Transcript_1/1_Conf_1.000	505	0							
Locus_1093_Transcript_1/1_Conf_1.000	785	20	5.45E-75	NP_671477.1	99	285.034	136	135	rRNA promoter binding protein
Locus_10930_Transcript_1/1_Conf_1.000	157	0							
Locus_10931_Transcript_1/1_Conf_1.000	1156	20	7.26E-145	XP_002638763.1	82	518.079	388	322	C. briggsae CBR-BLI-3 protein
Locus_10932_Transcript_1/1_Conf_1.000	163	0							
Locus_10933_Transcript_1/2_Conf_1.000	255	0							
Locus_10933_Transcript_2/2_Conf_1.000	209	0							
Locus_10934_Transcript_1/1_Conf_1.000	358	0							
Locus_10935_Transcript_1/1_Conf_1.000	554	20	1.51E-24	NP_500522.1	66	116.316	130	86	TransThyretin-Related family domain family member (ttr-20)
Locus_10936_Transcript_1/1_Conf_1.000	428	1	5.09E-14	NP_502212.1	63	80.8777	111	70	hypothetical protein ZK792.5
Locus_10937_Transcript_1/1_Conf_1.000	340	0							
Locus_10938_Transcript_1/1_Conf_1.000	784	20	5.50E-43	EFO19864.1	79	178.718	139	111	hypothetical protein LOAG_08632

Locus_10939_Transcript_1/1_Conf_1.000	411	20	2.91E-54	NP_001022641.1	83	214.542	136	113	LEThal family member (let-805)
Locus_1094_Transcript_1/1_Conf_1.000	533	20	4.89E-67	NP_500005.1	89	257.299	156	139	MAP kinase Activated protein Kinase family member (mak-2)
Locus_10940_Transcript_1/1_Conf_1.000	139	0							
Locus_10941_Transcript_1/1_Conf_1.000	181	2	1.68E-04	XP_001949404.1	71	49.2914	39	28	PREDICTED: similar to GA19830-PA
Locus_10942_Transcript_1/1_Conf_1.000	320	20	1.71E-17	ADI61822.1	61	92.4337	93	57	endonuclease-reverse transcriptase
Locus_10943_Transcript_1/1_Conf_1.000	1180	20	4.76E-99	XP_002642360.1	89	365.925	214	192	C. briggsae CBR-RAB-30 protein
Locus_10944_Transcript_1/1_Conf_1.000	835	0							
Locus_10945_Transcript_1/1_Conf_1.000	432	20	4.09E-48	2WS2	90	194.126	116	105	The 2 AngstromStructure Of A Nu-Class Gst From Haemonchus Contortus
Locus_10946_Transcript_1/1_Conf_1.000	281	0							
Locus_10947_Transcript_1/1_Conf_1.000	316	20	1.49E-29	NP_741839.2	69	132.494	105	73	hypothetical protein F48E3.8
Locus_10948_Transcript_1/1_Conf_1.000	134	0							
Locus_10949_Transcript_1/2_Conf_1.000	442	20	5.13E-22	AAO63576.1	56	107.457	150	85	secreted protein 4 precursor
Locus_10949_Transcript_2/2_Conf_1.000	442	20	6.69E-22	AAO63576.1	56	107.071	150	85	secreted protein 4 precursor
Locus_1095_Transcript_1/1_Conf_1.000	383	7	1.01E-38	XP_002639089.1	74	162.925	134	100	C. briggsae CBR-TAG-163 protein
Locus_10950_Transcript_1/2_Conf_1.000	671	20	2.58E-34	EFO27619.1	62	149.443	216	134	hypothetical protein LOAG_00870
Locus_10950_Transcript_2/2_Conf_1.000	487	6	1.10E-16	EFO27619.1	52	89.7373	155	81	hypothetical protein LOAG_00870
Locus_10951_Transcript_1/1_Conf_1.000	458	0							

Locus_10952_Transcript_1/1_Conf_1.000	320	20	1.82E-27	XP_513188.2	63	125.561	106	67	PREDICTED: complement component 1, q subcomponent, gamma polypeptide
Locus_10953_Transcript_1/1_Conf_1.000	1854	20	0	XP_002644381.1	86	868.226	578	498	C. briggsae CBR-SAX-3 protein
Locus_10954_Transcript_1/1_Conf_1.000	864	20	2.49E-66	XP_002640643.1	68	256.529	251	171	C. briggsae CBR-TAG-271 protein
Locus_10955_Transcript_1/4_Conf_0.429	538	20	7.17E-66	XP_508190.1	99	253.447	126	125	PREDICTED: interferon induced transmembrane protein 2 (1-8D) isoform 9
Locus_10955_Transcript_2/4_Conf_0.571	657	20	3.03E-64	AAX37033.1	99	248.825	125	124	interferon induced transmembrane protein 1
Locus_10955_Transcript_3/4_Conf_0.571	563	20	1.30E-63	AAP36548.1	100	246.128	133	133	Homo sapiens interferon induced transmembrane protein 3 (1-8U)
Locus_10955_Transcript_4/4_Conf_0.571	603	20	3.09E-75	XP_508190.1	97	285.034	146	142	PREDICTED: interferon induced transmembrane protein 2 (1-8D) isoform 9
Locus_10956_Transcript_1/1_Conf_1.000	908	20	3.74E-84	NP_495106.1	70	315.849	301	213	FUcosyl Transferase family member (fut-3)
Locus_10957_Transcript_1/1_Conf_1.000	290	20	3.69E-12	XP_002639821.1	61	74.7146	76	47	C. briggsae CBR-ERS-2 protein

Locus_10958_Transcript_1/2_Conf_1.000	314	20	7.70E-26	XP_002640523.1	82	120.168	81	67	Hypothetical protein CBG18685
Locus_10958_Transcript_2/2_Conf_1.000	385	20	7.51E-26	XP_002640523.1	82	120.168	81	67	Hypothetical protein CBG18685
Locus_10959_Transcript_1/1_Conf_1.000	311	20	1.18E-39	NP_001040812.1	85	166.007	103	88	hypothetical protein T27A1.5
Locus_1096_Transcript_1/1_Conf_1.000	1771	20	3.88E-40	NP_490728.2	74	171.014	213	158	TAF (TBP-associated transcription factor) family member (taf-4)
Locus_10960_Transcript_1/1_Conf_1.000	588	20	2.99E-40	XP_001898597.1	64	168.703	184	118	Steroid receptor seven-up type 2
Locus_10961_Transcript_1/1_Conf_1.000	665	0							
Locus_10962_Transcript_1/1_Conf_1.000	165	6	3.65E-04	NP_001020987.1	81	48.1358	38	31	UNCoordinated family member (unc-89)
Locus_10963_Transcript_1/1_Conf_1.000	323	12	1.53E-26	NP_001021703.1	87	122.479	107	94	EXOCyst component family member (exoc-8)
Locus_10964_Transcript_1/1_Conf_1.000	298	7	8.68E-14	NP_491337.1	70	80.1073	74	52	EXOCyst component family member (exoc-7)
Locus_10965_Transcript_1/1_Conf_1.000	240	0							

Locus_10966_Transcript_1/1_Conf_1.000	218	20	7.94E-28	XP_002929945.1	100	126.716	63	63	PREDICTED: endothelial differentiation-related factor 1-like
Locus_10967_Transcript_1/1_Conf_1.000	250	18	1.83E-24	XP_002636962.1	84	115.546	82	69	C. briggsae CBR-MAX-1 protein
Locus_10968_Transcript_1/1_Conf_1.000	179	20	1.27E-25	XP_002723429.1	100	119.398	59	59	PREDICTED: non-POU domain containing, octamer-binding-like
Locus_10969_Transcript_1/1_Conf_1.000	178	0							
Locus_1097_Transcript_1/1_Conf_1.000	1110	20	2.82E-114	CAT00983.1	80	416.387	336	271	C. elegans protein C34C6.2c, partially confirmed by transcript evidence
Locus_10970_Transcript_1/1_Conf_1.000	884	20	7.45E-66	EFO20497.1	64	254.988	297	191	serologically defined colon cancer antigen 1
Locus_10971_Transcript_1/1_Conf_1.000	179	20	3.58E-20	ACF22787.1	98	101.293	58	57	MDR-like ABC transporter
Locus_10972_Transcript_1/1_Conf_1.000	996	20	7.16E-111	NP_490929.1	95	404.831	252	240	mitochondrial ProHiBitin complex family member (phb-1)
Locus_10973_Transcript_1/1_Conf_1.000	528	0							
Locus_10974_Transcript_1/1_Conf_1.000	260	11	6.68E-30	XP_002631379.1	91	133.65	73	67	Hypothetical protein CBG03221
Locus_10975_Transcript_1/1_Conf_1.000	426	20	2.87E-33	NP_001129936.1	80	144.821	105	84	SMAll family member (sma-9)
Locus_10976_Transcript_1/1_Conf_1.000	132	3	2.59E-18	XP_002830627.1	93	95.1301	44	41	PREDICTED: hypothetical protein LOC100438967
Locus_10977_Transcript_1/1_Conf_1.000	482	4	5.71E-18	NP_503722.1	63	93.9745	105	67	hypothetical protein W02H5.2

Locus_10978_Transcript_1/1_Conf_1.000	694	20	1.79E-89	XP_002633161.1	77	332.798	231	179	C. briggsae CBR-TAG-224 protein
Locus_10979_Transcript_1/1_Conf_1.000	214	0							
Locus_1098_Transcript_1/2_Conf_1.000	1905	20	2.02E-98	NP_496095.1	63	364.77	401	256	WEE homolog family member (wee-1.3)
Locus_1098_Transcript_2/2_Conf_1.000	1905	20	2.02E-98	NP_496095.1	63	364.77	401	256	WEE homolog family member (wee-1.3)
Locus_10980_Transcript_1/1_Conf_1.000	247	0							
Locus_10981_Transcript_1/1_Conf_1.000	488	20	9.62E-21	NP_001040707.1	54	103.219	160	87	CDT (S. pombe CDC10 Dependent Transcript) homolog family member (cdt-1)
Locus_10982_Transcript_1/2_Conf_1.000	466	20	1.18E-10	XP_002641354.1	72	69.707	51	37	Hypothetical protein CBG13208
Locus_10982_Transcript_2/2_Conf_1.000	481	20	1.15E-10	XP_002641354.1	72	69.707	51	37	Hypothetical protein CBG13208
Locus_10983_Transcript_1/1_Conf_1.000	291	2	5.68E-05	NP_506635.1	55	50.8322	72	40	hypothetical protein Y50E8A.1
Locus_10984_Transcript_1/2_Conf_1.000	254	20	1.46E-08	NP_663214.1	70	62.7734	67	47	viral ubiquitin
Locus_10984_Transcript_2/2_Conf_1.000	204	20	2.52E-05	XP_321091.3	73	51.9878	46	34	AGAP001970-PA
Locus_10985_Transcript_1/1_Conf_1.000	680	20	4.15E-112	NP_492779.1	93	407.912	224	210	hypothetical protein B0511.6
Locus_10986_Transcript_1/1_Conf_1.000	612	2	5.99E-05	NP_035608.1	45	51.6026	122	55	small proline-rich protein 3
Locus_10987_Transcript_1/1_Conf_1.000	138	20	3.59E-20	XP_002928409.1	100	101.293	45	45	PREDICTED: heterogeneous nuclear ribonucleoprotein M-like

Locus_10988_Transcript_1/1_Conf_1.000	866	20	4.57E-44	EFO19733.1	60	182.57	243	148	hypothetical protein LOAG_08758
Locus_10989_Transcript_1/1_Conf_1.000	1446	20	1.50E-124	NP_501147.2	82	451.055	322	267	fatty acid ELOngation family member (elo-3)
Locus_1099_Transcript_1/2_Conf_1.000	833	20	1.14E-81	XP_002640453.1	93	307.375	186	173	C. briggsae CBR-RPL-17 protein
Locus_1099_Transcript_2/2_Conf_1.000	492	20	5.56E-37	NP_740781.1	89	157.147	91	81	Ribosomal Protein, Large subunit family member (rpl-17)
Locus_10990_Transcript_1/1_Conf_1.000	1051	20	1.23E-124	XP_002630800.1	84	450.669	268	227	Hypothetical protein CBG02500
Locus_10991_Transcript_1/1_Conf_1.000	331	1	1.63E-04	XP_001902364.1	60	49.2914	112	68	Myotubularin-related family protein
Locus_10992_Transcript_1/1_Conf_1.000	138	0							
Locus_10993_Transcript_1/1_Conf_1.000	1141	0							
Locus_10994_Transcript_1/1_Conf_1.000	479	0							
Locus_10995_Transcript_1/1_Conf_1.000	387	20	8.56E-22	EFO22859.1	96	106.686	61	59	hypothetical protein LOAG_05624
Locus_10996_Transcript_1/1_Conf_1.000	232	0							
Locus_10997_Transcript_1/2_Conf_1.000	182	0							
Locus_10997_Transcript_2/2_Conf_1.000	763	4	5.39E-32	NP_001122673.1	72	142.124	195	141	hypothetical protein B0353.1
Locus_10998_Transcript_1/1_Conf_1.000	406	4	1.09E-16	NP_001021652.1	57	89.7373	142	81	FANCI (Fanconi anemia complex component I) homolog family member (fnci-1)
Locus_10999_Transcript_1/1_Conf_1.000	464	20	2.69E-55	XP_002643394.1	84	218.009	148	125	Hypothetical protein CBG16008

Locus_11_Transcript_10/14_Conf_0.176	364	12	4.78E-09	NP_001023275.1	75	50.8322	45	34	VITellogenin structural genes (yolk protein genes) family member (vit-6)
Locus_11_Transcript_11/14_Conf_0.147	276	8	3.86E-06	NP_001023275.1	71	54.6842	46	33	VITellogenin structural genes (yolk protein genes) family member (vit-6)
Locus_11_Transcript_12/14_Conf_0.147	276	8	3.86E-06	NP_001023275.1	71	54.6842	46	33	VITellogenin structural genes (yolk protein genes) family member (vit-6)
Locus_11_Transcript_13/14_Conf_0.176	364	8	3.70E-07	Q94637.1	71	52.373	49	35	Vitellogenin-6
Locus_11_Transcript_14/14_Conf_0.176	364	20	4.36E-15	Q94637.1	76	68.5514	52	40	Vitellogenin-6
Locus_11_Transcript_5/14_Conf_0.088	407	20	4.57E-23	EFO25665.1	92	110.923	63	58	ribosomal protein S13
Locus_11_Transcript_6/14_Conf_0.059	354	20	4.58E-23	EFO25665.1	92	110.923	63	58	ribosomal protein S13
Locus_11_Transcript_7/14_Conf_0.176	364	20	1.11E-16	Q94637.1	78	73.9442	56	44	Vitellogenin-6

Locus_11_Transcript_8/14_Conf_0.088	448	20	6.38E-41	EFO25665.1	95	170.244	91	87	ribosomal protein S13
Locus_11_Transcript_9/14_Conf_0.088	448	20	6.38E-41	EFO25665.1	95	170.244	91	87	ribosomal protein S13
Locus_110_Transcript_1/3_Conf_0.833	457	20	1.56E-15	ADK91433.1	71	85.8853	73	52	c-type lectin 1
Locus_110_Transcript_2/3_Conf_0.722	452	20	1.58E-15	ADK91433.1	71	85.8853	73	52	c-type lectin 1
Locus_110_Transcript_3/3_Conf_0.889	394	20	1.60E-15	ADK91433.1	71	85.8853	73	52	c-type lectin 1

Locus_1100_Transcript_1/1_Conf_1.000	742	20	1.18E-44	XP_002644771.1	80	184.111	129	104	C. briggsae CBR-MIG-23 protein
Locus_11000_Transcript_1/1_Conf_1.000	752	20	1.68E-70	NP_001023373.1	75	270.011	240	180	Histidyl tRNA Synthetase family member (hrs-1)
Locus_11001_Transcript_1/1_Conf_1.000	481	20	2.93E-22	XP_001898035.1	56	108.227	176	99	hypothetical protein Bm1_32955
Locus_11002_Transcript_1/1_Conf_1.000	410	20	2.94E-38	XP_002643586.1	72	161.384	133	97	C. briggsae CBR-SYM-4 protein
Locus_11003_Transcript_1/1_Conf_1.000	284	6	1.56E-10	EFO21753.1	57	69.3218	97	56	hypothetical protein LOAG_06732
Locus_11004_Transcript_1/1_Conf_1.000	1122	20	1.72E-34	XP_002639508.1	52	151.369	382	199	Hypothetical protein CBG04113
Locus_11005_Transcript_1/1_Conf_1.000	156	0							
Locus_11006_Transcript_1/1_Conf_1.000	1610	20	6.01E-69	Q61CW2.3	62	266.544	361	225	Serine/threonine-protein kinase smg-1
Locus_11007_Transcript_1/1_Conf_1.000	421	20	1.82E-19	NP_502282.1	77	98.9821	85	66	hypothetical protein T12G3.4
Locus_11008_Transcript_1/1_Conf_1.000	524	2	1.11E-04	XP_422062.2	46	50.0618	102	47	PREDICTED: similar to mKIAA0236 protein
Locus_11009_Transcript_1/1_Conf_1.000	342	16	4.97E-25	XP_002646276.1	82	117.472	74	61	C. briggsae CBR-ABF-2 protein
Locus_1101_Transcript_1/10_Conf_0.250	306	20	3.70E-41	CAI17777.2	100	171.014	101	101	major histocompatibility complex, class I, A
Locus_1101_Transcript_10/10_Conf_0.321	716	20	7.08E-69	XP_002746334.1	88	208.764	150	132	PREDICTED: CHLA class I histocompatibility antigen, A-2 alpha chain-like

Locus_1101_Transcript_2/10_Conf_0.250	575	20	9.48E-30	CAQ09232.1	100	100.908	73	73	major histocompatibility complex, class I, C
Locus_1101_Transcript_3/10_Conf_0.321	368	20	3.26E-67	CBW44123.1	94	182.57	91	86	MHC class I antigen
Locus_1101_Transcript_4/10_Conf_0.286	246	20	5.43E-42	CBW44123.1	100	98.5969	37	37	MHC class I antigen
Locus_1101_Transcript_5/10_Conf_0.321	779	20	2.94E-76	ABQ95441.1	92	238.424	166	153	MHC class I antigen
Locus_1101_Transcript_6/10_Conf_0.107	465	20	3.27E-61	CAA34947.1	99	237.654	138	137	leukocyte antigen F

Locus_1101_Transcript_7/10_Conf_0.393	716	20	1.41E-60	CBM41445.1	100	167.933	76	76	MHC class I antigen
Locus_1101_Transcript_8/10_Conf_0.250	246	20	2.45E-42	CBW44123.1	100	98.5969	37	37	MHC class I antigen
Locus_1101_Transcript_9/10_Conf_0.250	718	20	3.53E-77	CAM24816.1	100	214.157	118	118	major histocompatibility complex, class I, C
Locus_11010_Transcript_1/1_Conf_1.000	303	0							
Locus_11011_Transcript_1/1_Conf_1.000	654	20	7.31E-95	NP_502560.1	86	350.517	217	187	FATty acid desaturase family member (fat-2)
Locus_11012_Transcript_1/1_Conf_1.000	643	20	1.23E-83	XP_002630183.1	89	313.153	212	189	C. briggsae CBR-FLI-1 protein
Locus_11013_Transcript_1/1_Conf_1.000	291	2	1.03E-06	NP_506151.1	70	56.6102	51	36	hypothetical protein C14C10.4
Locus_11014_Transcript_1/1_Conf_1.000	403								
Locus_11015_Transcript_1/1_Conf_1.000	590	2	1.49E-31	NP_497506.3	60	139.813	194	118	hypothetical protein Y48G9A.3

Locus_11016_Transcript_1/1_Conf_1.000	412	20	2.82E-57	NP_741553.1	88	224.557	136	120	ALdehyde deHydrogenase family member (alh-4)
Locus_11017_Transcript_1/1_Conf_1.000	1942	20	6.58E-105	XP_002644943.1	57	386.341	627	362	Hypothetical protein CBG10898
Locus_11018_Transcript_1/1_Conf_1.000	377	7	2.29E-14	AAC61752.1	57	82.0333	121	69	nuclear hormone receptor
Locus_11019_Transcript_1/1_Conf_1.000	442	20	1.35E-30	NP_498057.1	66	135.961	141	94	hypothetical protein C27F2.10
Locus_1102_Transcript_1/1_Conf_1.000	2206	20	0	XP_002633545.1	76	638.647	693	531	Hypothetical protein CBG05413
Locus_11020_Transcript_1/1_Conf_1.000	427	2	1.29E-33	XP_002636965.1	78	145.976	106	83	Hypothetical protein CBG09443
Locus_11021_Transcript_1/1_Conf_1.000	576	20	4.29E-36	EFO19461.1	90	154.836	90	81	hypothetical protein LOAG_09031
Locus_11022_Transcript_1/1_Conf_1.000	627	1	4.81E-05	XP_002645117.1	52	51.9878	93	49	C. briggsae CBR-XPC-1 protein
Locus_11023_Transcript_1/1_Conf_1.000	371	0							
Locus_11024_Transcript_1/1_Conf_1.000	441	20	6.03E-39	NP_872248.2	72	163.696	138	100	hypothetical protein R57.1
Locus_11025_Transcript_1/1_Conf_1.000	154	0							
Locus_11026_Transcript_1/1_Conf_1.000	376	0							
Locus_11027_Transcript_1/1_Conf_1.000	560	20	2.11E-50	NP_495951.2	84	202.216	136	115	hypothetical protein W07A12.4
Locus_11028_Transcript_1/1_Conf_1.000	338	9	3.60E-12	AAN61521.1	72	74.7146	66	48	301KDa_2 protein
Locus_11029_Transcript_1/1_Conf_1.000	259	20	3.22E-16	EFO26239.1	67	88.1965	85	57	hypothetical protein LOAG_02251
Locus_1103_Transcript_1/1_Conf_1.000	386	0							
Locus_11030_Transcript_1/1_Conf_1.000	572	0							
Locus_11031_Transcript_1/2_Conf_1.000	184	0							
Locus_11031_Transcript_2/2_Conf_1.000	435	0							

Locus_11032_Transcript_1/1_Conf_1.000	516	20	5.62E-22	NP_495931.2	56	107.457	156	88	hypothetical protein T24B8.7
Locus_11033_Transcript_1/1_Conf_1.000	168	4	8.36E-09	XP_002633975.1	75	63.5438	45	34	Hypothetical protein CBG20077
Locus_11034_Transcript_1/1_Conf_1.000	329	0							
Locus_11035_Transcript_1/1_Conf_1.000	433	0							
Locus_11036_Transcript_1/1_Conf_1.000	309	0							
Locus_11037_Transcript_1/1_Conf_1.000	729	20	4.08E-18	EFO19311.1	72	95.9005	83	60	hypothetical protein LOAG_09182
Locus_11038_Transcript_1/3_Conf_0.667	611	0							
Locus_11038_Transcript_2/3_Conf_0.667	808	0							
Locus_11038_Transcript_3/3_Conf_0.667	799	0							
Locus_11039_Transcript_1/1_Conf_1.000	795	20	1.57E-101	XP_002643079.1	91	373.244	224	204	C. briggsae CBR-ABCE-1 protein
Locus_1104_Transcript_1/1_Conf_1.000	695	20	1.52E-72	XP_002647023.1	92	276.559	150	139	C. briggsae CBR-MLC-3 protein
Locus_11040_Transcript_1/1_Conf_1.000	274	0							
Locus_11041_Transcript_1/1_Conf_1.000	232	0							

Locus_11042_Transcript_1/1_Conf_1.000	1063	20	1.56E-58	XP_002635593.1	81	231.106	161	132	Hypothetical protein CBG20581
Locus_11043_Transcript_1/1_Conf_1.000	543	20	7.55E-26	NP_498946.1	76	120.553	106	81	hypothetical protein F54F2.7
Locus_11044_Transcript_1/1_Conf_1.000	282	0							
Locus_11045_Transcript_1/1_Conf_1.000	248	0							
Locus_11046_Transcript_1/2_Conf_1.000	981	20	3.94E-122	NP_500161.1	84	442.195	326	275	hypothetical protein R05C11.3
Locus_11046_Transcript_2/2_Conf_1.000	981	20	3.94E-122	NP_500161.1	84	442.195	326	275	hypothetical protein R05C11.3
Locus_11047_Transcript_1/1_Conf_1.000	159	0							
Locus_11048_Transcript_1/1_Conf_1.000	377	0							
Locus_11049_Transcript_1/2_Conf_1.000	395	20	1.83E-19	XP_002640352.1	61	98.9821	116	71	C. briggsae CBR-ARI-1 protein
Locus_11049_Transcript_2/2_Conf_1.000	461	20	4.99E-22	XP_002640352.1	68	107.457	105	72	C. briggsae CBR-ARI-1 protein
Locus_1105_Transcript_1/1_Conf_1.000	223	0							
Locus_11050_Transcript_1/1_Conf_1.000	624	20	2.47E-78	NP_001122513.1	90	295.434	172	156	UNCoordinated family member (unc-57)
Locus_11051_Transcript_1/1_Conf_1.000	289	20	2.54E-29	NP_490714.1	92	131.724	96	89	hypothetical protein C53D5.5
Locus_11052_Transcript_1/1_Conf_1.000	167	0							
Locus_11053_Transcript_1/1_Conf_1.000	829	0							
Locus_11054_Transcript_1/1_Conf_1.000	245	20	2.66E-23	NP_510625.2	75	111.694	79	60	hypothetical protein T27A8.1
Locus_11055_Transcript_1/1_Conf_1.000	644	20	2.27E-53	XP_001899300.1	71	212.616	212	152	Negative elongation factor B homolog
Locus_11056_Transcript_1/1_Conf_1.000	183	10	6.56E-09	EFO27462.1	63	63.929	61	39	hypothetical protein LOAG_01021
Locus_11057_Transcript_1/1_Conf_1.000	299	20	1.02E-46	XP_002750287.1	100	189.504	94	94	PREDICTED: elongation factor 1-beta-like
Locus_11058_Transcript_1/1_Conf_1.000	488	20	5.77E-58	XP_002639764.1	80	226.868	153	123	Hypothetical protein CBG02210

Locus_11059_Transcript_1/1_Conf_1.000	975	20	2.06E-22	EFO20991.1	54	110.923	205	112	hypothetical protein LOAG_07497
Locus_1106_Transcript_1/1_Conf_1.000	460	20	1.15E-18	CBH29662.1	72	96.2857	88	64	C. elegans protein F44G4.4c, confirmed by transcript evidence
Locus_11060_Transcript_1/1_Conf_1.000	293	20	7.64E-18	XP_002631109.1	94	93.5893	52	49	Hypothetical protein CBG02884
Locus_11061_Transcript_1/1_Conf_1.000	720	20	1.51E-17	CAA10734.1	83	93.9745	66	55	centaurin beta 1A
Locus_11062_Transcript_1/1_Conf_1.000	588	20	9.82E-84	EFO22295.1	91	313.153	180	165	hypothetical protein LOAG_06193
Locus_11063_Transcript_1/2_Conf_1.000	906	20	3.34E-16	XP_001891812.1	60	90.1225	108	65	hypothetical protein Bm1_01480
Locus_11063_Transcript_2/2_Conf_1.000	840	20	2.93E-16	XP_001891812.1	60	90.1225	108	65	hypothetical protein Bm1_01480
Locus_11064_Transcript_1/1_Conf_1.000	235	0							
Locus_11065_Transcript_1/1_Conf_1.000	389	4	5.00E-30	NP_497649.1	87	134.035	85	74	hypothetical protein Y55D5A.4
Locus_11066_Transcript_1/1_Conf_1.000	336	3	5.74E-10	CAR63610.1	55	67.3958	93	52	putative IQ calmodulin-binding motif domain protein

Locus_11067_Transcript_1/2_Conf_1.000	1594	20	4.50E-101	NP_497068.2	69	373.244	389	271	TBC (Tre-2/Bub2/Cdc16) domain family member (tbc-20)
Locus_11067_Transcript_2/2_Conf_1.000	1588	20	9.98E-101	NP_497068.2	71	372.089	370	263	TBC (Tre-2/Bub2/Cdc16) domain family member (tbc-20)
Locus_11068_Transcript_1/1_Conf_1.000	312	20	4.36E-29	CAR63568.1	89	130.954	83	74	putative Tubulin-specific chaperone A
Locus_11069_Transcript_1/1_Conf_1.000	219	0							
Locus_1107_Transcript_1/2_Conf_1.000	2145	20	0	NP_509671.3	83	827.78	597	500	hypothetical protein ZC506.1
Locus_1107_Transcript_2/2_Conf_1.000	2009	20	0	NP_509671.3	81	854.744	645	527	hypothetical protein ZC506.1
Locus_11070_Transcript_1/1_Conf_1.000	569	20	7.71E-27	XP_001896497.1	66	124.02	126	84	pold2-prov protein
Locus_11071_Transcript_1/2_Conf_1.000	1137	0							
Locus_11071_Transcript_2/2_Conf_1.000	1135	0							
Locus_11072_Transcript_1/1_Conf_1.000	972	20	9.41E-60	NP_500420.3	62	234.958	329	204	hypothetical protein M02B7.5
Locus_11073_Transcript_1/1_Conf_1.000	330	20	7.08E-08	XP_001301920.1	68	60.4622	60	41	ankyrin repeat protein
Locus_11074_Transcript_1/1_Conf_1.000	418	0							
Locus_11075_Transcript_1/1_Conf_1.000	236	20	5.24E-27	XP_002643972.1	88	124.02	78	69	C. briggsae CBR-SLO-2 protein

Locus_11076_Transcript_1/1_Conf_1.000	729	20	6.66E-53	XP_002630580.1	61	211.46	244	151	Hypothetical protein CBG13036
Locus_11077_Transcript_1/1_Conf_1.000	1623	1	1.93E-06	XP_002416346.1	45	58.9214	199	90	conserved hypothetical protein
Locus_11078_Transcript_1/1_Conf_1.000	130	0							
Locus_11079_Transcript_1/1_Conf_1.000	1000								
Locus_1108_Transcript_1/1_Conf_1.000	1100	20	1.77E-36	EFO17908.1	51	157.918	293	151	hypothetical protein LOAG_10591
Locus_11080_Transcript_1/1_Conf_1.000	460	20	1.26E-57	XP_002639234.1	85	225.713	149	128	Hypothetical protein CBG03790
Locus_11081_Transcript_1/1_Conf_1.000	428	0							
Locus_11082_Transcript_1/1_Conf_1.000	146	0							
Locus_11083_Transcript_1/1_Conf_1.000	433	1	7.30E-05	XP_002638904.1	43	50.447	116	50	Hypothetical protein CBG22130
Locus_11084_Transcript_1/1_Conf_1.000	920	20	5.64E-128	XP_001897894.1	84	461.455	313	265	ancient conserved domain protein 4
Locus_11085_Transcript_1/1_Conf_1.000	177	0							
Locus_11086_Transcript_1/1_Conf_1.000	356	0							
Locus_11087_Transcript_1/1_Conf_1.000	1777	20	2.46E-135	NP_500645.1	63	487.263	541	341	Egl-1 suppressor/DiO uptake defective/raf enhancer family member (eor-1)
Locus_11088_Transcript_1/1_Conf_1.000	679	20	1.51E-37	XP_002631497.1	76	160.229	143	110	Hypothetical protein CBG20661
Locus_11089_Transcript_1/1_Conf_1.000	199	0							
Locus_1109_Transcript_1/4_Conf_0.556	596	20	4.78E-25	XP_002635171.1	91	118.242	67	61	Hypothetical protein CBG11408
Locus_1109_Transcript_2/4_Conf_0.667	2042	20	0	NP_001041134.1	93	769.615	433	406	hypothetical protein F58E10.3

Locus_1109_Transcript_3/4_Conf_0.222	1916	20	0	XP_002635171.1	94	660.218	366	346	Hypothetical protein CBG11408
Locus_1109_Transcript_4/4_Conf_0.667	2028	20	0	NP_001041134.1	93	769.615	433	406	hypothetical protein F58E10.3
Locus_11090_Transcript_1/1_Conf_1.000	1154	2	6.29E-48	NP_507188.3	48	196.052	391	191	hypothetical protein Y32B12B.2
Locus_11091_Transcript_1/1_Conf_1.000	592	2	1.52E-15	XP_002630921.1	76	86.6557	75	57	Hypothetical protein CBG02647
Locus_11092_Transcript_1/1_Conf_1.000	243	0							
Locus_11093_Transcript_1/2_Conf_1.000	661	0							
Locus_11093_Transcript_2/2_Conf_1.000	657	0							
Locus_11094_Transcript_1/2_Conf_1.000	514	3	7.44E-11	EFO17966.1	69	70.4774	66	46	hypothetical protein LOAG_10533
Locus_11094_Transcript_2/2_Conf_1.000	258	3	1.11E-08	EFO17966.1	69	63.1586	59	41	hypothetical protein LOAG_10533
Locus_11095_Transcript_1/1_Conf_1.000	376	0							
Locus_11096_Transcript_1/1_Conf_1.000	693	20	9.69E-19	XP_001895742.1	74	97.8265	97	72	KH domain containing protein
Locus_11097_Transcript_1/1_Conf_1.000	362	0							
Locus_11098_Transcript_1/1_Conf_1.000	455	7	2.42E-16	NP_509836.1	51	88.5817	155	80	VEGF (vascular endothelial growth factor) Receptor family member (ver-3)
Locus_11099_Transcript_1/1_Conf_1.000	249	20	4.81E-33	XP_002630901.1	86	144.05	87	75	Hypothetical protein CBG02625
Locus_111_Transcript_1/1_Conf_1.000	1415	20	0	XP_002647388.1	81	655.981	465	381	Hypothetical protein CBG06453
Locus_1110_Transcript_1/2_Conf_1.000	3146	5	6.29E-10	NP_498207.1	41	71.633	272	112	Germline-enhanced AT-HooK protein family member (gak-1)

Locus_1110_Transcript_2/2_Conf_1.000	3035	5	6.08E-10	NP_498207.1	41	71.633	272	112	Germline-enhanced AT-HooK protein family member (gak-1)
Locus_11100_Transcript_1/1_Conf_1.000	347	0							
Locus_11101_Transcript_1/1_Conf_1.000	466	20	5.58E-61	ACJ65180.1	87	236.884	154	135	Gaba b receptor subunit protein 2, confirmed by transcript evidence
Locus_11102_Transcript_1/1_Conf_1.000	713	7	1.62E-08	XP_002641190.1	66	63.929	54	36	Hypothetical protein CBG09051
Locus_11103_Transcript_1/1_Conf_1.000	150	0							
Locus_11104_Transcript_1/1_Conf_1.000	946	20	2.64E-51	XP_002641428.1	59	206.838	276	164	C. briggsae CBR-MAA-1 protein
Locus_11105_Transcript_1/1_Conf_1.000	595	0							
Locus_11106_Transcript_1/1_Conf_1.000	233	0							
Locus_11107_Transcript_1/1_Conf_1.000	302	20	2.75E-52	AAO85518.1	96	207.994	100	96	AF496634_1putative serine/threonine phosphatase
Locus_11108_Transcript_1/1_Conf_1.000	312	20	3.02E-30	EFO25269.1	91	134.806	95	87	HT004 protein
Locus_11109_Transcript_1/1_Conf_1.000	130	20	1.20E-15	NP_499263.1	93	86.2705	43	40	hypothetical protein T20G5.4
Locus_1111_Transcript_1/1_Conf_1.000	1166	4	4.48E-09	NP_498170.2	45	67.0106	244	111	hypothetical protein R02F2.7
Locus_11110_Transcript_1/1_Conf_1.000	175	20	1.16E-10	XP_002631813.1	86	69.707	44	38	Hypothetical protein CBG21034
Locus_11111_Transcript_1/1_Conf_1.000	311	0							
Locus_11112_Transcript_1/1_Conf_1.000	184	20	5.92E-18	CBA12962.1	78	93.9745	61	48	LEV-9 protein
Locus_11113_Transcript_1/1_Conf_1.000	1147	20	6.79E-103	XP_002642274.1	64	378.637	334	217	C. briggsae CBR-PDR-1 protein
Locus_11114_Transcript_1/1_Conf_1.000	405	20	1.52E-18	XP_001901920.1	88	95.9005	51	45	hypothetical protein Bm1_52260

Locus_11115_Transcript_1/1_Conf_1.000	558	20	1.98E-40	XP_002639086.1	89	169.088	106	95	C. briggsae CBR-VHA-10 protein
Locus_11116_Transcript_1/1_Conf_1.000	783	20	1.83E-46	XP_002642305.1	59	190.274	267	158	Hypothetical protein CBG18297
Locus_11117_Transcript_1/1_Conf_1.000	139	20	1.01E-14	P29190.1	94	83.1889	39	37	Phosphoenolpyruvate carboxylase
Locus_11118_Transcript_1/1_Conf_1.000	511	20	1.55E-37	NP_495841.1	65	159.073	163	106	hypothetical protein D2085.3
Locus_11119_Transcript_1/1_Conf_1.000	371	20	4.95E-33	XP_002631287.1	98	144.05	89	88	C. briggsae CBR-TNC-2 protein
Locus_1112_Transcript_1/1_Conf_1.000	557	3	3.21E-06	XP_002642465.1	59	55.4546	89	53	C. briggsae CBR-LIN-9 protein
Locus_11120_Transcript_1/1_Conf_1.000	490	20	2.20E-33	XP_001898147.1	76	145.206	125	96	SRB protein.
Locus_11121_Transcript_1/1_Conf_1.000	759	4	2.81E-65	NP_498072.1	67	252.677	248	168	hypothetical protein C45G9.5
Locus_11122_Transcript_1/1_Conf_1.000	570	20	4.50E-99	CAR63542.1	96	363.999	189	182	putative Pre-mRNA splicing protein
Locus_11123_Transcript_1/1_Conf_1.000	200	0							
Locus_11124_Transcript_1/1_Conf_1.000	593	0							
Locus_11125_Transcript_1/1_Conf_1.000	339	2	3.03E-11	XP_002629898.1	55	71.633	100	55	Hypothetical protein CBG21936
Locus_11126_Transcript_1/1_Conf_1.000	294	2	4.79E-04	XP_001554686.1	50	47.7506	101	51	hypothetical protein BC1G_06829

Locus_11127_Transcript_1/1_Conf_1.000	224	10	2.64E-26	NP_001022643.1	86	121.709	74	64	LEThal family member (let-805)
Locus_11128_Transcript_1/1_Conf_1.000	407	8	4.01E-19	EFO26895.1	61	97.8265	123	76	organic solute transporter alpha-like protein
Locus_11129_Transcript_1/1_Conf_1.000	155	0							
Locus_1113_Transcript_1/1_Conf_1.000	1578	20	0	CAR63639.1	98	686.797	354	347	hypothetical protein
Locus_11130_Transcript_1/2_Conf_1.000	525	0							
Locus_11130_Transcript_2/2_Conf_1.000	525	0							
Locus_11131_Transcript_1/1_Conf_1.000	447	0							
Locus_11132_Transcript_1/1_Conf_1.000	481	20	2.25E-14	EFO24820.1	62	82.0333	116	72	hypothetical protein LOAG_03664
Locus_11133_Transcript_1/2_Conf_1.000	1221	20	3.06E-80	XP_001898803.1	69	303.523	371	256	G-patch domain containing protein
Locus_11133_Transcript_2/2_Conf_1.000	1221	20	3.06E-80	XP_001898803.1	69	303.523	371	256	G-patch domain containing protein
Locus_11134_Transcript_1/1_Conf_1.000	584	20	9.06E-98	CAI40836.1	100	359.762	194	194	prosaposin

Locus_11135_Transcript_1/1_Conf_1.000	610	20	4.01E-78	NP_496338.1	91	294.664	183	167	hypothetical protein F59E10.3
Locus_11136_Transcript_1/1_Conf_1.000	532	4	1.27E-06	NP_493601.2	40	56.6102	190	76	FERM domain (protein4.1-ezrin-radixin-moesin) family member (frm-1)
Locus_11137_Transcript_1/1_Conf_1.000	461	20	3.09E-64	NP_502290.1	93	247.669	153	143	hypothetical protein F11A10.2
Locus_11138_Transcript_1/1_Conf_1.000	1540	20	2.51E-24	XP_001894571.1	48	118.242	400	192	UBX domain containing protein
Locus_11139_Transcript_1/1_Conf_1.000	338	4	7.01E-16	NP_491339.2	63	87.0409	105	67	hypothetical protein C43E11.11
Locus_1114_Transcript_1/1_Conf_1.000	541	1	2.48E-05	CAR63546.1	55	52.373	65	36	hypothetical protein
Locus_11140_Transcript_1/1_Conf_1.000	901	0							
Locus_11141_Transcript_1/1_Conf_1.000	497	20	2.54E-74	NP_491989.1	93	281.182	165	155	hypothetical protein C30F12.7
Locus_11142_Transcript_1/1_Conf_1.000	248	0							
Locus_11143_Transcript_1/1_Conf_1.000	333	20	8.57E-22	NP_499157.2	87	106.686	110	96	hypothetical protein T05G5.8
Locus_11144_Transcript_1/1_Conf_1.000	292	0							
Locus_11145_Transcript_1/1_Conf_1.000	506	0							

Locus_11146_Transcript_1/1_Conf_1.000	962	20	4.30E-41	XP_002631725.1	51	172.94	301	155	Hypothetical protein CBG20927
Locus_11147_Transcript_1/1_Conf_1.000	639	20	4.25E-36	XP_002630784.1	70	155.221	144	101	Hypothetical protein CBG02480
Locus_11148_Transcript_1/1_Conf_1.000	902	20	4.99E-81	NP_492213.1	79	305.449	221	176	Acyl protein THioesterase family member (ath-1)
Locus_11149_Transcript_1/1_Conf_1.000	215	0							
Locus_1115_Transcript_1/1_Conf_1.000	113	0							
Locus_11150_Transcript_1/1_Conf_1.000	1900	20	2.99E-102	EFO23042.1	57	377.481	622	356	hypothetical protein LOAG_05445
Locus_11151_Transcript_1/1_Conf_1.000	724	0							
Locus_11152_Transcript_1/1_Conf_1.000	910	20	1.41E-131	NP_502028.1	87	473.396	298	260	hypothetical protein ZK596.2
Locus_11153_Transcript_1/1_Conf_1.000	350	20	1.74E-46	EFO20855.1	88	188.734	115	102	hypothetical protein LOAG_07635
Locus_11154_Transcript_1/1_Conf_1.000	261	20	7.13E-24	XP_001900101.1	82	113.62	80	66	ADP-specific Phosphofructokinase/Glucokinase conserved region family protein
Locus_11155_Transcript_1/1_Conf_1.000	3521	20	2.71E-33	NP_491539.1	40	149.443	1174	475	SPindle Defective family member (spd-5)
Locus_11156_Transcript_1/1_Conf_1.000	162	20	8.40E-17	EFO20302.1	86	90.1225	53	46	hypothetical protein LOAG_08188
Locus_11157_Transcript_1/1_Conf_1.000	232	20	2.15E-12	NP_001022541.1	73	75.485	60	44	hypothetical protein ZK970.8
Locus_11158_Transcript_1/1_Conf_1.000	143	0							
Locus_11159_Transcript_1/1_Conf_1.000	238	0							
Locus_1116_Transcript_1/1_Conf_1.000	1338	20	2.04E-72	EFO21147.1	59	277.715	386	229	RNA binding protein
Locus_11160_Transcript_1/1_Conf_1.000	252	2	3.25E-08	NP_001023399.1	88	61.6178	34	30	hypothetical protein T23B5.4
Locus_11161_Transcript_1/1_Conf_1.000	636	20	2.34E-87	XP_002639436.1	84	325.479	209	177	Hypothetical protein CBG04029

Locus_11162_Transcript_1/3_Conf_0.667	681	0							
Locus_11162_Transcript_2/3_Conf_0.667	666	1	7.99E-04	ZP_04667639.1	42	48.1358	212	90	1,4-alpha-glucan branching enzyme
Locus_11162_Transcript_3/3_Conf_0.667	666	0							
Locus_11163_Transcript_1/1_Conf_1.000	608	20	3.56E-87	NP_497886.2	95	324.709	161	153	hypothetical protein R07E5.4
Locus_11164_Transcript_1/1_Conf_1.000	481	20	1.56E-15	XP_002638710.1	81	85.8853	59	48	Hypothetical protein CBG00291
Locus_11165_Transcript_1/1_Conf_1.000	180	2	7.53E-05	XP_002642697.1	59	50.447	59	35	C. briggsae CBR-NPP-15 protein
Locus_11166_Transcript_1/1_Conf_1.000	153	0							
Locus_11167_Transcript_1/1_Conf_1.000	253	20	6.73E-30	XP_002647042.1	86	133.65	84	73	Hypothetical protein CBG03560
Locus_11168_Transcript_1/1_Conf_1.000	559	20	5.32E-94	CAR63641.1	96	347.051	185	179	putative 26S proteasome regulatory chain 4
Locus_11169_Transcript_1/1_Conf_1.000	1069	8	4.80E-15	NP_497463.3	45	86.6557	288	131	hypothetical protein Y39A3CL.1
Locus_1117_Transcript_1/6_Conf_0.250	340	0							
Locus_1117_Transcript_3/6_Conf_0.708	1535	0							
Locus_1117_Transcript_4/6_Conf_0.542	1276	0							
Locus_1117_Transcript_5/6_Conf_0.667	1547	0							
Locus_1117_Transcript_6/6_Conf_0.667	1547	0							
Locus_11170_Transcript_1/1_Conf_1.000	667	0							
Locus_11171_Transcript_1/1_Conf_1.000	129	0							
Locus_11172_Transcript_1/1_Conf_1.000	314	0							
Locus_11173_Transcript_1/1_Conf_1.000	303	20	2.49E-37	NP_501339.2	88	158.303	99	88	neuRonal IGCAM family member (rig-4)
Locus_11174_Transcript_1/1_Conf_1.000	1037	20	3.15E-56	EFO24512.1	77	223.402	204	159	hypothetical protein LOAG_03972
Locus_11175_Transcript_1/1_Conf_1.000	404	20	1.37E-43	CAX65056.1	78	179.104	136	107	C. elegans protein F25C8.3d, partially confirmed by transcript evidence
Locus_11176_Transcript_1/1_Conf_1.000	409	20	3.04E-35	XP_002638650.1	77	151.369	135	105	C. briggsae CBR-TGT-2 protein
Locus_11177_Transcript_1/1_Conf_1.000	261	0							
Locus_11178_Transcript_1/1_Conf_1.000	209	0							
Locus_11179_Transcript_1/3_Conf_0.600	489	20	1.91E-61	CAR63538.1	75	238.424	162	123	putative MFP2
Locus_11179_Transcript_2/3_Conf_0.600	843	20	7.07E-103	CAR63538.1	79	377.867	249	198	putative MFP2
Locus_11179_Transcript_3/3_Conf_0.600	843	20	1.21E-102	CAR63538.1	79	377.096	249	198	putative MFP2

Locus_1118_Transcript_1/2_Conf_1.000	4155	20	0	ABA18180.1	90	1613.59	925	841	argonaute-like
Locus_1118_Transcript_2/2_Conf_1.000	4149	20	0	ABA18180.1	90	1613.59	925	841	argonaute-like
Locus_11180_Transcript_1/1_Conf_1.000	215	20	1.84E-16	XP_002642051.1	66	88.9669	72	48	Hypothetical protein CBG17988
Locus_11181_Transcript_1/1_Conf_1.000	181	5	2.49E-24	EFO16149.1	93	115.161	59	55	hypothetical protein LOAG_12360
Locus_11182_Transcript_1/1_Conf_1.000	974	20	2.56E-57	NP_498602.1	73	226.868	223	164	hypothetical protein B0361.6
Locus_11183_Transcript_1/1_Conf_1.000	173	0							
Locus_11184_Transcript_1/1_Conf_1.000	145	0							
Locus_11185_Transcript_1/1_Conf_1.000	988	20	3.98E-122	NP_508530.1	84	442.195	328	276	yeast SEC homolog family member (sec-3)
Locus_11186_Transcript_1/1_Conf_1.000	582	5	7.11E-10	XP_002637083.1	56	67.781	127	72	Hypothetical protein CBG09582
Locus_11187_Transcript_1/2_Conf_1.000	645	20	5.62E-76	NP_502165.2	87	287.73	219	192	hypothetical protein C10C6.6
Locus_11187_Transcript_2/2_Conf_1.000	645	20	5.62E-76	NP_502165.2	87	287.73	219	192	hypothetical protein C10C6.6
Locus_11188_Transcript_1/1_Conf_1.000	530	20	4.71E-14	EFO26499.1	95	81.2629	45	43	Cab39 protein
Locus_11189_Transcript_1/1_Conf_1.000	154	0							
Locus_1119_Transcript_1/1_Conf_1.000	521	20	2.57E-38	NP_001022966.1	93	161.77	116	109	hypothetical protein Y82E9BR.3

Locus_11190_Transcript_1/1_Conf_1.000	178	20	1.90E-13	EFO22275.1	80	78.9518	56	45	hypothetical protein LOAG_06211
Locus_11191_Transcript_1/1_Conf_1.000	228	0							
Locus_11192_Transcript_1/1_Conf_1.000	352	20	5.80E-26	NP_510321.1	69	120.553	91	63	Erythroid-Like Transcription factor family member (elt-3)
Locus_11193_Transcript_1/1_Conf_1.000	425	20	6.23E-20	XP_002640260.1	67	100.523	139	94	Hypothetical protein CBG12785
Locus_11194_Transcript_1/1_Conf_1.000	598	5	1.46E-29	XP_002639411.1	62	133.265	161	100	Hypothetical protein CBG04000
Locus_11195_Transcript_1/1_Conf_1.000	891	20	2.44E-64	ACO15781.1	72	249.98	238	172	Hypothetical protein F40G9.17
Locus_11196_Transcript_1/1_Conf_1.000	251	1	2.31E-27	NP_001024262.1	83	125.176	83	69	hypothetical protein Y51A2D.21
Locus_11197_Transcript_1/1_Conf_1.000	618	20	6.48E-55	ACJ65179.1	92	217.624	153	142	Hypothetical protein Y67D8C.10d
Locus_11198_Transcript_1/2_Conf_1.000	955	20	1.46E-33	NP_496477.2	50	147.902	296	150	hypothetical protein D1043.1
Locus_11198_Transcript_2/2_Conf_1.000	622	16	7.20E-22	NP_496477.2	53	107.842	186	99	hypothetical protein D1043.1
Locus_11199_Transcript_1/1_Conf_1.000	582	0							
Locus_112_Transcript_1/2_Conf_1.000	899	3	1.24E-15	XP_002630206.1	59	88.1965	144	86	Hypothetical protein CBG00616
Locus_112_Transcript_2/2_Conf_1.000	601	3	1.59E-15	XP_002630206.1	60	86.6557	141	85	Hypothetical protein CBG00616

Locus_1120_Transcript_1/1_Conf_1.000	249	0							
Locus_11200_Transcript_1/1_Conf_1.000	299	0							
Locus_11201_Transcript_1/4_Conf_0.571	334	20	7.74E-31	NP_498870.1	77	136.732	110	85	hypothetical protein C30C11.1
Locus_11201_Transcript_2/4_Conf_0.571	469	20	3.87E-38	NP_498870.1	79	160.999	116	92	hypothetical protein C30C11.1
Locus_11201_Transcript_3/4_Conf_0.429	334	20	7.74E-31	NP_498870.1	77	136.732	110	85	hypothetical protein C30C11.1
Locus_11201_Transcript_4/4_Conf_0.571	469	20	3.87E-38	NP_498870.1	79	160.999	116	92	hypothetical protein C30C11.1
Locus_11202_Transcript_1/1_Conf_1.000	191	0							
Locus_11203_Transcript_1/1_Conf_1.000	341	0							
Locus_11204_Transcript_1/1_Conf_1.000	232	0							
Locus_11205_Transcript_1/1_Conf_1.000	267	4	2.70E-07	XP_001894559.1	66	58.5362	56	37	Bromodomain containing protein
Locus_11206_Transcript_1/1_Conf_1.000	904	20	9.15E-83	NP_496402.1	82	311.227	220	182	hypothetical protein T06D8.5

Locus_11207_Transcript_1/1_Conf_1.000	581	20	3.48E-118	3K9M	100	427.557	193	193	Cathepsin B In Complex With Stefin A
Locus_11208_Transcript_1/1_Conf_1.000	899	0							
Locus_11209_Transcript_1/1_Conf_1.000	249	20	1.97E-10	XP_002845397.1	67	68.9366	73	49	phosphoethanolamine transferase 7
Locus_1121_Transcript_1/1_Conf_1.000	588	6	1.40E-21	NP_001023357.2	68	106.686	163	111	hypothetical protein T04C4.1
Locus_11210_Transcript_1/1_Conf_1.000	328	0							
Locus_11211_Transcript_1/2_Conf_1.000	204	0							
Locus_11211_Transcript_2/2_Conf_1.000	216	0							
Locus_11212_Transcript_1/1_Conf_1.000	170	0							
Locus_11213_Transcript_1/1_Conf_1.000	1483	20	3.34E-127	NP_506619.1	81	459.914	365	299	RFC (DNA replication factor) family member (rfc-1)
Locus_11214_Transcript_1/1_Conf_1.000	404	0							
Locus_11215_Transcript_1/1_Conf_1.000	355	0							
Locus_11216_Transcript_1/1_Conf_1.000	258	0							

Locus_11217_Transcript_1/1_Conf_1.000	628	20	3.73E-82	NP_508190.1	85	308.145	209	179	DiacylGlycerol Kinase family member (dgk-1)
Locus_11218_Transcript_1/1_Conf_1.000	1034	5	2.04E-39	XP_002641460.1	54	167.548	340	186	Hypothetical protein CBG13329
Locus_11219_Transcript_1/1_Conf_1.000	552	20	2.30E-57	Q09261.2	79	225.328	152	121	Uncharacterized protein C32A3.2
Locus_1122_Transcript_1/1_Conf_1.000	771	0							
Locus_11220_Transcript_1/1_Conf_1.000	236	20	9.30E-08	BAH16150.1	100	60.077	51	51	NADH dehydrogenase subunit 6
Locus_11221_Transcript_1/1_Conf_1.000	281	0							
Locus_11222_Transcript_1/1_Conf_1.000	242	20	1.92E-21	XP_002642159.1	78	105.531	79	62	Hypothetical protein CBG18119
Locus_11223_Transcript_1/1_Conf_1.000	1356	20	0	XP_002644007.1	90	706.057	410	371	Hypothetical protein CBG17397
Locus_11224_Transcript_1/1_Conf_1.000	188	0							
Locus_11225_Transcript_1/1_Conf_1.000	1096	2	7.91E-45	XP_002644320.1	52	185.652	330	174	Hypothetical protein CBG14129
Locus_11226_Transcript_1/1_Conf_1.000	586	20	5.11E-56	NP_498463.1	79	221.09	174	138	hypothetical protein C13B9.3
Locus_11227_Transcript_1/1_Conf_1.000	481	20	3.93E-43	XP_002640121.1	79	177.563	123	98	C. briggsae CBR-RBX-2 protein

Locus_11228_Transcript_1/1_Conf_1.000	1204	2	1.50E-47	NP_500551.2	52	194.897	412	215	hypothetical protein F55F10.1
Locus_11229_Transcript_1/1_Conf_1.000	566	0							
Locus_1123_Transcript_1/1_Conf_1.000	956	20	1.17E-107	ACI49193.1	75	394.045	317	239	hypothetical protein Csp3_JD03.002
Locus_11230_Transcript_1/1_Conf_1.000	523	7	1.31E-29	XP_001891702.1	65	132.88	132	87	Hypothetical 30.5 kDa protein ZK1321.3 in chromosome II, putative
Locus_11231_Transcript_1/1_Conf_1.000	287	7	9.11E-11	NP_504680.1	56	70.0922	94	53	hypothetical protein ZK1055.7
Locus_11232_Transcript_1/1_Conf_1.000	149	0							
Locus_11233_Transcript_1/1_Conf_1.000	340	20	2.38E-40	XP_002631516.1	83	168.318	112	94	Hypothetical protein CBG20680
Locus_11234_Transcript_1/1_Conf_1.000	988	20	1.03E-77	NP_499890.2	69	294.664	267	186	hypothetical protein T21D12.3
Locus_11235_Transcript_1/1_Conf_1.000	183	3	1.51E-05	XP_001901405.1	83	52.7582	37	31	Conserved hypothetical protein
Locus_11236_Transcript_1/1_Conf_1.000	1171	4	1.14E-28	NP_493404.2	50	132.109	320	160	hypothetical protein Y6B3B.9
Locus_11237_Transcript_1/1_Conf_1.000	170	0							
Locus_11238_Transcript_1/2_Conf_1.000	750	20	1.15E-103	NP_001021395.1	87	380.178	246	216	Receptor Mediated Endocytosis family member (rme-8)
Locus_11238_Transcript_2/2_Conf_1.000	538	20	1.65E-70	NP_001021395.1	88	268.855	176	155	Receptor Mediated Endocytosis family member (rme-8)
Locus_11239_Transcript_1/1_Conf_1.000	1041	20	1.40E-104	NP_001033378.1	78	384.03	315	247	Acyl CoA DeHydrogenase family member (acdh-11)
Locus_1124_Transcript_1/1_Conf_1.000	857	20	3.68E-30	NP_495106.1	72	136.346	102	74	FUcosyl Transferase family member (fut-3)
Locus_11240_Transcript_1/1_Conf_1.000	317	0							
Locus_11241_Transcript_1/1_Conf_1.000	604	20	3.56E-47	CAR63674.1	79	191.815	157	125	putative PeRoXisome assembly factor
Locus_11242_Transcript_1/1_Conf_1.000	947	20	0	NP_492020.1	99	672.159	315	314	hypothetical protein K10D3.4
Locus_11243_Transcript_1/1_Conf_1.000	340	0							
Locus_11244_Transcript_1/2_Conf_0.667	168	0							

Locus_11244_Transcript_2/2_Conf_0.667	168	0							
Locus_11245_Transcript_1/3_Conf_0.667	1205	20	3.06E-08	XP_001900670.1	46	64.3142	191	89	BRCA2 repeat family protein
Locus_11245_Transcript_2/3_Conf_0.500	743	20	1.67E-06	YP_001158279.1	35	57.3806	202	72	hypothetical protein Strop_1435
Locus_11245_Transcript_3/3_Conf_0.667	1151	20	3.48E-06	YP_001158279.1	35	57.3806	202	72	hypothetical protein Strop_1435
Locus_11246_Transcript_1/1_Conf_1.000	671	20	2.31E-67	XP_002633298.1	78	259.225	209	165	C. briggsae CBR-PRX-14 protein
Locus_11247_Transcript_1/1_Conf_1.000	526	20	8.93E-34	XP_001949820.1	63	146.747	152	96	PREDICTED: similar to conserved hypothetical protein
Locus_11248_Transcript_1/1_Conf_1.000	377	0							
Locus_11249_Transcript_1/1_Conf_1.000	249	0							
Locus_1125_Transcript_1/1_Conf_1.000	253	3	3.35E-21	NP_001041068.1	80	104.76	73	59	hypothetical protein ZK822.5
Locus_11250_Transcript_1/1_Conf_1.000	318	0							
Locus_11251_Transcript_1/1_Conf_1.000	334	3	1.62E-04	NP_492725.2	40	49.2914	84	34	hypothetical protein F25D7.5
Locus_11252_Transcript_1/1_Conf_1.000	792	20	2.08E-29	XP_001892702.1	51	133.65	267	137	zyg-9 protein
Locus_11253_Transcript_1/1_Conf_1.000	813	20	7.93E-40	NP_001022052.1	61	168.318	244	149	SREBP Cleavage activating Protein (SCAP) homolog family member (scp-1)
Locus_11254_Transcript_1/1_Conf_1.000	387	0							
Locus_11255_Transcript_1/1_Conf_1.000	317	4	1.50E-05	NP_741096.1	55	52.7582	65	36	hypothetical protein W04B5.3
Locus_11256_Transcript_1/1_Conf_1.000	1021	20	8.10E-57	NP_001023357.2	64	225.328	265	172	hypothetical protein T04C4.1
Locus_11257_Transcript_1/1_Conf_1.000	891	0							

Locus_11258_Transcript_1/1_Conf_1.000	433	20	3.35E-42	AAA27985.1	90	174.481	102	92	alpha-collagen
Locus_11259_Transcript_1/1_Conf_1.000	338	10	1.16E-10	EFO17726.1	54	69.707	112	61	hypothetical protein LOAG_10772
Locus_1126_Transcript_1/3_Conf_0.500	1243	7	9.87E-42	NP_001123026.1	45	175.637	499	225	RETiculon protein family member (ret-1)
Locus_1126_Transcript_2/3_Conf_0.667	2209	20	2.04E-89	NP_506656.2	50	335.109	718	366	RETiculon protein family member (ret-1)
Locus_1126_Transcript_3/3_Conf_0.333	1027	20	2.30E-59	NP_506657.3	74	233.802	249	185	RETiculon protein family member (ret-1)
Locus_11260_Transcript_1/1_Conf_1.000	372	20	2.79E-44	NP_491777.3	80	181.415	118	95	hypothetical protein T09B4.8
Locus_11261_Transcript_1/1_Conf_1.000	509	20	2.09E-66		93	254.988	169	158	hypothetical protein Y18D10A.15 - Caenorhabditis elegans
Locus_11262_Transcript_1/1_Conf_1.000	692	20	2.18E-63	NP_001021719.1	73	246.128	218	160	hypothetical protein Y110A7A.9
Locus_11263_Transcript_1/1_Conf_1.000	135	0							
Locus_11264_Transcript_1/1_Conf_1.000	187	10	5.00E-09	NP_001022133.1	59	64.3142	62	37	hypothetical protein F32A5.1
Locus_11265_Transcript_1/1_Conf_1.000	195	20	8.70E-22	XP_002604687.1	85	106.686	64	55	hypothetical protein BRAFLDRAFT_282362
Locus_11266_Transcript_1/1_Conf_1.000	154	0							
Locus_11267_Transcript_1/1_Conf_1.000	381	20	5.58E-29	XP_002632484.1	73	130.568	126	93	Hypothetical protein CBG13719

Locus_11268_Transcript_1/1_Conf_1.000	238	3	3.63E-12	EFO17234.1	75	74.7146	62	47	RecQ helicase
Locus_11269_Transcript_1/1_Conf_1.000	142	0							
Locus_1127_Transcript_1/1_Conf_1.000	854	20	1.30E-35	NP_502208.1	61	154.451	173	107	AuTophaGy (yeast Atg homolog) family member (atg-4.2)
Locus_11270_Transcript_1/1_Conf_1.000	682	20	4.72E-55	ACI49113.1	86	218.394	131	113	hypothetical protein Cbre_JD14.001
Locus_11271_Transcript_1/1_Conf_1.000	186	0							
Locus_11272_Transcript_1/1_Conf_1.000	278	20	6.51E-46	BAE88120.1	100	186.808	92	92	unnamed protein product
Locus_11273_Transcript_1/1_Conf_1.000	250	20	2.74E-20	NP_490990.2	78	101.679	83	65	hypothetical protein Y23H5B.5
Locus_11274_Transcript_1/2_Conf_1.000	602	1	2.15E-04	EFO27879.1	43	49.6766	133	58	hypothetical protein LOAG_00601
Locus_11274_Transcript_2/2_Conf_1.000	602	1	2.15E-04	EFO27879.1	43	49.6766	133	58	hypothetical protein LOAG_00601
Locus_11275_Transcript_1/1_Conf_1.000	577	20	2.21E-24	XP_310936.4	79	115.931	84	67	AGAP000199-PA
Locus_11276_Transcript_1/1_Conf_1.000	133	0							
Locus_11277_Transcript_1/1_Conf_1.000	436	20	2.09E-44	XP_002640736.1	84	181.8	119	101	Hypothetical protein CBG19806
Locus_11278_Transcript_1/1_Conf_1.000	779	20	3.85E-65	NP_509509.1	83	252.292	167	140	hypothetical protein D1009.1

Locus_11279_Transcript_1/1_Conf_1.000	858	20	9.30E-82	NP_495015.1	78	307.76	257	202	NuDiX family member (ndx-6)
Locus_1128_Transcript_1/1_Conf_1.000	118	0							
Locus_11280_Transcript_1/1_Conf_1.000	153	20	3.44E-18	NP_491363.1	98	94.7449	50	49	Dynein Heavy Chain family member (dhc-1)
Locus_11281_Transcript_1/1_Conf_1.000	257	0							
Locus_11282_Transcript_1/1_Conf_1.000	709	15	8.25E-05	XP_002318326.1	39	51.6026	258	103	predicted protein
Locus_11283_Transcript_1/1_Conf_1.000	518	3	9.29E-17	NP_001129848.1	64	90.1225	109	70	hypothetical protein C27H2.2
Locus_11284_Transcript_1/1_Conf_1.000	257	0							
Locus_11285_Transcript_1/1_Conf_1.000	495	0							
Locus_11286_Transcript_1/1_Conf_1.000	227	3	7.16E-24	NP_503052.1	79	113.62	78	62	hypothetical protein C52D10.12
Locus_11287_Transcript_1/1_Conf_1.000	136	0							
Locus_11288_Transcript_1/1_Conf_1.000	804	20	9.06E-121	EFO21494.1	86	437.187	265	228	hypothetical protein LOAG_06995
Locus_11289_Transcript_1/1_Conf_1.000	328	20	2.85E-49	3LQZ	100	197.978	109	109	CrystalStructure Of Hla-Dp2
Locus_1129_Transcript_1/1_Conf_1.000	1118	20	1.32E-103	CAV31790.1	84	380.948	248	210	C. elegans protein Y105E8B.8c, confirmed by transcript evidence

Locus_11290_Transcript_1/1_Conf_1.000	292	0							
Locus_11291_Transcript_1/1_Conf_1.000	458	0							
Locus_11292_Transcript_1/1_Conf_1.000	151	5	7.45E-13	XP_002643017.1	84	77.0258	50	42	C. briggsae CBR-POLK-1 protein
Locus_11293_Transcript_1/1_Conf_1.000	288	20	2.46E-24	XP_002632657.1	84	115.161	85	72	C. briggsae CBR-TRA-3 protein
Locus_11294_Transcript_1/1_Conf_1.000	253	20	2.16E-28	XP_002644773.1	94	128.642	67	63	Hypothetical protein CBG14786
Locus_11295_Transcript_1/2_Conf_1.000	627	0							
Locus_11295_Transcript_2/2_Conf_1.000	335	1	2.77E-04	XP_001892902.1	52	48.521	71	37	ATPase, AAA family protein
Locus_11296_Transcript_1/1_Conf_1.000	278	0							
Locus_11297_Transcript_1/1_Conf_1.000	842	20	1.59E-46	XP_002644816.1	60	190.66	265	161	Hypothetical protein CBG14834
Locus_11298_Transcript_1/1_Conf_1.000	656	0							
Locus_11299_Transcript_1/1_Conf_1.000	1014	20	2.26E-51	NP_495391.1	81	207.223	159	130	hypothetical protein F31E8.4
Locus_113_Transcript_1/2_Conf_1.000	919	5	2.13E-26	NP_492097.1	63	124.02	261	166	hypothetical protein ZK524.4
Locus_113_Transcript_2/2_Conf_1.000	787	5	2.34E-25	NP_492097.1	63	120.168	259	164	hypothetical protein ZK524.4
Locus_1130_Transcript_1/1_Conf_1.000	612	4	1.29E-15	XP_002639202.1	65	87.0409	104	68	Hypothetical protein CBG03746
Locus_11300_Transcript_1/1_Conf_1.000	403	0							
Locus_11301_Transcript_1/1_Conf_1.000	408	20	5.31E-72	BAG62064.1	100	273.478	135	135	unnamed protein product
Locus_11302_Transcript_1/1_Conf_1.000	301	2	2.60E-18	NP_493074.2	69	95.1301	99	69	hypothetical protein R05D7.1
Locus_11303_Transcript_1/1_Conf_1.000	185	0							
Locus_11304_Transcript_1/1_Conf_1.000	214	0							
Locus_11305_Transcript_1/1_Conf_1.000	226	0							

Locus_11306_Transcript_1/1_Conf_1.000	276	20	1.03E-22	XP_001900667.1	92	102.064	57	53	Hypothetical 26.6 kDa protein T19C3.4 in chromosome III, putative
Locus_11307_Transcript_1/1_Conf_1.000	578	20	5.04E-53	EFO20071.1	77	211.075	171	133	hypothetical protein LOAG_08420
Locus_11308_Transcript_1/1_Conf_1.000	471	0							
Locus_11309_Transcript_1/1_Conf_1.000	653	20	1.66E-107	NP_508927.2	92	392.504	217	200	DihydroPYrimidine Dehydrogenase family member (dpyd-1)
Locus_1131_Transcript_1/1_Conf_1.000	1513	20	6.24E-137	XP_002635005.1	70	492.271	458	323	C. briggsae CBR-ERS-3 protein
Locus_11310_Transcript_1/1_Conf_1.000	477	20	2.81E-65	NP_001122979.1	96	251.136	132	127	hypothetical protein M03F8.3
Locus_11311_Transcript_1/1_Conf_1.000	357	20	3.50E-15	NP_493404.2	64	84.7297	113	73	hypothetical protein Y6B3B.9
Locus_11312_Transcript_1/1_Conf_1.000	252	20	2.65E-18	NP_001023351.1	67	95.1301	74	50	hypothetical protein T01G1.4
Locus_11313_Transcript_1/1_Conf_1.000	233	2	1.76E-14	XP_002643270.1	79	82.4185	62	49	Hypothetical protein CBG08142
Locus_11314_Transcript_1/1_Conf_1.000	329	20	2.86E-33	NP_495799.1	79	144.821	106	84	hypothetical protein T13H5.4
Locus_11315_Transcript_1/1_Conf_1.000	167	0							

Locus_11316_Transcript_1/1_Conf_1.000	557	20	2.48E-91	A8X4H1.2	91	338.191	185	170	Dual specificity tyrosine-phosphorylation-regulated kinase mbk-1
Locus_11317_Transcript_1/1_Conf_1.000	314	0							
Locus_11318_Transcript_1/1_Conf_1.000	375	0							
Locus_11319_Transcript_1/1_Conf_1.000	629	0							
Locus_1132_Transcript_1/1_Conf_1.000	992	20	8.54E-40	XP_001897511.1	77	168.703	130	101	hypothetical protein Bm1_30365
Locus_11320_Transcript_1/1_Conf_1.000	423	0							
Locus_11321_Transcript_1/1_Conf_1.000	252	0							
Locus_11322_Transcript_1/1_Conf_1.000	979	20	3.55E-123	AAA03517.1	91	445.662	320	293	kinesin-related protein
Locus_11323_Transcript_1/1_Conf_1.000	390	0							
Locus_11324_Transcript_1/1_Conf_1.000	643	20	1.06E-42	XP_002631498.1	62	177.178	169	106	C. briggsae CBR-JMJD-2 protein
Locus_11325_Transcript_1/1_Conf_1.000	372	20	1.70E-17	XP_002647384.1	92	92.4337	51	47	Hypothetical protein CBG06449
Locus_11326_Transcript_1/1_Conf_1.000	977	20	1.40E-95	XP_002631498.1	68	353.984	320	220	C. briggsae CBR-JMJD-2 protein
Locus_11327_Transcript_1/1_Conf_1.000	696	20	1.33E-116	NP_496968.1	93	422.935	231	217	hypothetical protein Y48B6A.12
Locus_11328_Transcript_1/1_Conf_1.000	471	0							
Locus_11329_Transcript_1/1_Conf_1.000	283	0							

Locus_1133_Transcript_1/1_Conf_1.000	457	20	3.79E-62	XP_002638971.1	93	240.736	133	125	C. briggsae CBR-RPL-27 protein
Locus_11330_Transcript_1/1_Conf_1.000	619	4	9.11E-33	EFO26206.1	60	144.05	170	103	hypothetical protein LOAG_02278
Locus_11331_Transcript_1/1_Conf_1.000	349	7	3.30E-29	ADI24623.1	77	131.339	119	92	Copine domain protein, atypical protein 2, isoform c, partially confirmed by transcript evidence
Locus_11332_Transcript_1/1_Conf_1.000	757	20	2.61E-55	CBA11992.1	61	219.55	250	154	endonuclease-reverse transcriptase HmRTE-e01
Locus_11333_Transcript_1/1_Conf_1.000	618	20	4.77E-74	NP_506610.1	79	281.182	203	162	Patterned Expression Site family member (pes-9)
Locus_11334_Transcript_1/2_Conf_1.000	141	0							
Locus_11334_Transcript_2/2_Conf_1.000	165	0							
Locus_11335_Transcript_1/1_Conf_1.000	299	0							
Locus_11336_Transcript_1/1_Conf_1.000	389	20	2.18E-17	NP_507807.1	80	92.0485	71	57	hypothetical protein Y43F8C.7
Locus_11337_Transcript_1/1_Conf_1.000	486	20	7.30E-53	NP_495988.1	79	209.92	161	128	Eukaryotic Initiation Factor family member (eif-3.F)
Locus_11338_Transcript_1/1_Conf_1.000	161	20	1.44E-08	XP_002643286.1	71	62.7734	53	38	Hypothetical protein CBG08162
Locus_11339_Transcript_1/1_Conf_1.000	559	3	9.28E-14	XP_002641618.1	56	80.4925	187	105	Hypothetical protein CBG09938
Locus_1134_Transcript_1/6_Conf_0.357	495	20	1.60E-52	NP_509242.1	77	208.764	164	127	hypothetical protein C07D8.6

Locus_1134_Transcript_2/6_Conf_0.357	537	20	1.83E-53	NP_509242.1	77	212.231	166	129	hypothetical protein C07D8.6
Locus_1134_Transcript_3/6_Conf_0.357	1046	20	6.96E-104	NP_509242.1	76	381.719	306	235	hypothetical protein C07D8.6
Locus_1134_Transcript_4/6_Conf_0.357	1046	20	6.96E-104	NP_509242.1	76	381.719	306	235	hypothetical protein C07D8.6
Locus_1134_Transcript_5/6_Conf_0.357	1046	20	1.07E-104	NP_509242.1	76	384.415	306	235	hypothetical protein C07D8.6
Locus_1134_Transcript_6/6_Conf_0.357	1046	20	1.07E-104	NP_509242.1	76	384.415	306	235	hypothetical protein C07D8.6
Locus_11340_Transcript_1/1_Conf_1.000	559	20	4.00E-41	NP_505918.2	66	171.4	197	131	Tubulin Tyrosine Ligase Like family member (ttll-5)
Locus_11341_Transcript_1/1_Conf_1.000	932								
Locus_11342_Transcript_1/1_Conf_1.000	323	0							
Locus_11343_Transcript_1/2_Conf_1.000	688	20	4.46E-93	XP_002630033.1	84	344.739	226	191	C. briggsae CBR-PUF-12 protein
Locus_11343_Transcript_2/2_Conf_1.000	688	20	7.60E-93	XP_002630033.1	84	343.969	226	191	C. briggsae CBR-PUF-12 protein
Locus_11344_Transcript_1/1_Conf_1.000	1079	20	6.98E-38	EFO17895.1	52	162.54	260	137	hypothetical protein LOAG_10603
Locus_11345_Transcript_1/1_Conf_1.000	223	0							
Locus_11346_Transcript_1/1_Conf_1.000	354	0							
Locus_11347_Transcript_1/1_Conf_1.000	550	0							
Locus_11348_Transcript_1/1_Conf_1.000	502	20	1.64E-52	XP_002636901.1	80	208.764	166	134	Hypothetical protein CBG09363
Locus_11349_Transcript_1/1_Conf_1.000	222	0							
Locus_1135_Transcript_1/1_Conf_1.000	997	20	1.40E-98	NP_498051.1	80	363.999	283	228	hypothetical protein C27F2.4
Locus_11350_Transcript_1/1_Conf_1.000	648	0							
Locus_11351_Transcript_1/1_Conf_1.000	250	0							
Locus_11352_Transcript_1/1_Conf_1.000	325	4	6.39E-41	EFO17984.1	84	170.244	107	90	hypothetical protein LOAG_10513
Locus_11353_Transcript_1/1_Conf_1.000	307	2	1.67E-17	XP_002631009.1	60	92.4337	113	68	Hypothetical protein CBG02761
Locus_11354_Transcript_1/1_Conf_1.000	377	20	1.52E-58	ADG29194.1	100	228.794	114	114	40S ribosomal protein S23

Locus_11355_Transcript_1/1_Conf_1.000	777	20	6.88E-22	EFO23574.1	59	108.612	126	75	hypothetical protein LOAG_04910
Locus_11356_Transcript_1/1_Conf_1.000	944	20	5.23E-92	NP_871684.1	87	342.043	231	201	COenzyme Q (ubiquinone) biosynthesis family member (coq-2)
Locus_11357_Transcript_1/1_Conf_1.000	178	20	2.94E-14	XP_002643972.1	81	81.6481	61	50	C. briggsae CBR-SLO-2 protein
Locus_11358_Transcript_1/1_Conf_1.000	438	0							
Locus_11359_Transcript_1/1_Conf_1.000	329	20	6.62E-22	NP_001041137.1	82	107.071	101	83	Alpha MANnosidase family member (aman-2)
Locus_1136_Transcript_1/1_Conf_1.000	1684	4	2.30E-34	NP_490917.3	55	151.754	207	114	hypothetical protein Y20F4.2
Locus_11360_Transcript_1/1_Conf_1.000	687	20	5.54E-35	EFO23859.1	63	151.754	183	116	hypothetical protein LOAG_04629
Locus_11361_Transcript_1/1_Conf_1.000	169	0							
Locus_11362_Transcript_1/1_Conf_1.000	359	0							
Locus_11363_Transcript_1/1_Conf_1.000	395	0							
Locus_11364_Transcript_1/2_Conf_1.000	691	20	3.40E-24	NP_509021.2	51	115.931	239	122	hypothetical protein C15H9.4
Locus_11364_Transcript_2/2_Conf_1.000	679	20	5.56E-24	XP_002644813.1	54	115.161	242	131	Hypothetical protein CBG14831
Locus_11365_Transcript_1/1_Conf_1.000	137	1	4.27E-05	NP_494994.1	62	51.2174	45	28	hypothetical protein ZK622.1
Locus_11366_Transcript_1/1_Conf_1.000	937	2	8.69E-23	NP_510225.2	52	112.079	317	167	hypothetical protein C49F8.2
Locus_11367_Transcript_1/1_Conf_1.000	404	2	2.07E-07	NP_509527.1	47	58.9214	120	57	Sodium:Neurotransmitter symporter Family family member (snf-12)
Locus_11368_Transcript_1/1_Conf_1.000	529	20	7.45E-44	XP_002642085.1	70	180.259	151	107	Hypothetical protein CBG18026

Locus_11369_Transcript_1/1_Conf_1.000	2162	20	0	NP_492839.4	82	769.615	580	476	Leucine-rich repeats, Ras-like domain, Kinase family member (lrk-1)
Locus_1137_Transcript_1/1_Conf_1.000	1703	20	0	NP_498568.1	86	863.988	560	484	fatty Acid CoA Synthetase family member (acs-16)
Locus_11370_Transcript_1/1_Conf_1.000	461	20	1.61E-20	NP_497688.2	62	102.449	134	84	hypothetical protein Y53G8AR.5
Locus_11371_Transcript_1/1_Conf_1.000	237	2	3.40E-10	XP_001898035.1	61	68.1662	77	47	hypothetical protein Bm1_32955
Locus_11372_Transcript_1/1_Conf_1.000	168	0							
Locus_11373_Transcript_1/3_Conf_0.500	171	0							
Locus_11373_Transcript_2/3_Conf_0.500	171	0							
Locus_11373_Transcript_3/3_Conf_0.667	171	0							
Locus_11374_Transcript_1/1_Conf_1.000	195	0							
Locus_11375_Transcript_1/1_Conf_1.000	753	14	1.86E-45	NP_506662.1	59	186.808	231	137	hypothetical protein ZC412.3
Locus_11376_Transcript_1/1_Conf_1.000	1024	4	7.69E-23	XP_002629901.1	52	112.464	252	132	Hypothetical protein CBG21942
Locus_11377_Transcript_1/1_Conf_1.000	733	2	2.67E-09	CAP34328.1	66	66.6254	59	39	Hypothetical protein CBG16019
Locus_11378_Transcript_1/1_Conf_1.000	233	0							
Locus_11379_Transcript_1/1_Conf_1.000	299	20	6.16E-44	NP_502268.1	89	180.259	99	89	TRNA Guanine Transglycosylase family member (tgt-1)
Locus_1138_Transcript_1/1_Conf_1.000	1471	20	0	XP_002640255.1	86	706.442	435	378	C. briggsae CBR-UNC-87 protein
Locus_11380_Transcript_1/1_Conf_1.000	252	9	2.25E-09	XP_001896064.1	69	65.4698	59	41	hypothetical protein Bm1_23035
Locus_11381_Transcript_1/1_Conf_1.000	361	3	1.02E-14	NP_491456.2	70	83.1889	75	53	hypothetical protein F57C9.6
Locus_11382_Transcript_1/1_Conf_1.000	354	2	4.31E-05	NP_508627.5	74	51.2174	39	29	Sensory AXon guidance family member (sax-1)
Locus_11383_Transcript_1/1_Conf_1.000	327	6	9.25E-16	NP_490834.1	60	86.6557	100	60	hypothetical protein Y48G8AL.1
Locus_11384_Transcript_1/1_Conf_1.000	198	0							
Locus_11385_Transcript_1/1_Conf_1.000	652	20	5.56E-79	XP_002633800.1	81	297.745	219	178	C. briggsae CBR-RBD-1 protein
Locus_11386_Transcript_1/1_Conf_1.000	1033	0							
Locus_11387_Transcript_1/1_Conf_1.000	568	20	5.10E-71	NP_493701.1	80	270.781	189	152	hypothetical protein K01A2.5

Locus_11388_Transcript_1/1_Conf_1.000	239	8	9.85E-26	NP_001040987.1	84	119.783	79	67	ALP/Enigma encoding family member (alp-1)
Locus_11389_Transcript_1/1_Conf_1.000	589	20	2.37E-37	NP_503059.2	88	159.073	92	81	hypothetical protein ZK550.3
Locus_1139_Transcript_1/1_Conf_1.000	1014	20	4.79E-102	EFO22864.1	81	375.555	274	223	3'-phosphoadenosine 5'-phosphosulfate synthase 2
Locus_11390_Transcript_1/1_Conf_1.000	178	0							
Locus_11391_Transcript_1/1_Conf_1.000	309	20	5.15E-35	XP_001900807.1	84	150.599	102	86	peptidyl-prolyl cis-trans isomerase, FKBP-type family protein
Locus_11392_Transcript_1/1_Conf_1.000	546	20	2.91E-41	XP_002646691.1	78	171.785	134	105	Hypothetical protein CBG13068
Locus_11393_Transcript_1/1_Conf_1.000	639	20	1.76E-90	EFO23380.1	92	335.88	193	178	BTB/POZ domain-containing protein
Locus_11394_Transcript_1/1_Conf_1.000	609	0							
Locus_11395_Transcript_1/1_Conf_1.000	289	0							
Locus_11396_Transcript_1/1_Conf_1.000	354	20	1.37E-43	XP_002630114.1	86	179.104	111	96	C. briggsae CBR-PYR-1 protein
Locus_11397_Transcript_1/1_Conf_1.000	243	1	2.42E-08	CAR63594.1	62	62.003	79	49	hypothetical protein
Locus_11398_Transcript_1/1_Conf_1.000	2886	20	1.65E-158	NP_510290.1	63	565.074	807	511	Germinal Center Kinase family member (gck-4)
Locus_11399_Transcript_1/1_Conf_1.000	787	0							
Locus_114_Transcript_1/1_Conf_1.000	1512	20	1.35E-123	NP_497506.3	64	447.973	540	346	hypothetical protein Y48G9A.3

Locus_1140_Transcript_1/1_Conf_1.000	961	20	1.04E-95	XP_002634374.1	100	354.369	177	177	C. briggsae CBR-ARF-3 protein
Locus_11400_Transcript_1/1_Conf_1.000	134	0							
Locus_11401_Transcript_1/1_Conf_1.000	1973	20	0	NP_499392.1	82	837.025	625	516	OXidative stress Induced family member (oxi-1)
Locus_11402_Transcript_1/1_Conf_1.000	562	20	1.13E-91	AAT02163.1	96	339.347	176	169	hypothetical protein L3ni56 isoform a
Locus_11403_Transcript_1/1_Conf_1.000	397	0							
Locus_11404_Transcript_1/1_Conf_1.000	485	0							
Locus_11405_Transcript_1/1_Conf_1.000	664	20	3.23E-98	XP_002646363.1	90	361.688	220	200	Hypothetical protein CBG12078
Locus_11406_Transcript_1/1_Conf_1.000	441	2	1.43E-48	CAR63706.1	93	195.667	138	129	putative FOS (B-Zip transcription factor) homolog family member
Locus_11407_Transcript_1/1_Conf_1.000	565	20	3.30E-22	EFO23808.1	61	108.612	136	84	hypothetical protein LOAG_04674
Locus_11408_Transcript_1/1_Conf_1.000	478	5	1.24E-04	XP_805431.1	43	49.6766	112	49	hypothetical protein
Locus_11409_Transcript_1/1_Conf_1.000	1904	20	0	NP_504245.3	72	738.799	636	464	hypothetical protein Y61A9LA.10
Locus_1141_Transcript_1/1_Conf_1.000	259	0							
Locus_11410_Transcript_1/1_Conf_1.000	613	20	4.47E-93	XP_001896600.1	93	344.354	183	172	peptidyl-prolyl cis-trans isomerase 11
Locus_11411_Transcript_1/1_Conf_1.000	363	0							
Locus_11412_Transcript_1/1_Conf_1.000	855	20	2.09E-25	CAZ65529.1	69	120.553	133	92	C. elegans protein T28C6.7b, partially confirmed by transcript evidence

Locus_11413_Transcript_1/1_Conf_1.000	523	20	5.46E-44	EFO22205.1	94	180.644	113	107	small Nuclear Ribonucleoprotein family member
Locus_11414_Transcript_1/1_Conf_1.000	673	20	3.30E-29	XP_002642913.1	58	132.494	176	103	C. briggsae CBR-SMI-1 protein
Locus_11415_Transcript_1/1_Conf_1.000	1268	9	6.57E-25	ABJ99064.1	44	119.783	427	192	Hypothetical protein W03A3.2
Locus_11416_Transcript_1/1_Conf_1.000	341	4	4.82E-25	XP_002635120.1	67	117.472	110	74	Hypothetical protein CBG11342
Locus_11417_Transcript_1/1_Conf_1.000	998	20	3.96E-85	XP_002631495.1	68	319.316	329	226	Hypothetical protein CBG20655
Locus_11418_Transcript_1/1_Conf_1.000	573	5	3.23E-36	EFO27097.1	72	155.221	131	95	hypothetical protein LOAG_01386
Locus_11419_Transcript_1/1_Conf_1.000	569	6	8.80E-31	NP_001122953.1	73	137.117	142	104	hypothetical protein F53H10.2
Locus_1142_Transcript_1/1_Conf_1.000	1041	20	2.18E-65	XP_001891854.1	65	253.832	353	230	Conserved oligomeric Golgi complex component 4
Locus_11420_Transcript_1/1_Conf_1.000	630	3	1.78E-31	NP_508493.1	60	139.813	215	131	protein KINase family member (kin-29)
Locus_11421_Transcript_1/1_Conf_1.000	326	20	8.40E-17	XP_001896013.1	66	90.1225	115	76	Protein kinase domain containing protein
Locus_11422_Transcript_1/1_Conf_1.000	256	20	5.31E-27	NP_001041301.1	82	124.02	85	70	hypothetical protein ZK54.1
Locus_11423_Transcript_1/1_Conf_1.000	240	0							
Locus_11424_Transcript_1/1_Conf_1.000	1067	20	1.45E-96	NP_510510.1	73	357.451	282	208	DHHC-types zinc finger transcription factor family member (dhhc-1)
Locus_11425_Transcript_1/1_Conf_1.000	142	0							
Locus_11426_Transcript_1/1_Conf_1.000	491	20	1.47E-45	NP_509186.3	72	185.652	165	120	Carbonic AnHydrase family member (cah-5)
Locus_11427_Transcript_1/1_Conf_1.000	133	0							
Locus_11428_Transcript_1/1_Conf_1.000	271	0							
Locus_11429_Transcript_1/1_Conf_1.000	289	0							

Locus_1143_Transcript_1/1_Conf_1.000	1662	20	1.56E-51	EFO23026.1	46	208.764	447	208	MYND finger family protein
Locus_11430_Transcript_1/1_Conf_1.000	481	0							
Locus_11431_Transcript_1/1_Conf_1.000	239	0							
Locus_11432_Transcript_1/1_Conf_1.000	299	0							
Locus_11433_Transcript_1/1_Conf_1.000	1881	20	0	XP_001896664.1	85	874.389	583	496	Protein kinase domain containing protein
Locus_11434_Transcript_1/1_Conf_1.000	908	20	3.88E-73	CAE12199.1	64	279.256	286	185	aspartyl protease precursor
Locus_11435_Transcript_1/1_Conf_1.000	854	20	3.38E-76	NP_508767.1	99	289.271	142	141	AdaPtin, Small chain (clathrin associated complex) family member (aps-2)
Locus_11436_Transcript_1/1_Conf_1.000	337	20	6.34E-17	Q61CX7.2	63	90.5077	96	61	Protein lin-28
Locus_11437_Transcript_1/1_Conf_1.000	268	4	2.07E-07	NP_498921.3	64	58.9214	88	57	hypothetical protein B0303.11
Locus_11438_Transcript_1/1_Conf_1.000	936	20	1.11E-102	EFO20614.1	80	377.481	302	243	hypothetical protein LOAG_07877

Locus_11439_Transcript_1/1_Conf_1.000	379	0							
Locus_1144_Transcript_1/1_Conf_1.000	856	20	3.76E-68	NP_497103.1	75	232.646	244	185	hypothetical protein Y53F4B.18
Locus_11440_Transcript_1/2_Conf_1.000	350	0							
Locus_11440_Transcript_2/2_Conf_1.000	683	0							
Locus_11441_Transcript_1/1_Conf_1.000	942	20	5.78E-91	CAR97821.1	75	338.576	273	206	C. elegans protein F11C1.5d, partially confirmed by transcript evidence
Locus_11442_Transcript_1/2_Conf_1.000	357	0							
Locus_11442_Transcript_2/2_Conf_1.000	300	0							
Locus_11443_Transcript_1/1_Conf_1.000	528	20	3.69E-51	XP_002636692.1	72	204.527	158	115	Hypothetical protein CBG23406
Locus_11444_Transcript_1/1_Conf_1.000	376	0							
Locus_11445_Transcript_1/1_Conf_1.000	1420	20	0	CAR64255.1	86	659.062	454	391	protein RIO1 kinase
Locus_11446_Transcript_1/1_Conf_1.000	570	20	6.16E-56	NP_497037.1	91	220.705	141	129	ARF-Like family member (arl-3)
Locus_11447_Transcript_1/1_Conf_1.000	662	8	4.10E-45	XP_002639056.1	68	185.267	170	117	C. briggsae CBR-HOT-5 protein
Locus_11448_Transcript_1/1_Conf_1.000	1248	20	0	XP_001895795.1	92	640.573	371	343	actin 1
Locus_11449_Transcript_1/1_Conf_1.000	460	20	1.59E-52	NP_491634.1	85	208.764	154	131	hypothetical protein M01E11.2
Locus_1145_Transcript_1/2_Conf_1.000	777	4	2.29E-17	NP_504957.2	55	93.5893	164	91	hypothetical protein C50E3.5

Locus_1145_Transcript_2/2_Conf_1.000	1739	6	8.99E-50	NP_504957.2	54	202.986	396	217	hypothetical protein C50E3.5
Locus_11450_Transcript_1/1_Conf_1.000	474	0							
Locus_11451_Transcript_1/1_Conf_1.000	616	20	2.69E-53	AAX29387.1	100	212.231	156	156	ribosomal protein L29
Locus_11452_Transcript_1/1_Conf_1.000	741	5	1.56E-04	XP_001950169.1	38	50.8322	144	56	PREDICTED: similar to replication factors MCM
Locus_11453_Transcript_1/1_Conf_1.000	270	0							
Locus_11454_Transcript_1/1_Conf_1.000	399	0							
Locus_11455_Transcript_1/1_Conf_1.000	414	20	1.27E-25	XP_001233556.1	62	119.398	140	87	PREDICTED: hypothetical protein
Locus_11456_Transcript_1/1_Conf_1.000	513	20	6.42E-63	NP_871854.1	87	243.432	167	146	SCP(Small C-terminal domain Phosphatase)-Like phosphatase family member (scpl-3)
Locus_11457_Transcript_1/1_Conf_1.000	537	20	9.35E-74	NP_498688.1	84	279.641	178	151	Prolyl Carboxy Peptidase like family member (pcp-1)
Locus_11458_Transcript_1/1_Conf_1.000	189	5	7.96E-07	NP_506519.1	72	56.9954	51	37	hypothetical protein T16A9.5
Locus_11459_Transcript_1/1_Conf_1.000	237	0							
Locus_1146_Transcript_1/1_Conf_1.000	969	0							
Locus_11460_Transcript_1/1_Conf_1.000	914	20	2.21E-100	XP_001893912.1	81	369.777	274	222	mRNA capping enzyme, C-terminal domain containing protein
Locus_11461_Transcript_1/1_Conf_1.000	174	0							
Locus_11462_Transcript_1/1_Conf_1.000	942	4	1.31E-18	A8WZU5.2	48	98.2117	290	141	Fanconi-associated nuclease 1 homolog
Locus_11463_Transcript_1/1_Conf_1.000	421	20	6.46E-25	NP_001040864.1	69	117.087	107	74	SMAll family member (sma-4)
Locus_11464_Transcript_1/1_Conf_1.000	1249	20	3.51E-63	XP_001897220.1	58	246.899	397	232	P120
Locus_11465_Transcript_1/1_Conf_1.000	365	4	2.75E-12	XP_001895046.1	62	75.0998	118	74	hypothetical protein
Locus_11466_Transcript_1/1_Conf_1.000	225	0							

Locus_11467_Transcript_1/1_Conf_1.000	152	0							
Locus_11468_Transcript_1/1_Conf_1.000	414	20	2.18E-09	XP_002638816.1	55	65.4698	99	55	Hypothetical protein CBG22019
Locus_11469_Transcript_1/1_Conf_1.000	140	0							
Locus_1147_Transcript_1/2_Conf_1.000	375	20	2.88E-33	ABA00169.1	66	144.821	124	83	Plexin protein 1
Locus_1147_Transcript_2/2_Conf_1.000	375	20	2.88E-33	ABA00169.1	66	144.821	124	83	Plexin protein 1
Locus_11470_Transcript_1/1_Conf_1.000	650	20	3.71E-51	XP_002636678.1	66	205.297	216	144	C. briggsae CBR-CHE-11 protein
Locus_11471_Transcript_1/1_Conf_1.000	412	20	1.24E-12	NP_001020168.1	49	76.2554	159	79	coiled-coil domain-containing protein 93
Locus_11472_Transcript_1/1_Conf_1.000	1419	20	1.43E-79	XP_002645548.1	55	301.597	467	260	Hypothetical protein CBG05229
Locus_11473_Transcript_1/1_Conf_1.000	1166	20	7.30E-52	XP_001893792.1	50	209.149	375	189	Zinc finger, C2H2 type family protein
Locus_11474_Transcript_1/1_Conf_1.000	740	20	2.06E-41	XP_001900557.1	51	173.326	277	143	Bromodomain containing protein
Locus_11475_Transcript_1/1_Conf_1.000	357	0							
Locus_11476_Transcript_1/1_Conf_1.000	1183	20	2.21E-104	NP_501491.3	75	383.645	301	228	Heparan SulphoTransferase family member (hst-1)
Locus_11477_Transcript_1/1_Conf_1.000	239	8	9.26E-08	XP_002636450.1	75	60.077	48	36	Hypothetical protein CBG23111
Locus_11478_Transcript_1/1_Conf_1.000	177	0							
Locus_11479_Transcript_1/1_Conf_1.000	359	0							
Locus_1148_Transcript_1/1_Conf_1.000	324	0							

Locus_11480_Transcript_1/1_Conf_1.000	987	20	5.99E-94	XP_002632141.1	69	348.591	309	215	C. briggsae CBR-TRE-5 protein
Locus_11481_Transcript_1/1_Conf_1.000	284	2	2.48E-16	XP_002631194.1	78	88.5817	66	52	C. briggsae CBR-NLP-18 protein
Locus_11482_Transcript_1/2_Conf_1.000	501	0							
Locus_11482_Transcript_2/2_Conf_1.000	501	0							
Locus_11483_Transcript_1/2_Conf_1.000	480	20	2.56E-26	EFO22039.1	64	121.709	146	94	hypothetical protein LOAG_06449
Locus_11483_Transcript_2/2_Conf_1.000	480	20	3.34E-26	EFO22039.1	64	121.324	146	94	hypothetical protein LOAG_06449
Locus_11484_Transcript_1/1_Conf_1.000	841	0							
Locus_11485_Transcript_1/1_Conf_1.000	178	2	1.01E-06	XP_002630757.1	66	56.6102	59	39	Hypothetical protein CBG02451
Locus_11486_Transcript_1/1_Conf_1.000	193	0							
Locus_11487_Transcript_1/1_Conf_1.000	893	20	5.09E-62	ACI49172.1	67	242.276	262	176	hypothetical protein Csp3_JD01.004
Locus_11488_Transcript_1/1_Conf_1.000	385	20	3.72E-33	NP_490883.1	100	144.436	74	74	LSM Sm-like protein family member (lsm-6)

Locus_11489_Transcript_1/1_Conf_1.000	301	2	6.63E-06	NP_495103.1	69	53.9138	55	38	ZYGote defective: embryonic lethal family member (zyg-1)
Locus_1149_Transcript_1/1_Conf_1.000	1404	20	2.92E-85	NP_494767.1	58	320.472	466	273	hypothetical protein H20J04.2
Locus_11490_Transcript_1/1_Conf_1.000	441	20	4.61E-39	XP_002638772.1	73	164.081	142	105	C. briggsae CBR-PTR-21 protein
Locus_11491_Transcript_1/1_Conf_1.000	478	20	1.31E-38	XP_002643084.1	76	162.54	119	91	C. briggsae CBR-TAG-174 protein
Locus_11492_Transcript_1/1_Conf_1.000	689	20	8.68E-97	ABS50363.1	91	357.066	229	210	LIM domain protein variant
Locus_11493_Transcript_1/1_Conf_1.000	494	0							
Locus_11494_Transcript_1/1_Conf_1.000	580	0							
Locus_11495_Transcript_1/1_Conf_1.000	297	20	3.89E-22	NP_001024903.1	67	107.842	93	63	abnormal DAuer Formation family member (daf-9)
Locus_11496_Transcript_1/1_Conf_1.000	195	20	2.21E-25	XP_002640668.1	96	118.627	64	62	C. briggsae CBR-UNC-54 protein
Locus_11497_Transcript_1/1_Conf_1.000	448	4	4.92E-17	NP_740830.2	47	90.8929	184	88	hypothetical protein Y47G6A.29
Locus_11498_Transcript_1/1_Conf_1.000	146	0							
Locus_11499_Transcript_1/1_Conf_1.000	187	0							
Locus_115_Transcript_1/6_Conf_0.235	1107	20	0	CAR63627.1	99	652.129	326	324	putative Elongation FacTor

Locus_115_Transcript_2/6_Conf_0.235	770	20	5.37E-96	NP_001021266.1	72	354.755	306	222	UNCoordinated family member (unc-44)
Locus_115_Transcript_3/6_Conf_0.412	3662	20	0	NP_001021268.1	77	1289.63	1034	802	UNCoordinated family member (unc-44)
Locus_115_Transcript_4/6_Conf_0.118	1655	5	9.39E-41	NP_001021266.1	65	172.94	283	185	UNCoordinated family member (unc-44)
Locus_115_Transcript_5/6_Conf_0.412	3644	20	0	NP_500898.1	77	1278.46	1028	796	UNCoordinated family member (unc-44)
Locus_115_Transcript_6/6_Conf_0.353	2780	20	0	NP_492457.1	96	1558.12	852	824	Elongation FacTor family member (eft-2)
Locus_1150_Transcript_1/3_Conf_0.750	2164	2	6.08E-22	XP_002635564.1	44	110.923	347	156	C. briggsae CBR-TAM-1 protein
Locus_1150_Transcript_2/3_Conf_0.750	2188	2	6.17E-22	XP_002635564.1	44	110.923	347	156	C. briggsae CBR-TAM-1 protein
Locus_1150_Transcript_3/3_Conf_0.750	2176	2	6.13E-22	XP_002635564.1	44	110.923	347	156	C. briggsae CBR-TAM-1 protein
Locus_11500_Transcript_1/2_Conf_1.000	857	20	3.13E-13	XP_002646949.1	52	80.1073	177	93	C. briggsae CBR-APD-3 protein
Locus_11500_Transcript_2/2_Conf_1.000	670	20	1.47E-13	XP_002646949.1	52	80.4925	177	93	C. briggsae CBR-APD-3 protein
Locus_11501_Transcript_1/1_Conf_1.000	602	3	3.90E-22	NP_491469.2	52	108.612	200	104	hypothetical protein F25F8.1
Locus_11502_Transcript_1/2_Conf_1.000	830	20	2.27E-106	NP_001022869.1	84	389.423	256	217	hypothetical protein Y42G9A.4

Locus_11502_Transcript_2/2_Conf_1.000	767	20	7.67E-111	NP_001022869.1	92	404.06	235	218	hypothetical protein Y42G9A.4
Locus_11503_Transcript_1/1_Conf_1.000	512	20	1.20E-21	NP_001024866.1	55	106.301	177	98	hypothetical protein R57.1
Locus_11504_Transcript_1/4_Conf_0.333	548	20	4.24E-08	XP_001956624.1	50	61.6178	142	71	GF24494
Locus_11504_Transcript_2/4_Conf_0.333	720	19	3.97E-10	NP_496398.2	43	69.3218	246	107	hypothetical protein T06D8.1
Locus_11504_Transcript_3/4_Conf_0.222	702	0							
Locus_11504_Transcript_4/4_Conf_0.333	378	3	5.10E-06	NP_496398.2	52	54.299	97	51	hypothetical protein T06D8.1
Locus_11505_Transcript_1/1_Conf_1.000	398	0							
Locus_11506_Transcript_1/1_Conf_1.000	281	20	1.59E-52	XP_002930069.1	100	208.764	93	93	PREDICTED: casein kinase II subunit beta-like isoform 1

Locus_11507_Transcript_1/1_Conf_1.000	526	20	3.98E-58	AAF34687.1	81	227.639	175	143	AF223064_1putative microtubule severing protein katanin p60 subunit
Locus_11508_Transcript_1/1_Conf_1.000	816	20	2.24E-42	XP_002117005.1	55	176.792	240	134	hypothetical protein TRIADDRAFT_60996
Locus_11509_Transcript_1/1_Conf_1.000	307	1	4.72E-04	EFA84933.1	58	47.7506	58	34	hypothetical protein PPL_01926
Locus_1151_Transcript_1/3_Conf_0.667	2997	20	1.12E-165	XP_002630883.1	66	588.956	735	486	Hypothetical protein CBG02604
Locus_1151_Transcript_2/3_Conf_0.667	2997	20	6.54E-166	XP_002630883.1	66	589.726	735	487	Hypothetical protein CBG02604
Locus_1151_Transcript_3/3_Conf_0.667	2997	20	2.49E-165	XP_002630883.1	66	587.8	735	486	Hypothetical protein CBG02604
Locus_11510_Transcript_1/1_Conf_1.000	213	0							
Locus_11511_Transcript_1/1_Conf_1.000	227	0							
Locus_11512_Transcript_1/1_Conf_1.000	327	0							
Locus_11513_Transcript_1/2_Conf_1.000	1022	20	9.58E-50	XP_001309767.1	54	201.83	323	176	ankyrin repeat protein
Locus_11513_Transcript_2/2_Conf_1.000	1022	20	9.58E-50	XP_001309767.1	54	201.83	323	176	ankyrin repeat protein

Locus_11514_Transcript_1/1_Conf_1.000	828	20	6.47E-61	NP_499648.3	71	238.424	228	162	ELongator complex Protein Component family member (elpc-2)
Locus_11515_Transcript_1/1_Conf_1.000	128	0							
Locus_11516_Transcript_1/1_Conf_1.000	781	20	5.87E-21	EFO28351.1	65	105.531	111	73	2Fe-2S iron-sulfur cluster binding domain-containing protein
Locus_11517_Transcript_1/1_Conf_1.000	426	20	5.82E-10	XP_002595762.1	49	67.3958	143	71	hypothetical protein BRAFLDRAFT_200800
Locus_11518_Transcript_1/1_Conf_1.000	263	20	3.11E-21	EDL15956.1	85	63.929	40	34	procollagen, type I, alpha 1, isoform CRA_a
Locus_11519_Transcript_1/1_Conf_1.000	217	0							
Locus_1152_Transcript_1/4_Conf_0.750	1007	20	7.93E-41	AAN05752.1	71	172.17	147	105	heat shock protein 20
Locus_1152_Transcript_2/4_Conf_0.750	1007	20	1.00E-43	CAG25499.1	73	181.8	157	115	heat shock protein 20
Locus_1152_Transcript_3/4_Conf_0.450	584	20	3.38E-44	CAG25499.1	73	181.8	157	115	heat shock protein 20
Locus_1152_Transcript_4/4_Conf_0.750	993	20	9.81E-44	CAG25499.1	73	181.8	157	115	heat shock protein 20
Locus_11520_Transcript_1/2_Conf_1.000	426	0							
Locus_11520_Transcript_2/2_Conf_1.000	455	0							
Locus_11521_Transcript_1/1_Conf_1.000	337	0							
Locus_11522_Transcript_1/1_Conf_1.000	144	0							
Locus_11523_Transcript_1/1_Conf_1.000	619	3	2.18E-18	NP_498056.2	57	96.2857	141	81	hypothetical protein C27F2.7
Locus_11524_Transcript_1/1_Conf_1.000	293	20	3.64E-44	ACC44546.1	96	181.03	97	94	SPC-1
Locus_11525_Transcript_1/1_Conf_1.000	196	0							

Locus_11526_Transcript_1/1_Conf_1.000	227	20	1.10E-24	XP_002637346.1	84	116.316	75	63	Hypothetical protein CBG19044
Locus_11527_Transcript_1/1_Conf_1.000	426	0							
Locus_11528_Transcript_1/1_Conf_1.000	1200	20	1.01E-19	AAP48996.1	41	102.449	395	162	cellulosomal scaffoldin anchoring protein C
Locus_11529_Transcript_1/1_Conf_1.000	227	0							
Locus_1153_Transcript_1/1_Conf_1.000	784	4	4.38E-24	NP_508979.2	48	115.931	233	112	DAF-16/FOXO Controlled, germline Tumor affecting family member (dct-11)
Locus_11530_Transcript_1/1_Conf_1.000	595	5	2.82E-09	NP_505962.2	42	65.855	198	85	Nuclear Pore complex Protein family member (npp-22)
Locus_11531_Transcript_1/1_Conf_1.000	253	0							
Locus_11532_Transcript_1/1_Conf_1.000	197	20	6.47E-09	EFO25376.1	69	63.929	65	45	hypothetical protein LOAG_03111
Locus_11533_Transcript_1/1_Conf_1.000	534	0							
Locus_11534_Transcript_1/1_Conf_1.000	832	20	1.85E-31	NP_508153.1	58	140.584	178	105	hypothetical protein T04G9.4
Locus_11535_Transcript_1/1_Conf_1.000	570	20	2.05E-51	NP_504500.1	79	205.682	133	106	C-type LECtin family member (clec-1)
Locus_11536_Transcript_1/1_Conf_1.000	743	20	1.31E-27	NP_510604.1	95	127.487	65	62	hypothetical protein F59F4.2
Locus_11537_Transcript_1/1_Conf_1.000	305	1	6.19E-04	CAH23216.1	45	47.3654	97	44	putative L3 ES protein

Locus_11538_Transcript_1/1_Conf_1.000	594	20	9.92E-39	XP_002640158.1	86	163.696	110	95	C. briggsae CBR-TRE-1 protein
Locus_11539_Transcript_1/1_Conf_1.000	310	20	2.92E-30	XP_002645186.1	89	134.806	102	91	Hypothetical protein CBG16916
Locus_1154_Transcript_1/1_Conf_1.000	335	13	8.83E-35	NP_492132.1	79	149.828	108	86	Enhancer of Glp-One (glp-1) family member (ego-1)
Locus_11540_Transcript_1/1_Conf_1.000	262	20	4.93E-33	EFO21345.1	90	144.05	87	79	hypothetical protein LOAG_07143
Locus_11541_Transcript_1/1_Conf_1.000	151	0							
Locus_11542_Transcript_1/1_Conf_1.000	324	0							
Locus_11543_Transcript_1/1_Conf_1.000	790	20	2.29E-12	EFO26136.1	53	77.0258	195	104	hypothetical protein LOAG_02353
Locus_11544_Transcript_1/1_Conf_1.000	267	0							
Locus_11545_Transcript_1/1_Conf_1.000	138	15	1.84E-16	EAW72008.1	100	88.9669	39	39	natural killer cell group 7 sequence, isoform CRA_c
Locus_11546_Transcript_1/1_Conf_1.000	518	0							
Locus_11547_Transcript_1/1_Conf_1.000	237	0							
Locus_11548_Transcript_1/1_Conf_1.000	715	20	1.62E-48	XP_002637050.1	73	196.823	183	135	Hypothetical protein CBG09545
Locus_11549_Transcript_1/1_Conf_1.000	888	0							
Locus_1155_Transcript_1/1_Conf_1.000	519	20	3.46E-43	NP_492582.1	78	177.948	127	100	Farnesylated-proteins Converting Enzyme (FACE) family member (fce-1)
Locus_11550_Transcript_1/1_Conf_1.000	1195	20	1.16E-76	XP_002636710.1	67	291.582	317	214	C. briggsae CBR-TSFM-1 protein
Locus_11551_Transcript_1/1_Conf_1.000	295	0							
Locus_11552_Transcript_1/1_Conf_1.000	405	0							
Locus_11553_Transcript_1/1_Conf_1.000	388	20	2.67E-15	NP_495088.1	55	85.1149	127	71	hypothetical protein C17G10.1
Locus_11554_Transcript_1/1_Conf_1.000	582	20	6.19E-30	NP_490812.1	89	134.42	104	93	GLutaRedoXin family member (glrx-10)

Locus_11555_Transcript_1/1_Conf_1.000	1338	20	3.00E-132	XP_002633301.1	82	476.478	342	283	Hypothetical protein CBG06032
Locus_11556_Transcript_1/1_Conf_1.000	190	0							
Locus_11557_Transcript_1/1_Conf_1.000	225	0							
Locus_11558_Transcript_1/1_Conf_1.000	1590	20	6.37E-47	XP_002640788.1	45	193.356	552	252	C. briggsae CBR-FBXA-1 protein
Locus_11559_Transcript_1/1_Conf_1.000	262	20	2.70E-31	XP_001896078.1	90	138.272	83	75	A-macroglobulin complement component family protein
Locus_1156_Transcript_1/1_Conf_1.000	412	0							
Locus_11560_Transcript_1/1_Conf_1.000	777	12	2.84E-84	AAA96224.2	73	315.849	245	181	Hypothetical protein T07H6.4
Locus_11561_Transcript_1/1_Conf_1.000	143	9	2.74E-12	NP_001122601.1	91	75.0998	47	43	Multiple PDZ domain protein family member (mpz-1)
Locus_11562_Transcript_1/1_Conf_1.000	782	20	2.31E-134	AAX28980.1	100	482.256	243	243	ribosomal protein S3
Locus_11563_Transcript_1/1_Conf_1.000	294	20	1.39E-11	XP_002637534.1	64	72.7886	88	57	C. briggsae CBR-TRY-5 protein
Locus_11564_Transcript_1/1_Conf_1.000	1581	20	3.22E-75	EFO23010.1	56	287.345	536	305	hypothetical protein LOAG_05474

Locus_11565_Transcript_1/1_Conf_1.000	580								
Locus_11566_Transcript_1/1_Conf_1.000	424	20	2.60E-34	EFO19620.1	81	148.288	111	91	histone acetyltransferase
Locus_11567_Transcript_1/1_Conf_1.000	793	0							
Locus_11568_Transcript_1/1_Conf_1.000	674	20	3.72E-73	XP_002644648.1	79	278.485	224	179	Hypothetical protein CBG14624
Locus_11569_Transcript_1/1_Conf_1.000	1232	20	4.45E-95	NP_497827.1	75	352.829	282	213	GLyOxalase Domain containing family member (glod-4)
Locus_1157_Transcript_1/3_Conf_0.714	1297	2	2.51E-11	NP_499710.1	59	74.7146	148	88	hypothetical protein Y39E4B.6
Locus_1157_Transcript_2/3_Conf_0.571	1513	2	3.10E-11	NP_499710.1	59	74.7146	148	88	hypothetical protein Y39E4B.6
Locus_1157_Transcript_3/3_Conf_0.571	1235	20	2.12E-12	NP_499710.1	57	78.1814	215	124	hypothetical protein Y39E4B.6
Locus_11570_Transcript_1/1_Conf_1.000	713	0							
Locus_11571_Transcript_1/1_Conf_1.000	788	20	1.18E-77	XP_002637336.1	79	293.893	215	170	Hypothetical protein CBG19031
Locus_11572_Transcript_1/1_Conf_1.000	227	0							
Locus_11573_Transcript_1/1_Conf_1.000	157	0							
Locus_11574_Transcript_1/2_Conf_1.000	586	20	1.23E-17	NP_495042.2	50	93.5893	165	83	hypothetical protein F56D1.1
Locus_11574_Transcript_2/2_Conf_1.000	586	20	2.48E-18	XP_002630725.1	46	95.9005	156	73	Hypothetical protein CBG02409
Locus_11575_Transcript_1/1_Conf_1.000	437	20	1.79E-11	XP_002641852.1	77	72.4034	49	38	C. briggsae CBR-LARP-1 protein
Locus_11576_Transcript_1/1_Conf_1.000	215	0							
Locus_11577_Transcript_1/1_Conf_1.000	809	20	8.82E-124	XP_002630114.1	87	447.203	269	236	C. briggsae CBR-PYR-1 protein
Locus_11578_Transcript_1/2_Conf_1.000	479	2	1.62E-04	ZP_05026437.1	53	49.2914	113	61	DNA sulfur modification protein DndD
Locus_11578_Transcript_2/2_Conf_1.000	479	1	3.61E-04	XP_689920.3	54	48.1358	91	50	PREDICTED: cingulin-like
Locus_11579_Transcript_1/1_Conf_1.000	251	0							

Locus_1158_Transcript_1/1_Conf_1.000	762	20	2.88E-118	NP_491363.1	91	428.713	253	232	Dynein Heavy Chain family member (dhc-1)
Locus_11580_Transcript_1/1_Conf_1.000	289	10	2.73E-07	XP_002641560.1	51	58.5362	96	49	Hypothetical protein CBG09859
Locus_11581_Transcript_1/1_Conf_1.000	680	0							
Locus_11582_Transcript_1/1_Conf_1.000	204	0							
Locus_11583_Transcript_1/1_Conf_1.000	682	0							
Locus_11584_Transcript_1/1_Conf_1.000	727	20	1.01E-85	A8XKG6.2	83	320.472	242	203	DPYD_CAEBRRecName: Full=Probable dihydropyrimidine dehydrogenase
Locus_11585_Transcript_1/1_Conf_1.000	513	6	9.35E-30	CAR97833.1	69	133.265	134	93	C. elegans protein F46G10.5b, partially confirmed by transcript evidence
Locus_11586_Transcript_1/1_Conf_1.000	279	20	2.39E-32	XP_002639664.1	86	141.739	92	80	C. briggsae CBR-HUM-1 protein
Locus_11587_Transcript_1/1_Conf_1.000	274	0							
Locus_11588_Transcript_1/1_Conf_1.000	225	0							
Locus_11589_Transcript_1/1_Conf_1.000	225	2	5.88E-10	NP_492200.1	64	67.3958	71	46	hypothetical protein C54G4.5
Locus_1159_Transcript_1/1_Conf_1.000	1346	4	4.33E-38	NP_499275.2	63	163.696	242	154	hypothetical protein K10G9.2
Locus_11590_Transcript_1/1_Conf_1.000	208	0							
Locus_11591_Transcript_1/1_Conf_1.000	364	18	6.74E-35	NP_741076.1	78	150.214	120	94	GEX Interacting protein family member (gei-16)
Locus_11592_Transcript_1/1_Conf_1.000	773	20	7.15E-64	XP_002630082.1	90	248.054	153	138	Hypothetical protein CBG13461

Locus_11593_Transcript_1/1_Conf_1.000	275	20	1.08E-24	XP_002634119.1	84	116.316	71	60	Hypothetical protein CBG01673
Locus_11594_Transcript_1/1_Conf_1.000	370	20	1.49E-29	XP_002640278.1	85	132.494	85	73	Hypothetical protein CBG12804
Locus_11595_Transcript_1/1_Conf_1.000	365	20	5.00E-30	NP_498090.1	95	134.035	84	80	Temporarily Assigned Gene name family member (tag-262)
Locus_11596_Transcript_1/1_Conf_1.000	613	20	9.52E-19	XP_973445.1	51	97.4413	195	101	PREDICTED: similar to vesicular mannose-binding lectin
Locus_11597_Transcript_1/1_Conf_1.000	683	0							
Locus_11598_Transcript_1/1_Conf_1.000	179	0							
Locus_11599_Transcript_1/1_Conf_1.000	1092	20	1.34E-52	XP_002635267.1	69	211.46	266	185	C. briggsae CBR-LETM-1 protein
Locus_116_Transcript_1/1_Conf_1.000	550	20	3.26E-56	NP_498030.1	79	221.476	183	145	hypothetical protein F26F4.12
Locus_1160_Transcript_1/2_Conf_1.000	386	20	6.59E-14	EFO23006.1	70	80.4925	87	61	mast family protein
Locus_1160_Transcript_2/2_Conf_1.000	1120	20	4.47E-59	XP_001900462.1	74	233.032	222	165	CLASP1
Locus_11600_Transcript_1/1_Conf_1.000	497	1	5.59E-05	XP_001476928.1	53	50.8322	97	52	PREDICTED: hypothetical protein
Locus_11601_Transcript_1/1_Conf_1.000	201	0							
Locus_11602_Transcript_1/1_Conf_1.000	496	20	1.96E-42	XP_001902364.1	73	175.252	159	117	Myotubularin-related family protein
Locus_11603_Transcript_1/1_Conf_1.000	157	0							

Locus_11604_Transcript_1/1_Conf_1.000	351	7	4.30E-29	NP_001022438.1	87	130.954	97	85	Ligand-Gated ion Channel family member (lgc-35)
Locus_11605_Transcript_1/1_Conf_1.000	213	20	2.66E-15	NP_501562.1	73	85.1149	67	49	hypothetical protein C53B4.6
Locus_11606_Transcript_1/1_Conf_1.000	183	20	1.83E-27	2XDU	100	125.561	60	60	Structre Of Hsp90 With Small Molecule Inhibitor Bound
Locus_11607_Transcript_1/1_Conf_1.000	438	2	2.40E-08	NP_491834.1	55	62.003	101	56	MUTator family member (mut-2)
Locus_11608_Transcript_1/1_Conf_1.000	1236	20	5.27E-112	XP_002640687.1	75	409.068	352	264	Hypothetical protein CBG19749
Locus_11609_Transcript_1/1_Conf_1.000	348	20	5.58E-61	2I07	100	236.884	115	115	Human Complement Component C3b
Locus_1161_Transcript_1/1_Conf_1.000	881	20	1.63E-113	NP_001122649.1	77	413.305	294	229	abnormal cell LINeage family member (lin-29)
Locus_11610_Transcript_1/1_Conf_1.000	586	20	2.44E-66	NP_493947.1	80	255.373	194	157	hypothetical protein F56D12.6
Locus_11611_Transcript_1/1_Conf_1.000	488	20	2.79E-28	XP_001601941.1	66	128.257	136	91	PREDICTED: similar to rCG44212

Locus_11612_Transcript_1/1_Conf_1.000	358	20	3.73E-33	NP_001122663.1	73	144.436	115	85	hypothetical protein Y53F4B.39
Locus_11613_Transcript_1/1_Conf_1.000	409	20	4.86E-33	EFO26089.1	82	144.05	98	81	hypothetical protein LOAG_02401
Locus_11614_Transcript_1/1_Conf_1.000	369	20	3.01E-22	NP_505803.1	78	108.227	114	90	hypothetical protein F53B7.3
Locus_11615_Transcript_1/1_Conf_1.000	1161	20	1.48E-137	NP_491777.3	83	493.812	330	277	hypothetical protein T09B4.8
Locus_11616_Transcript_1/1_Conf_1.000	412	0							
Locus_11617_Transcript_1/1_Conf_1.000	149	20	2.40E-19	XP_002930267.1	100	98.5969	49	49	PREDICTED: histone H2A type 2-B-like isoform 1
Locus_11618_Transcript_1/1_Conf_1.000	233	3	1.59E-07	XP_002647560.1	69	59.3066	66	46	Hypothetical protein CBG06646
Locus_11619_Transcript_1/1_Conf_1.000	265	20	3.91E-14	XP_418636.2	80	81.2629	61	49	PREDICTED: similar to ABC transporter protein; P-glycoprotein
Locus_1162_Transcript_1/1_Conf_1.000	981	20	7.12E-156	XP_002641617.1	95	554.288	326	312	C. briggsae CBR-MOG-1 protein
Locus_11620_Transcript_1/1_Conf_1.000	1363	20	0	NP_509898.1	86	699.893	454	393	ACOnitase family member (aco-1)
Locus_11621_Transcript_1/2_Conf_1.000	378	20	2.50E-45	XP_002643138.1	84	184.882	123	104	Hypothetical protein CBG15316
Locus_11621_Transcript_2/2_Conf_1.000	384	20	2.03E-47	XP_002643138.1	85	191.815	123	105	Hypothetical protein CBG15316
Locus_11622_Transcript_1/1_Conf_1.000	297	20	1.74E-22	NP_499461.1	72	108.997	100	72	hypothetical protein T28D6.4
Locus_11623_Transcript_1/1_Conf_1.000	228	0							
Locus_11624_Transcript_1/1_Conf_1.000	244								
Locus_11625_Transcript_1/1_Conf_1.000	224	0							
Locus_11626_Transcript_1/1_Conf_1.000	138	0							
Locus_11627_Transcript_1/1_Conf_1.000	491	20	1.84E-64	XP_002630183.1	89	248.44	162	145	C. briggsae CBR-FLI-1 protein

Locus_11628_Transcript_1/1_Conf_1.000	230	20	1.95E-05	YP_743833.1	86	52.373	36	31	tRNA (5-carboxymethylaminomethyl-2-thiouridylate) synthase
Locus_11629_Transcript_1/1_Conf_1.000	626	0							
Locus_1163_Transcript_1/1_Conf_1.000	360	0							
Locus_11630_Transcript_1/1_Conf_1.000	132	0							
Locus_11631_Transcript_1/1_Conf_1.000	150	0							
Locus_11632_Transcript_1/1_Conf_1.000	342	2	1.45E-08	XP_002636650.1	52	62.7734	97	51	Hypothetical protein CBG23361
Locus_11633_Transcript_1/1_Conf_1.000	290	4	1.60E-15	XP_002633091.1	74	85.8853	78	58	Hypothetical protein CBG05778
Locus_11634_Transcript_1/1_Conf_1.000	879	20	8.66E-99	NP_500551.2	77	364.385	292	225	hypothetical protein F55F10.1
Locus_11635_Transcript_1/1_Conf_1.000	532	0							
Locus_11636_Transcript_1/1_Conf_1.000	507	16	1.38E-09	XP_002129449.1	50	66.2402	163	83	PREDICTED: hypothetical protein
Locus_11637_Transcript_1/1_Conf_1.000	389	0							
Locus_11638_Transcript_1/1_Conf_1.000	478	20	1.39E-64	XP_002633391.1	90	248.825	160	144	Hypothetical protein CBG06150
Locus_11639_Transcript_1/1_Conf_1.000	1464	20	0	NP_497853.1	97	892.493	488	477	hypothetical protein T08A11.2
Locus_1164_Transcript_1/2_Conf_1.000	401	20	3.41E-34	XP_002638772.1	70	147.902	133	94	C. briggsae CBR-PTR-21 protein

Locus_1164_Transcript_2/2_Conf_1.000	291	20	1.35E-22	NP_490751.1	75	109.383	91	69	PaTched Related family member (ptr-21)
Locus_11640_Transcript_1/1_Conf_1.000	629	0							
Locus_11641_Transcript_1/1_Conf_1.000	667	20	3.31E-58	EFO27604.1	74	228.794	221	164	hypothetical protein LOAG_00873
Locus_11642_Transcript_1/1_Conf_1.000	378	4	1.75E-14	XP_002633359.1	94	82.4185	50	47	Hypothetical protein CBG06103
Locus_11643_Transcript_1/1_Conf_1.000	134	4	3.74E-09	XP_002643366.1	79	64.6994	44	35	Hypothetical protein CBG15976
Locus_11644_Transcript_1/1_Conf_1.000	268	2	2.29E-06	XP_002636286.1	63	55.4546	73	46	Hypothetical protein CBG08576
Locus_11645_Transcript_1/1_Conf_1.000	823	0							
Locus_11646_Transcript_1/1_Conf_1.000	667	6	2.62E-55	XP_002637345.1	64	219.164	232	149	C. briggsae CBR-UNC-68 protein
Locus_11647_Transcript_1/2_Conf_1.000	1354	20	1.08E-145	NP_492121.1	72	521.161	456	330	Piwi (fruitfly) Related Gene family member (prg-1)
Locus_11647_Transcript_2/2_Conf_1.000	1354	20	1.08E-145	NP_492121.1	72	521.161	456	330	Piwi (fruitfly) Related Gene family member (prg-1)
Locus_11648_Transcript_1/1_Conf_1.000	479	0							
Locus_11649_Transcript_1/1_Conf_1.000	734	20	2.72E-62	EFO22517.1	73	242.662	204	149	DREV methyltransferase
Locus_1165_Transcript_1/1_Conf_1.000	412	20	6.92E-64	XP_002634177.1	93	246.514	132	124	C. briggsae CBR-RPL-20 protein
Locus_11650_Transcript_1/1_Conf_1.000	404	13	5.10E-06	XP_001900016.1	47	54.299	134	64	Leucine Rich Repeat family protein
Locus_11651_Transcript_1/1_Conf_1.000	452	15	7.58E-10	XP_001897754.1	49	67.0106	158	78	Poly

Locus_11652_Transcript_1/2_Conf_1.000	688	20	1.67E-23	XP_002646274.1	72	113.62	106	77	Hypothetical protein CBG11979
Locus_11652_Transcript_2/2_Conf_1.000	646	20	6.87E-74	XP_002646274.1	80	280.796	210	169	Hypothetical protein CBG11979
Locus_11653_Transcript_1/1_Conf_1.000	349	0							
Locus_11654_Transcript_1/1_Conf_1.000	1089	20	4.85E-95	XP_002645831.1	63	352.443	404	257	C. briggsae CBR-RBC-1 protein
Locus_11655_Transcript_1/1_Conf_1.000	294	20	5.43E-32	NP_001123000.1	84	140.584	96	81	hypothetical protein T05C3.6
Locus_11656_Transcript_1/1_Conf_1.000	335	20	8.56E-30	NP_507684.4	78	133.265	107	84	abnormal EMBroygenesis family member (emb-4)
Locus_11657_Transcript_1/1_Conf_1.000	291	4	2.23E-09	XP_002637600.1	72	65.4698	68	49	C. briggsae CBR-SULP-8 protein
Locus_11658_Transcript_1/1_Conf_1.000	1545	1	8.37E-04	XP_001604445.1	37	50.0618	354	132	PREDICTED: hypothetical protein
Locus_11659_Transcript_1/2_Conf_1.000	625	3	5.82E-13	CAR63732.1	62	67.3958	82	51	hypothetical protein
Locus_11659_Transcript_2/2_Conf_1.000	575	3	1.84E-15	CAR63732.1	51	86.2705	152	78	hypothetical protein
Locus_1166_Transcript_1/4_Conf_0.222	262	0							
Locus_1166_Transcript_2/4_Conf_0.222	900	1	9.95E-05	NP_505827.1	50	51.9878	102	52	hypothetical protein H19N07.3
Locus_1166_Transcript_3/4_Conf_0.222	892	20	1.48E-61	NP_491562.2	60	240.736	294	179	LEThal family member (let-526)
Locus_1166_Transcript_4/4_Conf_0.444	2031	0							
Locus_11660_Transcript_1/1_Conf_1.000	146	6	1.51E-13	NP_871966.2	89	79.337	48	43	hypothetical protein Y48B6A.6
Locus_11661_Transcript_1/1_Conf_1.000	256	0							
Locus_11662_Transcript_1/1_Conf_1.000	131	0							
Locus_11663_Transcript_1/1_Conf_1.000	770	20	1.68E-73	NP_501418.1	97	280.026	142	138	SQuashed Vulva family member (sqv-1)
Locus_11664_Transcript_1/1_Conf_1.000	427	20	7.56E-26	XP_002642911.1	83	120.168	77	64	Hypothetical protein CBG15186
Locus_11665_Transcript_1/1_Conf_1.000	1134	3	1.53E-30	CAA91299.3	46	138.272	400	187	C. elegans protein T01B7.6, confirmed by transcript evidence
Locus_11666_Transcript_1/1_Conf_1.000	174	20	1.78E-27	NP_001163801.1	100	125.561	57	57	hypothetical protein LOC401152 isoform 1
Locus_11667_Transcript_1/2_Conf_1.000	803	2	2.88E-18	NP_505117.2	68	96.6709	116	79	hypothetical protein K07C11.8
Locus_11667_Transcript_2/2_Conf_1.000	526	2	1.06E-18	NP_505117.2	68	96.6709	116	79	hypothetical protein K07C11.8

Locus_11668_Transcript_1/1_Conf_1.000	786	20	3.25E-43	XP_002640253.1	53	179.489	269	145	C. briggsae CBR-CYE-1 protein
Locus_11669_Transcript_1/1_Conf_1.000	434	5	9.75E-42	NP_495343.1	76	172.94	144	110	hypothetical protein C56C10.12
Locus_1167_Transcript_1/2_Conf_1.000	577	0							
Locus_1167_Transcript_2/2_Conf_1.000	577	0							
Locus_11670_Transcript_1/2_Conf_1.000	308	0							
Locus_11670_Transcript_2/2_Conf_1.000	307	0							
Locus_11671_Transcript_1/1_Conf_1.000	448	0							
Locus_11672_Transcript_1/1_Conf_1.000	611	20	7.54E-85	NP_491342.1	92	317.005	178	165	hypothetical protein C43E11.9
Locus_11673_Transcript_1/1_Conf_1.000	307								
Locus_11674_Transcript_1/1_Conf_1.000	328	20	4.75E-12	NP_495768.1	52	74.3294	117	61	hypothetical protein F49E12.1

Locus_11675_Transcript_1/1_Conf_1.000	238	20	2.97E-22	XP_002723288.1	82	108.227	63	52	PREDICTED: COX6B protein (predicted)-like
Locus_11676_Transcript_1/1_Conf_1.000	509	0							
Locus_11677_Transcript_1/1_Conf_1.000	260	20	2.39E-11	XP_002643075.1	58	72.0182	87	51	Hypothetical protein CBG22995
Locus_11678_Transcript_1/1_Conf_1.000	140	20	7.74E-15	NP_496814.1	93	83.5741	46	43	Member of AAA family binding CED-4 family member (mac-1)
Locus_11679_Transcript_1/1_Conf_1.000	370	1	1.11E-08	EFO23989.1	59	63.1586	91	54	hypothetical protein LOAG_04493
Locus_1168_Transcript_1/1_Conf_1.000	1984	20	9.92E-165	XP_002643237.1	62	585.104	650	405	C. briggsae CBR-IGCM-1 protein
Locus_11680_Transcript_1/1_Conf_1.000	1479	20	0	CBJ25106.1	86	700.664	494	425	C. elegans protein Y105C5B.21d, partially confirmed by transcript evidence
Locus_11681_Transcript_1/1_Conf_1.000	1026	20	5.25E-88	XP_002635050.1	65	328.946	360	234	Hypothetical protein CBG11250
Locus_11682_Transcript_1/1_Conf_1.000	818	20	3.81E-58	XP_002644069.1	69	229.18	198	137	C. briggsae CBR-PXN-2 protein
Locus_11683_Transcript_1/1_Conf_1.000	371	20	7.14E-40	NP_498263.2	80	166.777	110	88	ALdehyde deHydrogenase family member (alh-9)
Locus_11684_Transcript_1/1_Conf_1.000	133	0							
Locus_11685_Transcript_1/1_Conf_1.000	517	0							
Locus_11686_Transcript_1/1_Conf_1.000	451	2	1.25E-04	NP_501585.1	58	49.6766	58	34	hypothetical protein C01F6.2
Locus_11687_Transcript_1/1_Conf_1.000	921	20	4.58E-61	XP_001891577.1	82	239.195	172	142	Protein set-1
Locus_11688_Transcript_1/1_Conf_1.000	216	0							
Locus_11689_Transcript_1/1_Conf_1.000	126	0							
Locus_1169_Transcript_1/1_Conf_1.000	728	0							
Locus_11690_Transcript_1/1_Conf_1.000	447	2	1.94E-05	EFO16740.1	49	52.373	77	38	hypothetical protein LOAG_11764
Locus_11691_Transcript_1/1_Conf_1.000	1172	20	4.64E-147	XP_002645119.1	84	525.398	393	331	Hypothetical protein CBG16813
Locus_11692_Transcript_1/1_Conf_1.000	837	20	3.01E-13	NP_492529.2	46	80.1073	239	111	SET (trithorax/polycomb) domain containing family member (set-32)
Locus_11693_Transcript_1/1_Conf_1.000	347	6	7.94E-07	XP_002129449.1	46	56.9954	115	54	PREDICTED: hypothetical protein

Locus_11694_Transcript_1/1_Conf_1.000	271	0							
Locus_11695_Transcript_1/1_Conf_1.000	1172	20	1.03E-146	NP_507860.3	85	524.242	362	308	DeHydrogenases, Short chain family member (dhs-24)
Locus_11696_Transcript_1/1_Conf_1.000	390	20	4.06E-48	XP_002639529.1	85	194.126	130	111	Hypothetical protein CBG04158
Locus_11697_Transcript_1/1_Conf_1.000	226	3	2.91E-25	NP_500037.2	85	118.242	74	63	hypothetical protein Y55F3AR.1
Locus_11698_Transcript_1/1_Conf_1.000	446	20	8.17E-12	XP_002631215.1	56	73.559	96	54	C. briggsae CBR-ECT-2 protein
Locus_11699_Transcript_1/1_Conf_1.000	696	20	5.80E-96	EFO22056.1	86	354.369	232	200	hypothetical protein LOAG_06429
Locus_117_Transcript_1/1_Conf_1.000	191	0							
Locus_1170_Transcript_1/1_Conf_1.000	1015	0							

Locus_11700_Transcript_1/1_Conf_1.000	1894	20	1.95E-77	EFO28277.1	52	295.049	578	302	piwi domain-containing protein
Locus_11701_Transcript_1/1_Conf_1.000	150	5	3.46E-10	A8XKF2.2	83	68.1662	43	36	Choline transporter-like protein 1
Locus_11702_Transcript_1/1_Conf_1.000	231	4	4.47E-10	NP_492367.1	77	67.781	57	44	Glycogen Synthase Kinase Alpha subunit family member (gska-3)
Locus_11703_Transcript_1/1_Conf_1.000	551	20	3.87E-41	NP_001040716.1	69	171.4	183	127	hypothetical protein ZC328.3
Locus_11704_Transcript_1/1_Conf_1.000	210	0							
Locus_11705_Transcript_1/1_Conf_1.000	700	20	3.14E-65	NP_505697.2	73	252.292	234	172	hypothetical protein C35A5.7
Locus_11706_Transcript_1/1_Conf_1.000	757	8	5.54E-106	AAT02162.1	89	387.882	249	222	hypothetical protein L3ni51
Locus_11707_Transcript_1/1_Conf_1.000	682	20	7.46E-85	NP_496454.1	82	317.39	223	185	hypothetical protein B0334.3
Locus_11708_Transcript_1/1_Conf_1.000	344	1	2.10E-07	NP_001122817.1	67	58.9214	56	38	hypothetical protein Y54G2A.52
Locus_11709_Transcript_1/1_Conf_1.000	692	20	2.13E-34	XP_001898340.1	67	149.828	169	114	LD47622p
Locus_1171_Transcript_1/1_Conf_1.000	1900	20	7.84E-119	XP_002640096.1	71	432.565	440	313	C. briggsae CBR-PNK-1 protein
Locus_11710_Transcript_1/2_Conf_1.000	1819	20	2.14E-25	NP_504250.2	43	122.094	497	216	Suppressor Of Clr family member (soc-1)

Locus_11710_Transcript_2/2_Conf_1.000	1801	20	1.62E-25	NP_504250.2	44	122.479	496	219	Suppressor Of Clr family member (soc-1)
Locus_11711_Transcript_1/1_Conf_1.000	243	0							
Locus_11712_Transcript_1/1_Conf_1.000	164	5	1.88E-08	NP_497046.1	66	62.3882	53	35	UNCoordinated family member (unc-52)
Locus_11713_Transcript_1/1_Conf_1.000	375	7	1.95E-05	XP_001895231.1	88	52.373	34	30	Bucentaur or craniofacial development family protein
Locus_11714_Transcript_1/1_Conf_1.000	386	20	1.37E-11	XP_001902350.1	60	72.7886	119	72	Myosin XVIIIA
Locus_11715_Transcript_1/1_Conf_1.000	322	0							
Locus_11716_Transcript_1/1_Conf_1.000	320	0							
Locus_11717_Transcript_1/1_Conf_1.000	168	20	9.83E-26	BAH14701.1	100	119.783	55	55	unnamed protein product
Locus_11718_Transcript_1/1_Conf_1.000	982	20	1.68E-64	NP_492260.1	64	250.751	304	197	hypothetical protein F52B5.3
Locus_11719_Transcript_1/1_Conf_1.000	364	3	8.25E-25	NP_508493.1	74	116.701	122	91	protein KINase family member (kin-29)

Locus_1172_Transcript_1/1_Conf_1.000	503	20	1.34E-38	XP_002637575.1	75	162.54	148	111	C. briggsae CBR-EHBP-1 protein
Locus_11720_Transcript_1/1_Conf_1.000	150	0							
Locus_11721_Transcript_1/1_Conf_1.000	476	20	3.50E-15	XP_002199801.1	62	84.7297	86	54	PREDICTED: ELMO/CED-12 domain containing 1
Locus_11722_Transcript_1/1_Conf_1.000	805	20	1.43E-41	XP_002408201.1	62	174.096	265	165	Ran-binding protein, putative
Locus_11723_Transcript_1/1_Conf_1.000	569	0							
Locus_11724_Transcript_1/1_Conf_1.000	395	0							
Locus_11725_Transcript_1/2_Conf_1.000	635	20	4.02E-23	XP_001900825.1	78	112.079	89	70	CG3579-PA
Locus_11725_Transcript_2/2_Conf_1.000	635	20	4.02E-23	XP_001900825.1	78	112.079	89	70	CG3579-PA
Locus_11726_Transcript_1/2_Conf_1.000	1272	0							
Locus_11726_Transcript_2/2_Conf_1.000	1272	0							
Locus_11727_Transcript_1/1_Conf_1.000	303	20	5.03E-30	EFO21314.1	81	134.035	100	81	male sterility protein
Locus_11728_Transcript_1/1_Conf_1.000	222	6	2.64E-18	XP_001896269.1	85	95.1301	57	49	BTB/POZ domain containing protein
Locus_11729_Transcript_1/1_Conf_1.000	727	20	7.24E-76	XP_002647628.1	74	287.73	227	169	Hypothetical protein CBG06721
Locus_1173_Transcript_1/1_Conf_1.000	2987	20	0	XP_001900046.1	66	670.618	769	515	Kinesin motor domain containing protein
Locus_11730_Transcript_1/1_Conf_1.000	663	0							
Locus_11731_Transcript_1/1_Conf_1.000	353	4	1.75E-14	NP_496498.1	63	82.4185	99	63	hypothetical protein C47D12.8
Locus_11732_Transcript_1/1_Conf_1.000	1115	20	2.19E-74	CAX32485.1	67	283.878	359	243	C. elegans protein T20D3.11b, partially confirmed by transcript evidence
Locus_11733_Transcript_1/1_Conf_1.000	877	0							
Locus_11734_Transcript_1/1_Conf_1.000	469	2	8.13E-12	XP_002638516.1	46	73.559	139	65	Hypothetical protein CBG05542
Locus_11735_Transcript_1/1_Conf_1.000	332	20	8.89E-27	NP_496968.1	96	123.25	63	61	hypothetical protein Y48B6A.12

Locus_11736_Transcript_1/1_Conf_1.000	393	1	9.74E-05	NP_499759.1	72	50.0618	44	32	DNaJ domain (prokaryotic heat shock protein) family member (dnj-17)
Locus_11737_Transcript_1/1_Conf_1.000	608	20	3.48E-50	NP_497589.3	68	201.83	196	134	hypothetical protein Y71H2B.5
Locus_11738_Transcript_1/1_Conf_1.000	675	20	5.67E-37	EFO18191.1	71	158.303	168	120	hypothetical protein LOAG_10303
Locus_11739_Transcript_1/1_Conf_1.000	273	20	4.56E-23	EFO18946.1	74	110.923	90	67	hypothetical protein LOAG_09552
Locus_1174_Transcript_1/1_Conf_1.000	663	20	2.85E-70	XP_002640874.1	83	268.855	173	144	C. briggsae CBR-CCO-2 protein
Locus_11740_Transcript_1/1_Conf_1.000	202	0							
Locus_11741_Transcript_1/1_Conf_1.000	323	20	2.98E-38	NP_495409.3	86	161.384	108	93	hypothetical protein C44B7.10
Locus_11742_Transcript_1/1_Conf_1.000	553	20	1.81E-78	NP_493616.1	87	295.434	184	161	hypothetical protein F33H2.5
Locus_11743_Transcript_1/1_Conf_1.000	799	20	2.01E-72	EFO27128.1	77	276.559	244	188	cyclin domain-containing protein
Locus_11744_Transcript_1/1_Conf_1.000	154	20	3.01E-14	XP_002919374.1	100	81.6481	38	38	PREDICTED: pleckstrin homology domain-containing family O member 1-like
Locus_11745_Transcript_1/1_Conf_1.000	514	20	8.44E-39	XP_001894255.1	82	163.31	128	105	trafficking protein particle complex subunit 1

Locus_11746_Transcript_1/1_Conf_1.000	283	20	1.66E-20	XP_002192510.1	100	102.449	80	80	PREDICTED: heterogeneous nuclear ribonucleoprotein K
Locus_11747_Transcript_1/1_Conf_1.000	390	20	4.65E-36	NP_500022.1	71	154.066	127	91	Inner Mitochondrial Membrane Protease family member (immp-2)
Locus_11748_Transcript_1/1_Conf_1.000	251	20	2.63E-39	ADN23570.1	100	164.851	83	83	ubiquitin
Locus_11749_Transcript_1/1_Conf_1.000	509	20	5.75E-32	EFO22933.1	66	140.584	171	113	hypothetical protein LOAG_05552
Locus_1175_Transcript_1/1_Conf_1.000	807	20	2.18E-114	ACI49174.1	91	416.001	245	225	hypothetical protein Csp3_JD02.002
Locus_11750_Transcript_1/1_Conf_1.000	468	20	5.21E-51	NP_498688.1	72	203.756	153	111	Prolyl Carboxy Peptidase like family member (pcp-1)

Locus_11751_Transcript_1/1_Conf_1.000	205	20	7.53E-26	NP_495261.1	89	120.168	67	60	hypothetical protein F13H8.7
Locus_11752_Transcript_1/1_Conf_1.000	614	20	5.21E-25	NP_502214.2	53	118.242	186	100	hypothetical protein ZK792.7
Locus_11753_Transcript_1/1_Conf_1.000	800	20	2.58E-27	EFO17580.1	69	126.716	137	95	hypothetical protein LOAG_10920
Locus_11754_Transcript_1/1_Conf_1.000	589	3	2.01E-28	NP_493625.4	56	129.413	185	105	hypothetical protein F31C3.3
Locus_11755_Transcript_1/2_Conf_1.000	312	0							
Locus_11755_Transcript_2/2_Conf_1.000	279	0							
Locus_11756_Transcript_1/1_Conf_1.000	678	20	1.35E-78	NP_502573.1	78	296.59	223	176	hypothetical protein Y62E10A.6
Locus_11757_Transcript_1/1_Conf_1.000	303	0							
Locus_11758_Transcript_1/1_Conf_1.000	608	20	9.13E-67	XP_002641059.1	79	256.914	193	153	Hypothetical protein CBG22470
Locus_11759_Transcript_1/1_Conf_1.000	313	20	3.92E-54	XP_002760567.1	100	214.157	104	104	PREDICTED: 60S ribosomal protein L5-like isoform 1
Locus_1176_Transcript_1/2_Conf_1.000	708	20	1.49E-38	XP_001896392.1	63	163.696	215	136	Dual specificity phosphatase, catalytic domain containing protein
Locus_1176_Transcript_2/2_Conf_1.000	708	20	1.14E-38	XP_001896392.1	63	164.081	213	136	Dual specificity phosphatase, catalytic domain containing protein
Locus_11760_Transcript_1/1_Conf_1.000	1085	20	7.27E-160	CBI70492.1	93	567.77	361	337	vacuolar ATPase a subunit
Locus_11761_Transcript_1/2_Conf_1.000	263	0							
Locus_11761_Transcript_2/2_Conf_1.000	530	0							
Locus_11762_Transcript_1/1_Conf_1.000	273	6	1.37E-19	XP_002632822.1	70	99.3673	91	64	C. briggsae CBR-NHR-97 protein
Locus_11763_Transcript_1/1_Conf_1.000	217	0							

Locus_11764_Transcript_1/1_Conf_1.000	887	20	4.96E-110	XP_002636649.1	79	401.749	296	235	Hypothetical protein CBG23360
Locus_11765_Transcript_1/1_Conf_1.000	400	2	4.95E-09	XP_002639986.1	78	64.3142	42	33	Hypothetical protein CBG10814
Locus_11766_Transcript_1/1_Conf_1.000	307	0							
Locus_11767_Transcript_1/1_Conf_1.000	244	7	4.71E-12	NP_001122977.1	76	74.3294	80	61	Variable ABnormal morphology family member (vab-8)
Locus_11768_Transcript_1/1_Conf_1.000	1119	20	3.70E-138	CBL87054.2	86	495.738	311	270	C. elegans protein F54E4.1, partially confirmed by transcript evidence
Locus_11769_Transcript_1/1_Conf_1.000	545	14	2.77E-36	NP_001123010.1	68	155.221	157	107	related to yeast Vacuolar Protein Sorting factor family member (vps-39)
Locus_1177_Transcript_1/1_Conf_1.000	472	20	5.00E-62	XP_002646355.1	83	240.35	154	128	Hypothetical protein CBG12069
Locus_11770_Transcript_1/1_Conf_1.000	181	0							
Locus_11771_Transcript_1/2_Conf_1.000	272	0							
Locus_11771_Transcript_2/2_Conf_1.000	268	0							
Locus_11772_Transcript_1/1_Conf_1.000	628	1	1.22E-08	NP_001021391.1	56	63.929	144	81	hypothetical protein F16C3.3
Locus_11773_Transcript_1/1_Conf_1.000	434	3	1.92E-13	XP_002636820.1	58	78.9518	148	86	Hypothetical protein CBG09264
Locus_11774_Transcript_1/1_Conf_1.000	801	20	3.81E-87	NP_498566.3	84	325.479	234	198	hypothetical protein K04G7.11
Locus_11775_Transcript_1/1_Conf_1.000	188	0							
Locus_11776_Transcript_1/1_Conf_1.000	268	20	1.47E-37	XP_002641474.1	88	159.073	87	77	C. briggsae CBR-PTP-1 protein

Locus_11777_Transcript_1/1_Conf_1.000	410	20	2.91E-70	NP_501549.1	100	267.7	134	134	RAP homolog (vertebrate Rap GTPase family) family member (rap-1)
Locus_11778_Transcript_1/1_Conf_1.000	990	20	5.38E-26	NP_501282.1	49	122.865	289	143	hypothetical protein C33H5.8
Locus_11779_Transcript_1/1_Conf_1.000	314	0							
Locus_1178_Transcript_1/2_Conf_1.000	643	20	2.04E-78	NP_497574.2	89	295.819	174	156	hypothetical protein Y54F10AM.5
Locus_1178_Transcript_2/2_Conf_1.000	643	20	2.04E-78	NP_497574.2	89	295.819	174	156	hypothetical protein Y54F10AM.5
Locus_11780_Transcript_1/2_Conf_1.000	933	0							
Locus_11780_Transcript_2/2_Conf_1.000	581	0							
Locus_11781_Transcript_1/2_Conf_1.000	652	20	1.02E-56	XP_002638616.1	84	223.787	171	144	Hypothetical protein CBG05668
Locus_11781_Transcript_2/2_Conf_1.000	885	20	8.03E-60	XP_002638616.1	78	234.958	213	167	Hypothetical protein CBG05668
Locus_11782_Transcript_1/1_Conf_1.000	696	7	7.46E-35	XP_002641835.1	60	151.369	230	138	C. briggsae CBR-CYK-1 protein
Locus_11783_Transcript_1/1_Conf_1.000	518	20	6.39E-42	NP_494918.2	75	173.711	171	129	hypothetical protein T27F7.3
Locus_11784_Transcript_1/1_Conf_1.000	197	0							
Locus_11785_Transcript_1/1_Conf_1.000	217	0							
Locus_11786_Transcript_1/1_Conf_1.000	183	0							
Locus_11787_Transcript_1/1_Conf_1.000	245	0							
Locus_11788_Transcript_1/1_Conf_1.000	319	0							
Locus_11789_Transcript_1/1_Conf_1.000	309	20	7.71E-23	XP_002639369.1	66	110.153	96	64	C. briggsae CBR-ZIG-7 protein
Locus_1179_Transcript_1/1_Conf_1.000	2249	5	5.22E-24	XP_002636796.1	45	117.857	389	178	C. briggsae CBR-RIL-2 protein
Locus_11790_Transcript_1/1_Conf_1.000	279	0							

Locus_11791_Transcript_1/1_Conf_1.000	1017	20	1.02E-59	EFO16811.1	63	234.958	264	167	hypothetical protein LOAG_11692
Locus_11792_Transcript_1/1_Conf_1.000	188	0							
Locus_11793_Transcript_1/1_Conf_1.000	359	5	2.42E-24	XP_002636405.1	96	115.161	58	56	Hypothetical protein CBG23057
Locus_11794_Transcript_1/1_Conf_1.000	1503	20	0	NP_001024792.2	87	655.596	422	371	yeast SMF (divalent cation transporter) homolog family member (smf-1)
Locus_11795_Transcript_1/1_Conf_1.000	1026	20	3.84E-14	XP_002129449.1	47	83.5741	184	87	PREDICTED: hypothetical protein
Locus_11796_Transcript_1/1_Conf_1.000	432	2	5.59E-05	NP_740989.1	54	50.8322	141	77	hypothetical protein F07F6.8
Locus_11797_Transcript_1/1_Conf_1.000	164	0							
Locus_11798_Transcript_1/1_Conf_1.000	435	20	1.03E-67	XP_002644717.1	93	259.225	145	136	Hypothetical protein CBG14711
Locus_11799_Transcript_1/1_Conf_1.000	252	3	8.53E-17	XP_001898467.1	78	90.1225	80	63	FYVE zinc finger family protein
Locus_118_Transcript_1/1_Conf_1.000	471	0							
Locus_1180_Transcript_1/1_Conf_1.000	1449	20	1.23E-118	Q5QQ52.1	68	431.409	402	277	Xylosyltransferase sqv-6
Locus_11800_Transcript_1/1_Conf_1.000	266	0							
Locus_11801_Transcript_1/1_Conf_1.000	142	0							
Locus_11802_Transcript_1/1_Conf_1.000	487	0							
Locus_11803_Transcript_1/1_Conf_1.000	202	0							
Locus_11804_Transcript_1/1_Conf_1.000	316	5	5.17E-06	NP_001021675.1	71	54.299	63	45	hypothetical protein W10C8.6
Locus_11805_Transcript_1/1_Conf_1.000	152	0							
Locus_11806_Transcript_1/1_Conf_1.000	227	20	4.48E-26	NP_503148.1	90	120.939	66	60	hypothetical protein Y108G3AL.2
Locus_11807_Transcript_1/1_Conf_1.000	183	20	6.11E-23	XP_002640829.1	96	110.538	58	56	C. briggsae CBR-ADS-1 protein

Locus_11808_Transcript_1/2_Conf_1.000	449	2	8.42E-09	XP_002642114.1	48	63.5438	141	69	C. briggsae CBR-PQN-45 protein
Locus_11808_Transcript_2/2_Conf_1.000	449	2	1.75E-06	XP_002642114.1	48	55.8398	141	68	C. briggsae CBR-PQN-45 protein
Locus_11809_Transcript_1/1_Conf_1.000	372	0							
Locus_1181_Transcript_1/1_Conf_1.000	1290	20	5.04E-113	XP_002638266.1	87	412.535	275	240	C. briggsae CBR-HAF-3 protein
Locus_11810_Transcript_1/1_Conf_1.000	748	20	1.37E-40	NP_001022051.1	59	170.629	250	148	SREBP Cleavage activating Protein (SCAP) homolog family member (scp-1)
Locus_11811_Transcript_1/1_Conf_1.000	143	0							
Locus_11812_Transcript_1/2_Conf_1.000	367	0							
Locus_11812_Transcript_2/2_Conf_1.000	367	0							
Locus_11813_Transcript_1/1_Conf_1.000	604	20	9.93E-74	CAA86821.1	90	280.026	178	161	excretory/secretory antigen
Locus_11814_Transcript_1/1_Conf_1.000	1129	20	2.94E-50	XP_002634649.1	71	203.756	225	161	C. briggsae CBR-DGK-4 protein
Locus_11815_Transcript_1/1_Conf_1.000	319	7	1.71E-09	XP_001898068.1	69	65.855	71	49	Homeobox domain containing protein
Locus_11816_Transcript_1/1_Conf_1.000	291	4	2.63E-10	NP_491254.1	58	68.5514	80	47	hypothetical protein C50F2.4
Locus_11817_Transcript_1/1_Conf_1.000	143	0							
Locus_11818_Transcript_1/1_Conf_1.000	636	12	1.45E-20	NP_499391.1	76	103.605	86	66	hypothetical protein Y39A1C.1
Locus_11819_Transcript_1/1_Conf_1.000	232	12	6.03E-15	XP_002631617.1	72	83.9593	75	54	Hypothetical protein CBG20802
Locus_1182_Transcript_1/1_Conf_1.000	231	8	6.88E-19	XP_002631304.1	92	97.0561	53	49	Hypothetical protein CBG03118
Locus_11820_Transcript_1/1_Conf_1.000	283	0							
Locus_11821_Transcript_1/1_Conf_1.000	713	20	2.21E-98	EFO22809.1	88	362.459	237	210	hypothetical protein LOAG_05677
Locus_11822_Transcript_1/1_Conf_1.000	750	20	7.74E-92	XP_002630011.1	80	340.887	250	201	Hypothetical protein CBG13376

Locus_11823_Transcript_1/1_Conf_1.000	414	20	2.38E-40	NP_497425.1	72	168.318	136	99	SphingoMyelin Synthase family member (sms-3)
Locus_11824_Transcript_1/1_Conf_1.000	566	20	1.02E-23	XP_001902442.1	60	113.62	169	103	hypothetical protein Bm1_54925
Locus_11825_Transcript_1/1_Conf_1.000	823	20	4.09E-92	NP_505433.3	80	342.043	243	196	Heavy chain, Unconventional Myosin family member (hum-2)
Locus_11826_Transcript_1/1_Conf_1.000	300	0							
Locus_11827_Transcript_1/1_Conf_1.000	527	4	1.74E-37	CAB07693.3	74	159.073	131	97	C. elegans protein Y48E1B.7, partially confirmed by transcript evidence
Locus_11828_Transcript_1/2_Conf_1.000	831	20	2.39E-71	NP_493713.2	81	273.092	204	167	CalPoNin family member (cpn-2)
Locus_11828_Transcript_2/2_Conf_1.000	734	20	1.88E-71	NP_493713.2	81	273.092	204	167	CalPoNin family member (cpn-2)
Locus_11829_Transcript_1/1_Conf_1.000	607	20	2.77E-31	XP_002643253.1	75	139.043	128	96	C. briggsae CBR-AEX-3 protein
Locus_1183_Transcript_1/1_Conf_1.000	965	20	1.70E-37	XP_002189824.1	55	160.999	280	156	PREDICTED: centrosomal protein 97kDa
Locus_11830_Transcript_1/1_Conf_1.000	935	20	3.77E-119	NP_510560.2	81	432.18	304	249	Gut OBstructed or defective family member (gob-1)
Locus_11831_Transcript_1/1_Conf_1.000	183	20	6.53E-25	XP_002637927.1	96	117.087	61	59	Hypothetical protein CBG04739

Locus_11832_Transcript_1/1_Conf_1.000	339	0							
Locus_11833_Transcript_1/1_Conf_1.000	756	20	2.43E-77	EFO21654.1	76	292.738	249	191	hypothetical protein LOAG_06832
Locus_11834_Transcript_1/1_Conf_1.000	209	0							
Locus_11835_Transcript_1/1_Conf_1.000	281	0							
Locus_11836_Transcript_1/1_Conf_1.000	160	0							
Locus_11837_Transcript_1/1_Conf_1.000	1289	20	3.26E-104	XP_001898591.1	70	383.259	396	279	Polyprenyl synthetase family protein
Locus_11838_Transcript_1/1_Conf_1.000	765	20	4.93E-25	NP_496945.3	62	119.013	166	103	XRN (mouse/S. cerevisiae) ribonuclease related family member (xrn-1)
Locus_11839_Transcript_1/1_Conf_1.000	600	20	1.04E-99	AAV38432.1	100	366.311	173	173	tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)
Locus_1184_Transcript_1/1_Conf_1.000	621	20	6.01E-69	NP_001023176.1	91	264.233	157	143	hypothetical protein F33D4.8
Locus_11840_Transcript_1/1_Conf_1.000	493	17	4.43E-18	XP_002632297.1	56	94.3597	151	85	C. briggsae CBR-NOL-6 protein
Locus_11841_Transcript_1/1_Conf_1.000	441	0							
Locus_11842_Transcript_1/1_Conf_1.000	681	20	1.91E-72	XP_001896094.1	74	276.174	225	168	Protein kinase domain containing protein
Locus_11843_Transcript_1/1_Conf_1.000	133	6	9.22E-08	XP_002642608.1	82	60.077	41	34	C. briggsae CBR-LIG-4 protein
Locus_11844_Transcript_1/1_Conf_1.000	1224	0							
Locus_11845_Transcript_1/1_Conf_1.000	1117	20	6.22E-61	CAB01684.2	74	239.195	201	150	C. elegans protein C35C5.3a, confirmed by transcript evidence
Locus_11846_Transcript_1/1_Conf_1.000	234	0							

Locus_11847_Transcript_1/1_Conf_1.000	625	20	4.48E-96	EFO19031.1	91	354.369	208	190	hypothetical protein LOAG_09464
Locus_11848_Transcript_1/1_Conf_1.000	401	20	3.08E-35	XP_002639450.1	96	151.369	80	77	Hypothetical protein CBG04045
Locus_11849_Transcript_1/1_Conf_1.000	181	0							
Locus_1185_Transcript_1/1_Conf_1.000	2272	20	6.64E-43	XP_002644054.1	83	180.644	132	110	Hypothetical protein CBG17518
Locus_11850_Transcript_1/1_Conf_1.000	131	0							
Locus_11851_Transcript_1/1_Conf_1.000	495	0							
Locus_11852_Transcript_1/1_Conf_1.000	348	20	1.52E-50	NP_506259.2	92	202.216	115	106	hypothetical protein W07G4.3
Locus_11853_Transcript_1/1_Conf_1.000	889	4	1.98E-82	XP_002643042.1	77	310.071	289	223	Hypothetical protein CBG22957
Locus_11854_Transcript_1/1_Conf_1.000	410	3	7.49E-34	A8WRV1.2	75	146.747	128	96	Serine/threonine-protein kinase kin-29
Locus_11855_Transcript_1/1_Conf_1.000	368	0							
Locus_11856_Transcript_1/1_Conf_1.000	203	0							
Locus_11857_Transcript_1/1_Conf_1.000	222	20	2.02E-18	NP_001021770.1	92	95.5153	54	50	hypothetical protein Y47G6A.7
Locus_11858_Transcript_1/1_Conf_1.000	557	20	2.99E-20	NP_499961.2	73	102.064	82	60	Nuclear Hormone Receptor family member (nhr-76)
Locus_11859_Transcript_1/1_Conf_1.000	675	20	2.28E-70	NP_506561.1	87	269.24	170	149	CYclophyliN family member (cyn-1)

Locus_1186_Transcript_1/1_Conf_1.000	677	20	1.94E-61	NP_490749.1	92	239.58	166	153	hypothetical protein Y65B4BR.5
Locus_11860_Transcript_1/1_Conf_1.000	897	20	2.11E-31	XP_001892919.1	53	140.584	240	129	TPR Domain containing protein
Locus_11861_Transcript_1/1_Conf_1.000	524	20	3.22E-28	ACI49081.1	67	128.257	137	93	hypothetical protein Cbre_JD11.005
Locus_11862_Transcript_1/1_Conf_1.000	201	0							
Locus_11863_Transcript_1/1_Conf_1.000	297	0							
Locus_11864_Transcript_1/1_Conf_1.000	621	12	2.72E-45	NP_505034.1	79	185.652	204	163	hypothetical protein F40A3.7
Locus_11865_Transcript_1/1_Conf_1.000	2213	20	5.02E-88	XP_001893141.1	62	330.487	466	289	DEAD/DEAH box helicase family protein
Locus_11866_Transcript_1/1_Conf_1.000	650	2	2.68E-25	NP_492698.2	54	119.398	183	100	hypothetical protein ZC247.1
Locus_11867_Transcript_1/1_Conf_1.000	389	2	1.91E-13	NP_491039.1	55	78.9518	118	65	hypothetical protein Y71F9B.1
Locus_11868_Transcript_1/1_Conf_1.000	555	20	2.01E-16	NP_496567.2	48	89.3521	184	90	hypothetical protein Y17G7B.11
Locus_11869_Transcript_1/1_Conf_1.000	526	2	3.18E-23	XP_001895430.1	53	111.694	186	100	hypothetical protein Bm1_19875
Locus_1187_Transcript_1/1_Conf_1.000	825	0							
Locus_11870_Transcript_1/1_Conf_1.000	661	20	6.91E-85	NP_510667.2	87	317.39	217	189	TBC (Tre-2/Bub2/Cdc16) domain family member (tbc-4)
Locus_11871_Transcript_1/2_Conf_1.000	860	9	7.20E-42	XP_002642351.1	66	175.252	170	113	Hypothetical protein CBG18348
Locus_11871_Transcript_2/2_Conf_1.000	860	9	1.60E-41	XP_002642351.1	66	174.096	170	113	Hypothetical protein CBG18348
Locus_11872_Transcript_1/1_Conf_1.000	307	20	4.68E-36	NP_490795.2	82	154.066	102	84	Nematode AStacin protease family member (nas-30)
Locus_11873_Transcript_1/1_Conf_1.000	302	20	1.33E-30	XP_002634824.1	82	135.961	86	71	Hypothetical protein CBG13932

Locus_11874_Transcript_1/1_Conf_1.000	265	20	3.63E-36	NP_505689.1	91	154.451	87	80	hypothetical protein Y32F6B.1
Locus_11875_Transcript_1/1_Conf_1.000	764	20	1.17E-18	ABB53347.1	51	97.8265	183	95	secreted protein 5 precursor
Locus_11876_Transcript_1/1_Conf_1.000	221	0							
Locus_11877_Transcript_1/1_Conf_1.000	194	20	5.47E-24	NP_500274.2	92	114.005	63	58	hypothetical protein Y54G2A.4
Locus_11878_Transcript_1/1_Conf_1.000	333	9	8.87E-19	NP_509416.2	77	96.6709	103	80	hypothetical protein F55E10.7
Locus_11879_Transcript_1/1_Conf_1.000	141	0							
Locus_1188_Transcript_1/1_Conf_1.000	817	20	1.77E-47	XP_002637575.1	60	193.741	269	162	C. briggsae CBR-EHBP-1 protein
Locus_11880_Transcript_1/1_Conf_1.000	200	0							
Locus_11881_Transcript_1/1_Conf_1.000	615	20	7.66E-08	NP_001021233.1	76	61.2326	47	36	hypothetical protein D2045.9
Locus_11882_Transcript_1/1_Conf_1.000	1167	20	9.61E-153	NP_504650.1	78	544.273	389	304	hypothetical protein W01A11.1
Locus_11883_Transcript_1/1_Conf_1.000	481	0							
Locus_11884_Transcript_1/1_Conf_1.000	166	0							
Locus_11885_Transcript_1/1_Conf_1.000	1563	20	0	AAV27339.1	80	653.67	521	420	Hc38
Locus_11886_Transcript_1/1_Conf_1.000	434	0							
Locus_11887_Transcript_1/1_Conf_1.000	342	20	1.31E-33	NP_502290.1	98	145.976	70	69	hypothetical protein F11A10.2

Locus_11888_Transcript_1/1_Conf_1.000	429	20	8.58E-38	NP_001040974.1	81	159.844	141	115	hypothetical protein K09B11.9
Locus_11889_Transcript_1/1_Conf_1.000	491	20	1.63E-36	CAA21622.4	62	155.606	176	110	C. elegans protein Y43F8C.12, partially confirmed by transcript evidence
Locus_1189_Transcript_1/1_Conf_1.000	1045	20	6.25E-129	XP_002644986.1	86	464.922	316	273	C. briggsae CBR-TAG-320 protein
Locus_11890_Transcript_1/1_Conf_1.000	257	3	1.19E-10	XP_002632648.1	69	69.707	59	41	Hypothetical protein CBG21570
Locus_11891_Transcript_1/1_Conf_1.000	223	0							
Locus_11892_Transcript_1/1_Conf_1.000	646	11	3.33E-36	NP_501400.1	67	155.606	192	130	hypothetical protein F35H10.10
Locus_11893_Transcript_1/1_Conf_1.000	581	20	3.00E-61	XP_002648243.1	85	238.424	163	139	Hypothetical protein CBG24373
Locus_11894_Transcript_1/1_Conf_1.000	595	0							
Locus_11895_Transcript_1/1_Conf_1.000	681	3	1.54E-05	XP_002648983.1	83	53.9138	37	31	Hypothetical protein CBG21314
Locus_11896_Transcript_1/1_Conf_1.000	783	20	2.46E-51	NP_001024128.1	77	206.453	164	127	EEA1 (Early Endosome Antigen, Rab effector) homolog family member (eea-1)

Locus_11897_Transcript_1/1_Conf_1.000	550	20	5.55E-64	NP_491714.1	76	247.284	181	138	Aurora/Ipl1 Related kinase family member (air-2)
Locus_11898_Transcript_1/1_Conf_1.000	739	2	2.70E-41	NP_499274.3	61	172.94	212	131	Connector/eNhancer of KSR family member (cnk-1)
Locus_11899_Transcript_1/1_Conf_1.000	1098	20	3.42E-72	XP_001898576.1	64	276.559	303	195	Fructosamine kinase family protein
Locus_119_Transcript_1/10_Conf_0.167	708	20	9.80E-99	CAD22112.1	97	363.614	200	195	tubulin

Locus_119_Transcript_10/10_Conf_0.542	2840	20	0	XP_002646073.1	96	807.364	441	424	Hypothetical protein CBG07939
Locus_119_Transcript_2/10_Conf_0.167	666	20	5.04E-99	CAD22112.1	97	364.385	198	194	tubulin
Locus_119_Transcript_3/10_Conf_0.542	2940	20	0	XP_002646073.1	96	807.364	441	424	Hypothetical protein CBG07939

Locus_119_Transcript_4/10_Conf_0.542	2940	20	0	XP_002646073.1	96	807.364	441	424	Hypothetical protein CBG07939
Locus_119_Transcript_5/10_Conf_0.083	1395	20	4.88E-125	CBL87050.1	79	452.595	334	265	C. elegans protein C50F4.14b, confirmed by transcript evidence
Locus_119_Transcript_6/10_Conf_0.083	1395	20	4.88E-125	CBL87050.1	79	452.595	334	265	C. elegans protein C50F4.14b, confirmed by transcript evidence
Locus_119_Transcript_7/10_Conf_0.542	2840	20	0	XP_002646073.1	96	809.29	441	424	Hypothetical protein CBG07939
Locus_119_Transcript_8/10_Conf_0.292	1992	20	0	XP_002646073.1	95	655.596	360	344	Hypothetical protein CBG07939

Locus_119_Transcript_9/10_Conf_0.292	1992	20	0	XP_002646073.1	95	653.67	360	344	Hypothetical protein CBG07939
Locus_1190_Transcript_1/1_Conf_1.000	362	7	8.28E-25	NP_001022814.1	70	116.701	119	84	ODoRant response abnormal family member (odr-4)
Locus_11900_Transcript_1/3_Conf_0.600	666	20	6.19E-81	NP_491093.1	93	304.294	174	163	RNA Polymerase II (B) subunit family member (rpb-7)
Locus_11900_Transcript_2/3_Conf_0.400	353	20	2.59E-50	NP_491093.1	96	201.445	115	111	RNA Polymerase II (B) subunit family member (rpb-7)

Locus_11900_Transcript_3/3_Conf_0.600	646	20	5.80E-81	NP_491093.1	93	304.294	174	163	RNA Polymerase II (B) subunit family member (rpb-7)
Locus_11901_Transcript_1/1_Conf_1.000	293	2	6.25E-20	EFO16669.1	71	100.523	96	69	BTB/POZ domain-containing protein
Locus_11902_Transcript_1/2_Conf_1.000	277	0							
Locus_11902_Transcript_2/2_Conf_1.000	283	0							
Locus_11903_Transcript_1/1_Conf_1.000	347	0							
Locus_11904_Transcript_1/1_Conf_1.000	379	2	4.46E-10	XP_002630789.1	55	67.781	113	63	Hypothetical protein CBG02486
Locus_11905_Transcript_1/1_Conf_1.000	305	0							
Locus_11906_Transcript_1/1_Conf_1.000	134	0							
Locus_11907_Transcript_1/1_Conf_1.000	1126	20	5.49E-73	NP_491118.2	61	279.256	367	226	hypothetical protein Y54E10A.11
Locus_11908_Transcript_1/1_Conf_1.000	318	20	1.64E-28	NP_500157.2	75	129.028	106	80	Cleavage and Polyadenylation Specificity Factor family member (cpsf-1)
Locus_11909_Transcript_1/1_Conf_1.000	115	0							
Locus_1191_Transcript_1/1_Conf_1.000	455	20	1.20E-23	NP_509947.1	68	112.849	117	80	hypothetical protein T04F8.2
Locus_11910_Transcript_1/1_Conf_1.000	1299	20	8.65E-12	XP_002151267.1	50	76.2554	114	58	histone acetyltransferase, putative
Locus_11911_Transcript_1/1_Conf_1.000	185	0							
Locus_11912_Transcript_1/1_Conf_1.000	165	0							
Locus_11913_Transcript_1/1_Conf_1.000	696	20	1.15E-27	XP_001902469.1	54	127.487	231	125	G protein pathway suppressor 1

Locus_11914_Transcript_1/2_Conf_1.000	1426	20	3.73E-11	XP_002643523.1	45	74.3294	183	83	Hypothetical protein CBG16200
Locus_11914_Transcript_2/2_Conf_1.000	1401	20	8.09E-19	NP_741906.1	40	99.7525	509	206	Maternal Effect Sterile family member (mes-1)

Locus_11915_Transcript_1/1_Conf_1.000	1677	20	1.25E-40	AAA93318.1	56	172.555	278	156	serine/threonine kinase
Locus_11916_Transcript_1/2_Conf_1.000	763	0							
Locus_11916_Transcript_2/2_Conf_1.000	288	0							
Locus_11917_Transcript_1/1_Conf_1.000	299	0							
Locus_11918_Transcript_1/1_Conf_1.000	785	20	3.77E-76	XP_002639317.1	72	288.886	250	181	C. briggsae CBR-ABT-2 protein
Locus_11919_Transcript_1/1_Conf_1.000	305	0							
Locus_1192_Transcript_1/3_Conf_0.714	752	0							
Locus_1192_Transcript_2/3_Conf_0.714	804	0							
Locus_1192_Transcript_3/3_Conf_0.714	752	0							
Locus_11920_Transcript_1/1_Conf_1.000	836	20	1.31E-85	XP_002633781.1	73	320.472	278	205	Hypothetical protein CBG03472
Locus_11921_Transcript_1/2_Conf_1.000	492	20	2.95E-38	ACI49052.1	70	161.384	144	102	hypothetical protein Cbre_JD08.004
Locus_11921_Transcript_2/2_Conf_1.000	492	20	6.57E-38	ACI49052.1	70	160.229	144	102	hypothetical protein Cbre_JD08.004
Locus_11922_Transcript_1/1_Conf_1.000	996	20	1.01E-64	NP_504952.1	76	251.521	224	171	hypothetical protein F19F10.9
Locus_11923_Transcript_1/1_Conf_1.000	362	20	7.46E-42	NP_510509.2	88	173.326	94	83	hypothetical protein F09B12.3
Locus_11924_Transcript_1/1_Conf_1.000	175	0							

Locus_11925_Transcript_1/1_Conf_1.000	560	20	1.01E-60	ACI49101.1	77	236.498	189	146	hypothetical protein Cbre_JD13.003
Locus_11926_Transcript_1/1_Conf_1.000	498	3	8.29E-09	XP_002630376.1	67	63.5438	78	53	Hypothetical protein CBG04315
Locus_11927_Transcript_1/1_Conf_1.000	159	0							
Locus_11928_Transcript_1/2_Conf_1.000	638	0							
Locus_11928_Transcript_2/2_Conf_1.000	438	0							
Locus_11929_Transcript_1/1_Conf_1.000	884	0							
Locus_1193_Transcript_1/1_Conf_1.000	995	20	5.93E-166	ABC86838.1	93	587.8	331	311	depsiphilin
Locus_11930_Transcript_1/1_Conf_1.000	246	0							
Locus_11931_Transcript_1/1_Conf_1.000	175	4	7.26E-13	XP_002645979.1	78	77.0258	56	44	C. briggsae CBR-NHR-48 protein
Locus_11932_Transcript_1/1_Conf_1.000	482	0							
Locus_11933_Transcript_1/1_Conf_1.000	567	7	1.78E-15	XP_001898423.1	47	86.2705	189	90	Mediator complex subunit rgr-1
Locus_11934_Transcript_1/1_Conf_1.000	522	20	1.76E-34	XP_002642109.1	73	149.058	132	97	C. briggsae CBR-CDH-4 protein
Locus_11935_Transcript_1/2_Conf_1.000	339	0							
Locus_11935_Transcript_2/2_Conf_1.000	470	0							
Locus_11936_Transcript_1/1_Conf_1.000	681	0							
Locus_11937_Transcript_1/1_Conf_1.000	302	0							
Locus_11938_Transcript_1/1_Conf_1.000	315	5	9.10E-11	ADG63133.1	59	70.0922	105	62	calcium-dependent apyrase
Locus_11939_Transcript_1/1_Conf_1.000	704	20	4.72E-69	NP_508706.2	69	265.003	247	172	NCK (Non-Catalytic region of tyrosine Kinase) adaptor protein family member (nck-1)
Locus_1194_Transcript_1/1_Conf_1.000	1108	20	2.06E-24	ACI49169.1	62	117.857	148	92	hypothetical protein Csp3_JD01.001
Locus_11940_Transcript_1/1_Conf_1.000	311	9	5.01E-14	XP_002632974.1	61	80.8777	105	65	Hypothetical protein CBG21734

Locus_11941_Transcript_1/1_Conf_1.000	896	20	4.96E-57	XP_002630704.1	59	225.713	304	180	C. briggsae CBR-PINK-1 protein
Locus_11942_Transcript_1/1_Conf_1.000	556	20	5.06E-52	NP_501797.1	79	207.608	141	112	DiHydroPyrimidinase family member (dhp-2)
Locus_11943_Transcript_1/1_Conf_1.000	278	0							
Locus_11944_Transcript_1/1_Conf_1.000	362	0							
Locus_11945_Transcript_1/1_Conf_1.000	248	14	6.55E-14	ACT34056.1	92	80.4925	50	46	glutamate dehydrogenase
Locus_11946_Transcript_1/1_Conf_1.000	352	0							
Locus_11947_Transcript_1/1_Conf_1.000	390	20	1.04E-27	XP_002646193.1	72	126.331	103	75	Hypothetical protein CBG24498
Locus_11948_Transcript_1/2_Conf_1.000	1448	2	4.20E-18	XP_001891812.1	52	97.4413	218	114	hypothetical protein Bm1_01480
Locus_11948_Transcript_2/2_Conf_1.000	1448	2	4.20E-18	XP_001891812.1	52	97.4413	218	114	hypothetical protein Bm1_01480
Locus_11949_Transcript_1/1_Conf_1.000	359	3	1.02E-14	XP_002647546.1	60	83.1889	102	62	C. briggsae CBR-PME-5 protein
Locus_1195_Transcript_1/1_Conf_1.000	439	20	2.22E-54	NP_491454.2	84	214.927	132	111	hypothetical protein F54D7.2
Locus_11950_Transcript_1/1_Conf_1.000	538	20	3.93E-72	XP_002634910.1	84	274.248	172	145	Hypothetical protein CBG22508
Locus_11951_Transcript_1/1_Conf_1.000	728	0							

Locus_11952_Transcript_1/1_Conf_1.000	384	20	3.62E-12	NP_496283.1	60	74.7146	94	57	Cell-death-Related Nuclease family member (crn-3)
Locus_11953_Transcript_1/1_Conf_1.000	819	0							
Locus_11954_Transcript_1/1_Conf_1.000	330	0							
Locus_11955_Transcript_1/1_Conf_1.000	309	0							
Locus_11956_Transcript_1/1_Conf_1.000	228	0							
Locus_11957_Transcript_1/1_Conf_1.000	366	20	5.51E-21	XP_002634905.1	84	103.99	73	62	Hypothetical protein CBG22501
Locus_11958_Transcript_1/1_Conf_1.000	211	0							
Locus_11959_Transcript_1/1_Conf_1.000	454	20	3.72E-33	EFO18399.1	74	144.436	136	101	geranylgeranyl pyrophosphate synthetase
Locus_1196_Transcript_1/1_Conf_1.000	391	18	1.19E-15	NP_001122782.1	62	86.2705	123	77	hypothetical protein F58G6.9
Locus_11960_Transcript_1/1_Conf_1.000	147	7	2.49E-08	XP_002641319.1	72	62.003	48	35	Hypothetical protein CBG24620
Locus_11961_Transcript_1/1_Conf_1.000	430	20	7.46E-58	NP_491864.2	90	226.483	140	126	hypothetical protein K06A5.8
Locus_11962_Transcript_1/1_Conf_1.000	713	20	5.10E-87	XP_002637195.1	81	324.709	233	189	C. briggsae CBR-LIG-1 protein
Locus_11963_Transcript_1/1_Conf_1.000	198	20	9.61E-13	EFO27986.1	73	76.6406	60	44	hypothetical protein LOAG_00494

Locus_11964_Transcript_1/1_Conf_1.000	365	20	2.75E-20	XP_002639618.1	69	101.679	110	76	Hypothetical protein CBG12331
Locus_11965_Transcript_1/1_Conf_1.000	321	20	1.33E-46	NP_492433.1	87	189.119	106	93	HomoGentisate Oxidase family member (hgo-1)
Locus_11966_Transcript_1/1_Conf_1.000	352	20	2.36E-27	XP_002640036.1	74	125.176	115	86	Hypothetical protein CBG12508
Locus_11967_Transcript_1/1_Conf_1.000	551	0							
Locus_11968_Transcript_1/1_Conf_1.000	205	0							
Locus_11969_Transcript_1/1_Conf_1.000	303	20	1.08E-24	NP_508181.1	81	116.316	82	67	hypothetical protein F53H8.3
Locus_1197_Transcript_1/1_Conf_1.000	2172	6	6.52E-32	XP_002639900.1	44	144.05	510	227	C. briggsae CBR-APR-1 protein
Locus_11970_Transcript_1/1_Conf_1.000	713	3	9.84E-06	AAZ42336.1	66	54.6842	57	38	twitchin kinase
Locus_11971_Transcript_1/1_Conf_1.000	334	2	4.73E-04	XP_001894907.1	71	47.7506	45	32	RNA binding protein
Locus_11972_Transcript_1/1_Conf_1.000	1334	7	3.94E-92	XP_002631715.1	60	343.199	450	273	Hypothetical protein CBG20916
Locus_11973_Transcript_1/1_Conf_1.000	693	15	6.71E-20	CAN99691.2	50	101.679	222	112	C. elegans protein F54B3.1b, partially confirmed by transcript evidence
Locus_11974_Transcript_1/1_Conf_1.000	530	3	9.51E-07	Q60YF6.3	51	56.9954	102	53	Mediator of RNA polymerase II transcription subunit 29
Locus_11975_Transcript_1/1_Conf_1.000	278	0							
Locus_11976_Transcript_1/1_Conf_1.000	689	4	3.49E-13	NP_001023362.1	72	79.337	103	75	Temporarily Assigned Gene name family member (tag-261)

Locus_11977_Transcript_1/3_Conf_0.600	421	20	2.29E-30	NP_492796.1	72	135.191	117	85	hypothetical protein C34B2.6
Locus_11977_Transcript_2/3_Conf_0.600	526	20	3.51E-30	NP_492796.1	74	134.806	113	84	hypothetical protein C34B2.6

Locus_11977_Transcript_3/3_Conf_0.600	421	20	2.29E-30	NP_492796.1	72	135.191	117	85	hypothetical protein C34B2.6
Locus_11978_Transcript_1/1_Conf_1.000	387	20	2.16E-49	A8XV40.2	85	198.364	128	110	Probable spastin homolog spas-1
Locus_11979_Transcript_1/1_Conf_1.000	938	20	5.02E-79	XP_002636597.1	87	298.901	194	169	C. briggsae CBR-SKP-1 protein
Locus_1198_Transcript_1/1_Conf_1.000	1408	20	0	XP_002642332.1	91	777.704	468	429	Hypothetical protein CBG18327
Locus_11980_Transcript_1/1_Conf_1.000	231	8	2.99E-14	NP_502273.2	81	81.6481	74	60	UNCoordinated family member (unc-22)

Locus_11981_Transcript_1/1_Conf_1.000	217	3	8.24E-17	XP_001900400.1	73	90.1225	69	51	Zinc finger, C2H2 type family protein
Locus_11982_Transcript_1/1_Conf_1.000	363	20	2.10E-28	NP_507513.2	68	128.642	120	82	hypothetical protein E01B7.1
Locus_11983_Transcript_1/1_Conf_1.000	602	20	2.15E-12	XP_002633896.1	51	76.2554	208	107	Hypothetical protein CBG19958
Locus_11984_Transcript_1/1_Conf_1.000	178	0							
Locus_11985_Transcript_1/1_Conf_1.000	620	0							
Locus_11986_Transcript_1/1_Conf_1.000	281	0							
Locus_11987_Transcript_1/1_Conf_1.000	638	6	2.55E-25	EFO27989.1	56	119.398	148	83	hypothetical protein LOAG_00497
Locus_11988_Transcript_1/1_Conf_1.000	856	0							
Locus_11989_Transcript_1/2_Conf_1.000	558	0							
Locus_11989_Transcript_2/2_Conf_1.000	561	0							
Locus_1199_Transcript_1/2_Conf_1.000	2933	20	0	NP_001040844.1	68	730.709	792	540	Tousled-Like Kinase family member (tlk-1)
Locus_1199_Transcript_2/2_Conf_1.000	2912	20	0	NP_001040844.1	68	733.791	785	541	Tousled-Like Kinase family member (tlk-1)
Locus_11990_Transcript_1/1_Conf_1.000	453	0							
Locus_11991_Transcript_1/1_Conf_1.000	791	20	1.00E-92	NP_495958.1	80	343.969	257	208	yeast SEC homolog family member (sec-5)
Locus_11992_Transcript_1/1_Conf_1.000	374	0							
Locus_11993_Transcript_1/1_Conf_1.000	296	0							
Locus_11994_Transcript_1/1_Conf_1.000	292	0							
Locus_11995_Transcript_1/1_Conf_1.000	363	2	6.78E-11	XP_002635317.1	62	70.4774	80	50	C. briggsae CBR-TAG-196 protein
Locus_11996_Transcript_1/1_Conf_1.000	754	4	1.81E-24	NP_508542.1	85	117.087	121	103	hypothetical protein C15C7.5
Locus_11997_Transcript_1/1_Conf_1.000	614	20	2.09E-74	NP_491711.2	78	282.337	205	161	hypothetical protein C34G6.1
Locus_11998_Transcript_1/1_Conf_1.000	304	20	4.55E-31	XP_002424477.1	94	137.502	79	75	Surfeit locus protein, putative

Locus_11999_Transcript_1/1_Conf_1.000	236	0							
Locus_12_Transcript_1/1_Conf_1.000	1554	20	7.66E-106	NP_492481.1	95	389.037	208	199	RAB family member (rab-5)
Locus_120_Transcript_1/8_Conf_0.410	575	20	3.03E-26	AAO63576.1	54	122.094	199	108	secreted protein 4 precursor
Locus_120_Transcript_2/8_Conf_0.308	404	16	9.93E-10	AAO63576.1	51	66.6254	137	71	secreted protein 4 precursor
Locus_120_Transcript_3/8_Conf_0.179	166	0							
Locus_120_Transcript_4/8_Conf_0.179	179	0							
Locus_120_Transcript_5/8_Conf_0.436	584	20	5.42E-26	AAO63576.1	54	121.324	199	108	secreted protein 4 precursor
Locus_120_Transcript_6/8_Conf_0.462	584	20	3.51E-25	AAO63576.1	53	118.627	199	106	secreted protein 4 precursor
Locus_120_Transcript_8/8_Conf_0.462	584	20	3.18E-26	AAO63576.1	54	122.094	199	108	secreted protein 4 precursor
Locus_1200_Transcript_1/2_Conf_1.000	705	7	1.94E-06	XP_001897045.1	52	56.9954	159	84	hypothetical protein Bm1_27970
Locus_1200_Transcript_2/2_Conf_1.000	917	20	1.02E-28	NP_498671.2	80	131.724	83	67	Uridine PhosPhorylase family member (upp-1)
Locus_12000_Transcript_1/1_Conf_1.000	415	2	6.56E-06	XP_002637729.1	57	53.9138	84	48	Hypothetical protein CBG11595
Locus_12001_Transcript_1/1_Conf_1.000	1113	4	4.65E-16	EFO27437.1	45	90.1225	341	156	origin recognition complex subunit 5
Locus_12002_Transcript_1/1_Conf_1.000	573	0							
Locus_12003_Transcript_1/1_Conf_1.000	183	0							
Locus_12004_Transcript_1/1_Conf_1.000	140	0							
Locus_12005_Transcript_1/1_Conf_1.000	345	0							
Locus_12006_Transcript_1/1_Conf_1.000	249	0							
Locus_12007_Transcript_1/2_Conf_1.000	1111	1	1.82E-04	NP_498338.1	53	51.6026	76	41	hypothetical protein F42A10.5
Locus_12007_Transcript_2/2_Conf_1.000	1105	1	1.38E-04	NP_498338.1	55	51.9878	76	42	hypothetical protein F42A10.5
Locus_12008_Transcript_1/1_Conf_1.000	138	0							

Locus_12009_Transcript_1/1_Conf_1.000	805	20	3.42E-27	NP_501545.1	59	126.331	267	159	RADiation sensitivity abnormal/yeast RAD-related family member (rad-26)
Locus_1201_Transcript_1/1_Conf_1.000	930	20	1.95E-67	EFO26146.1	72	260.381	237	172	hypothetical protein LOAG_02340
Locus_12010_Transcript_1/1_Conf_1.000	634	5	6.44E-13	XP_002639170.1	72	78.1814	80	58	Hypothetical protein CBG03709
Locus_12011_Transcript_1/1_Conf_1.000	415	20	1.14E-50	CAA84656.2	84	202.601	132	112	C. elegans protein F10F2.2, confirmed by transcript evidence
Locus_12012_Transcript_1/1_Conf_1.000	621	0							
Locus_12013_Transcript_1/1_Conf_1.000	254	0							
Locus_12014_Transcript_1/2_Conf_1.000	440	3	2.03E-15	NP_492118.1	56	85.5001	146	82	hypothetical protein D2030.3
Locus_12014_Transcript_2/2_Conf_1.000	440	3	1.55E-15	NP_492118.1	56	85.8853	146	83	hypothetical protein D2030.3
Locus_12015_Transcript_1/1_Conf_1.000	428	20	5.04E-46	XP_002743343.1	100	187.193	96	96	PREDICTED: hypothetical protein LOC100413255
Locus_12016_Transcript_1/1_Conf_1.000	334	3	4.12E-16	XP_002631490.1	71	87.8113	70	50	C. briggsae CBR-EGG-3 protein
Locus_12017_Transcript_1/1_Conf_1.000	740	20	6.09E-110	NP_498645.1	80	400.979	246	198	MUscle Positioning family member (mup-4)
Locus_12018_Transcript_1/1_Conf_1.000	217	0							
Locus_12019_Transcript_1/1_Conf_1.000	392	0							
Locus_1202_Transcript_1/1_Conf_1.000	179	20	1.72E-22	NP_491853.2	94	108.997	57	54	SyNapTotagmin family member (snt-4)
Locus_12020_Transcript_1/1_Conf_1.000	152	0							

Locus_12021_Transcript_1/1_Conf_1.000	486	8	4.74E-44	XP_002631275.1	66	180.644	163	108	Hypothetical protein CBG03085
Locus_12022_Transcript_1/1_Conf_1.000	274	20	6.34E-33	NP_498117.3	86	143.665	91	79	Gro-1 OPeron gene family member (gop-1)
Locus_12023_Transcript_1/1_Conf_1.000	393	20	2.02E-18	NP_494788.2	58	95.5153	137	80	related to yeast Vacuolar Protein Sorting factor family member (vps-18)
Locus_12024_Transcript_1/1_Conf_1.000	305	0							
Locus_12025_Transcript_1/1_Conf_1.000	863	20	1.27E-62	BAE91269.1	100	244.202	116	116	unnamed protein product
Locus_12026_Transcript_1/1_Conf_1.000	309	20	2.32E-19	XP_002633895.1	69	98.5969	92	64	C. briggsae CBR-SAND-1 protein
Locus_12027_Transcript_1/1_Conf_1.000	162	0							
Locus_12028_Transcript_1/1_Conf_1.000	585	0							
Locus_12029_Transcript_1/1_Conf_1.000	529	0							
Locus_1203_Transcript_1/2_Conf_1.000	3600	20	1.36E-64	NP_497706.1	45	253.447	1002	459	hypothetical protein F59A2.6
Locus_1203_Transcript_2/2_Conf_1.000	3525	20	3.89E-56	NP_497706.1	44	225.328	984	436	hypothetical protein F59A2.6
Locus_12030_Transcript_1/1_Conf_1.000	430	0							
Locus_12031_Transcript_1/1_Conf_1.000	592	20	5.21E-24	XP_001892273.1	54	114.775	202	110	hypothetical protein
Locus_12032_Transcript_1/1_Conf_1.000	210	20	1.12E-13	XP_002755896.1	70	79.7221	68	48	PREDICTED: dnaJ homolog subfamily A member 3, mitochondrial
Locus_12033_Transcript_1/1_Conf_1.000	407	2	2.20E-09	NP_501176.1	80	65.4698	47	38	hypothetical protein T12B3.3
Locus_12034_Transcript_1/1_Conf_1.000	250	3	1.84E-16	AAC39119.1	67	88.9669	83	56	low-affinity peptide transporter
Locus_12035_Transcript_1/1_Conf_1.000	277	0							
Locus_12036_Transcript_1/1_Conf_1.000	1417	20	4.58E-78	NP_508977.1	57	296.59	402	230	hypothetical protein F13D11.1
Locus_12037_Transcript_1/1_Conf_1.000	269	9	6.66E-06	CBM41222.1	50	53.9138	63	32	C. elegans protein T10G3.3b, partially confirmed by transcript evidence
Locus_12038_Transcript_1/1_Conf_1.000	203	0							
Locus_12039_Transcript_1/1_Conf_1.000	574	10	1.54E-54	XP_002629691.1	74	216.083	194	144	Hypothetical protein CBG00912

Locus_1204_Transcript_1/2_Conf_1.000	4436	20	0	NP_001021649.1	81	1652.88	1207	982	HaMmeRhead embryonic lethal family member (hmr-1)
Locus_1204_Transcript_2/2_Conf_1.000	4558	20	0	NP_001021649.1	81	1652.88	1207	982	HaMmeRhead embryonic lethal family member (hmr-1)
Locus_12040_Transcript_1/1_Conf_1.000	296	0							
Locus_12041_Transcript_1/1_Conf_1.000	975	20	5.20E-167	XP_001898368.1	93	591.267	324	303	cpsf3-prov protein
Locus_12042_Transcript_1/1_Conf_1.000	824	8	3.52E-35	CAX51629.1	57	152.91	266	152	C. elegans protein C48B4.4d, partially confirmed by transcript evidence
Locus_12043_Transcript_1/1_Conf_1.000	794	20	1.16E-96	CAA45963.1	100	357.066	208	208	BBC1
Locus_12044_Transcript_1/1_Conf_1.000	835	20	4.68E-75	NP_495741.2	88	285.419	210	186	hypothetical protein K01C8.1
Locus_12045_Transcript_1/1_Conf_1.000	171	0							
Locus_12046_Transcript_1/1_Conf_1.000	308	20	7.46E-34	XP_002636068.1	79	146.747	102	81	Hypothetical protein CBG01308
Locus_12047_Transcript_1/1_Conf_1.000	967	20	2.03E-22	XP_001702729.1	70	110.923	100	70	ubiquitin-related modifier
Locus_12048_Transcript_1/1_Conf_1.000	380	0							

Locus_12049_Transcript_1/1_Conf_1.000	240	20	1.57E-15	NP_510155.3	73	85.8853	78	57	PIP Kinase family member (ppk-3)
Locus_1205_Transcript_1/1_Conf_1.000	205	7	3.40E-10	EFO26077.1	80	68.1662	51	41	leucine Rich Repeat family protein
Locus_12050_Transcript_1/1_Conf_1.000	2566	20	3.31E-179	XP_002639041.1	73	633.639	596	437	C. briggsae CBR-XNP-1 protein
Locus_12051_Transcript_1/1_Conf_1.000	750	20	1.14E-18	NP_499886.1	50	97.8265	196	98	hypothetical protein R02D3.7
Locus_12052_Transcript_1/1_Conf_1.000	645	20	6.67E-61	NP_498248.2	67	237.654	214	144	hypothetical protein Y37B11A.2
Locus_12053_Transcript_1/1_Conf_1.000	188	0							
Locus_12054_Transcript_1/1_Conf_1.000	687	20	8.18E-71	NP_504753.3	77	270.781	239	185	UNCoordinated family member (unc-68)
Locus_12055_Transcript_1/1_Conf_1.000	464	20	9.22E-72	XP_001900091.1	90	272.707	153	139	U5 small nuclear ribonucleoprotein 200 kDa helicase
Locus_12056_Transcript_1/1_Conf_1.000	688	20	2.90E-76	CAR63592.1	82	288.886	194	160	hypothetical protein

Locus_12057_Transcript_1/1_Conf_1.000	214	20	2.48E-21	NP_499949.2	87	105.145	71	62	Gut on EXterior family member (gex-2)
Locus_12058_Transcript_1/1_Conf_1.000	280	20	5.14E-43	NP_492127.1	95	177.178	93	89	Low-density lipoprotein Receptor Related family member (lrp-1)
Locus_12059_Transcript_1/1_Conf_1.000	619	20	4.21E-46	EFO25304.1	70	188.348	211	149	leucine Rich Repeat family protein
Locus_1206_Transcript_1/4_Conf_0.625	596	20	1.59E-20	XP_001895554.1	56	103.219	158	90	SWIRM domain containing protein
Locus_1206_Transcript_2/4_Conf_0.625	592	20	1.46E-26	XP_001895554.1	62	123.25	155	97	SWIRM domain containing protein
Locus_1206_Transcript_3/4_Conf_0.625	732	20	8.83E-29	EFO20641.1	63	131.339	154	98	hypothetical protein LOAG_07849

Locus_1206_Transcript_4/4_Conf_0.625	592	20	4.12E-29	EFO20641.1	63	131.724	156	99	hypothetical protein LOAG_07849
Locus_12060_Transcript_1/1_Conf_1.000	580	20	1.23E-14	XP_001900371.1	51	83.5741	198	102	hypothetical protein
Locus_12061_Transcript_1/1_Conf_1.000	152	0							
Locus_12062_Transcript_1/1_Conf_1.000	755	20	6.33E-78	NP_506083.1	77	294.664	254	196	hypothetical protein F55C5.8
Locus_12063_Transcript_1/1_Conf_1.000	264	9	6.24E-12	NP_001022773.1	58	73.9442	107	63	Myc and Mondo-Like family member (mml-1)
Locus_12064_Transcript_1/1_Conf_1.000	1005	20	2.87E-91	EFO27641.1	75	339.732	333	251	symplekin
Locus_12065_Transcript_1/1_Conf_1.000	586	0							
Locus_12066_Transcript_1/1_Conf_1.000	653	0							
Locus_12067_Transcript_1/1_Conf_1.000	386	20	1.24E-28	XP_002643566.1	69	129.413	114	79	Hypothetical protein CBG16268
Locus_12068_Transcript_1/1_Conf_1.000	446	2	3.93E-06	XP_001900477.1	64	54.6842	57	37	HMG box family protein
Locus_12069_Transcript_1/1_Conf_1.000	286	3	2.47E-24	XP_002631432.1	90	115.161	76	69	Hypothetical protein CBG03290
Locus_1207_Transcript_1/1_Conf_1.000	199	1	1.94E-05	XP_001624571.1	73	52.373	42	31	predicted protein
Locus_12070_Transcript_1/1_Conf_1.000	502	20	3.92E-30	XP_002629838.1	86	134.42	83	72	Hypothetical protein CBG18727
Locus_12071_Transcript_1/1_Conf_1.000	350	0							
Locus_12072_Transcript_1/2_Conf_1.000	1412	7	1.86E-47	XP_002635238.1	58	194.897	258	151	Hypothetical protein CBG11482
Locus_12072_Transcript_2/2_Conf_1.000	1388	7	1.08E-47	XP_002635238.1	56	195.667	279	159	Hypothetical protein CBG11482

Locus_12073_Transcript_1/1_Conf_1.000	1207	20	3.07E-117	XP_001897522.1	81	426.402	306	248	Zinc knuckle family protein
Locus_12074_Transcript_1/2_Conf_1.000	538	20	7.22E-42	XP_002399529.1	75	173.711	140	105	tpr repeat nuclear phosphoprotein, putative
Locus_12074_Transcript_2/2_Conf_1.000	776	4	6.81E-30	CAX51623.1	61	135.191	202	125	C. elegans protein B0464.2d, partially confirmed by transcript evidence
Locus_12075_Transcript_1/1_Conf_1.000	183	0							
Locus_12076_Transcript_1/1_Conf_1.000	147	0							
Locus_12077_Transcript_1/1_Conf_1.000	1383	20	5.17E-143	NP_496090.1	76	512.301	435	333	hypothetical protein ZK1320.9
Locus_12078_Transcript_1/1_Conf_1.000	483	20	4.19E-24	XP_001899004.1	65	114.39	122	80	co-chaperone protein HscB, mitochondrial precursor
Locus_12079_Transcript_1/1_Conf_1.000	193	0							
Locus_1208_Transcript_1/1_Conf_1.000	610	20	5.58E-88	NP_508413.1	96	327.405	191	185	Ribosomal Protein, Large subunit family member (rpl-11.2)
Locus_12080_Transcript_1/1_Conf_1.000	1569	20	4.79E-164	XP_002634686.1	74	582.408	522	390	Hypothetical protein CBG19672
Locus_12081_Transcript_1/1_Conf_1.000	803	20	1.19E-64	NP_502781.1	84	250.751	224	190	hypothetical protein Y57G11C.4
Locus_12082_Transcript_1/1_Conf_1.000	1005	20	9.39E-34	EFO13829.1	65	148.673	156	102	hypothetical protein LOAG_14699
Locus_12083_Transcript_1/1_Conf_1.000	460	20	1.15E-10	EFO17978.1	69	69.707	49	34	dual specificity phosphatase

Locus_12084_Transcript_1/1_Conf_1.000	301	0							
Locus_12085_Transcript_1/2_Conf_1.000	475	0							
Locus_12085_Transcript_2/2_Conf_1.000	489	0							
Locus_12086_Transcript_1/1_Conf_1.000	161	0							
Locus_12087_Transcript_1/1_Conf_1.000	464	0							
Locus_12088_Transcript_1/1_Conf_1.000	776	0							
Locus_12089_Transcript_1/1_Conf_1.000	290	0							
Locus_1209_Transcript_1/1_Conf_1.000	779	20	1.17E-37	NP_494880.1	74	160.999	204	151	COLlagen family member (col-73)
Locus_12090_Transcript_1/1_Conf_1.000	1134	20	2.51E-57	NP_497893.1	76	227.254	185	141	hypothetical protein R07E5.1
Locus_12091_Transcript_1/2_Conf_1.000	195	0							
Locus_12091_Transcript_2/2_Conf_1.000	397	0							
Locus_12092_Transcript_1/1_Conf_1.000	814	0							
Locus_12093_Transcript_1/1_Conf_1.000	309	0							
Locus_12094_Transcript_1/1_Conf_1.000	428	20	2.42E-48	EFO18868.1	84	194.897	130	110	hypothetical protein LOAG_09629
Locus_12095_Transcript_1/1_Conf_1.000	134	0							
Locus_12096_Transcript_1/1_Conf_1.000	559	3	1.69E-15	NP_500893.2	84	86.2705	50	42	hypothetical protein K02B2.1
Locus_12097_Transcript_1/2_Conf_1.000	1557	3	1.52E-53	NP_498952.1	68	215.312	199	136	hypothetical protein F44E2.4
Locus_12097_Transcript_2/2_Conf_1.000	1554	3	1.52E-53	NP_498952.1	68	215.312	199	136	hypothetical protein F44E2.4
Locus_12098_Transcript_1/1_Conf_1.000	1068	20	4.85E-100	NP_495424.2	75	369.007	299	226	hypothetical protein F22D3.6
Locus_12099_Transcript_1/1_Conf_1.000	426	0							
Locus_121_Transcript_1/7_Conf_0.375	150	0							
Locus_121_Transcript_2/7_Conf_0.375	156	0							
Locus_121_Transcript_3/7_Conf_0.375	310	0							
Locus_121_Transcript_4/7_Conf_0.667	423	0							
Locus_121_Transcript_5/7_Conf_0.167	162	0							
Locus_121_Transcript_6/7_Conf_0.375	259	0							
Locus_121_Transcript_7/7_Conf_0.375	150	0							
Locus_1210_Transcript_1/1_Conf_1.000	736	6	1.09E-26	NP_500907.1	63	124.405	135	86	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-22)
Locus_12100_Transcript_1/1_Conf_1.000	360	0							
Locus_12101_Transcript_1/1_Conf_1.000	444	0							
Locus_12102_Transcript_1/1_Conf_1.000	532	20	3.16E-82	XP_002638801.1	89	307.76	177	159	Hypothetical protein CBG05158
Locus_12103_Transcript_1/1_Conf_1.000	1160	20	9.14E-55	XP_002632325.1	76	218.779	184	140	Hypothetical protein CBG00332

Locus_12104_Transcript_1/1_Conf_1.000	235	3	4.91E-25	XP_002644048.1	55	117.472	128	71	Hypothetical protein CBG17510
Locus_12105_Transcript_1/1_Conf_1.000	210	0							
Locus_12106_Transcript_1/1_Conf_1.000	438	20	8.76E-35	EFO24963.1	82	149.828	111	92	hypothetical protein LOAG_03520
Locus_12107_Transcript_1/1_Conf_1.000	358	20	9.17E-32	XP_002642780.1	75	139.813	115	87	Hypothetical protein CBG21174
Locus_12108_Transcript_1/1_Conf_1.000	287	20	1.31E-25	CAA22110.2	78	119.398	91	71	C. elegans protein Y75B8A.26, partially confirmed by transcript evidence
Locus_12109_Transcript_1/1_Conf_1.000	323	20	4.47E-18	XP_002637707.1	67	94.3597	107	72	Hypothetical protein CBG11572
Locus_1211_Transcript_1/1_Conf_1.000	1856	20	0	EFO19100.1	95	1095.49	605	575	U5 snRNP-specific protein
Locus_12110_Transcript_1/1_Conf_1.000	578	0							
Locus_12111_Transcript_1/1_Conf_1.000	406	0							
Locus_12112_Transcript_1/1_Conf_1.000	486	4	3.41E-26	XP_002639317.1	63	121.324	144	92	C. briggsae CBR-ABT-2 protein
Locus_12113_Transcript_1/1_Conf_1.000	390	4	2.10E-20	XP_002646179.1	65	102.064	125	82	Hypothetical protein CBG23745
Locus_12114_Transcript_1/1_Conf_1.000	1113	20	4.80E-21	XP_001892006.1	60	106.686	172	104	1300013D05Rik protein
Locus_12115_Transcript_1/1_Conf_1.000	182	0							

Locus_12116_Transcript_1/1_Conf_1.000	201	20	1.09E-24	NP_001822.2	100	116.316	66	66	clusterin isoform 1
Locus_12117_Transcript_1/1_Conf_1.000	1033	4	1.74E-22	ABS19466.2	46	111.309	305	142	Hypothetical protein F49D11.10
Locus_12118_Transcript_1/1_Conf_1.000	692	0							
Locus_12119_Transcript_1/1_Conf_1.000	657	0							
Locus_1212_Transcript_1/2_Conf_1.000	1732	6	1.80E-58	NP_494278.3	52	231.876	336	177	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-42)
Locus_1212_Transcript_2/2_Conf_1.000	1179	6	4.07E-58	NP_494278.3	52	229.95	324	171	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-42)
Locus_12120_Transcript_1/1_Conf_1.000	227	0							
Locus_12121_Transcript_1/1_Conf_1.000	257	20	4.07E-27	XP_001898425.1	89	124.405	85	76	RuvB-like 2
Locus_12122_Transcript_1/1_Conf_1.000	388	20	2.85E-09	NP_001007899.1	54	65.0846	96	52	methyltransferase like 9
Locus_12123_Transcript_1/1_Conf_1.000	343	20	2.72E-31	CBM41226.1	76	138.272	113	87	C. elegans protein T21C9.2b, confirmed by transcript evidence
Locus_12124_Transcript_1/1_Conf_1.000	408	20	5.32E-64	XP_002636978.1	92	246.899	134	124	Hypothetical protein CBG09461

Locus_12125_Transcript_1/1_Conf_1.000	496	20	9.42E-45	XP_001895465.1	70	182.956	164	115	EGF-like domain containing protein
Locus_12126_Transcript_1/1_Conf_1.000	236	20	1.34E-14	ADI61822.1	70	82.8037	77	54	endonuclease-reverse transcriptase
Locus_12127_Transcript_1/1_Conf_1.000	531	20	4.31E-47	XP_002633395.1	84	191.045	167	141	C. briggsae CBR-KIN-4 protein
Locus_12128_Transcript_1/1_Conf_1.000	510	20	3.03E-33	NP_504831.1	76	144.821	117	90	hypothetical protein C13F10.2
Locus_12129_Transcript_1/1_Conf_1.000	149	20	1.56E-10	NP_491508.2	79	69.3218	48	38	PHAryngeal gland Toxin-related family member (phat-1)
Locus_1213_Transcript_1/4_Conf_0.375	536	20	1.58E-30	XP_002630755.1	64	132.494	122	79	C. briggsae CBR-LYS-8 protein
Locus_1213_Transcript_2/4_Conf_0.250	234	0							
Locus_1213_Transcript_3/4_Conf_0.500	968	20	4.18E-60	XP_002630755.1	67	236.113	208	140	C. briggsae CBR-LYS-8 protein
Locus_1213_Transcript_4/4_Conf_0.500	962	20	1.28E-61	XP_002630755.1	67	241.121	206	140	C. briggsae CBR-LYS-8 protein
Locus_12130_Transcript_1/1_Conf_1.000	249	20	6.53E-14	XP_002631442.1	80	80.4925	81	65	Hypothetical protein CBG03304
Locus_12131_Transcript_1/1_Conf_1.000	592	0							
Locus_12132_Transcript_1/1_Conf_1.000	377	0							
Locus_12133_Transcript_1/1_Conf_1.000	411	0							
Locus_12134_Transcript_1/2_Conf_1.000	962								
Locus_12134_Transcript_2/2_Conf_1.000	978								
Locus_12135_Transcript_1/1_Conf_1.000	407	0							

Locus_12136_Transcript_1/1_Conf_1.000	880	20	1.23E-153	NP_494939.1	93	546.584	292	274	PhosphoLipase D family member (pld-1)
Locus_12137_Transcript_1/1_Conf_1.000	729	20	3.98E-45	NP_505512.3	65	152.14	195	128	AQuaPorin or aquaglyceroporin related family member (aqp-4)
Locus_12138_Transcript_1/1_Conf_1.000	757	20	1.05E-96	NP_502164.1	85	357.066	239	204	WHiTe (Drosophila) related ABC transporte family member (wht-2)
Locus_12139_Transcript_1/1_Conf_1.000	204	0							
Locus_1214_Transcript_1/2_Conf_1.000	493	20	5.93E-47	NP_499522.2	93	190.274	121	113	GBF1(Golgi-specific Brefeldin-A-resistant Factor 1) homolog family member (gbf-1)

Locus_1214_Transcript_2/2_Conf_1.000	493	20	5.93E-47	NP_499522.2	93	190.274	121	113	GBF1(Golgi-specific Brefeldin-A-resistant Factor 1) homolog family member (gbf-1)
Locus_12140_Transcript_1/1_Conf_1.000	1133	0							
Locus_12141_Transcript_1/1_Conf_1.000	409	5	3.38E-18	NP_491750.3	64	94.7449	134	87	hypothetical protein C27A12.9
Locus_12142_Transcript_1/1_Conf_1.000	463	1	8.49E-09	NP_498245.2	57	63.5438	142	81	related to Islet cell Diabetes Autoantigen family member (ida-1)
Locus_12143_Transcript_1/1_Conf_1.000	181	0							
Locus_12144_Transcript_1/1_Conf_1.000	1954	20	1.00E-60	NP_494841.3	49	239.58	643	316	hypothetical protein F10G7.10
Locus_12145_Transcript_1/1_Conf_1.000	751	20	2.86E-78	EFO16473.1	76	295.819	226	173	zinc finger protein
Locus_12146_Transcript_1/1_Conf_1.000	646	20	4.81E-35	XP_002640142.1	66	151.754	160	107	C. briggsae CBR-DBR-1 protein
Locus_12147_Transcript_1/1_Conf_1.000	558	20	2.26E-44	EFO25953.1	64	182.185	189	122	TK/Met protein kinase
Locus_12148_Transcript_1/1_Conf_1.000	345	20	2.90E-33	NP_498634.1	80	144.821	111	89	hypothetical protein T20B12.3

Locus_12149_Transcript_1/1_Conf_1.000	252	4	2.57E-13	XP_001894170.1	64	78.5666	82	53	Ribonucleases P/MRP protein subunit POP1 containing protein
Locus_1215_Transcript_1/3_Conf_0.600	1864	20	0	CAB40412.1	91	759.214	472	434	hexokinase
Locus_1215_Transcript_2/3_Conf_0.400	1728	20	0	CAB40412.1	94	750.74	448	423	hexokinase
Locus_1215_Transcript_3/3_Conf_0.600	1863	20	0	CAB40412.1	92	775.778	483	446	hexokinase
Locus_12150_Transcript_1/1_Conf_1.000	331	0							
Locus_12151_Transcript_1/1_Conf_1.000	575	0							
Locus_12152_Transcript_1/1_Conf_1.000	451	20	2.96E-30	NP_001041050.1	70	134.806	117	82	hypothetical protein Y57G11C.3
Locus_12153_Transcript_1/1_Conf_1.000	1755	20	1.86E-127	NP_496546.2	68	461.07	487	336	hypothetical protein W03C9.6
Locus_12154_Transcript_1/1_Conf_1.000	397	20	2.38E-11	XP_002638990.1	61	72.0182	88	54	Hypothetical protein CBG22236
Locus_12155_Transcript_1/1_Conf_1.000	503	20	1.71E-25	XP_002641945.1	64	119.013	121	78	C. briggsae CBR-TAG-198 protein
Locus_12156_Transcript_1/1_Conf_1.000	665	20	1.75E-27	XP_001894040.1	56	126.716	166	93	F-box domain containing protein
Locus_12157_Transcript_1/1_Conf_1.000	138	0							

Locus_12158_Transcript_1/1_Conf_1.000	875	20	2.11E-20	XP_002640302.1	48	103.99	286	139	Hypothetical protein CBG12832
Locus_12159_Transcript_1/1_Conf_1.000	1760	20	1.15E-169	XP_002634860.1	72	601.282	536	386	Hypothetical protein CBG13978
Locus_1216_Transcript_1/1_Conf_1.000	1826	20	1.18E-124	NP_509391.1	58	451.825	569	335	hypothetical protein M60.2
Locus_12160_Transcript_1/1_Conf_1.000	422	0							
Locus_12161_Transcript_1/2_Conf_1.000	925	20	2.16E-34	NP_499533.1	85	150.599	91	78	SR Protein (splicing factor) family member (rsp-8)
Locus_12161_Transcript_2/2_Conf_1.000	318	0							
Locus_12162_Transcript_1/1_Conf_1.000	454	13	4.12E-24	NP_492324.2	58	114.39	138	81	hypothetical protein R05D11.9
Locus_12163_Transcript_1/1_Conf_1.000	407	20	8.63E-22	EFO25480.1	65	106.686	117	77	hypothetical protein LOAG_03009
Locus_12164_Transcript_1/1_Conf_1.000	146	0							

Locus_12165_Transcript_1/1_Conf_1.000	128	20	7.83E-15	XP_001110023.2	100	83.5741	42	42	PREDICTED: sentrin-specific protease 3-like isoform 3
Locus_12166_Transcript_1/1_Conf_1.000	593	20	2.57E-47	NP_501908.2	67	192.2	182	123	hypothetical protein Y43C5B.3
Locus_12167_Transcript_1/1_Conf_1.000	470	20	3.59E-68	XP_001231438.1	100	260.766	148	148	PREDICTED: similar to ribosomal protein L26 isoform 1
Locus_12168_Transcript_1/1_Conf_1.000	313	0							
Locus_12169_Transcript_1/1_Conf_1.000	355	0							
Locus_1217_Transcript_1/1_Conf_1.000	1216	20	1.67E-70	EFO17798.1	60	271.166	346	210	hypothetical protein LOAG_10699
Locus_12170_Transcript_1/1_Conf_1.000	279	0							
Locus_12171_Transcript_1/1_Conf_1.000	442	0							
Locus_12172_Transcript_1/1_Conf_1.000	217	20	5.89E-23	NP_499273.3	84	110.538	71	60	hypothetical protein R01H10.7
Locus_12173_Transcript_1/1_Conf_1.000	251	3	2.25E-06	EFO15975.1	64	55.4546	68	44	hypothetical protein LOAG_12534
Locus_12174_Transcript_1/2_Conf_1.000	1249	2	1.31E-17	NP_507948.2	48	95.5153	179	87	DAF-16/FOXO Controlled, germline Tumor affecting family member (dct-10)
Locus_12174_Transcript_2/2_Conf_1.000	1249	2	2.64E-18	NP_507948.2	48	97.8265	179	87	DAF-16/FOXO Controlled, germline Tumor affecting family member (dct-10)
Locus_12175_Transcript_1/1_Conf_1.000	989	20	1.58E-78	XP_002641183.1	89	297.36	213	191	Hypothetical protein CBG09044
Locus_12176_Transcript_1/1_Conf_1.000	412	4	2.50E-05	XP_001900130.1	68	51.9878	44	30	hypothetical protein
Locus_12177_Transcript_1/1_Conf_1.000	403	0							

Locus_12178_Transcript_1/1_Conf_1.000	822	20	1.72E-90	XP_002640833.1	85	336.65	276	236	C. briggsae CBR-KLP-20 protein
Locus_12179_Transcript_1/1_Conf_1.000	566	0							
Locus_1218_Transcript_1/1_Conf_1.000	4106	20	0	XP_001893907.1	68	1054.66	1287	886	hypothetical protein
Locus_12180_Transcript_1/1_Conf_1.000	188	20	4.24E-08	P34569.4	60	61.2326	61	37	Kelch repeat-containing protein kel-10
Locus_12181_Transcript_1/1_Conf_1.000	371	20	3.43E-34	NP_497510.2	80	147.902	111	89	hypothetical protein C39B5.6
Locus_12182_Transcript_1/1_Conf_1.000	133	0							
Locus_12183_Transcript_1/1_Conf_1.000	593	2	2.06E-04	EFO24041.1	56	49.6766	55	31	hypothetical protein LOAG_04441
Locus_12184_Transcript_1/2_Conf_1.000	1770	20	1.13E-39	EFO23952.1	45	169.474	526	237	hypothetical protein LOAG_04537

Locus_12184_Transcript_2/2_Conf_1.000	1770	20	1.13E-39	EFO23952.1	45	169.474	526	237	hypothetical protein LOAG_04537
Locus_12185_Transcript_1/1_Conf_1.000	528	20	2.64E-57	NP_501339.2	77	224.942	171	132	neuRonal IGCAM family member (rig-4)
Locus_12186_Transcript_1/1_Conf_1.000	390	1	7.48E-10	NP_001129792.1	73	67.0106	56	41	hypothetical protein T23G11.11
Locus_12187_Transcript_1/1_Conf_1.000	896	3	1.12E-16	NP_500551.2	62	91.6633	293	183	hypothetical protein F55F10.1
Locus_12188_Transcript_1/1_Conf_1.000	299	0							
Locus_12189_Transcript_1/1_Conf_1.000	723	19	8.04E-27	NP_503051.1	72	124.79	123	89	FMRF-Like Peptide family member (flp-17)
Locus_1219_Transcript_1/1_Conf_1.000	177	0							
Locus_12190_Transcript_1/1_Conf_1.000	187	0							
Locus_12191_Transcript_1/2_Conf_1.000	1129	20	1.78E-55	XP_002636552.1	62	221.09	297	185	C. briggsae CBR-SULP-4 protein
Locus_12191_Transcript_2/2_Conf_1.000	494	20	2.78E-12	NP_505493.1	68	75.0998	74	51	SULfate Permease family member (sulp-8)
Locus_12192_Transcript_1/1_Conf_1.000	757	20	6.67E-43	ABC69942.1	63	178.333	190	120	STIP
Locus_12193_Transcript_1/1_Conf_1.000	425	20	5.82E-26	NP_494922.1	59	120.553	127	76	hypothetical protein F59A6.4
Locus_12194_Transcript_1/1_Conf_1.000	276	20	5.74E-18	NP_495183.1	80	93.9745	66	53	FRataxin (involved in human Friedrich's ataxia) Homolog family member (frh-1)

Locus_12195_Transcript_1/1_Conf_1.000	1120	20	1.15E-155	NP_497603.3	88	553.903	373	329	hypothetical protein Y71H2AM.9
Locus_12196_Transcript_1/1_Conf_1.000	315	20	1.59E-31	XP_002637541.1	78	139.043	104	82	C. briggsae CBR-HUM-2 protein
Locus_12197_Transcript_1/1_Conf_1.000	138	1	1.62E-04	NP_500104.1	81	49.2914	43	35	Nuclear Pore complex Protein family member (npp-8)
Locus_12198_Transcript_1/1_Conf_1.000	370	20	3.01E-22	XP_002632893.1	82	108.227	74	61	Hypothetical protein CBG15101
Locus_12199_Transcript_1/1_Conf_1.000	578	0							
Locus_122_Transcript_1/10_Conf_0.500	1018	20	3.88E-43	NP_509305.1	72	179.874	170	124	VITellogenin structural genes (yolk protein genes) family member (vit-1)
Locus_122_Transcript_10/10_Conf_0.312	573	20	1.00E-45	NP_509305.1	69	186.808	191	133	VITellogenin structural genes (yolk protein genes) family member (vit-1)
Locus_122_Transcript_2/10_Conf_0.500	1018	20	2.87E-46	NP_509305.1	72	190.274	182	132	VITellogenin structural genes (yolk protein genes) family member (vit-1)
Locus_122_Transcript_3/10_Conf_0.312	244	2	7.29E-05	NP_509305.1	77	50.447	45	35	VITellogenin structural genes (yolk protein genes) family member (vit-1)
Locus_122_Transcript_4/10_Conf_0.312	244	13	1.57E-07	NP_509305.1	73	59.3066	57	42	VITellogenin structural genes (yolk protein genes) family member (vit-1)

Locus_122_Transcript_5/10_Conf_0.281	1052	20	1.77E-30	NP_509305.1	75	137.887	119	90	VITellogenin structural genes (yolk protein genes) family member (vit-1)
Locus_122_Transcript_6/10_Conf_0.281	1094	20	1.39E-33	NP_509305.1	74	148.288	131	98	VITellogenin structural genes (yolk protein genes) family member (vit-1)
Locus_122_Transcript_7/10_Conf_0.281	1052	20	1.77E-30	NP_509305.1	75	137.887	119	90	VITellogenin structural genes (yolk protein genes) family member (vit-1)
Locus_122_Transcript_8/10_Conf_0.062	564	6	3.91E-07	NP_001040703.1	66	58.5362	74	49	bZIP transcription factor family member (zip-4)
Locus_122_Transcript_9/10_Conf_0.312	573	20	1.82E-47	NP_509305.1	69	192.586	198	138	VITellogenin structural genes (yolk protein genes) family member (vit-1)
Locus_1220_Transcript_1/2_Conf_1.000	486	20	1.82E-11	CAD26968.1	52	72.4034	106	56	transposase
Locus_1220_Transcript_2/2_Conf_1.000	317	20	7.44E-13	CAD26968.1	58	77.0258	89	52	transposase
Locus_12200_Transcript_1/1_Conf_1.000	194	0							
Locus_12201_Transcript_1/1_Conf_1.000	1099	20	4.97E-55	NP_496426.1	77	219.55	175	135	hypothetical protein B0491.1
Locus_12202_Transcript_1/1_Conf_1.000	241	20	1.16E-18	EFO26239.1	77	96.2857	71	55	hypothetical protein LOAG_02251
Locus_12203_Transcript_1/1_Conf_1.000	270	0							
Locus_12204_Transcript_1/1_Conf_1.000	291	4	4.19E-16	XP_002646250.1	65	87.8113	91	60	C. briggsae CBR-AEX-1 protein

Locus_12205_Transcript_1/1_Conf_1.000	528	20	2.38E-66	NP_498192.2	95	254.988	144	137	hypothetical protein F09F7.3
Locus_12206_Transcript_1/1_Conf_1.000	242	6	1.13E-05	XP_001897023.1	53	53.1434	76	41	RNA dependent RNA polymerase family protein
Locus_12207_Transcript_1/1_Conf_1.000	524	0							
Locus_12208_Transcript_1/1_Conf_1.000	562	20	1.65E-50	XP_002633700.1	77	202.601	173	134	Hypothetical protein CBG03383
Locus_12209_Transcript_1/1_Conf_1.000	293	20	2.29E-22	XP_002639062.1	70	108.612	95	67	Hypothetical protein CBG14873
Locus_1221_Transcript_1/1_Conf_1.000	260	0							
Locus_12210_Transcript_1/1_Conf_1.000	1963	20	3.52E-122	EFO20200.1	59	443.736	620	370	hypothetical protein LOAG_08289
Locus_12211_Transcript_1/1_Conf_1.000	252	0							
Locus_12212_Transcript_1/2_Conf_1.000	336	0							
Locus_12212_Transcript_2/2_Conf_1.000	833	20	2.50E-28	XP_001896132.1	78	130.183	108	85	hypothetical protein
Locus_12213_Transcript_1/1_Conf_1.000	686	0							
Locus_12214_Transcript_1/1_Conf_1.000	401	5	4.15E-40	XP_001898210.1	76	167.548	117	89	hypothetical protein Bm1_33815
Locus_12215_Transcript_1/1_Conf_1.000	391	20	2.82E-33		67	144.821	121	82	DNA topoisomerase II
Locus_12216_Transcript_1/3_Conf_0.429	449	20	4.44E-26	NP_491633.1	73	120.939	101	74	Kinesin-Like Protein family member (klp-15)
Locus_12216_Transcript_2/3_Conf_0.429	847	20	7.21E-63	NP_491633.1	63	244.973	274	173	Kinesin-Like Protein family member (klp-15)

Locus_12216_Transcript_3/3_Conf_0.286	416	20	2.48E-21	NP_491633.1	72	105.145	90	65	Kinesin-Like Protein family member (klp-15)
Locus_12217_Transcript_1/1_Conf_1.000	444	12	5.64E-21	NP_871630.1	69	103.99	123	85	Nuclear Hormone Receptor family member (nhr-80)
Locus_12218_Transcript_1/1_Conf_1.000	348	20	1.29E-41	NP_055217.2	100	172.555	82	82	cytochrome b-c1 complex subunit 8
Locus_12219_Transcript_1/1_Conf_1.000	274	2	1.73E-22	NP_498411.1	81	108.997	91	74	related to yeast Vacuolar Protein Sorting factor family member (vps-16)
Locus_1222_Transcript_1/1_Conf_1.000	1102	20	1.66E-167	XP_002647836.1	91	593.193	350	319	Hypothetical protein CBG23625
Locus_12220_Transcript_1/1_Conf_1.000	139	0							
Locus_12221_Transcript_1/1_Conf_1.000	643	20	4.70E-75	NP_493334.1	87	284.648	213	187	hypothetical protein M01E5.2
Locus_12222_Transcript_1/1_Conf_1.000	553	0							
Locus_12223_Transcript_1/1_Conf_1.000	549	20	5.34E-83	BAG61260.1	100	310.457	181	181	unnamed protein product
Locus_12224_Transcript_1/1_Conf_1.000	418	20	3.11E-27	XP_002637376.1	69	124.79	135	94	Hypothetical protein CBG19078

Locus_12225_Transcript_1/1_Conf_1.000	1107	20	1.02E-23	XP_001638909.1	49	115.546	236	117	predicted protein
Locus_12226_Transcript_1/1_Conf_1.000	766	20	3.96E-91	XP_002630470.1	77	338.576	259	201	Hypothetical protein CBG11204
Locus_12227_Transcript_1/1_Conf_1.000	147	0							
Locus_12228_Transcript_1/1_Conf_1.000	508	20	5.33E-62	NP_505267.1	80	240.35	168	136	Regulator of Presynaptic Morphology family member (rpm-1)
Locus_12229_Transcript_1/1_Conf_1.000	844	0							
Locus_1223_Transcript_1/1_Conf_1.000	286	18	3.12E-27	NP_499455.1	79	124.79	94	75	Tumorous Enhancer of Glp-1(gf) family member (teg-1)
Locus_12230_Transcript_1/1_Conf_1.000	147	0							
Locus_12231_Transcript_1/1_Conf_1.000	151	0							
Locus_12232_Transcript_1/1_Conf_1.000	405	0							
Locus_12233_Transcript_1/1_Conf_1.000	229	2	2.08E-15	BAE00363.1	97	85.5001	40	39	unnamed protein product
Locus_12234_Transcript_1/1_Conf_1.000	292	20	3.19E-40	XP_002642536.1	86	167.933	95	82	C. briggsae CBR-LRS-1 protein
Locus_12235_Transcript_1/1_Conf_1.000	958	20	4.24E-65	XP_001895121.1	61	252.677	309	191	hypothetical protein
Locus_12236_Transcript_1/1_Conf_1.000	1034	20	4.23E-178	AAB99830.2	93	628.246	332	309	thrombospondin
Locus_12237_Transcript_1/1_Conf_1.000	139	0							
Locus_12238_Transcript_1/1_Conf_1.000	195	20	6.90E-19	XP_001899845.1	88	97.0561	51	45	CG7224
Locus_12239_Transcript_1/1_Conf_1.000	168	2	7.08E-08	CAA21622.4	73	60.4622	56	41	C. elegans protein Y43F8C.12, partially confirmed by transcript evidence
Locus_1224_Transcript_1/1_Conf_1.000	2034	20	4.79E-29	AAO63577.1	47	134.42	250	118	secreted protein 5 precursor
Locus_12240_Transcript_1/1_Conf_1.000	208	0							

Locus_12241_Transcript_1/1_Conf_1.000	937	20	7.28E-62	NP_500367.1	61	241.891	318	196	hypothetical protein M57.2
Locus_12242_Transcript_1/1_Conf_1.000	689	20	1.08E-22	XP_002645890.1	51	110.923	179	93	Hypothetical protein CBG07640
Locus_12243_Transcript_1/1_Conf_1.000	389	4	7.76E-15	XP_002631400.1	76	83.5741	64	49	Hypothetical protein CBG03250
Locus_12244_Transcript_1/1_Conf_1.000	226	0							
Locus_12245_Transcript_1/1_Conf_1.000	325	0							
Locus_12246_Transcript_1/1_Conf_1.000	194	0							
Locus_12247_Transcript_1/1_Conf_1.000	240	0							
Locus_12248_Transcript_1/1_Conf_1.000	608	0							
Locus_12249_Transcript_1/1_Conf_1.000	260	8	1.23E-07	ABB53347.1	51	59.6918	81	42	secreted protein 5 precursor
Locus_1225_Transcript_1/3_Conf_0.750	707	15	4.82E-25	ACU24256.1	100	88.1965	41	41	unknown
Locus_1225_Transcript_2/3_Conf_0.750	772	19	1.93E-21	XP_002118239.1	81	68.5514	86	70	predicted protein
Locus_1225_Transcript_3/3_Conf_0.750	708	19	1.63E-21	XP_002118239.1	81	68.5514	86	70	predicted protein
Locus_12250_Transcript_1/1_Conf_1.000	992	20	4.85E-35	EFO19997.1	54	152.91	339	184	hypothetical protein LOAG_08495
Locus_12251_Transcript_1/1_Conf_1.000	743	0							
Locus_12252_Transcript_1/1_Conf_1.000	292	0							
Locus_12253_Transcript_1/1_Conf_1.000	168	2	1.48E-05	NP_509318.1	62	52.7582	54	34	ADAM (disintegrin plus metalloprotease) family member (adm-4)
Locus_12254_Transcript_1/1_Conf_1.000	253	20	2.24E-17	XP_001896328.1	94	92.0485	85	80	calcium ATPase
Locus_12255_Transcript_1/1_Conf_1.000	420	0							
Locus_12256_Transcript_1/1_Conf_1.000	321	0							
Locus_12257_Transcript_1/1_Conf_1.000	659	20	4.01E-24	CBI63237.1	57	115.546	203	117	C. elegans protein Y111B2A.4a, partially confirmed by transcript evidence
Locus_12258_Transcript_1/1_Conf_1.000	936	20	2.19E-58	EFO25095.1	65	230.335	252	165	hypothetical protein LOAG_03392
Locus_12259_Transcript_1/1_Conf_1.000	195	0							

Locus_1226_Transcript_1/3_Conf_0.667	2576	20	1.23E-157	XP_002640115.1	67	561.992	544	365	C. briggsae CBR-GLD-2 protein
Locus_1226_Transcript_2/3_Conf_0.667	2278	20	1.82E-149	XP_002640115.1	74	534.643	422	315	C. briggsae CBR-GLD-2 protein
Locus_1226_Transcript_3/3_Conf_0.667	2654	20	2.18E-149	XP_002640115.1	74	534.643	422	315	C. briggsae CBR-GLD-2 protein
Locus_12260_Transcript_1/1_Conf_1.000	130	0							
Locus_12261_Transcript_1/1_Conf_1.000	563	20	3.18E-56	ACI48999.1	85	173.326	113	97	hypothetical protein Cbre_JD01.006
Locus_12262_Transcript_1/1_Conf_1.000	559	20	4.53E-69	NP_495779.1	84	264.233	184	155	abnormal Eversion of VuLva family member (evl-20)
Locus_12263_Transcript_1/1_Conf_1.000	612	20	1.72E-52	CBL43463.1	73	209.534	165	122	C. elegans protein Y52B11C.1, partially confirmed by transcript evidence

Locus_12264_Transcript_1/1_Conf_1.000	212	20	3.60E-20	NP_497809.1	87	101.293	70	61	Heavy chain, Unconventional Myosin family member (hum-5)
Locus_12265_Transcript_1/1_Conf_1.000	214	0							
Locus_12266_Transcript_1/1_Conf_1.000	237	0							
Locus_12267_Transcript_1/1_Conf_1.000	568	20	1.35E-47	XP_002633481.1	93	192.971	103	96	C. briggsae CBR-PHY-2 protein
Locus_12268_Transcript_1/1_Conf_1.000	205	0							
Locus_12269_Transcript_1/1_Conf_1.000	386	20	2.33E-22	XP_001269594.1	75	72.0182	54	41	hypothetical protein ACLA_028940
Locus_1227_Transcript_1/1_Conf_1.000	326	0							
Locus_12270_Transcript_1/1_Conf_1.000	151	4	1.36E-06	NP_499647.1	95	56.225	46	44	TAF (TBP-associated transcription factor) family member (taf-7.2)
Locus_12271_Transcript_1/1_Conf_1.000	161	20	5.46E-16	NP_492067.1	88	87.4261	52	46	hypothetical protein F13G3.11
Locus_12272_Transcript_1/1_Conf_1.000	138	0							
Locus_12273_Transcript_1/1_Conf_1.000	437	20	7.64E-63	BAG59449.1	100	243.047	119	119	unnamed protein product
Locus_12274_Transcript_1/2_Conf_1.000	1580	20	0	XP_002647008.1	82	690.649	515	427	Hypothetical protein CBG23794
Locus_12274_Transcript_2/2_Conf_1.000	573	20	1.59E-59	NP_499267.1	81	232.646	186	151	hypothetical protein Y70G10A.3

Locus_12275_Transcript_1/1_Conf_1.000	954	20	6.19E-125	ACY39994.1	76	451.44	351	268	C. elegans FLN-2 protein, isoform d
Locus_12276_Transcript_1/1_Conf_1.000	235	20	4.92E-17	NP_506788.1	67	90.8929	77	52	CYtochrome P450 family member (cyp-34A2)
Locus_12277_Transcript_1/1_Conf_1.000	201	20	3.28E-29	XP_002819700.1	100	131.339	67	67	PREDICTED: stomatin-like protein 2-like isoform 2
Locus_12278_Transcript_1/1_Conf_1.000	159	20	7.90E-07	CAD99040.1	83	56.9954	37	31	putative scj1 protein
Locus_12279_Transcript_1/1_Conf_1.000	212	20	1.73E-22	EFO21588.1	82	108.997	70	58	coiled-coil domain-containing protein 101
Locus_1228_Transcript_1/1_Conf_1.000	1671	20	0	XP_002637091.1	89	723.391	475	424	Hypothetical protein CBG09590
Locus_12280_Transcript_1/1_Conf_1.000	214	0							
Locus_12281_Transcript_1/1_Conf_1.000	781	20	7.18E-19	NP_498090.1	48	98.5969	258	125	Temporarily Assigned Gene name family member (tag-262)
Locus_12282_Transcript_1/1_Conf_1.000	197	0							
Locus_12283_Transcript_1/1_Conf_1.000	293	0							
Locus_12284_Transcript_1/1_Conf_1.000	274	2	6.81E-19	XP_002636840.1	70	97.0561	91	64	Hypothetical protein CBG09291
Locus_12285_Transcript_1/1_Conf_1.000	1973	7	2.83E-95	NP_510336.2	53	354.369	617	330	TBC (Tre-2/Bub2/Cdc16) domain family member (tbc-19)
Locus_12286_Transcript_1/1_Conf_1.000	143	2	1.32E-06	XP_002632345.1	76	56.225	43	33	Hypothetical protein CBG00357
Locus_12287_Transcript_1/1_Conf_1.000	252	0							
Locus_12288_Transcript_1/1_Conf_1.000	171	0							
Locus_12289_Transcript_1/1_Conf_1.000	196	0							
Locus_1229_Transcript_1/1_Conf_1.000	2030	20	4.67E-101	XP_001894842.1	62	373.629	481	301	Dual specificity phosphatase, catalytic domain containing protein
Locus_12290_Transcript_1/1_Conf_1.000	188	4	2.17E-20	NP_505746.2	93	102.064	62	58	hypothetical protein F28H7.8
Locus_12291_Transcript_1/1_Conf_1.000	356	20	2.42E-40	NP_510442.2	93	168.318	90	84	hypothetical protein F40E10.6
Locus_12292_Transcript_1/1_Conf_1.000	530	0							
Locus_12293_Transcript_1/1_Conf_1.000	528	20	2.75E-30	XP_001897467.1	63	135.191	177	113	CAP-Gly domain containing protein
Locus_12294_Transcript_1/1_Conf_1.000	136	0							
Locus_12295_Transcript_1/1_Conf_1.000	143	0							

Locus_12296_Transcript_1/1_Conf_1.000	383	20	1.33E-30	NP_498702.1	83	135.961	123	103	Ribosomal Protein, Large subunit family member (rpl-35)
Locus_12297_Transcript_1/1_Conf_1.000	807	20	2.11E-101	NP_001023058.1	77	372.859	263	204	hypothetical protein C42C1.11
Locus_12298_Transcript_1/1_Conf_1.000	363	20	1.01E-30	NP_497603.3	87	136.346	85	74	hypothetical protein Y71H2AM.9
Locus_12299_Transcript_1/1_Conf_1.000	430	3	1.09E-16	XP_002639154.1	92	89.7373	55	51	Hypothetical protein CBG14981
Locus_123_Transcript_1/8_Conf_0.267	1728	20	8.41E-141	ADI54942.1	98	505.368	263	258	heat shock protein 70
Locus_123_Transcript_2/8_Conf_0.267	1728	20	8.41E-141	ADI54942.1	98	505.368	263	258	heat shock protein 70
Locus_123_Transcript_3/8_Conf_0.167	477	20	4.50E-47	BAI81971.1	100	190.66	99	99	heat shock protein 70
Locus_123_Transcript_4/8_Conf_0.167	519	20	6.08E-56	BAI81971.1	100	220.32	113	113	heat shock protein 70
Locus_123_Transcript_5/8_Conf_0.267	1739	20	0	XP_002632429.1	98	846.655	478	473	C. briggsae CBR-HSP-1 protein

Locus_123_Transcript_6/8_Conf_0.267	1739	20	0	XP_002632429.1	98	840.877	478	473	C. briggsae CBR-HSP-1 protein
Locus_123_Transcript_7/8_Conf_0.400	1830	20	0	NP_503068.1	98	1019.22	574	565	Heat Shock Protein family member (hsp-1)
Locus_123_Transcript_8/8_Conf_0.400	1872	20	0	NP_503068.1	98	1039.64	588	579	Heat Shock Protein family member (hsp-1)
Locus_1230_Transcript_1/4_Conf_0.300	1373	20	5.97E-67	XP_002632730.1	72	259.61	245	178	C. briggsae CBR-LST-3 protein
Locus_1230_Transcript_2/4_Conf_0.700	3319	20	9.72E-110	XP_001901214.1	58	403.29	787	462	SAP domain containing protein
Locus_1230_Transcript_3/4_Conf_0.700	3320	20	9.72E-110	XP_001901214.1	58	403.29	787	462	SAP domain containing protein
Locus_1230_Transcript_4/4_Conf_0.700	3320	20	9.72E-110	XP_001901214.1	58	403.29	787	462	SAP domain containing protein
Locus_12300_Transcript_1/1_Conf_1.000	340	20	1.55E-31	XP_002633760.1	63	139.043	117	74	C. briggsae CBR-GON-1 protein
Locus_12301_Transcript_1/1_Conf_1.000	231	0							
Locus_12302_Transcript_1/2_Conf_1.000	252	0							
Locus_12302_Transcript_2/2_Conf_1.000	387	0							
Locus_12303_Transcript_1/1_Conf_1.000	248	3	7.74E-15	XP_002639235.1	59	83.5741	82	49	Hypothetical protein CBG03793
Locus_12304_Transcript_1/1_Conf_1.000	763	20	1.32E-54	NP_001022234.1	69	217.238	237	164	hypothetical protein K05F1.6

Locus_12305_Transcript_1/1_Conf_1.000	552	2	1.32E-28	NP_505498.1	59	129.798	162	97	hypothetical protein ZK287.7
Locus_12306_Transcript_1/1_Conf_1.000	1228	20	8.71E-67	NP_001122711.1	52	258.84	405	213	CBP/p300 homolog family member (cbp-1)
Locus_12307_Transcript_1/2_Conf_1.000	668	20	6.91E-48	EFO24728.1	67	194.512	219	148	blistered cuticle protein 3
Locus_12307_Transcript_2/2_Conf_1.000	668	20	6.91E-48	EFO24728.1	67	194.512	219	148	blistered cuticle protein 3
Locus_12308_Transcript_1/1_Conf_1.000	309	0							
Locus_12309_Transcript_1/1_Conf_1.000	342	20	1.87E-56	AAZ82849.1	96	221.861	113	109	Cam kinase kinase protein 1, isoform b
Locus_1231_Transcript_1/1_Conf_1.000	712	20	1.62E-16	XP_001656054.1	48	90.5077	233	112	brain chitinase and chia
Locus_12310_Transcript_1/1_Conf_1.000	161	0							
Locus_12311_Transcript_1/1_Conf_1.000	585	0							
Locus_12312_Transcript_1/1_Conf_1.000	553	0							

Locus_12313_Transcript_1/2_Conf_1.000	1509	20	8.47E-110	NP_502354.2	73	402.134	334	244	yeast SEC homolog family member (sec-24.2)
Locus_12313_Transcript_2/2_Conf_1.000	1509	20	8.47E-110	NP_502354.2	73	402.134	334	244	yeast SEC homolog family member (sec-24.2)
Locus_12314_Transcript_1/1_Conf_1.000	243	2	1.16E-10	XP_002643753.1	76	69.707	64	49	C. briggsae CBR-PSSY-1 protein
Locus_12315_Transcript_1/1_Conf_1.000	235	4	5.44E-16	XP_002644415.1	66	87.4261	75	50	C. briggsae CBR-TSP-17 protein
Locus_12316_Transcript_1/1_Conf_1.000	309	0							
Locus_12317_Transcript_1/1_Conf_1.000	887	0							
Locus_12318_Transcript_1/1_Conf_1.000	507	0							
Locus_12319_Transcript_1/1_Conf_1.000	171	0							
Locus_1232_Transcript_1/1_Conf_1.000	520	20	3.83E-42	NP_510335.2	78	174.481	129	101	hypothetical protein C31E10.7
Locus_12320_Transcript_1/1_Conf_1.000	486	14	2.46E-08	XP_002648923.1	49	62.003	160	79	Hypothetical protein CBG17840
Locus_12321_Transcript_1/1_Conf_1.000	527	0							
Locus_12322_Transcript_1/1_Conf_1.000	612	20	5.54E-43	NP_499696.2	77	177.948	160	124	hypothetical protein ZK1010.3

Locus_12323_Transcript_1/1_Conf_1.000	685	20	4.40E-101	NP_001023295.1	95	371.318	196	187	UNCoordinated family member (unc-43)
Locus_12324_Transcript_1/1_Conf_1.000	241	5	4.90E-09	XP_001898554.1	84	64.3142	38	32	DOMON domain containing protein
Locus_12325_Transcript_1/1_Conf_1.000	264	20	1.64E-20	NP_001022870.1	79	102.449	87	69	hypothetical protein Y43F4A.1
Locus_12326_Transcript_1/1_Conf_1.000	592	20	2.17E-54	NP_504292.2	76	215.698	198	151	hypothetical protein C37H5.5
Locus_12327_Transcript_1/1_Conf_1.000	852	0							
Locus_12328_Transcript_1/1_Conf_1.000	354	4	2.35E-27	XP_002641855.1	72	125.176	106	77	Hypothetical protein CBG16529
Locus_12329_Transcript_1/1_Conf_1.000	181	0							
Locus_1233_Transcript_1/1_Conf_1.000	510	20	8.51E-44	ACI49119.1	85	179.874	115	98	hypothetical protein Cbre_JD14.007
Locus_12330_Transcript_1/1_Conf_1.000	683	20	8.43E-12	EFA08418.1	47	74.7146	223	106	hypothetical protein TcasGA2_TC006065
Locus_12331_Transcript_1/1_Conf_1.000	356	20	4.73E-28	XP_002074576.1	64	127.487	118	76	GK23146
Locus_12332_Transcript_1/1_Conf_1.000	232	1	1.81E-19	EFO17857.1	68	98.9821	77	53	CK1/TTBK protein kinase
Locus_12333_Transcript_1/1_Conf_1.000	814	4	1.72E-18	CAB54509.2	48	97.4413	215	104	C. elegans protein Y79H2A.3a, partially confirmed by transcript evidence
Locus_12334_Transcript_1/1_Conf_1.000	609	0							
Locus_12335_Transcript_1/1_Conf_1.000	194	4	4.20E-16	NP_497814.3	82	87.8113	56	46	UNCoordinated family member (unc-79)
Locus_12336_Transcript_1/1_Conf_1.000	419	3	1.27E-04	NP_001084750.1	60	49.6766	58	35	TSC22 domain family, member 2
Locus_12337_Transcript_1/1_Conf_1.000	342	20	6.46E-41	NP_491314.1	82	170.244	108	89	INneXin family member (inx-16)

Locus_12338_Transcript_1/1_Conf_1.000	165	0							
Locus_12339_Transcript_1/1_Conf_1.000	434	3	2.67E-23	XP_002647006.1	62	111.694	155	97	Hypothetical protein CBG22464
Locus_1234_Transcript_1/1_Conf_1.000	310	20	3.84E-14	XP_001847954.1	72	81.2629	74	54	shc transforming protein
Locus_12340_Transcript_1/1_Conf_1.000	248	0							
Locus_12341_Transcript_1/1_Conf_1.000	492	0							
Locus_12342_Transcript_1/1_Conf_1.000	646	15	9.65E-52	XP_002644812.1	66	207.223	219	146	Hypothetical protein CBG14830
Locus_12343_Transcript_1/1_Conf_1.000	210	20	7.76E-15	XP_002595182.1	68	83.5741	69	47	hypothetical protein BRAFLDRAFT_285565
Locus_12344_Transcript_1/1_Conf_1.000	165	0							
Locus_12345_Transcript_1/1_Conf_1.000	1449	20	6.31E-123	XP_002640311.1	68	445.662	510	347	C. briggsae CBR-LET-363 protein
Locus_12346_Transcript_1/1_Conf_1.000	866	20	2.24E-91	XP_002644316.1	74	339.732	289	214	C. briggsae CBR-TAG-312 protein
Locus_12347_Transcript_1/1_Conf_1.000	334	0							
Locus_12348_Transcript_1/1_Conf_1.000	682	20	8.31E-60	NP_497539.3	71	234.187	198	142	F-box A protein family member (fbxa-1)
Locus_12349_Transcript_1/1_Conf_1.000	326	20	2.21E-25	NP_496059.2	81	118.627	91	74	UDP-GlucuronosylTransferase family member (ugt-58)
Locus_1235_Transcript_1/1_Conf_1.000	728	20	2.20E-40	XP_002639923.1	59	169.859	251	149	C. briggsae CBR-JPH-1 protein
Locus_12350_Transcript_1/1_Conf_1.000	436	0							
Locus_12351_Transcript_1/1_Conf_1.000	247	0							
Locus_12352_Transcript_1/1_Conf_1.000	382	20	9.47E-45	NP_510091.2	90	182.956	114	103	hypothetical protein T18D3.3
Locus_12353_Transcript_1/1_Conf_1.000	367	0							

Locus_12354_Transcript_1/1_Conf_1.000	496	20	6.32E-41	XP_002641474.1	69	170.244	162	112	C. briggsae CBR-PTP-1 protein
Locus_12355_Transcript_1/1_Conf_1.000	751	20	2.84E-102	EFO15747.1	95	375.555	205	196	RPB-5 protein
Locus_12356_Transcript_1/1_Conf_1.000	1087	14	2.21E-23	EFO22475.1	49	114.39	314	154	PH domain-containing protein
Locus_12357_Transcript_1/1_Conf_1.000	390	20	6.31E-25	XP_002639764.1	85	117.087	101	86	Hypothetical protein CBG02210
Locus_12358_Transcript_1/1_Conf_1.000	875	20	7.48E-26	EFO26243.1	50	122.094	287	146	ku P80 DNA helicase
Locus_12359_Transcript_1/1_Conf_1.000	165	0							
Locus_1236_Transcript_1/1_Conf_1.000	1606	20	9.23E-78	EFO24996.1	65	295.819	423	276	hypothetical protein LOAG_03490
Locus_12360_Transcript_1/1_Conf_1.000	316	3	2.10E-07	CBM41222.1	51	58.9214	86	44	C. elegans protein T10G3.3b, partially confirmed by transcript evidence
Locus_12361_Transcript_1/1_Conf_1.000	939	20	2.43E-65	NP_001040941.1	72	253.447	202	147	PhosphatidylSerine Receptor family member (psr-1)
Locus_12362_Transcript_1/1_Conf_1.000	235	0							
Locus_12363_Transcript_1/1_Conf_1.000	274	20	1.67E-25	XP_002643815.1	78	119.013	90	71	Hypothetical protein CBG02030
Locus_12364_Transcript_1/1_Conf_1.000	510	0							
Locus_12365_Transcript_1/1_Conf_1.000	459	20	1.60E-28	XP_002639084.1	62	129.028	151	95	Hypothetical protein CBG14902
Locus_12366_Transcript_1/1_Conf_1.000	133	0							
Locus_12367_Transcript_1/1_Conf_1.000	492	8	7.07E-16	XP_002629751.1	86	87.0409	50	43	Hypothetical protein CBG00985

Locus_12368_Transcript_1/1_Conf_1.000	441	20	7.61E-42	XP_001899686.1	73	173.326	145	106	Abnormal embryonic partitioning of cytoplasm protein 3, isoform b
Locus_12369_Transcript_1/2_Conf_1.000	1028	20	2.59E-111	XP_002634540.1	85	406.371	265	226	C. briggsae CBR-EGL-21 protein
Locus_12369_Transcript_2/2_Conf_1.000	1028	20	2.59E-111	XP_002634540.1	85	406.371	265	226	C. briggsae CBR-EGL-21 protein
Locus_1237_Transcript_1/2_Conf_1.000	1379	20	5.70E-17	XP_002639868.1	43	93.5893	181	79	C. briggsae CBR-DAO-5 protein
Locus_1237_Transcript_2/2_Conf_1.000	1567	20	4.36E-16	XP_002639868.1	52	90.8929	165	87	C. briggsae CBR-DAO-5 protein
Locus_12370_Transcript_1/1_Conf_1.000	224	0							
Locus_12371_Transcript_1/1_Conf_1.000	363	0							
Locus_12372_Transcript_1/1_Conf_1.000	906	20	1.42E-91	NP_741241.1	73	340.502	302	222	Dipeptidyl Peptidase Four (IV) family member (dpf-6)
Locus_12373_Transcript_1/1_Conf_1.000	171	0							
Locus_12374_Transcript_1/1_Conf_1.000	516	20	1.52E-51	XP_002647980.1	72	205.682	172	125	C. briggsae CBR-PUS-1 protein
Locus_12375_Transcript_1/1_Conf_1.000	445	20	6.85E-43	NP_510130.2	85	176.792	105	90	hypothetical protein F22E10.5
Locus_12376_Transcript_1/1_Conf_1.000	154	20	1.18E-18	XP_002920956.1	100	96.2857	46	46	PREDICTED: RNA-binding protein 42-like isoform 2
Locus_12377_Transcript_1/1_Conf_1.000	373	0							
Locus_12378_Transcript_1/1_Conf_1.000	594	0							
Locus_12379_Transcript_1/1_Conf_1.000	132	4	4.42E-10	NP_001021692.1	88	67.781	42	37	EATing: abnormal pharyngeal pumping family member (eat-18)
Locus_1238_Transcript_1/1_Conf_1.000	1257	20	7.26E-101	XP_002630425.1	76	372.089	303	231	Hypothetical protein CBG11150

Locus_12380_Transcript_1/1_Conf_1.000	374	20	1.21E-39	XP_002642385.1	83	166.007	126	105	Hypothetical protein CBG18389
Locus_12381_Transcript_1/1_Conf_1.000	589	0							
Locus_12382_Transcript_1/1_Conf_1.000	213	15	2.66E-15	NP_001022735.1	73	85.1149	71	52	hypothetical protein R155.1
Locus_12383_Transcript_1/1_Conf_1.000	650	0							
Locus_12384_Transcript_1/1_Conf_1.000	694	20	1.83E-09	XP_002642093.1	52	67.0106	174	91	C. briggsae CBR-SMC-4 protein
Locus_12385_Transcript_1/1_Conf_1.000	304	0							
Locus_12386_Transcript_1/1_Conf_1.000	625	20	1.56E-56	NP_001023008.1	72	223.016	197	143	CULlin family member (cul-2)
Locus_12387_Transcript_1/1_Conf_1.000	897	20	3.44E-74	NP_495578.2	68	282.722	260	177	hypothetical protein ZK1290.5
Locus_12388_Transcript_1/1_Conf_1.000	226	1	1.27E-12	NP_499274.3	74	76.2554	67	50	Connector/eNhancer of KSR family member (cnk-1)
Locus_12389_Transcript_1/1_Conf_1.000	474	14	7.46E-50	EFO27980.1	79	199.904	158	125	hypothetical protein LOAG_00505
Locus_1239_Transcript_1/1_Conf_1.000	159	0							
Locus_12390_Transcript_1/1_Conf_1.000	329	0							
Locus_12391_Transcript_1/1_Conf_1.000	363	20	6.35E-09	XP_002176123.1	67	63.929	55	37	chromo domain-containing protein

Locus_12392_Transcript_1/1_Conf_1.000	353	20	9.25E-32	NP_509229.1	75	139.813	114	86	SUppressor of activated let-60 Ras family member (sur-5)
Locus_12393_Transcript_1/1_Conf_1.000	138	16	2.11E-12	XP_002631560.1	86	75.485	46	40	Hypothetical protein CBG20736
Locus_12394_Transcript_1/1_Conf_1.000	177	20	3.70E-25	NP_501715.1	96	117.857	58	56	Acetylcholine-gated Chloride Channel family member (acc-1)
Locus_12395_Transcript_1/1_Conf_1.000	502	20	5.42E-64	XP_001154691.1	99	246.899	125	124	PREDICTED: hypothetical protein isoform 2
Locus_12396_Transcript_1/1_Conf_1.000	202	20	1.29E-25	XP_002818734.1	100	119.398	58	58	PREDICTED: chondroitin sulfate glucuronyltransferase-like isoform 2
Locus_12397_Transcript_1/1_Conf_1.000	376	20	8.89E-59	NP_492127.1	89	229.565	126	113	Low-density lipoprotein Receptor Related family member (lrp-1)
Locus_12398_Transcript_1/1_Conf_1.000	177	0							
Locus_12399_Transcript_1/1_Conf_1.000	229	0							
Locus_124_Transcript_1/1_Conf_1.000	237	0							
Locus_1240_Transcript_1/1_Conf_1.000	2279	20	1.82E-32	XP_001901591.1	67	145.976	159	107	WH1 domain containing protein
Locus_12400_Transcript_1/1_Conf_1.000	980	20	1.81E-34	NP_490916.4	47	150.984	381	182	GTPase Activating Protein family member (gap-3)
Locus_12401_Transcript_1/1_Conf_1.000	1105	20	2.38E-97	XP_001895783.1	73	360.147	342	252	BTB/POZ domain containing protein 9

Locus_12402_Transcript_1/1_Conf_1.000	453	20	2.11E-36	XP_002645055.1	67	155.221	152	102	Hypothetical protein CBG16715
Locus_12403_Transcript_1/1_Conf_1.000	224	0							
Locus_12404_Transcript_1/1_Conf_1.000	197	0							
Locus_12405_Transcript_1/1_Conf_1.000	352	20	3.63E-36	NP_491357.1	88	154.451	93	82	hypothetical protein ZK973.3
Locus_12406_Transcript_1/2_Conf_1.000	635	20	1.69E-29	XP_001902631.1	56	133.265	211	119	ARID/BRIGHT DNA binding domain containing protein
Locus_12406_Transcript_2/2_Conf_1.000	292	20	3.66E-20	EFO18078.1	83	101.293	59	49	arid/bright DNA binding domain-containing protein
Locus_12407_Transcript_1/1_Conf_1.000	1137	20	2.25E-98	XP_002643956.1	64	363.614	380	246	Hypothetical protein CBG17315
Locus_12408_Transcript_1/1_Conf_1.000	181	20	1.12E-24	XP_002646598.1	94	116.316	59	56	Hypothetical protein CBG20482
Locus_12409_Transcript_1/1_Conf_1.000	1260	20	1.50E-21	XP_001364696.1	52	108.612	266	140	PREDICTED: similar to SCY1-like 3 (S. cerevisiae)
Locus_1241_Transcript_1/1_Conf_1.000	1559	5	6.60E-57	NP_493282.1	74	226.483	179	134	hypothetical protein W05B5.1
Locus_12410_Transcript_1/1_Conf_1.000	306	0							
Locus_12411_Transcript_1/1_Conf_1.000	520	3	3.06E-07	NP_491907.1	52	58.5362	88	46	Protein Phosphatase Four Regulatory subunit family member (ppfr-2)
Locus_12412_Transcript_1/1_Conf_1.000	254	1	2.25E-09	EFO23711.1	55	65.4698	84	47	hypothetical protein LOAG_04772
Locus_12413_Transcript_1/1_Conf_1.000	374	0							
Locus_12414_Transcript_1/1_Conf_1.000	714	20	4.38E-70	XP_002645904.1	76	268.47	217	167	C. briggsae CBR-MRP-5 protein
Locus_12415_Transcript_1/1_Conf_1.000	164	0							
Locus_12416_Transcript_1/1_Conf_1.000	438	20	5.15E-27	NP_492346.2	70	124.02	116	82	hypothetical protein F39H2.3

Locus_12417_Transcript_1/1_Conf_1.000	585	20	4.04E-61	EFO19790.1	74	238.039	197	147	exostosin-1
Locus_12418_Transcript_1/1_Conf_1.000	686	5	6.46E-44	NP_001023038.1	74	181.415	156	116	EXCretory canal abnormal family member (exc-5)
Locus_12419_Transcript_1/1_Conf_1.000	222	2	4.38E-05	CAR63563.1	80	51.2174	35	28	hypothetical protein
Locus_1242_Transcript_1/1_Conf_1.000	2496	20	0	NP_491559.1	88	840.877	572	509	Ezrin/Radixin/Moesin family member (erm-1)
Locus_12420_Transcript_1/1_Conf_1.000	713	20	9.99E-67	NP_001041123.2	68	257.299	238	163	hypothetical protein F55A11.6
Locus_12421_Transcript_1/1_Conf_1.000	139	0							
Locus_12422_Transcript_1/1_Conf_1.000	851	20	2.50E-55	XP_002629711.1	72	219.935	220	159	C. briggsae CBR-RHY-1 protein
Locus_12423_Transcript_1/2_Conf_1.000	729	20	1.03E-53	XP_002636561.1	64	214.157	214	139	Hypothetical protein CBG23253
Locus_12423_Transcript_2/2_Conf_1.000	526	20	2.69E-30	XP_002636561.1	61	135.191	147	91	Hypothetical protein CBG23253
Locus_12424_Transcript_1/1_Conf_1.000	692	0							
Locus_12425_Transcript_1/1_Conf_1.000	235	0							

Locus_12426_Transcript_1/1_Conf_1.000	488	20	1.13E-53	NP_497733.1	87	212.616	131	115	Protein Tyrosine Phosphatase family member (ptp-1)
Locus_12427_Transcript_1/2_Conf_1.000	470	2	2.07E-07	XP_001892427.1	70	58.9214	55	39	hypothetical protein Bm1_04745
Locus_12427_Transcript_2/2_Conf_1.000	632	2	6.80E-07	EFO16594.1	72	58.151	51	37	hypothetical protein LOAG_11910
Locus_12428_Transcript_1/1_Conf_1.000	237	0							
Locus_12429_Transcript_1/1_Conf_1.000	1179	20	3.74E-120	ACI49192.1	74	436.032	393	292	hypothetical protein Csp3_JD03.001
Locus_1243_Transcript_1/1_Conf_1.000	353	20	9.92E-18	BAE87571.1	60	93.2041	110	66	unnamed protein product
Locus_12430_Transcript_1/1_Conf_1.000	224	5	3.22E-24	NP_001022641.1	82	114.775	75	62	LEThal family member (let-805)
Locus_12431_Transcript_1/1_Conf_1.000	291	0							
Locus_12432_Transcript_1/1_Conf_1.000	342	20	1.65E-36	EFO24987.1	84	155.606	108	91	hypothetical protein LOAG_03502
Locus_12433_Transcript_1/1_Conf_1.000	289	4	3.33E-13	XP_002638865.1	72	78.1814	65	47	Hypothetical protein CBG22082
Locus_12434_Transcript_1/1_Conf_1.000	263	0							
Locus_12435_Transcript_1/1_Conf_1.000	145	0							
Locus_12436_Transcript_1/1_Conf_1.000	380	19	5.42E-24	NP_494788.2	69	114.005	133	93	related to yeast Vacuolar Protein Sorting factor family member (vps-18)
Locus_12437_Transcript_1/1_Conf_1.000	476	0							
Locus_12438_Transcript_1/1_Conf_1.000	139	0							
Locus_12439_Transcript_1/1_Conf_1.000	716	20	7.45E-78	AAN11402.1	75	294.278	235	178	secreted-protein 1 precursor
Locus_1244_Transcript_1/1_Conf_1.000	2806	20	1.07E-53	NP_741023.2	47	216.853	768	361	Nuclear Pore complex Protein family member (npp-21)
Locus_12440_Transcript_1/1_Conf_1.000	485	0							
Locus_12441_Transcript_1/1_Conf_1.000	243	0							
Locus_12442_Transcript_1/1_Conf_1.000	467	4	4.96E-09	EFO27500.1	50	64.3142	144	72	hypothetical protein LOAG_00978

Locus_12443_Transcript_1/1_Conf_1.000	477	20	1.36E-43	NP_501913.1	76	179.104	151	115	hypothetical protein R11A8.5
Locus_12444_Transcript_1/1_Conf_1.000	1002	20	2.97E-72	XP_002634026.1	83	276.559	187	156	C. briggsae CBR-PCT-1 protein
Locus_12445_Transcript_1/1_Conf_1.000	308	2	2.18E-25	XP_002631591.1	82	118.627	92	76	C. briggsae CBR-DRR-1 protein
Locus_12446_Transcript_1/1_Conf_1.000	895	6	6.11E-31	NP_001122672.1	58	139.043	202	119	Regulator of G protein Signaling family member (rgs-5)
Locus_12447_Transcript_1/1_Conf_1.000	280	0							
Locus_12448_Transcript_1/1_Conf_1.000	1022	20	1.89E-122	NP_503577.1	81	443.351	320	261	hypothetical protein F22F7.1
Locus_12449_Transcript_1/1_Conf_1.000	497	16	2.84E-33	XP_002832705.1	96	144.821	89	86	PREDICTED: hypothetical protein LOC100439353, partial
Locus_1245_Transcript_1/3_Conf_0.818	3794	20	1.53E-90	NP_741537.1	53	339.732	653	348	human MLK (Mixed Lineage Kinase) homolog family member (mlk-1)
Locus_1245_Transcript_2/3_Conf_0.818	3818	20	1.54E-90	NP_741537.1	53	339.732	653	348	human MLK (Mixed Lineage Kinase) homolog family member (mlk-1)
Locus_1245_Transcript_3/3_Conf_0.455	640	0							
Locus_12450_Transcript_1/1_Conf_1.000	505	2	1.94E-08	XP_002643645.1	78	62.3882	51	40	Hypothetical protein CBG16393

Locus_12451_Transcript_1/1_Conf_1.000	280	0							
Locus_12452_Transcript_1/1_Conf_1.000	670	0							
Locus_12453_Transcript_1/3_Conf_0.714	1973	20	3.64E-26	XP_001900501.1	51	124.79	291	150	hypothetical protein Bm1_45195
Locus_12453_Transcript_2/3_Conf_0.714	1973	20	3.64E-26	XP_001900501.1	51	124.79	291	150	hypothetical protein Bm1_45195
Locus_12453_Transcript_3/3_Conf_0.714	1973	20	3.64E-26	XP_001900501.1	51	124.79	291	150	hypothetical protein Bm1_45195
Locus_12454_Transcript_1/2_Conf_1.000	526	0							
Locus_12454_Transcript_2/2_Conf_1.000	532	0							
Locus_12455_Transcript_1/1_Conf_1.000	729	4	1.08E-10	XP_001894822.1	51	71.2478	176	91	SNF2 family N-terminal domain containing protein
Locus_12456_Transcript_1/1_Conf_1.000	386	20	1.66E-49	XP_002643641.1	89	198.749	128	115	C. briggsae CBR-IFA-3 protein

Locus_12457_Transcript_1/1_Conf_1.000	380	0							
Locus_12458_Transcript_1/1_Conf_1.000	132	0							
Locus_12459_Transcript_1/1_Conf_1.000	145	0							
Locus_1246_Transcript_1/2_Conf_1.000	920	1	1.54E-08	XP_002643611.1	48	64.6994	170	82	C. briggsae CBR-AIN-1 protein
Locus_1246_Transcript_2/2_Conf_1.000	842	1	2.25E-08	XP_002643611.1	44	63.929	165	74	C. briggsae CBR-AIN-1 protein
Locus_12460_Transcript_1/1_Conf_1.000	262	19	3.43E-10	XP_002633069.1	87	68.1662	40	35	C. briggsae CBR-TIN-9.1 protein
Locus_12461_Transcript_1/1_Conf_1.000	355	0							
Locus_12462_Transcript_1/1_Conf_1.000	665	20	1.47E-58	NP_492769.1	69	229.95	213	149	RTEL (mammalian Regulator of TELomere length) homolog family member (rtel-1)
Locus_12463_Transcript_1/1_Conf_1.000	274	0							
Locus_12464_Transcript_1/1_Conf_1.000	130	20	1.93E-05	XP_002576412.1	76	52.373	43	33	tyrosine kinase
Locus_12465_Transcript_1/1_Conf_1.000	621	0							
Locus_12466_Transcript_1/1_Conf_1.000	134	0							
Locus_12467_Transcript_1/1_Conf_1.000	279	0							
Locus_12468_Transcript_1/3_Conf_0.714	1279	20	2.22E-129	NP_499995.2	83	466.848	369	309	hypothetical protein Y55F3BL.2
Locus_12468_Transcript_2/3_Conf_0.714	1279	20	2.22E-129	NP_499995.2	83	466.848	369	309	hypothetical protein Y55F3BL.2
Locus_12468_Transcript_3/3_Conf_0.714	1279	20	2.22E-129	NP_499995.2	83	466.848	369	309	hypothetical protein Y55F3BL.2

Locus_12469_Transcript_1/1_Conf_1.000	447	0							
Locus_1247_Transcript_1/2_Conf_1.000	429	20	3.58E-60	ABJ97284.1	99	234.187	110	109	major sperm protein
Locus_1247_Transcript_2/2_Conf_1.000	534	20	4.57E-57	BAI81973.1	100	224.172	104	104	major sperm protein 1
Locus_12470_Transcript_1/1_Conf_1.000	390	20	4.20E-45	XP_002636522.1	86	184.111	115	99	Hypothetical protein CBG23203
Locus_12471_Transcript_1/1_Conf_1.000	405	20	8.61E-30	XP_002634543.1	70	133.265	134	94	C. briggsae CBR-CED-5 protein
Locus_12472_Transcript_1/1_Conf_1.000	479	19	1.01E-22	XP_002640716.1	59	109.768	152	90	Hypothetical protein CBG19783
Locus_12473_Transcript_1/1_Conf_1.000	875	20	8.77E-51	XP_001902022.1	64	204.912	293	188	hypothetical protein Bm1_52770
Locus_12474_Transcript_1/1_Conf_1.000	131	20	1.57E-15	XP_002742370.1	95	85.8853	43	41	PREDICTED: urocanase domain containing 1-like
Locus_12475_Transcript_1/1_Conf_1.000	540	20	2.80E-41	XP_001896506.1	68	171.785	179	123	Cullin family protein
Locus_12476_Transcript_1/1_Conf_1.000	212	20	5.55E-21	XP_002927000.1	100	103.99	49	49	PREDICTED: LOW QUALITY PROTEIN: lamin-A/C-like
Locus_12477_Transcript_1/1_Conf_1.000	152	0							
Locus_12478_Transcript_1/1_Conf_1.000	375	0							
Locus_12479_Transcript_1/1_Conf_1.000	1504	20	8.66E-14	BAA36710.1	42	83.1889	375	161	DEAD-Box Protein

Locus_1248_Transcript_1/1_Conf_1.000	465	5	1.34E-22	NP_497291.1	66	109.383	100	66	hypothetical protein F23H11.5
Locus_12480_Transcript_1/1_Conf_1.000	859	0							
Locus_12481_Transcript_1/1_Conf_1.000	877	20	1.91E-106	XP_002640662.1	85	389.808	275	235	Hypothetical protein CBG19722
Locus_12482_Transcript_1/1_Conf_1.000	179	0							
Locus_12483_Transcript_1/1_Conf_1.000	422	0							
Locus_12484_Transcript_1/1_Conf_1.000	1238	0							
Locus_12485_Transcript_1/1_Conf_1.000	595	5	8.44E-22	XP_002648817.1	60	107.457	123	74	Hypothetical protein CBG15628
Locus_12486_Transcript_1/1_Conf_1.000	1033	10	1.31E-86	NP_505475.2	88	324.324	218	192	hypothetical protein K09G1.1
Locus_12487_Transcript_1/1_Conf_1.000	325	20	3.89E-22	XP_001902301.1	84	107.842	73	62	ubiquitin-like protein
Locus_12488_Transcript_1/1_Conf_1.000	577	20	2.09E-07	XP_001122201.1	79	53.9138	43	34	PREDICTED: similar to Lysine-specific histone demethylase 1 (Amine oxidase flavin-containing domain protein 2) (BRAF35-HDAC complex protein BHC110)
Locus_12489_Transcript_1/1_Conf_1.000	453	0							
Locus_1249_Transcript_1/4_Conf_0.667	1470	20	0	NP_001021985.1	93	720.694	409	384	HELicase family member (hel-1)

Locus_1249_Transcript_2/4_Conf_0.222	961	20	1.50E-110	NP_001021986.1	91	403.675	230	210	HELicase family member (hel-1)
Locus_1249_Transcript_3/4_Conf_0.667	1470	20	0	NP_001021985.1	93	720.694	409	384	HELicase family member (hel-1)

Locus_1249_Transcript_4/4_Conf_0.667	1470	20	0	NP_001021985.1	93	720.694	409	384	HELicase family member (hel-1)
Locus_12490_Transcript_1/3_Conf_0.429	1555	20	1.44E-11	EAX02636.1	44	75.8702	310	137	glycosyltransferase 28 domain containing 1, isoform CRA_c
Locus_12490_Transcript_2/3_Conf_0.286	1364	20	1.21E-11	BAH13833.1	44	75.8702	310	137	unnamed protein product
Locus_12490_Transcript_3/3_Conf_0.571	274	0							
Locus_12491_Transcript_1/1_Conf_1.000	391	20	1.45E-37	BAA08309.1	80	159.073	120	96	ryanodine receptor
Locus_12492_Transcript_1/1_Conf_1.000	606	0							
Locus_12493_Transcript_1/1_Conf_1.000	278	5	8.25E-33	XP_002637129.1	85	143.28	91	78	Hypothetical protein CBG09631
Locus_12494_Transcript_1/1_Conf_1.000	352	20	1.48E-21	XP_001898517.1	63	105.916	117	74	DRIM protein

Locus_12495_Transcript_1/1_Conf_1.000	349	17	1.18E-10	NP_493130.2	51	69.707	133	68	hypothetical protein T09E11.6
Locus_12496_Transcript_1/2_Conf_1.000	237	20	2.51E-21	EFO19548.1	75	105.145	78	59	ubiquinone biosynthesis O-methyltransferase
Locus_12496_Transcript_2/2_Conf_1.000	243	20	8.02E-20	EFO19548.1	73	100.138	80	59	ubiquinone biosynthesis O-methyltransferase
Locus_12497_Transcript_1/1_Conf_1.000	706	15	3.19E-25	NP_501506.1	65	119.398	135	88	hypothetical protein F21D5.6
Locus_12498_Transcript_1/1_Conf_1.000	301	20	3.17E-24	NP_502574.1	70	114.775	99	70	MAternally affected Uncoordination family member (mau-8)
Locus_12499_Transcript_1/1_Conf_1.000	445	0							
Locus_125_Transcript_1/2_Conf_1.000	970	20	4.14E-108	AAC48257.3	90	395.586	252	228	Pcna (proliferating cell nuclear antigen) homolog protein 1, confirmed by transcript evidence
Locus_125_Transcript_2/2_Conf_1.000	970	20	4.14E-108	AAC48257.3	90	395.586	252	228	Pcna (proliferating cell nuclear antigen) homolog protein 1, confirmed by transcript evidence
Locus_1250_Transcript_1/1_Conf_1.000	1214	2	4.04E-08	XP_002640249.1	68	63.929	61	42	C. briggsae CBR-PQN-20 protein
Locus_12500_Transcript_1/1_Conf_1.000	399	0							
Locus_12501_Transcript_1/1_Conf_1.000	130	0							
Locus_12502_Transcript_1/1_Conf_1.000	170	20	1.68E-25	ACJ65168.1	98	119.013	56	55	Uncoordinated protein 68, isoform b, partially confirmed by transcript evidence
Locus_12503_Transcript_1/1_Conf_1.000	237	1	2.70E-07	NP_491118.2	52	58.5362	78	41	hypothetical protein Y54E10A.11

Locus_12504_Transcript_1/2_Conf_1.000	810	20	2.59E-67	NP_491541.1	78	259.61	187	146	hypothetical protein F56A3.2
Locus_12504_Transcript_2/2_Conf_1.000	781	20	2.43E-67	NP_491541.1	78	259.61	187	146	hypothetical protein F56A3.2
Locus_12505_Transcript_1/1_Conf_1.000	344	0							
Locus_12506_Transcript_1/1_Conf_1.000	175	0							
Locus_12507_Transcript_1/1_Conf_1.000	280	8	3.97E-11	XP_001894571.1	70	71.2478	62	44	UBX domain containing protein
Locus_12508_Transcript_1/1_Conf_1.000	931	20	8.44E-87	NP_497567.1	88	324.709	234	206	hypothetical protein Y54F10AL.1
Locus_12509_Transcript_1/1_Conf_1.000	232	0							
Locus_1251_Transcript_1/1_Conf_1.000	499	0							
Locus_12510_Transcript_1/1_Conf_1.000	564	0							
Locus_12511_Transcript_1/1_Conf_1.000	932	20	1.96E-59	NP_491606.2	60	233.802	316	192	hypothetical protein C09D4.4
Locus_12512_Transcript_1/1_Conf_1.000	201	20	1.25E-20	NP_499993.1	89	102.834	66	59	Enoyl-CoA Hydratase family member (ech-5)
Locus_12513_Transcript_1/1_Conf_1.000	1304	20	2.20E-140	NP_001040974.1	80	503.442	435	348	hypothetical protein K09B11.9
Locus_12514_Transcript_1/1_Conf_1.000	391	20	6.33E-09	AAA97925.1	79	63.929	39	31	hum-1
Locus_12515_Transcript_1/1_Conf_1.000	1130	20	2.58E-46	XP_001898245.1	57	190.66	379	217	Protein kinase domain containing protein
Locus_12516_Transcript_1/1_Conf_1.000	182	0							
Locus_12517_Transcript_1/1_Conf_1.000	130	0							

Locus_12518_Transcript_1/1_Conf_1.000	390	20	2.30E-51	NP_001022641.1	86	204.912	130	112	LEThal family member (let-805)
Locus_12519_Transcript_1/1_Conf_1.000	193	0							
Locus_1252_Transcript_1/5_Conf_0.333	1413	1	4.36E-04	XP_002639136.1	53	50.8322	128	68	C. briggsae CBR-TAG-63 protein
Locus_1252_Transcript_2/5_Conf_0.222	385	0							
Locus_1252_Transcript_3/5_Conf_0.222	1257	0							
Locus_1252_Transcript_4/5_Conf_0.222	2044	20	0	XP_002638874.1	84	843.958	571	483	Hypothetical protein CBG22093
Locus_1252_Transcript_5/5_Conf_0.333	1566	20	2.03E-05	XP_002813170.1	40	55.4546	230	92	PREDICTED: hypothetical protein LOC100442257
Locus_12520_Transcript_1/1_Conf_1.000	195	0							
Locus_12521_Transcript_1/1_Conf_1.000	332	8	1.86E-08	XP_002639634.1	62	62.3882	94	59	C. briggsae CBR-CLE-1 protein
Locus_12522_Transcript_1/1_Conf_1.000	210	4	3.86E-06	XP_001898470.1	55	54.6842	84	47	hypothetical protein Bm1_35105
Locus_12523_Transcript_1/1_Conf_1.000	662	2	5.74E-31	NP_505701.2	62	138.272	225	140	hypothetical protein F25D1.2
Locus_12524_Transcript_1/2_Conf_1.000	442	1	1.50E-05	YP_003009133.1	44	52.7582	92	41	Collagen triple helix repeat protein
Locus_12524_Transcript_2/2_Conf_1.000	365	1	4.71E-04	YP_003009133.1	44	47.7506	86	38	Collagen triple helix repeat protein
Locus_12525_Transcript_1/1_Conf_1.000	171	0							
Locus_12526_Transcript_1/1_Conf_1.000	129	0							
Locus_12527_Transcript_1/1_Conf_1.000	282	4	3.59E-15	XP_001895046.1	72	84.7297	70	51	hypothetical protein
Locus_12528_Transcript_1/1_Conf_1.000	679	20	2.76E-31	NP_492764.2	91	139.428	82	75	UBiquitin Conjugating enzyme family member (ubc-25)
Locus_12529_Transcript_1/1_Conf_1.000	134	16	1.68E-09	XP_001898554.1	75	65.855	45	34	DOMON domain containing protein
Locus_1253_Transcript_1/2_Conf_1.000	487	0							
Locus_1253_Transcript_2/2_Conf_1.000	487	1	1.49E-05	XP_002738888.1	41	52.7582	128	53	PREDICTED: selectin, platelet-like
Locus_12530_Transcript_1/1_Conf_1.000	367	0							
Locus_12531_Transcript_1/1_Conf_1.000	280	2	3.15E-08	XP_002630287.1	86	61.6178	44	38	Hypothetical protein CBG00720
Locus_12532_Transcript_1/1_Conf_1.000	145	0							
Locus_12533_Transcript_1/1_Conf_1.000	843	0							

Locus_12534_Transcript_1/1_Conf_1.000	733	20	1.57E-126	XP_002647010.1	93	456.062	242	227	C. briggsae CBR-COR-1 protein
Locus_12535_Transcript_1/1_Conf_1.000	787	0							
Locus_12536_Transcript_1/1_Conf_1.000	1674	2	1.88E-04	XP_002505186.1	38	52.373	236	90	predicted protein
Locus_12537_Transcript_1/1_Conf_1.000	553	20	2.04E-05	XP_790476.1	54	52.7582	130	71	PREDICTED: hypothetical protein
Locus_12538_Transcript_1/1_Conf_1.000	338	20	2.57E-18	EFA09973.1	64	95.1301	110	71	hypothetical protein TcasGA2_TC012131
Locus_12539_Transcript_1/1_Conf_1.000	438	8	1.11E-13	CBA11608.1	57	79.7221	137	79	C. elegans protein F45H7.2d, partially confirmed by transcript evidence
Locus_1254_Transcript_1/4_Conf_0.667	797	0							
Locus_1254_Transcript_2/4_Conf_0.444	271	0							
Locus_1254_Transcript_3/4_Conf_0.667	848	0							
Locus_1254_Transcript_4/4_Conf_0.667	788	0							
Locus_12540_Transcript_1/1_Conf_1.000	429	5	3.89E-06	XP_002636697.1	47	54.6842	141	67	Hypothetical protein CBG23415
Locus_12541_Transcript_1/1_Conf_1.000	2523	14	2.06E-08	XP_002666563.1	37	66.2402	325	121	PREDICTED: wu:fo94f09
Locus_12542_Transcript_1/1_Conf_1.000	391	20	1.26E-41	XP_002639098.1	78	172.555	129	101	C. briggsae CBR-UNC-40 protein
Locus_12543_Transcript_1/1_Conf_1.000	746	20	2.82E-62	CBM41226.1	66	242.662	263	175	C. elegans protein T21C9.2b, confirmed by transcript evidence
Locus_12544_Transcript_1/1_Conf_1.000	574	4	1.37E-10	XP_001900000.1	58	70.0922	92	54	60S ribosomal protein L44
Locus_12545_Transcript_1/1_Conf_1.000	313	20	4.23E-16	XP_002641332.1	61	87.8113	99	61	Hypothetical protein CBG13180
Locus_12546_Transcript_1/1_Conf_1.000	438	3	8.55E-06	NP_001023785.1	45	53.5286	150	68	hypothetical protein F11A3.2

Locus_12547_Transcript_1/1_Conf_1.000	994	20	1.13E-116	NP_494571.1	82	424.091	328	269	AdaPtin, Delta chain (clathrin associated complex) family member (apd-3)
Locus_12548_Transcript_1/1_Conf_1.000	890	20	5.58E-69	XP_002630482.1	65	265.388	306	200	Hypothetical protein CBG11218
Locus_12549_Transcript_1/1_Conf_1.000	225	3	2.64E-10	P0C656.2	62	68.5514	72	45	Mediator of RNA polymerase II transcription subunit 12
Locus_1255_Transcript_1/1_Conf_1.000	612	20	3.71E-47	XP_002642127.1	78	191.815	142	112	C. briggsae CBR-RNP-4 protein
Locus_12550_Transcript_1/1_Conf_1.000	709	20	3.10E-44	NP_001021008.1	72	182.57	184	133	PolyBRoMo domain containing family member (pbrm-1)
Locus_12551_Transcript_1/1_Conf_1.000	294	1	6.90E-11	NP_001129840.1	69	70.4774	63	44	hypothetical protein R08D7.4
Locus_12552_Transcript_1/1_Conf_1.000	544	5	5.05E-30	XP_002630594.1	63	134.42	195	123	C. briggsae CBR-AKA-1 protein
Locus_12553_Transcript_1/1_Conf_1.000	237	0							

Locus_12554_Transcript_1/1_Conf_1.000	1477	20	8.09E-158	XP_002641701.1	81	561.607	438	356	C. briggsae CBR-TBG-1 protein
Locus_12555_Transcript_1/1_Conf_1.000	302	0							
Locus_12556_Transcript_1/1_Conf_1.000	282	20	3.81E-41	XP_002630326.1	96	171.014	93	90	Hypothetical protein CBG04253
Locus_12557_Transcript_1/1_Conf_1.000	380	0							
Locus_12558_Transcript_1/1_Conf_1.000	273	0							
Locus_12559_Transcript_1/1_Conf_1.000	235	3	1.30E-09	XP_002639005.1	60	66.2402	80	48	Hypothetical protein CBG22251
Locus_1256_Transcript_1/1_Conf_1.000	1268	20	2.92E-57	NP_503731.1	63	227.254	269	171	hypothetical protein Y45G12B.2
Locus_12560_Transcript_1/1_Conf_1.000	594	0							
Locus_12561_Transcript_1/1_Conf_1.000	531	20	1.49E-23	EFO15643.1	89	112.849	68	61	K+ channel tetramerisation domain-containing protein
Locus_12562_Transcript_1/1_Conf_1.000	312	0							
Locus_12563_Transcript_1/1_Conf_1.000	295	20	4.15E-40	XP_002834805.1	100	167.548	86	86	PREDICTED: cytochrome c oxidase subunit 6C-like
Locus_12564_Transcript_1/1_Conf_1.000	813	0							
Locus_12565_Transcript_1/1_Conf_1.000	268	0							
Locus_12566_Transcript_1/2_Conf_1.000	634	0							
Locus_12566_Transcript_2/2_Conf_1.000	619	0							
Locus_12567_Transcript_1/1_Conf_1.000	194	0							
Locus_12568_Transcript_1/1_Conf_1.000	181	0							
Locus_12569_Transcript_1/1_Conf_1.000	130	0							
Locus_1257_Transcript_1/1_Conf_1.000	240	0							
Locus_12570_Transcript_1/1_Conf_1.000	257	0							
Locus_12571_Transcript_1/1_Conf_1.000	682	20	1.06E-22	EFO19565.1	60	110.923	108	65	hypothetical protein LOAG_08928
Locus_12572_Transcript_1/1_Conf_1.000	624	20	1.32E-55	XP_002630212.1	89	219.935	129	115	Hypothetical protein CBG00622
Locus_12573_Transcript_1/1_Conf_1.000	276	0							
Locus_12574_Transcript_1/1_Conf_1.000	1074	20	3.50E-98	NP_494995.1	72	362.844	362	261	Guanylyl CYclase family member (gcy-12)

Locus_12575_Transcript_1/1_Conf_1.000	984	20	5.53E-07	XP_001581848.1	42	59.6918	339	143	hypothetical protein
Locus_12576_Transcript_1/1_Conf_1.000	164	0							
Locus_12577_Transcript_1/1_Conf_1.000	351	20	6.66E-14	EFO26156.1	65	80.4925	106	69	hypothetical protein LOAG_02329
Locus_12578_Transcript_1/1_Conf_1.000	450	0							
Locus_12579_Transcript_1/1_Conf_1.000	465	1	1.04E-43	XP_001164327.1	95	129.798	86	82	PREDICTED: prolyl 4-hydroxylase, beta subunit isoform 5
Locus_1258_Transcript_1/1_Conf_1.000	1433	20	6.74E-61	XP_001900112.1	58	239.58	355	208	UV excision repair protein Rad23 containing protein
Locus_12580_Transcript_1/2_Conf_1.000	1040	20	3.04E-51	EFO25759.1	60	206.838	279	168	hypothetical protein LOAG_02720
Locus_12580_Transcript_2/2_Conf_1.000	1040	20	3.04E-51	EFO25759.1	60	206.838	279	168	hypothetical protein LOAG_02720
Locus_12581_Transcript_1/1_Conf_1.000	358	5	2.43E-16	XP_002632410.1	56	88.5817	121	68	Hypothetical protein CBG00435
Locus_12582_Transcript_1/1_Conf_1.000	278	0							
Locus_12583_Transcript_1/1_Conf_1.000	915	20	1.77E-73	XP_001896686.1	68	280.411	310	211	hypothetical protein
Locus_12584_Transcript_1/1_Conf_1.000	526	0							
Locus_12585_Transcript_1/1_Conf_1.000	296	2	2.71E-07	XP_002639374.1	57	58.5362	76	44	Hypothetical protein CBG03958
Locus_12586_Transcript_1/1_Conf_1.000	336	20	6.99E-24	NP_496444.1	67	113.62	106	72	Alanyl tRNA Synthetase family member (ars-1)

Locus_12587_Transcript_1/1_Conf_1.000	949	20	1.21E-112	XP_002646059.1	92	410.609	239	221	C. briggsae CBR-PMR-1 protein
Locus_12588_Transcript_1/1_Conf_1.000	398	2	3.09E-35	NP_500395.2	76	151.369	131	100	hypothetical protein Y37E11AL.6
Locus_12589_Transcript_1/1_Conf_1.000	131	0							
Locus_1259_Transcript_1/4_Conf_0.400	276	14	1.12E-05	NP_001174125.1	40	53.1434	88	36	Os04g0654400
Locus_1259_Transcript_2/4_Conf_0.500	399	20	1.14E-05	BAJ05299.1	39	53.1434	138	54	oocyte maturation arresting factor
Locus_1259_Transcript_3/4_Conf_0.300	399	0							
Locus_1259_Transcript_4/4_Conf_0.600	522	6	4.23E-04	ZP_06212340.1	46	48.1358	83	39	UreE urease accessory domain protein
Locus_12590_Transcript_1/1_Conf_1.000	2848	20	0	XP_001900373.1	71	875.159	832	597	TPR Domain containing protein
Locus_12591_Transcript_1/1_Conf_1.000	353	20	4.45E-26	XP_002640398.1	60	120.939	120	73	Hypothetical protein CBG08444
Locus_12592_Transcript_1/1_Conf_1.000	223	20	1.27E-20	XP_002637343.1	78	102.834	70	55	Hypothetical protein CBG19039
Locus_12593_Transcript_1/1_Conf_1.000	429	0							
Locus_12594_Transcript_1/1_Conf_1.000	290	0							

Locus_12595_Transcript_1/1_Conf_1.000	283	0							
Locus_12596_Transcript_1/1_Conf_1.000	423	20	1.64E-28	NP_497201.1	75	129.028	133	101	hypothetical protein Y55B1BR.4
Locus_12597_Transcript_1/1_Conf_1.000	1170	20	1.71E-125	NP_491652.1	75	453.751	395	299	hypothetical protein F55F8.2
Locus_12598_Transcript_1/1_Conf_1.000	771	20	1.03E-78	XP_001900477.1	79	297.36	240	190	HMG box family protein
Locus_12599_Transcript_1/1_Conf_1.000	220	0							
Locus_126_Transcript_1/1_Conf_1.000	2058	20	6.05E-80	XP_001896711.1	65	303.523	317	209	Dcp2, box A domain containing protein
Locus_1260_Transcript_1/1_Conf_1.000	1398	20	1.13E-129	XP_002635578.1	86	468.003	301	260	C. briggsae CBR-TAG-253 protein
Locus_12600_Transcript_1/1_Conf_1.000	1892	20	6.35E-20	XP_002647615.1	43	103.99	301	132	C. briggsae CBR-MES-4 protein
Locus_12601_Transcript_1/1_Conf_1.000	725	20	3.35E-57	XP_002634017.1	71	225.713	225	161	C. briggsae CBR-SPH-1 protein
Locus_12602_Transcript_1/1_Conf_1.000	459	4	5.91E-15	NP_490674.3	53	83.9593	156	84	hypothetical protein Y48G1C.8
Locus_12603_Transcript_1/1_Conf_1.000	623	20	2.45E-62	XP_002639152.1	75	242.276	196	148	Hypothetical protein CBG14979
Locus_12604_Transcript_1/1_Conf_1.000	368	20	6.91E-48	XP_002641646.1	84	193.356	123	104	C. briggsae CBR-CBP-1 protein

Locus_12605_Transcript_1/1_Conf_1.000	231	20	1.80E-35	NP_510459.1	98	152.14	76	75	EPsiN (endocytic protein) homolog family member (epn-1)
Locus_12606_Transcript_1/1_Conf_1.000	516	0							
Locus_12607_Transcript_1/1_Conf_1.000	379	0							
Locus_12608_Transcript_1/1_Conf_1.000	261	0							
Locus_12609_Transcript_1/1_Conf_1.000	199	20	6.64E-22	XP_002927828.1	100	107.071	50	50	PREDICTED: 60S ribosomal protein L17-like
Locus_1261_Transcript_1/3_Conf_0.625	360	20	1.24E-12	AAD51334.1	72	76.2554	59	43	Kunitz type serine protease inhibitor
Locus_1261_Transcript_2/3_Conf_0.250	1504	20	2.78E-137	NP_506041.1	74	493.426	430	319	hypothetical protein C13C4.5
Locus_1261_Transcript_3/3_Conf_0.625	1417	20	2.65E-118	XP_001898133.1	77	430.254	354	274	Innexin family protein
Locus_12610_Transcript_1/1_Conf_1.000	481	0							
Locus_12611_Transcript_1/1_Conf_1.000	411	20	6.33E-25	XP_002636649.1	60	117.087	124	75	Hypothetical protein CBG23360
Locus_12612_Transcript_1/1_Conf_1.000	764	0							
Locus_12613_Transcript_1/1_Conf_1.000	652	20	1.09E-66	NP_490879.2	75	256.914	203	154	hypothetical protein Y71G12B.17
Locus_12614_Transcript_1/1_Conf_1.000	371	0							

Locus_12615_Transcript_1/1_Conf_1.000	179	20	5.72E-18	XP_002813487.1	100	93.9745	44	44	PREDICTED: protein SEC13 homolog isoform 4
Locus_12616_Transcript_1/1_Conf_1.000	474	20	1.08E-24	XP_002630102.1	69	116.316	155	107	Hypothetical protein CBG13485
Locus_12617_Transcript_1/2_Conf_1.000	566	20	3.28E-38	EFO27624.1	69	161.77	129	90	hypothetical protein LOAG_00857
Locus_12617_Transcript_2/2_Conf_1.000	795	20	7.18E-38	EFO27624.1	69	161.77	129	90	hypothetical protein LOAG_00857
Locus_12618_Transcript_1/2_Conf_1.000	546	0							
Locus_12618_Transcript_2/2_Conf_1.000	254	0							
Locus_12619_Transcript_1/1_Conf_1.000	421	0							
Locus_1262_Transcript_1/1_Conf_1.000	1527	20	2.45E-72	XP_002635160.1	64	277.715	391	252	Hypothetical protein CBG11393
Locus_12620_Transcript_1/1_Conf_1.000	311	0							
Locus_12621_Transcript_1/1_Conf_1.000	638	0							
Locus_12622_Transcript_1/1_Conf_1.000	303	0							
Locus_12623_Transcript_1/1_Conf_1.000	393	0							
Locus_12624_Transcript_1/1_Conf_1.000	209	2	1.13E-05	NP_495673.2	79	53.1434	69	55	hypothetical protein DH11.4
Locus_12625_Transcript_1/1_Conf_1.000	401	0							
Locus_12626_Transcript_1/2_Conf_0.500	1445	2	4.07E-05	XP_002647016.1	38	54.299	338	129	Hypothetical protein CBG24039
Locus_12626_Transcript_2/2_Conf_0.500	919	0							
Locus_12627_Transcript_1/1_Conf_1.000	458	20	9.39E-45	XP_001895623.1	83	182.956	120	100	DNA-directed RNA polymerase II 33 kDa polypeptide
Locus_12628_Transcript_1/1_Conf_1.000	494	20	1.09E-08	ZP_07656264.1	53	63.1586	136	73	chromosome segregation protein SMC

Locus_12629_Transcript_1/1_Conf_1.000	870	2	7.21E-13	XP_002639099.1	44	78.9518	295	132	C. briggsae CBR-NPP-7 protein
Locus_1263_Transcript_1/1_Conf_1.000	979	0							
Locus_12630_Transcript_1/1_Conf_1.000	615	0							
Locus_12631_Transcript_1/1_Conf_1.000	314	3	6.77E-06	XP_002642902.1	47	53.9138	117	55	Hypothetical protein CBG15176
Locus_12632_Transcript_1/1_Conf_1.000	944	20	2.87E-90	NP_493664.2	77	336.265	271	210	hypothetical protein K10B4.3
Locus_12633_Transcript_1/1_Conf_1.000	1558	20	5.25E-155	NP_495455.2	84	552.362	390	331	3-Ketoacyl-coA Thiolase family member (kat-1)
Locus_12634_Transcript_1/1_Conf_1.000	273	20	2.10E-44	XP_002749580.1	100	181.8	89	89	PREDICTED: 60S ribosomal protein L10a-like isoform 1
Locus_12635_Transcript_1/1_Conf_1.000	743	6	2.48E-18	EFO22616.1	43	96.6709	341	147	TK/ABL protein kinase
Locus_12636_Transcript_1/1_Conf_1.000	1284	20	1.85E-91	XP_001895766.1	68	340.887	389	265	double-strand break repair protein mre-11

Locus_12637_Transcript_1/1_Conf_1.000	912	20	9.17E-22	CAX65090.1	55	108.612	177	98	C. elegans protein Y56A3A.4b, confirmed by transcript evidence
Locus_12638_Transcript_1/3_Conf_0.600	546	20	1.35E-38	XP_002643489.1	83	162.925	106	88	C. briggsae CBR-APA-2 protein
Locus_12638_Transcript_2/3_Conf_0.600	551	20	1.38E-38	XP_002643489.1	83	162.925	106	88	C. briggsae CBR-APA-2 protein

Locus_12638_Transcript_3/3_Conf_0.600	551	20	1.38E-38	XP_002643489.1	83	162.925	106	88	C. briggsae CBR-APA-2 protein
Locus_12639_Transcript_1/1_Conf_1.000	813	0							
Locus_1264_Transcript_1/2_Conf_1.000	674	20	9.52E-53	XP_002631659.1	90	210.69	116	105	C. briggsae CBR-MEX-1 protein
Locus_1264_Transcript_2/2_Conf_1.000	680	20	9.73E-53	XP_002631659.1	90	210.69	116	105	C. briggsae CBR-MEX-1 protein
Locus_12640_Transcript_1/1_Conf_1.000	597	20	5.71E-42	NP_001024929.1	69	174.481	191	132	Choline Kinase C family member (ckc-1)
Locus_12641_Transcript_1/2_Conf_1.000	244	0							
Locus_12641_Transcript_2/2_Conf_1.000	244	0							
Locus_12642_Transcript_1/1_Conf_1.000	398	0							
Locus_12643_Transcript_1/1_Conf_1.000	1113	20	6.49E-127	NP_001122812.1	79	458.373	359	287	TBC (Tre-2/Bub2/Cdc16) domain family member (tbc-9)
Locus_12644_Transcript_1/1_Conf_1.000	227	0							
Locus_12645_Transcript_1/1_Conf_1.000	475	20	9.70E-66	EFO26601.1	83	252.677	156	131	CK1/WORM6 protein kinase
Locus_12646_Transcript_1/1_Conf_1.000	283	0							
Locus_12647_Transcript_1/1_Conf_1.000	402	0							
Locus_12648_Transcript_1/1_Conf_1.000	1086	2	2.71E-13	XP_001900007.1	42	80.8777	288	121	hypothetical protein Bm1_42720
Locus_12649_Transcript_1/1_Conf_1.000	186	0							
Locus_1265_Transcript_1/2_Conf_0.333	2359	20	3.74E-113	XP_001898107.1	65	414.075	464	303	PDZ-domain protein scribble
Locus_1265_Transcript_2/2_Conf_0.667	1272	20	5.40E-144	NP_491319.1	90	515.383	323	292	proteasome Regulatory Particle, Non-ATPase-like family member (rpn-8)

Locus_12650_Transcript_1/1_Conf_1.000	190	2	1.66E-04	XP_002410801.1	56	49.2914	60	34	factor for adipocyte differentiation, putative
Locus_12651_Transcript_1/1_Conf_1.000	344	20	2.23E-25	NP_499570.1	87	118.627	79	69	ARp2/3 compleX component family member (arx-3)
Locus_12652_Transcript_1/1_Conf_1.000	438	0							
Locus_12653_Transcript_1/1_Conf_1.000	154	2	3.34E-05	XP_002643365.1	64	51.6026	57	37	C. briggsae CBR-PQN-34 protein
Locus_12654_Transcript_1/2_Conf_1.000	1788	20	0	NP_495749.1	80	681.404	552	447	mammalian NucleoSTemin (stem cell marker) related family member (nst-1)
Locus_12654_Transcript_2/2_Conf_1.000	1788	20	0	NP_495749.1	81	681.404	552	448	mammalian NucleoSTemin (stem cell marker) related family member (nst-1)
Locus_12655_Transcript_1/1_Conf_1.000	366	20	3.01E-35	NP_001129924.1	90	151.369	121	110	SLOwpoke potassium channel family member (slo-2)
Locus_12656_Transcript_1/1_Conf_1.000	256	0							
Locus_12657_Transcript_1/1_Conf_1.000	265	0							
Locus_12658_Transcript_1/1_Conf_1.000	411	6	2.41E-16	XP_001901424.1	72	88.5817	127	92	tRNA modification GTPase TrmE family protein
Locus_12659_Transcript_1/1_Conf_1.000	510	0							
Locus_1266_Transcript_1/1_Conf_1.000	900	20	2.63E-106	NP_001022302.1	92	389.423	259	239	MethylMalonic Aciduria type A protein family member (mmaa-1)
Locus_12660_Transcript_1/1_Conf_1.000	247	3	1.46E-05	NP_491382.1	75	52.7582	48	36	hypothetical protein Y119C1B.5
Locus_12661_Transcript_1/1_Conf_1.000	507	0							
Locus_12662_Transcript_1/1_Conf_1.000	694	20	5.13E-28	XP_001891849.1	58	128.642	173	102	Retinoblastoma-associated protein A domain containing protein
Locus_12663_Transcript_1/1_Conf_1.000	889	0							
Locus_12664_Transcript_1/1_Conf_1.000	133	0							
Locus_12665_Transcript_1/1_Conf_1.000	1434	20	1.51E-177	NP_506191.1	81	627.091	433	351	hypothetical protein F18E2.1
Locus_12666_Transcript_1/1_Conf_1.000	235	0							
Locus_12667_Transcript_1/1_Conf_1.000	321	0							

Locus_12668_Transcript_1/1_Conf_1.000	375	0							
Locus_12669_Transcript_1/1_Conf_1.000	340	0							
Locus_1267_Transcript_1/2_Conf_1.000	2235	20	0	XP_002640959.1	94	882.478	528	497	C. briggsae CBR-HSP-60 protein
Locus_1267_Transcript_2/2_Conf_1.000	937	0							
Locus_12670_Transcript_1/1_Conf_1.000	1490	0							
Locus_12671_Transcript_1/3_Conf_0.600	849	20	3.13E-90	NP_741744.2	78	335.88	274	214	hypothetical protein C15C7.7
Locus_12671_Transcript_2/3_Conf_0.600	773	20	2.07E-87	NP_741744.2	79	326.25	250	199	hypothetical protein C15C7.7

Locus_12671_Transcript_3/3_Conf_0.600	849	20	5.70E-92	NP_741744.2	78	341.658	274	216	hypothetical protein C15C7.7
Locus_12672_Transcript_1/1_Conf_1.000	394	0							
Locus_12673_Transcript_1/1_Conf_1.000	233	18	7.37E-13	NP_741861.2	83	77.0258	53	44	Nuclear Hormone Receptor family member (nhr-14)
Locus_12674_Transcript_1/1_Conf_1.000	701	13	5.22E-36	ACV31115.1	81	155.221	126	103	Hypothetical protein H06I04.6b
Locus_12675_Transcript_1/1_Conf_1.000	379	0							
Locus_12676_Transcript_1/1_Conf_1.000	210	0							
Locus_12677_Transcript_1/1_Conf_1.000	295	0							
Locus_12678_Transcript_1/1_Conf_1.000	438	20	1.58E-68	XP_002639744.1	83	261.922	142	118	C. briggsae CBR-LAM-3 protein
Locus_12679_Transcript_1/1_Conf_1.000	1321	20	0	NP_497570.1	86	693.345	416	359	hypothetical protein Y54F10AM.8
Locus_1268_Transcript_1/1_Conf_1.000	164	19	4.45E-18	XP_001894499.1	94	94.3597	51	48	unc-45 protein
Locus_12680_Transcript_1/1_Conf_1.000	241	3	1.86E-08	NP_508175.1	94	62.3882	38	36	Suppressor/Enhancer of Lin-12 family member (sel-12)
Locus_12681_Transcript_1/2_Conf_1.000	534	20	5.60E-47	XP_002634543.1	74	190.66	169	126	C. briggsae CBR-CED-5 protein

Locus_12681_Transcript_2/2_Conf_1.000	534	20	5.60E-47	XP_002634543.1	74	190.66	169	126	C. briggsae CBR-CED-5 protein
Locus_12682_Transcript_1/1_Conf_1.000	386	4	6.16E-20	EFO26621.1	53	100.523	151	81	AIDA-1b
Locus_12683_Transcript_1/1_Conf_1.000	316	0							
Locus_12684_Transcript_1/1_Conf_1.000	137	12	4.27E-05	XP_002609440.1	60	51.2174	43	26	hypothetical protein BRAFLDRAFT_93487
Locus_12685_Transcript_1/1_Conf_1.000	413	20	5.19E-19	CAL53402.1	59	97.4413	108	64	putative SMC protein (ISS)
Locus_12686_Transcript_1/1_Conf_1.000	133	0							
Locus_12687_Transcript_1/1_Conf_1.000	207	0							
Locus_12688_Transcript_1/1_Conf_1.000	219	0							
Locus_12689_Transcript_1/1_Conf_1.000	175	0							
Locus_1269_Transcript_1/1_Conf_1.000	803	20	5.86E-96	XP_002633299.1	83	354.755	240	200	Hypothetical protein CBG06029
Locus_12690_Transcript_1/1_Conf_1.000	250	0							
Locus_12691_Transcript_1/1_Conf_1.000	457	3	4.87E-09	NP_498641.1	53	64.3142	89	48	hypothetical protein H14A12.3
Locus_12692_Transcript_1/3_Conf_0.714	953	20	2.99E-79	NP_502288.1	80	299.671	211	170	hypothetical protein K08E4.6
Locus_12692_Transcript_2/3_Conf_0.714	953	20	6.03E-80	NP_502288.1	81	301.982	211	171	hypothetical protein K08E4.6
Locus_12692_Transcript_3/3_Conf_0.714	953	20	6.03E-80	NP_502288.1	81	301.982	211	171	hypothetical protein K08E4.6
Locus_12693_Transcript_1/1_Conf_1.000	546	4	2.00E-66	NP_001033357.2	82	255.373	181	150	DAF-16/FOXO Controlled, germline Tumor affecting family member (dct-6)
Locus_12694_Transcript_1/1_Conf_1.000	464	0							
Locus_12695_Transcript_1/1_Conf_1.000	242	0							
Locus_12696_Transcript_1/3_Conf_0.333	224	0							

Locus_12696_Transcript_2/3_Conf_0.667	751	0							
Locus_12696_Transcript_3/3_Conf_0.500	566	0							
Locus_12697_Transcript_1/1_Conf_1.000	224	2	9.73E-13	XP_002632085.1	88	76.6406	42	37	Hypothetical protein CBG17053
Locus_12698_Transcript_1/1_Conf_1.000	264	0							
Locus_12699_Transcript_1/1_Conf_1.000	500	20	9.04E-56	XP_002632430.1	81	219.55	166	136	Hypothetical protein CBG00458
Locus_127_Transcript_1/4_Conf_0.250	497	20	2.80E-81	DAA05878.1	98	304.294	151	148	TPA_inf: eukaryotic translation elongation factor 1A
Locus_127_Transcript_2/4_Conf_0.250	539	20	3.54E-81	DAA05878.1	98	304.294	151	148	TPA_inf: eukaryotic translation elongation factor 1A
Locus_127_Transcript_3/4_Conf_0.450	1010	20	6.93E-178	ABX79382.1	97	627.476	323	315	elongation factor 1 alpha
Locus_127_Transcript_4/4_Conf_0.450	1010	20	6.93E-178	ABX79382.1	97	627.476	323	315	elongation factor 1 alpha
Locus_1270_Transcript_1/1_Conf_1.000	1122	20	5.19E-23	NP_001023207.1	62	113.235	176	110	MiniBrain Kinase (Drosophila) homolog family member (mbk-2)
Locus_12700_Transcript_1/1_Conf_1.000	396	0							

Locus_12701_Transcript_1/1_Conf_1.000	600	16	2.13E-36	ACI49203.1	92	155.992	92	85	hypothetical protein Csp3_JD04.002
Locus_12702_Transcript_1/1_Conf_1.000	148	20	7.72E-18	NP_508515.2	93	93.5893	48	45	AQuaPorin or aquaglyceroporin related family member (aqp-7)
Locus_12703_Transcript_1/1_Conf_1.000	408	3	2.35E-11	NP_498613.2	53	72.0182	114	61	hypothetical protein F56C9.8
Locus_12704_Transcript_1/1_Conf_1.000	778	20	7.04E-59	XP_002639543.1	75	231.491	244	185	Hypothetical protein CBG04172
Locus_12705_Transcript_1/1_Conf_1.000	389	0							
Locus_12706_Transcript_1/1_Conf_1.000	474	0							
Locus_12707_Transcript_1/1_Conf_1.000	285	0							
Locus_12708_Transcript_1/1_Conf_1.000	632	20	3.99E-07	ABA06434.1	48	58.9214	129	63	telomerase reverse transcriptase
Locus_12709_Transcript_1/1_Conf_1.000	379	20	1.39E-11	ACM79010.1	64	72.7886	67	43	Kunitz protein 8
Locus_1271_Transcript_1/1_Conf_1.000	645	20	6.41E-80	NP_001022987.1	89	300.827	183	164	related to yeast Vacuolar Protein Sorting factor family member (vps-29)

Locus_12710_Transcript_1/1_Conf_1.000	230	20	8.14E-28	AAY84711.2	86	126.716	74	64	dual oxidase
Locus_12711_Transcript_1/1_Conf_1.000	1057	20	2.33E-22	XP_001894604.1	50	110.923	240	121	exonuclease family protein
Locus_12712_Transcript_1/1_Conf_1.000	239	0							
Locus_12713_Transcript_1/1_Conf_1.000	232	2	2.45E-08	NP_494772.1	71	62.003	66	47	NOT-Like (yeast CCR4/NOT complex component) family member (ntl-2)
Locus_12714_Transcript_1/1_Conf_1.000	397	20	3.31E-29	EFO19311.1	63	131.339	128	81	hypothetical protein LOAG_09182
Locus_12715_Transcript_1/1_Conf_1.000	203	11	1.34E-06	ADI61824.1	59	56.225	67	40	endonuclease-reverse transcriptase
Locus_12716_Transcript_1/1_Conf_1.000	1234	20	1.23E-177	CAA06162.1	89	627.091	397	354	CB-CYP-4

Locus_12717_Transcript_1/1_Conf_1.000	397	20	2.09E-07	XP_002630114.1	97	58.9214	34	33	C. briggsae CBR-PYR-1 protein
Locus_12718_Transcript_1/1_Conf_1.000	428	20	6.79E-51	NP_504643.1	80	203.371	142	115	ACyLtransferase-like family member (acl-8)
Locus_12719_Transcript_1/1_Conf_1.000	158	0							
Locus_1272_Transcript_1/1_Conf_1.000	689	20	2.36E-102	NP_498785.1	93	375.555	205	192	yeast PRP (splicing factor) related family member (prp-8)
Locus_12720_Transcript_1/1_Conf_1.000	294	0							
Locus_12721_Transcript_1/1_Conf_1.000	205	0							
Locus_12722_Transcript_1/1_Conf_1.000	353	0							
Locus_12723_Transcript_1/1_Conf_1.000	277	0							
Locus_12724_Transcript_1/1_Conf_1.000	158	0							
Locus_12725_Transcript_1/1_Conf_1.000	471	20	6.82E-27	NP_505188.3	60	123.635	160	96	PeroXidasiN (Drosophila peroxidase) homolog family member (pxn-1)

Locus_12726_Transcript_1/1_Conf_1.000	591	20	2.82E-62	NP_001023646.1	80	241.891	196	158	AKT kinase family member (akt-1)
Locus_12727_Transcript_1/1_Conf_1.000	882	20	3.52E-124	BAG63399.1	100	448.743	222	222	unnamed protein product
Locus_12728_Transcript_1/1_Conf_1.000	945	20	2.81E-61	EFA79727.1	64	239.965	266	171	hypothetical protein PPL_07418
Locus_12729_Transcript_1/1_Conf_1.000	170	0							
Locus_1273_Transcript_1/1_Conf_1.000	692	20	8.85E-65	XP_002631500.1	81	250.751	200	162	Hypothetical protein CBG20664
Locus_12730_Transcript_1/1_Conf_1.000	380	1	2.07E-07	NP_499670.1	75	58.9214	45	34	hypothetical protein Y37D8A.4
Locus_12731_Transcript_1/1_Conf_1.000	364	20	4.23E-29	NP_507527.2	83	130.954	112	93	hypothetical protein Y59A8B.8
Locus_12732_Transcript_1/1_Conf_1.000	168	0							
Locus_12733_Transcript_1/1_Conf_1.000	917	1	3.19E-06	XP_001900252.1	40	56.9954	333	134	hypothetical protein Bm1_43950

Locus_12734_Transcript_1/1_Conf_1.000	608	20	7.02E-51	NP_506230.1	84	204.142	157	132	hypothetical protein F54F3.4
Locus_12735_Transcript_1/1_Conf_1.000	133	0							
Locus_12736_Transcript_1/1_Conf_1.000	380	0							
Locus_12737_Transcript_1/1_Conf_1.000	361	0							
Locus_12738_Transcript_1/1_Conf_1.000	272	20	7.50E-42	XP_002637342.1	97	173.326	90	88	C. briggsae CBR-UNC-70 protein
Locus_12739_Transcript_1/1_Conf_1.000	333	1	1.24E-12	EFO14895.1	85	76.2554	49	42	CMGC/CDK/CDK9 protein kinase
Locus_1274_Transcript_1/1_Conf_1.000	520	20	1.19E-35	XP_002634275.1	68	152.91	168	115	Hypothetical protein CBG01851
Locus_12740_Transcript_1/1_Conf_1.000	367	3	2.66E-07	NP_001021652.1	46	58.5362	118	55	FANCI (Fanconi anemia complex component I) homolog family member (fnci-1)
Locus_12741_Transcript_1/1_Conf_1.000	290	0							
Locus_12742_Transcript_1/2_Conf_1.000	808	20	3.94E-23	XP_002640836.1	56	112.849	230	131	Hypothetical protein CBG15724
Locus_12742_Transcript_2/2_Conf_1.000	808	20	3.94E-23	XP_002640836.1	56	112.849	230	131	Hypothetical protein CBG15724
Locus_12743_Transcript_1/1_Conf_1.000	671	20	3.45E-63	XP_002639870.1	69	245.358	223	155	C. briggsae CBR-IRS-2 protein
Locus_12744_Transcript_1/1_Conf_1.000	537	20	6.55E-35	XP_002633331.1	70	150.599	139	98	Hypothetical protein CBG06070
Locus_12745_Transcript_1/1_Conf_1.000	600	0							

Locus_12746_Transcript_1/1_Conf_1.000	419	20	1.09E-72	NP_001122711.1	94	275.789	136	129	CBP/p300 homolog family member (cbp-1)
Locus_12747_Transcript_1/1_Conf_1.000	446	4	3.65E-28	XP_002634339.1	72	127.872	134	97	C. briggsae CBR-RIC-3 protein
Locus_12748_Transcript_1/1_Conf_1.000	133	0							
Locus_12749_Transcript_1/1_Conf_1.000	257	0							
Locus_1275_Transcript_1/2_Conf_1.000	212	6	1.16E-10	NP_001023274.1	64	69.707	70	45	VITellogenin structural genes (yolk protein genes) family member (vit-6)
Locus_1275_Transcript_2/2_Conf_1.000	205	6	3.40E-10	NP_001023274.1	64	68.1662	68	44	VITellogenin structural genes (yolk protein genes) family member (vit-6)
Locus_12750_Transcript_1/1_Conf_1.000	178	0							
Locus_12751_Transcript_1/1_Conf_1.000	271	7	1.25E-12	CAD44516.1	65	76.2554	89	58	VAB-10B protein
Locus_12752_Transcript_1/1_Conf_1.000	924	20	3.21E-46	XP_002636564.1	80	189.889	149	120	Hypothetical protein CBG23256
Locus_12753_Transcript_1/1_Conf_1.000	237	0							
Locus_12754_Transcript_1/1_Conf_1.000	601	20	1.06E-35	NP_496466.1	79	153.68	116	92	hypothetical protein F54D5.11
Locus_12755_Transcript_1/1_Conf_1.000	264	20	2.29E-14	NP_502268.1	64	82.0333	82	53	TRNA Guanine Transglycosylase family member (tgt-1)
Locus_12756_Transcript_1/2_Conf_1.000	695	4	3.31E-35	XP_002639709.1	62	152.525	202	127	Hypothetical protein CBG12430
Locus_12756_Transcript_2/2_Conf_1.000	695	4	2.54E-35	XP_002639709.1	63	152.91	202	128	Hypothetical protein CBG12430

Locus_12757_Transcript_1/1_Conf_1.000	219	3	3.70E-20	CAR63585.1	91	101.293	72	66	putative MAD-Like family member
Locus_12758_Transcript_1/1_Conf_1.000	433	20	1.50E-42	NP_499178.1	87	175.637	132	115	ARF-Like family member (arl-5)
Locus_12759_Transcript_1/1_Conf_1.000	417	20	1.54E-42	XP_001896370.1	80	175.637	138	111	hypothetical protein
Locus_1276_Transcript_1/1_Conf_1.000	221	4	2.74E-15	XP_002631558.1	75	85.1149	73	55	Hypothetical protein CBG20734
Locus_12760_Transcript_1/1_Conf_1.000	271	1	1.68E-17	EAW48404.1	100	92.4337	42	42	hCG2030753
Locus_12761_Transcript_1/1_Conf_1.000	304	20	1.42E-16	EFO22213.1	72	89.3521	101	73	arginine-tRNA-protein transferase
Locus_12762_Transcript_1/1_Conf_1.000	663	20	4.47E-15	XP_001897733.1	48	85.5001	219	107	hypothetical protein Bm1_31440
Locus_12763_Transcript_1/1_Conf_1.000	235	7	8.70E-06	XP_002631981.1	75	53.5286	37	28	Hypothetical protein CBG10259
Locus_12764_Transcript_1/1_Conf_1.000	246	1	4.71E-04	NP_505419.3	69	47.7506	42	29	hypothetical protein K07B1.7

Locus_12765_Transcript_1/1_Conf_1.000	676	20	4.44E-74	AAL06642.1	80	281.567	201	162	serine-threonine protein kinase
Locus_12766_Transcript_1/1_Conf_1.000	452	0							
Locus_12767_Transcript_1/1_Conf_1.000	158	9	5.29E-19	XP_002488965.1	91	97.4413	46	42	hypothetical protein SORBIDRAFT_1138s002030
Locus_12768_Transcript_1/1_Conf_1.000	215	16	1.97E-10	NP_493125.2	66	68.9366	63	42	hypothetical protein T09E11.9
Locus_12769_Transcript_1/1_Conf_1.000	387	0							
Locus_1277_Transcript_1/1_Conf_1.000	519	20	1.15E-46	XP_002633893.1	77	189.504	132	102	C. briggsae CBR-ELO-5 protein
Locus_12770_Transcript_1/1_Conf_1.000	748	20	2.09E-97	NP_001021052.1	88	359.377	218	192	UDP-GALactose 4-Epimerase family member (gale-1)
Locus_12771_Transcript_1/1_Conf_1.000	259	0							
Locus_12772_Transcript_1/1_Conf_1.000	198	0							
Locus_12773_Transcript_1/1_Conf_1.000	477	20	3.92E-67	EFO21314.1	87	257.299	159	139	male sterility protein
Locus_12774_Transcript_1/1_Conf_1.000	1144	20	3.39E-70	XP_002639112.1	57	270.011	411	236	Hypothetical protein CBG14931
Locus_12775_Transcript_1/1_Conf_1.000	282	20	7.24E-08	XP_002630318.1	71	60.4622	69	49	Hypothetical protein CBG04241
Locus_12776_Transcript_1/2_Conf_1.000	523	0							
Locus_12776_Transcript_2/2_Conf_1.000	450	0							
Locus_12777_Transcript_1/1_Conf_1.000	177	20	1.85E-08	ZP_04173150.1	60	62.3882	56	34	LPXTG-motif cell wall anchor domain protein
Locus_12778_Transcript_1/1_Conf_1.000	502	1	8.24E-04	XP_002123338.1	56	46.9802	79	45	PREDICTED: similar to phosphatidylinositol glycan anchor biosynthesis, class G
Locus_12779_Transcript_1/1_Conf_1.000	264	3	9.65E-05	AAD37914.1	51	50.0618	102	53	R151.8B protein
Locus_1278_Transcript_1/1_Conf_1.000	707	20	2.78E-37	XP_001898151.1	70	159.458	140	98	Conserved hypothetical protein
Locus_12780_Transcript_1/1_Conf_1.000	306	20	2.25E-22	NP_001022063.1	72	108.612	101	73	Acyl CoA DeHydrogenase family member (acdh-12)
Locus_12781_Transcript_1/1_Conf_1.000	397	20	1.63E-60	XP_002634622.1	93	235.343	132	123	Hypothetical protein CBG18478
Locus_12782_Transcript_1/1_Conf_1.000	138	3	4.69E-12	CBA10134.1	82	74.3294	47	39	DAF-16A transcription factor

Locus_12783_Transcript_1/1_Conf_1.000	740	6	5.80E-44	NP_001032983.1	57	181.8	277	160	hypothetical protein W05F2.4
Locus_12784_Transcript_1/1_Conf_1.000	386	0							
Locus_12785_Transcript_1/1_Conf_1.000	219	0							
Locus_12786_Transcript_1/1_Conf_1.000	535	0							
Locus_12787_Transcript_1/1_Conf_1.000	206	0							
Locus_12788_Transcript_1/2_Conf_1.000	3164	20	1.68E-103	NP_500284.2	55	382.489	732	409	Enhancer of EfL-1 mutant phenotype family member (eel-1)
Locus_12788_Transcript_2/2_Conf_1.000	3164	20	1.68E-103	NP_500284.2	55	382.489	732	409	Enhancer of EfL-1 mutant phenotype family member (eel-1)
Locus_12789_Transcript_1/1_Conf_1.000	1004	20	1.09E-82	NP_500551.2	75	311.227	305	229	hypothetical protein F55F10.1
Locus_1279_Transcript_1/1_Conf_1.000	970	20	4.07E-55	XP_002637784.1	59	219.55	326	194	C. briggsae CBR-RFC-1 protein
Locus_12790_Transcript_1/1_Conf_1.000	150	0							
Locus_12791_Transcript_1/2_Conf_1.000	754	20	1.10E-13	XP_002646295.1	47	81.2629	165	79	Hypothetical protein CBG12001
Locus_12791_Transcript_2/2_Conf_1.000	742	20	7.46E-15	XP_002646295.1	52	85.1149	175	91	Hypothetical protein CBG12001
Locus_12792_Transcript_1/1_Conf_1.000	494	4	2.13E-12	NP_502353.1	67	75.485	84	57	hypothetical protein ZC518.1
Locus_12793_Transcript_1/1_Conf_1.000	378	20	2.97E-30	XP_002631828.1	78	134.806	100	78	Hypothetical protein CBG17763
Locus_12794_Transcript_1/1_Conf_1.000	314	0							
Locus_12795_Transcript_1/1_Conf_1.000	405	0							
Locus_12796_Transcript_1/1_Conf_1.000	635	1	4.04E-07	EFO17551.1	67	58.9214	71	48	hypothetical protein LOAG_10948
Locus_12797_Transcript_1/1_Conf_1.000	710	20	9.01E-44	AAD00842.1	66	181.03	195	130	OvB8

Locus_12798_Transcript_1/1_Conf_1.000	917	4	1.46E-51	NP_510523.1	66	207.608	245	162	hypothetical protein T10B10.3
Locus_12799_Transcript_1/1_Conf_1.000	357	20	3.73E-25	XP_002630560.1	71	117.857	115	82	C. briggsae CBR-NPP-21 protein
Locus_128_Transcript_1/1_Conf_1.000	148	0							
Locus_1280_Transcript_1/1_Conf_1.000	519	20	2.25E-42	EFO20386.1	65	175.252	157	103	hypothetical protein LOAG_08104
Locus_12800_Transcript_1/1_Conf_1.000	373	0							
Locus_12801_Transcript_1/1_Conf_1.000	790	15	7.81E-37	NP_506593.2	57	158.303	240	139	hypothetical protein R02D5.3
Locus_12802_Transcript_1/1_Conf_1.000	296	20	1.48E-29	EFO21682.1	75	132.494	95	72	hypothetical protein LOAG_06805
Locus_12803_Transcript_1/1_Conf_1.000	265	0							
Locus_12804_Transcript_1/1_Conf_1.000	128	0							
Locus_12805_Transcript_1/1_Conf_1.000	184	0							
Locus_12806_Transcript_1/2_Conf_0.667	1081	20	2.19E-31	XP_002600898.1	59	140.969	191	113	hypothetical protein BRAFLDRAFT_215136
Locus_12806_Transcript_2/2_Conf_0.833	1482	20	3.43E-31	XP_002600898.1	59	140.969	191	113	hypothetical protein BRAFLDRAFT_215136
Locus_12807_Transcript_1/1_Conf_1.000	229	20	6.25E-20	XP_002645118.1	80	100.523	75	60	Hypothetical protein CBG16811
Locus_12808_Transcript_1/1_Conf_1.000	556	20	1.38E-41	XP_002632423.1	55	172.94	205	114	C. briggsae CBR-SNF-9 protein
Locus_12809_Transcript_1/1_Conf_1.000	958	20	1.46E-65	NP_498963.1	61	254.218	322	197	Temporarily Assigned Gene name family member (tag-256)
Locus_1281_Transcript_1/1_Conf_1.000	342	20	9.65E-37	XP_002633235.1	79	156.377	116	92	Hypothetical protein CBG05956
Locus_12810_Transcript_1/1_Conf_1.000	444	0							
Locus_12811_Transcript_1/1_Conf_1.000	247	10	3.14E-16	XP_001892618.1	74	88.1965	79	59	Acyltransferase family protein

Locus_12812_Transcript_1/1_Conf_1.000	357	19	3.49E-31	NP_496395.1	75	137.887	95	72	LIn-26 Related family member (lir-3)
Locus_12813_Transcript_1/2_Conf_1.000	321	0							
Locus_12813_Transcript_2/2_Conf_1.000	793	20	3.54E-29	XP_001902329.1	54	132.88	250	136	TPR Domain containing protein
Locus_12814_Transcript_1/1_Conf_1.000	402	0							
Locus_12815_Transcript_1/1_Conf_1.000	524	20	1.38E-71	XP_002638567.1	87	272.322	174	152	Hypothetical protein CBG05609
Locus_12816_Transcript_1/1_Conf_1.000	484	20	1.02E-78	XP_002640630.1	95	295.819	161	154	C. briggsae CBR-APG-1 protein
Locus_12817_Transcript_1/1_Conf_1.000	553	20	1.59E-66	EFO24958.1	83	255.758	183	153	hypothetical protein LOAG_03524
Locus_12818_Transcript_1/1_Conf_1.000	386	0							
Locus_12819_Transcript_1/3_Conf_0.667	1139	20	6.73E-119	ADE60689.1	80	431.795	309	250	Larp (rna binding la related protein) homolog protein 1, isoform a, partially confirmed by transcript evidence
Locus_12819_Transcript_2/3_Conf_0.333	438	20	2.70E-68	ADE60689.1	90	261.151	146	132	Larp (rna binding la related protein) homolog protein 1, isoform a, partially confirmed by transcript evidence
Locus_12819_Transcript_3/3_Conf_0.667	1322	20	1.37E-129	ADE60688.1	77	467.618	373	289	Larp (rna binding la related protein) homolog protein 1, isoform b, partially confirmed by transcript evidence
Locus_1282_Transcript_1/1_Conf_1.000	501	20	2.70E-47	NP_492215.1	77	191.43	167	129	hypothetical protein K04G2.6
Locus_12820_Transcript_1/1_Conf_1.000	134	0							
Locus_12821_Transcript_1/1_Conf_1.000	232	20	7.37E-13	NP_497336.3	79	77.0258	74	59	hypothetical protein Y71D11A.3
Locus_12822_Transcript_1/1_Conf_1.000	571	20	1.13E-25	NP_741242.1	72	120.168	100	72	Dipeptidyl Peptidase Four (IV) family member (dpf-6)
Locus_12823_Transcript_1/1_Conf_1.000	401	20	1.43E-40	NP_505591.1	78	169.088	133	104	hypothetical protein R04B5.5
Locus_12824_Transcript_1/1_Conf_1.000	155	0							

Locus_12825_Transcript_1/1_Conf_1.000	333	20	1.67E-33	AAB23867.2	79	145.591	110	87	UNC-5
Locus_12826_Transcript_1/1_Conf_1.000	876	0							
Locus_12827_Transcript_1/1_Conf_1.000	297	0							
Locus_12828_Transcript_1/1_Conf_1.000	134	20	6.59E-14	YP_003434088.1	93	80.4925	44	41	cytochrome c oxidase subunit III
Locus_12829_Transcript_1/1_Conf_1.000	537	20	7.24E-34	XP_002633416.1	67	147.132	178	120	Hypothetical protein CBG06181
Locus_1283_Transcript_1/1_Conf_1.000	1057	20	3.46E-50	XP_002633732.1	55	203.371	372	206	Hypothetical protein CBG03417
Locus_12830_Transcript_1/1_Conf_1.000	258	7	7.42E-13	CAA10033.1	71	77.0258	78	56	DYS-1 protein
Locus_12831_Transcript_1/1_Conf_1.000	249	0							
Locus_12832_Transcript_1/1_Conf_1.000	584	20	1.07E-82	XP_002639182.1	93	309.686	184	172	C. briggsae CBR-TAG-316 protein
Locus_12833_Transcript_1/1_Conf_1.000	317	0							
Locus_12834_Transcript_1/1_Conf_1.000	157	3	6.25E-20	CAR63690.1	92	100.523	52	48	putative Sna protein
Locus_12835_Transcript_1/1_Conf_1.000	282	4	1.61E-07	EFO25881.1	56	59.3066	96	54	SPRY domain-containing protein
Locus_12836_Transcript_1/2_Conf_1.000	760	20	2.91E-54	XP_002634768.1	74	216.083	243	182	C. briggsae CBR-HLH-30 protein

Locus_12836_Transcript_2/2_Conf_1.000	751	20	6.84E-56	XP_002634768.1	75	221.476	240	182	C. briggsae CBR-HLH-30 protein
Locus_12837_Transcript_1/1_Conf_1.000	159	0							
Locus_12838_Transcript_1/1_Conf_1.000	568	3	8.56E-10	NP_001023556.1	88	67.3958	42	37	Membrane Calcium ATPase family member (mca-3)
Locus_12839_Transcript_1/1_Conf_1.000	153	0							
Locus_1284_Transcript_1/2_Conf_1.000	1061	7	1.51E-37	NP_492729.1	54	161.384	231	126	hypothetical protein Y106G6H.4
Locus_1284_Transcript_2/2_Conf_1.000	920	7	1.38E-41	NP_492729.1	65	174.481	184	121	hypothetical protein Y106G6H.4
Locus_12840_Transcript_1/1_Conf_1.000	495	20	1.78E-35	AAC78238.2	89	152.14	102	91	Guanylyl cyclase protein 28, isoform d
Locus_12841_Transcript_1/1_Conf_1.000	1362	20	3.25E-174	NP_501303.1	83	615.92	416	347	hypothetical protein C06A6.5
Locus_12842_Transcript_1/1_Conf_1.000	152	0							
Locus_12843_Transcript_1/1_Conf_1.000	360	4	1.28E-17	XP_002639414.1	79	92.8189	73	58	C. briggsae CBR-EIF-3.H protein
Locus_12844_Transcript_1/1_Conf_1.000	1312	20	1.77E-129	XP_002633684.1	70	467.233	455	319	C. briggsae CBR-EEL-1 protein

Locus_12845_Transcript_1/1_Conf_1.000	845	20	6.15E-123	XP_002635231.1	88	444.506	280	248	Hypothetical protein CBG11474
Locus_12846_Transcript_1/1_Conf_1.000	333	20	6.51E-54	NP_001138309.1	100	213.386	110	110	keratin, type I cytoskeletal 17
Locus_12847_Transcript_1/1_Conf_1.000	134	2	7.30E-05	XP_002645884.1	69	50.447	43	30	Hypothetical protein CBG07632
Locus_12848_Transcript_1/1_Conf_1.000	269	0							
Locus_12849_Transcript_1/1_Conf_1.000	154	0							
Locus_1285_Transcript_1/1_Conf_1.000	2370	20	0	XP_002638699.1	93	1173.3	690	642	Hypothetical protein CBG11896
Locus_12850_Transcript_1/1_Conf_1.000	407	20	5.04E-38	EFO20415.1	69	160.614	142	99	hyaluronidase
Locus_12851_Transcript_1/2_Conf_1.000	475	20	4.25E-29	P34578.3	66	130.954	149	99	Rap guanine nucleotide exchange factor 1
Locus_12851_Transcript_2/2_Conf_1.000	881	20	4.51E-47	P34578.3	56	192.586	308	173	Rap guanine nucleotide exchange factor 1
Locus_12852_Transcript_1/1_Conf_1.000	133	0							
Locus_12853_Transcript_1/1_Conf_1.000	246	0							

Locus_12854_Transcript_1/1_Conf_1.000	228	2	3.93E-06	NP_490772.2	62	54.6842	74	46	hypothetical protein Y18H1A.3
Locus_12855_Transcript_1/1_Conf_1.000	687	2	5.04E-12	EFO22475.1	55	75.485	135	75	PH domain-containing protein
Locus_12856_Transcript_1/1_Conf_1.000	1229	20	7.08E-93	EFO21585.1	65	345.51	413	271	hypothetical protein LOAG_06905
Locus_12857_Transcript_1/1_Conf_1.000	158	0							
Locus_12858_Transcript_1/1_Conf_1.000	676	4	1.15E-21	XP_002640452.1	58	107.457	198	115	Hypothetical protein CBG08509
Locus_12859_Transcript_1/1_Conf_1.000	819	2	1.43E-12	XP_002639525.1	43	77.7962	252	110	Hypothetical protein CBG04150
Locus_1286_Transcript_1/3_Conf_0.714	2169	20	4.10E-127	XP_002636551.1	58	460.299	652	383	Hypothetical protein CBG23241
Locus_1286_Transcript_2/3_Conf_0.714	2169	20	1.84E-127	AAX34423.1	58	461.455	653	381	anion transporter SULP-5
Locus_1286_Transcript_3/3_Conf_0.714	2169	20	1.08E-127	XP_002636551.1	58	462.225	652	384	Hypothetical protein CBG23241
Locus_12860_Transcript_1/1_Conf_1.000	406	0							
Locus_12861_Transcript_1/1_Conf_1.000	288	0							
Locus_12862_Transcript_1/1_Conf_1.000	305	20	1.12E-29	XP_002639182.1	93	132.88	79	74	C. briggsae CBR-TAG-316 protein
Locus_12863_Transcript_1/1_Conf_1.000	472	20	4.25E-45	XP_001900983.1	85	184.111	132	113	La domain containing protein
Locus_12864_Transcript_1/1_Conf_1.000	322	0							
Locus_12865_Transcript_1/1_Conf_1.000	686	20	3.29E-72	NP_508530.1	75	275.404	228	173	yeast SEC homolog family member (sec-3)

Locus_12866_Transcript_1/1_Conf_1.000	449	20	2.49E-61	NP_496269.1	89	238.039	152	136	hypothetical protein R166.2
Locus_12867_Transcript_1/1_Conf_1.000	421	20	2.52E-53	EFO17199.1	90	211.46	117	106	histone methyltransferase
Locus_12868_Transcript_1/1_Conf_1.000	843	20	5.34E-151	XP_537399.1	99	537.724	266	265	PREDICTED: similar to 40S ribosomal protein S4, X isoform
Locus_12869_Transcript_1/1_Conf_1.000	327	20	2.77E-36	XP_002637153.1	84	154.836	104	88	Hypothetical protein CBG09655
Locus_1287_Transcript_1/1_Conf_1.000	255	20	4.96E-33	XP_002698352.1	87	144.05	85	74	PREDICTED: hypothetical protein
Locus_12870_Transcript_1/1_Conf_1.000	642	20	3.29E-36	XP_001899664.1	69	155.606	136	95	Smad1
Locus_12871_Transcript_1/1_Conf_1.000	298	20	7.77E-47	XP_002644145.1	92	189.889	98	91	C. briggsae CBR-DAF-12 protein
Locus_12872_Transcript_1/1_Conf_1.000	356	20	2.13E-12	CAB07705.2	76	75.485	52	40	C. elegans protein ZC101.1, partially confirmed by transcript evidence
Locus_12873_Transcript_1/1_Conf_1.000	788	0							
Locus_12874_Transcript_1/1_Conf_1.000	467	0							
Locus_12875_Transcript_1/1_Conf_1.000	285	18	5.00E-09	NP_501190.1	82	64.3142	39	32	Temporarily Assigned Gene name family member (tag-224)

Locus_12876_Transcript_1/1_Conf_1.000	637	20	1.40E-23	AAA51433.1	95	113.62	63	60	guanine nucleotide regulatory protein
Locus_12877_Transcript_1/1_Conf_1.000	1310	20	7.19E-107	XP_001897028.1	67	392.119	394	267	Peptidase family M1 containing protein
Locus_12878_Transcript_1/1_Conf_1.000	366	0							

Locus_12879_Transcript_1/1_Conf_1.000	844	20	1.28E-11	NP_497036.1	62	74.7146	91	57	hypothetical protein F19H8.2
Locus_1288_Transcript_1/1_Conf_1.000	804	20	1.22E-16	EFO16079.1	49	91.2781	186	92	hypothetical protein LOAG_12429
Locus_12880_Transcript_1/1_Conf_1.000	128	20	5.09E-06	ZP_01004740.1	66	54.299	45	30	ribosomal RNA large subunit methyltransferase J
Locus_12881_Transcript_1/1_Conf_1.000	1570	20	1.15E-133	XP_002643167.1	73	481.485	435	319	Hypothetical protein CBG15348
Locus_12882_Transcript_1/1_Conf_1.000	291	0							
Locus_12883_Transcript_1/1_Conf_1.000	1272	0							

Locus_12884_Transcript_1/1_Conf_1.000	202	20	2.06E-23	AAA18956.1	91	112.079	62	57	Sur-1 MAP kinase
Locus_12885_Transcript_1/1_Conf_1.000	375	20	1.30E-17	XP_001901741.1	66	92.8189	125	83	Eukaryotic-type DNA primase, large subunit family protein
Locus_12886_Transcript_1/1_Conf_1.000	348	20	3.28E-53	XP_002646356.1	91	211.075	116	106	Hypothetical protein CBG12070
Locus_12887_Transcript_1/1_Conf_1.000	475	4	5.92E-39	NP_491915.2	88	163.696	157	139	hypothetical protein ZC581.9
Locus_12888_Transcript_1/1_Conf_1.000	804	20	3.90E-31	NP_001184122.1	73	139.428	116	85	sestrin-3
Locus_12889_Transcript_1/1_Conf_1.000	681	20	3.65E-23	EFO19714.1	70	112.464	106	75	hypothetical protein LOAG_08776
Locus_1289_Transcript_1/1_Conf_1.000	357	20	2.50E-29	NP_499668.1	71	131.724	111	79	hypothetical protein Y37D8A.2
Locus_12890_Transcript_1/1_Conf_1.000	138	20	1.05E-11	NP_509287.1	88	73.1738	42	37	hypothetical protein C44E12.1
Locus_12891_Transcript_1/1_Conf_1.000	372	8	1.49E-29	EFO20596.1	97	132.494	69	67	MYND finger family protein
Locus_12892_Transcript_1/1_Conf_1.000	448	0							

Locus_12893_Transcript_1/1_Conf_1.000	241	19	1.12E-21	NP_492014.4	75	106.301	79	60	hypothetical protein F22D6.11
Locus_12894_Transcript_1/1_Conf_1.000	345	0							
Locus_12895_Transcript_1/1_Conf_1.000	544	4	2.87E-25	NP_508889.1	61	118.627	168	103	hypothetical protein Y34B4A.7
Locus_12896_Transcript_1/1_Conf_1.000	822	0							
Locus_12897_Transcript_1/1_Conf_1.000	1391	20	9.61E-73	XP_002641571.1	66	278.87	294	196	Hypothetical protein CBG09872
Locus_12898_Transcript_1/1_Conf_1.000	128	20	1.29E-17	XP_002813872.1	100	92.8189	42	42	PREDICTED: lactotransferrin-like isoform 2
Locus_12899_Transcript_1/1_Conf_1.000	608	3	1.30E-04	XP_968882.1	45	50.447	203	93	PREDICTED: similar to cp27, putative
Locus_129_Transcript_1/1_Conf_1.000	197	6	3.77E-25	NP_492295.1	95	117.857	65	62	hypothetical protein F10D11.6
Locus_1290_Transcript_1/1_Conf_1.000	304	1	2.35E-11	NP_490917.3	50	72.0182	104	53	hypothetical protein Y20F4.2
Locus_12900_Transcript_1/1_Conf_1.000	266	20	3.39E-42	NP_508537.1	100	174.481	88	88	SPeCtrin family member (spc-1)
Locus_12901_Transcript_1/1_Conf_1.000	148	0							
Locus_12902_Transcript_1/1_Conf_1.000	334	1	1.74E-06	XP_002803306.1	48	55.8398	92	45	PREDICTED: hypothetical protein LOC100426317
Locus_12903_Transcript_1/1_Conf_1.000	696	0							
Locus_12904_Transcript_1/1_Conf_1.000	601	16	9.29E-24	EFO26799.1	51	114.005	185	95	HMG box family protein
Locus_12905_Transcript_1/1_Conf_1.000	604	20	1.14E-69	NP_500088.1	85	266.544	174	148	hypothetical protein Y77E11A.1
Locus_12906_Transcript_1/1_Conf_1.000	209	0							
Locus_12907_Transcript_1/1_Conf_1.000	264	17	2.08E-07	CAA88613.1	45	58.9214	73	33	salivary gland secretion protein 4

Locus_12908_Transcript_1/1_Conf_1.000	189	20	1.11E-24	XP_001898310.1	95	116.316	62	59	DNA-directed RNA polymerase II largest subunit
Locus_12909_Transcript_1/1_Conf_1.000	165	20	1.38E-19	XP_002912840.1	94	99.3673	54	51	PREDICTED: LOW QUALITY PROTEIN: protein unc-13 homolog A-like
Locus_1291_Transcript_1/1_Conf_1.000	855	20	3.78E-51	NP_001122835.1	69	206.068	195	135	UNCoordinated family member (unc-22)
Locus_12910_Transcript_1/2_Conf_1.000	275	0							
Locus_12910_Transcript_2/2_Conf_1.000	248	0							
Locus_12911_Transcript_1/1_Conf_1.000	292	0							
Locus_12912_Transcript_1/1_Conf_1.000	696	20	2.32E-36	NP_001022303.1	80	156.377	114	92	MethylMalonic Aciduria type A protein family member (mmaa-1)
Locus_12913_Transcript_1/1_Conf_1.000	451	1	4.76E-04	XP_001901417.1	63	47.7506	66	42	hypothetical protein Bm1_49755
Locus_12914_Transcript_1/1_Conf_1.000	346	6	1.65E-20	CAR63710.1	86	102.449	65	56	putative C2 domain containing protein
Locus_12915_Transcript_1/1_Conf_1.000	161	0							
Locus_12916_Transcript_1/1_Conf_1.000	367	0							
Locus_12917_Transcript_1/2_Conf_1.000	988	0							
Locus_12917_Transcript_2/2_Conf_1.000	859	0							
Locus_12918_Transcript_1/1_Conf_1.000	190	15	1.04E-14	NP_496066.2	80	83.1889	60	48	Nuclear Hormone Receptor family member (nhr-19)
Locus_12919_Transcript_1/1_Conf_1.000	757	20	7.13E-45	NP_509296.1	63	184.882	257	164	hypothetical protein F27D9.2
Locus_1292_Transcript_1/2_Conf_1.000	1832	0							
Locus_1292_Transcript_2/2_Conf_1.000	1826	0							
Locus_12920_Transcript_1/1_Conf_1.000	376	3	4.02E-35	NP_502233.2	77	150.984	117	91	hypothetical protein H01G02.1
Locus_12921_Transcript_1/1_Conf_1.000	148	0							
Locus_12922_Transcript_1/1_Conf_1.000	229	0							
Locus_12923_Transcript_1/1_Conf_1.000	164	0							
Locus_12924_Transcript_1/1_Conf_1.000	383	0							

Locus_12925_Transcript_1/1_Conf_1.000	405	20	1.98E-26	NP_001119697.1	74	122.094	89	66	casein kinase II beta subunit
Locus_12926_Transcript_1/1_Conf_1.000	651	6	1.28E-91	CAR63586.1	89	339.732	217	195	hypothetical protein
Locus_12927_Transcript_1/1_Conf_1.000	355	20	1.34E-06	XP_001894185.1	46	56.225	107	50	Major Sperm Protein (MSP) cytoskeletal MSP
Locus_12928_Transcript_1/1_Conf_1.000	142	3	1.78E-11	NP_508432.1	85	72.4034	47	40	hypothetical protein F47G3.1
Locus_12929_Transcript_1/2_Conf_1.000	764	0							
Locus_12929_Transcript_2/2_Conf_1.000	383	0							
Locus_1293_Transcript_1/1_Conf_1.000	679	20	1.44E-80	XP_002632216.1	78	303.138	225	176	Hypothetical protein CBG07084
Locus_12930_Transcript_1/1_Conf_1.000	233	0							
Locus_12931_Transcript_1/1_Conf_1.000	208	0							
Locus_12932_Transcript_1/1_Conf_1.000	588	20	6.02E-49	XP_002631639.1	67	197.593	187	126	Hypothetical protein CBG20828
Locus_12933_Transcript_1/1_Conf_1.000	298	0							
Locus_12934_Transcript_1/1_Conf_1.000	135	0							

Locus_12935_Transcript_1/1_Conf_1.000	347	20	8.78E-06	NP_001128605.1	46	53.5286	123	57	breast cancer anti-estrogen resistance 1
Locus_12936_Transcript_1/1_Conf_1.000	213	7	2.17E-25	EFO23509.1	95	118.627	69	66	STAT protein
Locus_12937_Transcript_1/1_Conf_1.000	735	20	3.68E-83	XP_001898650.1	82	311.997	243	201	SD04925p
Locus_12938_Transcript_1/1_Conf_1.000	685	20	2.70E-66	NP_496968.1	80	255.758	185	149	hypothetical protein Y48B6A.12
Locus_12939_Transcript_1/1_Conf_1.000	133	0							

Locus_1294_Transcript_1/2_Conf_1.000	1511	20	6.79E-176	AAF00540.1	99	621.698	319	318	AF187691_1casein kinase I
Locus_1294_Transcript_2/2_Conf_1.000	1501	20	6.74E-176	AAF00540.1	99	621.698	319	318	AF187691_1casein kinase I
Locus_12940_Transcript_1/1_Conf_1.000	833	20	2.40E-55	XP_002635067.1	75	219.935	239	180	Hypothetical protein CBG11281
Locus_12941_Transcript_1/1_Conf_1.000	945	20	3.43E-67	XP_002629865.1	65	259.61	242	158	C. briggsae CBR-ZTF-2 protein
Locus_12942_Transcript_1/1_Conf_1.000	196	0							
Locus_12943_Transcript_1/1_Conf_1.000	729	20	5.63E-52	XP_002645831.1	65	208.379	230	151	C. briggsae CBR-RBC-1 protein
Locus_12944_Transcript_1/1_Conf_1.000	207	0							
Locus_12945_Transcript_1/1_Conf_1.000	307	0							
Locus_12946_Transcript_1/1_Conf_1.000	385	3	2.68E-15	AAT12422.1	73	85.1149	105	77	hypothetical protein isoform a

Locus_12947_Transcript_1/1_Conf_1.000	542	6	4.65E-20	NP_491731.2	72	101.293	86	62	hypothetical protein C06A5.3
Locus_12948_Transcript_1/1_Conf_1.000	483	20	4.46E-42	NP_500460.1	72	174.096	155	113	hypothetical protein W02C12.1
Locus_12949_Transcript_1/1_Conf_1.000	351	0							
Locus_1295_Transcript_1/1_Conf_1.000	564	20	2.04E-64	NP_001021182.1	82	248.825	188	155	hypothetical protein C24A1.3
Locus_12950_Transcript_1/1_Conf_1.000	369								
Locus_12951_Transcript_1/1_Conf_1.000	300	0							
Locus_12952_Transcript_1/1_Conf_1.000	449	3	6.67E-06	ZP_06280939.1	45	53.9138	79	36	LPXTG-motif cell wall anchor domain protein
Locus_12953_Transcript_1/1_Conf_1.000	356	20	7.32E-21	XP_002644943.1	81	103.605	111	90	Hypothetical protein CBG10898
Locus_12954_Transcript_1/1_Conf_1.000	918	20	2.25E-76	ACM46026.1	68	290.041	304	208	Temporarily assigned gene name protein 233, isoform a, partially confirmed by transcript evidence
Locus_12955_Transcript_1/1_Conf_1.000	178	0							
Locus_12956_Transcript_1/1_Conf_1.000	421	2	1.35E-06	XP_002641991.1	51	56.225	147	75	Hypothetical protein CBG09214
Locus_12957_Transcript_1/1_Conf_1.000	558	0							
Locus_12958_Transcript_1/1_Conf_1.000	210	20	9.47E-21	EAX00648.1	100	103.219	50	50	hCG23722
Locus_12959_Transcript_1/1_Conf_1.000	177	20	2.75E-12	XP_002629697.1	77	75.0998	59	46	C. briggsae CBR-AQP-2 protein
Locus_1296_Transcript_1/1_Conf_1.000	429	0							
Locus_12960_Transcript_1/1_Conf_1.000	167	0							
Locus_12961_Transcript_1/1_Conf_1.000	360	0							
Locus_12962_Transcript_1/1_Conf_1.000	329	20	7.80E-31	NP_493554.1	81	136.732	98	80	hypothetical protein Y54E5A.6
Locus_12963_Transcript_1/1_Conf_1.000	131	0							
Locus_12964_Transcript_1/1_Conf_1.000	302	7	2.12E-28	XP_002635247.1	73	128.642	99	73	Hypothetical protein CBG11491
Locus_12965_Transcript_1/1_Conf_1.000	436	2	7.01E-16	NP_504797.1	49	87.0409	144	71	hypothetical protein VC5.2
Locus_12966_Transcript_1/1_Conf_1.000	277	20	3.59E-28	NP_500389.1	85	127.872	90	77	hypothetical protein ZC416.1
Locus_12967_Transcript_1/1_Conf_1.000	326	1	2.22E-09	NP_502613.2	64	65.4698	73	47	QUInine non-avoider family member (qui-1)
Locus_12968_Transcript_1/1_Conf_1.000	495	0							

Locus_12969_Transcript_1/1_Conf_1.000	156	0							
Locus_1297_Transcript_1/1_Conf_1.000	957	20	6.30E-85	NP_492334.1	87	318.546	214	187	hypothetical protein F43G9.5
Locus_12970_Transcript_1/1_Conf_1.000	421	0							
Locus_12971_Transcript_1/1_Conf_1.000	564	20	1.29E-26	NP_505444.1	63	123.25	138	87	FMRF-Like Peptide family member (flp-6)
Locus_12972_Transcript_1/1_Conf_1.000	424	20	2.12E-52	XP_002643051.1	83	208.379	139	116	C. briggsae CBR-DPF-6 protein
Locus_12973_Transcript_1/1_Conf_1.000	899	20	4.40E-37	XP_001900313.1	61	159.458	219	134	Piwi domain containing protein
Locus_12974_Transcript_1/1_Conf_1.000	539	0							
Locus_12975_Transcript_1/1_Conf_1.000	790	20	3.57E-90	XP_001896878.1	80	335.495	250	201	vesicle-fusing ATPase
Locus_12976_Transcript_1/1_Conf_1.000	250	0							
Locus_12977_Transcript_1/1_Conf_1.000	604	4	1.78E-14	EFO26702.1	61	83.1889	142	88	GTP-ase activating protein for Arf containing protein
Locus_12978_Transcript_1/1_Conf_1.000	432	0							
Locus_12979_Transcript_1/1_Conf_1.000	171	20	5.38E-24	NP_001024141.1	98	114.005	56	55	Germinal Center Kinase family member (gck-1)
Locus_1298_Transcript_1/3_Conf_0.667	577	3	4.16E-23	NP_495792.1	65	111.694	123	81	hypothetical protein M05D6.6
Locus_1298_Transcript_2/3_Conf_0.667	565	3	1.34E-23	NP_495792.1	65	113.235	123	81	hypothetical protein M05D6.6
Locus_1298_Transcript_3/3_Conf_0.667	565	3	3.89E-23	NP_495792.1	65	111.694	123	81	hypothetical protein M05D6.6
Locus_12980_Transcript_1/1_Conf_1.000	458	20	5.36E-24	XP_001900529.1	56	114.005	141	79	CG17219-PA
Locus_12981_Transcript_1/1_Conf_1.000	698	20	1.60E-53	NP_502420.2	76	213.386	194	149	hypothetical protein C26H9A.2
Locus_12982_Transcript_1/1_Conf_1.000	1663	20	6.14E-149	NP_495532.2	80	532.332	454	366	hypothetical protein F21D12.3
Locus_12983_Transcript_1/1_Conf_1.000	644	2	4.93E-24	NP_001033409.1	65	115.161	152	100	hypothetical protein F29B9.12

Locus_12984_Transcript_1/1_Conf_1.000	256	20	7.18E-24	NP_001022680.1	83	113.62	77	64	hypothetical protein K11H3.6
Locus_12985_Transcript_1/1_Conf_1.000	182	0							
Locus_12986_Transcript_1/1_Conf_1.000	479	4	1.08E-08	NP_492518.1	88	63.1586	36	32	hypothetical protein F30A10.6
Locus_12987_Transcript_1/1_Conf_1.000	185	0							
Locus_12988_Transcript_1/1_Conf_1.000	149	20	1.08E-11	XP_002640991.1	75	73.1738	48	36	Hypothetical protein CBG11740
Locus_12989_Transcript_1/1_Conf_1.000	228	0							
Locus_1299_Transcript_1/1_Conf_1.000	1862	20	8.03E-60	NP_506181.2	56	236.498	420	238	hypothetical protein R11D1.10
Locus_12990_Transcript_1/1_Conf_1.000	1454	20	0	XP_001898240.1	84	707.212	483	410	XPA-binding protein 2
Locus_12991_Transcript_1/1_Conf_1.000	215	0							
Locus_12992_Transcript_1/1_Conf_1.000	162	0							
Locus_12993_Transcript_1/1_Conf_1.000	175	0							
Locus_12994_Transcript_1/1_Conf_1.000	391	0							
Locus_12995_Transcript_1/1_Conf_1.000	367	4	1.00E-30	XP_002639732.1	68	136.346	124	85	C. briggsae CBR-TAG-264 protein
Locus_12996_Transcript_1/1_Conf_1.000	878	20	3.34E-26	XP_001892273.1	48	123.25	294	144	hypothetical protein
Locus_12997_Transcript_1/1_Conf_1.000	879	0							
Locus_12998_Transcript_1/2_Conf_1.000	2488	20	4.26E-99	XP_002636770.1	56	367.466	651	365	Hypothetical protein CBG23501
Locus_12998_Transcript_2/2_Conf_1.000	2473	20	6.31E-95	XP_002636770.1	55	353.599	651	361	Hypothetical protein CBG23501
Locus_12999_Transcript_1/1_Conf_1.000	274	0							
Locus_13_Transcript_1/1_Conf_1.000	251	0							
Locus_130_Transcript_1/6_Conf_0.250	885	20	5.66E-114	XP_002634359.1	96	414.846	221	214	C. briggsae CBR-RPS-2 protein

Locus_130_Transcript_2/6_Conf_0.375	1992	20	4.50E-149	XP_002636413.1	78	533.102	392	307	Hypothetical protein CBG23066
Locus_130_Transcript_3/6_Conf_0.250	1031	20	1.47E-114	XP_002634359.1	96	417.157	222	215	C. briggsae CBR-RPS-2 protein
Locus_130_Transcript_4/6_Conf_0.375	2180	20	5.00E-149	XP_002636413.1	78	533.102	392	307	Hypothetical protein CBG23066
Locus_130_Transcript_5/6_Conf_0.250	1031	20	7.31E-114	XP_002634359.1	96	414.846	221	214	C. briggsae CBR-RPS-2 protein
Locus_130_Transcript_6/6_Conf_0.375	2180	20	5.00E-149	XP_002636413.1	78	533.102	392	307	Hypothetical protein CBG23066
Locus_1300_Transcript_1/1_Conf_1.000	983	0							
Locus_13000_Transcript_1/1_Conf_1.000	301	0							

Locus_13001_Transcript_1/1_Conf_1.000	391	20	1.30E-62	1LYA	100	242.276	117	117	CrystalStructures Of Native And Inhibited Forms Of Human Cathepsin D: Implications For Lysosomal Targeting And Drug Design
Locus_13002_Transcript_1/1_Conf_1.000	178	0							
Locus_13003_Transcript_1/1_Conf_1.000	299	20	1.13E-21	NP_495836.2	80	106.301	89	72	Variable ABnormal morphology family member (vab-9)
Locus_13004_Transcript_1/1_Conf_1.000	406	20	2.05E-23	ACI49193.1	84	112.079	72	61	hypothetical protein Csp3_JD03.002
Locus_13005_Transcript_1/1_Conf_1.000	248	0							
Locus_13006_Transcript_1/1_Conf_1.000	218	9	2.57E-10	CAD28559.2	81	68.5514	48	39	metalloprotease I
Locus_13007_Transcript_1/1_Conf_1.000	228	0							
Locus_13008_Transcript_1/1_Conf_1.000	433	20	8.29E-25	NP_504567.1	61	116.701	143	88	hypothetical protein R01B10.4
Locus_13009_Transcript_1/1_Conf_1.000	307	0							
Locus_1301_Transcript_1/1_Conf_1.000	1108	4	3.28E-38	XP_002643523.1	51	163.696	345	177	Hypothetical protein CBG16200
Locus_13010_Transcript_1/1_Conf_1.000	289	0							
Locus_13011_Transcript_1/1_Conf_1.000	628	2	1.34E-31	NP_506277.1	54	140.198	214	116	High Incidence of Males (increased X chromosome loss) family member (him-17)
Locus_13012_Transcript_1/1_Conf_1.000	296	0							
Locus_13013_Transcript_1/1_Conf_1.000	752								
Locus_13014_Transcript_1/1_Conf_1.000	203	0							
Locus_13015_Transcript_1/1_Conf_1.000	550	1	2.22E-04	XP_002637364.1	56	49.2914	69	39	Hypothetical protein CBG19064
Locus_13016_Transcript_1/1_Conf_1.000	175	0							
Locus_13017_Transcript_1/1_Conf_1.000	584	20	3.19E-18	ACJ01664.1	67	95.5153	81	55	DAF-12 C4
Locus_13018_Transcript_1/1_Conf_1.000	204	0							
Locus_13019_Transcript_1/1_Conf_1.000	276	0							
Locus_1302_Transcript_1/2_Conf_1.000	1289	0							
Locus_1302_Transcript_2/2_Conf_1.000	1279	0							
Locus_13020_Transcript_1/1_Conf_1.000	139	4	1.24E-12	NP_505034.1	73	76.2554	46	34	hypothetical protein F40A3.7
Locus_13021_Transcript_1/1_Conf_1.000	468	4	6.44E-09	XP_002630296.1	58	63.929	98	57	C. briggsae CBR-EMB-27 protein
Locus_13022_Transcript_1/1_Conf_1.000	645	3	2.83E-19	XP_001902425.1	58	99.3673	144	84	hypothetical protein Bm1_54835
Locus_13023_Transcript_1/1_Conf_1.000	327	0							

Locus_13024_Transcript_1/1_Conf_1.000	753	20	2.95E-67	XP_001899456.1	73	259.225	248	182	Tetraspanin family protein
Locus_13025_Transcript_1/1_Conf_1.000	365	20	1.12E-21	XP_002633316.1	78	106.301	85	67	C. briggsae CBR-GTL-2 protein
Locus_13026_Transcript_1/1_Conf_1.000	257	0							
Locus_13027_Transcript_1/1_Conf_1.000	741	20	9.52E-95	NP_494897.3	79	350.517	249	197	hypothetical protein R05F9.12
Locus_13028_Transcript_1/1_Conf_1.000	268	16	1.93E-13	XP_002629956.1	88	78.9518	45	40	C. briggsae CBR-MLT-7 protein
Locus_13029_Transcript_1/1_Conf_1.000	289	20	5.87E-18	NP_495990.1	63	93.9745	95	60	Tubulin Tyrosine Ligase Like family member (ttll-12)
Locus_1303_Transcript_1/1_Conf_1.000	1421	20	3.62E-91	NP_496549.1	94	340.117	190	179	RAB family member (rab-7)
Locus_13030_Transcript_1/1_Conf_1.000	263	0							
Locus_13031_Transcript_1/1_Conf_1.000	788	20	1.56E-45	ABB88219.1	72	187.193	168	121	Hypothetical protein Y48G1C.12
Locus_13032_Transcript_1/1_Conf_1.000	1755	20	1.26E-91	XP_001901778.1	65	342.043	430	281	Probable molybdopterin binding domain containing protein
Locus_13033_Transcript_1/1_Conf_1.000	1226	20	0	XP_001118006.2	100	673.315	327	327	PREDICTED: elongation factor 2
Locus_13034_Transcript_1/1_Conf_1.000	796	1	1.61E-05	CBI55964.1	42	54.299	156	66	unnamed protein product
Locus_13035_Transcript_1/1_Conf_1.000	848	0							

Locus_13036_Transcript_1/1_Conf_1.000	576	20	1.03E-05	YP_002522680.1	51	53.9138	127	66	hypothetical protein trd_1477
Locus_13037_Transcript_1/1_Conf_1.000	248	2	1.32E-06	NP_502588.1	59	56.225	74	44	NucleOLar protein family member (nol-9)
Locus_13038_Transcript_1/1_Conf_1.000	316	0							
Locus_13039_Transcript_1/1_Conf_1.000	480	20	3.12E-32	EFO26003.1	68	141.354	157	107	SPRY domain-containing protein
Locus_1304_Transcript_1/1_Conf_1.000	769	20	1.49E-29	XP_002648943.1	60	134.035	165	99	Hypothetical protein CBG21256
Locus_13040_Transcript_1/1_Conf_1.000	710	20	1.20E-96	NP_498704.1	85	356.681	233	199	COenzyme Q (ubiquinone) biosynthesis family member (coq-5)
Locus_13041_Transcript_1/1_Conf_1.000	297	0							
Locus_13042_Transcript_1/2_Conf_1.000	302	0							
Locus_13042_Transcript_2/2_Conf_1.000	441	0							
Locus_13043_Transcript_1/1_Conf_1.000	139	0							
Locus_13044_Transcript_1/2_Conf_1.000	238	0							
Locus_13044_Transcript_2/2_Conf_1.000	376	0							
Locus_13045_Transcript_1/1_Conf_1.000	878	20	7.09E-77	NP_505070.2	68	291.582	296	202	Valyl tRNA Synthetase family member (vrs-1)
Locus_13046_Transcript_1/1_Conf_1.000	567	0							
Locus_13047_Transcript_1/1_Conf_1.000	211	2	1.67E-09	EFO27604.1	71	65.855	70	50	hypothetical protein LOAG_00873
Locus_13048_Transcript_1/1_Conf_1.000	1552	20	0	XP_002647888.1	87	853.588	516	450	C. briggsae CBR-IRS-1 protein
Locus_13049_Transcript_1/1_Conf_1.000	393	6	1.19E-18	NP_001021427.1	82	96.2857	119	98	hypothetical protein F28H1.4

Locus_1305_Transcript_1/2_Conf_1.000	2638	19	4.39E-09	YP_867496.1	38	68.5514	565	218	Zinc finger-domain-containing protein
Locus_1305_Transcript_2/2_Conf_1.000	472	0							
Locus_13050_Transcript_1/1_Conf_1.000	355	20	1.47E-29	NP_503604.2	78	132.494	114	90	hypothetical protein F44C8.7
Locus_13051_Transcript_1/1_Conf_1.000	415	0							
Locus_13052_Transcript_1/1_Conf_1.000	1019	20	8.53E-91	NP_001021798.2	74	338.191	327	243	Arf-1 Guanine nucleotide Exchange Factor homolog family member (agef-1)
Locus_13053_Transcript_1/1_Conf_1.000	368	20	9.96E-55	BAA08392.1	100	216.083	107	107	vacuolar ATPase
Locus_13054_Transcript_1/1_Conf_1.000	501	5	7.60E-50	NP_496398.2	79	199.904	140	111	hypothetical protein T06D8.1
Locus_13055_Transcript_1/1_Conf_1.000	396	0							
Locus_13056_Transcript_1/1_Conf_1.000	305	8	9.52E-13	XP_001900282.1	68	76.6406	67	46	hypothetical protein Bm1_44100
Locus_13057_Transcript_1/1_Conf_1.000	838	20	4.39E-89	NP_001022911.1	76	332.028	279	214	HELicase family member (hel-308)
Locus_13058_Transcript_1/1_Conf_1.000	472	20	1.16E-50	NP_492624.2	77	202.601	158	122	hypothetical protein F52F12.7
Locus_13059_Transcript_1/1_Conf_1.000	146	3	8.27E-20	EEE74739.1	100	100.138	48	48	predicted protein

Locus_1306_Transcript_1/1_Conf_1.000	1387	20	5.91E-38	EFO24120.1	61	163.31	239	148	CAMK/TRBL protein kinase
Locus_13060_Transcript_1/1_Conf_1.000	144	0							
Locus_13061_Transcript_1/1_Conf_1.000	419	20	1.22E-39	NP_510447.1	74	166.007	139	103	hypothetical protein C05G5.1
Locus_13062_Transcript_1/1_Conf_1.000	721	20	1.55E-38	XP_002641616.1	60	163.696	252	152	C. briggsae CBR-ALX-1 protein
Locus_13063_Transcript_1/1_Conf_1.000	433	20	7.73E-39	NP_490837.2	79	163.31	129	103	GRainyHead (Drosophila transcription factor) homolog family member (grh-1)
Locus_13064_Transcript_1/1_Conf_1.000	181	0							
Locus_13065_Transcript_1/3_Conf_0.667	797	20	6.81E-105	NP_496077.1	80	384.415	268	216	hypothetical protein ZK1307.9
Locus_13065_Transcript_2/3_Conf_0.556	821	20	1.39E-108	NP_496077.1	81	396.741	274	222	hypothetical protein ZK1307.9
Locus_13065_Transcript_3/3_Conf_0.667	821	20	1.39E-108	NP_496077.1	81	396.741	274	222	hypothetical protein ZK1307.9
Locus_13066_Transcript_1/1_Conf_1.000	737	8	3.28E-23	XP_002642159.1	50	112.849	217	110	Hypothetical protein CBG18119
Locus_13067_Transcript_1/1_Conf_1.000	732	5	6.33E-27	A8WN14.3	57	125.176	248	143	E3 UFM1-protein ligase 1 homolog
Locus_13068_Transcript_1/2_Conf_1.000	343	20	1.45E-16	EFO27351.1	66	89.3521	89	59	hypothetical protein LOAG_01121
Locus_13068_Transcript_2/2_Conf_1.000	771	20	2.74E-31	EFO27351.1	65	139.813	144	95	hypothetical protein LOAG_01121
Locus_13069_Transcript_1/1_Conf_1.000	393	0							
Locus_1307_Transcript_1/1_Conf_1.000	498	20	1.22E-44	NP_500024.1	76	182.57	133	102	AuTophaGy (yeast Atg homolog) family member (atg-3)
Locus_13070_Transcript_1/2_Conf_1.000	1052	20	1.49E-37	EFO27069.1	58	161.384	203	119	Ulp1 protease

Locus_13070_Transcript_2/2_Conf_1.000	995	20	1.37E-37	EFO27069.1	58	161.384	203	119	Ulp1 protease
Locus_13071_Transcript_1/1_Conf_1.000	796	20	5.87E-40	EFO26083.1	76	168.703	142	108	hypothetical protein LOAG_02395
Locus_13072_Transcript_1/1_Conf_1.000	272	0							
Locus_13073_Transcript_1/1_Conf_1.000	168	3	3.29E-05	XP_002630736.1	66	51.6026	54	36	Hypothetical protein CBG02420
Locus_13074_Transcript_1/1_Conf_1.000	396	20	3.75E-57	NP_001021410.2	88	224.172	132	117	LIM domain family member (lim-9)
Locus_13075_Transcript_1/1_Conf_1.000	191	0							
Locus_13076_Transcript_1/1_Conf_1.000	837	0							
Locus_13077_Transcript_1/1_Conf_1.000	297	20	9.57E-21	AAF36480.1	88	103.219	61	54	glutathione S-transferase 2
Locus_13078_Transcript_1/1_Conf_1.000	887	20	3.17E-48	EFO25981.1	64	196.438	214	139	MBD3 protein
Locus_13079_Transcript_1/1_Conf_1.000	463	20	2.21E-41	EFO25969.1	77	171.785	148	115	abnormal epIthelia family member
Locus_1308_Transcript_1/1_Conf_1.000	353	2	2.71E-07	XP_002643980.1	53	58.5362	101	54	C. briggsae CBR-OCT-2 protein
Locus_13080_Transcript_1/1_Conf_1.000	521	3	6.82E-07	XP_002647552.1	55	57.3806	95	53	Hypothetical protein CBG06638
Locus_13081_Transcript_1/1_Conf_1.000	2063	20	0	EFO26190.1	76	647.121	510	390	BTB/POZ domain-containing protein 2
Locus_13082_Transcript_1/2_Conf_1.000	895	20	3.45E-50	EFO21942.1	75	202.986	160	121	kynurenine-oxoglutarate transaminase
Locus_13082_Transcript_2/2_Conf_1.000	895	20	3.45E-50	EFO21942.1	75	202.986	160	121	kynurenine-oxoglutarate transaminase
Locus_13083_Transcript_1/1_Conf_1.000	790	0							
Locus_13084_Transcript_1/1_Conf_1.000	193	2	7.92E-15	NP_498089.2	77	83.5741	62	48	hypothetical protein Y54H5A.2
Locus_13085_Transcript_1/1_Conf_1.000	880	20	6.31E-41	XP_001900446.1	95	172.17	86	82	MYND finger family protein
Locus_13086_Transcript_1/1_Conf_1.000	229	20	4.63E-15	NP_500708.1	71	84.3445	63	45	hypothetical protein C09B9.4
Locus_13087_Transcript_1/1_Conf_1.000	372	0							

Locus_13088_Transcript_1/1_Conf_1.000	479	20	1.50E-34	NP_503037.2	72	149.058	121	88	ITSN (intersectin) family member (itsn-1)
Locus_13089_Transcript_1/1_Conf_1.000	406	0							
Locus_1309_Transcript_1/1_Conf_1.000	2613	20	0	XP_002637775.1	90	640.958	390	351	C. briggsae CBR-UNC-112 protein
Locus_13090_Transcript_1/1_Conf_1.000	526	18	4.91E-24	XP_002643238.1	88	114.39	70	62	Hypothetical protein CBG08105
Locus_13091_Transcript_1/1_Conf_1.000	530	0							
Locus_13092_Transcript_1/1_Conf_1.000	334	0							
Locus_13093_Transcript_1/2_Conf_1.000	579	20	3.25E-10	NP_502107.1	65	62.7734	55	36	COLlagen family member (col-125)
Locus_13093_Transcript_2/2_Conf_1.000	579	20	1.49E-10	NP_502107.1	65	63.929	55	36	COLlagen family member (col-125)
Locus_13094_Transcript_1/1_Conf_1.000	176	20	1.20E-15	XP_001898544.1	84	86.2705	58	49	Probable methylenetetrahydrofolate reductase
Locus_13095_Transcript_1/1_Conf_1.000	305	0							
Locus_13096_Transcript_1/1_Conf_1.000	310	0							
Locus_13097_Transcript_1/1_Conf_1.000	460	20	1.19E-23	CAV31771.1	96	112.849	52	50	C. elegans protein F25D7.3b, partially confirmed by transcript evidence
Locus_13098_Transcript_1/1_Conf_1.000	473	5	2.97E-22	NP_497202.2	65	108.227	110	72	hypothetical protein F10C5.2
Locus_13099_Transcript_1/1_Conf_1.000	322	0							

Locus_131_Transcript_1/1_Conf_1.000	1566	20	2.64E-130	ADD54353.1	97	470.315	385	375	NADH dehydrogenase subunit 4
Locus_1310_Transcript_1/2_Conf_0.857	546	19	3.36E-05	EFO26634.1	40	51.9878	106	43	hypothetical protein LOAG_01858
Locus_1310_Transcript_2/2_Conf_0.857	516	5	1.07E-04	XP_539701.2	54	50.0618	55	30	PREDICTED: similar to CG31690-PB, isoform B
Locus_13100_Transcript_1/1_Conf_1.000	315	20	2.71E-39	NP_001041037.1	86	164.851	105	91	GLYcosylation related family member (gly-10)
Locus_13101_Transcript_1/1_Conf_1.000	440	20	9.96E-55	NP_508530.1	85	216.083	138	118	yeast SEC homolog family member (sec-3)
Locus_13102_Transcript_1/1_Conf_1.000	207	4	1.20E-15	XP_002642004.1	100	86.2705	41	41	C. briggsae CBR-TOH-1 protein
Locus_13103_Transcript_1/1_Conf_1.000	253	20	3.81E-33	XP_002640505.1	91	144.436	84	77	Hypothetical protein CBG13644
Locus_13104_Transcript_1/1_Conf_1.000	161	20	1.45E-21	CAB93148.1	97	79.337	35	34	HDJ2 protein
Locus_13105_Transcript_1/1_Conf_1.000	174	0							
Locus_13106_Transcript_1/1_Conf_1.000	579	2	1.19E-09	XP_002642979.1	80	67.0106	50	40	Hypothetical protein CBG15263

Locus_13107_Transcript_1/1_Conf_1.000	301	20	5.03E-38	XP_001899774.1	92	160.614	93	86	Guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif family protein
Locus_13108_Transcript_1/1_Conf_1.000	241	0							
Locus_13109_Transcript_1/1_Conf_1.000	1259	20	5.19E-107	NP_496341.1	68	392.504	393	268	EGG sterile (unfertilizable) family member (egg-3)
Locus_1311_Transcript_1/1_Conf_1.000	1046	18	4.94E-17	ABB53347.1	38	93.2041	306	119	secreted protein 5 precursor
Locus_13110_Transcript_1/1_Conf_1.000	328	8	3.17E-32	NP_001024859.1	79	141.354	110	87	hypothetical protein R11G1.6
Locus_13111_Transcript_1/1_Conf_1.000	219	0							
Locus_13112_Transcript_1/1_Conf_1.000	185	11	1.36E-14	XP_002631488.1	80	82.8037	61	49	C. briggsae CBR-PTR-8 protein
Locus_13113_Transcript_1/1_Conf_1.000	414	2	2.48E-21	XP_002633521.1	76	105.145	86	66	Hypothetical protein CBG05384
Locus_13114_Transcript_1/1_Conf_1.000	929	20	7.07E-102	NP_001024859.1	75	374.785	317	239	hypothetical protein R11G1.6
Locus_13115_Transcript_1/2_Conf_1.000	785	20	4.39E-16	XP_002158068.1	51	89.3521	176	90	PREDICTED: similar to Forkhead box protein J1
Locus_13115_Transcript_2/2_Conf_1.000	776	20	6.61E-17	XP_002158068.1	50	92.0485	173	87	PREDICTED: similar to Forkhead box protein J1

Locus_13116_Transcript_1/1_Conf_1.000	597	20	8.14E-81	CAB07859.3	83	303.523	206	173	C. elegans protein W09D10.2, partially confirmed by transcript evidence
Locus_13117_Transcript_1/1_Conf_1.000	234	0							
Locus_13118_Transcript_1/1_Conf_1.000	464	20	5.99E-63	NP_502809.2	88	243.432	153	135	hypothetical protein Y41E3.3
Locus_13119_Transcript_1/1_Conf_1.000	502	20	8.96E-59	XP_002630065.1	82	229.565	156	129	Hypothetical protein CBG13441
Locus_1312_Transcript_1/4_Conf_0.250	1458	5	7.02E-13	XP_002642206.1	40	80.1073	228	92	C. briggsae CBR-BRP-1 protein
Locus_1312_Transcript_2/4_Conf_0.250	1496	5	7.27E-13	XP_002642206.1	40	80.1073	228	92	C. briggsae CBR-BRP-1 protein
Locus_1312_Transcript_3/4_Conf_0.667	1503	5	7.33E-13	XP_002642206.1	40	80.1073	228	92	C. briggsae CBR-BRP-1 protein
Locus_1312_Transcript_4/4_Conf_0.667	1509	5	7.37E-13	XP_002642206.1	40	80.1073	228	92	C. briggsae CBR-BRP-1 protein
Locus_13120_Transcript_1/1_Conf_1.000	205	0							
Locus_13121_Transcript_1/1_Conf_1.000	261	0							
Locus_13122_Transcript_1/1_Conf_1.000	451	5	1.25E-12	XP_001901679.1	89	76.2554	46	41	Immunoglobulin I-set domain containing protein
Locus_13123_Transcript_1/1_Conf_1.000	750	20	7.85E-44	NP_001122771.1	59	181.415	251	149	hypothetical protein F13H10.4
Locus_13124_Transcript_1/1_Conf_1.000	610	20	5.60E-72	XP_002637344.1	83	274.248	181	152	C. briggsae CBR-ODC-1 protein
Locus_13125_Transcript_1/1_Conf_1.000	563	20	4.00E-97	EFB27138.1	100	357.451	175	175	hypothetical protein PANDA_001098

Locus_13126_Transcript_1/1_Conf_1.000	329	20	3.25E-53	EAW77587.1	100	211.075	109	109	annexin A2, isoform CRA_c
Locus_13127_Transcript_1/1_Conf_1.000	284	0							
Locus_13128_Transcript_1/2_Conf_1.000	417	0							
Locus_13128_Transcript_2/2_Conf_1.000	869	6	1.44E-21	XP_002635348.1	57	107.842	208	120	C. briggsae CBR-DNJ-22 protein
Locus_13129_Transcript_1/1_Conf_1.000	437	13	6.14E-12	XP_002412316.1	59	73.9442	105	62	conserved hypothetical protein
Locus_1313_Transcript_1/2_Conf_1.000	1167	20	1.16E-73	XP_002641912.1	82	281.567	242	200	C. briggsae CBR-RNP-7 protein
Locus_1313_Transcript_2/2_Conf_1.000	835	20	3.77E-16	XP_001896769.1	69	89.7373	95	66	hypothetical protein Bm1_26580
Locus_13130_Transcript_1/1_Conf_1.000	129	20	6.40E-09	XP_002603055.1	86	63.929	38	33	hypothetical protein BRAFLDRAFT_274883

Locus_13131_Transcript_1/1_Conf_1.000	261	0							
Locus_13132_Transcript_1/1_Conf_1.000	645	15	3.83E-16	XP_002646317.1	68	88.9669	147	101	Hypothetical protein CBG12024
Locus_13133_Transcript_1/1_Conf_1.000	281	2	1.01E-06	XP_002639296.1	54	56.6102	95	52	Hypothetical protein CBG03866
Locus_13134_Transcript_1/1_Conf_1.000	768	20	9.91E-58	XP_001893225.1	64	227.639	257	165	Myb-like DNA-binding domain containing protein
Locus_13135_Transcript_1/1_Conf_1.000	410	20	6.34E-33	XP_002632976.1	70	143.665	122	86	Hypothetical protein CBG21736
Locus_13136_Transcript_1/1_Conf_1.000	203	20	7.11E-08	NP_001079447.1	69	60.4622	56	39	phosphatidylinositol-specific phospholipase C, X domain containing 2
Locus_13137_Transcript_1/1_Conf_1.000	1025	0							
Locus_13138_Transcript_1/1_Conf_1.000	130	4	5.78E-18	NP_001022641.1	95	93.9745	43	41	LEThal family member (let-805)
Locus_13139_Transcript_1/1_Conf_1.000	239	20	4.41E-34	NP_496717.1	98	147.517	79	78	hypothetical protein Y46G5A.12
Locus_1314_Transcript_1/1_Conf_1.000	933	4	1.75E-07	NP_741911.1	65	61.2326	66	43	Suppressor of Constitutive Dauer formation family member (scd-1)
Locus_13140_Transcript_1/1_Conf_1.000	275	7	1.47E-05	NP_740998.1	63	52.7582	46	29	hypothetical protein C25H3.7
Locus_13141_Transcript_1/1_Conf_1.000	143	20	1.32E-06	CAB00874.2	63	56.225	47	30	C. elegans protein R09H10.5, partially confirmed by transcript evidence

Locus_13142_Transcript_1/1_Conf_1.000	148	8	7.72E-18	XP_002640908.1	95	93.5893	48	46	Hypothetical protein CBG00466
Locus_13143_Transcript_1/1_Conf_1.000	239	0							
Locus_13144_Transcript_1/1_Conf_1.000	312	20	4.20E-40		87	167.548	102	89	protein K10D6.2b
Locus_13145_Transcript_1/2_Conf_1.000	787	20	2.22E-92	XP_002631607.1	78	342.813	261	204	Hypothetical protein CBG20788
Locus_13145_Transcript_2/2_Conf_1.000	787	20	4.94E-92	XP_002631607.1	77	341.658	261	203	Hypothetical protein CBG20788
Locus_13146_Transcript_1/1_Conf_1.000	661	20	1.31E-67	XP_002641643.1	81	259.996	180	147	C. briggsae CBR-SQV-3 protein
Locus_13147_Transcript_1/1_Conf_1.000	181	0							
Locus_13148_Transcript_1/1_Conf_1.000	450	0							
Locus_13149_Transcript_1/1_Conf_1.000	598	1	8.06E-04	XP_002063859.1	40	47.7506	159	64	GK15899
Locus_1315_Transcript_1/1_Conf_1.000	1262	0							
Locus_13150_Transcript_1/2_Conf_1.000	374	0							
Locus_13150_Transcript_2/2_Conf_1.000	281	0							
Locus_13151_Transcript_1/1_Conf_1.000	720	20	3.04E-10	XP_001323102.1	48	69.707	235	115	viral A-type inclusion protein
Locus_13152_Transcript_1/1_Conf_1.000	288	2	1.66E-04	XP_001898158.1	53	49.2914	86	46	hypothetical protein Bm1_33560
Locus_13153_Transcript_1/2_Conf_1.000	1066	20	1.62E-71	NP_509394.1	78	274.248	224	175	hypothetical protein M60.7
Locus_13153_Transcript_2/2_Conf_1.000	1065	20	1.62E-71	NP_509394.1	78	274.248	224	175	hypothetical protein M60.7
Locus_13154_Transcript_1/1_Conf_1.000	331	20	3.85E-38	NP_492132.1	90	160.999	110	99	Enhancer of Glp-One (glp-1) family member (ego-1)
Locus_13155_Transcript_1/2_Conf_1.000	584	0							
Locus_13155_Transcript_2/2_Conf_1.000	584	0							
Locus_13156_Transcript_1/1_Conf_1.000	197	0							
Locus_13157_Transcript_1/1_Conf_1.000	135	20	1.24E-12	XP_002643051.1	88	76.2554	45	40	C. briggsae CBR-DPF-6 protein
Locus_13158_Transcript_1/1_Conf_1.000	168	0							

Locus_13159_Transcript_1/1_Conf_1.000	581	20	1.34E-77	NP_501968.2	83	292.738	193	161	Flavin-containing MonoOxygenase family member (fmo-1)
Locus_1316_Transcript_1/1_Conf_1.000	1659	20	0	CAD29445.1	90	844.729	488	440	protein disulfide isomerase 1
Locus_13160_Transcript_1/1_Conf_1.000	151	0							
Locus_13161_Transcript_1/1_Conf_1.000	533	2	3.56E-17	XP_002632168.1	64	91.6633	127	82	C. briggsae CBR-PQN-85 protein
Locus_13162_Transcript_1/1_Conf_1.000	369	20	2.47E-16	XP_001626861.1	67	88.5817	87	59	predicted protein
Locus_13163_Transcript_1/2_Conf_1.000	507	20	1.57E-21	XP_002926282.1	61	105.916	131	81	PREDICTED: poly(ADP-ribose) glycohydrolase-like
Locus_13163_Transcript_2/2_Conf_1.000	507	20	5.39E-22	XP_002926282.1	61	107.457	131	81	PREDICTED: poly(ADP-ribose) glycohydrolase-like
Locus_13164_Transcript_1/1_Conf_1.000	146	9	6.55E-17	XP_002805525.1	100	90.5077	42	42	PREDICTED: hypothetical protein LOC100426852
Locus_13165_Transcript_1/1_Conf_1.000	399	0							
Locus_13166_Transcript_1/1_Conf_1.000	472	20	7.26E-45	XP_002645831.1	72	183.341	162	117	C. briggsae CBR-RBC-1 protein
Locus_13167_Transcript_1/1_Conf_1.000	412	0							
Locus_13168_Transcript_1/1_Conf_1.000	195	1	2.08E-15	EAW79999.1	97	85.5001	40	39	MYC-associated zinc finger protein (purine-binding transcription factor), isoform CRA_f
Locus_13169_Transcript_1/1_Conf_1.000	539	0							
Locus_1317_Transcript_1/2_Conf_1.000	3302	20	0	NP_507869.1	68	815.839	899	615	UNCoordinated family member (unc-51)

Locus_1317_Transcript_2/2_Conf_1.000	3296	20	0	NP_507869.1	66	815.068	917	612	UNCoordinated family member (unc-51)
Locus_13170_Transcript_1/1_Conf_1.000	475	0							
Locus_13171_Transcript_1/1_Conf_1.000	438	0							
Locus_13172_Transcript_1/1_Conf_1.000	320	20	2.63E-18	XP_002635663.1	72	95.1301	79	57	Hypothetical protein CBG21858
Locus_13173_Transcript_1/1_Conf_1.000	823	20	1.19E-99	XP_002643926.1	87	367.081	244	214	C. briggsae CBR-SFXN-1.5 protein
Locus_13174_Transcript_1/1_Conf_1.000	445	0							
Locus_13175_Transcript_1/2_Conf_1.000	537	20	7.99E-41	NP_501090.1	72	170.244	166	121	hypothetical protein C06G3.9
Locus_13175_Transcript_2/2_Conf_1.000	537	20	3.04E-40	NP_501090.1	71	168.318	166	119	hypothetical protein C06G3.9
Locus_13176_Transcript_1/1_Conf_1.000	686	0							
Locus_13177_Transcript_1/1_Conf_1.000	390	20	6.95E-32	NP_501302.1	78	140.198	125	98	MVB (yeast MultiVesicular Body sorting factor) related family member (mvb-12)

Locus_13178_Transcript_1/1_Conf_1.000	1520	20	2.12E-84	XP_002636129.1	61	317.775	396	243	C. briggsae CBR-ATGR-9 protein
Locus_13179_Transcript_1/1_Conf_1.000	199	0							
Locus_1318_Transcript_1/1_Conf_1.000	553	20	1.31E-44	NP_741320.1	65	182.956	183	119	SET (trithorax/polycomb) domain containing family member (set-23)
Locus_13180_Transcript_1/1_Conf_1.000	843	20	6.24E-75	XP_002639128.1	78	285.034	223	174	C. briggsae CBR-SPG-7 protein
Locus_13181_Transcript_1/1_Conf_1.000	866	20	1.28E-62	XP_002637088.1	67	244.202	248	168	Hypothetical protein CBG09587
Locus_13182_Transcript_1/1_Conf_1.000	721	20	1.81E-79	NP_508983.2	75	299.671	253	192	CTBP (CtBP) transcriptional co-repressor homolog family member (ctbp-1)
Locus_13183_Transcript_1/1_Conf_1.000	267	0							
Locus_13184_Transcript_1/1_Conf_1.000	333	0							
Locus_13185_Transcript_1/1_Conf_1.000	425	0							
Locus_13186_Transcript_1/1_Conf_1.000	196	0							
Locus_13187_Transcript_1/1_Conf_1.000	807	0							
Locus_13188_Transcript_1/1_Conf_1.000	344	4	1.83E-11	NP_504395.2	56	72.4034	115	65	hypothetical protein Y47A7.1
Locus_13189_Transcript_1/2_Conf_1.000	280	2	1.24E-04	EFO19653.1	80	49.6766	41	33	pre-B cell enhancing factor
Locus_13189_Transcript_2/2_Conf_1.000	222	0							
Locus_1319_Transcript_1/2_Conf_1.000	999	20	6.04E-142	XP_002630817.1	88	508.064	311	276	C. briggsae CBR-LEC-5 protein
Locus_1319_Transcript_2/2_Conf_1.000	1023	20	1.27E-118	XP_002630817.1	79	430.639	319	254	C. briggsae CBR-LEC-5 protein
Locus_13190_Transcript_1/1_Conf_1.000	170	0							
Locus_13191_Transcript_1/1_Conf_1.000	217	0							
Locus_13192_Transcript_1/1_Conf_1.000	318	0							
Locus_13193_Transcript_1/1_Conf_1.000	269	20	1.25E-20	NP_001129924.1	80	102.834	89	72	SLOwpoke potassium channel family member (slo-2)
Locus_13194_Transcript_1/1_Conf_1.000	995	5	6.55E-56	EFO22136.1	64	222.246	273	176	hypothetical protein LOAG_06352
Locus_13195_Transcript_1/1_Conf_1.000	286	0							
Locus_13196_Transcript_1/1_Conf_1.000	332	0							

Locus_13197_Transcript_1/1_Conf_1.000	306	4	7.04E-08	XP_002637153.1	81	60.4622	37	30	Hypothetical protein CBG09655
Locus_13198_Transcript_1/1_Conf_1.000	220	20	3.03E-22	XP_002630183.1	80	108.227	73	59	C. briggsae CBR-FLI-1 protein
Locus_13199_Transcript_1/1_Conf_1.000	520	2	8.34E-05	XP_002644141.1	56	50.447	65	37	C. briggsae CBR-FLP-19 protein
Locus_132_Transcript_1/3_Conf_0.600	418	20	1.03E-30	XP_002635598.1	80	136.346	130	105	C. briggsae CBR-RPS-30 protein
Locus_132_Transcript_2/3_Conf_0.600	478	20	1.01E-30	XP_002635598.1	80	136.346	130	105	C. briggsae CBR-RPS-30 protein
Locus_132_Transcript_3/3_Conf_0.600	487	20	1.02E-30	XP_002635598.1	80	136.346	130	105	C. briggsae CBR-RPS-30 protein
Locus_1320_Transcript_1/1_Conf_1.000	360	4	2.50E-13	NP_504235.2	64	78.5666	117	75	Drosophila SOS homolog family member (sos-1)
Locus_13200_Transcript_1/1_Conf_1.000	247	0							
Locus_13201_Transcript_1/1_Conf_1.000	555	4	3.52E-37	NP_493486.2	83	158.303	130	108	hypothetical protein C49A1.10
Locus_13202_Transcript_1/1_Conf_1.000	345	0							
Locus_13203_Transcript_1/1_Conf_1.000	221	0							
Locus_13204_Transcript_1/1_Conf_1.000	451	6	6.85E-11	XP_002632899.1	79	70.4774	54	43	C. briggsae CBR-DAF-15 protein
Locus_13205_Transcript_1/2_Conf_1.000	231	20	2.07E-15	XP_001898420.1	82	85.5001	64	53	ATP-dependent DNA helicase, RecQ family protein
Locus_13205_Transcript_2/2_Conf_1.000	236	20	7.85E-15	XP_001898420.1	82	83.5741	63	52	ATP-dependent DNA helicase, RecQ family protein
Locus_13206_Transcript_1/1_Conf_1.000	218	0							
Locus_13207_Transcript_1/1_Conf_1.000	423	0							
Locus_13208_Transcript_1/1_Conf_1.000	616	20	2.70E-37	EFO15564.1	60	159.073	202	123	hypothetical protein LOAG_12944

Locus_13209_Transcript_1/1_Conf_1.000	358	20	2.76E-28	NP_505501.1	72	128.257	119	86	Temporarily Assigned Gene name family member (tag-120)
Locus_1321_Transcript_1/2_Conf_1.000	1618	20	6.21E-98	NP_500797.1	81	362.844	246	200	fatty acid ELOngation family member (elo-6)
Locus_1321_Transcript_2/2_Conf_1.000	1618	20	6.21E-98	NP_500797.1	81	362.844	246	200	fatty acid ELOngation family member (elo-6)
Locus_13210_Transcript_1/1_Conf_1.000	362	20	1.32E-38	NP_497625.3	87	162.54	101	88	hypothetical protein Y71H2AM.1
Locus_13211_Transcript_1/1_Conf_1.000	236	0							
Locus_13212_Transcript_1/1_Conf_1.000	201	0							
Locus_13213_Transcript_1/1_Conf_1.000	178	2	5.03E-06	XP_002639575.1	65	54.299	60	39	C. briggsae CBR-BAM-2 protein
Locus_13214_Transcript_1/1_Conf_1.000	663	20	1.86E-53	NP_001024840.1	74	213.001	213	159	hypothetical protein R07E4.1
Locus_13215_Transcript_1/1_Conf_1.000	606	20	1.43E-11	XP_002632653.1	46	73.559	188	88	Hypothetical protein CBG21575
Locus_13216_Transcript_1/1_Conf_1.000	418	0							
Locus_13217_Transcript_1/1_Conf_1.000	563	0							
Locus_13218_Transcript_1/1_Conf_1.000	320	0							
Locus_13219_Transcript_1/1_Conf_1.000	166	0							
Locus_1322_Transcript_1/1_Conf_1.000	1273	20	2.72E-95	NP_504655.1	91	353.599	202	184	DumPY : shorter than wild-type family member (dpy-11)
Locus_13220_Transcript_1/1_Conf_1.000	333	0							
Locus_13221_Transcript_1/1_Conf_1.000	400	20	2.90E-09	XP_002720026.1	53	65.0846	94	50	PREDICTED: heterochromatin protein 1-beta-like
Locus_13222_Transcript_1/1_Conf_1.000	369	0							
Locus_13223_Transcript_1/2_Conf_1.000	497	20	1.22E-68	ACY40004.1	87	262.307	162	142	K+/cl- cotransporter protein 2, isoform c

Locus_13223_Transcript_2/2_Conf_1.000	497	20	1.22E-68	ACY40004.1	87	262.307	162	142	K+/cl- cotransporter protein 2, isoform c
Locus_13224_Transcript_1/1_Conf_1.000	236	3	1.87E-08	NP_001024264.1	58	62.3882	77	45	hypothetical protein Y58G8A.4
Locus_13225_Transcript_1/1_Conf_1.000	303	0							
Locus_13226_Transcript_1/1_Conf_1.000	276	0							
Locus_13227_Transcript_1/1_Conf_1.000	377	20	2.37E-19	EFO22101.1	68	98.5969	95	65	hypothetical protein LOAG_06386
Locus_13228_Transcript_1/1_Conf_1.000	175	0							
Locus_13229_Transcript_1/1_Conf_1.000	352	20	5.64E-13	EFO19207.1	78	77.411	60	47	hypothetical protein LOAG_09288
Locus_1323_Transcript_1/2_Conf_1.000	261	20	5.83E-26	EFO20001.1	80	120.553	86	69	Sel1l protein
Locus_1323_Transcript_2/2_Conf_1.000	261	20	5.83E-26	EFO20001.1	80	120.553	86	69	Sel1l protein
Locus_13230_Transcript_1/1_Conf_1.000	304	2	7.26E-29	NP_508948.2	80	130.183	100	80	hypothetical protein T21F4.1
Locus_13231_Transcript_1/1_Conf_1.000	418	20	4.21E-16	XP_001893741.1	60	87.8113	110	67	LIM domain containing protein
Locus_13232_Transcript_1/1_Conf_1.000	305	4	7.03E-24	XP_002636973.1	68	113.62	101	69	Hypothetical protein CBG09454
Locus_13233_Transcript_1/1_Conf_1.000	178	0							
Locus_13234_Transcript_1/1_Conf_1.000	248	0							

Locus_13235_Transcript_1/1_Conf_1.000	542	20	1.52E-79	XP_002630154.1	95	298.901	160	153	C. briggsae CBR-ARL-1 protein
Locus_13236_Transcript_1/1_Conf_1.000	1407	20	4.01E-42	XP_002632130.1	75	177.178	185	140	C. briggsae CBR-COL-68 protein
Locus_13237_Transcript_1/1_Conf_1.000	413	20	4.99E-38	NP_491552.2	87	160.614	137	120	LEThal family member (let-363)
Locus_13238_Transcript_1/1_Conf_1.000	349	20	6.85E-43	XP_002760231.1	98	176.792	114	112	PREDICTED: prefoldin subunit 2-like
Locus_13239_Transcript_1/1_Conf_1.000	155	2	3.34E-05	NP_498595.1	66	51.6026	53	35	hypothetical protein T20H4.5
Locus_1324_Transcript_1/1_Conf_1.000	370	0							
Locus_13240_Transcript_1/1_Conf_1.000	134	0							
Locus_13241_Transcript_1/1_Conf_1.000	483	20	3.44E-18	XP_002639738.1	63	94.7449	101	64	Hypothetical protein CBG12466
Locus_13242_Transcript_1/1_Conf_1.000	391	20	6.31E-25	XP_002639033.1	77	117.087	93	72	Hypothetical protein CBG22282
Locus_13243_Transcript_1/1_Conf_1.000	748	4	5.58E-42	XP_001892872.1	71	175.252	170	121	hypothetical protein Bm1_07015
Locus_13244_Transcript_1/1_Conf_1.000	265	7	2.22E-09	XP_001901023.1	95	65.4698	40	38	hypothetical protein Bm1_47805
Locus_13245_Transcript_1/1_Conf_1.000	575	20	6.01E-83	NP_493544.2	90	310.457	181	164	hypothetical protein Y105E8B.3

Locus_13246_Transcript_1/2_Conf_1.000	558	10	3.30E-11	NP_499177.3	41	72.0182	198	82	hypothetical protein ZK632.7
Locus_13246_Transcript_2/2_Conf_1.000	522	14	9.41E-12	NP_499177.3	40	73.559	202	82	hypothetical protein ZK632.7
Locus_13247_Transcript_1/1_Conf_1.000	178	0							
Locus_13248_Transcript_1/1_Conf_1.000	424	1	2.15E-04	AAK18978.3	53	48.9062	125	67	Hypothetical protein T20F7.1
Locus_13249_Transcript_1/1_Conf_1.000	728	20	5.90E-94	AAV70493.1	82	347.821	230	190	acetylcholine/choline transporter
Locus_1325_Transcript_1/1_Conf_1.000	679	20	6.08E-63	XP_002631415.1	70	244.588	217	154	Hypothetical protein CBG03266
Locus_13250_Transcript_1/2_Conf_1.000	1727	20	0	XP_002640216.1	81	750.74	529	433	Hypothetical protein CBG12727
Locus_13250_Transcript_2/2_Conf_1.000	1023	20	1.19E-140	XP_002640216.1	83	503.827	323	271	Hypothetical protein CBG12727
Locus_13251_Transcript_1/1_Conf_1.000	401	0							
Locus_13252_Transcript_1/1_Conf_1.000	442	0							
Locus_13253_Transcript_1/1_Conf_1.000	185	0							
Locus_13254_Transcript_1/1_Conf_1.000	255	3	3.82E-09	XP_002640308.1	75	64.6994	57	43	Hypothetical protein CBG12847

Locus_13255_Transcript_1/2_Conf_1.000	251	20	1.55E-23	XP_001901686.1	83	112.464	83	69	Cohesin subunit SA-1
Locus_13255_Transcript_2/2_Conf_1.000	251	20	1.55E-23	XP_001901686.1	83	112.464	83	69	Cohesin subunit SA-1
Locus_13256_Transcript_1/1_Conf_1.000	325	0							
Locus_13257_Transcript_1/1_Conf_1.000	316	0							

Locus_13258_Transcript_1/1_Conf_1.000	690	20	7.06E-38	EFO24692.1	65	161.384	164	108	protein-tyrosine phosphatase
Locus_13259_Transcript_1/1_Conf_1.000	1507	20	3.66E-113	XP_002630297.1	72	413.305	410	299	C. briggsae CBR-PCH-2 protein
Locus_1326_Transcript_1/1_Conf_1.000	1316	20	1.64E-50	NP_499287.2	57	204.912	254	147	T BoX family member (tbx-8)
Locus_13260_Transcript_1/1_Conf_1.000	2594	3	7.10E-04	NP_001032352.2	51	51.2174	105	54	tripartite motif-containing protein 71
Locus_13261_Transcript_1/1_Conf_1.000	2647	12	7.76E-14	CAR63553.1	43	84.3445	252	110	putative major allergen
Locus_13262_Transcript_1/1_Conf_1.000	167	0							
Locus_13263_Transcript_1/1_Conf_1.000	482	20	3.83E-14	XP_001902194.1	57	81.2629	138	79	3'-5' exoribonuclease CSL4 homolog
Locus_13264_Transcript_1/1_Conf_1.000	441	20	1.49E-29	NP_497626.1	65	132.494	125	82	hypothetical protein Y71H2AR.1
Locus_13265_Transcript_1/1_Conf_1.000	746	0							
Locus_13266_Transcript_1/1_Conf_1.000	271	20	6.15E-36	CAR63585.1	95	153.68	88	84	putative MAD-Like family member
Locus_13267_Transcript_1/1_Conf_1.000	315	0							
Locus_13268_Transcript_1/1_Conf_1.000	311	5	1.40E-40	NP_495954.1	93	169.088	103	96	Regulator of HYpoxia-inducible factor (hif-1) family member (rhy-1)

Locus_13269_Transcript_1/1_Conf_1.000	875	20	5.87E-55	NP_498653.2	56	218.779	298	169	LIGase family member (lig-4)
Locus_1327_Transcript_1/1_Conf_1.000	1858	20	1.51E-50	EFO27065.1	54	205.682	362	196	hypothetical protein LOAG_01420
Locus_13270_Transcript_1/1_Conf_1.000	1352	20	6.71E-47	NP_499810.2	52	192.971	437	228	hypothetical protein T25C8.1
Locus_13271_Transcript_1/1_Conf_1.000	361	1	3.04E-27	NP_493572.2	68	124.79	118	81	hypothetical protein F39B2.8
Locus_13272_Transcript_1/1_Conf_1.000	849	20	2.30E-109	XP_002646355.1	81	399.438	283	230	Hypothetical protein CBG12069
Locus_13273_Transcript_1/1_Conf_1.000	306	0							
Locus_13274_Transcript_1/1_Conf_1.000	231	8	3.10E-11	AAT72456.1	72	71.633	59	43	FOG-3
Locus_13275_Transcript_1/1_Conf_1.000	727	2	2.61E-25	XP_002636407.1	63	119.783	157	99	Hypothetical protein CBG23059
Locus_13276_Transcript_1/1_Conf_1.000	303	20	3.49E-23	EFO20885.1	80	111.309	76	61	hypothetical protein LOAG_07603
Locus_13277_Transcript_1/1_Conf_1.000	247	0							
Locus_13278_Transcript_1/1_Conf_1.000	197	0							
Locus_13279_Transcript_1/1_Conf_1.000	1020	0							
Locus_1328_Transcript_1/2_Conf_0.500	1269	20	0	NP_509217.2	89	652.129	381	341	hypothetical protein F46H5.3
Locus_1328_Transcript_2/2_Conf_0.500	1269	20	0	NP_509217.2	89	649.047	381	340	hypothetical protein F46H5.3
Locus_13280_Transcript_1/1_Conf_1.000	233	10	1.88E-16	XP_002642915.1	68	88.9669	76	52	Hypothetical protein CBG15190
Locus_13281_Transcript_1/1_Conf_1.000	350	6	1.75E-22	XP_002636985.1	77	108.997	105	81	Hypothetical protein CBG09473
Locus_13282_Transcript_1/1_Conf_1.000	536	20	9.77E-84	NP_000230.1	100	312.768	148	148	lysozyme C precursor
Locus_13283_Transcript_1/1_Conf_1.000	142	9	7.98E-12	XP_002647278.1	82	73.559	46	38	C. briggsae CBR-KETN-1 protein

Locus_13284_Transcript_1/1_Conf_1.000	508	20	9.74E-56	NP_496100.1	79	219.55	173	137	hypothetical protein Y53C12B.1
Locus_13285_Transcript_1/1_Conf_1.000	564	20	9.16E-65	AAP36795.1	100	249.98	128	128	Homo sapiens CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344)
Locus_13286_Transcript_1/1_Conf_1.000	588	12	1.14E-39	XP_002638395.1	58	166.777	201	117	Hypothetical protein CBG18604
Locus_13287_Transcript_1/2_Conf_1.000	1848	20	0	XP_001896443.1	79	755.747	568	451	DNA topoisomerase III beta-1
Locus_13287_Transcript_2/2_Conf_1.000	1848	20	0	XP_001896443.1	79	754.977	568	450	DNA topoisomerase III beta-1
Locus_13288_Transcript_1/1_Conf_1.000	156	20	1.31E-09	AAK31527.3	80	66.2402	52	42	Neuronal symmetry protein 1, partially confirmed by transcript evidence
Locus_13289_Transcript_1/1_Conf_1.000	488								
Locus_1329_Transcript_1/2_Conf_1.000	458	20	1.08E-24	AAX30301.1	96	116.316	55	53	unknown
Locus_1329_Transcript_2/2_Conf_1.000	469	20	1.86E-32	BAA10929.1	74	142.124	120	89	cytochrome P450 like_TBP
Locus_13290_Transcript_1/1_Conf_1.000	137	0							
Locus_13291_Transcript_1/1_Conf_1.000	146	20	1.56E-10	XP_002640635.1	76	69.3218	46	35	Hypothetical protein CBG08753
Locus_13292_Transcript_1/1_Conf_1.000	832	20	1.76E-82	NP_498112.1	74	310.071	241	179	PRotein arginine MethylTransferase family member (prmt-5)
Locus_13293_Transcript_1/1_Conf_1.000	460	20	1.31E-22	EFO19933.1	63	109.383	138	87	helix-loop-helix DNA-binding domain-containing protein
Locus_13294_Transcript_1/1_Conf_1.000	152	0							
Locus_13295_Transcript_1/1_Conf_1.000	315	0							
Locus_13296_Transcript_1/1_Conf_1.000	822	20	8.96E-39	NP_501996.2	54	164.851	282	155	UDP-GlucuronosylTransferase family member (ugt-54)

Locus_13297_Transcript_1/1_Conf_1.000	632	20	2.85E-21	CAR97823.1	54	105.916	166	91	C. elegans protein F26H11.2i, partially confirmed by transcript evidence
Locus_13298_Transcript_1/1_Conf_1.000	463	20	2.35E-59	XP_002634350.1	85	231.491	131	112	C. briggsae CBR-ILYS-4 protein
Locus_13299_Transcript_1/1_Conf_1.000	392	0							
Locus_133_Transcript_1/1_Conf_1.000	1211	20	3.47E-52	NP_493028.2	59	210.305	373	222	WAVE (actin cytoskeleton modulator) homolog family member (wve-1)
Locus_1330_Transcript_1/1_Conf_1.000	1727	20	0	NP_740787.2	78	707.597	556	438	hypothetical protein C53H9.2
Locus_13300_Transcript_1/1_Conf_1.000	624	0							
Locus_13301_Transcript_1/1_Conf_1.000	610	20	1.64E-55	NP_741176.2	67	219.55	210	141	hypothetical protein C23G10.7
Locus_13302_Transcript_1/1_Conf_1.000	185	0							
Locus_13303_Transcript_1/1_Conf_1.000	885	20	2.23E-110	NP_496279.1	84	402.905	266	224	Temporarily Assigned Gene name family member (tag-242)
Locus_13304_Transcript_1/1_Conf_1.000	815	20	7.38E-54	CAA92456.3	71	214.927	203	146	C. elegans protein C53B4.4b, partially confirmed by transcript evidence
Locus_13305_Transcript_1/1_Conf_1.000	484	20	9.99E-31	NP_490911.1	68	130.183	150	103	SCAMP (synaptic vesicle protein) homolog family member (scm-1)
Locus_13306_Transcript_1/1_Conf_1.000	153	0							
Locus_13307_Transcript_1/1_Conf_1.000	140	0							
Locus_13308_Transcript_1/1_Conf_1.000	177	0							
Locus_13309_Transcript_1/1_Conf_1.000	205	0							
Locus_1331_Transcript_1/1_Conf_1.000	811	20	3.27E-78	NP_509260.1	71	295.819	248	178	ACyLtransferase-like family member (acl-12)

Locus_13310_Transcript_1/1_Conf_1.000	389	20	7.21E-37	EFO23898.1	78	156.762	120	94	FolC protein
Locus_13311_Transcript_1/1_Conf_1.000	1583	20	9.77E-40	NP_498165.2	46	169.474	458	213	hypothetical protein F48E8.2
Locus_13312_Transcript_1/2_Conf_1.000	221	0							
Locus_13312_Transcript_2/2_Conf_1.000	173	0							
Locus_13313_Transcript_1/1_Conf_1.000	735	20	2.32E-61	NP_509122.1	70	239.58	244	173	hypothetical protein F38B6.4
Locus_13314_Transcript_1/1_Conf_1.000	241	7	3.37E-26	XP_002631168.1	84	121.324	70	59	C. briggsae CBR-PQM-1 protein
Locus_13315_Transcript_1/1_Conf_1.000	413	20	1.61E-36	NP_501320.2	74	155.606	135	100	eXPOrtin (nuclear export receptor) family member (xpo-3)
Locus_13316_Transcript_1/1_Conf_1.000	362	20	2.85E-17	AAO63576.1	59	91.6633	111	66	secreted protein 4 precursor
Locus_13317_Transcript_1/1_Conf_1.000	203	20	8.11E-12	NP_001021562.1	67	73.559	74	50	hypothetical protein K07A3.3
Locus_13318_Transcript_1/1_Conf_1.000	384	0							
Locus_13319_Transcript_1/1_Conf_1.000	572	0							
Locus_1332_Transcript_1/1_Conf_1.000	622	15	4.24E-06	XP_002637664.1	47	55.4546	143	68	Hypothetical protein CBG19420
Locus_13320_Transcript_1/1_Conf_1.000	279	0							
Locus_13321_Transcript_1/1_Conf_1.000	633	6	9.27E-20	NP_510700.3	57	100.908	227	131	Histone DeAcetylase family member (hda-4)
Locus_13322_Transcript_1/1_Conf_1.000	513	20	8.15E-42	XP_001951535.1	70	173.326	172	122	PREDICTED: similar to dynein heavy chain
Locus_13323_Transcript_1/1_Conf_1.000	184	3	3.71E-12	NP_491803.1	87	74.7146	48	42	SaPosin-like Protein family member (spp-15)
Locus_13324_Transcript_1/1_Conf_1.000	472	3	2.34E-35	NP_501123.1	74	151.754	157	117	COLlagen family member (col-113)
Locus_13325_Transcript_1/1_Conf_1.000	646	4	2.63E-41	XP_001897455.1	80	172.555	123	99	hypothetical protein
Locus_13326_Transcript_1/1_Conf_1.000	170	0							
Locus_13327_Transcript_1/2_Conf_1.000	1263	2	2.33E-22	NP_499581.2	54	111.309	211	116	hypothetical protein Y75B8A.8
Locus_13327_Transcript_2/2_Conf_1.000	1263	2	2.33E-22	NP_499581.2	54	111.309	211	116	hypothetical protein Y75B8A.8
Locus_13328_Transcript_1/1_Conf_1.000	185	0							

Locus_13329_Transcript_1/1_Conf_1.000	293	3	9.66E-13	CAA92756.3	75	76.6406	62	47	C. elegans protein T24B8.4, partially confirmed by transcript evidence
Locus_1333_Transcript_1/3_Conf_0.714	1891	20	0	XP_002640606.1	94	917.916	529	499	Hypothetical protein CBG08717
Locus_1333_Transcript_2/3_Conf_0.714	1891	20	0	XP_002640606.1	94	917.916	529	499	Hypothetical protein CBG08717
Locus_1333_Transcript_3/3_Conf_0.714	1891	20	0	XP_002640606.1	94	917.916	529	499	Hypothetical protein CBG08717
Locus_13330_Transcript_1/1_Conf_1.000	343	0							
Locus_13331_Transcript_1/1_Conf_1.000	547	2	1.15E-13	NP_001033437.1	60	80.1073	87	53	hypothetical protein W09G12.10
Locus_13332_Transcript_1/1_Conf_1.000	158	0							
Locus_13333_Transcript_1/1_Conf_1.000	129	0							

Locus_13334_Transcript_1/1_Conf_1.000	239	20	5.95E-39	BAG65521.1	100	163.696	79	79	unnamed protein product
Locus_13335_Transcript_1/1_Conf_1.000	153	0							
Locus_13336_Transcript_1/1_Conf_1.000	363	4	1.56E-23	XP_002631126.1	81	112.464	125	102	C. briggsae CBR-SHN-1 protein
Locus_13337_Transcript_1/1_Conf_1.000	164	0							
Locus_13338_Transcript_1/1_Conf_1.000	1913	20	8.31E-177	NP_491489.1	69	625.165	613	425	AminoPeptidase P family member (app-1)
Locus_13339_Transcript_1/1_Conf_1.000	136	0							
Locus_1334_Transcript_1/1_Conf_1.000	1090	20	3.95E-105	XP_002629729.1	71	385.956	325	231	C. briggsae CBR-TAG-124 protein
Locus_13340_Transcript_1/1_Conf_1.000	353	0							
Locus_13341_Transcript_1/1_Conf_1.000	1304	20	1.16E-157	NP_506859.2	79	560.836	437	347	hypothetical protein C06B8.7
Locus_13342_Transcript_1/1_Conf_1.000	606	2	6.63E-17	NP_500233.1	58	91.2781	110	64	hypothetical protein Y69A2AR.28
Locus_13343_Transcript_1/1_Conf_1.000	289	2	1.36E-06	XP_001894940.1	51	56.225	95	49	Trypsin family protein
Locus_13344_Transcript_1/1_Conf_1.000	139	0							
Locus_13345_Transcript_1/1_Conf_1.000	240	0							
Locus_13346_Transcript_1/2_Conf_1.000	501	6	5.29E-35	NP_495914.1	57	150.599	167	96	hypothetical protein C18E9.8
Locus_13346_Transcript_2/2_Conf_1.000	501	6	5.29E-35	NP_495914.1	57	150.599	167	96	hypothetical protein C18E9.8
Locus_13347_Transcript_1/1_Conf_1.000	174	0							

Locus_13348_Transcript_1/1_Conf_1.000	1009	20	5.79E-108	NP_497663.1	80	395.201	304	245	MEChanosensory abnormality family member (mec-12)
Locus_13349_Transcript_1/1_Conf_1.000	555	0							
Locus_1335_Transcript_1/1_Conf_1.000	570	20	9.13E-76	ACD88888.1	97	286.574	149	145	troponin C
Locus_13350_Transcript_1/1_Conf_1.000	145	0							
Locus_13351_Transcript_1/1_Conf_1.000	437	0							
Locus_13352_Transcript_1/2_Conf_1.000	233	20	7.88E-15	ZP_04113472.1	64	83.5741	76	49	LPXTG-motif cell wall anchor domain protein
Locus_13352_Transcript_2/2_Conf_1.000	676	20	6.09E-23	ZP_04113472.1	53	111.694	130	69	LPXTG-motif cell wall anchor domain protein
Locus_13353_Transcript_1/1_Conf_1.000	985	20	7.47E-121	NP_494897.3	75	437.958	328	248	hypothetical protein R05F9.12
Locus_13354_Transcript_1/1_Conf_1.000	377	0							
Locus_13355_Transcript_1/1_Conf_1.000	299	0							
Locus_13356_Transcript_1/1_Conf_1.000	228	0							
Locus_13357_Transcript_1/1_Conf_1.000	250	0							
Locus_13358_Transcript_1/4_Conf_0.375	367	20	6.44E-62	EFO26582.1	100	239.965	122	122	TATA-box binding protein
Locus_13358_Transcript_2/4_Conf_0.625	925	20	3.50E-93	XP_002642588.1	73	345.895	320	235	C. briggsae CBR-TBP-1 protein

Locus_13358_Transcript_3/4_Conf_0.625	925	20	3.50E-93	XP_002642588.1	73	345.895	320	235	C. briggsae CBR-TBP-1 protein
Locus_13358_Transcript_4/4_Conf_0.625	925	20	3.50E-93	XP_002642588.1	73	345.895	320	235	C. briggsae CBR-TBP-1 protein
Locus_13359_Transcript_1/1_Conf_1.000	154	4	9.08E-11	EFO21130.1	88	70.0922	42	37	hypothetical protein LOAG_07358
Locus_1336_Transcript_1/1_Conf_1.000	190	0							
Locus_13360_Transcript_1/1_Conf_1.000	219	0							
Locus_13361_Transcript_1/1_Conf_1.000	639	0							
Locus_13362_Transcript_1/1_Conf_1.000	717	20	1.29E-45	EFO23663.1	63	187.193	228	144	myosin xviiia
Locus_13363_Transcript_1/1_Conf_1.000	221	0							
Locus_13364_Transcript_1/1_Conf_1.000	380	20	9.53E-37	NP_492244.1	78	156.377	113	89	hypothetical protein ZK265.3
Locus_13365_Transcript_1/1_Conf_1.000	254	20	3.12E-27	NP_495261.1	83	124.79	80	67	hypothetical protein F13H8.7
Locus_13366_Transcript_1/1_Conf_1.000	161	16	3.20E-16	AAS49411.1	86	88.1965	51	44	putative neuromuscular acetylcholinesterase
Locus_13367_Transcript_1/1_Conf_1.000	325	6	1.52E-34	NP_492775.2	84	149.058	105	89	LAMinin related. See also lmb- family member (lam-3)
Locus_13368_Transcript_1/1_Conf_1.000	132	0							
Locus_13369_Transcript_1/1_Conf_1.000	785	20	3.74E-108	XP_002631013.1	88	395.201	260	230	C. briggsae CBR-PTR-18 protein
Locus_1337_Transcript_1/3_Conf_0.667	921	0							
Locus_1337_Transcript_2/3_Conf_0.667	967	0							
Locus_1337_Transcript_3/3_Conf_0.667	969	0							

Locus_13370_Transcript_1/1_Conf_1.000	451	20	5.38E-40	NP_496146.1	68	167.162	149	102	Ubiquitin Fusion Degradation (yeast UFD homolog) family member (ufd-3)
Locus_13371_Transcript_1/1_Conf_1.000	204	0							
Locus_13372_Transcript_1/1_Conf_1.000	395	20	1.54E-34	XP_002644371.1	72	149.058	129	94	C. briggsae CBR-DHS-27 protein
Locus_13373_Transcript_1/1_Conf_1.000	477	20	4.99E-38	XP_001898260.1	74	160.614	125	93	MSP domain containing protein
Locus_13374_Transcript_1/1_Conf_1.000	281	20	1.54E-47	BAG51482.1	100	192.2	88	88	unnamed protein product
Locus_13375_Transcript_1/1_Conf_1.000	730	20	1.87E-63	NP_510828.1	93	246.514	152	142	Myosin Light Chain family member (mlc-2)
Locus_13376_Transcript_1/1_Conf_1.000	271	0							
Locus_13377_Transcript_1/1_Conf_1.000	617	3	5.44E-38	XP_002631029.1	71	161.384	151	108	Hypothetical protein CBG02786
Locus_13378_Transcript_1/1_Conf_1.000	888	6	4.31E-45	XP_002641960.1	66	186.037	201	134	C. briggsae CBR-UNC-36 protein
Locus_13379_Transcript_1/1_Conf_1.000	236	2	7.37E-05	EFO22556.1	58	50.447	77	45	hypothetical protein LOAG_05929
Locus_1338_Transcript_1/1_Conf_1.000	535	18	7.08E-42	NP_001040754.1	65	173.711	177	116	DNaJ domain (prokaryotic heat shock protein) family member (dnj-8)
Locus_13380_Transcript_1/1_Conf_1.000	697	0							
Locus_13381_Transcript_1/1_Conf_1.000	348	0							
Locus_13382_Transcript_1/1_Conf_1.000	332	5	2.27E-22	NP_491451.2	64	108.612	109	70	2 (Zwei) IG-domain protein family member (zig-7)
Locus_13383_Transcript_1/1_Conf_1.000	1055	20	1.17E-74	AAK29933.3	67	284.648	308	208	Rab connectin related protein 2, partially confirmed by transcript evidence
Locus_13384_Transcript_1/1_Conf_1.000	379	0							
Locus_13385_Transcript_1/1_Conf_1.000	306	6	1.28E-25	AAT02161.1	80	119.398	76	61	hypothetical protein L3ni22
Locus_13386_Transcript_1/1_Conf_1.000	136	0							
Locus_13387_Transcript_1/1_Conf_1.000	1009	20	1.47E-127	NP_506318.1	81	460.299	301	245	CathePsin Z family member (cpz-2)
Locus_13388_Transcript_1/1_Conf_1.000	523	20	1.63E-64	XP_002631314.1	84	248.825	163	137	C. briggsae CBR-LDH-1 protein
Locus_13389_Transcript_1/1_Conf_1.000	177	0							

Locus_1339_Transcript_1/1_Conf_1.000	612	0							
Locus_13390_Transcript_1/1_Conf_1.000	175	20	2.66E-23	XP_002642408.1	92	111.694	57	53	C. briggsae CBR-NHL-1 protein
Locus_13391_Transcript_1/1_Conf_1.000	247	20	2.10E-28	XP_001900058.1	82	128.642	80	66	Immunoglobulin I-set domain containing protein
Locus_13392_Transcript_1/1_Conf_1.000	170	0							
Locus_13393_Transcript_1/1_Conf_1.000	1188	3	9.40E-95	XP_002639760.1	69	351.673	312	216	Hypothetical protein CBG02206
Locus_13394_Transcript_1/2_Conf_1.000	307	0							
Locus_13394_Transcript_2/2_Conf_1.000	310	0							
Locus_13395_Transcript_1/1_Conf_1.000	484	17	1.60E-07	NP_001133980.1	71	59.3066	45	32	SH2 domain-containing protein 4A
Locus_13396_Transcript_1/1_Conf_1.000	300	20	2.76E-44	EFO23652.1	92	181.415	99	92	vacuolar proton pump
Locus_13397_Transcript_1/1_Conf_1.000	172	0							
Locus_13398_Transcript_1/1_Conf_1.000	481	6	1.70E-62	XP_002636539.1	80	241.891	160	129	Hypothetical protein CBG23226
Locus_13399_Transcript_1/1_Conf_1.000	362	20	4.87E-17	XP_002630266.1	60	90.8929	126	76	Hypothetical protein CBG00693
Locus_134_Transcript_1/1_Conf_1.000	716	4	2.79E-16	NP_001022219.1	50	89.7373	182	92	hypothetical protein F59B10.4
Locus_1340_Transcript_1/5_Conf_0.444	1411	0							
Locus_1340_Transcript_2/5_Conf_0.556	1507	0							
Locus_1340_Transcript_3/5_Conf_0.444	1429	0							
Locus_1340_Transcript_4/5_Conf_0.556	1501	0							
Locus_1340_Transcript_5/5_Conf_0.556	1507	0							
Locus_13400_Transcript_1/1_Conf_1.000	477	3	1.79E-11	NP_494767.1	63	72.4034	112	71	hypothetical protein H20J04.2
Locus_13401_Transcript_1/2_Conf_1.000	847	20	2.05E-17	NP_510460.2	66	93.9745	83	55	MiniBrain Kinase (Drosophila) homolog family member (mbk-1)
Locus_13401_Transcript_2/2_Conf_1.000	771	20	1.73E-17	NP_510460.2	66	93.9745	83	55	MiniBrain Kinase (Drosophila) homolog family member (mbk-1)
Locus_13402_Transcript_1/1_Conf_1.000	450	0							

Locus_13403_Transcript_1/1_Conf_1.000	578	20	2.95E-53	XP_002643681.1	72	211.846	182	132	Hypothetical protein CBG01860
Locus_13404_Transcript_1/1_Conf_1.000	134	0							
Locus_13405_Transcript_1/1_Conf_1.000	967	20	5.27E-63	XP_002639862.1	63	245.743	320	204	C. briggsae CBR-CED-12 protein
Locus_13406_Transcript_1/1_Conf_1.000	208	0							
Locus_13407_Transcript_1/1_Conf_1.000	1122	8	3.04E-31	CAR63527.1	94	140.584	108	102	putative TolA protein
Locus_13408_Transcript_1/1_Conf_1.000	256	0							
Locus_13409_Transcript_1/1_Conf_1.000	607	20	2.74E-71	XP_002633090.1	95	271.937	164	156	C. briggsae CBR-CYN-12 protein
Locus_1341_Transcript_1/1_Conf_1.000	285	20	4.08E-19	XP_001898944.1	67	97.8265	94	63	Protein kinase domain containing protein
Locus_13410_Transcript_1/1_Conf_1.000	641	2	1.92E-04	DAA21469.1	36	50.0618	158	57	complement factor H precursor
Locus_13411_Transcript_1/1_Conf_1.000	186	0							

Locus_13412_Transcript_1/2_Conf_1.000	372	20	1.07E-19	NP_506362.1	64	99.7525	99	64	BIR (baculovirus inhibitory repeat) family member (bir-2)
Locus_13412_Transcript_2/2_Conf_1.000	644	20	3.31E-20	NP_506362.1	60	102.449	128	77	BIR (baculovirus inhibitory repeat) family member (bir-2)
Locus_13413_Transcript_1/1_Conf_1.000	251	0							
Locus_13414_Transcript_1/2_Conf_1.000	299	2	7.87E-07	XP_002647590.1	61	56.9954	77	47	Hypothetical protein CBG06678
Locus_13414_Transcript_2/2_Conf_1.000	367	2	1.32E-06	XP_002647590.1	61	56.225	77	47	Hypothetical protein CBG06678

Locus_13415_Transcript_1/1_Conf_1.000	643	20	1.46E-76	CAA21686.2	81	289.656	216	177	C. elegans protein Y54E2A.4, partially confirmed by transcript evidence
Locus_13416_Transcript_1/1_Conf_1.000	830	8	1.32E-13	EFO16199.1	50	81.2629	175	89	acetyltransferase
Locus_13417_Transcript_1/1_Conf_1.000	378	0							
Locus_13418_Transcript_1/1_Conf_1.000	250	0							
Locus_13419_Transcript_1/1_Conf_1.000	257	0							
Locus_1342_Transcript_1/1_Conf_1.000	454	20	5.72E-42	O01358.1	93	173.711	125	117	60S ribosomal protein L27a
Locus_13420_Transcript_1/1_Conf_1.000	302	0							
Locus_13421_Transcript_1/1_Conf_1.000	475	17	5.39E-16	ACI49188.1	67	87.4261	97	65	hypothetical protein Csp3_JD02.016
Locus_13422_Transcript_1/1_Conf_1.000	285	0							
Locus_13423_Transcript_1/1_Conf_1.000	196	0							
Locus_13424_Transcript_1/1_Conf_1.000	422	20	3.01E-14	XP_002660885.1	68	81.6481	88	60	PREDICTED: hypothetical protein
Locus_13425_Transcript_1/1_Conf_1.000	1300	20	8.71E-105	AAM18101.1	74	385.185	347	257	AF497823_1putative Na-H exchanger isoform 1
Locus_13426_Transcript_1/1_Conf_1.000	297	20	6.22E-12	ACD12702.1	85	73.9442	48	41	histone H1
Locus_13427_Transcript_1/1_Conf_1.000	331	0							
Locus_13428_Transcript_1/1_Conf_1.000	1601	20	4.84E-103	NP_508710.2	60	379.793	529	319	Multidrug Resistance Protein family member (mrp-6)
Locus_13429_Transcript_1/1_Conf_1.000	163	0							
Locus_1343_Transcript_1/1_Conf_1.000	499	20	2.38E-56	XP_002648101.1	85	221.476	152	130	C. briggsae CBR-DHS-13 protein
Locus_13430_Transcript_1/1_Conf_1.000	388	0							
Locus_13431_Transcript_1/2_Conf_1.000	551	20	4.41E-53	NP_499799.1	77	211.075	180	140	fatty Acid CoA Synthetase family member (acs-14)

Locus_13431_Transcript_2/2_Conf_1.000	534	20	8.92E-53	NP_499799.1	78	209.92	175	138	fatty Acid CoA Synthetase family member (acs-14)
Locus_13432_Transcript_1/1_Conf_1.000	945	3	5.54E-25	CAB03203.2	55	119.398	245	135	C. elegans protein M02B1.4, partially confirmed by transcript evidence
Locus_13433_Transcript_1/1_Conf_1.000	542	15	2.87E-70	XP_002642952.1	82	268.085	180	148	Hypothetical protein CBG15235
Locus_13434_Transcript_1/1_Conf_1.000	128	0							
Locus_13435_Transcript_1/1_Conf_1.000	402	20	2.33E-59	XP_002642823.1	92	231.491	131	121	Hypothetical protein CBG21221
Locus_13436_Transcript_1/1_Conf_1.000	370	0							
Locus_13437_Transcript_1/1_Conf_1.000	429	20	2.33E-43	XP_002639695.1	78	178.333	146	114	C. briggsae CBR-FCP-1 protein
Locus_13438_Transcript_1/1_Conf_1.000	654	20	7.25E-10	XP_002634943.1	44	68.1662	134	60	Hypothetical protein CBG22545
Locus_13439_Transcript_1/1_Conf_1.000	992	20	1.31E-173	ADF56003.1	99	613.224	310	309	nicotinic acetylcholine receptor alpha subunit 63b
Locus_1344_Transcript_1/1_Conf_1.000	1056	20	8.92E-115	Q94125.6	72	417.927	375	272	Phosphatidylinositol 3-kinase age-1

Locus_13440_Transcript_1/1_Conf_1.000	221	20	3.34E-29	XP_002629937.1	89	131.339	73	65	Hypothetical protein CBG03655
Locus_13441_Transcript_1/1_Conf_1.000	230	0							
Locus_13442_Transcript_1/1_Conf_1.000	163	0							
Locus_13443_Transcript_1/1_Conf_1.000	220	0							
Locus_13444_Transcript_1/1_Conf_1.000	701	10	2.06E-16	XP_001891682.1	47	90.1225	225	106	MRG family protein
Locus_13445_Transcript_1/1_Conf_1.000	225	0							
Locus_13446_Transcript_1/1_Conf_1.000	404	20	3.98E-59	XP_002630309.1	92	230.72	131	121	Hypothetical protein CBG00745
Locus_13447_Transcript_1/1_Conf_1.000	246	0							
Locus_13448_Transcript_1/1_Conf_1.000	481	0							
Locus_13449_Transcript_1/1_Conf_1.000	192	0							
Locus_1345_Transcript_1/1_Conf_1.000	288	0							
Locus_13450_Transcript_1/1_Conf_1.000	446	20	1.75E-22	XP_002635322.1	59	108.997	145	86	Hypothetical protein CBG01489
Locus_13451_Transcript_1/1_Conf_1.000	357	0							
Locus_13452_Transcript_1/1_Conf_1.000	459	4	2.75E-04	XP_002547545.1	42	48.521	147	62	predicted protein
Locus_13453_Transcript_1/1_Conf_1.000	255	0							
Locus_13454_Transcript_1/1_Conf_1.000	1224	20	0	NP_001021621.1	89	686.026	403	361	Nuclear/nucleolar GTP-binding Protein family member (ngp-1)
Locus_13455_Transcript_1/1_Conf_1.000	146	0							
Locus_13456_Transcript_1/1_Conf_1.000	403	2	1.59E-07	NP_509349.1	65	59.3066	58	38	hypothetical protein F45E1.1
Locus_13457_Transcript_1/1_Conf_1.000	600	20	2.88E-33	EFO23325.1	63	145.591	149	94	hypothetical protein LOAG_05163
Locus_13458_Transcript_1/1_Conf_1.000	870	0							
Locus_13459_Transcript_1/1_Conf_1.000	612	0							

Locus_1346_Transcript_1/3_Conf_0.714	1080	20	1.88E-91	NP_493246.1	68	340.502	407	278	hypothetical protein Y18D10A.8
Locus_1346_Transcript_2/3_Conf_0.714	1086	20	5.15E-97	NP_493246.1	69	358.992	407	281	hypothetical protein Y18D10A.8
Locus_1346_Transcript_3/3_Conf_0.714	1110	20	4.37E-99	NP_493246.1	70	365.925	407	287	hypothetical protein Y18D10A.8
Locus_13460_Transcript_1/1_Conf_1.000	475	0							
Locus_13461_Transcript_1/1_Conf_1.000	2719	20	0	XP_002638375.1	78	1257.66	963	754	Hypothetical protein CBG18580
Locus_13462_Transcript_1/1_Conf_1.000	216	5	8.82E-11	NP_001021862.1	57	70.0922	101	58	PMR-type Golgi ATPase family member (pmr-1)
Locus_13463_Transcript_1/1_Conf_1.000	1376	20	0	NP_740958.1	94	647.506	366	345	protein KINase family member (kin-1)
Locus_13464_Transcript_1/1_Conf_1.000	526	0							
Locus_13465_Transcript_1/1_Conf_1.000	319	0							

Locus_13466_Transcript_1/1_Conf_1.000	602	20	1.46E-85	AAU87825.2	88	319.316	186	165	Hypothetical protein C54E4.5
Locus_13467_Transcript_1/1_Conf_1.000	547	1	8.28E-04	XP_640723.1	62	47.3654	95	59	hypothetical protein DDB_G0281503
Locus_13468_Transcript_1/1_Conf_1.000	300	20	7.78E-31	EFO26621.1	81	136.732	93	76	AIDA-1b
Locus_13469_Transcript_1/1_Conf_1.000	701	20	3.22E-86	XP_001895373.1	81	322.013	233	189	PCI domain containing protein
Locus_1347_Transcript_1/1_Conf_1.000	1004	20	3.25E-103	A8WLV5.2	80	379.407	267	215	Probable eukaryotic translation initiation factor 3 subunit G
Locus_13470_Transcript_1/1_Conf_1.000	216	20	2.24E-14	ADF56007.1	95	82.0333	70	67	nicotinic acetylcholine receptor non-alpha subunit 29.3
Locus_13471_Transcript_1/1_Conf_1.000	383	20	8.61E-30	XP_002640484.1	90	133.265	85	77	C. briggsae CBR-TAF-1 protein
Locus_13472_Transcript_1/1_Conf_1.000	238	8	1.34E-06	CAR63562.1	67	56.225	78	53	putative COLlagen
Locus_13473_Transcript_1/1_Conf_1.000	144	0							
Locus_13474_Transcript_1/1_Conf_1.000	306	1	1.28E-09	EFO19473.1	67	66.2402	99	67	AGC/DMPK/GEK protein kinase
Locus_13475_Transcript_1/2_Conf_1.000	170	0							
Locus_13475_Transcript_2/2_Conf_1.000	991	0							
Locus_13476_Transcript_1/1_Conf_1.000	138	19	3.72E-09	EFO15479.1	91	64.6994	34	31	hypothetical protein LOAG_13032
Locus_13477_Transcript_1/1_Conf_1.000	564	7	4.05E-04	XP_002935260.1	42	48.521	171	72	PREDICTED: bromodomain-containing protein 3
Locus_13478_Transcript_1/1_Conf_1.000	352	0							

Locus_13479_Transcript_1/1_Conf_1.000	158	0							
Locus_1348_Transcript_1/1_Conf_1.000	289	0							
Locus_13480_Transcript_1/1_Conf_1.000	130	7	1.58E-07	NP_510233.1	73	59.3066	42	31	CYtochrome P450 family member (cyp-13B1)
Locus_13481_Transcript_1/1_Conf_1.000	128	0							
Locus_13482_Transcript_1/1_Conf_1.000	509	20	5.67E-80	XP_002633437.1	91	300.056	169	155	C. briggsae CBR-UNC-22 protein
Locus_13483_Transcript_1/1_Conf_1.000	380	20	7.05E-40	NP_497647.1	78	166.777	127	100	hypothetical protein Y55D5A.3
Locus_13484_Transcript_1/1_Conf_1.000	132	0							
Locus_13485_Transcript_1/1_Conf_1.000	838	20	2.89E-32	XP_001897363.1	52	143.28	226	119	hypothetical protein Bm1_29605
Locus_13486_Transcript_1/1_Conf_1.000	132	0							
Locus_13487_Transcript_1/1_Conf_1.000	354	20	6.18E-28	NP_001021940.1	70	127.102	121	85	hypothetical protein C08H9.3
Locus_13488_Transcript_1/1_Conf_1.000	224	0							
Locus_13489_Transcript_1/1_Conf_1.000	845	20	9.65E-68	NP_001021145.1	72	261.151	239	174	hypothetical protein C05D11.1
Locus_1349_Transcript_1/1_Conf_1.000	1533	3	3.63E-116	NP_502736.1	60	423.32	520	314	hypothetical protein Y64G10A.6
Locus_13490_Transcript_1/1_Conf_1.000	267	0							
Locus_13491_Transcript_1/1_Conf_1.000	305	0							
Locus_13492_Transcript_1/1_Conf_1.000	452	20	1.12E-53	NP_493642.1	86	212.616	150	129	hypothetical protein F23F1.6
Locus_13493_Transcript_1/1_Conf_1.000	1078	20	6.21E-95	EFO23108.1	66	352.058	363	243	Paf1 family protein
Locus_13494_Transcript_1/2_Conf_1.000	1385	20	0	NP_001021410.2	98	698.738	319	313	LIM domain family member (lim-9)
Locus_13494_Transcript_2/2_Conf_1.000	1385	20	0	NP_001021410.2	98	698.738	319	313	LIM domain family member (lim-9)
Locus_13495_Transcript_1/1_Conf_1.000	150	0							
Locus_13496_Transcript_1/2_Conf_1.000	230	20	2.01E-10	ACA30304.1	63	68.9366	74	47	serine protease

Locus_13496_Transcript_2/2_Conf_1.000	256	20	3.13E-11	ACA30304.1	64	71.633	78	50	serine protease
Locus_13497_Transcript_1/1_Conf_1.000	372	0							
Locus_13498_Transcript_1/1_Conf_1.000	153	0							
Locus_13499_Transcript_1/1_Conf_1.000	142	0							
Locus_135_Transcript_1/1_Conf_1.000	1283	20	1.43E-168	ABX79385.1	96	597.045	341	330	glyceraldehyde-3-phosphate dehydrogenase
Locus_1350_Transcript_1/1_Conf_1.000	1668	20	9.88E-139	XP_001900571.1	69	498.434	495	342	HIRA protein.
Locus_13500_Transcript_1/1_Conf_1.000	689	20	1.94E-80	NP_496210.2	85	302.753	235	200	hypothetical protein F54B3.3
Locus_13501_Transcript_1/1_Conf_1.000	363	1	4.71E-04	XP_758895.1	52	47.7506	67	35	hypothetical protein UM02748.1
Locus_13502_Transcript_1/1_Conf_1.000	330	0							
Locus_13503_Transcript_1/1_Conf_1.000	286	0							
Locus_13504_Transcript_1/1_Conf_1.000	340	0							
Locus_13505_Transcript_1/1_Conf_1.000	786	4	3.37E-32	XP_002630374.1	54	142.895	269	147	Hypothetical protein CBG04313
Locus_13506_Transcript_1/1_Conf_1.000	1287	1	4.67E-18	NP_491884.1	41	97.0561	449	185	hypothetical protein T10E9.2
Locus_13507_Transcript_1/1_Conf_1.000	220	0							

Locus_13508_Transcript_1/1_Conf_1.000	1148	20	1.34E-175	NP_509023.1	86	620.157	382	331	hypothetical protein C15H9.7
Locus_13509_Transcript_1/1_Conf_1.000	443	0							
Locus_1351_Transcript_1/1_Conf_1.000	2915	20	0	XP_002641964.1	98	1678.3	858	841	C. briggsae CBR-PRP-8 protein
Locus_13510_Transcript_1/1_Conf_1.000	865	2	9.01E-08	EFO28197.1	56	62.003	92	52	hypothetical protein LOAG_00279
Locus_13511_Transcript_1/1_Conf_1.000	182	0							
Locus_13512_Transcript_1/1_Conf_1.000	378	0							
Locus_13513_Transcript_1/1_Conf_1.000	148	0							
Locus_13514_Transcript_1/1_Conf_1.000	640	2	3.16E-15	NP_001041016.1	79	85.8853	63	50	hypothetical protein Y116A8C.30
Locus_13515_Transcript_1/1_Conf_1.000	170	0							
Locus_13516_Transcript_1/1_Conf_1.000	388	4	8.31E-09	NP_001022032.1	46	63.5438	121	56	TRRAP-like (transcription/transformation domain-associated protein) family member (trr-1)
Locus_13517_Transcript_1/1_Conf_1.000	573	0							
Locus_13518_Transcript_1/1_Conf_1.000	145	2	4.41E-05	XP_002642155.1	70	51.2174	48	34	C. briggsae CBR-GLR-1 protein
Locus_13519_Transcript_1/1_Conf_1.000	135	0							
Locus_1352_Transcript_1/1_Conf_1.000	587	20	9.11E-13	XP_002195631.1	58	77.411	129	76	PREDICTED: RAD51-like 3 (S. cerevisiae)

Locus_13520_Transcript_1/1_Conf_1.000	346	2	6.08E-07	NP_502515.1	53	57.3806	103	55	hypothetical protein C39E9.11
Locus_13521_Transcript_1/1_Conf_1.000	1096	20	1.21E-77	EFO19790.1	61	294.664	378	232	exostosin-1
Locus_13522_Transcript_1/1_Conf_1.000	441	20	3.66E-36	XP_002640257.1	67	154.451	149	100	Hypothetical protein CBG12782
Locus_13523_Transcript_1/1_Conf_1.000	527	20	6.82E-42	EFO20779.1	66	173.711	175	117	hypothetical protein LOAG_07709
Locus_13524_Transcript_1/1_Conf_1.000	385	20	2.49E-37	XP_002641238.1	74	158.303	133	99	C. briggsae CBR-THOC-2 protein
Locus_13525_Transcript_1/1_Conf_1.000	243	0							
Locus_13526_Transcript_1/1_Conf_1.000	487	0							
Locus_13527_Transcript_1/1_Conf_1.000	265	0							
Locus_13528_Transcript_1/1_Conf_1.000	492	0							
Locus_13529_Transcript_1/1_Conf_1.000	363	0							
Locus_1353_Transcript_2/3_Conf_0.667	798	20	8.63E-116	NP_001076672.1	89	420.624	249	224	hypothetical protein F01G4.6
Locus_1353_Transcript_3/3_Conf_0.667	798	20	8.64E-116	NP_001076672.1	89	420.624	249	224	hypothetical protein F01G4.6
Locus_13530_Transcript_1/1_Conf_1.000	955	1	6.55E-42	CAG28316.1	65	175.637	202	132	spindle assembly abnormal protein 5, SAS-5
Locus_13531_Transcript_1/2_Conf_1.000	470	0							
Locus_13531_Transcript_2/2_Conf_1.000	470	0							
Locus_13532_Transcript_1/1_Conf_1.000	331	2	2.78E-12	NP_508464.2	64	75.0998	96	62	hypothetical protein F52H2.7

Locus_13533_Transcript_1/1_Conf_1.000	475	3	2.68E-07	NP_001021054.1	48	58.5362	154	75	Suppressor with Morphological effect on Genitalia family member (smg-1)
Locus_13534_Transcript_1/1_Conf_1.000	486	0							
Locus_13535_Transcript_1/1_Conf_1.000	155	2	1.66E-04	XP_002634292.1	72	49.2914	51	37	C. briggsae CBR-UGT-54 protein
Locus_13536_Transcript_1/1_Conf_1.000	230	0							
Locus_13537_Transcript_1/1_Conf_1.000	400	20	9.23E-48	XP_001898337.1	82	192.971	133	110	oxidoreductase, short chain dehydrogenase/reductase family protein
Locus_13538_Transcript_1/1_Conf_1.000	895	20	2.30E-70	Q610N4.2	77	270.011	253	195	Transmembrane protein 104 homolog
Locus_13539_Transcript_1/1_Conf_1.000	381	0							
Locus_1354_Transcript_1/1_Conf_1.000	472	20	2.11E-44	XP_002634364.1	96	181.8	82	79	C. briggsae CBR-EXC-9 protein
Locus_13540_Transcript_1/1_Conf_1.000	438	20	4.04E-56	XP_002637802.1	94	220.705	137	130	C. briggsae CBR-HDA-1 protein
Locus_13541_Transcript_1/1_Conf_1.000	686	0							
Locus_13542_Transcript_1/1_Conf_1.000	161	0							
Locus_13543_Transcript_1/1_Conf_1.000	465	20	3.29E-37	XP_002631639.1	77	157.918	149	116	Hypothetical protein CBG20828
Locus_13544_Transcript_1/1_Conf_1.000	145	2	1.08E-11	NP_492142.1	85	73.1738	47	40	hypothetical protein T23G11.4
Locus_13545_Transcript_1/1_Conf_1.000	149	0							
Locus_13546_Transcript_1/1_Conf_1.000	145	0							
Locus_13547_Transcript_1/1_Conf_1.000	497	6	6.75E-43	NP_498388.1	69	176.792	166	116	hypothetical protein C56G2.3
Locus_13548_Transcript_1/1_Conf_1.000	688	20	1.54E-85	XP_002636924.1	81	319.701	229	186	C. briggsae CBR-ACL-6 protein
Locus_13549_Transcript_1/1_Conf_1.000	201	4	1.99E-26	XP_002632215.1	95	122.094	66	63	Hypothetical protein CBG07083
Locus_1355_Transcript_1/1_Conf_1.000	229	0							
Locus_13550_Transcript_1/1_Conf_1.000	248	0							
Locus_13551_Transcript_1/1_Conf_1.000	382	0							

Locus_13552_Transcript_1/1_Conf_1.000	570	20	3.37E-62	ACA81684.1	84	241.506	161	136	cholecystokinin receptor 2 splice isoform b
Locus_13553_Transcript_1/1_Conf_1.000	263	0							
Locus_13554_Transcript_1/1_Conf_1.000	631	20	2.10E-32	EFO24248.1	61	142.895	175	107	repair protein Rad1/Rec1/Rad17 containing protein
Locus_13555_Transcript_1/1_Conf_1.000	514	20	3.54E-37	CAR63581.1	77	157.918	143	111	putative COLlagen
Locus_13556_Transcript_1/1_Conf_1.000	295	7	5.45E-16	NP_490710.2	75	87.4261	80	60	hypothetical protein C53D5.2
Locus_13557_Transcript_1/1_Conf_1.000	268	20	1.64E-04	DAA32996.1	44	49.2914	83	37	ubiquitin-associated and SH3 domain-containing protein A
Locus_13558_Transcript_1/1_Conf_1.000	547	20	1.27E-12	XP_001704397.1	47	76.6406	141	67	Tenascin-X precursor
Locus_13559_Transcript_1/2_Conf_1.000	1350	20	9.68E-163	XP_002638613.1	83	577.785	407	340	C. briggsae CBR-PGP-9 protein
Locus_13559_Transcript_2/2_Conf_1.000	1350	20	9.68E-163	XP_002638613.1	83	577.785	407	340	C. briggsae CBR-PGP-9 protein

Locus_1356_Transcript_1/2_Conf_1.000	2814	20	0	NP_490865.3	78	1028.08	758	592	hypothetical protein Y92H12A.2
Locus_1356_Transcript_2/2_Conf_1.000	2754	20	0	NP_490865.3	80	1030.78	743	598	hypothetical protein Y92H12A.2
Locus_13560_Transcript_1/1_Conf_1.000	326	0							

Locus_13561_Transcript_1/1_Conf_1.000	1146	20	1.69E-69	EFO24820.1	66	267.7	296	196	hypothetical protein LOAG_03664
Locus_13562_Transcript_1/1_Conf_1.000	221	3	1.16E-05	NP_492441.1	52	53.1434	70	37	related to vertebrate MEF2 transcription factor family member (mef-2)
Locus_13563_Transcript_1/1_Conf_1.000	231	2	1.49E-05	XP_002630854.1	68	52.7582	50	34	C. briggsae CBR-RAN-5 protein
Locus_13564_Transcript_1/1_Conf_1.000	265	20	8.66E-30	XP_002629838.1	85	133.265	87	74	Hypothetical protein CBG18727
Locus_13565_Transcript_1/1_Conf_1.000	128	2	6.42E-09	XP_002636472.1	80	63.929	42	34	Hypothetical protein CBG23143
Locus_13566_Transcript_1/1_Conf_1.000	319	4	3.09E-35	CAR63626.1	89	151.369	108	97	hypothetical protein
Locus_13567_Transcript_1/1_Conf_1.000	347	0							
Locus_13568_Transcript_1/1_Conf_1.000	484	5	6.92E-19	NP_509847.1	60	97.0561	128	77	CLaudin-like in Caenorhabditis family member (clc-1)
Locus_13569_Transcript_1/1_Conf_1.000	243	0							
Locus_1357_Transcript_1/5_Conf_0.688	3471	20	9.63E-92	XP_002641165.1	57	343.584	600	347	C. briggsae CBR-NPP-10 protein
Locus_1357_Transcript_2/5_Conf_0.125	492	5	9.25E-08	XP_002641165.1	55	60.077	85	47	C. briggsae CBR-NPP-10 protein
Locus_1357_Transcript_3/5_Conf_0.188	1343	20	2.37E-36	ACZ54696.1	64	157.918	242	156	Nuclear pore complex protein protein 10, isoform c, partially confirmed by transcript evidence
Locus_1357_Transcript_4/5_Conf_0.562	2980	20	6.44E-81	XP_002641165.1	63	307.375	417	264	C. briggsae CBR-NPP-10 protein
Locus_1357_Transcript_5/5_Conf_0.688	3492	20	9.69E-92	XP_002641165.1	57	343.584	600	347	C. briggsae CBR-NPP-10 protein
Locus_13570_Transcript_1/1_Conf_1.000	221	20	6.73E-30	XP_002826714.1	100	133.65	63	63	PREDICTED: 60S ribosomal protein L21-like isoform 1
Locus_13571_Transcript_1/1_Conf_1.000	211	0							
Locus_13572_Transcript_1/1_Conf_1.000	591	1	2.87E-06	NP_504410.1	48	55.8398	108	52	hypothetical protein B0238.11
Locus_13573_Transcript_1/1_Conf_1.000	185	19	7.48E-13	NP_491270.2	79	77.0258	48	38	Low-density lipoprotein Receptor Related family member (lrp-2)
Locus_13574_Transcript_1/1_Conf_1.000	211	1	6.16E-04	XP_002646401.1	58	47.3654	70	41	C. briggsae CBR-DYS-1 protein

Locus_13575_Transcript_1/1_Conf_1.000	676	20	1.79E-107	NP_497185.1	93	392.504	223	208	Alkyl-Dihydroxyacetonephosphate Synthase family member (ads-1)
Locus_13576_Transcript_1/1_Conf_1.000	574	20	1.83E-39	EFO22852.1	65	166.007	194	127	WD domain-containing protein
Locus_13577_Transcript_1/3_Conf_0.667	1150	20	1.10E-177	XP_002641484.1	89	627.091	386	345	Hypothetical protein CBG09775
Locus_13577_Transcript_2/3_Conf_0.667	1150	20	3.00E-175	XP_002641484.1	89	619.002	385	344	Hypothetical protein CBG09775
Locus_13577_Transcript_3/3_Conf_0.667	1150	20	3.00E-175	XP_002641484.1	89	619.002	385	344	Hypothetical protein CBG09775
Locus_13578_Transcript_1/1_Conf_1.000	203	0							
Locus_13579_Transcript_1/2_Conf_1.000	631	20	3.13E-36	CBA11992.1	72	155.606	122	89	endonuclease-reverse transcriptase HmRTE-e01
Locus_13579_Transcript_2/2_Conf_1.000	313	2	6.77E-06	XP_002632164.1	68	53.9138	60	41	Hypothetical protein CBG07023
Locus_1358_Transcript_1/6_Conf_0.286	753	20	5.14E-104	NP_741155.2	95	381.333	227	216	hypothetical protein F01F1.12
Locus_1358_Transcript_2/6_Conf_0.286	711	20	1.34E-103	NP_741155.2	95	379.793	224	213	hypothetical protein F01F1.12
Locus_1358_Transcript_3/6_Conf_0.357	1287	20	2.85E-108	XP_002641199.1	94	396.741	228	215	Hypothetical protein CBG09060

Locus_1358_Transcript_4/6_Conf_0.357	1287	20	1.42E-107	XP_002641199.1	94	394.43	228	215	Hypothetical protein CBG09060
Locus_1358_Transcript_5/6_Conf_0.357	1288	20	6.04E-167	NP_001021240.1	94	591.652	361	340	hypothetical protein F01F1.12
Locus_1358_Transcript_6/6_Conf_0.357	1288	20	1.49E-165	NP_001021240.1	94	587.03	361	340	hypothetical protein F01F1.12
Locus_13580_Transcript_1/1_Conf_1.000	326	0							
Locus_13581_Transcript_1/1_Conf_1.000	685	0							
Locus_13582_Transcript_1/1_Conf_1.000	494	20	4.86E-41	XP_001901777.1	80	170.629	110	88	Melibiase family protein
Locus_13583_Transcript_1/1_Conf_1.000	175	0							
Locus_13584_Transcript_1/1_Conf_1.000	171	20	4.55E-23	AAF59456.4	96	110.923	57	55	Smg-associated and lethal protein 2, partially confirmed by transcript evidence
Locus_13585_Transcript_1/1_Conf_1.000	439	0							
Locus_13586_Transcript_1/1_Conf_1.000	502	0							
Locus_13588_Transcript_1/1_Conf_1.000	541	20	6.96E-08	ZP_04297130.1	45	60.8474	140	63	Cell divisionFtsK/SpoIIIE
Locus_13589_Transcript_1/1_Conf_1.000	316	5	7.46E-05	EFO12242.1	66	50.447	56	37	hypothetical protein LOAG_16291
Locus_1359_Transcript_1/5_Conf_0.444	887	20	5.77E-50	CBA11992.1	59	202.216	264	158	endonuclease-reverse transcriptase HmRTE-e01

Locus_1359_Transcript_2/5_Conf_0.444	673	13	2.21E-25	CBA11992.1	58	119.783	163	96	endonuclease-reverse transcriptase HmRTE-e01
Locus_1359_Transcript_3/5_Conf_0.222	271	0							
Locus_1359_Transcript_4/5_Conf_0.333	1219	20	9.52E-66	CBA11992.1	55	255.373	358	199	endonuclease-reverse transcriptase HmRTE-e01
Locus_1359_Transcript_5/5_Conf_0.444	953	20	5.03E-50	CBA11992.1	60	202.601	265	159	endonuclease-reverse transcriptase HmRTE-e01
Locus_13590_Transcript_1/1_Conf_1.000	189	0							
Locus_13591_Transcript_1/2_Conf_1.000	774	3	1.80E-22	NP_001022822.1	42	110.538	328	140	hypothetical protein Y111B2A.9
Locus_13591_Transcript_2/2_Conf_1.000	774	3	1.37E-22	NP_001022822.1	42	110.923	328	140	hypothetical protein Y111B2A.9
Locus_13592_Transcript_1/2_Conf_1.000	1066	20	6.87E-147	XP_001899040.1	92	524.628	336	310	vinculin
Locus_13592_Transcript_2/2_Conf_1.000	1066	20	6.87E-147	XP_001899040.1	92	524.628	336	310	vinculin
Locus_13593_Transcript_1/1_Conf_1.000	481	20	1.27E-33	XP_002636940.1	92	145.976	79	73	Hypothetical protein CBG09413
Locus_13594_Transcript_1/1_Conf_1.000	501	3	7.43E-13	CAR63585.1	76	77.0258	56	43	putative MAD-Like family member
Locus_13595_Transcript_1/2_Conf_1.000	152	0							
Locus_13595_Transcript_2/2_Conf_1.000	144	0							
Locus_13596_Transcript_1/1_Conf_1.000	172	0							
Locus_13597_Transcript_1/1_Conf_1.000	227	0							
Locus_13598_Transcript_1/1_Conf_1.000	454	20	1.52E-18	NP_509240.2	57	95.9005	142	81	TransThyretin-Related family domain family member (ttr-30)
Locus_13599_Transcript_1/1_Conf_1.000	230	0							
Locus_136_Transcript_1/2_Conf_1.000	645	0							
Locus_136_Transcript_2/2_Conf_1.000	907	0							
Locus_1360_Transcript_1/1_Conf_1.000	294	0							
Locus_13600_Transcript_1/1_Conf_1.000	358	0							
Locus_13601_Transcript_1/1_Conf_1.000	356	0							

Locus_13602_Transcript_1/1_Conf_1.000	177	20	4.83E-25	2XA7	100	117.472	58	58	Ap2 Clathrin Adaptor Core In Active Complex With Cargo Peptides
Locus_13603_Transcript_1/2_Conf_1.000	644	0							
Locus_13603_Transcript_2/2_Conf_1.000	641	0							
Locus_13604_Transcript_1/2_Conf_1.000	578	4	1.54E-09	XP_002641258.1	94	66.6254	35	33	Hypothetical protein CBG05169
Locus_13604_Transcript_2/2_Conf_1.000	488	4	9.98E-10	XP_002641258.1	94	66.6254	35	33	Hypothetical protein CBG05169
Locus_13605_Transcript_1/2_Conf_1.000	344	0							
Locus_13605_Transcript_2/2_Conf_1.000	344	0							
Locus_13606_Transcript_1/1_Conf_1.000	860	20	3.01E-56	CAA22108.2	63	223.016	300	189	C. elegans protein Y75B8A.24, partially confirmed by transcript evidence
Locus_13607_Transcript_1/1_Conf_1.000	405	20	3.48E-47	XP_002641892.1	83	191.045	130	109	Hypothetical protein CBG16586
Locus_13608_Transcript_1/1_Conf_1.000	891	20	1.22E-31	EFO23701.1	52	141.354	291	153	TPR Domain containing protein
Locus_13609_Transcript_1/1_Conf_1.000	880	20	3.50E-07	XP_692550.3	42	60.077	325	138	PREDICTED: si:dkey-230p4.1
Locus_1361_Transcript_1/1_Conf_1.000	1005	20	2.30E-56	NP_001022708.1	56	223.787	352	199	Inhibitor of NFKappaB Kinase Epsilon subunit homolog family member (ikke-1)
Locus_13610_Transcript_1/1_Conf_1.000	310	0							
Locus_13611_Transcript_1/1_Conf_1.000	837	20	1.75E-37	EFO26887.1	53	160.614	247	132	hypothetical protein LOAG_01595
Locus_13612_Transcript_1/1_Conf_1.000	450	0							

Locus_13613_Transcript_1/1_Conf_1.000	494	1	4.75E-04	EFO15567.1	48	47.7506	78	38	hypothetical protein LOAG_12942
Locus_13614_Transcript_1/1_Conf_1.000	728	2	9.00E-18	NP_502746.1	50	94.7449	253	128	hypothetical protein Y67A10A.9
Locus_13615_Transcript_1/1_Conf_1.000	416	20	1.35E-51	EFO20693.1	87	205.682	139	121	hypothetical protein LOAG_07794
Locus_13616_Transcript_1/1_Conf_1.000	237	0							
Locus_13617_Transcript_1/1_Conf_1.000	185	20	6.75E-22	EFO21414.1	91	107.071	61	56	hypothetical protein LOAG_07072
Locus_13618_Transcript_1/1_Conf_1.000	200	20	1.06E-19	EFO24572.1	78	99.7525	65	51	carboxyl transferase domain-containing protein
Locus_13619_Transcript_1/1_Conf_1.000	204	20	5.22E-27	CAR63646.1	88	124.02	67	59	putative Homeobox family member
Locus_1362_Transcript_1/1_Conf_1.000	135	2	3.27E-05	NP_492659.1	78	51.6026	41	32	hypothetical protein B0379.1
Locus_13620_Transcript_1/1_Conf_1.000	263	0							
Locus_13621_Transcript_1/1_Conf_1.000	395	20	2.21E-57	XP_002644998.1	89	224.942	131	117	C. briggsae CBR-LAM-2 protein
Locus_13622_Transcript_1/1_Conf_1.000	300	0							

Locus_13623_Transcript_1/1_Conf_1.000	214	20	6.34E-09	NP_491270.2	59	63.929	71	42	Low-density lipoprotein Receptor Related family member (lrp-2)
Locus_13624_Transcript_1/1_Conf_1.000	346	4	1.30E-33	XP_002641415.1	83	145.976	101	84	Hypothetical protein CBG13282
Locus_13625_Transcript_1/1_Conf_1.000	431	20	7.05E-24	XP_002631495.1	72	113.62	144	105	Hypothetical protein CBG20655
Locus_13626_Transcript_1/1_Conf_1.000	392	0							
Locus_13627_Transcript_1/1_Conf_1.000	983	20	3.23E-116	XP_002647755.1	75	422.55	328	247	C. briggsae CBR-ASP-1 protein
Locus_13628_Transcript_1/2_Conf_1.000	712	0							
Locus_13628_Transcript_2/2_Conf_1.000	1566	0							
Locus_13629_Transcript_1/1_Conf_1.000	904	20	6.12E-87	XP_002640327.1	70	325.094	301	213	C. briggsae CBR-GLH-1 protein
Locus_1363_Transcript_1/1_Conf_1.000	514	2	2.74E-05	XP_002631254.1	51	51.9878	116	60	Hypothetical protein CBG03058
Locus_13630_Transcript_1/1_Conf_1.000	624	0							
Locus_13631_Transcript_1/1_Conf_1.000	1361	1	2.13E-08	XP_001901492.1	44	65.0846	213	94	hypothetical protein
Locus_13632_Transcript_1/1_Conf_1.000	272	0							
Locus_13633_Transcript_1/1_Conf_1.000	329	2	2.98E-06	XP_002636840.1	68	55.0694	61	42	Hypothetical protein CBG09291

Locus_13634_Transcript_1/1_Conf_1.000	499	20	3.24E-29	NP_505373.1	57	131.339	153	88	hypothetical protein B0222.5
Locus_13635_Transcript_1/1_Conf_1.000	146	0							
Locus_13636_Transcript_1/1_Conf_1.000	192	0							
Locus_13637_Transcript_1/1_Conf_1.000	1292	20	0	AAR07614.1	99	801.586	408	406	UNC-18
Locus_13638_Transcript_1/1_Conf_1.000	159	0							
Locus_13639_Transcript_1/1_Conf_1.000	422	5	9.67E-13	XP_002645040.1	54	76.6406	142	77	C. briggsae CBR-CLC-5 protein
Locus_1364_Transcript_1/1_Conf_1.000	348	20	2.22E-17	NP_491097.3	75	92.0485	73	55	hypothetical protein Y54E10BR.1
Locus_13640_Transcript_1/1_Conf_1.000	181	0							
Locus_13641_Transcript_1/1_Conf_1.000	321	0							
Locus_13642_Transcript_1/1_Conf_1.000	559	20	2.13E-26	XP_002637392.1	64	122.479	145	93	Hypothetical protein CBG19099
Locus_13643_Transcript_1/1_Conf_1.000	179	0							
Locus_13644_Transcript_1/1_Conf_1.000	186	20	3.70E-12	XP_002631121.1	72	74.7146	58	42	Hypothetical protein CBG02899
Locus_13645_Transcript_1/1_Conf_1.000	172	20	2.41E-24	XP_002758725.1	100	115.161	57	57	PREDICTED: dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1-like isoform 2
Locus_13646_Transcript_1/2_Conf_1.000	504	0							
Locus_13646_Transcript_2/2_Conf_1.000	477	0							
Locus_13647_Transcript_1/1_Conf_1.000	170	0							
Locus_13648_Transcript_1/1_Conf_1.000	176	0							
Locus_13649_Transcript_1/1_Conf_1.000	229	0							
Locus_1365_Transcript_1/5_Conf_0.222	672	20	2.19E-65	AAG36874.1	83	252.677	182	152	AF242767_1SF2
Locus_1365_Transcript_2/5_Conf_0.333	534	0							
Locus_1365_Transcript_3/5_Conf_0.222	748	20	2.75E-65	AAG36874.1	83	252.677	182	152	AF242767_1SF2

Locus_1365_Transcript_4/5_Conf_0.556	1140	20	6.14E-72	AAG36874.1	83	275.789	198	165	AF242767_1SF2
Locus_1365_Transcript_5/5_Conf_0.556	975	20	4.83E-72	AAG36874.1	83	275.789	198	165	AF242767_1SF2
Locus_13650_Transcript_1/1_Conf_1.000	142	0							
Locus_13651_Transcript_1/1_Conf_1.000	395	20	1.26E-28	XP_001901742.1	77	129.413	94	73	PWI domain containing protein
Locus_13652_Transcript_1/1_Conf_1.000	377	20	6.63E-38	NP_001023236.1	80	160.229	125	101	hypothetical protein F56H11.1
Locus_13653_Transcript_1/1_Conf_1.000	459	14	8.77E-35	XP_002640654.1	72	149.828	153	111	Hypothetical protein CBG19712
Locus_13654_Transcript_1/1_Conf_1.000	339	0							
Locus_13655_Transcript_1/1_Conf_1.000	366	20	6.28E-33	NP_001022691.1	87	143.665	94	82	AVEugle (Drosophila eye differentation) homolog family member (ave-1)
Locus_13656_Transcript_1/1_Conf_1.000	258	4	5.50E-08	EFO22604.1	67	60.8474	76	51	RPN-3 protein
Locus_13657_Transcript_1/1_Conf_1.000	171	5	9.20E-16	NP_495035.1	83	86.6557	55	46	DeHydrogenases, Short chain family member (dhs-5)
Locus_13658_Transcript_1/1_Conf_1.000	952	20	5.77E-115	XP_002645892.1	82	418.313	317	260	Hypothetical protein CBG07642
Locus_13659_Transcript_1/1_Conf_1.000	721	2	1.78E-10	EFO16155.1	50	70.4774	145	73	hypothetical protein LOAG_12354
Locus_1366_Transcript_1/1_Conf_1.000	362	5	3.72E-25	CAR63528.1	96	117.857	64	62	hypothetical protein

Locus_13660_Transcript_1/1_Conf_1.000	420	20	1.64E-36	XP_002636220.1	70	155.606	128	90	Hypothetical protein CBG12141
Locus_13661_Transcript_1/1_Conf_1.000	131	0							
Locus_13662_Transcript_1/1_Conf_1.000	314	0							
Locus_13663_Transcript_1/1_Conf_1.000	194	0							
Locus_13664_Transcript_1/1_Conf_1.000	957	2	1.10E-04	XP_001270159.1	40	51.9878	275	112	GAS2 domain protein
Locus_13665_Transcript_1/2_Conf_1.000	1756	20	1.06E-114	XP_001898777.1	73	418.698	343	251	daf-18 protein

Locus_13665_Transcript_2/2_Conf_1.000	1666	20	9.93E-115	XP_001898777.1	73	418.698	343	251	daf-18 protein
Locus_13666_Transcript_1/1_Conf_1.000	138	0							
Locus_13667_Transcript_1/1_Conf_1.000	152	0							
Locus_13668_Transcript_1/1_Conf_1.000	760	20	5.15E-43	NP_001123112.1	78	178.718	119	94	hypothetical protein C17H11.6
Locus_13669_Transcript_1/1_Conf_1.000	381	20	8.63E-22	XP_001899513.1	66	106.686	116	77	AIDA-1b
Locus_1367_Transcript_1/3_Conf_0.714	1556	0							
Locus_1367_Transcript_2/3_Conf_0.571	1020	0							
Locus_1367_Transcript_3/3_Conf_0.714	1553	0							
Locus_13670_Transcript_1/1_Conf_1.000	493	20	4.09E-64	EFO26413.1	91	247.284	135	123	F-box only protein 11
Locus_13671_Transcript_1/1_Conf_1.000	130	0							
Locus_13672_Transcript_1/1_Conf_1.000	231	0							
Locus_13673_Transcript_1/1_Conf_1.000	138	0							
Locus_13674_Transcript_1/1_Conf_1.000	379	20	1.24E-36	NP_509879.2	81	155.992	125	102	hypothetical protein C03A3.2
Locus_13675_Transcript_1/1_Conf_1.000	268	0							
Locus_13676_Transcript_1/1_Conf_1.000	328	0							
Locus_13677_Transcript_1/1_Conf_1.000	237	5	4.58E-23	XP_002631799.1	81	110.923	79	64	Hypothetical protein CBG21018
Locus_13678_Transcript_1/1_Conf_1.000	452	7	2.35E-19	CAB60494.2	63	98.5969	136	87	C. elegans protein Y39C12A.1, partially confirmed by transcript evidence

Locus_13679_Transcript_1/1_Conf_1.000	846	20	1.45E-63	NP_503370.1	65	247.284	238	155	hypothetical protein K10C9.3
Locus_1368_Transcript_1/1_Conf_1.000	838	20	2.77E-67	XP_002630597.1	73	259.61	236	174	Hypothetical protein CBG13057
Locus_13680_Transcript_1/1_Conf_1.000	145	20	1.08E-11	XP_002630906.1	75	73.1738	48	36	Hypothetical protein CBG02630
Locus_13681_Transcript_1/1_Conf_1.000	609	0							
Locus_13682_Transcript_1/1_Conf_1.000	312	0							
Locus_13683_Transcript_1/1_Conf_1.000	553	20	4.53E-21	EFO23361.1	59	104.76	140	83	cyclin domain-containing protein
Locus_13684_Transcript_1/1_Conf_1.000	203	0							
Locus_13685_Transcript_1/1_Conf_1.000	410	20	1.46E-45	XP_001896252.1	82	185.652	134	110	MED7 protein
Locus_13686_Transcript_1/1_Conf_1.000	280	20	3.46E-31	XP_001897202.1	86	137.887	93	80	CG8090-PA
Locus_13687_Transcript_1/1_Conf_1.000	274	2	1.37E-11	NP_495410.4	62	72.7886	82	51	hypothetical protein C44B7.11
Locus_13688_Transcript_1/1_Conf_1.000	308	0							
Locus_13689_Transcript_1/1_Conf_1.000	593	20	1.71E-67	XP_002641317.1	80	259.225	200	160	C. briggsae CBR-PAD-2 protein
Locus_1369_Transcript_1/1_Conf_1.000	616	20	3.87E-60	NP_496176.1	74	234.958	203	151	beta-LACTamase domain containing family member (lact-2)
Locus_13690_Transcript_1/1_Conf_1.000	1069	20	8.71E-33	XP_002647217.1	68	145.591	208	142	Hypothetical protein CBG22401
Locus_13691_Transcript_1/1_Conf_1.000	279	20	2.04E-15	EFO22882.1	76	85.5001	60	46	TK/FER protein kinase
Locus_13692_Transcript_1/1_Conf_1.000	707	20	4.59E-32	XP_002643629.1	88	142.124	124	110	C. briggsae CBR-LET-2 protein

Locus_13693_Transcript_1/1_Conf_1.000	551	0							
Locus_13694_Transcript_1/1_Conf_1.000	461	20	2.08E-44	NP_510159.1	83	181.8	118	98	hypothetical protein F11C1.1
Locus_13695_Transcript_1/1_Conf_1.000	633	20	3.04E-71	XP_001902705.1	86	271.937	181	157	Ras-related protein Rab-11B
Locus_13696_Transcript_1/1_Conf_1.000	525	20	1.05E-50	NP_491216.2	76	202.986	171	130	Resistance to Inhibitors of Cholinesterase family member (ric-19)
Locus_13697_Transcript_1/1_Conf_1.000	734	20	5.14E-53	NP_493372.1	70	211.846	220	155	NuDiX family member (ndx-8)
Locus_13698_Transcript_1/2_Conf_1.000	296	0							
Locus_13698_Transcript_2/2_Conf_1.000	308	0							
Locus_13699_Transcript_1/2_Conf_1.000	783	20	9.29E-75	AAN11401.1	69	284.263	259	181	metalloprotease 1 precursor
Locus_13699_Transcript_2/2_Conf_1.000	783	20	4.17E-75	AAN11401.1	70	285.419	259	182	metalloprotease 1 precursor
Locus_137_Transcript_10/15_Conf_0.375	380	20	1.56E-55	ABM92348.1	99	218.779	106	105	beta tubulin isotype 1
Locus_137_Transcript_11/15_Conf_0.375	380	20	1.56E-55	ABM92348.1	99	218.779	106	105	beta tubulin isotype 1
Locus_137_Transcript_12/15_Conf_0.375	380	20	1.56E-55	ABM92348.1	99	218.779	106	105	beta tubulin isotype 1

Locus_137_Transcript_13/15_Conf_0.375	380	20	1.56E-55	ABM92348.1	99	218.779	106	105	beta tubulin isotype 1
Locus_137_Transcript_14/15_Conf_0.375	380	20	1.56E-55	ABM92348.1	99	218.779	106	105	beta tubulin isotype 1
Locus_137_Transcript_15/15_Conf_0.375	380	20	1.56E-55	ABM92348.1	99	218.779	106	105	beta tubulin isotype 1
Locus_137_Transcript_2/15_Conf_1.000	1082	20	1.66E-180	AAP20434.1	99	636.336	333	332	beta-tubulin isotype 1
Locus_137_Transcript_3/15_Conf_1.000	1082	20	0	AAP20434.1	99	638.262	333	332	beta-tubulin isotype 1
Locus_137_Transcript_4/15_Conf_1.000	167	20	4.89E-25	ACS50329.1	100	117.472	55	55	beta-tubulin
Locus_137_Transcript_5/15_Conf_1.000	221	20	9.41E-24	ABM92348.1	98	113.235	53	52	beta tubulin isotype 1
Locus_137_Transcript_6/15_Conf_0.375	380	20	1.56E-55	ABM92348.1	99	218.779	106	105	beta tubulin isotype 1
Locus_137_Transcript_7/15_Conf_0.375	380	20	1.56E-55	ABM92348.1	99	218.779	106	105	beta tubulin isotype 1

Locus_137_Transcript_8/15_Conf_0.375	380	20	1.56E-55	ABM92348.1	99	218.779	106	105	beta tubulin isotype 1
Locus_137_Transcript_9/15_Conf_0.375	380	20	1.56E-55	ABM92348.1	99	218.779	106	105	beta tubulin isotype 1
Locus_1370_Transcript_1/2_Conf_1.000	1722	20	3.34E-89	NP_505054.1	71	333.954	292	210	hypothetical protein Y97E10AL.2
Locus_1370_Transcript_2/2_Conf_1.000	1722	20	3.34E-89	NP_505054.1	71	333.954	292	210	hypothetical protein Y97E10AL.2
Locus_13700_Transcript_1/1_Conf_1.000	141	0							
Locus_13701_Transcript_1/1_Conf_1.000	173	0							
Locus_13702_Transcript_1/1_Conf_1.000	512	0							
Locus_13703_Transcript_1/1_Conf_1.000	155	2	2.39E-11	NP_501239.3	72	72.0182	51	37	hypothetical protein F45E4.5
Locus_13704_Transcript_1/1_Conf_1.000	367	19	1.97E-10	XP_002631639.1	55	68.9366	103	57	Hypothetical protein CBG20828
Locus_13705_Transcript_1/1_Conf_1.000	405	20	1.42E-40	NP_496968.1	83	169.088	135	113	hypothetical protein Y48B6A.12
Locus_13706_Transcript_1/1_Conf_1.000	237	0							
Locus_13707_Transcript_1/1_Conf_1.000	357	0							
Locus_13708_Transcript_1/1_Conf_1.000	137	0							
Locus_13709_Transcript_1/1_Conf_1.000	465	20	1.92E-61	NP_491989.1	91	238.424	136	124	hypothetical protein C30F12.7

Locus_1371_Transcript_1/1_Conf_1.000	488	20	6.86E-35	XP_002636128.1	70	150.214	134	94	Hypothetical protein CBG01378
Locus_13710_Transcript_1/1_Conf_1.000	128	20	1.58E-07	AAD01617.2	92	59.3066	42	39	cyclophilin-16
Locus_13711_Transcript_1/1_Conf_1.000	407	0							
Locus_13712_Transcript_1/1_Conf_1.000	341	20	3.13E-24	EFO24293.1	80	114.775	85	68	hypothetical protein LOAG_04190
Locus_13713_Transcript_1/1_Conf_1.000	177	0							
Locus_13714_Transcript_1/1_Conf_1.000	145	0							
Locus_13715_Transcript_1/1_Conf_1.000	309	14	1.72E-14	CAD44516.1	59	82.4185	102	61	VAB-10B protein
Locus_13716_Transcript_1/1_Conf_1.000	954	20	4.09E-60	NP_500156.2	78	236.113	184	145	XPC (Xeroderma Pigmentosum group C) DNA repair gene homolog family member (xpc-1)
Locus_13717_Transcript_1/1_Conf_1.000	461	20	1.35E-51	XP_002631622.1	76	205.682	151	116	Hypothetical protein CBG20808
Locus_13718_Transcript_1/1_Conf_1.000	498	0							
Locus_13719_Transcript_1/1_Conf_1.000	180	0							
Locus_1372_Transcript_1/1_Conf_1.000	1716	20	1.61E-91	EFO25336.1	68	341.658	317	218	EBF3-S
Locus_13720_Transcript_1/1_Conf_1.000	864	20	6.66E-11	EFN66847.1	49	72.4034	131	65	hypothetical protein EAG_08499
Locus_13721_Transcript_1/1_Conf_1.000	230	0							
Locus_13722_Transcript_1/1_Conf_1.000	464	8	1.30E-25	NP_507480.1	69	119.398	129	90	TWiK family of potassium channels family member (twk-33)
Locus_13723_Transcript_1/1_Conf_1.000	391	0							

Locus_13724_Transcript_1/1_Conf_1.000	382	3	1.34E-06	XP_002643776.1	67	56.225	43	29	C. briggsae CBR-FLP-2 protein
Locus_13725_Transcript_1/1_Conf_1.000	152	20	4.67E-15	NP_505261.2	84	84.3445	50	42	hypothetical protein B0507.2
Locus_13726_Transcript_1/1_Conf_1.000	254	0							
Locus_13727_Transcript_1/1_Conf_1.000	657	1	1.21E-12	XP_002647382.1	45	77.411	200	91	Hypothetical protein CBG06447
Locus_13728_Transcript_1/1_Conf_1.000	244	0							
Locus_13729_Transcript_1/1_Conf_1.000	1080	20	4.78E-95	AAA97973.2	64	352.443	363	233	Hypothetical protein F21C10.7
Locus_1373_Transcript_1/1_Conf_1.000	993	20	6.49E-88	NP_001122884.1	69	328.561	291	203	Temporarily Assigned Gene name family member (tag-333)
Locus_13730_Transcript_1/1_Conf_1.000	460	16	3.47E-15	NP_495156.1	66	84.7297	112	74	TBC (Tre-2/Bub2/Cdc16) domain family member (tbc-2)
Locus_13731_Transcript_1/1_Conf_1.000	397	2	1.40E-11	XP_002640811.1	52	72.7886	116	61	Hypothetical protein CBG15695
Locus_13732_Transcript_1/1_Conf_1.000	180	0							
Locus_13733_Transcript_1/1_Conf_1.000	256	0							
Locus_13734_Transcript_1/1_Conf_1.000	220	6	1.46E-08	EFO21023.1	70	62.7734	51	36	hypothetical protein LOAG_07466
Locus_13735_Transcript_1/1_Conf_1.000	770	0							
Locus_13736_Transcript_1/1_Conf_1.000	187	5	2.16E-28	NP_502312.2	98	128.642	62	61	Neurexin Like receptor family member (nlr-1)
Locus_13737_Transcript_1/1_Conf_1.000	158	20	1.07E-11	CAQ48388.2	80	73.1738	51	41	C. elegans protein C26H9A.1b, confirmed by transcript evidence
Locus_13738_Transcript_1/1_Conf_1.000	948	19	1.20E-35	NP_001129935.1	55	154.836	229	128	SMAll family member (sma-9)
Locus_13739_Transcript_1/1_Conf_1.000	376	20	9.52E-53	XP_001086913.2	100	209.534	103	103	PREDICTED: translocon-associated protein subunit delta isoform 2
Locus_1374_Transcript_1/2_Conf_1.000	513	1	3.58E-05	CAR63546.1	52	51.6026	93	49	hypothetical protein
Locus_1374_Transcript_2/2_Conf_1.000	404	1	3.31E-05	CAR63546.1	52	51.6026	93	49	hypothetical protein
Locus_13740_Transcript_1/1_Conf_1.000	975	13	5.06E-29	XP_002634908.1	89	132.88	85	76	Hypothetical protein CBG22506
Locus_13741_Transcript_1/1_Conf_1.000	253	0							
Locus_13742_Transcript_1/1_Conf_1.000	404	0							
Locus_13743_Transcript_1/1_Conf_1.000	134	0							
Locus_13744_Transcript_1/1_Conf_1.000	454	0							
Locus_13745_Transcript_1/1_Conf_1.000	198	2	4.33E-05	NP_497805.2	86	51.2174	36	31	hypothetical protein C36E8.4

Locus_13746_Transcript_1/1_Conf_1.000	413	20	2.25E-22	NP_001153506.1	73	108.612	87	64	uridine-cytidine kinase 2
Locus_13747_Transcript_1/2_Conf_1.000	273	0							
Locus_13747_Transcript_2/2_Conf_1.000	273	0							
Locus_13748_Transcript_1/1_Conf_1.000	357	0							
Locus_13749_Transcript_1/1_Conf_1.000	547	0							
Locus_1375_Transcript_1/4_Conf_0.667	3239	2	4.99E-10	XP_001891820.1	52	72.0182	114	60	GRAM domain containing protein
Locus_1375_Transcript_2/4_Conf_0.667	3293	2	5.08E-10	XP_001891820.1	52	72.0182	114	60	GRAM domain containing protein
Locus_1375_Transcript_3/4_Conf_0.667	3293	2	5.08E-10	XP_001891820.1	52	72.0182	114	60	GRAM domain containing protein
Locus_1375_Transcript_4/4_Conf_0.667	3293	2	5.08E-10	XP_001891820.1	52	72.0182	114	60	GRAM domain containing protein
Locus_13750_Transcript_1/1_Conf_1.000	134	0							
Locus_13751_Transcript_1/1_Conf_1.000	332	4	1.17E-10	NP_498501.1	62	69.707	114	71	hypothetical protein T07E3.4
Locus_13752_Transcript_1/1_Conf_1.000	227	0							
Locus_13753_Transcript_1/3_Conf_0.667	916	20	1.38E-118	XP_002639923.1	89	430.254	257	230	C. briggsae CBR-JPH-1 protein
Locus_13753_Transcript_2/3_Conf_0.667	865	20	5.30E-109	XP_002639923.1	89	398.282	239	213	C. briggsae CBR-JPH-1 protein
Locus_13753_Transcript_3/3_Conf_0.667	865	20	5.30E-109	XP_002639923.1	89	398.282	239	213	C. briggsae CBR-JPH-1 protein
Locus_13754_Transcript_1/1_Conf_1.000	135	0							
Locus_13755_Transcript_1/1_Conf_1.000	691	20	5.60E-35	XP_002631614.1	57	151.754	238	136	C. briggsae CBR-MAC-1 protein
Locus_13756_Transcript_1/1_Conf_1.000	211	0							
Locus_13757_Transcript_1/1_Conf_1.000	1383	10	1.47E-113	ACP34146.1	70	414.461	435	306	Hypothetical protein F56B3.4a
Locus_13758_Transcript_1/1_Conf_1.000	534	9	2.54E-07	XP_002639002.1	62	58.9214	56	35	Hypothetical protein CBG22248
Locus_13759_Transcript_1/1_Conf_1.000	303	0							
Locus_1376_Transcript_1/1_Conf_1.000	526	2	3.26E-60	CAR63590.1	72	234.572	170	123	hypothetical protein
Locus_13760_Transcript_1/1_Conf_1.000	340	0							
Locus_13761_Transcript_1/1_Conf_1.000	1057	0							

Locus_13762_Transcript_1/1_Conf_1.000	429	20	5.57E-29	EFO19478.1	78	130.568	96	75	U5 snRNP-associated protein
Locus_13763_Transcript_1/1_Conf_1.000	336	20	1.66E-33	XP_002631318.1	79	145.591	106	84	Hypothetical protein CBG03140
Locus_13764_Transcript_1/1_Conf_1.000	452	20	6.84E-19	NP_491248.1	90	97.0561	55	50	hypothetical protein T03F1.1
Locus_13765_Transcript_1/1_Conf_1.000	977	20	7.97E-75	CAR63535.1	67	285.034	309	208	putative transcription factor yin yang 2
Locus_13766_Transcript_1/1_Conf_1.000	439	20	2.45E-53	XP_002631343.1	88	211.46	143	127	C. briggsae CBR-SGN-1 protein
Locus_13767_Transcript_1/1_Conf_1.000	984	20	5.42E-79	XP_002631146.1	64	298.901	343	221	Hypothetical protein CBG02930
Locus_13768_Transcript_1/1_Conf_1.000	356	6	1.25E-12	NP_741018.1	65	76.2554	85	56	Homeobox family member (ceh-38)
Locus_13769_Transcript_1/1_Conf_1.000	810	20	8.08E-61	XP_002630102.1	69	238.039	270	187	Hypothetical protein CBG13485
Locus_1377_Transcript_1/1_Conf_1.000	2561	4	1.15E-14	XP_002638877.1	38	87.0409	708	272	Hypothetical protein CBG22096
Locus_13770_Transcript_1/1_Conf_1.000	256	0							

Locus_13771_Transcript_1/1_Conf_1.000	942	20	7.05E-97	NP_001129916.1	77	358.221	294	227	TWiK family of potassium channels family member (twk-46)
Locus_13772_Transcript_1/1_Conf_1.000	235	0							
Locus_13773_Transcript_1/1_Conf_1.000	143	20	2.56E-18	XP_002816314.1	100	95.1301	47	47	PREDICTED: PRELI domain-containing protein 1, mitochondrial-like isoform 2
Locus_13774_Transcript_1/1_Conf_1.000	930	20	3.52E-109	NP_494780.1	84	399.053	301	254	Temporarily Assigned Gene name family member (tag-231)
Locus_13775_Transcript_1/1_Conf_1.000	232	20	1.06E-27	NP_497182.2	89	126.331	76	68	hypothetical protein Y50D7A.2
Locus_13776_Transcript_1/1_Conf_1.000	466	0							
Locus_13777_Transcript_1/1_Conf_1.000	268	4	1.17E-10	NP_497704.1	57	69.707	88	51	hypothetical protein F59A2.5
Locus_13778_Transcript_1/1_Conf_1.000	543	20	4.59E-15	XP_421797.2	63	84.7297	110	70	PREDICTED: hypothetical protein
Locus_13779_Transcript_1/1_Conf_1.000	130	3	1.99E-10	NP_491646.3	80	68.9366	42	34	hypothetical protein F46F11.7
Locus_1378_Transcript_1/1_Conf_1.000	170	0							
Locus_13780_Transcript_1/1_Conf_1.000	495	4	1.84E-32	NP_497919.1	73	142.124	110	81	hypothetical protein M88.2
Locus_13781_Transcript_1/1_Conf_1.000	334	0							
Locus_13782_Transcript_1/1_Conf_1.000	157	0							
Locus_13783_Transcript_1/1_Conf_1.000	436	20	4.38E-26	XP_002821384.1	100	120.939	62	62	PREDICTED: 60S acidic ribosomal protein P2-like
Locus_13784_Transcript_1/1_Conf_1.000	550	20	5.08E-25	NP_491930.1	76	117.857	90	69	DiHydroOrotate Dehydrogenas family member (dhod-1)
Locus_13785_Transcript_1/1_Conf_1.000	444	20	7.37E-21	XP_002639995.1	62	103.605	147	92	C. briggsae CBR-ELPC-1 protein
Locus_13786_Transcript_1/1_Conf_1.000	406	3	2.79E-04	A8WRV1.2	56	48.521	81	46	Serine/threonine-protein kinase kin-29
Locus_13787_Transcript_1/1_Conf_1.000	478	0							

Locus_13788_Transcript_1/1_Conf_1.000	692	20	1.49E-120	AAL06642.1	97	436.032	230	225	serine-threonine protein kinase
Locus_13789_Transcript_1/1_Conf_1.000	1181	0							
Locus_1379_Transcript_1/1_Conf_1.000	700	0							
Locus_13790_Transcript_1/1_Conf_1.000	572	20	1.12E-49	CBA11992.1	68	199.904	187	128	endonuclease-reverse transcriptase HmRTE-e01
Locus_13791_Transcript_1/1_Conf_1.000	437	4	1.04E-27	NP_001023419.1	78	126.331	104	82	hypothetical protein W03F8.10
Locus_13792_Transcript_1/1_Conf_1.000	690	5	1.80E-33	XP_002641216.1	64	146.747	167	107	Hypothetical protein CBG09080
Locus_13793_Transcript_1/1_Conf_1.000	214	0							
Locus_13794_Transcript_1/1_Conf_1.000	266	0							
Locus_13795_Transcript_1/1_Conf_1.000	1514	20	9.32E-133	Q24702.1	75	478.404	453	342	DVA-1 polyprotein
Locus_13796_Transcript_1/1_Conf_1.000	164	0							
Locus_13797_Transcript_1/1_Conf_1.000	355	20	3.08E-11	NP_001122952.1	67	71.633	70	47	hypothetical protein F53H10.2
Locus_13798_Transcript_1/1_Conf_1.000	232	0							
Locus_13799_Transcript_1/1_Conf_1.000	525	20	4.24E-68	NP_509350.2	96	260.766	125	120	hypothetical protein C34D10.2

Locus_138_Transcript_1/1_Conf_1.000	2455	20	3.09E-110	EFO16992.1	80	404.445	298	241	CCR4-NOT transcription complex component
Locus_1380_Transcript_1/2_Conf_1.000	1408	20	5.30E-119	NP_492252.1	71	432.565	410	292	hypothetical protein T01G9.2
Locus_1380_Transcript_2/2_Conf_1.000	1408	20	2.63E-118	NP_492252.1	70	430.254	410	291	hypothetical protein T01G9.2
Locus_13800_Transcript_1/1_Conf_1.000	365	20	1.07E-56	XP_001135032.1	99	222.631	121	120	PREDICTED: similar to Ribosomal protein L14
Locus_13801_Transcript_1/1_Conf_1.000	424	0							
Locus_13802_Transcript_1/1_Conf_1.000	148	0							
Locus_13803_Transcript_1/1_Conf_1.000	372	4	3.54E-23	NP_493560.1	77	111.309	87	67	hypothetical protein K05C4.11
Locus_13804_Transcript_1/1_Conf_1.000	177	0							
Locus_13805_Transcript_1/1_Conf_1.000	179	0							
Locus_13806_Transcript_1/2_Conf_1.000	360	1	2.77E-04	XP_002634943.1	44	48.521	109	48	Hypothetical protein CBG22545
Locus_13806_Transcript_2/2_Conf_1.000	1075	20	5.55E-11	XP_002634943.1	42	73.1738	198	85	Hypothetical protein CBG22545
Locus_13807_Transcript_1/1_Conf_1.000	432	0							
Locus_13808_Transcript_1/1_Conf_1.000	533	4	3.53E-41	XP_002636840.1	70	171.4	178	126	Hypothetical protein CBG09291
Locus_13809_Transcript_1/1_Conf_1.000	134	0							
Locus_1381_Transcript_1/1_Conf_1.000	541	0							
Locus_13810_Transcript_1/1_Conf_1.000	171	2	4.73E-04	CAX65058.1	66	47.7506	48	32	C. elegans protein F55D12.2b, confirmed by transcript evidence
Locus_13811_Transcript_1/1_Conf_1.000	1124	20	2.78E-101	NP_001021584.1	74	373.244	285	212	EXOnuclease family member (exo-3)
Locus_13812_Transcript_1/1_Conf_1.000	199	1	2.15E-04	XP_002643566.1	73	48.9062	46	34	Hypothetical protein CBG16268
Locus_13813_Transcript_1/1_Conf_1.000	165	0							
Locus_13814_Transcript_1/1_Conf_1.000	982	2	1.04E-13	NP_504241.1	75	82.0333	68	51	hypothetical protein Y61A9LA.3
Locus_13815_Transcript_1/1_Conf_1.000	665	20	4.07E-109	NP_510020.2	91	397.897	221	203	hypothetical protein W03G11.3
Locus_13816_Transcript_1/1_Conf_1.000	1056	20	4.60E-103	NP_490719.1	71	379.022	343	244	hypothetical protein Y48G1A.3
Locus_13817_Transcript_1/1_Conf_1.000	401	0							
Locus_13818_Transcript_1/1_Conf_1.000	192	0							
Locus_13819_Transcript_1/1_Conf_1.000	726	2	6.69E-05	XP_001901708.1	47	51.9878	134	63	F-box domain containing protein

Locus_1382_Transcript_1/1_Conf_1.000	672	20	1.80E-51	XP_002644536.1	88	206.453	125	110	C. briggsae CBR-DPY-23 protein
Locus_13820_Transcript_1/2_Conf_1.000	434	20	8.58E-22	NP_497868.1	79	106.686	74	59	Temporarily Assigned Gene name family member (tag-131)
Locus_13820_Transcript_2/2_Conf_1.000	434	20	8.58E-22	NP_497868.1	79	106.686	74	59	Temporarily Assigned Gene name family member (tag-131)
Locus_13821_Transcript_1/1_Conf_1.000	332	0							
Locus_13822_Transcript_1/1_Conf_1.000	682	20	4.67E-87		90	324.709	199	180	hypothetical protein C25H3.9 - Caenorhabditis elegans
Locus_13823_Transcript_1/1_Conf_1.000	142	4	6.99E-08	NP_500284.2	84	60.4622	39	33	Enhancer of EfL-1 mutant phenotype family member (eel-1)
Locus_13824_Transcript_1/1_Conf_1.000	660	0							
Locus_13825_Transcript_1/1_Conf_1.000	651	20	1.20E-65	ADE60684.1	78	253.447	182	142	Diacylglycerol kinase protein 4, isoform b, partially confirmed by transcript evidence
Locus_13826_Transcript_1/1_Conf_1.000	757	20	7.03E-93	NP_496968.1	90	344.354	202	183	hypothetical protein Y48B6A.12
Locus_13827_Transcript_1/1_Conf_1.000	327	0							
Locus_13828_Transcript_1/1_Conf_1.000	1116	20	1.07E-129	NP_497714.2	83	467.618	304	254	Protein PHosphatase family member (pph-6)
Locus_13829_Transcript_1/1_Conf_1.000	561	20	8.25E-18	XP_392369.1	97	93.9745	43	42	PREDICTED: similar to Protein yippee-like 1
Locus_1383_Transcript_1/1_Conf_1.000	1683	0							
Locus_13830_Transcript_1/1_Conf_1.000	213	0							
Locus_13831_Transcript_1/1_Conf_1.000	418	20	3.56E-23	XP_001893552.1	75	111.309	86	65	haloacid dehalogenase-like hydrolase domain containing 2, putative
Locus_13832_Transcript_1/1_Conf_1.000	353	20	2.87E-41	3MNG	100	171.4	85	85	Wild Type Human Prxv With Dtt Bound As A Competitive Inhibitor

Locus_13833_Transcript_1/1_Conf_1.000	229	20	2.45E-32	NP_741109.1	90	141.739	75	68	FERM domain (protein4.1-ezrin-radixin-moesin) family member (frm-8)
Locus_13834_Transcript_1/1_Conf_1.000	296	20	4.02E-35	XP_002632369.1	87	150.984	98	86	C. briggsae CBR-PMP-4 protein
Locus_13835_Transcript_1/1_Conf_1.000	667	0							
Locus_13836_Transcript_1/1_Conf_1.000	332	2	1.48E-05	XP_002643723.1	62	52.7582	53	33	Hypothetical protein CBG01914
Locus_13837_Transcript_1/1_Conf_1.000	880	20	2.17E-33	XP_001984068.1	84	147.132	82	69	GH15211
Locus_13838_Transcript_1/1_Conf_1.000	858	20	2.08E-73	XP_001894604.1	67	280.026	273	185	exonuclease family protein
Locus_13839_Transcript_1/1_Conf_1.000	657	0							
Locus_1384_Transcript_1/1_Conf_1.000	466	20	3.86E-62	BAG54741.1	100	240.736	146	146	unnamed protein product
Locus_13840_Transcript_1/1_Conf_1.000	150	0							
Locus_13841_Transcript_1/2_Conf_1.000	295	0							
Locus_13841_Transcript_2/2_Conf_1.000	295	0							
Locus_13842_Transcript_1/1_Conf_1.000	557	20	9.60E-27	NP_495774.1	58	123.635	176	103	hypothetical protein F14E5.4
Locus_13843_Transcript_1/1_Conf_1.000	377	20	1.75E-30	NP_509361.1	81	135.576	124	101	hypothetical protein K07E3.4
Locus_13844_Transcript_1/1_Conf_1.000	179	3	9.46E-13	NP_495112.1	77	76.6406	57	44	hypothetical protein C25H3.11

Locus_13845_Transcript_1/1_Conf_1.000	298	20	1.09E-24	XP_002632973.1	78	116.316	84	66	Hypothetical protein CBG21733
Locus_13846_Transcript_1/1_Conf_1.000	461	0							
Locus_13847_Transcript_1/1_Conf_1.000	397	0							
Locus_13848_Transcript_1/1_Conf_1.000	142	0							
Locus_13849_Transcript_1/1_Conf_1.000	131	5	3.29E-05	AAK71410.2	63	51.6026	41	26	AC024881_1Hypothetical protein Y97E10B.1
Locus_1385_Transcript_1/1_Conf_1.000	537	3	2.68E-04	XP_002939048.1	47	48.9062	130	62	PREDICTED: macrophage mannose receptor 1-like
Locus_13850_Transcript_1/2_Conf_1.000	385	20	1.37E-27	XP_002128408.1	93	125.946	91	85	PREDICTED: similar to U6 snRNA-associated Sm-like protein LSm3
Locus_13850_Transcript_2/2_Conf_1.000	385	20	1.37E-27	XP_002128408.1	93	125.946	91	85	PREDICTED: similar to U6 snRNA-associated Sm-like protein LSm3
Locus_13851_Transcript_1/2_Conf_1.000	585	20	3.31E-55	XP_002632393.1	73	218.394	192	142	Hypothetical protein CBG00415
Locus_13851_Transcript_2/2_Conf_1.000	585	20	3.31E-55	XP_002632393.1	73	218.394	192	142	Hypothetical protein CBG00415
Locus_13852_Transcript_1/1_Conf_1.000	430	20	1.72E-46	NP_001020988.1	81	188.734	137	111	UNCoordinated family member (unc-89)
Locus_13853_Transcript_1/2_Conf_1.000	598	20	2.85E-25	XP_002740677.1	70	119.013	104	73	PREDICTED: cyclin-dependent kinase 2-like
Locus_13853_Transcript_2/2_Conf_1.000	276	0							
Locus_13854_Transcript_1/1_Conf_1.000	259	20	3.42E-34	NP_492433.1	86	147.902	86	74	HomoGentisate Oxidase family member (hgo-1)
Locus_13855_Transcript_1/1_Conf_1.000	1287	20	3.91E-57	NP_001020983.1	57	226.868	405	233	TOLl (Drosophila) family member (tol-1)
Locus_13856_Transcript_1/1_Conf_1.000	453	20	7.75E-31	XP_002648358.1	84	136.732	92	78	Hypothetical protein CBG24564
Locus_13857_Transcript_1/1_Conf_1.000	212	0							

Locus_13858_Transcript_1/1_Conf_1.000	243	20	3.05E-19	XP_002632237.1	81	98.2117	64	52	Hypothetical protein CBG07111
Locus_13859_Transcript_1/1_Conf_1.000	609	20	9.41E-11	XP_001899546.1	44	70.8626	207	93	hypothetical protein
Locus_1386_Transcript_1/1_Conf_1.000	1651	20	2.99E-180	XP_002639432.1	74	636.336	483	361	C. briggsae CBR-TYR-4 protein
Locus_13860_Transcript_1/1_Conf_1.000	677	20	1.95E-37	NP_504260.1	65	159.844	177	116	TAF (TBP-associated transcription factor) family member (taf-10)
Locus_13861_Transcript_1/1_Conf_1.000	217	20	6.31E-17	DAA16569.1	100	90.5077	72	72	heat shock protein HSP 90-beta
Locus_13862_Transcript_1/1_Conf_1.000	313	0							
Locus_13863_Transcript_1/1_Conf_1.000	762	20	1.68E-142	NP_001164609.1	100	509.22	239	239	clusterin isoform 3
Locus_13864_Transcript_1/1_Conf_1.000	552	0							
Locus_13865_Transcript_1/1_Conf_1.000	268	0							
Locus_13866_Transcript_1/1_Conf_1.000	440	20	8.78E-27	XP_002633460.1	71	123.25	142	101	Hypothetical protein CBG06228
Locus_13867_Transcript_1/1_Conf_1.000	1178	20	3.95E-37	NP_492228.1	61	160.229	210	129	MAternally affected Uncoordination family member (mau-2)
Locus_13868_Transcript_1/1_Conf_1.000	246	4	1.91E-13	NP_497420.1	77	78.9518	61	47	hypothetical protein Y67D2.6

Locus_13869_Transcript_1/1_Conf_1.000	157	20	3.11E-11	NP_491902.3	88	71.633	44	39	hypothetical protein D2092.5
Locus_1387_Transcript_1/3_Conf_0.286	322	0							
Locus_1387_Transcript_2/3_Conf_0.714	1422	20	5.15E-37	NP_502566.1	47	160.229	381	182	Muscle EXcess family member (mex-5)
Locus_1387_Transcript_3/3_Conf_0.714	1422	20	5.15E-37	NP_502566.1	47	160.229	381	182	Muscle EXcess family member (mex-5)
Locus_13870_Transcript_1/1_Conf_1.000	399	2	2.62E-18	XP_002642086.1	78	95.1301	132	104	Hypothetical protein CBG18027
Locus_13871_Transcript_1/1_Conf_1.000	227	0							
Locus_13872_Transcript_1/1_Conf_1.000	233	20	1.87E-32	NP_502000.1	90	142.124	76	69	hypothetical protein C06G8.1
Locus_13873_Transcript_1/1_Conf_1.000	672	20	1.73E-62	NP_492446.3	76	243.047	221	168	hypothetical protein ZK858.1
Locus_13874_Transcript_1/1_Conf_1.000	379	20	2.51E-29	XP_002644672.1	69	131.724	126	87	C. briggsae CBR-VPS-41 protein
Locus_13875_Transcript_1/1_Conf_1.000	204	0							
Locus_13876_Transcript_1/1_Conf_1.000	911	20	1.89E-35	NP_509877.2	54	154.066	266	144	hypothetical protein C34F6.10
Locus_13877_Transcript_1/1_Conf_1.000	671	0							
Locus_13878_Transcript_1/1_Conf_1.000	302	20	5.59E-21	XP_002632832.1	53	103.99	143	76	Hypothetical protein CBG15024

Locus_13879_Transcript_1/1_Conf_1.000	425	20	6.64E-30	NP_001040880.1	79	133.65	89	71	hypothetical protein Y39A3CL.4
Locus_1388_Transcript_1/1_Conf_1.000	941	0							
Locus_13880_Transcript_1/1_Conf_1.000	410	0							
Locus_13881_Transcript_1/1_Conf_1.000	358	20	1.51E-34	Q9BI88.2	74	149.058	109	81	UPF0587 protein F46B6.12
Locus_13882_Transcript_1/1_Conf_1.000	520	20	8.83E-39	NP_001021589.1	64	163.31	171	111	hypothetical protein R11A5.4
Locus_13883_Transcript_1/1_Conf_1.000	185	0							
Locus_13884_Transcript_1/1_Conf_1.000	655	0							
Locus_13885_Transcript_1/1_Conf_1.000	213	0							
Locus_13886_Transcript_1/1_Conf_1.000	345	2	7.44E-05	XP_002647702.1	55	50.447	93	52	Hypothetical protein CBG17891
Locus_13887_Transcript_1/1_Conf_1.000	176	0							
Locus_13888_Transcript_1/1_Conf_1.000	497	1	2.77E-04	ABI21593.1	53	39.2762	45	24	hypothetical protein
Locus_13889_Transcript_1/1_Conf_1.000	309	20	2.74E-28	EFO23898.1	74	128.257	99	74	FolC protein
Locus_1389_Transcript_1/1_Conf_1.000	567	20	2.84E-13	XP_002637364.1	50	78.9518	183	93	Hypothetical protein CBG19064
Locus_13890_Transcript_1/1_Conf_1.000	692	0							
Locus_13891_Transcript_1/1_Conf_1.000	162	0							
Locus_13892_Transcript_1/1_Conf_1.000	203	0							
Locus_13893_Transcript_1/1_Conf_1.000	295	20	5.80E-34	XP_002636626.1	90	147.132	98	89	C. briggsae CBR-AMAN-2 protein
Locus_13894_Transcript_1/1_Conf_1.000	392	20	2.02E-31	XP_001898856.1	77	138.658	129	100	cation channel family protein
Locus_13895_Transcript_1/1_Conf_1.000	814	0							

Locus_13896_Transcript_1/1_Conf_1.000	324	20	7.55E-42	XP_002629880.1	84	173.326	104	88	Hypothetical protein CBG21917
Locus_13897_Transcript_1/1_Conf_1.000	347	0							
Locus_13898_Transcript_1/1_Conf_1.000	498	4	1.19E-39	NP_498063.1	71	166.007	151	108	hypothetical protein R144.11
Locus_13899_Transcript_1/1_Conf_1.000	395	20	1.22E-31	XP_002642778.1	70	139.428	131	93	C. briggsae CBR-PRMT-5 protein
Locus_139_Transcript_1/1_Conf_1.000	1544	20	8.25E-44	XP_002647887.1	61	182.956	239	148	Hypothetical protein CBG23753
Locus_1390_Transcript_1/2_Conf_1.000	711	5	1.67E-21	XP_002641213.1	77	107.071	80	62	C. briggsae CBR-MDT-15 protein
Locus_1390_Transcript_2/2_Conf_1.000	893	9	4.64E-39	XP_001902687.1	67	166.007	154	104	hypothetical protein

Locus_13900_Transcript_1/1_Conf_1.000	797	9	1.41E-17	NP_491541.1	64	94.3597	102	66	hypothetical protein F56A3.2
Locus_13901_Transcript_1/1_Conf_1.000	315	20	6.52E-09	XP_002113412.1	57	63.929	97	56	hypothetical protein TRIADDRAFT_57554
Locus_13902_Transcript_1/2_Conf_1.000	899	20	1.09E-112	XP_002631657.1	88	410.609	261	230	Hypothetical protein CBG20848
Locus_13902_Transcript_2/2_Conf_1.000	874	20	5.41E-109	XP_002631657.1	88	398.282	252	222	Hypothetical protein CBG20848
Locus_13903_Transcript_1/1_Conf_1.000	186	0							
Locus_13904_Transcript_1/2_Conf_1.000	251	0							
Locus_13904_Transcript_2/2_Conf_1.000	257	0							
Locus_13905_Transcript_1/2_Conf_1.000	627	20	4.31E-38	XP_002640628.1	60	161.77	200	120	C. briggsae CBR-EAT-18 protein
Locus_13905_Transcript_2/2_Conf_1.000	483	20	3.30E-45	XP_002640628.1	78	184.496	152	120	C. briggsae CBR-EAT-18 protein
Locus_13906_Transcript_1/1_Conf_1.000	648	20	2.51E-23	NP_001129749.1	95	112.849	60	57	abnormal cell LINeage family member (lin-10)
Locus_13907_Transcript_1/1_Conf_1.000	484	20	7.31E-61	XP_002642567.1	89	236.498	161	144	C. briggsae CBR-UNC-79 protein
Locus_13908_Transcript_1/1_Conf_1.000	132	0							
Locus_13909_Transcript_1/1_Conf_1.000	200	0							
Locus_1391_Transcript_1/1_Conf_1.000	311	0							
Locus_13910_Transcript_1/1_Conf_1.000	264	0							
Locus_13911_Transcript_1/1_Conf_1.000	293	20	6.04E-23	AAN05752.1	75	110.538	95	72	heat shock protein 20
Locus_13912_Transcript_1/1_Conf_1.000	318	20	2.80E-28	XP_002645500.1	70	128.257	106	75	Hypothetical protein CBG22750
Locus_13913_Transcript_1/1_Conf_1.000	372	20	2.73E-07	NP_491642.2	53	58.5362	129	69	hypothetical protein F46F11.9
Locus_13914_Transcript_1/1_Conf_1.000	368	0							
Locus_13915_Transcript_1/1_Conf_1.000	589	20	6.00E-57	XP_002644776.1	74	224.172	199	149	Hypothetical protein CBG14789
Locus_13916_Transcript_1/1_Conf_1.000	458	0							
Locus_13917_Transcript_1/1_Conf_1.000	131	0							
Locus_13918_Transcript_1/1_Conf_1.000	580	20	2.62E-65	NP_508919.2	77	251.906	192	148	hypothetical protein C03F11.3
Locus_13919_Transcript_1/1_Conf_1.000	207	0							
Locus_1392_Transcript_1/1_Conf_1.000	946	20	4.19E-65	XP_001623486.1	65	252.677	310	204	predicted protein

Locus_13920_Transcript_1/1_Conf_1.000	755	5	3.21E-05	XP_001895157.1	63	53.1434	55	35	TAZ zinc finger family protein
Locus_13921_Transcript_1/1_Conf_1.000	1344	20	7.87E-165	XP_002636651.1	78	584.719	451	353	C. briggsae CBR-DRS-2 protein
Locus_13922_Transcript_1/1_Conf_1.000	264	0							
Locus_13923_Transcript_1/1_Conf_1.000	325	0							
Locus_13924_Transcript_1/1_Conf_1.000	616	20	1.29E-39	XP_002642330.1	72	166.777	153	111	Hypothetical protein CBG18325
Locus_13925_Transcript_1/1_Conf_1.000	191	0							
Locus_13926_Transcript_1/1_Conf_1.000	254	20	1.04E-38	A8XJL7.2	97	162.925	84	82	Serine/threonine-protein kinase sax-1
Locus_13927_Transcript_1/2_Conf_1.000	1105	20	1.87E-110	XP_002634178.1	79	403.675	311	246	Hypothetical protein CBG01746
Locus_13927_Transcript_2/2_Conf_1.000	1106	20	2.45E-110	XP_002634178.1	79	403.29	311	246	Hypothetical protein CBG01746
Locus_13928_Transcript_1/1_Conf_1.000	833	1	3.29E-04	XP_002405770.1	40	50.0618	170	68	secreted mucin MUC17, putative
Locus_13929_Transcript_1/1_Conf_1.000	213	0							
Locus_1393_Transcript_1/1_Conf_1.000	509	2	1.33E-04	NP_683559.2	42	49.6766	118	50	RNA recognition motif (RRM)-containing protein
Locus_13930_Transcript_1/1_Conf_1.000	703	20	1.54E-19	NP_001076765.1	70	100.523	100	70	Phasmid Socket Absent family member (psa-3)

Locus_13931_Transcript_1/1_Conf_1.000	712	20	2.78E-101	NP_001024342.1	92	372.089	237	219	Aboc, EXpulsion defective family member (aex-3)
Locus_13932_Transcript_1/1_Conf_1.000	458	20	3.95E-43	EFO23801.1	79	177.563	144	114	replication factor C
Locus_13933_Transcript_1/1_Conf_1.000	275	2	1.24E-12	NP_495888.2	62	76.2554	88	55	hypothetical protein T07D4.1
Locus_13934_Transcript_1/1_Conf_1.000	348	20	4.60E-39	NP_491924.1	79	164.081	116	92	hypothetical protein W02D3.4
Locus_13935_Transcript_1/1_Conf_1.000	195	0							
Locus_13936_Transcript_1/1_Conf_1.000	145	2	1.46E-08	NP_501792.2	70	62.7734	47	33	abnormal GONad development family member (gon-1)
Locus_13937_Transcript_1/1_Conf_1.000	151	0							
Locus_13938_Transcript_1/1_Conf_1.000	594	0							
Locus_13939_Transcript_1/1_Conf_1.000	205	10	3.63E-12	XP_002639106.1	73	74.7146	63	46	Hypothetical protein CBG14925
Locus_1394_Transcript_1/1_Conf_1.000	936	20	7.42E-107	NP_501650.1	76	391.349	301	230	hypothetical protein C10C5.3
Locus_13940_Transcript_1/1_Conf_1.000	455	0							
Locus_13941_Transcript_1/1_Conf_1.000	427	20	4.60E-15	NP_495055.1	57	84.3445	143	82	hypothetical protein ZK177.8
Locus_13942_Transcript_1/1_Conf_1.000	184	0							
Locus_13944_Transcript_1/1_Conf_1.000	185	4	1.84E-11	XP_002630706.1	74	72.4034	63	47	C. briggsae CBR-MOG-5 protein
Locus_13945_Transcript_1/1_Conf_1.000	260	3	6.93E-19	XP_002638537.1	90	97.0561	52	47	Hypothetical protein CBG05572
Locus_13946_Transcript_1/1_Conf_1.000	534	0							

Locus_13947_Transcript_1/1_Conf_1.000	398	20	9.86E-66	EFO27677.1	96	252.677	130	126	hypothetical protein LOAG_00808
Locus_13948_Transcript_1/1_Conf_1.000	324	0							
Locus_13949_Transcript_1/1_Conf_1.000	151	0							
Locus_1395_Transcript_1/2_Conf_1.000	820	20	1.15E-62	NP_498755.1	81	244.202	178	145	hypothetical protein K12H4.4
Locus_1395_Transcript_2/2_Conf_1.000	821	20	1.15E-62	NP_498755.1	81	244.202	178	145	hypothetical protein K12H4.4
Locus_13950_Transcript_1/2_Conf_1.000	431	20	2.96E-30	XP_002641823.1	70	134.806	144	101	Hypothetical protein CBG16490
Locus_13950_Transcript_2/2_Conf_1.000	423	20	1.13E-29	XP_002641823.1	70	132.88	141	99	Hypothetical protein CBG16490
Locus_13951_Transcript_1/1_Conf_1.000	537	0							
Locus_13952_Transcript_1/1_Conf_1.000	145	0							
Locus_13953_Transcript_1/1_Conf_1.000	170	0							
Locus_13954_Transcript_1/1_Conf_1.000	461	20	3.14E-16	XP_002612934.1	55	88.1965	102	57	hypothetical protein BRAFLDRAFT_278667
Locus_13955_Transcript_1/1_Conf_1.000	887	20	8.92E-43	XP_002665162.1	55	178.333	271	150	PREDICTED: kelch-like 10-like
Locus_13956_Transcript_1/1_Conf_1.000	440	0							
Locus_13957_Transcript_1/1_Conf_1.000	135	4	7.50E-18	EFO16626.1	100	93.5893	44	44	INX-1 protein
Locus_13958_Transcript_1/1_Conf_1.000	141	0							

Locus_13959_Transcript_1/1_Conf_1.000	216	20	2.56E-18	XP_002640829.1	75	95.1301	70	53	C. briggsae CBR-ADS-1 protein
Locus_1396_Transcript_1/1_Conf_1.000	1615	6	2.82E-50	EFO24916.1	48	204.527	512	246	hypothetical protein LOAG_03568
Locus_13960_Transcript_1/1_Conf_1.000	240	0							
Locus_13961_Transcript_1/1_Conf_1.000	399	20	4.43E-50	NP_001022450.1	86	200.675	132	114	hypothetical protein Y48E1A.1
Locus_13962_Transcript_1/1_Conf_1.000	170	0							
Locus_13963_Transcript_1/1_Conf_1.000	425	20	7.53E-58	EFO26325.1	85	226.483	140	119	hypothetical protein LOAG_02163
Locus_13964_Transcript_1/1_Conf_1.000	186	0							
Locus_13965_Transcript_1/1_Conf_1.000	131	20	6.39E-17	XP_002713121.1	100	90.5077	43	43	PREDICTED: beta-catenin

Locus_13966_Transcript_1/3_Conf_0.500	1025	20	1.53E-55	NP_510746.2	69	221.09	199	138	hypothetical protein K02H8.1
Locus_13966_Transcript_2/3_Conf_0.333	627	20	1.06E-60	NP_001129932.1	70	236.884	211	149	hypothetical protein K02H8.1
Locus_13966_Transcript_3/3_Conf_0.500	692	8	1.26E-10	NP_001129931.1	60	70.8626	83	50	hypothetical protein K02H8.1
Locus_13967_Transcript_1/1_Conf_1.000	207	0							
Locus_13968_Transcript_1/1_Conf_1.000	237	20	4.15E-16	XP_002632592.1	71	87.8113	78	56	C. briggsae CBR-EPS-8 protein
Locus_13969_Transcript_1/1_Conf_1.000	477	20	2.56E-42	CAN99691.2	65	174.866	167	110	C. elegans protein F54B3.1b, partially confirmed by transcript evidence
Locus_1397_Transcript_1/2_Conf_1.000	3125	20	4.35E-104	NP_001041165.1	56	384.415	707	401	hypothetical protein T09E8.1
Locus_1397_Transcript_2/2_Conf_1.000	1860	20	6.13E-68	XP_002636951.1	64	263.462	357	230	Hypothetical protein CBG09427
Locus_13970_Transcript_1/1_Conf_1.000	162	3	8.69E-14	NP_508964.2	90	80.1073	52	47	Regulator of G protein Signaling family member (rgs-6)
Locus_13971_Transcript_1/1_Conf_1.000	134	0							
Locus_13972_Transcript_1/1_Conf_1.000	379	1	8.70E-06	XP_001892617.1	55	53.5286	58	32	Protein kinase domain containing protein
Locus_13973_Transcript_1/1_Conf_1.000	980	0							
Locus_13974_Transcript_1/1_Conf_1.000	259	0							
Locus_13975_Transcript_1/1_Conf_1.000	256	5	1.11E-08	XP_002639252.1	94	63.1586	39	37	C. briggsae CBR-GFI-2 protein
Locus_13976_Transcript_1/1_Conf_1.000	226	0							
Locus_13977_Transcript_1/1_Conf_1.000	334	2	5.40E-08	NP_495385.1	78	60.8474	42	33	hypothetical protein F41G3.1

Locus_13978_Transcript_1/1_Conf_1.000	155	20	6.48E-25	NP_001158888.1	100	117.087	51	51	L-lactate dehydrogenase A chain isoform 5
Locus_13979_Transcript_1/1_Conf_1.000	214	20	1.50E-34	XP_002927231.1	100	149.058	71	71	PREDICTED: tubulin alpha-1B chain-like
Locus_1398_Transcript_1/2_Conf_1.000	1828	20	7.68E-132	NP_502079.1	70	475.707	431	303	IntraMembrane Protease (IMPAS) family member (imp-2)
Locus_1398_Transcript_2/2_Conf_1.000	1809	20	5.85E-128	NP_502079.1	74	389.037	313	234	IntraMembrane Protease (IMPAS) family member (imp-2)
Locus_13980_Transcript_1/1_Conf_1.000	139	0							
Locus_13981_Transcript_1/1_Conf_1.000	308	4	1.20E-15	XP_002639235.1	69	86.2705	65	45	Hypothetical protein CBG03793

Locus_13982_Transcript_1/1_Conf_1.000	388	20	2.91E-54	EFO19497.1	89	214.542	128	115	DNA polymerase epsilon catalytic subunit
Locus_13983_Transcript_1/1_Conf_1.000	248	9	1.01E-14	NP_506678.2	65	83.1889	78	51	hypothetical protein W09D12.1
Locus_13984_Transcript_1/1_Conf_1.000	337	0							
Locus_13985_Transcript_1/1_Conf_1.000	361	0							
Locus_13986_Transcript_1/1_Conf_1.000	735	20	9.50E-39	XP_002641664.1	64	164.466	216	139	Hypothetical protein CBG09992
Locus_13987_Transcript_1/1_Conf_1.000	444	20	1.38E-51	XP_002640280.1	83	205.682	121	101	Hypothetical protein CBG12806
Locus_13988_Transcript_1/1_Conf_1.000	839	20	1.17E-49	NP_494767.1	58	201.06	286	166	hypothetical protein H20J04.2

Locus_13989_Transcript_1/1_Conf_1.000	1524	20	5.44E-72		54	276.559	508	278	hypothetical protein Y106G6D.5
Locus_1399_Transcript_1/3_Conf_0.500	1802	4	1.41E-37	NP_001122735.1	57	162.54	407	236	hypothetical protein Y56A3A.7
Locus_1399_Transcript_2/3_Conf_0.625	1579	5	2.03E-45	NP_001122735.1	58	188.348	448	261	hypothetical protein Y56A3A.7
Locus_1399_Transcript_3/3_Conf_0.500	1870	5	2.52E-45	NP_001122735.1	58	188.348	448	261	hypothetical protein Y56A3A.7
Locus_13990_Transcript_1/1_Conf_1.000	220	0							
Locus_13991_Transcript_1/1_Conf_1.000	335	0							
Locus_13992_Transcript_1/1_Conf_1.000	729	20	1.47E-84	XP_002647042.1	76	316.62	247	190	Hypothetical protein CBG03560
Locus_13993_Transcript_1/1_Conf_1.000	162	0							
Locus_13994_Transcript_1/1_Conf_1.000	357	20	2.75E-44	EFO19977.1	91	181.415	117	107	hypothetical protein LOAG_08511
Locus_13995_Transcript_1/1_Conf_1.000	151	20	8.78E-22	XP_002638784.1	96	106.686	50	48	Hypothetical protein CBG05137
Locus_13996_Transcript_1/1_Conf_1.000	576	20	2.79E-19	NP_508889.1	52	98.9821	155	82	hypothetical protein Y34B4A.7
Locus_13997_Transcript_1/1_Conf_1.000	978	20	1.86E-39	EFO19488.1	60	167.548	233	142	hypothetical protein LOAG_09005
Locus_13998_Transcript_1/1_Conf_1.000	211	0							
Locus_13999_Transcript_1/1_Conf_1.000	402	4	4.78E-04	XP_001899942.1	54	47.7506	97	53	hypothetical protein Bm1_42390

Locus_14_Transcript_1/1_Conf_1.000	2309	20	0	XP_002641511.1	94	973.77	599	569	C. briggsae CBR-CHC-1 protein
Locus_140_Transcript_1/1_Conf_1.000	1282	20	0	AAS55927.1	96	765.763	399	386	cytoskeletal beta actin
Locus_1400_Transcript_1/1_Conf_1.000	893	0							
Locus_14000_Transcript_1/1_Conf_1.000	349	20	2.52E-37	XP_002636973.1	86	158.303	115	99	Hypothetical protein CBG09454
Locus_14001_Transcript_1/1_Conf_1.000	259	20	1.31E-17	XP_002641885.1	73	92.8189	86	63	Hypothetical protein CBG16572

Locus_14002_Transcript_1/1_Conf_1.000	960	20	2.10E-138	XP_001155090.1	98	381.333	197	195	PREDICTED: similar to ANXA2 protein
Locus_14003_Transcript_1/1_Conf_1.000	335	0							
Locus_14004_Transcript_1/1_Conf_1.000	191	0							
Locus_14005_Transcript_1/1_Conf_1.000	151	1	6.32E-04	XP_002642982.1	58	47.3654	50	29	Hypothetical protein CBG15266
Locus_14006_Transcript_1/1_Conf_1.000	148	0							
Locus_14007_Transcript_1/1_Conf_1.000	266	1	8.17E-04	XP_001901545.1	64	46.9802	54	35	hypothetical protein Bm1_50385
Locus_14008_Transcript_1/1_Conf_1.000	574	20	1.17E-70	XP_001895692.1	74	269.626	204	152	jmjC domain containing protein
Locus_14009_Transcript_1/1_Conf_1.000	139	20	9.14E-16	EFO23246.1	95	86.6557	45	43	degenerin unc-8
Locus_1401_Transcript_1/1_Conf_1.000	1167	20	1.73E-85	XP_002641620.1	60	320.857	392	239	C. briggsae CBR-BUB-1 protein
Locus_14010_Transcript_1/1_Conf_1.000	388	0							
Locus_14011_Transcript_1/1_Conf_1.000	448	0							
Locus_14012_Transcript_1/1_Conf_1.000	423	0							
Locus_14013_Transcript_1/1_Conf_1.000	161	0							

Locus_14014_Transcript_1/1_Conf_1.000	619	20	3.19E-86	XP_001896258.1	81	321.627	205	167	Cytoplasmic polyadenylation element binding protein 1
Locus_14015_Transcript_1/1_Conf_1.000	669	0							
Locus_14016_Transcript_1/3_Conf_0.600	335	1	2.51E-05	NP_491118.2	56	51.9878	110	62	hypothetical protein Y54E10A.11
Locus_14016_Transcript_2/3_Conf_0.600	342	1	4.38E-05	NP_491118.2	55	51.2174	110	61	hypothetical protein Y54E10A.11
Locus_14016_Transcript_3/3_Conf_0.600	335	1	4.28E-05	NP_491118.2	55	51.2174	110	61	hypothetical protein Y54E10A.11
Locus_14017_Transcript_1/1_Conf_1.000	440	10	3.79E-46	NP_001129848.1	79	187.578	144	114	hypothetical protein C27H2.2
Locus_14018_Transcript_1/1_Conf_1.000	476	20	3.16E-24	XP_317488.4	76	114.775	89	68	AGAP007978-PA
Locus_14019_Transcript_1/1_Conf_1.000	161	0							
Locus_1402_Transcript_1/1_Conf_1.000	560	20	1.72E-60	XP_002639413.1	85	235.728	151	129	C. briggsae CBR-CPS-6 protein
Locus_14020_Transcript_1/1_Conf_1.000	270	6	5.60E-13	AAK31527.3	57	77.411	113	65	Neuronal symmetry protein 1, partially confirmed by transcript evidence
Locus_14021_Transcript_1/1_Conf_1.000	149	20	1.66E-12	XP_001899592.1	85	75.8702	48	41	C2 domain containing protein
Locus_14022_Transcript_1/1_Conf_1.000	128	0							
Locus_14023_Transcript_1/1_Conf_1.000	458	20	2.94E-22	NP_498986.2	68	108.227	128	88	hypothetical protein R08D7.5
Locus_14024_Transcript_1/1_Conf_1.000	333	18	1.24E-28	NP_506118.1	81	129.413	90	73	hypothetical protein C54D10.5
Locus_14025_Transcript_1/1_Conf_1.000	395	20	1.27E-20	XP_002638798.1	74	102.834	111	83	C. briggsae CBR-PIF-1 protein
Locus_14026_Transcript_1/1_Conf_1.000	173	0							
Locus_14027_Transcript_1/1_Conf_1.000	194	20	2.30E-14	XP_002646723.1	75	82.0333	58	44	C. briggsae CBR-CLH-3 protein
Locus_14028_Transcript_1/1_Conf_1.000	146	0							
Locus_14029_Transcript_1/1_Conf_1.000	496	0							

Locus_1403_Transcript_1/1_Conf_1.000	302	2	4.30E-05	XP_002642297.1	58	51.2174	51	30	Hypothetical protein CBG18289
Locus_14030_Transcript_1/1_Conf_1.000	148	0							
Locus_14031_Transcript_1/1_Conf_1.000	283	0							
Locus_14032_Transcript_1/1_Conf_1.000	392	20	4.50E-39	EFO23299.1	73	164.081	130	96	hypothetical protein LOAG_05186
Locus_14033_Transcript_1/2_Conf_1.000	1212	20	1.14E-95	XP_002636970.1	60	354.755	446	271	Hypothetical protein CBG09451
Locus_14033_Transcript_2/2_Conf_1.000	1212	20	1.14E-95	XP_002636970.1	60	354.755	446	271	Hypothetical protein CBG09451
Locus_14034_Transcript_1/1_Conf_1.000	1029	20	8.42E-86	XP_002634139.1	73	321.627	300	221	Hypothetical protein CBG01700
Locus_14035_Transcript_1/1_Conf_1.000	270	20	7.54E-26	EFO21211.1	78	120.168	89	70	hypothetical protein LOAG_07280
Locus_14036_Transcript_1/1_Conf_1.000	496	0							
Locus_14037_Transcript_1/1_Conf_1.000	147	20	2.17E-20	3IE3	100	102.064	48	48	l Basis ForThe Binding OfThe Anti-Cancer Compound 6-(7-Nitro-2
Locus_14038_Transcript_1/1_Conf_1.000	595	20	1.85E-69	XP_002630445.1	81	265.774	180	146	Hypothetical protein CBG11178
Locus_14039_Transcript_1/1_Conf_1.000	950	7	6.37E-21	XP_001894575.1	57	105.916	158	91	MGC80099 protein
Locus_1404_Transcript_1/1_Conf_1.000	302	20	2.33E-43	AAO85518.1	100	178.333	87	87	AF496634_1putative serine/threonine phosphatase
Locus_14040_Transcript_1/1_Conf_1.000	399	20	5.44E-32	ABQ01576.1	72	140.584	109	79	scramblase 1
Locus_14041_Transcript_1/1_Conf_1.000	320	0							

Locus_14042_Transcript_1/1_Conf_1.000	184	20	2.17E-28	EFB20679.1	100	128.642	60	60	hypothetical protein PANDA_013768
Locus_14043_Transcript_1/1_Conf_1.000	131	0							
Locus_14044_Transcript_1/1_Conf_1.000	430	20	2.31E-67	AAO85518.1	98	258.07	127	125	AF496634_1putative serine/threonine phosphatase
Locus_14045_Transcript_1/1_Conf_1.000	194	6	2.30E-14	NP_510479.1	93	82.0333	63	59	Multidrug Resistance Protein family member (mrp-5)
Locus_14046_Transcript_1/1_Conf_1.000	172	20	2.19E-09	XP_001897369.1	75	65.4698	52	39	Protein kinase domain containing protein
Locus_14047_Transcript_1/1_Conf_1.000	165	3	2.88E-09	XP_002646710.1	74	65.0846	43	32	C. briggsae CBR-MAOC-1 protein
Locus_14048_Transcript_1/1_Conf_1.000	1358	20	6.92E-76	NP_001041223.1	67	289.271	300	201	mammalian VAV (oncogene) related family member (vav-1)
Locus_14049_Transcript_1/1_Conf_1.000	531	4	1.18E-12	NP_500378.1	65	76.6406	78	51	TAF (TBP-associated transcription factor) family member (taf-2)
Locus_1405_Transcript_1/1_Conf_1.000	1277	20	6.07E-103	EFO28398.1	72	379.022	425	307	hypothetical protein LOAG_00087
Locus_14050_Transcript_1/1_Conf_1.000	190	0							
Locus_14051_Transcript_1/1_Conf_1.000	934	3	1.81E-12	XP_001896205.1	57	77.7962	90	52	hypothetical protein Bm1_23740
Locus_14052_Transcript_1/1_Conf_1.000	146	0							

Locus_14053_Transcript_1/1_Conf_1.000	192	20	5.66E-21	NP_493596.1	100	103.99	53	53	UNCoordinated family member (unc-54)
Locus_14054_Transcript_1/1_Conf_1.000	267	0							
Locus_14055_Transcript_1/1_Conf_1.000	204	0							
Locus_14056_Transcript_1/1_Conf_1.000	811	20	9.91E-51	NP_001024382.1	83	204.527	157	131	DiacylGlycerol Kinase family member (dgk-1)
Locus_14057_Transcript_1/1_Conf_1.000	177	1	3.60E-04	NP_492172.1	71	48.1358	49	35	Aspergillus NUclear Division related family member (nud-2)
Locus_14058_Transcript_1/1_Conf_1.000	408	0							
Locus_14059_Transcript_1/1_Conf_1.000	309	19	5.93E-07	CAB40845.1	52	57.3806	75	39	conidiospore surface protein
Locus_1406_Transcript_1/1_Conf_1.000	1498	20	1.06E-96	XP_001899812.1	67	358.607	410	276	hypothetical protein Bm1_41765
Locus_14060_Transcript_1/1_Conf_1.000	534	20	1.25E-38	XP_001897852.1	56	162.925	177	100	notch-like transmembrane receptor

Locus_14061_Transcript_1/1_Conf_1.000	410	0							
Locus_14062_Transcript_1/1_Conf_1.000	139	1	2.58E-10	AAT12422.1	83	68.5514	42	35	hypothetical protein isoform a
Locus_14063_Transcript_1/1_Conf_1.000	479	5	9.18E-08	XP_002638736.1	56	60.077	90	51	C. briggsae CBR-EGO-1 protein
Locus_14064_Transcript_1/1_Conf_1.000	260	20	8.17E-28	NP_498761.1	86	126.716	86	74	DiCer Related family member (dcr-1)
Locus_14065_Transcript_1/1_Conf_1.000	161	8	1.95E-05	NP_001020988.1	84	52.373	53	45	UNCoordinated family member (unc-89)
Locus_14066_Transcript_1/1_Conf_1.000	355	0							
Locus_14067_Transcript_1/1_Conf_1.000	634	20	4.15E-28	XP_002641256.1	85	128.642	82	70	Hypothetical protein CBG05167
Locus_14068_Transcript_1/1_Conf_1.000	177	0							
Locus_14069_Transcript_1/1_Conf_1.000	914	20	1.64E-87	EFO27866.1	76	327.02	283	216	GTPase activating protein and VPS9 domains 1
Locus_1407_Transcript_1/2_Conf_1.000	706	20	1.49E-107	CAR63530.1	98	392.889	197	195	putative synaptic vesicle 2-related protein
Locus_1407_Transcript_2/2_Conf_1.000	861	20	2.97E-128	CAR63530.1	97	462.225	243	236	putative synaptic vesicle 2-related protein
Locus_14070_Transcript_1/1_Conf_1.000	387	20	2.84E-33	XP_002642740.1	79	144.821	112	89	Hypothetical protein CBG21119
Locus_14071_Transcript_1/1_Conf_1.000	372	0							
Locus_14072_Transcript_1/1_Conf_1.000	293	6	5.12E-14	XP_002639127.1	71	80.8777	83	59	Hypothetical protein CBG14946

Locus_14073_Transcript_1/1_Conf_1.000	478	20	1.76E-67	XP_002912365.1	100	258.455	129	129	PREDICTED: 60S ribosomal protein L23a-like
Locus_14074_Transcript_1/1_Conf_1.000	345	9	1.39E-35	XP_002641524.1	87	152.525	87	76	Hypothetical protein CBG09820
Locus_14075_Transcript_1/1_Conf_1.000	364	0							
Locus_14076_Transcript_1/1_Conf_1.000	483	2	1.40E-19	XP_002639186.1	57	99.3673	173	99	C. briggsae CBR-LEM-3 protein
Locus_14077_Transcript_1/1_Conf_1.000	351	0							
Locus_14078_Transcript_1/1_Conf_1.000	285	0							
Locus_14079_Transcript_1/1_Conf_1.000	415	20	3.57E-28	NP_001022052.1	64	127.872	134	87	SREBP Cleavage activating Protein (SCAP) homolog family member (scp-1)
Locus_1408_Transcript_1/2_Conf_1.000	317	20	1.23E-15	P82968.1	79	86.2705	53	42	Four-domain proteases inhibitor
Locus_1408_Transcript_2/2_Conf_1.000	316	20	2.09E-15	P82968.1	79	85.5001	53	42	Four-domain proteases inhibitor
Locus_14080_Transcript_1/1_Conf_1.000	471	20	1.98E-42	XP_002648986.1	76	175.252	160	122	C. briggsae CBR-SAX-2 protein
Locus_14081_Transcript_1/1_Conf_1.000	383	20	4.01E-19	XP_395372.2	59	97.8265	127	76	PREDICTED: similar to CG7565-PA
Locus_14082_Transcript_1/1_Conf_1.000	622	20	2.62E-56	XP_001894163.1	76	222.246	193	148	hypothetical protein Bm1_13490
Locus_14083_Transcript_1/2_Conf_1.000	649	20	1.19E-49	NP_502541.2	78	200.29	149	117	hypothetical protein JC8.2
Locus_14083_Transcript_2/2_Conf_1.000	626	20	1.08E-49	NP_502541.2	78	200.29	149	117	hypothetical protein JC8.2
Locus_14084_Transcript_1/1_Conf_1.000	812	20	2.86E-82	XP_002631390.1	84	309.301	258	217	Hypothetical protein CBG03232

Locus_14085_Transcript_1/1_Conf_1.000	162	0							
Locus_14086_Transcript_1/1_Conf_1.000	630	0							
Locus_14087_Transcript_1/2_Conf_1.000	428	0							
Locus_14087_Transcript_2/2_Conf_1.000	428	0							
Locus_14088_Transcript_1/1_Conf_1.000	672	20	4.02E-35	CAB16467.2	63	152.14	180	115	C. elegans protein W10C6.1, partially confirmed by transcript evidence
Locus_14089_Transcript_1/1_Conf_1.000	254	20	5.89E-26	EFO25124.1	80	120.553	83	67	bromodomain containing protein
Locus_1409_Transcript_1/1_Conf_1.000	616	20	3.45E-109	BAG61974.1	100	397.897	192	192	unnamed protein product
Locus_14090_Transcript_1/1_Conf_1.000	224	13	8.50E-17	XP_002641658.1	74	90.1225	71	53	Hypothetical protein CBG09986
Locus_14091_Transcript_1/1_Conf_1.000	225	0							
Locus_14092_Transcript_1/1_Conf_1.000	246	0							
Locus_14093_Transcript_1/1_Conf_1.000	439	20	1.15E-18	XP_002646219.1	65	96.2857	101	66	Hypothetical protein CBG11908
Locus_14094_Transcript_1/1_Conf_1.000	144	20	6.35E-12	CAF98408.1	83	73.9442	48	40	unnamed protein product
Locus_14095_Transcript_1/1_Conf_1.000	157	0							
Locus_14096_Transcript_1/2_Conf_1.000	621	20	5.51E-22	XP_002632140.1	74	108.227	105	78	C. briggsae CBR-SPTL-1 protein
Locus_14096_Transcript_2/2_Conf_1.000	260	0							
Locus_14097_Transcript_1/1_Conf_1.000	356	9	4.05E-49	XP_519474.2	96	126.716	62	60	PREDICTED: hepatocellular carcinoma-associated antigen 112
Locus_14098_Transcript_1/1_Conf_1.000	165	0							

Locus_14099_Transcript_1/1_Conf_1.000	275	20	6.39E-09	XP_001893875.1	61	63.929	81	50	Bromodomain associated family protein
Locus_141_Transcript_1/1_Conf_1.000	2163	20	4.62E-163	NP_872090.1	74	579.711	527	391	Lateral Signaling Target family member (lst-4)
Locus_1410_Transcript_1/1_Conf_1.000	200	0							
Locus_14100_Transcript_1/1_Conf_1.000	488	20	1.44E-08	NP_001021459.2	44	62.7734	159	71	hypothetical protein F36H2.3
Locus_14101_Transcript_1/1_Conf_1.000	212	0							
Locus_14102_Transcript_1/1_Conf_1.000	270	0							
Locus_14103_Transcript_1/1_Conf_1.000	439	20	2.29E-59	NP_004543.1	100	231.491	106	106	NADH dehydrogenase ubiquinone iron-sulfur protein 5
Locus_14104_Transcript_1/1_Conf_1.000	1783	20	2.65E-12	XP_002661927.1	41	78.5666	439	182	PREDICTED: hypothetical protein
Locus_14105_Transcript_1/1_Conf_1.000	369	0							
Locus_14106_Transcript_1/1_Conf_1.000	133	0							
Locus_14107_Transcript_1/1_Conf_1.000	132	0							
Locus_14108_Transcript_1/1_Conf_1.000	621	15	1.29E-87	NP_495267.1	89	326.25	191	171	hypothetical protein C29F5.1
Locus_14109_Transcript_1/1_Conf_1.000	222	0							
Locus_1411_Transcript_1/1_Conf_1.000	987	20	2.23E-48	XP_002634004.1	80	197.208	180	144	Hypothetical protein CBG20111
Locus_14110_Transcript_1/1_Conf_1.000	449	0							

Locus_14111_Transcript_1/1_Conf_1.000	339	20	2.17E-17	EFO24980.1	72	92.0485	79	57	hypothetical protein LOAG_03505
Locus_14112_Transcript_1/1_Conf_1.000	978	0							
Locus_14113_Transcript_1/1_Conf_1.000	667	20	5.18E-25	NP_502063.1	45	94.3597	163	74	hypothetical protein Y5F2A.4
Locus_14114_Transcript_1/1_Conf_1.000	189	20	7.69E-10	XP_002640423.1	73	67.0106	56	41	Hypothetical protein CBG08474
Locus_14115_Transcript_1/1_Conf_1.000	363	20	1.04E-35	XP_002631218.1	81	152.91	121	99	Hypothetical protein CBG03015
Locus_14116_Transcript_1/1_Conf_1.000	777	5	3.29E-32	NP_496398.2	76	142.895	102	78	hypothetical protein T06D8.1
Locus_14117_Transcript_1/1_Conf_1.000	336	0							
Locus_14118_Transcript_1/1_Conf_1.000	328	20	3.74E-33	ACD88896.1	81	144.436	91	74	conserved hypothetical protein
Locus_14119_Transcript_1/1_Conf_1.000	332	0							
Locus_1412_Transcript_1/1_Conf_1.000	1338	20	1.66E-90	XP_001894513.1	68	337.806	363	247	DZF family protein

Locus_14120_Transcript_1/1_Conf_1.000	442	20	1.25E-44	XP_002633800.1	79	182.57	147	117	C. briggsae CBR-RBD-1 protein
Locus_14121_Transcript_1/1_Conf_1.000	473	0							
Locus_14122_Transcript_1/1_Conf_1.000	652	20	1.56E-81	NP_001122814.1	82	306.22	217	178	STAT transcription factor family member (sta-1)
Locus_14123_Transcript_1/1_Conf_1.000	282	20	1.32E-09	CAJ98743.1	77	66.2402	54	42	serine/threonine phosphatase
Locus_14124_Transcript_1/1_Conf_1.000	267	0							
Locus_14125_Transcript_1/1_Conf_1.000	543	20	3.59E-60	NP_505435.1	84	234.572	175	148	hypothetical protein F36D4.2
Locus_14126_Transcript_1/1_Conf_1.000	289	0							
Locus_14127_Transcript_1/1_Conf_1.000	464	20	5.25E-59	NP_494756.1	84	230.335	154	130	hypothetical protein C01F1.1
Locus_14128_Transcript_1/1_Conf_1.000	310	20	2.03E-23	NP_493573.1	73	112.079	100	73	hypothetical protein F39B2.7
Locus_14129_Transcript_1/1_Conf_1.000	223	0							
Locus_1413_Transcript_1/1_Conf_1.000	1479	6	1.00E-14	NP_001129872.1	46	86.2705	366	169	hypothetical protein T23B5.3
Locus_14130_Transcript_1/1_Conf_1.000	566	20	3.59E-69	CBA12962.1	75	264.618	200	151	LEV-9 protein
Locus_14131_Transcript_1/1_Conf_1.000	313	0							
Locus_14132_Transcript_1/1_Conf_1.000	453	20	3.59E-36	NP_509859.1	73	154.451	118	87	hypothetical protein R08B4.3
Locus_14133_Transcript_1/1_Conf_1.000	132	0							

Locus_14134_Transcript_1/1_Conf_1.000	968	20	1.30E-61	XP_001896873.1	69	241.121	267	185	Origin recognition complex subunit 1
Locus_14135_Transcript_1/1_Conf_1.000	585	0							
Locus_14136_Transcript_1/1_Conf_1.000	1051	20	5.42E-80	NP_001023527.1	67	302.368	298	202	hypothetical protein Y57G11C.43
Locus_14137_Transcript_1/1_Conf_1.000	442	20	4.75E-52	AAX37111.1	100	207.223	118	118	small nuclear ribonucleoprotein D2 polypeptide
Locus_14138_Transcript_1/1_Conf_1.000	375	7	2.62E-10	ADI24623.1	64	68.5514	70	45	Copine domain protein, atypical protein 2, isoform c, partially confirmed by transcript evidence
Locus_14139_Transcript_1/1_Conf_1.000	963	20	2.30E-34	EFO26310.1	75	150.599	129	97	rap/ran-GAP family protein
Locus_1414_Transcript_1/1_Conf_1.000	790	20	5.30E-110	NP_001129887.1	86	401.364	262	227	SEC(selenocysteine)-tRNA Synthase family member (secs-1)
Locus_14140_Transcript_1/1_Conf_1.000	139	20	1.67E-17	BAG60581.1	100	92.4337	46	46	unnamed protein product
Locus_14141_Transcript_1/1_Conf_1.000	264								
Locus_14142_Transcript_1/1_Conf_1.000	448	20	9.61E-13	XP_002674131.1	55	76.6406	86	48	hypothetical protein NAEGRDRAFT_80725
Locus_14143_Transcript_1/1_Conf_1.000	168	0							
Locus_14144_Transcript_1/1_Conf_1.000	391	3	6.54E-14	NP_500183.2	75	80.4925	60	45	hypothetical protein M70.4
Locus_14145_Transcript_1/1_Conf_1.000	260	0							
Locus_14146_Transcript_1/1_Conf_1.000	266	20	1.13E-21	XP_002645292.1	73	106.301	88	65	C. briggsae CBR-SNF-12 protein
Locus_14147_Transcript_1/1_Conf_1.000	208	0							
Locus_14148_Transcript_1/1_Conf_1.000	1051	20	1.11E-08	XP_002635706.1	39	65.4698	215	85	Hypothetical protein CBG22445

Locus_14149_Transcript_1/1_Conf_1.000	366	4	2.09E-36	NP_001033357.2	79	155.221	118	94	DAF-16/FOXO Controlled, germline Tumor affecting family member (dct-6)
Locus_1415_Transcript_1/1_Conf_1.000	1034	20	9.68E-82	NP_492732.2	72	308.145	321	233	yeast SEC homolog family member (sec-8)
Locus_14150_Transcript_1/1_Conf_1.000	190	0							
Locus_14151_Transcript_1/1_Conf_1.000	146	13	1.98E-05	XP_001901649.1	74	52.373	47	35	WGR domain containing protein
Locus_14152_Transcript_1/1_Conf_1.000	138	0							
Locus_14153_Transcript_1/1_Conf_1.000	139	4	1.61E-12	CAA86821.1	95	75.8702	43	41	excretory/secretory antigen
Locus_14154_Transcript_1/1_Conf_1.000	342	0							
Locus_14155_Transcript_1/1_Conf_1.000	154	0							
Locus_14156_Transcript_1/1_Conf_1.000	525	20	9.48E-60	NP_492590.1	79	233.032	162	129	hypothetical protein K02A11.3
Locus_14157_Transcript_1/1_Conf_1.000	673	20	3.64E-36	EFO26611.1	60	155.606	220	134	hypothetical protein LOAG_01867
Locus_14158_Transcript_1/1_Conf_1.000	219	0							
Locus_14159_Transcript_1/1_Conf_1.000	234	20	2.88E-17	NP_501645.1	75	91.6633	69	52	hypothetical protein T20D3.8
Locus_1416_Transcript_1/1_Conf_1.000	508	2	1.40E-62	XP_001145371.1	98	242.276	118	116	PREDICTED: hypothetical protein
Locus_14160_Transcript_1/1_Conf_1.000	577	20	2.25E-69	NP_496170.1	80	265.388	191	154	LEThal family member (let-268)
Locus_14161_Transcript_1/1_Conf_1.000	800	20	2.77E-13	XP_001902864.1	65	80.1073	87	57	hypothetical protein Bm1_57035
Locus_14162_Transcript_1/1_Conf_1.000	842	20	4.07E-26	XP_002641927.1	63	122.865	138	88	Hypothetical protein CBG16626
Locus_14163_Transcript_1/1_Conf_1.000	128	20	1.48E-13	NP_503406.2	92	79.337	42	39	SyNapTotagmin family member (snt-3)
Locus_14164_Transcript_1/1_Conf_1.000	169	0							
Locus_14165_Transcript_1/1_Conf_1.000	254	0							
Locus_14166_Transcript_1/1_Conf_1.000	194	0							
Locus_14167_Transcript_1/1_Conf_1.000	226	4	5.13E-22	XP_002631267.1	80	107.457	75	60	C. briggsae CBR-PRO-1 protein
Locus_14168_Transcript_1/1_Conf_1.000	593	0							
Locus_14169_Transcript_1/1_Conf_1.000	198	0							

Locus_1417_Transcript_1/1_Conf_1.000	1934	20	1.35E-17	CAX12544.1	44	96.2857	258	114	nuclear oncoprotein skia
Locus_14170_Transcript_1/2_Conf_1.000	291	0							
Locus_14170_Transcript_2/2_Conf_1.000	333	0							
Locus_14171_Transcript_1/1_Conf_1.000	156	1	1.76E-22	XP_002343179.1	100	108.997	51	51	PREDICTED: hypothetical protein XP_002343179
Locus_14172_Transcript_1/1_Conf_1.000	570	3	9.97E-06	XP_002637821.1	51	53.9138	152	78	Hypothetical protein CBG04610
Locus_14173_Transcript_1/1_Conf_1.000	469	0							
Locus_14174_Transcript_1/1_Conf_1.000	322	11	1.70E-25	XP_002634211.1	83	119.013	90	75	C. briggsae CBR-MAU-8 protein
Locus_14175_Transcript_1/1_Conf_1.000	452	20	3.39E-26	NP_491902.3	69	121.324	120	83	hypothetical protein D2092.5
Locus_14176_Transcript_1/1_Conf_1.000	404	20	7.07E-32	NP_741383.1	74	140.198	111	83	tYrosinyl tRNA Synthetase family member (yrs-1)
Locus_14177_Transcript_1/1_Conf_1.000	164	0							
Locus_14178_Transcript_1/1_Conf_1.000	405	20	2.42E-32	NP_495663.1	72	141.739	134	97	REV1 (translesion DNA polymerase) homolog family member (rev-1)
Locus_14179_Transcript_1/1_Conf_1.000	913	20	8.32E-15	EFO17283.1	60	85.5001	202	122	hypothetical protein LOAG_11216
Locus_1418_Transcript_1/1_Conf_1.000	881	2	7.01E-24	NP_502443.2	51	115.546	257	133	hypothetical protein F07C6.4
Locus_14180_Transcript_1/1_Conf_1.000	370	20	1.89E-24	EFO19846.1	79	115.546	92	73	cleavage and polyadenylation specificity factor subunit 2
Locus_14181_Transcript_1/1_Conf_1.000	382	5	1.52E-18	XP_002643698.1	74	95.9005	78	58	Hypothetical protein CBG01887
Locus_14182_Transcript_1/1_Conf_1.000	694	20	1.65E-26	XP_001900728.1	75	123.635	96	72	RhoGAP domain containing protein
Locus_14183_Transcript_1/1_Conf_1.000	337	20	3.01E-51	AAD00776.1	89	204.527	112	100	2,5 dihydroxyphenylacetate oxidase
Locus_14184_Transcript_1/1_Conf_1.000	266	20	1.17E-42	XP_002347521.1	100	176.022	84	84	PREDICTED: hypothetical protein XP_002347521

Locus_14185_Transcript_1/1_Conf_1.000	194	2	9.06E-11	XP_002638788.1	84	70.0922	46	39	Hypothetical protein CBG05143
Locus_14186_Transcript_1/1_Conf_1.000	233	0							
Locus_14187_Transcript_1/1_Conf_1.000	408	0							
Locus_14188_Transcript_1/1_Conf_1.000	480	20	4.36E-26	XP_002634144.1	77	120.939	131	101	Hypothetical protein CBG01705
Locus_14189_Transcript_1/1_Conf_1.000	224	0							
Locus_1419_Transcript_1/1_Conf_1.000	588	20	5.41E-66	NP_499418.1	86	254.218	153	133	hypothetical protein Y48A6B.7
Locus_14190_Transcript_1/1_Conf_1.000	129	0							
Locus_14191_Transcript_1/1_Conf_1.000	335	0							
Locus_14192_Transcript_1/1_Conf_1.000	631	20	2.08E-21	XP_002633194.1	58	84.7297	105	61	Hypothetical protein CBG05911
Locus_14193_Transcript_1/2_Conf_1.000	631	2	5.39E-04	EFO27009.1	71	48.521	35	25	hypothetical protein LOAG_01466
Locus_14193_Transcript_2/2_Conf_1.000	571	2	4.19E-04	EFO27009.1	71	48.521	35	25	hypothetical protein LOAG_01466
Locus_14194_Transcript_1/1_Conf_1.000	358	4	1.56E-39	NP_496830.2	83	165.622	119	99	hypothetical protein Y48E1C.4
Locus_14195_Transcript_1/1_Conf_1.000	313	0							
Locus_14196_Transcript_1/1_Conf_1.000	194	0							
Locus_14197_Transcript_1/1_Conf_1.000	468	20	5.92E-71	AAC38987.1	91	270.011	156	142	P-glycoprotein
Locus_14198_Transcript_1/1_Conf_1.000	545	20	1.46E-45	XP_002640390.1	72	186.037	182	132	Hypothetical protein CBG08435
Locus_14199_Transcript_1/1_Conf_1.000	221	6	1.97E-05	XP_002639496.1	69	52.373	66	46	Hypothetical protein CBG04097

Locus_142_Transcript_1/1_Conf_1.000	1491	20	1.49E-66	NP_496763.1	59	258.455	337	200	CYclin D family member (cyd-1)
Locus_1420_Transcript_1/1_Conf_1.000	487	20	8.63E-46	NP_510298.1	68	186.422	160	110	AMP-Activated Kinase Beta subunit family member (aakb-1)
Locus_14200_Transcript_1/1_Conf_1.000	256	0							
Locus_14201_Transcript_1/1_Conf_1.000	154	0							
Locus_14202_Transcript_1/1_Conf_1.000	1023	1	1.96E-10	NP_498298.1	41	71.2478	321	134	hypothetical protein F25B5.2
Locus_14203_Transcript_1/1_Conf_1.000	202	0							
Locus_14204_Transcript_1/1_Conf_1.000	935	20	6.54E-63	NP_491315.1	64	245.358	304	197	INneXin family member (inx-17)
Locus_14205_Transcript_1/1_Conf_1.000	282	5	8.86E-06	XP_002631238.1	62	53.5286	64	40	Hypothetical protein CBG03041
Locus_14206_Transcript_1/1_Conf_1.000	685	20	4.59E-74	1TW9	84	281.567	204	172	Glutathione Transferase-2
Locus_14207_Transcript_1/1_Conf_1.000	424	0							
Locus_14208_Transcript_1/1_Conf_1.000	185	20	1.83E-27	XP_002914026.1	100	125.561	61	61	PREDICTED: polyadenylate-binding protein 1-like
Locus_14209_Transcript_1/1_Conf_1.000	362	0							
Locus_1421_Transcript_1/1_Conf_1.000	603	0							
Locus_14210_Transcript_1/1_Conf_1.000	264	20	1.21E-31	XP_001894470.1	86	139.428	87	75	GCD14 protein
Locus_14211_Transcript_1/1_Conf_1.000	468	9	9.54E-37	NP_499059.2	60	156.377	168	102	hypothetical protein K04H4.2

Locus_14212_Transcript_1/1_Conf_1.000	341	0							
Locus_14213_Transcript_1/1_Conf_1.000	901	20	9.16E-59	XP_002638852.1	63	231.491	290	184	Hypothetical protein CBG22064
Locus_14214_Transcript_1/1_Conf_1.000	204	0							
Locus_14215_Transcript_1/1_Conf_1.000	388	20	5.52E-37	NP_001040927.1	75	157.147	128	96	hypothetical protein C47A4.2
Locus_14216_Transcript_1/1_Conf_1.000	172	0							
Locus_14217_Transcript_1/1_Conf_1.000	274	20	1.42E-16	XP_002641416.1	78	89.3521	65	51	C. briggsae CBR-SBP-1 protein
Locus_14218_Transcript_1/1_Conf_1.000	222	0							
Locus_14219_Transcript_1/1_Conf_1.000	227	20	6.06E-23	XP_002606421.1	89	110.538	73	65	hypothetical protein BRAFLDRAFT_67673
Locus_1422_Transcript_1/1_Conf_1.000	865	20	3.31E-119	NP_871640.1	84	432.18	288	242	Glycyl tRNA Synthetase family member (grs-1)
Locus_14220_Transcript_1/1_Conf_1.000	364	20	6.06E-52	NP_001023252.1	91	206.838	120	110	Transbilayer Amphipath Transporters (subfamily IV P-type ATPase) family member (tat-2)
Locus_14221_Transcript_1/1_Conf_1.000	204	2	1.09E-08	NP_499474.1	85	63.1586	35	30	BED-type zinc finger transcription factor family member (bed-2)
Locus_14222_Transcript_1/1_Conf_1.000	396	20	4.73E-68	XP_002927413.1	100	260.381	131	131	PREDICTED: eukaryotic translation initiation factor 3 subunit C-like
Locus_14223_Transcript_1/1_Conf_1.000	390	6	4.53E-15	EFO16157.1	52	84.3445	142	74	ribonuclease P/MRP protein subunit POP1 containing protein

Locus_14224_Transcript_1/1_Conf_1.000	329	20	1.13E-29	XP_001900386.1	80	132.88	105	84	Phosphatidylcholine:ceramide cholinephosphotransferase 3, putative
Locus_14225_Transcript_1/1_Conf_1.000	266	17	1.86E-40	EFO27230.1	97	168.703	88	86	fasciclin domain-containing protein
Locus_14226_Transcript_1/1_Conf_1.000	432	2	6.60E-06	NP_499664.2	48	53.9138	116	56	hypothetical protein BE10.2
Locus_14227_Transcript_1/1_Conf_1.000	400	9	1.35E-06	XP_002630073.1	52	56.225	91	48	Hypothetical protein CBG13452
Locus_14228_Transcript_1/1_Conf_1.000	187	0							
Locus_14229_Transcript_1/1_Conf_1.000	197	0							
Locus_1423_Transcript_1/1_Conf_1.000	1472	20	1.30E-115	NP_001024665.1	67	421.394	449	303	SynDaPiN (synaptic dynamin binding protein) homolog family member (sdpn-1)
Locus_14230_Transcript_1/1_Conf_1.000	443	20	6.07E-15	XP_001520430.1	62	83.9593	80	50	PREDICTED: similar to N-acetylglucosaminyltransferase V, partial
Locus_14231_Transcript_1/1_Conf_1.000	505	0							
Locus_14232_Transcript_1/1_Conf_1.000	285	20	2.31E-22	NP_491075.2	77	108.612	94	73	hypothetical protein Y71F9AL.1
Locus_14233_Transcript_1/1_Conf_1.000	523	0							
Locus_14234_Transcript_1/1_Conf_1.000	741	20	2.38E-37	XP_001900728.1	51	159.844	269	139	RhoGAP domain containing protein
Locus_14235_Transcript_1/1_Conf_1.000	805	20	8.46E-10	XP_862879.1	44	68.5514	218	97	PREDICTED: similar to Syntaxin-18 isoform 4

Locus_14236_Transcript_1/1_Conf_1.000	250	20	2.09E-36	AAH02110.2	98	155.221	75	74	Rpl24 protein
Locus_14237_Transcript_1/1_Conf_1.000	283	3	4.99E-25	NP_001041206.1	75	117.472	96	72	hypothetical protein ZC487.1
Locus_14238_Transcript_1/1_Conf_1.000	361	20	8.32E-09	EFO24006.1	61	63.5438	72	44	hypothetical protein LOAG_04478
Locus_14239_Transcript_1/3_Conf_0.600	780	20	5.95E-90	XP_002631584.1	82	334.724	264	219	Hypothetical protein CBG20762
Locus_14239_Transcript_2/3_Conf_0.600	781	20	5.95E-90	XP_002631584.1	82	334.724	264	219	Hypothetical protein CBG20762
Locus_14239_Transcript_3/3_Conf_0.600	781	20	5.95E-90	XP_002631584.1	82	334.724	264	219	Hypothetical protein CBG20762
Locus_1424_Transcript_1/2_Conf_1.000	1073	5	1.70E-36	XP_002641061.1	72	157.918	154	112	Hypothetical protein CBG22473
Locus_1424_Transcript_2/2_Conf_1.000	1152	5	1.90E-36	XP_002641061.1	72	157.918	154	112	Hypothetical protein CBG22473
Locus_14240_Transcript_1/1_Conf_1.000	765	20	1.20E-55	XP_002631403.1	70	220.705	220	154	Hypothetical protein CBG03253
Locus_14241_Transcript_1/1_Conf_1.000	824	0							
Locus_14242_Transcript_1/1_Conf_1.000	364	0							
Locus_14243_Transcript_1/1_Conf_1.000	284	0							
Locus_14244_Transcript_1/1_Conf_1.000	202	4	2.61E-10	NP_499313.2	70	68.5514	67	47	hypothetical protein F43D9.1

Locus_14245_Transcript_1/1_Conf_1.000	373	20	6.17E-68	BAG59411.1	100	259.996	119	119	unnamed protein product
Locus_14246_Transcript_1/1_Conf_1.000	337	20	6.47E-62	CAA68491.1	100	239.965	112	112	glutathione peroxidase
Locus_14247_Transcript_1/1_Conf_1.000	326	0							

Locus_14248_Transcript_1/1_Conf_1.000	198	20	5.07E-30	XP_002923753.1	100	134.035	65	65	PREDICTED: rRNA 2'-O-methyltransferase fibrillarin-like
Locus_14249_Transcript_1/1_Conf_1.000	741	20	2.65E-12	XP_002416765.1	49	76.6406	147	73	Sin3p-Rpd3p histone-deacetylase complex, DNA binding subunit, putative
Locus_1425_Transcript_1/1_Conf_1.000	356	7	2.79E-04	XP_002782358.1	69	48.521	42	29	conserved hypothetical protein
Locus_14250_Transcript_1/1_Conf_1.000	483	0							
Locus_14251_Transcript_1/1_Conf_1.000	377	20	3.87E-54	XP_002638687.1	93	214.157	124	116	Hypothetical protein CBG11882
Locus_14252_Transcript_1/1_Conf_1.000	317	0							
Locus_14253_Transcript_1/1_Conf_1.000	258	0							
Locus_14254_Transcript_1/2_Conf_1.000	464	0							
Locus_14254_Transcript_2/2_Conf_1.000	351	0							
Locus_14255_Transcript_1/1_Conf_1.000	253	0							
Locus_14256_Transcript_1/1_Conf_1.000	181	0							
Locus_14257_Transcript_1/1_Conf_1.000	626	0							
Locus_14258_Transcript_1/1_Conf_1.000	465	20	3.63E-44	NP_490714.1	87	181.03	107	94	hypothetical protein C53D5.5
Locus_14259_Transcript_1/1_Conf_1.000	546	20	6.91E-51	XP_002631157.1	85	203.756	144	123	C. briggsae CBR-RPN-9 protein
Locus_1426_Transcript_1/1_Conf_1.000	180	0							
Locus_14260_Transcript_1/1_Conf_1.000	131	0							
Locus_14261_Transcript_1/1_Conf_1.000	195	0							
Locus_14262_Transcript_1/1_Conf_1.000	354	0							
Locus_14263_Transcript_1/1_Conf_1.000	341	20	5.14E-35	XP_002639310.1	87	150.599	113	99	Hypothetical protein CBG03881
Locus_14264_Transcript_1/1_Conf_1.000	178	0							
Locus_14265_Transcript_1/1_Conf_1.000	154	0							
Locus_14266_Transcript_1/1_Conf_1.000	1401	20	4.04E-111	XP_002631389.1	75	406.371	319	241	C. briggsae CBR-OOC-5 protein
Locus_14267_Transcript_1/1_Conf_1.000	676	1	7.48E-05	NP_505951.1	68	51.6026	89	61	hypothetical protein T27F2.4
Locus_14268_Transcript_1/1_Conf_1.000	138	0							
Locus_14269_Transcript_1/1_Conf_1.000	363	3	1.01E-06	NP_507800.2	70	56.6102	50	35	hypothetical protein B0399.1

Locus_1427_Transcript_1/1_Conf_1.000	1976	20	9.60E-144	NP_001033327.1	71	515.383	500	359	CAN cell Migration defective family member (cam-1)
Locus_14270_Transcript_1/1_Conf_1.000	175	14	4.71E-12	NP_505743.1	78	74.3294	56	44	hypothetical protein F28H7.3
Locus_14271_Transcript_1/1_Conf_1.000	284	0							
Locus_14272_Transcript_1/1_Conf_1.000	203	0							
Locus_14273_Transcript_1/1_Conf_1.000	212	6	9.51E-05	NP_001122663.1	59	50.0618	66	39	hypothetical protein Y53F4B.39
Locus_14274_Transcript_1/1_Conf_1.000	416	20	5.15E-35	XP_002634297.1	87	150.599	109	95	Hypothetical protein CBG17635
Locus_14275_Transcript_1/1_Conf_1.000	408	0							
Locus_14276_Transcript_1/1_Conf_1.000	725	20	2.45E-100	NP_491653.2	84	369.007	241	203	hypothetical protein F55F8.3
Locus_14277_Transcript_1/1_Conf_1.000	222	0							
Locus_14278_Transcript_1/2_Conf_1.000	202	0							
Locus_14278_Transcript_2/2_Conf_1.000	154	0							
Locus_14279_Transcript_1/1_Conf_1.000	182	0							
Locus_1428_Transcript_1/1_Conf_1.000	226	0							
Locus_14280_Transcript_1/1_Conf_1.000	301	0							
Locus_14281_Transcript_1/1_Conf_1.000	910	20	2.16E-39	EFO22896.1	62	167.162	260	163	hypothetical protein LOAG_05591
Locus_14282_Transcript_1/1_Conf_1.000	461	20	3.68E-41	CAD44516.1	76	171.014	152	117	VAB-10B protein

Locus_14283_Transcript_1/1_Conf_1.000	177	7	4.39E-10	NP_509266.1	72	67.781	58	42	hypothetical protein F48E3.2
Locus_14284_Transcript_1/1_Conf_1.000	582	4	6.42E-19	NP_491128.4	57	97.8265	192	111	Conserved Oligomeric Golgi (COG) Component family member (cogc-1)
Locus_14285_Transcript_1/1_Conf_1.000	460	20	2.48E-13	XP_001380323.1	53	78.5666	132	71	PREDICTED: hypothetical protein
Locus_14286_Transcript_1/1_Conf_1.000	622	0							
Locus_14287_Transcript_1/1_Conf_1.000	263	0							
Locus_14288_Transcript_1/1_Conf_1.000	407	20	2.34E-27	XP_002630954.1	69	125.176	143	100	C. briggsae CBR-TAG-184 protein
Locus_14289_Transcript_1/1_Conf_1.000	249	20	4.99E-22	XP_001902912.1	82	107.457	80	66	aminotransferase, class V family protein
Locus_1429_Transcript_1/1_Conf_1.000	524	20	2.06E-67	CAR63531.1	93	258.455	147	138	putative Prion-like-(Q/N-rich)-domain-bearing protein
Locus_14290_Transcript_1/1_Conf_1.000	193	20	1.49E-13	XP_002762172.1	100	79.337	38	38	PREDICTED: 26S protease regulatory subunit 6B
Locus_14291_Transcript_1/1_Conf_1.000	329	0							
Locus_14292_Transcript_1/2_Conf_1.000	922	20	5.23E-65	XP_002648431.1	84	252.292	217	183	C. briggsae CBR-LPD-8 protein
Locus_14292_Transcript_2/2_Conf_1.000	922	20	5.23E-65	XP_002648431.1	84	252.292	217	183	C. briggsae CBR-LPD-8 protein
Locus_14293_Transcript_1/2_Conf_1.000	442	3	9.07E-11	NP_001023436.1	55	70.0922	128	71	hypothetical protein Y37E11AL.3
Locus_14293_Transcript_2/2_Conf_1.000	442	3	9.07E-11	NP_001023436.1	55	70.0922	128	71	hypothetical protein Y37E11AL.3
Locus_14294_Transcript_1/1_Conf_1.000	458	4	2.50E-13	XP_002640105.1	52	78.5666	149	78	C. briggsae CBR-MUT-2 protein
Locus_14295_Transcript_1/1_Conf_1.000	551	20	1.02E-25	NP_498886.2	53	120.168	163	88	hypothetical protein C06E1.3
Locus_14296_Transcript_1/1_Conf_1.000	372	0							
Locus_14297_Transcript_1/1_Conf_1.000	279	1	2.85E-09	EAX01292.1	72	65.0846	47	34	hCG1648136
Locus_14298_Transcript_1/1_Conf_1.000	177	0							
Locus_14299_Transcript_1/1_Conf_1.000	185	0							

Locus_143_Transcript_1/4_Conf_0.727	3170	20	0	AAM73861.1	85	1433.31	1045	889	AF457202_1putative serine/threonine protein kinase
Locus_143_Transcript_2/4_Conf_0.727	3347	20	0	AAM73859.1	91	1497.26	963	884	AF457200_1putative serine/threonine protein kinase
Locus_143_Transcript_3/4_Conf_0.727	3251	20	0	AAM73861.1	91	1519.6	1030	940	AF457202_1putative serine/threonine protein kinase
Locus_143_Transcript_4/4_Conf_0.727	3125	20	0	AAM73861.1	86	1439.86	1030	895	AF457202_1putative serine/threonine protein kinase
Locus_1430_Transcript_1/1_Conf_1.000	539	3	3.83E-43	XP_002633338.1	77	177.948	144	112	Hypothetical protein CBG06077
Locus_14300_Transcript_1/1_Conf_1.000	206	0							
Locus_14301_Transcript_1/1_Conf_1.000	205	0							
Locus_14302_Transcript_1/1_Conf_1.000	265	0							
Locus_14303_Transcript_1/1_Conf_1.000	1465	20	1.09E-21	NP_001090490.1	66	109.383	89	59	inhibitor of growth family, member 1-like
Locus_14304_Transcript_1/1_Conf_1.000	146	17	1.37E-14	A8WQT4.2	92	82.8037	42	39	Calcium uptake protein 1 homolog
Locus_14305_Transcript_1/1_Conf_1.000	247	1	7.26E-05	NP_502613.2	56	50.447	80	45	QUInine non-avoider family member (qui-1)
Locus_14306_Transcript_1/1_Conf_1.000	838	20	2.56E-113	XP_002640628.1	84	412.535	279	236	C. briggsae CBR-EAT-18 protein
Locus_14307_Transcript_1/1_Conf_1.000	377	0							
Locus_14308_Transcript_1/1_Conf_1.000	323	5	1.03E-06	XP_001893560.1	74	56.6102	47	35	hypothetical protein Bm1_10440
Locus_14309_Transcript_1/1_Conf_1.000	224	0							

Locus_1431_Transcript_1/1_Conf_1.000	755	20	3.72E-70	XP_002640472.1	82	268.855	214	177	C. briggsae CBR-RPS-6 protein
Locus_14310_Transcript_1/2_Conf_1.000	997	20	1.02E-56	NP_741459.2	61	224.942	326	202	WASP (actin cytoskeleton modulator) homolog family member (wsp-1)
Locus_14310_Transcript_2/2_Conf_1.000	988	20	1.44E-55	NP_741459.2	60	221.09	323	197	WASP (actin cytoskeleton modulator) homolog family member (wsp-1)
Locus_14311_Transcript_1/1_Conf_1.000	172	0							
Locus_14312_Transcript_1/1_Conf_1.000	174	0							
Locus_14313_Transcript_1/1_Conf_1.000	500	3	8.50E-38	NP_493074.2	77	159.844	132	102	hypothetical protein R05D7.1
Locus_14314_Transcript_1/1_Conf_1.000	144	0							
Locus_14315_Transcript_1/1_Conf_1.000	256	2	1.72E-09	EFO18967.1	61	65.855	85	52	LIM domain-containing protein
Locus_14316_Transcript_1/1_Conf_1.000	624	0							

Locus_14317_Transcript_1/1_Conf_1.000	238	20	5.43E-08	XP_002930758.1	100	60.8474	45	45	PREDICTED: melanoma-associated antigen D1-like
Locus_14318_Transcript_1/2_Conf_1.000	651	0							
Locus_14318_Transcript_2/2_Conf_1.000	636	0							
Locus_14319_Transcript_1/1_Conf_1.000	1110	20	1.27E-106	NP_497939.2	76	390.963	341	260	Suppressor/Enhancer of Lin-12 family member (sel-2)
Locus_1432_Transcript_1/1_Conf_1.000	1709	20	3.59E-168	NP_502152.3	77	596.275	470	362	CYtochrome P450 family member (cyp-31A2)
Locus_14320_Transcript_1/2_Conf_1.000	352	20	1.06E-19	XP_001900152.1	62	99.7525	114	71	Actin family protein
Locus_14320_Transcript_2/2_Conf_1.000	427	20	2.69E-23	XP_002629986.1	81	111.694	79	64	Hypothetical protein CBG13348
Locus_14321_Transcript_1/1_Conf_1.000	853	20	1.81E-37	NP_496498.1	68	160.614	183	125	hypothetical protein C47D12.8
Locus_14322_Transcript_1/1_Conf_1.000	973	20	1.76E-82	XP_002638826.1	73	310.457	326	240	Hypothetical protein CBG22031
Locus_14323_Transcript_1/1_Conf_1.000	512	20	9.41E-43	ACI49172.1	68	176.407	168	115	hypothetical protein Csp3_JD01.004
Locus_14324_Transcript_1/1_Conf_1.000	156	0							
Locus_14325_Transcript_1/1_Conf_1.000	235	0							
Locus_14326_Transcript_1/1_Conf_1.000	772	0							
Locus_14327_Transcript_1/1_Conf_1.000	469	4	2.70E-15	XP_002639461.1	62	85.1149	91	57	Hypothetical protein CBG04056
Locus_14328_Transcript_1/1_Conf_1.000	213	0							
Locus_14329_Transcript_1/1_Conf_1.000	620	0							
Locus_1433_Transcript_1/1_Conf_1.000	202	20	8.38E-17	XP_002634622.1	77	90.1225	67	52	Hypothetical protein CBG18478
Locus_14330_Transcript_1/1_Conf_1.000	534	0							
Locus_14331_Transcript_1/1_Conf_1.000	229	0							

Locus_14332_Transcript_1/1_Conf_1.000	261	20	3.41E-34	NP_504245.3	95	147.902	86	82	hypothetical protein Y61A9LA.10
Locus_14333_Transcript_1/1_Conf_1.000	188	0							
Locus_14334_Transcript_1/1_Conf_1.000	816	20	8.97E-100	NP_001022287.1	79	367.466	272	216	hypothetical protein R53.1
Locus_14335_Transcript_1/1_Conf_1.000	368	20	9.69E-34	XP_002639434.1	82	146.362	112	92	Hypothetical protein CBG04027
Locus_14336_Transcript_1/1_Conf_1.000	442	20	9.91E-50	AAB59518.1	100	199.519	100	100	apolipoprotein E
Locus_14337_Transcript_1/1_Conf_1.000	578	20	7.50E-65	NP_001023936.1	81	250.366	192	157	hypothetical protein F46B6.6
Locus_14338_Transcript_1/1_Conf_1.000	180	0							
Locus_14339_Transcript_1/1_Conf_1.000	165	0							
Locus_1434_Transcript_1/2_Conf_1.000	1010	1	2.68E-04	XP_001899348.1	64	50.8322	54	35	Probable coatomer beta' subunit

Locus_1434_Transcript_2/2_Conf_1.000	959	1	2.45E-04	XP_001899348.1	64	50.8322	54	35	Probable coatomer beta' subunit
Locus_14340_Transcript_1/1_Conf_1.000	341	20	2.30E-51	XP_002638788.1	91	204.912	113	103	Hypothetical protein CBG05143
Locus_14341_Transcript_1/1_Conf_1.000	574	0							
Locus_14342_Transcript_1/1_Conf_1.000	192	0							
Locus_14343_Transcript_1/1_Conf_1.000	293	6	9.98E-18	Q8I0P7.3	75	93.2041	84	63	Probable 3',5'-cyclic phosphodiesterase pde-3
Locus_14344_Transcript_1/1_Conf_1.000	355	0							
Locus_14345_Transcript_1/1_Conf_1.000	305	6	8.61E-14	ADI24640.1	57	80.1073	96	55	Hypothetical protein C56E6.9
Locus_14346_Transcript_1/1_Conf_1.000	175	0							
Locus_14347_Transcript_1/1_Conf_1.000	221	20	9.07E-35	XP_002759394.1	100	149.828	73	73	PREDICTED: polyadenylate-binding protein 1-like
Locus_14348_Transcript_1/1_Conf_1.000	217	20	1.45E-13	ADI61822.1	68	79.337	69	47	endonuclease-reverse transcriptase
Locus_14349_Transcript_1/1_Conf_1.000	144	0							
Locus_1435_Transcript_1/1_Conf_1.000	718	0							
Locus_14350_Transcript_1/1_Conf_1.000	485	20	1.26E-28	NP_001076607.1	69	129.413	116	81	hypothetical protein K12C11.6
Locus_14351_Transcript_1/1_Conf_1.000	260	0							
Locus_14352_Transcript_1/1_Conf_1.000	723	20	7.17E-76	AAA28103.1	95	287.73	185	176	ras protein
Locus_14353_Transcript_1/2_Conf_1.000	663	20	1.15E-79	BAD92215.1	100	300.056	145	145	HLA class II histocompatibility antigen, DP beta chain precursor variant

Locus_14353_Transcript_2/2_Conf_1.000	553	20	7.35E-80	BAD92215.1	100	300.056	145	145	HLA class II histocompatibility antigen, DP beta chain precursor variant
Locus_14354_Transcript_1/1_Conf_1.000	258	20	9.94E-42	BAI45345.1	100	172.94	85	85	mannosidase, alpha, class 2B, member 1
Locus_14355_Transcript_1/1_Conf_1.000	513	3	3.78E-47	EFO27774.1	67	191.045	171	116	rap/ran-GAP family protein
Locus_14356_Transcript_1/1_Conf_1.000	686	20	5.95E-98	XP_001894292.1	87	360.918	226	198	cyclin-dependent kinase 7 homolog
Locus_14357_Transcript_1/1_Conf_1.000	544	20	1.08E-48	NP_504578.1	72	196.438	180	131	hypothetical protein F17A9.4
Locus_14358_Transcript_1/1_Conf_1.000	268	20	6.86E-19	NP_505920.1	72	97.0561	87	63	hypothetical protein C55A6.6
Locus_14359_Transcript_1/1_Conf_1.000	905	2	5.43E-43	NP_492185.2	59	179.104	295	175	SMG-associated and Lethal family member (smgl-1)
Locus_1436_Transcript_1/2_Conf_1.000	1214	20	1.17E-124	XP_002639724.1	84	451.055	354	299	C. briggsae CBR-MEL-26 protein

Locus_1436_Transcript_2/2_Conf_1.000	2114	20	2.42E-124	XP_002639724.1	84	451.055	354	299	C. briggsae CBR-MEL-26 protein
Locus_14360_Transcript_1/1_Conf_1.000	239	20	4.71E-36	XP_002640668.1	97	154.066	79	77	C. briggsae CBR-UNC-54 protein
Locus_14361_Transcript_1/1_Conf_1.000	534	8	2.37E-13	NP_496318.1	52	78.9518	171	89	ECT2 (mammalian Rho GEF) homolog family member (ect-2)
Locus_14362_Transcript_1/1_Conf_1.000	203	0							
Locus_14363_Transcript_1/1_Conf_1.000	333	2	2.25E-38	NP_498952.1	80	161.77	111	89	hypothetical protein F44E2.4
Locus_14364_Transcript_1/1_Conf_1.000	225	0							
Locus_14365_Transcript_1/1_Conf_1.000	262	20	1.76E-06	CAA85409.2	64	55.8398	45	29	C. elegans protein D2089.2, partially confirmed by transcript evidence
Locus_14366_Transcript_1/1_Conf_1.000	373	11	4.47E-26	NP_001021875.1	68	120.939	126	86	Leucyl tRNA Synthetase family member (lrs-2)
Locus_14367_Transcript_1/1_Conf_1.000	164	0							
Locus_14368_Transcript_1/1_Conf_1.000	269	0							
Locus_14369_Transcript_1/1_Conf_1.000	697	20	2.42E-09	XP_002631402.1	50	66.6254	180	90	Hypothetical protein CBG03252
Locus_1437_Transcript_1/1_Conf_1.000	955	20	3.37E-30	AAA92672.1	68	136.732	147	101	HMG CoA synthase
Locus_14370_Transcript_1/1_Conf_1.000	374	2	4.65E-07	XP_002647555.1	75	57.7658	48	36	Hypothetical protein CBG06641
Locus_14371_Transcript_1/1_Conf_1.000	709	0							
Locus_14372_Transcript_1/1_Conf_1.000	152	0							
Locus_14373_Transcript_1/1_Conf_1.000	132	0							
Locus_14374_Transcript_1/1_Conf_1.000	1714	20	3.62E-152	NP_496363.1	74	543.117	575	427	LEThal family member (let-858)

Locus_14375_Transcript_1/1_Conf_1.000	527	20	2.87E-32	NP_499126.1	63	141.739	157	99	DNA PRImase homolog family member (pri-1)
Locus_14376_Transcript_1/1_Conf_1.000	143	0							
Locus_14377_Transcript_1/1_Conf_1.000	180	19	3.97E-22	NP_498645.1	86	107.842	59	51	MUscle Positioning family member (mup-4)
Locus_14378_Transcript_1/1_Conf_1.000	562	20	8.46E-47	NP_001022572.1	69	190.274	195	136	Elongation Factor Kinase family member (efk-1)
Locus_14379_Transcript_1/1_Conf_1.000	271	0							
Locus_1438_Transcript_1/1_Conf_1.000	219	20	1.04E-38	XP_002762091.1	100	162.925	73	73	PREDICTED: glucose-6-phosphate isomerase-like, partial
Locus_14380_Transcript_1/1_Conf_1.000	417	0							
Locus_14381_Transcript_1/1_Conf_1.000	525	0							
Locus_14382_Transcript_1/1_Conf_1.000	248	3	9.49E-05	NP_508523.1	55	50.0618	83	46	Temporarily Assigned Gene name family member (tag-312)
Locus_14383_Transcript_1/1_Conf_1.000	509	20	1.84E-46	NP_001021940.1	72	188.734	168	122	hypothetical protein C08H9.3
Locus_14384_Transcript_1/1_Conf_1.000	401	0							
Locus_14385_Transcript_1/1_Conf_1.000	231	20	2.89E-25	XP_002639432.1	80	118.242	77	62	C. briggsae CBR-TYR-4 protein
Locus_14386_Transcript_1/1_Conf_1.000	652	20	7.03E-74	XP_001901411.1	70	280.796	223	157	Thioredoxin family protein
Locus_14387_Transcript_1/1_Conf_1.000	155	0							

Locus_14388_Transcript_1/1_Conf_1.000	705	20	2.85E-66	NP_001122776.1	87	255.758	148	130	hypothetical protein F35G2.1
Locus_14389_Transcript_1/1_Conf_1.000	598	20	9.67E-66	XP_001900850.1	79	253.447	198	157	ERCC4 domain containing protein
Locus_1439_Transcript_1/1_Conf_1.000	561	20	4.50E-40	XP_002639226.1	96	167.933	91	88	Hypothetical protein CBG03777
Locus_14390_Transcript_1/1_Conf_1.000	500	20	4.24E-21	Q61SU7.3	60	104.375	141	85	ATP-dependent RNA helicase SUV3 homolog
Locus_14391_Transcript_1/1_Conf_1.000	264	20	2.06E-31	XP_002646681.1	91	138.658	85	78	C. briggsae CBR-PRX-5 protein
Locus_14392_Transcript_1/1_Conf_1.000	1037	20	3.77E-17		46	93.5893	283	131	hypothetical protein ZC13.1
Locus_14393_Transcript_1/2_Conf_1.000	398	0							
Locus_14393_Transcript_2/2_Conf_1.000	398	0							
Locus_14394_Transcript_1/1_Conf_1.000	563	20	2.38E-49	XP_001901731.1	72	198.749	188	136	Guanine nucleotide-binding protein alpha-3 subunit

Locus_14395_Transcript_1/1_Conf_1.000	258	0							
Locus_14396_Transcript_1/1_Conf_1.000	458	0							
Locus_14397_Transcript_1/1_Conf_1.000	278	0							
Locus_14398_Transcript_1/1_Conf_1.000	133	20	2.50E-13	NP_001023736.1	90	78.5666	44	40	Na/H eXchanger family member (nhx-3)
Locus_14399_Transcript_1/1_Conf_1.000	139	0							
Locus_144_Transcript_1/1_Conf_1.000	1533	20	0	XP_001895190.1	81	681.404	483	396	Receptor family ligand binding region containing protein
Locus_1440_Transcript_1/1_Conf_1.000	1065	20	1.82E-123	XP_002637266.1	78	446.817	330	260	Hypothetical protein CBG18949
Locus_14400_Transcript_1/1_Conf_1.000	172	0							
Locus_14401_Transcript_1/1_Conf_1.000	262	0							
Locus_14402_Transcript_1/1_Conf_1.000	369	20	6.96E-11	NP_493178.1	67	70.4774	78	53	hypothetical protein W02D9.3
Locus_14403_Transcript_1/1_Conf_1.000	208	0							
Locus_14404_Transcript_1/1_Conf_1.000	767	0							
Locus_14405_Transcript_1/3_Conf_0.667	518	1	2.71E-08	NP_001122478.1	74	62.003	43	32	hypothetical protein F45H11.3
Locus_14405_Transcript_2/3_Conf_0.667	525	1	2.89E-08	NP_001122478.1	74	62.003	43	32	hypothetical protein F45H11.3
Locus_14405_Transcript_3/3_Conf_0.667	534	1	3.00E-08	NP_001122478.1	74	62.003	43	32	hypothetical protein F45H11.3
Locus_14406_Transcript_1/1_Conf_1.000	238	0							
Locus_14407_Transcript_1/1_Conf_1.000	243	0							
Locus_14408_Transcript_1/2_Conf_1.000	509	20	3.35E-48	NP_499553.1	85	194.512	123	105	yeast CCR4 Associated Factor family member (ccf-1)

Locus_14408_Transcript_2/2_Conf_1.000	509	20	3.35E-48	NP_499553.1	85	194.512	123	105	yeast CCR4 Associated Factor family member (ccf-1)
Locus_14409_Transcript_1/1_Conf_1.000	351	5	1.14E-13	XP_002639084.1	65	79.7221	88	58	Hypothetical protein CBG14902
Locus_1441_Transcript_1/1_Conf_1.000	856	20	8.07E-86	NP_499133.1	98	321.242	162	160	UBiquitin Conjugating enzyme family member (ubc-7)
Locus_14410_Transcript_1/1_Conf_1.000	432	20	6.54E-38	NP_498982.1	80	160.229	111	89	hypothetical protein R08D7.1
Locus_14411_Transcript_1/1_Conf_1.000	1595	20	0	XP_002643273.1	85	742.265	523	447	C. briggsae CBR-MRP-1 protein
Locus_14412_Transcript_1/1_Conf_1.000	539	18	5.31E-69	XP_002640063.1	90	263.848	166	151	Hypothetical protein CBG12545
Locus_14413_Transcript_1/1_Conf_1.000	767	20	1.62E-52	EFO24017.1	65	210.305	238	157	hypothetical protein LOAG_04469
Locus_14414_Transcript_1/1_Conf_1.000	1089	4	2.69E-53	NP_509401.2	54	213.772	339	184	hypothetical protein R09F10.3
Locus_14415_Transcript_1/1_Conf_1.000	310	0							
Locus_14416_Transcript_1/1_Conf_1.000	128	0							
Locus_14417_Transcript_1/1_Conf_1.000	257	19	5.50E-24	EFO18138.1	83	114.005	85	71	hypothetical protein LOAG_10361

Locus_14418_Transcript_1/1_Conf_1.000	318	4	2.55E-05	XP_001895677.1	86	51.9878	36	31	Actin family protein
Locus_14419_Transcript_1/1_Conf_1.000	451	20	2.25E-62	EFO28147.1	98	241.506	120	118	pre-mRNA splicing factor PRP8
Locus_1442_Transcript_1/1_Conf_1.000	1047	20	1.13E-45	NP_495323.1	56	188.348	352	199	Temporarily Assigned Gene name family member (tag-184)
Locus_14420_Transcript_1/1_Conf_1.000	152	2	8.52E-09	XP_002629821.1	81	63.5438	48	39	C. briggsae CBR-SQV-8 protein
Locus_14421_Transcript_1/2_Conf_1.000	448	0							
Locus_14421_Transcript_2/2_Conf_1.000	448	0							
Locus_14422_Transcript_1/1_Conf_1.000	168	20	5.60E-13	XP_001607068.1	81	77.411	60	49	PREDICTED: similar to polyribonucleotide nucleotidyltransferase
Locus_14423_Transcript_1/1_Conf_1.000	664	2	1.44E-11	NP_492348.1	51	73.559	117	60	hypothetical protein K07A12.2
Locus_14424_Transcript_1/1_Conf_1.000	502	20	1.03E-22	XP_002639569.1	82	109.768	112	92	Hypothetical protein CBG04200
Locus_14425_Transcript_1/2_Conf_1.000	666	20	4.07E-32	XP_002640276.1	72	142.124	177	128	Hypothetical protein CBG12801
Locus_14425_Transcript_2/2_Conf_1.000	587	20	1.11E-34	XP_002640276.1	72	150.214	170	123	Hypothetical protein CBG12801
Locus_14426_Transcript_1/1_Conf_1.000	558	0							
Locus_14427_Transcript_1/1_Conf_1.000	813	20	5.00E-18	XP_001623641.1	37	95.9005	264	99	predicted protein
Locus_14428_Transcript_1/1_Conf_1.000	264	0							
Locus_14429_Transcript_1/1_Conf_1.000	573	20	8.19E-48	CBA11992.1	62	193.741	191	120	endonuclease-reverse transcriptase HmRTE-e01
Locus_1443_Transcript_1/1_Conf_1.000	681	20	1.58E-34	NP_498150.1	64	150.214	170	110	hypothetical protein Y32H12A.7
Locus_14430_Transcript_1/1_Conf_1.000	277	4	3.61E-12	XP_001896695.1	62	74.7146	91	57	Hr1 repeat family protein
Locus_14431_Transcript_1/1_Conf_1.000	337	0							

Locus_14432_Transcript_1/1_Conf_1.000	241	3	2.42E-16	EFO23234.1	69	88.5817	66	46	hypothetical protein LOAG_05253
Locus_14433_Transcript_1/1_Conf_1.000	219	20	4.50E-34	EAW69389.1	100	147.517	71	71	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae), isoform CRA_a
Locus_14434_Transcript_1/1_Conf_1.000	261	2	1.14E-05	XP_002634568.1	84	53.1434	52	44	Hypothetical protein CBG08374
Locus_14435_Transcript_1/1_Conf_1.000	270	20	5.04E-30	XP_001898305.1	79	134.035	87	69	Transmembrane 9 superfamily protein member 2 precursor, putative
Locus_14436_Transcript_1/1_Conf_1.000	281	0							
Locus_14437_Transcript_1/1_Conf_1.000	338	0							
Locus_14438_Transcript_1/1_Conf_1.000	165	7	1.17E-18	XP_002639508.1	96	96.2857	51	49	Hypothetical protein CBG04113
Locus_14439_Transcript_1/1_Conf_1.000	221	20	1.50E-29	NP_494777.1	90	132.494	73	66	MoLTing defective family member (mlt-7)
Locus_1444_Transcript_1/2_Conf_1.000	800	20	2.46E-78	NP_498360.2	81	296.204	227	184	hypothetical protein T12A2.7
Locus_1444_Transcript_2/2_Conf_1.000	800	20	2.46E-78	NP_498360.2	81	296.204	227	184	hypothetical protein T12A2.7
Locus_14440_Transcript_1/1_Conf_1.000	394	20	9.94E-50	EFO26261.1	87	199.519	131	115	hypothetical protein LOAG_02219
Locus_14441_Transcript_1/1_Conf_1.000	251	3	4.49E-39	XP_002830960.1	95	164.081	83	79	PREDICTED: hypothetical protein LOC100438111
Locus_14442_Transcript_1/1_Conf_1.000	323	20	5.25E-43	XP_002633186.1	92	177.178	104	96	Hypothetical protein CBG05900
Locus_14443_Transcript_1/1_Conf_1.000	1117	20	4.32E-54	NP_741217.1	67	216.468	223	151	EXOSome (multiexonuclease complex) component family member (exos-9)
Locus_14444_Transcript_1/2_Conf_1.000	898	8	9.44E-48	NP_871881.1	70	194.897	244	172	hypothetical protein F30F8.9
Locus_14444_Transcript_2/2_Conf_1.000	568	10	7.43E-38	NP_492165.1	65	160.614	186	121	hypothetical protein F30F8.9

Locus_14445_Transcript_1/1_Conf_1.000	218	20	2.02E-23	XP_001898626.1	88	112.079	72	64	Pyruvate kinase, muscle isozyme
Locus_14446_Transcript_1/2_Conf_1.000	597	0							
Locus_14446_Transcript_2/2_Conf_1.000	511	0							
Locus_14447_Transcript_1/1_Conf_1.000	161	0							
Locus_14448_Transcript_1/1_Conf_1.000	129	0							
Locus_14449_Transcript_1/1_Conf_1.000	218	0							
Locus_1445_Transcript_1/2_Conf_1.000	2002	20	6.72E-93	XP_002643215.1	68	342.813	326	223	Hypothetical protein CBG08080
Locus_1445_Transcript_2/2_Conf_1.000	1973	20	4.66E-98	XP_002643215.1	66	363.614	365	242	Hypothetical protein CBG08080
Locus_14450_Transcript_1/1_Conf_1.000	186	0							
Locus_14451_Transcript_1/1_Conf_1.000	148	0							
Locus_14452_Transcript_1/1_Conf_1.000	200	20	2.89E-17	XP_002634283.1	78	91.6633	65	51	C. briggsae CBR-HRS-1 protein
Locus_14453_Transcript_1/1_Conf_1.000	922	20	4.39E-96	NP_509283.1	76	355.525	273	208	APYrase family member (apy-1)
Locus_14454_Transcript_1/1_Conf_1.000	130	2	9.57E-05	NP_498688.1	67	50.0618	43	29	Prolyl Carboxy Peptidase like family member (pcp-1)
Locus_14455_Transcript_1/1_Conf_1.000	886								
Locus_14456_Transcript_1/1_Conf_1.000	422	0							
Locus_14457_Transcript_1/1_Conf_1.000	572	20	6.34E-69	NP_505519.3	81	263.848	186	152	UNCoordinated family member (unc-42)
Locus_14458_Transcript_1/1_Conf_1.000	469	0							
Locus_14459_Transcript_1/1_Conf_1.000	477	2	1.08E-08	XP_002637934.1	48	63.1586	152	74	Hypothetical protein CBG04746

Locus_1446_Transcript_1/2_Conf_1.000	1659	20	3.77E-160	XP_001896639.1	93	557.755	309	289	hypothetical protein
Locus_1446_Transcript_2/2_Conf_1.000	1595	20	8.91E-166	XP_001896639.1	92	588.186	329	305	hypothetical protein
Locus_14460_Transcript_1/1_Conf_1.000	381	20	5.05E-30	NP_498764.1	70	134.035	125	88	GTP exchange factor for ARFs family member (grp-1)
Locus_14461_Transcript_1/1_Conf_1.000	270	0							
Locus_14462_Transcript_1/1_Conf_1.000	540	0							
Locus_14463_Transcript_1/1_Conf_1.000	490	0							
Locus_14464_Transcript_1/1_Conf_1.000	137	0							
Locus_14465_Transcript_1/1_Conf_1.000	258	20	8.74E-22	NP_506083.1	77	106.686	76	59	hypothetical protein F55C5.8
Locus_14466_Transcript_1/1_Conf_1.000	324	0							
Locus_14467_Transcript_1/1_Conf_1.000	166	20	2.44E-08	ACO51818.1	70	62.003	55	39	Rho GDP-dissociation inhibitor 2
Locus_14468_Transcript_1/1_Conf_1.000	262	0							

Locus_14469_Transcript_1/2_Conf_1.000	948	20	4.99E-58	XP_002638726.1	73	229.18	240	176	Hypothetical protein CBG00309
Locus_14469_Transcript_2/2_Conf_1.000	948	20	4.99E-58	XP_002638726.1	73	229.18	240	176	Hypothetical protein CBG00309
Locus_1447_Transcript_1/1_Conf_1.000	615	0							
Locus_14470_Transcript_1/1_Conf_1.000	151	0							
Locus_14471_Transcript_1/1_Conf_1.000	158	0							
Locus_14472_Transcript_1/1_Conf_1.000	132	0							
Locus_14473_Transcript_1/1_Conf_1.000	158	20	3.00E-22	XP_002814804.1	100	108.227	52	52	PREDICTED: insulin-like growth factor-binding protein 7-like
Locus_14474_Transcript_1/1_Conf_1.000	387	0							
Locus_14475_Transcript_1/1_Conf_1.000	206	0							
Locus_14476_Transcript_1/1_Conf_1.000	536	20	3.08E-37	EFO23539.1	71	158.303	156	111	hypothetical protein LOAG_04946
Locus_14477_Transcript_1/1_Conf_1.000	294	0							
Locus_14478_Transcript_1/1_Conf_1.000	231	0							
Locus_14479_Transcript_1/1_Conf_1.000	207	0							
Locus_1448_Transcript_1/1_Conf_1.000	618	20	9.05E-57	XP_002630759.1	68	223.787	206	141	Hypothetical protein CBG02453
Locus_14480_Transcript_1/1_Conf_1.000	890	20	1.99E-66	EFO26982.1	90	256.914	152	138	PAR-6 protein

Locus_14481_Transcript_1/1_Conf_1.000	708	20	8.65E-71	NP_509361.1	87	270.781	195	171	hypothetical protein K07E3.4
Locus_14482_Transcript_1/1_Conf_1.000	165	0							
Locus_14483_Transcript_1/1_Conf_1.000	264	3	8.72E-06	NP_504274.2	70	53.5286	50	35	UDP-GlucuronosylTransferase family member (ugt-61)
Locus_14484_Transcript_1/1_Conf_1.000	183	20	5.92E-18	NP_001022451.1	92	93.9745	54	50	hypothetical protein Y48E1A.1
Locus_14485_Transcript_1/1_Conf_1.000	244	20	6.79E-19	XP_001641772.1	74	97.0561	79	59	predicted protein
Locus_14486_Transcript_1/1_Conf_1.000	215	6	5.19E-11	AAL56427.1	77	70.8626	54	42	AF370722_1intracellular globin
Locus_14487_Transcript_1/1_Conf_1.000	416	0							
Locus_14488_Transcript_1/1_Conf_1.000	484	0							
Locus_14489_Transcript_1/1_Conf_1.000	630	20	6.93E-60	XP_002637479.1	72	234.187	211	152	Hypothetical protein CBG19196
Locus_1449_Transcript_1/1_Conf_1.000	667	0							
Locus_14490_Transcript_1/1_Conf_1.000	248	3	1.91E-13	XP_002647006.1	75	78.9518	64	48	Hypothetical protein CBG22464
Locus_14491_Transcript_1/1_Conf_1.000	261	1	4.34E-05	XP_001899770.1	54	51.2174	82	45	hAT family dimerisation domain containing protein
Locus_14492_Transcript_1/1_Conf_1.000	314	1	2.85E-04	NP_497581.3	50	48.521	81	41	hypothetical protein Y54F10AR.2
Locus_14493_Transcript_1/1_Conf_1.000	221	0							
Locus_14494_Transcript_1/2_Conf_1.000	160	0							
Locus_14494_Transcript_2/2_Conf_1.000	347	0							
Locus_14495_Transcript_1/1_Conf_1.000	183	5	3.47E-18	NP_001023620.1	81	94.7449	60	49	hypothetical protein ZK792.4
Locus_14496_Transcript_1/1_Conf_1.000	602	20	8.42E-17	EFO27042.1	46	90.8929	189	88	hypothetical protein LOAG_01440
Locus_14497_Transcript_1/1_Conf_1.000	386	0							
Locus_14498_Transcript_1/1_Conf_1.000	249	20	4.99E-22	XP_002427316.1	70	107.457	81	57	transportin-2, putative
Locus_14499_Transcript_1/1_Conf_1.000	200	0							

Locus_145_Transcript_1/3_Conf_0.600	897	0							
Locus_145_Transcript_2/3_Conf_0.600	1436	20	1.17E-12	NP_001021459.2	37	79.337	359	134	hypothetical protein F36H2.3
Locus_145_Transcript_3/3_Conf_0.600	908	0							
Locus_1450_Transcript_1/1_Conf_1.000	1424	20	0	NP_741215.1	83	681.789	436	366	NADH Ubiquinone Oxidoreductase family member (nuo-4)
Locus_14500_Transcript_1/1_Conf_1.000	417	20	9.98E-34	EFO21654.1	70	146.362	137	97	hypothetical protein LOAG_06832
Locus_14501_Transcript_1/1_Conf_1.000	401	3	1.39E-19	NP_507813.1	62	99.3673	116	72	hypothetical protein Y43F8C.13
Locus_14502_Transcript_1/1_Conf_1.000	264	9	5.65E-05	NP_504738.1	60	50.8322	70	42	COLlagen family member (col-143)
Locus_14503_Transcript_1/1_Conf_1.000	478	4	5.56E-13	EFO24423.1	63	77.411	119	76	hypothetical protein LOAG_04059
Locus_14504_Transcript_1/1_Conf_1.000	900	20	1.11E-80	NP_503421.1	73	304.294	278	204	Hydroxy-Acyl-CoA Dehydrogenase family member (hacd-1)
Locus_14505_Transcript_1/1_Conf_1.000	466	20	1.74E-54	AAD45606.1	92	215.312	124	115	galectin 3
Locus_14506_Transcript_1/1_Conf_1.000	139	0							
Locus_14507_Transcript_1/1_Conf_1.000	351	20	1.69E-33	NP_496144.1	94	145.591	87	82	hypothetical protein C05C10.3
Locus_14508_Transcript_1/1_Conf_1.000	190	20	6.07E-23	CAR63575.1	87	110.538	63	55	hypothetical protein
Locus_14509_Transcript_1/1_Conf_1.000	285	0							

Locus_1451_Transcript_1/2_Conf_1.000	1673	20	5.98E-35	XP_002635620.1	61	153.68	212	130	Hypothetical protein CBG21813
Locus_1451_Transcript_2/2_Conf_1.000	1673	20	5.98E-35	XP_002635620.1	61	153.68	212	130	Hypothetical protein CBG21813
Locus_14510_Transcript_1/1_Conf_1.000	137	2	2.11E-12	CAE17761.2	91	75.485	36	33	C. elegans protein C48D5.3, confirmed by transcript evidence
Locus_14511_Transcript_1/1_Conf_1.000	309	0							
Locus_14512_Transcript_1/1_Conf_1.000	409	20	1.50E-58	AAH71725.1	97	228.794	131	128	IGL@ protein
Locus_14513_Transcript_1/1_Conf_1.000	712	20	3.36E-30	NP_499239.1	78	135.961	85	67	hypothetical protein T16H12.4
Locus_14514_Transcript_1/1_Conf_1.000	938	20	1.05E-68	NP_499903.3	62	264.618	314	197	Defecation Suppressor of Clk-1 family member (dsc-4)
Locus_14515_Transcript_1/1_Conf_1.000	139	0							
Locus_14516_Transcript_1/1_Conf_1.000	556	0							
Locus_14517_Transcript_1/1_Conf_1.000	344	20	1.27E-12	EFO18793.1	69	76.2554	75	52	hypothetical protein LOAG_09702
Locus_14518_Transcript_1/1_Conf_1.000	149	0							
Locus_14519_Transcript_1/1_Conf_1.000	197	0							
Locus_1452_Transcript_1/1_Conf_1.000	545	20	1.93E-13	XP_001902112.1	95	79.337	40	38	Iron-sulfur cluster assembly accessory protein
Locus_14520_Transcript_1/1_Conf_1.000	607	0							
Locus_14521_Transcript_1/1_Conf_1.000	208	20	1.33E-06	XP_002739131.1	59	56.225	67	40	PREDICTED: major facilitator superfamily domain containing 5-like
Locus_14522_Transcript_1/1_Conf_1.000	565	4	3.64E-29	NP_510486.2	54	131.724	172	93	hypothetical protein F20D1.3

Locus_14523_Transcript_1/2_Conf_1.000	692	3	6.45E-07	EFO21590.1	43	58.5362	211	92	hypothetical protein LOAG_06899
Locus_14523_Transcript_2/2_Conf_1.000	692	4	2.89E-07	EFO21590.1	44	59.6918	211	93	hypothetical protein LOAG_06899
Locus_14524_Transcript_1/1_Conf_1.000	577	20	9.81E-57	XP_002629673.1	82	223.402	149	123	Hypothetical protein CBG00891
Locus_14525_Transcript_1/1_Conf_1.000	444	20	1.99E-50	NP_492361.2	78	201.83	148	116	RNA Polymerase II (B) subunit family member (rpb-3)
Locus_14526_Transcript_1/1_Conf_1.000	241	2	3.87E-14	XP_002643403.1	75	81.2629	58	44	Hypothetical protein CBG16021
Locus_14527_Transcript_1/1_Conf_1.000	210	0							
Locus_14528_Transcript_1/1_Conf_1.000	287	5	5.72E-05	XP_002637333.1	65	50.8322	49	32	C. briggsae CBR-COL-142 protein
Locus_14529_Transcript_1/1_Conf_1.000	684	20	6.82E-86	NP_499668.1	79	320.857	228	181	hypothetical protein Y37D8A.2
Locus_1453_Transcript_1/2_Conf_1.000	1438	20	7.44E-84	NP_504551.3	82	315.849	224	184	Protein Carboxymethyltransferase family member (pcm-1)
Locus_1453_Transcript_2/2_Conf_1.000	1482	20	7.78E-84	NP_504551.3	82	315.849	224	184	Protein Carboxymethyltransferase family member (pcm-1)
Locus_14530_Transcript_1/1_Conf_1.000	242	20	2.67E-23	XP_002709090.1	83	111.694	80	67	PREDICTED: N-acetyltransferase 10
Locus_14531_Transcript_1/1_Conf_1.000	235	0							
Locus_14532_Transcript_1/1_Conf_1.000	357	0							
Locus_14533_Transcript_1/1_Conf_1.000	299	20	5.05E-38	EFO27760.1	83	160.614	93	78	glycosyl hydrolase family 31 protein
Locus_14534_Transcript_1/1_Conf_1.000	239	20	6.39E-25	XP_002644187.1	87	117.087	73	64	Hypothetical protein CBG17169
Locus_14535_Transcript_1/1_Conf_1.000	221	0							
Locus_14536_Transcript_1/1_Conf_1.000	235	0							
Locus_14537_Transcript_1/2_Conf_1.000	1575	20	4.02E-94	NP_001022260.1	59	350.132	545	323	Initiation Factor 4G (eIF4G) family member (ifg-1)
Locus_14537_Transcript_2/2_Conf_1.000	1581	20	3.09E-94	NP_001022260.1	59	350.517	545	322	Initiation Factor 4G (eIF4G) family member (ifg-1)

Locus_14538_Transcript_1/1_Conf_1.000	180	5	8.59E-09	CAA16382.5	66	63.5438	60	40	C. elegans protein Y45F10D.7, partially confirmed by transcript evidence
Locus_14539_Transcript_1/1_Conf_1.000	303	20	4.25E-29	NP_509429.1	89	130.954	74	66	Temporarily Assigned Gene name family member (tag-123)
Locus_1454_Transcript_1/2_Conf_1.000	821	20	6.98E-68	XP_002635374.1	68	261.536	286	195	C. briggsae CBR-TAG-117 protein
Locus_1454_Transcript_2/2_Conf_1.000	1175	20	6.21E-75	XP_002635374.1	60	285.804	427	257	C. briggsae CBR-TAG-117 protein
Locus_14540_Transcript_1/1_Conf_1.000	730	20	7.01E-103	NP_001021145.1	85	377.481	240	206	hypothetical protein C05D11.1
Locus_14541_Transcript_1/1_Conf_1.000	189	20	4.80E-28	ACJ65168.1	96	127.487	62	60	Uncoordinated protein 68, isoform b, partially confirmed by transcript evidence
Locus_14542_Transcript_1/3_Conf_0.667	1307	20	1.48E-128	XP_001898423.1	74	464.151	434	323	Mediator complex subunit rgr-1
Locus_14542_Transcript_2/3_Conf_0.667	1467	20	1.24E-142	XP_001898423.1	73	511.146	490	360	Mediator complex subunit rgr-1
Locus_14542_Transcript_3/3_Conf_0.667	1467	20	1.24E-142	XP_001898423.1	73	511.146	490	360	Mediator complex subunit rgr-1
Locus_14543_Transcript_1/1_Conf_1.000	352	20	1.02E-38	XP_002631360.1	78	162.925	123	97	Hypothetical protein CBG03195

Locus_14544_Transcript_1/1_Conf_1.000	391	20	2.15E-49	AAN11401.1	81	198.364	128	104	metalloprotease 1 precursor
Locus_14545_Transcript_1/1_Conf_1.000	1738	20	1.46E-100	NP_001123105.1	64	371.703	487	312	CDC-42 Guanine nucleotide Exchange Factor family member (cgef-1)
Locus_14546_Transcript_1/1_Conf_1.000	315	20	1.60E-23	EFO20067.1	68	112.464	112	77	hypothetical protein LOAG_08425
Locus_14547_Transcript_1/1_Conf_1.000	283	20	3.71E-12	XP_002120612.1	60	74.7146	80	48	PREDICTED: similar to ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1, partial
Locus_14548_Transcript_1/1_Conf_1.000	191	0							
Locus_14549_Transcript_1/1_Conf_1.000	161	0							
Locus_1455_Transcript_1/1_Conf_1.000	496	20	8.78E-59	NP_497791.1	81	229.565	153	124	NITrilase family member (nit-1)
Locus_14550_Transcript_1/2_Conf_1.000	1052	20	2.34E-91	NP_500791.2	75	340.117	324	244	SAND endocytosis protein family member (sand-1)
Locus_14550_Transcript_2/2_Conf_1.000	459	20	3.46E-23	NP_500791.2	71	111.309	121	86	SAND endocytosis protein family member (sand-1)
Locus_14551_Transcript_1/1_Conf_1.000	302	20	2.28E-06	XP_002003728.1	49	55.4546	99	49	GI18068
Locus_14552_Transcript_1/1_Conf_1.000	152	3	1.50E-05	NP_494220.2	68	52.7582	50	34	hypothetical protein F54A3.1
Locus_14553_Transcript_1/1_Conf_1.000	238	20	3.75E-17	YP_003797541.1	80	91.2781	71	57	ATP-dependent protease La
Locus_14554_Transcript_1/1_Conf_1.000	525	20	2.97E-37	EFO26437.1	70	158.303	170	120	CK1 protein kinase
Locus_14555_Transcript_1/1_Conf_1.000	448	14	5.77E-42	NP_501544.1	79	173.711	121	96	hypothetical protein C27B7.2
Locus_14556_Transcript_1/1_Conf_1.000	258	0							
Locus_14557_Transcript_1/1_Conf_1.000	245	0							
Locus_14558_Transcript_1/1_Conf_1.000	247	2	1.19E-15	EFO24527.1	66	86.2705	80	53	hypothetical protein LOAG_03957
Locus_14559_Transcript_1/1_Conf_1.000	170	0							
Locus_1456_Transcript_1/1_Conf_1.000	302	1	1.48E-05	XP_002129449.1	53	52.7582	102	55	PREDICTED: hypothetical protein
Locus_14560_Transcript_1/1_Conf_1.000	640	20	3.23E-60	EFO27810.1	74	235.343	206	153	plasmid Maintenance protein containing protein
Locus_14561_Transcript_1/1_Conf_1.000	795	0							

Locus_14562_Transcript_1/1_Conf_1.000	1201	4	2.28E-88	XP_002635496.1	70	330.487	375	264	Hypothetical protein CBG08796
Locus_14563_Transcript_1/1_Conf_1.000	184	0							
Locus_14564_Transcript_1/1_Conf_1.000	552	20	5.32E-46	XP_002647377.1	93	187.578	133	124	Hypothetical protein CBG06437
Locus_14565_Transcript_1/1_Conf_1.000	423	20	8.97E-27	NP_502633.1	72	123.25	114	83	UDP-GlucuronosylTransferase family member (ugt-22)
Locus_14566_Transcript_1/2_Conf_1.000	228	0							
Locus_14566_Transcript_2/2_Conf_1.000	746	0							
Locus_14567_Transcript_1/1_Conf_1.000	303	0							
Locus_14568_Transcript_1/1_Conf_1.000	848	20	4.71E-30	3N9L	67	135.961	151	102	Cekdm7a From C.Elegans
Locus_14569_Transcript_1/1_Conf_1.000	340	0							
Locus_1457_Transcript_1/1_Conf_1.000	1198	20	7.36E-55	NP_741338.1	65	219.164	236	154	hypothetical protein Y69A2AR.7
Locus_14570_Transcript_1/1_Conf_1.000	138	6	2.41E-16	NP_872196.2	95	88.5817	46	44	hypothetical protein D1054.9
Locus_14571_Transcript_1/1_Conf_1.000	497	14	3.99E-19	NP_499088.1	72	97.8265	81	59	Neuropeptide-Like Protein family member (nlp-36)
Locus_14572_Transcript_1/1_Conf_1.000	380	0							
Locus_14573_Transcript_1/1_Conf_1.000	509	0							
Locus_14574_Transcript_1/2_Conf_1.000	619	20	1.51E-19	XP_001645325.1	47	100.138	204	97	hypothetical protein Kpol_1058p4

Locus_14574_Transcript_2/2_Conf_1.000	412	15	4.56E-07	XP_001645325.1	44	57.7658	134	60	hypothetical protein Kpol_1058p4
Locus_14575_Transcript_1/1_Conf_1.000	237	4	1.06E-11	EFO22550.1	67	73.1738	77	52	TATA binding protein associated factor
Locus_14576_Transcript_1/1_Conf_1.000	630	0							
Locus_14577_Transcript_1/1_Conf_1.000	654	20	1.57E-97	NP_498645.1	83	359.377	218	183	MUscle Positioning family member (mup-4)
Locus_14578_Transcript_1/1_Conf_1.000	178	8	3.84E-14	NP_504908.1	81	81.2629	59	48	hypothetical protein F18E3.7
Locus_14579_Transcript_1/1_Conf_1.000	1211	20	2.81E-94	XP_002640721.1	62	350.132	392	245	Hypothetical protein CBG19789
Locus_1458_Transcript_1/2_Conf_1.000	1009	20	3.08E-101	NP_492354.1	86	372.859	236	205	Proteasome Beta Subunit family member (pbs-7)
Locus_1458_Transcript_2/2_Conf_1.000	2245	20	3.79E-83	NP_741955.2	71	314.309	320	229	hypothetical protein H18N23.2

Locus_14580_Transcript_1/1_Conf_1.000	305	20	7.75E-31	XP_001891560.1	98	136.732	67	66	DNA-directed RNA polymerase II 7.6 kDa polypeptide
Locus_14581_Transcript_1/2_Conf_1.000	461	0							
Locus_14581_Transcript_2/2_Conf_1.000	460	0							
Locus_14582_Transcript_1/1_Conf_1.000	559	0							
Locus_14583_Transcript_1/1_Conf_1.000	429	20	4.12E-32	NP_495516.2	78	140.969	127	100	hypothetical protein F32A5.8
Locus_14584_Transcript_1/3_Conf_0.600	245	0							
Locus_14584_Transcript_2/3_Conf_0.400	376	0							
Locus_14584_Transcript_3/3_Conf_0.600	245	0							
Locus_14585_Transcript_1/1_Conf_1.000	198	0							
Locus_14586_Transcript_1/1_Conf_1.000	222	20	1.26E-28	NP_496968.1	94	129.413	74	70	hypothetical protein Y48B6A.12
Locus_14587_Transcript_1/1_Conf_1.000	448	20	1.12E-61	XP_002641528.1	84	239.195	149	126	Hypothetical protein CBG09825
Locus_14588_Transcript_1/1_Conf_1.000	277	20	2.11E-12	EFO21272.1	62	75.485	74	46	hypothetical protein LOAG_07212
Locus_14589_Transcript_1/1_Conf_1.000	195	0							
Locus_1459_Transcript_1/1_Conf_1.000	229	20	2.61E-34	XP_002925190.1	100	148.288	73	73	PREDICTED: 40S ribosomal protein S13-like
Locus_14590_Transcript_1/1_Conf_1.000	227	0							
Locus_14591_Transcript_1/2_Conf_1.000	233	0							
Locus_14591_Transcript_2/2_Conf_1.000	430	20	6.78E-43	NP_001021848.1	82	176.792	107	88	hypothetical protein ZC334.7
Locus_14592_Transcript_1/1_Conf_1.000	191	0							

Locus_14593_Transcript_1/1_Conf_1.000	254	20	2.74E-15	CAA84704.4	87	85.1149	57	50	C. elegans protein F43D9.3a, confirmed by transcript evidence
Locus_14594_Transcript_1/1_Conf_1.000	325	0							
Locus_14595_Transcript_1/1_Conf_1.000	379	20	1.46E-61	XP_002831613.1	100	238.81	114	114	PREDICTED: LOW QUALITY PROTEIN: ubiquitin-like modifier-activating enzyme 1-like
Locus_14596_Transcript_1/1_Conf_1.000	152	0							
Locus_14597_Transcript_1/1_Conf_1.000	154	0							
Locus_14598_Transcript_1/1_Conf_1.000	209	0							
Locus_14599_Transcript_1/1_Conf_1.000	1985	20	0	NP_001041007.1	71	662.529	655	468	Juxtamembrane domain-Associated Catenin family member (jac-1)
Locus_146_Transcript_1/1_Conf_1.000	2367	20	0	XP_002639688.1	93	1111.29	626	586	C. briggsae CBR-FASN-1 protein
Locus_1460_Transcript_1/1_Conf_1.000	294	4	8.71E-14	XP_002646111.1	72	80.1073	69	50	C. briggsae CBR-PAD-1 protein
Locus_14600_Transcript_1/2_Conf_1.000	657	6	2.00E-07	ZP_02160840.1	45	60.077	159	72	hypothetical protein KAOT1_18882
Locus_14600_Transcript_2/2_Conf_1.000	657	3	2.00E-07	ZP_02160840.1	45	60.077	159	72	hypothetical protein KAOT1_18882
Locus_14601_Transcript_1/1_Conf_1.000	128	0							
Locus_14602_Transcript_1/1_Conf_1.000	245	0							
Locus_14603_Transcript_1/1_Conf_1.000	450	20	2.76E-36	NP_494905.2	74	154.836	151	112	MeDiaTor family member (mdt-4)
Locus_14604_Transcript_1/1_Conf_1.000	245	4	2.04E-23	NP_741205.1	96	112.079	61	59	PDF (arthropod Pigment Dispersing Factor) homolog family member (pdf-1)
Locus_14605_Transcript_1/1_Conf_1.000	317	0							
Locus_14606_Transcript_1/1_Conf_1.000	280	20	4.22E-29	NP_501217.2	82	130.954	93	77	hypothetical protein R05G6.10
Locus_14607_Transcript_1/1_Conf_1.000	143	0							
Locus_14608_Transcript_1/1_Conf_1.000	250	0							

Locus_14609_Transcript_1/1_Conf_1.000	1321	2	6.15E-05	NP_495931.2	46	53.5286	213	98	hypothetical protein T24B8.7
Locus_1461_Transcript_1/2_Conf_1.000	909	20	5.33E-30	NP_498126.1	73	135.961	137	101	hypothetical protein ZC395.10
Locus_1461_Transcript_2/2_Conf_1.000	894	20	5.17E-30	NP_498126.1	73	135.961	137	101	hypothetical protein ZC395.10
Locus_14610_Transcript_1/1_Conf_1.000	442	20	2.81E-28	XP_002643824.1	69	128.257	123	86	Hypothetical protein CBG02040
Locus_14611_Transcript_1/1_Conf_1.000	312	20	6.10E-23	XP_001902677.1	76	110.538	97	74	5'-nucleotidase, cytosolic III
Locus_14612_Transcript_1/1_Conf_1.000	427	0							
Locus_14613_Transcript_1/1_Conf_1.000	136	0							
Locus_14614_Transcript_1/1_Conf_1.000	143	20	4.99E-22	BAG61003.1	100	107.457	47	47	unnamed protein product
Locus_14615_Transcript_1/1_Conf_1.000	383	2	4.42E-26	XP_002631382.1	69	120.939	126	87	Hypothetical protein CBG03224
Locus_14616_Transcript_1/2_Conf_1.000	210	9	1.12E-05	XP_002634231.1	74	53.1434	47	35	C. briggsae CBR-TTR-45 protein
Locus_14616_Transcript_2/2_Conf_1.000	216	19	9.13E-08	XP_002634231.1	76	60.077	47	36	C. briggsae CBR-TTR-45 protein
Locus_14617_Transcript_1/1_Conf_1.000	388	0							
Locus_14618_Transcript_1/1_Conf_1.000	177	0							
Locus_14619_Transcript_1/1_Conf_1.000	310	20	3.72E-09	CAF95080.1	61	64.6994	91	56	unnamed protein product
Locus_1462_Transcript_1/1_Conf_1.000	1438	8	1.77E-85	ADM53747.1	62	321.242	339	213	Zinc finger transcription factor family protein 12, isoform c
Locus_14620_Transcript_1/2_Conf_1.000	404	20	1.17E-18	XP_002591927.1	58	96.2857	134	78	hypothetical protein BRAFLDRAFT_265245
Locus_14620_Transcript_2/2_Conf_1.000	404	20	1.17E-18	XP_002591927.1	58	96.2857	134	78	hypothetical protein BRAFLDRAFT_265245

Locus_14621_Transcript_1/1_Conf_1.000	170	20	5.41E-16	ABE91946.1	88	87.4261	53	47	Ras GTPase; Sigma-54 factor, interaction region
Locus_14622_Transcript_1/1_Conf_1.000	804	0							
Locus_14623_Transcript_1/1_Conf_1.000	554	0							
Locus_14624_Transcript_1/1_Conf_1.000	167	0							
Locus_14625_Transcript_1/1_Conf_1.000	439	20	5.62E-74	NP_501665.1	97	280.026	144	141	hypothetical protein F59B8.2
Locus_14626_Transcript_1/1_Conf_1.000	149	5	1.11E-16	NP_491711.2	87	89.7373	49	43	hypothetical protein C34G6.1
Locus_14627_Transcript_1/1_Conf_1.000	977	20	2.32E-74	AAV41897.1	65	283.493	319	210	SAX-2
Locus_14628_Transcript_1/1_Conf_1.000	524	0							
Locus_14629_Transcript_1/1_Conf_1.000	585	20	1.60E-33	NP_496652.1	73	146.362	134	98	Temporarily Assigned Gene name family member (tag-281)
Locus_1463_Transcript_1/1_Conf_1.000	2295	20	0	NP_510527.1	79	679.093	535	423	hypothetical protein H03A11.1
Locus_14630_Transcript_1/1_Conf_1.000	294	20	1.25E-36	CAB57358.1	85	155.992	95	81	microsomal aminopeptidase
Locus_14631_Transcript_1/1_Conf_1.000	184	0							
Locus_14632_Transcript_1/1_Conf_1.000	282	6	3.97E-14	NP_495914.1	68	81.2629	74	51	hypothetical protein C18E9.8
Locus_14633_Transcript_1/1_Conf_1.000	418	0							
Locus_14634_Transcript_1/1_Conf_1.000	232	4	3.19E-24	XP_002630898.1	91	114.775	62	57	Hypothetical protein CBG02620
Locus_14635_Transcript_1/1_Conf_1.000	328	2	1.42E-32	NP_504605.1	77	142.51	109	84	hypothetical protein K12B6.4
Locus_14636_Transcript_1/1_Conf_1.000	181	0							
Locus_14637_Transcript_1/1_Conf_1.000	306	0							
Locus_14638_Transcript_1/1_Conf_1.000	671	20	1.49E-82	CAC10528.1	80	309.686	227	182	putative inositol 1,4,5-trisphosphate receptor

Locus_14639_Transcript_1/1_Conf_1.000	189	0							
Locus_1464_Transcript_2/4_Conf_0.667	3362	1	7.52E-09	NP_509922.2	35	68.1662	600	214	hypothetical protein F29G6.3
Locus_1464_Transcript_3/4_Conf_0.250	2174	0							
Locus_1464_Transcript_4/4_Conf_0.667	3317	1	9.05E-07	NP_509922.2	35	61.2326	579	208	hypothetical protein F29G6.3
Locus_14640_Transcript_1/1_Conf_1.000	164	0							
Locus_14641_Transcript_1/1_Conf_1.000	226	0							
Locus_14642_Transcript_1/1_Conf_1.000	255	0							
Locus_14643_Transcript_1/1_Conf_1.000	512	0							
Locus_14644_Transcript_1/1_Conf_1.000	196	20	2.45E-16	NP_494786.4	93	88.5817	63	59	TWiK family of potassium channels family member (twk-2)
Locus_14645_Transcript_1/1_Conf_1.000	246	1	3.61E-04	NP_509416.2	71	48.1358	42	30	hypothetical protein F55E10.7
Locus_14646_Transcript_1/1_Conf_1.000	428	20	5.18E-67	XP_002634991.1	99	256.914	125	124	Hypothetical protein CBG13531
Locus_14647_Transcript_1/1_Conf_1.000	576	0							
Locus_14648_Transcript_1/1_Conf_1.000	548	20	4.22E-24	XP_002642540.1	88	114.775	76	67	Hypothetical protein CBG20163
Locus_14649_Transcript_1/1_Conf_1.000	254	5	2.03E-10	NP_508729.2	66	68.9366	80	53	hypothetical protein C52B9.4
Locus_1465_Transcript_1/1_Conf_1.000	2135	20	2.59E-174	NP_499577.1	67	617.076	682	458	hypothetical protein Y75B8A.4
Locus_14650_Transcript_1/1_Conf_1.000	776	20	6.76E-54	XP_002640868.1	79	214.927	157	125	Hypothetical protein CBG15759
Locus_14651_Transcript_1/1_Conf_1.000	1026	20	1.30E-78	NP_492757.2	79	297.745	239	189	ToLlIp homolog family member (tli-1)

Locus_14652_Transcript_1/1_Conf_1.000	378	20	2.12E-36	BAG58382.1	100	155.221	74	74	unnamed protein product
Locus_14653_Transcript_1/1_Conf_1.000	153	0							
Locus_14654_Transcript_1/1_Conf_1.000	627	20	8.02E-85	ACO11472.1	83	317.005	201	167	Beta-ureidopropionase
Locus_14655_Transcript_1/1_Conf_1.000	140	3	8.57E-06	XP_002640263.1	67	53.5286	46	31	Hypothetical protein CBG12788
Locus_14656_Transcript_1/1_Conf_1.000	446	20	1.86E-56	XP_001894541.1	83	221.861	148	124	LIM domain containing protein
Locus_14657_Transcript_1/1_Conf_1.000	427	0							
Locus_14658_Transcript_1/1_Conf_1.000	366	6	5.89E-23	XP_002633327.1	86	110.538	90	78	C. briggsae CBR-DNJ-1 protein
Locus_14659_Transcript_1/1_Conf_1.000	156	0							
Locus_1466_Transcript_1/1_Conf_1.000	383	0							
Locus_14660_Transcript_1/1_Conf_1.000	349	0							
Locus_14661_Transcript_1/1_Conf_1.000	436	20	1.30E-62	CAL49442.3	91	242.276	144	132	C. elegans protein F36H1.2c, partially confirmed by transcript evidence
Locus_14662_Transcript_1/1_Conf_1.000	534	20	1.43E-42	EFO22680.1	77	176.022	126	98	hypothetical protein LOAG_05804
Locus_14663_Transcript_1/1_Conf_1.000	190	0							
Locus_14664_Transcript_1/1_Conf_1.000	152	0							
Locus_14665_Transcript_1/1_Conf_1.000	160	0							
Locus_14666_Transcript_1/1_Conf_1.000	503	20	2.87E-73	XP_001892755.1	89	277.715	167	149	TBC domain containing protein
Locus_14667_Transcript_1/1_Conf_1.000	623	20	1.87E-56	CAB66478.1	100	180.644	91	91	hypothetical protein
Locus_14668_Transcript_1/1_Conf_1.000	319	0							
Locus_14669_Transcript_1/1_Conf_1.000	372	0							

Locus_1467_Transcript_1/3_Conf_0.714	3136	20	9.44E-99	EFO28201.1	61	366.696	472	292	hypothetical protein LOAG_00283
Locus_1467_Transcript_2/3_Conf_0.714	3142	20	9.46E-99	EFO28201.1	61	366.696	472	292	hypothetical protein LOAG_00283
Locus_1467_Transcript_3/3_Conf_0.714	3142	20	9.46E-99	EFO28201.1	61	366.696	472	292	hypothetical protein LOAG_00283
Locus_14670_Transcript_1/1_Conf_1.000	466	20	1.80E-51	NP_001023266.1	81	205.297	156	127	UNCoordinated family member (unc-26)
Locus_14671_Transcript_1/2_Conf_1.000	435	20	9.64E-66	XP_002633333.1	92	252.677	145	134	Hypothetical protein CBG06072
Locus_14671_Transcript_2/2_Conf_1.000	435	20	9.64E-66	XP_002633333.1	92	252.677	145	134	Hypothetical protein CBG06072
Locus_14672_Transcript_1/1_Conf_1.000	223	0							
Locus_14673_Transcript_1/1_Conf_1.000	381	0							
Locus_14674_Transcript_1/1_Conf_1.000	216	20	1.27E-33	XP_002913180.1	100	145.976	72	72	PREDICTED: cyclin-dependent kinase 2-associated protein 1-like
Locus_14675_Transcript_1/1_Conf_1.000	300	20	2.19E-33	XP_002822876.1	100	145.206	71	71	PREDICTED: protein C10-like isoform 2
Locus_14676_Transcript_1/1_Conf_1.000	671	20	2.37E-88	CAA91463.2	86	328.946	223	192	C. elegans protein F42E11.1a, partially confirmed by transcript evidence
Locus_14677_Transcript_1/1_Conf_1.000	291	20	1.39E-27	NP_493472.1	75	125.946	92	69	hypothetical protein C37A5.1
Locus_14678_Transcript_1/2_Conf_1.000	430	20	3.50E-23	XP_002631584.1	74	111.309	108	80	Hypothetical protein CBG20762
Locus_14678_Transcript_2/2_Conf_1.000	430	20	2.96E-22	XP_002631584.1	73	108.227	108	79	Hypothetical protein CBG20762
Locus_14679_Transcript_1/1_Conf_1.000	268	0							
Locus_1468_Transcript_1/1_Conf_1.000	1016	0							
Locus_14680_Transcript_1/1_Conf_1.000	181	0							

Locus_14681_Transcript_1/1_Conf_1.000	316	20	8.77E-22	BAE75796.1	70	106.686	98	69	Slc26a6 A
Locus_14682_Transcript_1/1_Conf_1.000	304	0							
Locus_14683_Transcript_1/1_Conf_1.000	169	0							
Locus_14684_Transcript_1/1_Conf_1.000	612	20	1.70E-92	XP_002644330.1	90	342.428	203	183	C. briggsae CBR-SPC-1 protein
Locus_14685_Transcript_1/1_Conf_1.000	177	9	8.00E-12	EFO23504.1	71	73.559	59	42	TK protein kinase
Locus_14686_Transcript_1/1_Conf_1.000	487	20	1.38E-51	NP_502547.2	73	205.682	170	125	hypothetical protein JC8.5
Locus_14687_Transcript_1/1_Conf_1.000	724	20	8.06E-19	EFN63743.1	49	98.2117	220	109	RCC1 domain-containing protein 1
Locus_14688_Transcript_1/1_Conf_1.000	603	20	2.23E-41	NP_001023110.1	64	172.555	197	128	Homolog Of ELAC2 (cancer susceptibility locus) family member (hoe-1)
Locus_14689_Transcript_1/1_Conf_1.000	272	0							
Locus_1469_Transcript_1/1_Conf_1.000	498	0							
Locus_14690_Transcript_1/1_Conf_1.000	175	0							
Locus_14691_Transcript_1/1_Conf_1.000	132	0							

Locus_14692_Transcript_1/1_Conf_1.000	1236	20	6.00E-124	XP_002643227.1	74	448.743	423	315	C. briggsae CBR-SEL-12 protein
Locus_14693_Transcript_1/1_Conf_1.000	222	0							
Locus_14694_Transcript_1/1_Conf_1.000	206	0							
Locus_14695_Transcript_1/1_Conf_1.000	865								
Locus_14696_Transcript_1/1_Conf_1.000	197	0							
Locus_14697_Transcript_1/1_Conf_1.000	179	0							
Locus_14698_Transcript_1/1_Conf_1.000	423	4	9.97E-10	NP_493393.1	57	66.6254	135	78	hypothetical protein W09C5.7
Locus_14699_Transcript_1/1_Conf_1.000	602	20	4.11E-72	NP_001122494.1	84	274.633	179	152	TOMosyn synaptic protein family member (tom-1)
Locus_147_Transcript_1/1_Conf_1.000	1067	20	5.14E-110	XP_002642221.1	86	402.134	251	216	Hypothetical protein CBG18195
Locus_1470_Transcript_1/3_Conf_0.500	529	0							
Locus_1470_Transcript_2/3_Conf_0.500	516	0							
Locus_1470_Transcript_3/3_Conf_0.667	516	0							
Locus_14700_Transcript_1/1_Conf_1.000	471	2	3.74E-25	XP_002642486.1	61	117.857	127	78	Hypothetical protein CBG06905
Locus_14701_Transcript_1/1_Conf_1.000	283	3	1.04E-14	NP_001024665.1	86	83.1889	53	46	SynDaPiN (synaptic dynamin binding protein) homolog family member (sdpn-1)
Locus_14702_Transcript_1/1_Conf_1.000	144	0							
Locus_14703_Transcript_1/1_Conf_1.000	400	0							

Locus_14704_Transcript_1/1_Conf_1.000	881	20	2.61E-95	XP_002642921.1	83	352.829	296	248	Hypothetical protein CBG15197
Locus_14705_Transcript_1/1_Conf_1.000	1243	20	3.17E-165	NP_499162.2	83	585.874	405	338	hypothetical protein R10E11.3
Locus_14706_Transcript_1/1_Conf_1.000	1024	20	1.04E-11	CBH12501.1	45	75.485	341	156	kinesin K39, putative
Locus_14707_Transcript_1/4_Conf_0.250	239	0							
Locus_14707_Transcript_2/4_Conf_0.625	1388	20	1.72E-29	XP_001897896.1	45	135.191	397	181	RNA binding motif protein 21
Locus_14707_Transcript_3/4_Conf_0.625	1399	20	1.02E-29	XP_001897896.1	45	135.961	401	183	RNA binding motif protein 21

Locus_14707_Transcript_4/4_Conf_0.625	1399	20	1.02E-29	XP_001897896.1	45	135.961	401	183	RNA binding motif protein 21
Locus_14708_Transcript_1/1_Conf_1.000	467	0							
Locus_14709_Transcript_1/1_Conf_1.000	570	3	1.59E-11	NP_494749.2	56	73.1738	88	50	hypothetical protein C16A11.7
Locus_1471_Transcript_1/1_Conf_1.000	3092	20	1.17E-133	CAA78521.1	74	482.641	523	388	hypothetical polypeptide II
Locus_14710_Transcript_1/1_Conf_1.000	143	0							
Locus_14711_Transcript_1/1_Conf_1.000	197	0							
Locus_14712_Transcript_1/1_Conf_1.000	353	0							
Locus_14713_Transcript_1/1_Conf_1.000	756	20	1.37E-96	NP_504476.1	87	356.681	224	197	Cell-death-Related Nuclease family member (crn-2)
Locus_14714_Transcript_1/1_Conf_1.000	605	0							
Locus_14715_Transcript_1/1_Conf_1.000	804	20	3.06E-60	XP_002639513.1	61	236.113	265	164	Hypothetical protein CBG04119
Locus_14716_Transcript_1/1_Conf_1.000	413	0							
Locus_14717_Transcript_1/1_Conf_1.000	1313	20	0	NP_001023732.1	93	780.015	433	406	EGg Laying defective family member (egl-3)
Locus_14718_Transcript_1/1_Conf_1.000	173	0							
Locus_14719_Transcript_1/1_Conf_1.000	453	20	2.94E-38	XP_002640798.1	77	161.384	109	85	C. briggsae CBR-NHR-121 protein
Locus_1472_Transcript_1/1_Conf_1.000	384	0							
Locus_14720_Transcript_1/1_Conf_1.000	307	0							
Locus_14721_Transcript_1/1_Conf_1.000	575	20	7.65E-54	XP_002113404.1	73	213.772	160	117	hypothetical protein TRIADDRAFT_57530
Locus_14722_Transcript_1/1_Conf_1.000	254	0							
Locus_14723_Transcript_1/1_Conf_1.000	238	0							
Locus_14724_Transcript_1/1_Conf_1.000	610	20	3.81E-20	EFO20693.1	55	102.064	167	93	hypothetical protein LOAG_07794
Locus_14725_Transcript_1/1_Conf_1.000	263	0							

Locus_14726_Transcript_1/1_Conf_1.000	359	20	2.96E-22	NP_001041045.1	63	108.227	119	76	COenzyme Q (ubiquinone) biosynthesis family member (coq-3)
Locus_14727_Transcript_1/1_Conf_1.000	1012	20	1.28E-139	NP_494712.1	94	500.36	313	297	proteasome Regulatory Particle, Non-ATPase-like family member (rpn-11)
Locus_14728_Transcript_1/1_Conf_1.000	413	0							
Locus_14729_Transcript_1/1_Conf_1.000	137	20	2.85E-17	XP_001103566.2	100	91.6633	45	45	PREDICTED: fas-activated serine/threonine kinase
Locus_1473_Transcript_1/1_Conf_1.000	945	20	2.50E-126	XP_002633756.1	83	456.062	301	252	C. briggsae CBR-DHP-2 protein
Locus_14730_Transcript_1/1_Conf_1.000	147	0							
Locus_14731_Transcript_1/1_Conf_1.000	271	0							
Locus_14732_Transcript_1/1_Conf_1.000	333	13	6.81E-11	NP_491252.1	64	70.4774	62	40	AntiBacterial Factor related family member (abf-2)
Locus_14733_Transcript_1/1_Conf_1.000	418	20	3.30E-53	NP_493616.1	83	211.075	139	116	hypothetical protein F33H2.5
Locus_14734_Transcript_1/2_Conf_1.000	740	20	7.79E-65	NP_501092.1	73	251.136	228	167	Conserved Oligomeric Golgi (COG) Component family member (cogc-2)

Locus_14734_Transcript_2/2_Conf_1.000	740	20	7.79E-65	NP_501092.1	73	251.136	228	167	Conserved Oligomeric Golgi (COG) Component family member (cogc-2)
Locus_14735_Transcript_1/1_Conf_1.000	613	0							
Locus_14736_Transcript_1/1_Conf_1.000	311	20	4.67E-28	EFO27919.1	92	127.487	76	70	hypothetical protein LOAG_00556
Locus_14737_Transcript_1/1_Conf_1.000	425	20	2.28E-30	XP_002637013.1	65	135.191	146	96	C. briggsae CBR-NID-1 protein
Locus_14738_Transcript_1/1_Conf_1.000	142	20	4.23E-13	XP_002645201.1	91	77.7962	46	42	C. briggsae CBR-BCAT-1 protein
Locus_14739_Transcript_1/1_Conf_1.000	307	0							
Locus_1474_Transcript_1/2_Conf_1.000	1463	0							
Locus_1474_Transcript_2/2_Conf_1.000	1433	0							
Locus_14740_Transcript_1/1_Conf_1.000	814	20	4.47E-59	EFO26681.1	64	232.261	278	179	glycosyl transferase
Locus_14741_Transcript_1/1_Conf_1.000	448	20	8.91E-43	NP_001021685.1	94	176.407	100	94	ZO-1 (Zonula Occludens tight junctional protein) Ortholog family member (zoo-1)
Locus_14742_Transcript_1/1_Conf_1.000	544	20	1.09E-24	ADI24640.1	59	116.701	175	104	Hypothetical protein C56E6.9
Locus_14743_Transcript_1/1_Conf_1.000	219	20	5.89E-26	EFO13953.1	91	120.553	72	66	hypothetical protein LOAG_14573
Locus_14744_Transcript_1/1_Conf_1.000	402	0							
Locus_14745_Transcript_1/1_Conf_1.000	298	0							
Locus_14746_Transcript_1/1_Conf_1.000	234	0							
Locus_14747_Transcript_1/1_Conf_1.000	193	0							
Locus_14748_Transcript_1/1_Conf_1.000	182	0							
Locus_14749_Transcript_1/1_Conf_1.000	141	0							

Locus_1475_Transcript_1/1_Conf_1.000	826	20	9.88E-70	EFO26807.1	81	267.7	202	164	wnt-4 protein
Locus_14750_Transcript_1/1_Conf_1.000	261	0							
Locus_14751_Transcript_1/1_Conf_1.000	666	0							
Locus_14752_Transcript_1/1_Conf_1.000	281	2	8.57E-06	XP_002645909.1	64	53.5286	51	33	Hypothetical protein CBG07665
Locus_14753_Transcript_1/1_Conf_1.000	173	20	1.28E-25	ADM64582.1	100	119.398	56	56	ribosomal protein L27
Locus_14754_Transcript_1/1_Conf_1.000	177	0							
Locus_14755_Transcript_1/2_Conf_1.000	265	0							
Locus_14755_Transcript_2/2_Conf_1.000	265	0							
Locus_14756_Transcript_1/1_Conf_1.000	412	10	1.23E-28	NP_001123020.1	69	129.413	105	73	hypothetical protein T23B12.8
Locus_14757_Transcript_1/2_Conf_1.000	426	20	1.17E-18	EFO16664.1	53	96.2857	183	98	lenep protein
Locus_14757_Transcript_2/2_Conf_1.000	339	20	3.58E-20	XP_002629740.1	66	101.293	106	71	Hypothetical protein CBG00973
Locus_14758_Transcript_1/1_Conf_1.000	302	20	6.35E-41	NP_509597.1	91	170.244	100	91	GTPase Activating Protein family member (gap-2)

Locus_14759_Transcript_1/1_Conf_1.000	1202	20	4.81E-155	NP_495846.1	83	551.977	369	307	hypothetical protein C34C6.4
Locus_1476_Transcript_1/2_Conf_1.000	1330	0							
Locus_1476_Transcript_2/2_Conf_1.000	1330	0							
Locus_14760_Transcript_1/2_Conf_1.000	247	0							
Locus_14760_Transcript_2/2_Conf_1.000	360	0							
Locus_14761_Transcript_1/1_Conf_1.000	423	20	1.86E-40	NP_492533.2	74	168.703	136	101	IRoquois subclass of homeoboX family member (irx-1)
Locus_14762_Transcript_1/1_Conf_1.000	285	0							
Locus_14763_Transcript_1/1_Conf_1.000	651	20	5.29E-21	XP_002740067.1	58	105.145	140	82	PREDICTED: RETRotransposon-like family member (retr-1)-like, partial
Locus_14764_Transcript_1/1_Conf_1.000	356	20	7.04E-40	Q5K2C1.1	88	166.777	109	96	Alpha,alpha-trehalose-phosphate synthase UDP-forming 2
Locus_14765_Transcript_1/1_Conf_1.000	236	2	8.68E-14	XP_002647167.1	69	80.1073	78	54	Hypothetical protein CBG22317
Locus_14766_Transcript_1/2_Conf_1.000	517	4	1.29E-26	NP_506375.1	71	122.865	116	83	hypothetical protein F53F4.11
Locus_14766_Transcript_2/2_Conf_1.000	517	4	1.29E-26	NP_506375.1	71	122.865	116	83	hypothetical protein F53F4.11
Locus_14767_Transcript_1/1_Conf_1.000	677	0							
Locus_14768_Transcript_1/1_Conf_1.000	144	0							
Locus_14769_Transcript_1/1_Conf_1.000	590	20	9.54E-71	NP_001041018.1	80	270.011	196	158	hypothetical protein Y11D7A.3

Locus_1477_Transcript_1/3_Conf_0.714	3328	20	0	XP_002635268.1	69	780.015	789	547	Hypothetical protein CBG11512
Locus_1477_Transcript_2/3_Conf_0.714	3352	20	0	XP_002635268.1	70	778.474	790	556	Hypothetical protein CBG11512
Locus_1477_Transcript_3/3_Conf_0.714	3334	20	0	XP_002635268.1	69	781.556	790	548	Hypothetical protein CBG11512
Locus_14770_Transcript_1/1_Conf_1.000	536	20	2.21E-35	EFO24456.1	79	152.14	102	81	hypothetical protein LOAG_04032
Locus_14771_Transcript_1/1_Conf_1.000	228	11	1.03E-06	NP_001020992.1	76	56.6102	42	32	hypothetical protein C09D4.1

Locus_14772_Transcript_1/1_Conf_1.000	231	20	8.38E-33	NP_500265.2	93	143.28	76	71	hypothetical protein Y54G2A.17
Locus_14773_Transcript_1/1_Conf_1.000	214	0							
Locus_14774_Transcript_1/2_Conf_1.000	618	20	3.76E-95	NP_508927.2	85	351.288	218	187	DihydroPYrimidine Dehydrogenase family member (dpyd-1)
Locus_14774_Transcript_2/2_Conf_1.000	618	20	1.43E-94	NP_508927.2	85	349.362	218	187	DihydroPYrimidine Dehydrogenase family member (dpyd-1)
Locus_14775_Transcript_1/2_Conf_1.000	492	0							
Locus_14775_Transcript_2/2_Conf_1.000	479	0							
Locus_14776_Transcript_1/1_Conf_1.000	414	20	3.10E-56	XP_002642176.1	87	221.09	137	120	Hypothetical protein CBG18143
Locus_14777_Transcript_1/1_Conf_1.000	401	5	3.09E-19	NP_492332.1	64	98.2117	91	59	hypothetical protein F43G9.4
Locus_14778_Transcript_1/1_Conf_1.000	583	0							
Locus_14779_Transcript_1/1_Conf_1.000	527	0							
Locus_1478_Transcript_1/2_Conf_1.000	1381	20	1.25E-88	NP_001016570.1	66	331.643	322	213	aurora kinase A

Locus_1478_Transcript_2/2_Conf_1.000	1324	20	3.90E-92	NP_001081565.1	72	343.199	290	209	serine/threonine-protein kinase 6
Locus_14780_Transcript_1/1_Conf_1.000	927	2	6.57E-07	NP_502860.2	42	59.3066	185	78	hypothetical protein Y73F8A.25
Locus_14781_Transcript_1/1_Conf_1.000	493	0							
Locus_14782_Transcript_1/1_Conf_1.000	234	20	5.44E-16	AAK29933.3	71	87.4261	76	54	Rab connectin related protein 2, partially confirmed by transcript evidence
Locus_14783_Transcript_1/1_Conf_1.000	353	20	6.19E-36	XP_002646888.1	75	153.68	123	93	C. briggsae CBR-PTC-3 protein
Locus_14784_Transcript_1/1_Conf_1.000	250	20	1.40E-40	BAI45831.1	100	169.088	83	83	lipolysis stimulated lipoprotein receptor
Locus_14785_Transcript_1/1_Conf_1.000	186	0							
Locus_14786_Transcript_1/1_Conf_1.000	249	0							
Locus_14787_Transcript_1/1_Conf_1.000	169	0							
Locus_14788_Transcript_1/1_Conf_1.000	406	0							
Locus_14789_Transcript_1/1_Conf_1.000	658	0							
Locus_1479_Transcript_1/1_Conf_1.000	651	0							
Locus_14790_Transcript_1/1_Conf_1.000	357	20	6.98E-56	ACZ54691.1	96	219.935	118	114	Uncoordinated protein 82, isoform f
Locus_14791_Transcript_1/1_Conf_1.000	222	0							
Locus_14792_Transcript_1/1_Conf_1.000	640	19	4.40E-33	XP_002631813.1	54	145.206	208	114	Hypothetical protein CBG21034
Locus_14793_Transcript_1/1_Conf_1.000	1754	20	8.87E-138	NP_740853.2	79	495.352	435	347	TOMosyn synaptic protein family member (tom-1)
Locus_14794_Transcript_1/1_Conf_1.000	521	4	1.51E-30	XP_002631397.1	63	135.961	150	95	C. briggsae CBR-DEP-1 protein
Locus_14795_Transcript_1/1_Conf_1.000	222	0							
Locus_14796_Transcript_1/1_Conf_1.000	220	0							
Locus_14797_Transcript_1/1_Conf_1.000	496	0							

Locus_14798_Transcript_1/1_Conf_1.000	673	20	1.48E-37	XP_002629759.1	59	160.229	223	133	Hypothetical protein CBG00995
Locus_14799_Transcript_1/1_Conf_1.000	273	5	2.43E-08	XP_002634384.1	52	62.003	88	46	C. briggsae CBR-ELPC-4 protein
Locus_148_Transcript_1/4_Conf_0.545	557	0							
Locus_148_Transcript_2/4_Conf_0.545	553	0							
Locus_148_Transcript_3/4_Conf_0.545	359	0							
Locus_148_Transcript_4/4_Conf_0.545	563	0							
Locus_1480_Transcript_1/1_Conf_1.000	1606	20	0	NP_496376.1	94	885.174	474	447	NADH Ubiquinone Oxidoreductase family member (nuo-1)
Locus_14800_Transcript_1/1_Conf_1.000	258	20	1.94E-29	EFO25600.1	100	132.109	66	66	beige/BEACH domain-containing protein
Locus_14801_Transcript_1/1_Conf_1.000	1658	20	2.37E-84	NP_503398.1	62	317.775	452	281	hypothetical protein C39F7.5
Locus_14802_Transcript_1/2_Conf_1.000	1197	20	4.94E-168	AAV68383.1	85	595.119	391	335	antigen h11
Locus_14802_Transcript_2/2_Conf_1.000	1090	20	2.00E-157	CAB57358.1	86	559.681	355	307	microsomal aminopeptidase
Locus_14803_Transcript_1/1_Conf_1.000	1065	20	5.00E-89	NP_001022488.1	62	332.413	370	230	UNCoordinated family member (unc-52)
Locus_14804_Transcript_1/1_Conf_1.000	545	20	1.98E-34	EFO15307.1	72	149.058	133	97	hypothetical protein LOAG_13207
Locus_14805_Transcript_1/1_Conf_1.000	278	0							
Locus_14806_Transcript_1/1_Conf_1.000	205	0							
Locus_14807_Transcript_1/1_Conf_1.000	422	4	1.45E-08	NP_493601.2	54	62.7734	75	41	FERM domain (protein4.1-ezrin-radixin-moesin) family member (frm-1)
Locus_14808_Transcript_1/1_Conf_1.000	187	0							
Locus_14809_Transcript_1/2_Conf_1.000	180	0							
Locus_14809_Transcript_2/2_Conf_1.000	309	0							
Locus_1481_Transcript_1/1_Conf_1.000	400	7	5.06E-46	NP_501821.2	84	187.193	132	111	hypothetical protein T04B2.5
Locus_14810_Transcript_1/3_Conf_0.667	634	20	2.18E-61	CAA22108.2	75	239.195	213	161	C. elegans protein Y75B8A.24, partially confirmed by transcript evidence

Locus_14810_Transcript_2/3_Conf_0.500	962	20	9.12E-92	XP_002647048.1	75	341.273	325	244	Hypothetical protein CBG03566
Locus_14810_Transcript_3/3_Conf_0.667	1108	20	1.30E-111	XP_002647048.1	75	407.527	374	283	Hypothetical protein CBG03566
Locus_14811_Transcript_1/1_Conf_1.000	395	20	1.35E-38	NP_001023370.1	71	162.54	130	93	ALP/Enigma encoding family member (alp-1)
Locus_14812_Transcript_1/1_Conf_1.000	285	0							
Locus_14813_Transcript_1/1_Conf_1.000	185	2	3.37E-05	NP_497903.1	62	51.6026	59	37	anNEXin family member (nex-3)
Locus_14814_Transcript_1/1_Conf_1.000	574	0							
Locus_14815_Transcript_1/1_Conf_1.000	175	19	9.49E-13	XP_002636796.1	75	76.6406	57	43	C. briggsae CBR-RIL-2 protein
Locus_14816_Transcript_1/1_Conf_1.000	592	20	1.72E-43	EFN62425.1	80	179.489	125	101	Nuclear factor 1 A-type
Locus_14817_Transcript_1/1_Conf_1.000	741	0							
Locus_14818_Transcript_1/1_Conf_1.000	222	0							
Locus_14819_Transcript_1/1_Conf_1.000	206	4	6.41E-09	XP_001892631.1	83	63.929	65	54	hypothetical protein Bm1_05795
Locus_1482_Transcript_1/1_Conf_1.000	919	20	5.63E-19	EFO24485.1	76	99.3673	84	64	hypothetical protein LOAG_03999
Locus_14820_Transcript_1/1_Conf_1.000	616	20	1.13E-51	XP_002630011.1	79	206.838	179	142	Hypothetical protein CBG13376
Locus_14821_Transcript_1/1_Conf_1.000	269	20	1.33E-30	XP_002644858.1	81	135.961	86	70	Hypothetical protein CBG05031
Locus_14822_Transcript_1/1_Conf_1.000	144	0							
Locus_14823_Transcript_1/1_Conf_1.000	625	20	1.08E-41	EFO25741.1	75	173.711	150	113	hypothetical protein LOAG_02746
Locus_14824_Transcript_1/1_Conf_1.000	614	20	9.80E-32	NP_001041088.1	57	140.584	194	111	hypothetical protein C27A7.3

Locus_14825_Transcript_1/1_Conf_1.000	638	20	2.01E-46	NP_741492.1	64	189.504	214	139	hypothetical protein T12G3.8
Locus_14826_Transcript_1/1_Conf_1.000	454	20	2.31E-59	NP_498636.2	84	231.491	151	128	hypothetical protein T20B12.1
Locus_14827_Transcript_1/1_Conf_1.000	519	0							
Locus_14828_Transcript_1/1_Conf_1.000	357	20	1.08E-32	XP_002630470.1	73	142.895	116	85	Hypothetical protein CBG11204
Locus_14829_Transcript_1/1_Conf_1.000	193	0							
Locus_1483_Transcript_1/2_Conf_1.000	1709	20	7.27E-36	NP_001021928.1	60	156.762	264	160	Maternal Effect Lethal family member (mel-11)
Locus_1483_Transcript_2/2_Conf_1.000	1442	20	1.30E-19	NP_001021929.1	63	102.449	166	105	Maternal Effect Lethal family member (mel-11)
Locus_14830_Transcript_1/1_Conf_1.000	154	0							
Locus_14831_Transcript_1/1_Conf_1.000	154	0							
Locus_14832_Transcript_1/1_Conf_1.000	266	0							
Locus_14833_Transcript_1/1_Conf_1.000	720	20	1.11E-44	EFO25648.1	63	184.111	209	133	platelet-activating factor acetylhydrolase
Locus_14834_Transcript_1/1_Conf_1.000	471	20	3.75E-17	XP_001896547.1	64	91.2781	102	66	Transcription factor TFIIB repeat family protein
Locus_14835_Transcript_1/1_Conf_1.000	142	3	2.17E-09	XP_002631490.1	77	65.4698	45	35	C. briggsae CBR-EGG-3 protein
Locus_14836_Transcript_1/1_Conf_1.000	194	0							
Locus_14837_Transcript_1/1_Conf_1.000	193	0							
Locus_14838_Transcript_1/1_Conf_1.000	306	20	1.61E-20	NP_510072.1	69	102.449	99	69	hypothetical protein F42F12.4

Locus_14839_Transcript_1/2_Conf_1.000	605	20	2.35E-91	XP_002643185.1	97	338.576	168	164	Hypothetical protein CBG24154
Locus_14839_Transcript_2/2_Conf_1.000	501	20	3.17E-72	EFO25025.1	98	274.248	133	131	NADH-ubiquinone oxidoreductase 23 kDa subunit
Locus_1484_Transcript_1/1_Conf_1.000	1577	20	2.28E-89	NP_001022864.1	68	334.339	363	250	hypothetical protein Y42G9A.3
Locus_14840_Transcript_1/2_Conf_1.000	386	20	6.39E-09	XP_641859.1	53	63.929	128	69	hypothetical protein DDB_G0279091
Locus_14840_Transcript_2/2_Conf_1.000	212	0							
Locus_14841_Transcript_1/1_Conf_1.000	251	0							
Locus_14842_Transcript_1/1_Conf_1.000	366	13	3.31E-35	XP_849940.1	96	128.642	65	63	PREDICTED: similar to Small EDRK-rich factor 2 (4F5rel) isoform 2
Locus_14843_Transcript_1/1_Conf_1.000	310	0							
Locus_14844_Transcript_1/1_Conf_1.000	139	0							
Locus_14845_Transcript_1/1_Conf_1.000	399	20	2.79E-28	XP_002548749.1	83	128.257	101	84	ADP-ribosylation factor

Locus_14846_Transcript_1/2_Conf_1.000	478	20	7.46E-34	CAD56609.2	66	146.747	142	94	C. elegans protein Y39A1A.5, confirmed by transcript evidence
Locus_14846_Transcript_2/2_Conf_1.000	478	20	7.46E-34	CAD56609.2	66	146.747	142	94	C. elegans protein Y39A1A.5, confirmed by transcript evidence
Locus_14847_Transcript_1/1_Conf_1.000	532	0							
Locus_14848_Transcript_1/1_Conf_1.000	267	0							
Locus_14849_Transcript_1/1_Conf_1.000	134	0							
Locus_1485_Transcript_1/1_Conf_1.000	483	20	2.13E-52	NP_495985.1	84	208.379	152	129	Temporarily Assigned Gene name family member (tag-175)
Locus_14850_Transcript_1/1_Conf_1.000	555	20	2.41E-70	XP_002633243.1	95	268.47	141	135	Hypothetical protein CBG05964
Locus_14851_Transcript_1/1_Conf_1.000	154	0							
Locus_14852_Transcript_1/1_Conf_1.000	1020	20	2.27E-75	EFA02360.1	62	286.96	378	238	hypothetical protein TcasGA2_TC008035
Locus_14853_Transcript_1/1_Conf_1.000	353	20	1.38E-27	XP_002647028.1	76	125.946	115	88	C. briggsae CBR-EMB-8 protein
Locus_14854_Transcript_1/1_Conf_1.000	175	0							
Locus_14855_Transcript_1/1_Conf_1.000	207	5	4.14E-08	XP_002641493.1	86	61.2326	38	33	Hypothetical protein CBG09784

Locus_14856_Transcript_1/1_Conf_1.000	615	20	4.91E-47	XP_001899238.1	60	191.43	208	126	Low-density lipoprotein receptor repeat class B containing protein
Locus_14857_Transcript_1/1_Conf_1.000	296	0							
Locus_14858_Transcript_1/1_Conf_1.000	317	2	5.17E-06	XP_002642239.1	57	54.299	71	41	Hypothetical protein CBG18221
Locus_14859_Transcript_1/1_Conf_1.000	232	0							
Locus_1486_Transcript_1/3_Conf_0.667	1060	20	6.71E-78	EFO24879.1	67	295.434	325	218	hypothetical protein LOAG_03607
Locus_1486_Transcript_2/3_Conf_0.667	1134	20	9.79E-78	EFO24879.1	67	295.049	325	218	hypothetical protein LOAG_03607
Locus_1486_Transcript_3/3_Conf_0.667	1060	20	8.77E-78	EFO24879.1	67	295.049	325	218	hypothetical protein LOAG_03607
Locus_14860_Transcript_1/1_Conf_1.000	1048	20	1.52E-82	ACF74367.1	66	310.842	364	243	Hypothetical protein R13F6.4d
Locus_14861_Transcript_1/1_Conf_1.000	163	0							
Locus_14862_Transcript_1/1_Conf_1.000	254	11	2.17E-20	NP_001122684.1	76	102.064	76	58	UNCoordinated family member (unc-103)
Locus_14863_Transcript_1/1_Conf_1.000	154	0							
Locus_14864_Transcript_1/1_Conf_1.000	230	20	4.17E-32	XP_002638742.1	94	140.969	76	72	C. briggsae CBR-PDE-6 protein
Locus_14865_Transcript_1/1_Conf_1.000	132	0							
Locus_14866_Transcript_1/1_Conf_1.000	517	20	1.48E-30	NP_510020.2	69	135.961	141	98	hypothetical protein W03G11.3
Locus_14867_Transcript_1/1_Conf_1.000	179	0							
Locus_14868_Transcript_1/1_Conf_1.000	257	4	8.80E-14	EFO27378.1	76	80.1073	64	49	hypothetical protein LOAG_01103
Locus_14869_Transcript_1/1_Conf_1.000	140	0							
Locus_1487_Transcript_1/1_Conf_1.000	227	0							

Locus_14870_Transcript_1/1_Conf_1.000	140	16	1.37E-11	AAP36667.1	100	72.7886	36	36	Homo sapiens vesicle-associated membrane protein 8 (endobrevin)
Locus_14871_Transcript_1/1_Conf_1.000	665	0							
Locus_14872_Transcript_1/1_Conf_1.000	288	0							
Locus_14873_Transcript_1/1_Conf_1.000	144	1	2.57E-21	EAX03766.1	100	105.145	47	47	high mobility group AT-hook 1, isoform CRA_e
Locus_14874_Transcript_1/1_Conf_1.000	754	20	7.31E-42	CAA90662.2	62	174.866	205	129	C. elegans protein R166.1, partially confirmed by transcript evidence
Locus_14875_Transcript_1/1_Conf_1.000	169	3	1.58E-07	XP_002642375.1	70	59.3066	50	35	Hypothetical protein CBG18379
Locus_14876_Transcript_1/1_Conf_1.000	228	0							
Locus_14877_Transcript_1/1_Conf_1.000	147	0							
Locus_14878_Transcript_1/1_Conf_1.000	280	3	2.40E-16	NP_740874.1	81	88.5817	55	45	hypothetical protein F57B10.14
Locus_14879_Transcript_1/1_Conf_1.000	413	20	1.72E-30	NP_503523.2	73	135.576	126	93	hypothetical protein Y32G9A.8
Locus_1488_Transcript_1/1_Conf_1.000	1213	20	4.78E-118	NP_492517.2	86	429.098	322	279	STomatin-Like family member (stl-1)

Locus_14880_Transcript_1/1_Conf_1.000	212	20	1.73E-14	EFO26533.1	81	82.4185	58	47	hypothetical protein LOAG_01953
Locus_14881_Transcript_1/1_Conf_1.000	274	2	3.74E-09	NP_492101.1	61	64.6994	89	55	hypothetical protein T28F4.4
Locus_14882_Transcript_1/1_Conf_1.000	189	2	2.39E-19	NP_503543.1	85	98.5969	63	54	hypothetical protein T08B1.1
Locus_14883_Transcript_1/1_Conf_1.000	139	0							
Locus_14884_Transcript_1/1_Conf_1.000	359	0							
Locus_14885_Transcript_1/2_Conf_1.000	641	20	1.88E-84	EFO20001.1	84	315.849	213	181	Sel1l protein
Locus_14885_Transcript_2/2_Conf_1.000	641	20	1.88E-84	EFO20001.1	84	315.849	213	181	Sel1l protein
Locus_14886_Transcript_1/1_Conf_1.000	235	0							
Locus_14887_Transcript_1/1_Conf_1.000	256	20	7.41E-29	XP_002810117.1	100	130.183	73	73	PREDICTED: keratinocyte-associated protein 2-like isoform 1
Locus_14888_Transcript_1/1_Conf_1.000	134	0							
Locus_14889_Transcript_1/1_Conf_1.000	328	2	6.86E-11	NP_509148.2	86	70.4774	45	39	hypothetical protein F41B4.1
Locus_1489_Transcript_1/1_Conf_1.000	552	20	3.32E-56	EFO21483.1	81	221.476	155	126	inner mitochondrial membrane protease family member
Locus_14890_Transcript_1/1_Conf_1.000	295	0							
Locus_14891_Transcript_1/1_Conf_1.000	138	0							
Locus_14892_Transcript_1/1_Conf_1.000	243	20	3.36E-26	EFO16124.1	84	121.324	79	67	protein-tyrosine phosphatase
Locus_14893_Transcript_1/1_Conf_1.000	466								
Locus_14894_Transcript_1/1_Conf_1.000	745	20	7.59E-100	ACY40006.1	86	367.466	250	217	K+/cl- cotransporter protein 2, isoform a
Locus_14895_Transcript_1/1_Conf_1.000	197	0							

Locus_14896_Transcript_1/1_Conf_1.000	236	2	4.31E-13	NP_501715.1	74	77.7962	77	57	Acetylcholine-gated Chloride Channel family member (acc-1)
Locus_14897_Transcript_1/1_Conf_1.000	222	2	5.90E-10	NP_508526.2	81	67.3958	43	35	TWiK family of potassium channels family member (twk-16)
Locus_14898_Transcript_1/1_Conf_1.000	384	20	3.84E-38	CAA88959.2	75	160.999	119	90	C. elegans protein M03C11.2, partially confirmed by transcript evidence
Locus_14899_Transcript_1/2_Conf_1.000	584	0							
Locus_14899_Transcript_2/2_Conf_1.000	432	0							
Locus_149_Transcript_1/1_Conf_1.000	747	20	3.16E-45	XP_001896912.1	70	186.037	189	134	hypothetical protein
Locus_1490_Transcript_1/2_Conf_1.000	2340	7	2.01E-34	NP_001122680.1	57	152.525	190	109	hypothetical protein C29E4.13
Locus_1490_Transcript_2/2_Conf_1.000	2340	7	2.01E-34	NP_001122680.1	57	152.525	190	109	hypothetical protein C29E4.13
Locus_14900_Transcript_1/1_Conf_1.000	422	0							
Locus_14901_Transcript_1/1_Conf_1.000	205	4	1.74E-06	XP_001894167.1	75	55.8398	48	36	Rad9 family protein
Locus_14902_Transcript_1/1_Conf_1.000	176	0							
Locus_14903_Transcript_1/1_Conf_1.000	321	0							
Locus_14904_Transcript_1/1_Conf_1.000	185	0							
Locus_14905_Transcript_1/2_Conf_1.000	246	0							
Locus_14905_Transcript_2/2_Conf_1.000	255	0							
Locus_14906_Transcript_1/1_Conf_1.000	403	0							
Locus_14907_Transcript_1/1_Conf_1.000	144	20	2.49E-16	NP_499865.1	93	88.5817	48	45	hypothetical protein F29C4.6
Locus_14908_Transcript_1/1_Conf_1.000	507	0							
Locus_14909_Transcript_1/1_Conf_1.000	262	20	1.48E-29	NP_496100.1	87	132.494	87	76	hypothetical protein Y53C12B.1

Locus_1491_Transcript_1/2_Conf_1.000	286	20	6.74E-14	NP_501767.1	77	80.4925	66	51	Sperm-Specific family, class P family member (ssp-10)
Locus_1491_Transcript_2/2_Conf_1.000	284	20	6.76E-14	NP_501767.1	77	80.4925	66	51	Sperm-Specific family, class P family member (ssp-10)
Locus_14910_Transcript_1/1_Conf_1.000	227	0							
Locus_14911_Transcript_1/1_Conf_1.000	405	0							
Locus_14912_Transcript_1/1_Conf_1.000	230	0							
Locus_14913_Transcript_1/1_Conf_1.000	136	0							
Locus_14914_Transcript_1/1_Conf_1.000	330	20	2.04E-31	NP_001022715.1	87	138.658	109	95	ALIX (Apoptosis-linked gene 2 interacting protein X) homolog family member (alx-1)
Locus_14915_Transcript_1/1_Conf_1.000	349	0							
Locus_14916_Transcript_1/1_Conf_1.000	827	3	2.67E-91	CAR63525.1	78	339.347	265	207	hypothetical protein
Locus_14917_Transcript_1/1_Conf_1.000	514	0							
Locus_14918_Transcript_1/1_Conf_1.000	518	0							
Locus_14919_Transcript_1/1_Conf_1.000	289	20	4.33E-29	XP_002920245.1	100	130.954	61	61	PREDICTED: STIP1 homology and U box-containing protein 1-like
Locus_1492_Transcript_1/1_Conf_1.000	657	20	9.15E-53	NP_001040786.1	66	210.69	218	144	RNase H family member (rnh-1.0)

Locus_14920_Transcript_1/1_Conf_1.000	168	9	7.55E-18	ACI49073.1	92	93.5893	52	48	hypothetical protein Cbre_JD10.005
Locus_14921_Transcript_1/1_Conf_1.000	293	1	4.35E-05	NP_498089.2	48	51.2174	110	53	hypothetical protein Y54H5A.2
Locus_14922_Transcript_1/1_Conf_1.000	469	20	7.09E-24	NP_496299.1	64	113.62	117	75	beta-LACTamase domain containing family member (lact-3)
Locus_14923_Transcript_1/1_Conf_1.000	618	20	3.78E-71	EFO14607.1	78	271.552	205	160	TRE-2 protein
Locus_14924_Transcript_1/1_Conf_1.000	788	20	1.70E-84	EFO16211.1	73	316.62	261	193	oxidoreductase
Locus_14925_Transcript_1/1_Conf_1.000	680	2	3.62E-07	NP_502401.1	50	59.3066	136	69	HSN Abnormal Migration family member (ham-1)
Locus_14926_Transcript_1/1_Conf_1.000	362	20	1.78E-43	XP_002631054.1	89	178.718	107	96	C. briggsae CBR-BTF-1 protein
Locus_14927_Transcript_1/1_Conf_1.000	299	2	4.60E-15	NP_498014.2	64	84.3445	90	58	COenzyme Q (ubiquinone) biosynthesis family member (coq-8)
Locus_14928_Transcript_1/1_Conf_1.000	595	20	1.13E-42	XP_002647701.1	65	176.792	201	131	Hypothetical protein CBG17890
Locus_14929_Transcript_1/2_Conf_1.000	323	0							
Locus_14929_Transcript_2/2_Conf_1.000	323	0							
Locus_1493_Transcript_1/1_Conf_1.000	1584	20	2.64E-77	XP_002647056.1	55	294.278	454	250	Hypothetical protein CBG03577
Locus_14930_Transcript_1/1_Conf_1.000	144	20	7.74E-18	XP_002815470.1	100	93.5893	47	47	PREDICTED: t-complex protein 1 subunit epsilon-like
Locus_14931_Transcript_1/1_Conf_1.000	662	20	2.08E-81	CAD44515.1	84	305.834	220	186	VAB-10A protein
Locus_14932_Transcript_1/1_Conf_1.000	217	0							
Locus_14933_Transcript_1/1_Conf_1.000	437	5	8.28E-17	XP_002642061.1	65	90.1225	137	90	Hypothetical protein CBG17999
Locus_14934_Transcript_1/1_Conf_1.000	142	0							
Locus_14935_Transcript_1/1_Conf_1.000	303	0							
Locus_14936_Transcript_1/1_Conf_1.000	354	11	2.00E-10	EFO17518.1	56	68.9366	96	54	hypothetical protein LOAG_10981
Locus_14937_Transcript_1/1_Conf_1.000	215	1	1.62E-04	EFO24319.1	67	49.2914	49	33	hypothetical protein LOAG_04165

Locus_14938_Transcript_1/1_Conf_1.000	443	20	7.17E-16	EFO24199.1	57	87.0409	108	62	hypothetical protein LOAG_04289
Locus_14939_Transcript_1/1_Conf_1.000	322	2	3.00E-14	NP_491418.1	68	81.6481	74	51	hypothetical protein B0041.5
Locus_1494_Transcript_1/4_Conf_0.444	946	20	2.32E-31	XP_001896932.1	80	140.584	105	85	PDZ domain containing protein
Locus_1494_Transcript_2/4_Conf_0.444	1817	20	0	CAP24558.1	89	716.457	419	376	C. briggsae CBR-LIN-53 protein
Locus_1494_Transcript_3/4_Conf_0.333	1078	20	1.01E-31	EFO21602.1	79	132.494	107	85	hypothetical protein LOAG_06884

Locus_1494_Transcript_4/4_Conf_0.444	1817	20	0	CAP24558.1	89	716.457	419	376	C. briggsae CBR-LIN-53 protein
Locus_14940_Transcript_1/1_Conf_1.000	462	0							
Locus_14941_Transcript_1/1_Conf_1.000	277	0							
Locus_14942_Transcript_1/1_Conf_1.000	1104	7	6.14E-45	NP_493565.1	58	186.037	284	167	hypothetical protein K05C4.7
Locus_14943_Transcript_1/1_Conf_1.000	312	5	1.12E-08	NP_506662.1	54	63.1586	98	53	hypothetical protein ZC412.3
Locus_14944_Transcript_1/1_Conf_1.000	710	20	9.22E-81	NP_492436.1	78	303.908	241	189	hypothetical protein W06D4.4
Locus_14945_Transcript_1/1_Conf_1.000	566	20	2.99E-15	XP_002633158.1	86	85.5001	46	40	C. briggsae CBR-UNC-82 protein
Locus_14946_Transcript_1/1_Conf_1.000	297	4	5.99E-23	NP_741662.1	68	110.538	99	68	TRNA Guanine Transglycosylase family member (tgt-2)
Locus_14947_Transcript_1/1_Conf_1.000	170	0							
Locus_14948_Transcript_1/1_Conf_1.000	767	20	3.05E-67	NP_001021875.1	68	259.225	257	177	Leucyl tRNA Synthetase family member (lrs-2)

Locus_14949_Transcript_1/1_Conf_1.000	727	20	5.12E-05	XP_001950365.1	45	52.373	139	63	PREDICTED: similar to IRA1 protein
Locus_1495_Transcript_1/1_Conf_1.000	293	6	1.18E-18	CAD44516.1	74	96.2857	81	60	VAB-10B protein
Locus_14950_Transcript_1/1_Conf_1.000	612	20	9.71E-64	NP_001021995.1	77	246.899	181	140	hypothetical protein C27D6.11
Locus_14951_Transcript_1/1_Conf_1.000	679	20	2.11E-39	NP_495410.4	58	166.392	234	138	hypothetical protein C44B7.11
Locus_14952_Transcript_1/1_Conf_1.000	545	20	5.98E-23	XP_002641267.1	62	110.923	141	88	Hypothetical protein CBG05179
Locus_14953_Transcript_1/1_Conf_1.000	289	5	1.95E-21	NP_498783.1	72	105.531	91	66	hypothetical protein C50C3.7
Locus_14954_Transcript_1/1_Conf_1.000	188	20	6.29E-28	XP_002923753.1	100	127.102	62	62	PREDICTED: rRNA 2'-O-methyltransferase fibrillarin-like
Locus_14955_Transcript_1/1_Conf_1.000	195	16	6.90E-19	NP_500647.2	82	97.0561	64	53	Dipeptidyl Peptidase Four (IV) family member (dpf-5)
Locus_14956_Transcript_1/1_Conf_1.000	482	2	9.46E-05	AAO63578.1	37	50.0618	141	53	secreted protein 6 precursor

Locus_14957_Transcript_1/1_Conf_1.000	254	6	2.24E-25	NP_492295.1	88	118.627	75	66	hypothetical protein F10D11.6
Locus_14958_Transcript_1/1_Conf_1.000	508	20	1.71E-76	ADD13547.1	90	288.5	169	153	Inositol triphosphate receptor protein 1, isoform h
Locus_14959_Transcript_1/1_Conf_1.000	450	20	1.91E-53	XP_002638883.1	78	211.846	144	113	Hypothetical protein CBG22103
Locus_1496_Transcript_1/1_Conf_1.000	295	0							
Locus_14960_Transcript_1/1_Conf_1.000	339	2	3.59E-04	NP_001040692.2	50	48.1358	89	45	hypothetical protein T28B8.3
Locus_14961_Transcript_1/1_Conf_1.000	307	0							
Locus_14962_Transcript_1/1_Conf_1.000	423	0							
Locus_14963_Transcript_1/1_Conf_1.000	213	0							
Locus_14964_Transcript_1/1_Conf_1.000	161	0							
Locus_14965_Transcript_1/1_Conf_1.000	304	5	6.17E-12	CAB55048.3	56	73.9442	88	50	C. elegans protein Y50E8A.5, partially confirmed by transcript evidence
Locus_14966_Transcript_1/1_Conf_1.000	689	3	6.17E-10	NP_491340.2	49	68.5514	191	94	histone METhyltransferase-like family member (met-1)
Locus_14967_Transcript_1/1_Conf_1.000	148	0							
Locus_14968_Transcript_1/1_Conf_1.000	382	0							
Locus_14969_Transcript_1/1_Conf_1.000	324	5	2.34E-51	NP_740906.1	93	204.912	108	101	hypothetical protein F26E4.7
Locus_1497_Transcript_1/1_Conf_1.000	230	20	1.35E-06	XP_002643187.1	78	56.225	41	32	Hypothetical protein CBG24156
Locus_14970_Transcript_1/1_Conf_1.000	174	0							

Locus_14971_Transcript_1/1_Conf_1.000	242	20	1.32E-38	ADG03678.1	100	162.54	80	80	alpha actinin 4 short isoform
Locus_14972_Transcript_1/1_Conf_1.000	619	4	3.56E-53	NP_001033357.2	67	211.846	206	140	DAF-16/FOXO Controlled, germline Tumor affecting family member (dct-6)
Locus_14973_Transcript_1/1_Conf_1.000	143	20	9.41E-21	XP_002642408.1	100	103.219	47	47	C. briggsae CBR-NHL-1 protein
Locus_14974_Transcript_1/1_Conf_1.000	456	0							
Locus_14975_Transcript_1/1_Conf_1.000	869	20	2.14E-33	EFO16257.1	68	147.132	150	102	hypothetical protein LOAG_12250
Locus_14976_Transcript_1/1_Conf_1.000	158	5	1.82E-19	NP_001022619.1	88	98.9821	52	46	NorDiHydroGuaiaretic acid resistant family member (ndg-4)
Locus_14977_Transcript_1/1_Conf_1.000	761	0							
Locus_14978_Transcript_1/1_Conf_1.000	326	0							
Locus_14979_Transcript_1/1_Conf_1.000	400	0							
Locus_1498_Transcript_1/2_Conf_1.000	472	20	4.44E-10	P34473.3	59	67.781	89	53	Uncharacterized protein F58A4.6
Locus_1498_Transcript_2/2_Conf_1.000	472	20	3.40E-10	P34473.3	59	68.1662	89	53	Uncharacterized protein F58A4.6
Locus_14980_Transcript_1/1_Conf_1.000	398	2	4.21E-08	NP_001122443.1	91	61.2326	36	33	hypothetical protein F02E9.5
Locus_14981_Transcript_1/1_Conf_1.000	223	20	2.47E-16	XP_001902364.1	79	88.5817	74	59	Myotubularin-related family protein
Locus_14982_Transcript_1/1_Conf_1.000	419	0							
Locus_14983_Transcript_1/1_Conf_1.000	348	20	2.21E-33	CAR63547.1	72	145.206	118	86	putative COLlagen

Locus_14984_Transcript_1/1_Conf_1.000	310	20	2.17E-25	NP_001020988.1	83	118.627	103	86	UNCoordinated family member (unc-89)
Locus_14985_Transcript_1/1_Conf_1.000	236	0							
Locus_14986_Transcript_1/1_Conf_1.000	293	0							
Locus_14987_Transcript_1/1_Conf_1.000	241	0							
Locus_14988_Transcript_1/1_Conf_1.000	391	20	1.39E-48	XP_002632959.1	85	195.667	128	109	C. briggsae CBR-RAD-26 protein
Locus_14989_Transcript_1/1_Conf_1.000	314	20	3.02E-30	NP_499492.1	78	134.806	102	80	hypothetical protein Y66D12A.10
Locus_1499_Transcript_1/1_Conf_1.000	1283	20	7.71E-106	EFO24882.1	68	388.652	435	300	hypothetical protein LOAG_03599
Locus_14990_Transcript_1/1_Conf_1.000	163	0							
Locus_14991_Transcript_1/1_Conf_1.000	437	0							
Locus_14992_Transcript_1/1_Conf_1.000	251	20	6.10E-20	XP_002644341.1	71	100.523	85	61	Hypothetical protein CBG14163
Locus_14993_Transcript_1/1_Conf_1.000	374	20	2.53E-29	XP_002641856.1	69	131.724	116	81	Hypothetical protein CBG16531
Locus_14994_Transcript_1/1_Conf_1.000	475	0							
Locus_14995_Transcript_1/1_Conf_1.000	398	0							
Locus_14996_Transcript_1/1_Conf_1.000	144	0							
Locus_14997_Transcript_1/1_Conf_1.000	605	20	3.35E-21	XP_001950752.1	57	105.531	207	119	PREDICTED: similar to galactokinase 1
Locus_14998_Transcript_1/1_Conf_1.000	226	0							
Locus_14999_Transcript_1/1_Conf_1.000	380	20	9.55E-29	XP_002639263.1	83	129.798	84	70	C. briggsae CBR-MOM-5 protein
Locus_15_Transcript_1/3_Conf_0.429	424	0							
Locus_15_Transcript_2/3_Conf_0.429	598	0							
Locus_15_Transcript_3/3_Conf_0.500	349	0							
Locus_150_Transcript_1/6_Conf_0.500	1513	20	0	Q9N358.3	88	641.728	414	368	T-complex protein 1 subunitTheta
Locus_150_Transcript_2/6_Conf_0.571	1550	20	0	Q9N358.3	91	805.053	503	461	T-complex protein 1 subunitTheta

Locus_150_Transcript_3/6_Conf_0.571	1550	20	0	Q9N358.3	91	803.512	503	461	T-complex protein 1 subunitTheta
Locus_150_Transcript_4/6_Conf_0.571	1550	20	0	Q9N358.3	91	801.971	503	461	T-complex protein 1 subunitTheta
Locus_150_Transcript_5/6_Conf_0.143	2282	20	3.04E-104	XP_001900116.1	54	384.415	763	415	SMC proteins Flexible Hinge Domain containing protein
Locus_150_Transcript_6/6_Conf_0.571	1550	20	0	Q9N358.3	91	803.512	503	461	T-complex protein 1 subunitTheta
Locus_1500_Transcript_1/1_Conf_1.000	1364	20	0	NP_508841.1	99	758.444	376	375	ACTin family member (act-4)
Locus_15000_Transcript_1/1_Conf_1.000	136	0							
Locus_15001_Transcript_1/1_Conf_1.000	307	0							
Locus_15002_Transcript_1/1_Conf_1.000	180	0							
Locus_15003_Transcript_1/1_Conf_1.000	305	7	1.57E-15	XP_001894313.1	63	85.8853	86	55	NLI interacting factor-like phosphatase family protein
Locus_15004_Transcript_1/1_Conf_1.000	235	0							
Locus_15005_Transcript_1/1_Conf_1.000	571	0							
Locus_15006_Transcript_1/1_Conf_1.000	222	0							
Locus_15007_Transcript_1/1_Conf_1.000	267	0							
Locus_15008_Transcript_1/1_Conf_1.000	184	1	3.60E-07	EFO17857.1	67	58.151	61	41	CK1/TTBK protein kinase

Locus_15009_Transcript_1/1_Conf_1.000	1054	20	3.08E-91	XP_002640663.1	68	339.732	332	228	C. briggsae CBR-DOG-1 protein
Locus_1501_Transcript_1/3_Conf_0.667	1640	20	1.59E-16	ACX37244.1	40	92.4337	404	164	eIF4G
Locus_1501_Transcript_2/3_Conf_0.667	1634	20	2.07E-16	ACX37244.1	40	92.0485	402	164	eIF4G
Locus_1501_Transcript_3/3_Conf_0.333	366	0							
Locus_15010_Transcript_1/1_Conf_1.000	331	20	6.74E-59	BAF84240.1	100	229.95	109	109	unnamed protein product
Locus_15011_Transcript_1/1_Conf_1.000	345	2	8.18E-20	XP_001897339.1	65	100.138	101	66	Negative elongation factor A homolog
Locus_15012_Transcript_1/1_Conf_1.000	315	0							
Locus_15013_Transcript_1/1_Conf_1.000	479	20	1.51E-18	EFO24760.1	82	95.9005	76	63	hypothetical protein LOAG_03731
Locus_15014_Transcript_1/1_Conf_1.000	900	16	8.69E-09	XP_001921732.1	45	65.4698	170	77	PREDICTED: zonadhesin-like
Locus_15015_Transcript_1/1_Conf_1.000	239	0							
Locus_15016_Transcript_1/1_Conf_1.000	409	20	3.38E-18	XP_001362642.1	46	94.7449	122	57	PREDICTED: similar to OTTHUMP00000028801
Locus_15017_Transcript_1/1_Conf_1.000	406	6	2.20E-09	EFO22525.1	58	65.4698	77	45	hypothetical protein LOAG_05962
Locus_15018_Transcript_1/1_Conf_1.000	979	20	3.96E-90	NP_001076724.1	70	335.88	327	230	Na-K-Cl Cotransporter homolog family member (nkcc-1)
Locus_15019_Transcript_1/1_Conf_1.000	489	20	9.46E-61	XP_002637665.1	90	236.113	151	137	C. briggsae CBR-APT-10 protein

Locus_1502_Transcript_1/1_Conf_1.000	576	20	2.00E-25	XP_001901168.1	78	119.398	111	87	Groucho/TLE N-terminal Q-rich domain containing protein
Locus_15020_Transcript_1/1_Conf_1.000	615	9	9.37E-06	AAD13340.1	42	54.299	187	79	ancylostoma secreted protein 1 precursor
Locus_15021_Transcript_1/1_Conf_1.000	778	1	2.44E-27	NP_497506.3	55	126.716	246	137	hypothetical protein Y48G9A.3
Locus_15022_Transcript_1/1_Conf_1.000	391	0							
Locus_15023_Transcript_1/1_Conf_1.000	889	20	2.31E-115	NP_741249.1	82	419.468	297	245	hypothetical protein C02F5.7
Locus_15024_Transcript_1/1_Conf_1.000	252	20	1.36E-14	XP_002643359.1	57	82.8037	101	58	Hypothetical protein CBG15962
Locus_15025_Transcript_1/3_Conf_0.667	924	20	1.06E-49	NP_498711.1	62	201.445	199	124	TYRosinase family member (tyr-1)
Locus_15025_Transcript_2/3_Conf_0.667	924	20	1.06E-49	NP_498711.1	62	201.445	199	124	TYRosinase family member (tyr-1)
Locus_15025_Transcript_3/3_Conf_0.667	924	20	1.06E-49	NP_498711.1	62	201.445	199	124	TYRosinase family member (tyr-1)
Locus_15026_Transcript_1/1_Conf_1.000	544	4	2.11E-44	XP_002641787.1	71	182.185	152	109	Hypothetical protein CBG10134
Locus_15027_Transcript_1/1_Conf_1.000	130	2	1.09E-08	NP_491911.3	79	63.1586	43	34	hypothetical protein ZC581.3
Locus_15028_Transcript_1/1_Conf_1.000	1009	1	7.76E-20	NP_495158.3	45	102.449	320	147	hypothetical protein ZK1248.13
Locus_15029_Transcript_1/1_Conf_1.000	422	20	4.43E-58	ABS45067.1	94	227.254	140	132	latrophilin-like protein 2
Locus_1503_Transcript_1/1_Conf_1.000	2692	20	0	NP_741616.2	65	1031.55	913	597	CRiM (Cysteine RIch motor neuron protein) homolog family member (crm-1)
Locus_15030_Transcript_1/1_Conf_1.000	563	0							
Locus_15031_Transcript_1/1_Conf_1.000	479	20	2.56E-42	NP_501928.1	74	174.866	139	103	hypothetical protein F13B12.4
Locus_15032_Transcript_1/1_Conf_1.000	693	6	7.33E-59	NP_502752.1	64	231.106	211	137	hypothetical protein LLC1.2
Locus_15033_Transcript_1/1_Conf_1.000	156	0							
Locus_15034_Transcript_1/1_Conf_1.000	147	20	6.31E-20	XP_002833008.1	100	100.523	48	48	PREDICTED: heme-binding protein 2-like isoform 2
Locus_15035_Transcript_1/1_Conf_1.000	589	5	1.75E-40	NP_505776.1	85	169.474	149	127	hypothetical protein F32D8.5
Locus_15036_Transcript_1/1_Conf_1.000	843	2	5.95E-09	EFO24331.1	64	65.855	78	50	hypothetical protein LOAG_04146
Locus_15037_Transcript_1/1_Conf_1.000	193	20	4.97E-09	XP_002737095.1	70	64.3142	57	40	PREDICTED: glutathione S-transferase kappa 1-like

Locus_15038_Transcript_1/1_Conf_1.000	280	2	3.59E-12	XP_002631029.1	68	74.7146	67	46	Hypothetical protein CBG02786
Locus_15039_Transcript_1/1_Conf_1.000	288	20	3.32E-29	XP_002633438.1	82	131.339	95	78	Hypothetical protein CBG06206
Locus_1504_Transcript_1/1_Conf_1.000	1163	20	9.59E-129	XP_002636865.1	74	464.537	390	292	Hypothetical protein CBG09322
Locus_15040_Transcript_1/1_Conf_1.000	488	0							
Locus_15041_Transcript_1/1_Conf_1.000	257	20	6.11E-07	XP_002159471.1	50	57.3806	91	46	PREDICTED: similar to alkaline phosphatase, liver/bone/kidney, partial
Locus_15042_Transcript_1/1_Conf_1.000	303	0							
Locus_15043_Transcript_1/1_Conf_1.000	294	20	3.66E-12	NP_495668.1	56	74.7146	98	55	hypothetical protein ZK669.2
Locus_15044_Transcript_1/2_Conf_1.000	720	0							
Locus_15044_Transcript_2/2_Conf_1.000	485	0							

Locus_15045_Transcript_1/1_Conf_1.000	686	19	1.50E-16	XP_002648013.1	45	90.5077	212	97	Hypothetical protein CBG23963
Locus_15046_Transcript_1/1_Conf_1.000	331	20	1.45E-53	NP_491646.3	87	212.231	109	95	hypothetical protein F46F11.7
Locus_15047_Transcript_1/2_Conf_1.000	557	20	1.13E-51	XP_002647223.1	73	206.453	180	132	Hypothetical protein CBG23813
Locus_15047_Transcript_2/2_Conf_1.000	555	20	1.13E-51	XP_002647223.1	74	206.453	175	130	Hypothetical protein CBG23813
Locus_15048_Transcript_1/1_Conf_1.000	436	20	4.84E-25	XP_002972906.1	68	117.472	125	85	hypothetical protein SELMODRAFT_98330
Locus_15049_Transcript_1/1_Conf_1.000	557	20	1.85E-70	XP_002630469.1	86	268.855	166	143	C. briggsae CBR-SQV-7 protein
Locus_1505_Transcript_1/1_Conf_1.000	451	20	5.37E-48	XP_002640609.1	85	193.741	149	128	C. briggsae CBR-PRI-2 protein
Locus_15050_Transcript_1/1_Conf_1.000	327	0							
Locus_15051_Transcript_1/1_Conf_1.000	192	0							
Locus_15052_Transcript_1/1_Conf_1.000	303	0							
Locus_15053_Transcript_1/1_Conf_1.000	746	0							
Locus_15054_Transcript_1/1_Conf_1.000	340	6	3.71E-09	CBM41222.1	55	64.6994	90	50	C. elegans protein T10G3.3b, partially confirmed by transcript evidence
Locus_15055_Transcript_1/1_Conf_1.000	377	20	1.17E-26	XP_002641207.1	70	122.865	108	76	Hypothetical protein CBG09068
Locus_15056_Transcript_1/1_Conf_1.000	748	0							
Locus_15057_Transcript_1/1_Conf_1.000	198	13	1.81E-11	EFO18099.1	63	72.4034	63	40	hypothetical protein LOAG_10400
Locus_15058_Transcript_1/1_Conf_1.000	140	0							

Locus_15059_Transcript_1/1_Conf_1.000	439	20	1.55E-23	NP_509583.1	71	112.464	112	80	hypothetical protein B0272.4
Locus_1506_Transcript_1/1_Conf_1.000	419	20	7.93E-23	XP_002636649.1	80	110.153	70	56	Hypothetical protein CBG23360
Locus_15060_Transcript_1/1_Conf_1.000	129	2	2.35E-11	XP_002640624.1	88	72.0182	42	37	Hypothetical protein CBG08742
Locus_15061_Transcript_1/1_Conf_1.000	512	20	2.54E-64	XP_002641212.1	83	248.054	159	132	Hypothetical protein CBG09074
Locus_15062_Transcript_1/1_Conf_1.000	520	6	7.54E-06	XP_002598663.1	42	53.9138	124	53	hypothetical protein BRAFLDRAFT_67064
Locus_15063_Transcript_1/1_Conf_1.000	289	0							
Locus_15064_Transcript_1/1_Conf_1.000	388	20	1.91E-21	NP_497585.1	68	105.531	123	84	G Protein, Alpha subunit family member (gpa-17)

Locus_15065_Transcript_1/1_Conf_1.000	572	20	3.89E-26	CAA94882.2	60	121.709	193	117	C. elegans protein B0024.10, confirmed by transcript evidence
Locus_15066_Transcript_1/1_Conf_1.000	205	5	7.28E-29	CAR63715.1	100	130.183	67	67	putative NHL (ring finger b-box coiled coil) domain containing family member
Locus_15067_Transcript_1/1_Conf_1.000	533	20	8.44E-27	XP_002639475.1	61	123.635	172	105	Hypothetical protein CBG04073
Locus_15068_Transcript_1/1_Conf_1.000	237	6	3.88E-14	ACJ65180.1	73	81.2629	79	58	Gaba b receptor subunit protein 2, confirmed by transcript evidence
Locus_15069_Transcript_1/1_Conf_1.000	303	20	8.57E-30	XP_001898220.1	83	133.265	100	83	multidrug Resistance Protein family member (mrp-5)
Locus_1507_Transcript_1/2_Conf_1.000	1909	8	2.19E-44	XP_002641295.1	63	185.267	282	180	Hypothetical protein CBG05210
Locus_1507_Transcript_2/2_Conf_1.000	1215	8	1.21E-44	XP_002641295.1	63	185.267	282	180	Hypothetical protein CBG05210
Locus_15070_Transcript_1/1_Conf_1.000	163	20	2.53E-13	NP_493802.2	85	78.5666	54	46	SyNapTotagmin family member (snt-6)
Locus_15071_Transcript_1/1_Conf_1.000	140	0							
Locus_15072_Transcript_1/1_Conf_1.000	308	20	1.41E-24	AAL15593.1	72	115.931	103	75	AF322256_14Sim15
Locus_15073_Transcript_1/1_Conf_1.000	414	0							

Locus_15074_Transcript_1/1_Conf_1.000	513	20	5.10E-52	NP_496057.1	83	207.223	155	130	EXCretory canal abnormal family member (exc-7)
Locus_15075_Transcript_1/1_Conf_1.000	181	13	7.75E-18	NP_001021395.1	88	93.5893	52	46	Receptor Mediated Endocytosis family member (rme-8)
Locus_15076_Transcript_1/1_Conf_1.000	410	0							
Locus_15077_Transcript_1/1_Conf_1.000	755	20	4.72E-57	NP_499177.3	68	225.328	252	173	hypothetical protein ZK632.7
Locus_15078_Transcript_1/1_Conf_1.000	181	0							
Locus_15079_Transcript_1/1_Conf_1.000	186	0							
Locus_1508_Transcript_1/1_Conf_1.000	1272	20	3.15E-51	XP_002641264.1	72	207.223	211	152	C. briggsae CBR-DNJ-24 protein
Locus_15080_Transcript_1/1_Conf_1.000	286	3	2.24E-17	XP_002645893.1	78	92.0485	92	72	Hypothetical protein CBG07646
Locus_15081_Transcript_1/1_Conf_1.000	1005	20	3.31E-63	XP_001902019.1	62	246.514	295	184	PRPF39 protein
Locus_15082_Transcript_1/1_Conf_1.000	278	20	1.85E-08	CBI63218.1	76	62.3882	52	40	C. elegans protein F46G10.7c, confirmed by transcript evidence
Locus_15083_Transcript_1/1_Conf_1.000	425	1	1.65E-04	EFN74469.1	45	49.2914	81	37	hypothetical protein EAG_09297
Locus_15084_Transcript_1/1_Conf_1.000	350	0							
Locus_15085_Transcript_1/1_Conf_1.000	467	20	1.94E-29	XP_002639128.1	84	132.109	88	74	C. briggsae CBR-SPG-7 protein
Locus_15086_Transcript_1/1_Conf_1.000	810	0							
Locus_15087_Transcript_1/1_Conf_1.000	169	20	8.61E-22	NP_001076639.1	96	106.686	55	53	TWiK family of potassium channels family member (twk-39)
Locus_15088_Transcript_1/1_Conf_1.000	238	0							
Locus_15089_Transcript_1/1_Conf_1.000	138	0							
Locus_1509_Transcript_1/1_Conf_1.000	1131	20	1.05E-156	NP_001022735.1	84	557.37	376	316	hypothetical protein R155.1

Locus_15090_Transcript_1/1_Conf_1.000	500	20	7.90E-60	NP_509931.1	98	233.032	116	114	abnormal cell MIGration family member (mig-2)
Locus_15091_Transcript_1/1_Conf_1.000	290	0							
Locus_15092_Transcript_1/1_Conf_1.000	262	20	2.22E-17	XP_002632484.1	75	92.0485	70	53	Hypothetical protein CBG13719
Locus_15093_Transcript_1/1_Conf_1.000	389	0							
Locus_15094_Transcript_1/1_Conf_1.000	162	20	5.27E-11	NP_501217.2	81	70.8626	54	44	hypothetical protein R05G6.10
Locus_15095_Transcript_1/1_Conf_1.000	183	0							
Locus_15096_Transcript_1/1_Conf_1.000	409	0							
Locus_15097_Transcript_1/1_Conf_1.000	298	0							
Locus_15098_Transcript_1/1_Conf_1.000	183	20	9.15E-11	XP_002640025.1	87	70.0922	40	35	Hypothetical protein CBG12497
Locus_15099_Transcript_1/1_Conf_1.000	159	1	3.32E-05	EFO20471.1	69	51.6026	53	37	hypothetical protein LOAG_08020
Locus_151_Transcript_1/1_Conf_1.000	814	0							
Locus_1510_Transcript_1/1_Conf_1.000	1331	20	2.01E-88	XP_002639683.1	62	330.872	444	277	C. briggsae CBR-GEI-11 protein
Locus_15100_Transcript_1/1_Conf_1.000	128	2	3.65E-04	NP_499641.2	64	48.1358	37	24	hypothetical protein Y111B2A.10
Locus_15101_Transcript_1/1_Conf_1.000	879	20	5.20E-19	XP_002637508.1	75	99.3673	79	60	C. briggsae CBR-TAG-232 protein
Locus_15102_Transcript_1/1_Conf_1.000	314	0							
Locus_15103_Transcript_1/1_Conf_1.000	523	0							
Locus_15104_Transcript_1/1_Conf_1.000	350	20	1.87E-32	NP_508492.1	71	142.124	116	83	hypothetical protein Y71H10B.1

Locus_15105_Transcript_1/1_Conf_1.000	315	20	9.35E-32	AAL72637.1	73	139.813	105	77	AF411588_1inositol polyphosphate 5-phosphatase type I
Locus_15106_Transcript_1/1_Conf_1.000	326	20	3.40E-26	NP_492719.1	85	121.324	70	60	hypothetical protein F45H11.5
Locus_15107_Transcript_1/1_Conf_1.000	185	0							
Locus_15108_Transcript_1/1_Conf_1.000	196	0							
Locus_15109_Transcript_1/1_Conf_1.000	955	20	5.47E-89	CAB05198.3	80	332.028	240	193	C. elegans protein F52B11.2, partially confirmed by transcript evidence
Locus_1511_Transcript_1/2_Conf_1.000	1744	3	1.11E-23	XP_001898374.1	48	116.316	346	168	hypothetical protein Bm1_34635
Locus_1511_Transcript_2/2_Conf_1.000	1645	20	4.06E-28	NP_504644.1	80	130.954	94	76	ACyLtransferase-like family member (acl-9)
Locus_15110_Transcript_1/1_Conf_1.000	381	20	1.41E-48	XP_002648358.1	88	195.667	125	111	Hypothetical protein CBG24564
Locus_15111_Transcript_1/1_Conf_1.000	316	20	2.99E-54	CAI15061.1	100	214.542	105	105	guanylate kinase 1
Locus_15112_Transcript_1/1_Conf_1.000	176	0							
Locus_15113_Transcript_1/2_Conf_1.000	448	0							
Locus_15113_Transcript_2/2_Conf_1.000	472	0							
Locus_15114_Transcript_1/1_Conf_1.000	316	20	1.49E-37	NP_741746.1	98	159.073	105	103	Kinesin-Like Protein family member (klp-4)
Locus_15115_Transcript_1/1_Conf_1.000	1793	20	3.41E-76	NP_872042.1	58	290.812	499	294	hypothetical protein C27H5.2
Locus_15116_Transcript_1/1_Conf_1.000	352	2	3.09E-11	NP_495375.3	53	71.633	115	61	hypothetical protein T14B4.1
Locus_15117_Transcript_1/1_Conf_1.000	366	20	6.98E-16	EFO23847.1	72	87.0409	75	54	hypothetical protein LOAG_04634

Locus_15118_Transcript_1/1_Conf_1.000	157	20	1.50E-05	XP_002004206.1	69	52.7582	46	32	GI19788
Locus_15119_Transcript_1/1_Conf_1.000	271	8	9.89E-10	NP_491880.1	60	66.6254	82	50	hypothetical protein T10E9.6
Locus_1512_Transcript_1/1_Conf_1.000	2516	20	0	EFO26683.1	88	916.376	614	545	elongation factor Tu GTP binding domain-containing protein
Locus_15120_Transcript_1/1_Conf_1.000	263	5	3.66E-20	NP_001123142.1	74	101.293	81	60	related to yeast Vacuolar Protein Sorting factor family member (vps-41)
Locus_15121_Transcript_1/1_Conf_1.000	172	20	3.15E-24	XP_002631669.1	100	114.775	56	56	C. briggsae CBR-MOG-4 protein
Locus_15122_Transcript_1/3_Conf_0.571	674	0							
Locus_15122_Transcript_2/3_Conf_0.714	790	0							
Locus_15122_Transcript_3/3_Conf_0.714	789	0							
Locus_15123_Transcript_1/1_Conf_1.000	385	0							

Locus_15124_Transcript_1/1_Conf_1.000	1032	20	1.25E-121	XP_002643017.1	76	440.654	340	260	C. briggsae CBR-POLK-1 protein
Locus_15125_Transcript_1/1_Conf_1.000	620	2	5.89E-40	XP_002634811.1	77	167.933	120	93	Hypothetical protein CBG13916
Locus_15126_Transcript_1/1_Conf_1.000	697	20	1.28E-10	XP_002642710.1	70	70.8626	75	53	C. briggsae CBR-MCM-5 protein
Locus_15127_Transcript_1/1_Conf_1.000	297	0							
Locus_15128_Transcript_1/1_Conf_1.000	613	20	3.43E-85	XP_002645218.1	94	318.161	191	180	Hypothetical protein CBG00076
Locus_15129_Transcript_1/1_Conf_1.000	172	3	3.38E-10	XP_002642486.1	78	68.1662	55	43	Hypothetical protein CBG06905
Locus_1513_Transcript_1/2_Conf_1.000	593	0							
Locus_1513_Transcript_2/2_Conf_1.000	2315	20	1.12E-170	XP_002639813.1	63	605.134	665	422	C. briggsae CBR-WTS-1 protein
Locus_15130_Transcript_1/1_Conf_1.000	308	3	1.47E-05	XP_001607761.1	82	52.7582	34	28	PREDICTED: similar to ENSANGP00000004989
Locus_15131_Transcript_1/1_Conf_1.000	152	0							
Locus_15132_Transcript_1/1_Conf_1.000	184	0							
Locus_15133_Transcript_1/1_Conf_1.000	358	0							
Locus_15134_Transcript_1/1_Conf_1.000	171	20	4.41E-18	CAL38390.1	100	94.3597	45	45	hypothetical protein
Locus_15135_Transcript_1/1_Conf_1.000	421	20	1.35E-14	EFO20607.1	74	82.8037	71	53	hypothetical protein LOAG_07879
Locus_15136_Transcript_1/1_Conf_1.000	606	20	5.51E-80	XP_002636870.1	85	300.827	201	172	Hypothetical protein CBG09328
Locus_15137_Transcript_1/1_Conf_1.000	204	0							
Locus_15138_Transcript_1/1_Conf_1.000	255	0							
Locus_15139_Transcript_1/1_Conf_1.000	168	0							
Locus_1514_Transcript_1/1_Conf_1.000	1282	20	1.42E-83	NP_503108.1	81	314.694	230	187	hypothetical protein C06A12.3
Locus_15140_Transcript_1/1_Conf_1.000	293	0							
Locus_15141_Transcript_1/1_Conf_1.000	137	0							

Locus_15142_Transcript_1/1_Conf_1.000	768	20	5.13E-30	XP_002647111.1	63	135.576	158	100	C. briggsae CBR-HEH-1 protein
Locus_15143_Transcript_1/1_Conf_1.000	117	0							
Locus_15144_Transcript_1/1_Conf_1.000	470	0							
Locus_15145_Transcript_1/1_Conf_1.000	271	0							
Locus_15146_Transcript_1/1_Conf_1.000	348	0							
Locus_15147_Transcript_1/1_Conf_1.000	186	0							
Locus_15148_Transcript_1/1_Conf_1.000	303	20	1.67E-25	XP_001177751.1	81	119.013	101	82	PREDICTED: hypothetical protein
Locus_15149_Transcript_1/1_Conf_1.000	406	6	3.50E-23	XP_001898115.1	64	111.309	134	87	hypothetical protein
Locus_1515_Transcript_1/3_Conf_0.500	242	0							
Locus_1515_Transcript_2/3_Conf_0.667	352	0							
Locus_1515_Transcript_3/3_Conf_0.667	298	0							
Locus_15150_Transcript_1/1_Conf_1.000	137	0							
Locus_15151_Transcript_1/1_Conf_1.000	1100	20	1.29E-95	XP_002648242.1	86	354.369	227	196	C. briggsae CBR-SRF-3 protein
Locus_15152_Transcript_1/1_Conf_1.000	496	0							
Locus_15153_Transcript_1/1_Conf_1.000	479	0							
Locus_15154_Transcript_1/1_Conf_1.000	390	20	2.23E-38	XP_002832332.1	75	161.77	134	101	PREDICTED: host cell factor 1-like
Locus_15155_Transcript_1/1_Conf_1.000	684	0							
Locus_15156_Transcript_1/1_Conf_1.000	377	20	7.56E-42	AAH29482.1	100	173.326	83	83	Hypothetical protein HSPC152
Locus_15157_Transcript_1/1_Conf_1.000	553	6	2.26E-12	XP_002630815.1	53	75.8702	145	77	Hypothetical protein CBG02516
Locus_15158_Transcript_1/1_Conf_1.000	253	0							
Locus_15159_Transcript_1/1_Conf_1.000	985	20	1.74E-93	NP_496492.1	78	347.051	338	266	hypothetical protein C47D12.2
Locus_1516_Transcript_1/1_Conf_1.000	225	5	1.77E-14	XP_002631813.1	68	82.4185	73	50	Hypothetical protein CBG21034

Locus_15160_Transcript_1/1_Conf_1.000	420	10	5.47E-24	NP_500401.1	81	114.005	121	99	hypothetical protein Y37E11AL.1
Locus_15161_Transcript_1/1_Conf_1.000	338	14	6.78E-11		62	70.4774	85	53	hypothetical protein Y105C5B.d
Locus_15162_Transcript_1/1_Conf_1.000	185	0							
Locus_15163_Transcript_1/1_Conf_1.000	671	20	3.61E-20	XP_002630952.1	54	102.449	173	94	C. briggsae CBR-ABCX-1 protein
Locus_15164_Transcript_1/1_Conf_1.000	564	20	1.73E-55	NP_500586.2	81	219.164	185	150	hypothetical protein ZK185.2
Locus_15165_Transcript_1/1_Conf_1.000	220	0							
Locus_15166_Transcript_1/1_Conf_1.000	379	20	1.10E-16	EFO21580.1	66	89.7373	75	50	hypothetical protein LOAG_06910
Locus_15167_Transcript_1/1_Conf_1.000	440	20	5.49E-37	NP_504599.2	86	157.147	104	90	Myotonic dystrophy-Related, Cdc42-binding Kinase homolog family member (mrck-1)
Locus_15168_Transcript_1/1_Conf_1.000	264	4	1.53E-26	NP_491513.2	81	122.479	88	72	Formin HOmology Domain family member (fhod-1)
Locus_15169_Transcript_1/2_Conf_1.000	226	0							
Locus_15169_Transcript_2/2_Conf_1.000	127	0							
Locus_1517_Transcript_1/1_Conf_1.000	1362	20	4.44E-131	XP_002631365.1	69	472.626	459	321	C. briggsae CBR-RHA-1 protein
Locus_15170_Transcript_1/1_Conf_1.000	492	20	5.96E-31	EFO14143.1	64	137.117	164	106	hypothetical protein LOAG_14379
Locus_15171_Transcript_1/1_Conf_1.000	342	5	1.23E-07	XP_001892437.1	64	59.6918	64	41	Gem-associated protein 7
Locus_15172_Transcript_1/1_Conf_1.000	406	20	2.13E-20	NP_503751.1	63	102.064	119	75	hypothetical protein R05D8.7

Locus_15173_Transcript_1/1_Conf_1.000	186	4	5.52E-16	XP_002630757.1	77	87.4261	62	48	Hypothetical protein CBG02451
Locus_15174_Transcript_1/1_Conf_1.000	187	0							
Locus_15175_Transcript_1/1_Conf_1.000	418	1	3.23E-08	NP_491852.1	52	61.6178	125	65	hypothetical protein F37E3.3
Locus_15176_Transcript_1/1_Conf_1.000	709	5	4.35E-22	XP_002645124.1	60	108.997	130	78	Hypothetical protein CBG16818
Locus_15177_Transcript_1/1_Conf_1.000	281	0							
Locus_15178_Transcript_1/1_Conf_1.000	314	0							
Locus_15179_Transcript_1/1_Conf_1.000	169	0							
Locus_1518_Transcript_1/1_Conf_1.000	1195	20	7.42E-132	XP_002632159.1	89	474.937	304	271	Hypothetical protein CBG07018
Locus_15180_Transcript_1/1_Conf_1.000	1008	20	4.42E-116	XP_002638881.1	79	422.165	334	264	C. briggsae CBR-VPS-34 protein
Locus_15181_Transcript_1/1_Conf_1.000	146	0							
Locus_15182_Transcript_1/1_Conf_1.000	731	20	6.69E-37	NP_506278.1	89	158.303	87	78	hypothetical protein T09E8.3
Locus_15183_Transcript_1/1_Conf_1.000	704	2	1.95E-14	EFO28233.1	48	83.5741	246	120	TTK protein kinase
Locus_15184_Transcript_1/1_Conf_1.000	194	0							
Locus_15185_Transcript_1/1_Conf_1.000	321	0							
Locus_15186_Transcript_1/1_Conf_1.000	141	0							
Locus_15187_Transcript_1/1_Conf_1.000	262	0							
Locus_15188_Transcript_1/1_Conf_1.000	232	0							
Locus_15189_Transcript_1/1_Conf_1.000	401	20	1.62E-68	XP_002640864.1	96	261.922	133	129	C. briggsae CBR-UNC-25 protein
Locus_1519_Transcript_1/2_Conf_1.000	935	20	7.67E-88	NP_505412.2	85	328.176	206	176	ACyLtransferase-like family member (acl-14)
Locus_1519_Transcript_2/2_Conf_1.000	1107	20	2.40E-73	NP_505413.1	82	280.411	180	149	hypothetical protein K07B1.4

Locus_15190_Transcript_1/1_Conf_1.000	290	20	3.44E-18	XP_002818294.1	100	94.7449	96	96	PREDICTED: collagen alpha-2(I) chain-like
Locus_15191_Transcript_1/1_Conf_1.000	279	20	1.77E-27	XP_001900518.1	79	125.561	92	73	3'5'-cyclic nucleotide phosphodiesterase family protein
Locus_15192_Transcript_1/1_Conf_1.000	325	20	9.27E-24	AAP41124.1	78	113.235	84	66	aldose reductase
Locus_15193_Transcript_1/1_Conf_1.000	678	20	3.26E-24	XP_002640845.1	52	115.931	224	118	C. briggsae CBR-CDH-1 protein
Locus_15194_Transcript_1/2_Conf_1.000	283	20	1.32E-17	XP_002630522.1	63	92.8189	97	62	Hypothetical protein CBG12960
Locus_15194_Transcript_2/2_Conf_1.000	283	20	1.32E-17	XP_002630522.1	63	92.8189	97	62	Hypothetical protein CBG12960
Locus_15195_Transcript_1/1_Conf_1.000	265	0							
Locus_15196_Transcript_1/1_Conf_1.000	342	0							
Locus_15197_Transcript_1/1_Conf_1.000	132	20	2.87E-09	AAC72298.1	83	65.0846	43	36	reverse transcriptase
Locus_15198_Transcript_1/1_Conf_1.000	764	20	2.35E-11	EFN52362.1	43	73.559	250	109	hypothetical protein CHLNCDRAFT_138782
Locus_15199_Transcript_1/1_Conf_1.000	139	0							

Locus_152_Transcript_1/1_Conf_1.000	305	20	1.29E-09	XP_002122773.1	63	66.2402	63	40	PREDICTED: similar to glucosidase, beta, acid
Locus_1520_Transcript_1/1_Conf_1.000	357	20	2.04E-31	EFO22150.1	78	138.658	105	82	SET domain-containing protein
Locus_15200_Transcript_1/1_Conf_1.000	254	20	2.40E-19	XP_001998853.1	73	98.5969	76	56	GI23404
Locus_15201_Transcript_1/1_Conf_1.000	1292	20	3.09E-78	XP_001896605.1	62	296.975	402	251	HYPOTHETICAL 59.2KD PROTEIN IN PFK26-SGA1 INTERGENIC REGION, putative
Locus_15202_Transcript_1/1_Conf_1.000	179	0							
Locus_15203_Transcript_1/1_Conf_1.000	383	20	5.96E-31	NP_505237.1	68	137.117	126	86	human CLN (neuronal ceroid lipofuscinosis) related family member (cln-3.3)
Locus_15204_Transcript_1/1_Conf_1.000	989	20	7.11E-79	XP_001897597.1	84	298.516	200	169	Lung seven transmembrane receptor family protein
Locus_15205_Transcript_1/1_Conf_1.000	609	20	8.39E-60	EFO27604.1	75	233.802	203	153	hypothetical protein LOAG_00873
Locus_15206_Transcript_1/1_Conf_1.000	478	20	8.51E-38	EFO19811.1	75	159.844	132	99	hemimethylated DNA binding domain-containing protein
Locus_15207_Transcript_1/1_Conf_1.000	136	4	1.02E-06	XP_001896000.1	79	56.6102	44	35	hypothetical protein
Locus_15208_Transcript_1/1_Conf_1.000	277	20	2.24E-38	NP_492839.4	92	161.77	91	84	Leucine-rich repeats, Ras-like domain, Kinase family member (lrk-1)
Locus_15209_Transcript_1/2_Conf_1.000	1065	20	2.24E-97	XP_002646179.1	73	360.147	322	238	Hypothetical protein CBG23745

Locus_15209_Transcript_2/2_Conf_1.000	948	20	1.26E-77	XP_002646179.1	63	294.278	322	204	Hypothetical protein CBG23745
Locus_1521_Transcript_1/1_Conf_1.000	1019	20	3.84E-83	NP_496604.1	72	312.768	266	193	hypothetical protein Y57A10A.26
Locus_15210_Transcript_1/1_Conf_1.000	210	0							
Locus_15211_Transcript_1/1_Conf_1.000	352	20	1.21E-23	XP_002630751.1	63	112.849	114	72	Hypothetical protein CBG02443
Locus_15212_Transcript_1/1_Conf_1.000	460	5	4.54E-07	XP_002643565.1	66	57.7658	54	36	Hypothetical protein CBG16267
Locus_15213_Transcript_1/1_Conf_1.000	209	0							
Locus_15214_Transcript_1/1_Conf_1.000	138	0							
Locus_15215_Transcript_1/1_Conf_1.000	156	0							
Locus_15216_Transcript_1/1_Conf_1.000	471	20	8.26E-57	NP_500720.1	87	223.016	147	128	IsoValeryl-CoA Dehydrogenase family member (ivd-1)
Locus_15217_Transcript_1/1_Conf_1.000	529	20	1.61E-30	XP_002633897.1	66	135.961	168	112	Hypothetical protein CBG19959
Locus_15218_Transcript_1/1_Conf_1.000	182	0							
Locus_15219_Transcript_1/1_Conf_1.000	145	20	2.18E-20	XP_002759346.1	100	102.064	48	48	PREDICTED: eukaryotic translation initiation factor 3 subunit E
Locus_1522_Transcript_1/2_Conf_1.000	2182	20	7.02E-26	ZP_02995497.1	54	124.02	127	69	hypothetical protein CLOSPO_02619
Locus_1522_Transcript_2/2_Conf_1.000	2188	20	7.04E-26	ZP_02995497.1	54	124.02	127	69	hypothetical protein CLOSPO_02619
Locus_15220_Transcript_1/1_Conf_1.000	246	20	1.23E-20	XP_002646069.1	85	102.834	67	57	C. briggsae CBR-GALE-1 protein
Locus_15221_Transcript_1/2_Conf_1.000	343	0							
Locus_15221_Transcript_2/2_Conf_1.000	207	0							
Locus_15222_Transcript_1/1_Conf_1.000	436	20	5.16E-35	XP_001900114.1	70	150.599	132	93	MGC14327-like protein
Locus_15223_Transcript_1/2_Conf_1.000	431	20	1.01E-38	NP_498705.1	92	162.925	93	86	Temporarily Assigned Gene name family member (tag-277)

Locus_15223_Transcript_2/2_Conf_1.000	386	20	1.01E-38	NP_498705.1	92	162.925	93	86	Temporarily Assigned Gene name family member (tag-277)
Locus_15224_Transcript_1/1_Conf_1.000	224	0							
Locus_15225_Transcript_1/2_Conf_1.000	896	20	8.53E-33	NP_491838.1	74	145.206	114	85	hypothetical protein K04F10.7
Locus_15225_Transcript_2/2_Conf_1.000	896	20	8.53E-33	NP_491838.1	74	145.206	114	85	hypothetical protein K04F10.7
Locus_15226_Transcript_1/1_Conf_1.000	235	12	2.61E-18	NP_502380.1	85	95.1301	63	54	hypothetical protein C25G4.6
Locus_15227_Transcript_1/1_Conf_1.000	305	20	1.51E-26	XP_002832428.1	100	122.479	58	58	PREDICTED: neudesin-like
Locus_15228_Transcript_1/1_Conf_1.000	212	20	2.33E-19	EFO17543.1	87	98.5969	57	50	aspartate aminotransferase
Locus_15229_Transcript_1/1_Conf_1.000	359	16	6.35E-33	XP_002639055.1	82	143.665	103	85	C. briggsae CBR-GCY-28 protein
Locus_1523_Transcript_1/1_Conf_1.000	1218	20	9.22E-61	NP_498568.1	83	238.81	160	134	fatty Acid CoA Synthetase family member (acs-16)
Locus_15230_Transcript_1/1_Conf_1.000	190	20	2.56E-13	NP_498621.1	81	78.5666	64	52	GOlgi Snap Receptor complex member family member (gosr-1)
Locus_15231_Transcript_1/1_Conf_1.000	133	0							
Locus_15232_Transcript_1/1_Conf_1.000	725	20	1.23E-51	XP_001892945.1	71	207.223	239	170	exosome complex exonuclease RRP40
Locus_15233_Transcript_1/1_Conf_1.000	169	0							
Locus_15234_Transcript_1/1_Conf_1.000	491	0							
Locus_15235_Transcript_1/1_Conf_1.000	385	20	1.55E-55	NP_491165.2	99	218.779	128	127	human SPG (spastic paraplegia) family member (spg-7)

Locus_15236_Transcript_1/1_Conf_1.000	129	6	5.61E-05	ZP_01471425.1	79	50.8322	39	31	short-chain dehydrogenase/reductase (SDR) superfamily protein
Locus_15237_Transcript_1/1_Conf_1.000	385	20	7.24E-37	NP_491915.2	82	156.762	124	102	hypothetical protein ZC581.9
Locus_15238_Transcript_1/1_Conf_1.000	251	20	6.95E-32	XP_002644493.1	96	140.198	83	80	Hypothetical protein CBG14380
Locus_15239_Transcript_1/1_Conf_1.000	446	20	5.22E-59	XP_002633481.1	86	230.335	147	127	C. briggsae CBR-PHY-2 protein
Locus_1524_Transcript_1/2_Conf_1.000	607	3	8.62E-33	CAR63637.1	75	144.05	115	87	hypothetical protein
Locus_1524_Transcript_2/2_Conf_1.000	247	0							
Locus_15240_Transcript_1/1_Conf_1.000	223	0							
Locus_15241_Transcript_1/1_Conf_1.000	1252	0							
Locus_15242_Transcript_1/1_Conf_1.000	216	13	3.95E-19	XP_002639744.1	81	97.8265	70	57	C. briggsae CBR-LAM-3 protein
Locus_15243_Transcript_1/1_Conf_1.000	259	0							
Locus_15244_Transcript_1/1_Conf_1.000	959	20	2.20E-29	NP_001076617.1	63	134.035	131	83	hypothetical protein W01A8.8
Locus_15245_Transcript_1/1_Conf_1.000	346	16	3.02E-06	XP_002636866.1	66	55.0694	66	44	Hypothetical protein CBG09323
Locus_15246_Transcript_1/1_Conf_1.000	619	20	2.23E-55	CAO00417.1	71	219.164	190	135	two-domain activation associated secreted protein ASP4 precursor
Locus_15247_Transcript_1/1_Conf_1.000	489	20	2.24E-78	XP_002643972.1	96	294.664	162	156	C. briggsae CBR-SLO-2 protein
Locus_15248_Transcript_1/2_Conf_1.000	403	0							
Locus_15248_Transcript_2/2_Conf_1.000	397	0							

Locus_15249_Transcript_1/1_Conf_1.000	1090	20	3.36E-96	NP_501359.1	72	356.295	359	262	hypothetical protein F42G8.6
Locus_1525_Transcript_1/1_Conf_1.000	1322	20	4.25E-14	XP_001899731.1	81	83.9593	55	45	Protein cec-1.
Locus_15250_Transcript_1/1_Conf_1.000	365	20	1.08E-24	NP_495704.1	81	116.316	72	59	CysTiNoSin (lysosomal protein) homolog family member (ctns-1)
Locus_15251_Transcript_1/1_Conf_1.000	146	3	1.56E-10	XP_002641998.1	92	69.3218	39	36	Hypothetical protein CBG09222
Locus_15252_Transcript_1/1_Conf_1.000	247	20	8.01E-12	EFO25925.1	75	73.559	64	48	SMC protein Flexible Hinge Domain containing protein
Locus_15253_Transcript_1/1_Conf_1.000	575	0							
Locus_15254_Transcript_1/1_Conf_1.000	533	20	2.81E-22	ACS37721.1	51	108.612	175	90	C-type lectin-1
Locus_15255_Transcript_1/1_Conf_1.000	387	20	1.66E-41	A8XST1.2	76	172.17	128	98	Post-GPI attachment to proteins factor 2
Locus_15256_Transcript_1/1_Conf_1.000	307	0							
Locus_15257_Transcript_1/2_Conf_1.000	1142	4	5.86E-06	NP_505144.2	52	56.6102	119	62	hypothetical protein W02D7.6
Locus_15257_Transcript_2/2_Conf_1.000	1142	4	5.86E-06	NP_505144.2	52	56.6102	119	62	hypothetical protein W02D7.6
Locus_15258_Transcript_1/1_Conf_1.000	139	0							
Locus_15259_Transcript_1/1_Conf_1.000	190	0							
Locus_1526_Transcript_1/2_Conf_1.000	1264	20	1.90E-32	NP_507998.1	61	144.821	233	143	hypothetical protein F53F8.5
Locus_1526_Transcript_2/2_Conf_1.000	1177	20	2.04E-17	NP_507998.1	50	94.7449	233	118	hypothetical protein F53F8.5

Locus_15260_Transcript_1/1_Conf_1.000	256	20	5.70E-13	XP_002645055.1	54	77.411	82	45	Hypothetical protein CBG16715
Locus_15261_Transcript_1/1_Conf_1.000	227	0							
Locus_15262_Transcript_1/1_Conf_1.000	258	0							
Locus_15263_Transcript_1/1_Conf_1.000	329	0							
Locus_15264_Transcript_1/1_Conf_1.000	520	20	1.19E-43	XP_002630483.1	83	179.489	109	91	Hypothetical protein CBG11219
Locus_15265_Transcript_1/1_Conf_1.000	944	20	2.52E-70	EFO21354.1	67	270.011	313	210	hypothetical protein LOAG_07131
Locus_15266_Transcript_1/1_Conf_1.000	379	20	1.57E-47	XP_002634501.1	87	192.2	127	111	C. briggsae CBR-SMGL-2 protein
Locus_15267_Transcript_1/1_Conf_1.000	130	0							
Locus_15268_Transcript_1/1_Conf_1.000	499	20	2.91E-46	XP_001899325.1	72	187.963	165	120	GDP-fucose protein O-fucosyltransferase 2 precursor
Locus_15269_Transcript_1/1_Conf_1.000	438	20	7.40E-42	XP_002645831.1	77	173.326	142	110	C. briggsae CBR-RBC-1 protein
Locus_1527_Transcript_1/1_Conf_1.000	582	0							
Locus_15270_Transcript_1/1_Conf_1.000	203	0							
Locus_15271_Transcript_1/1_Conf_1.000	495	17	8.33E-09	EFN69196.1	60	63.5438	86	52	hypothetical protein EAG_13720
Locus_15272_Transcript_1/1_Conf_1.000	177	0							
Locus_15273_Transcript_1/1_Conf_1.000	449	13	7.11E-16	NP_496492.1	70	87.0409	75	53	hypothetical protein C47D12.2
Locus_15274_Transcript_1/1_Conf_1.000	284	3	2.10E-15	NP_497247.2	56	85.5001	93	53	GEX Interacting protein family member (gei-16)
Locus_15275_Transcript_1/1_Conf_1.000	235	0							

Locus_15276_Transcript_1/1_Conf_1.000	458	20	2.95E-06	NP_499181.1	54	55.0694	85	46	hypothetical protein ZK632.10
Locus_15277_Transcript_1/1_Conf_1.000	502	20	1.53E-50	NP_495899.1	81	202.216	140	114	hypothetical protein T21B10.1
Locus_15278_Transcript_1/1_Conf_1.000	272	0							
Locus_15279_Transcript_1/1_Conf_1.000	205	1	8.10E-04	NP_001023900.1	66	46.9802	66	44	hypothetical protein F39G3.5
Locus_1528_Transcript_1/1_Conf_1.000	430	20	2.86E-25	NP_001122693.1	73	118.242	117	86	POLK (DNA polymerase kappa) homolog family member (polk-1)
Locus_15280_Transcript_1/1_Conf_1.000	442	20	1.06E-35	XP_002643964.1	72	152.91	137	100	C. briggsae CBR-HUM-4 protein
Locus_15281_Transcript_1/2_Conf_1.000	1053	20	2.59E-114	NP_501835.2	73	416.387	356	263	DIS3 (yeast disjunction abnormal) exonuclease homolog family member (dis-3)
Locus_15281_Transcript_2/2_Conf_1.000	1011	20	6.26E-86	NP_501835.2	71	322.013	300	213	DIS3 (yeast disjunction abnormal) exonuclease homolog family member (dis-3)
Locus_15282_Transcript_1/1_Conf_1.000	243	0							
Locus_15283_Transcript_1/1_Conf_1.000	988	10	2.17E-35	ABF71718.3	69	154.066	297	205	Collagen protein 46, partially confirmed by transcript evidence
Locus_15284_Transcript_1/2_Conf_1.000	682	20	8.56E-73	EFO23808.1	78	277.33	227	179	hypothetical protein LOAG_04674
Locus_15284_Transcript_2/2_Conf_1.000	682	20	8.56E-73	EFO23808.1	78	277.33	227	179	hypothetical protein LOAG_04674
Locus_15285_Transcript_1/1_Conf_1.000	259	0							
Locus_15286_Transcript_1/1_Conf_1.000	1200	20	5.45E-74	XP_001896288.1	62	282.722	351	220	mbt repeat family protein
Locus_15287_Transcript_1/1_Conf_1.000	221	0							
Locus_15288_Transcript_1/1_Conf_1.000	227	20	2.24E-09	XP_002647659.1	70	65.4698	47	33	Hypothetical protein CBG06766
Locus_15289_Transcript_1/1_Conf_1.000	384	20	7.29E-13	ADI24665.1	63	77.0258	77	49	Hypothetical protein Y38C1AA.13

Locus_1529_Transcript_1/1_Conf_1.000	435	20	1.83E-32	XP_002641208.1	70	142.124	125	88	C. briggsae CBR-DPF-4 protein
Locus_15290_Transcript_1/1_Conf_1.000	199	0							
Locus_15291_Transcript_1/2_Conf_1.000	413	0							
Locus_15291_Transcript_2/2_Conf_1.000	413	0							
Locus_15292_Transcript_1/1_Conf_1.000	160	0							
Locus_15293_Transcript_1/1_Conf_1.000	810	20	6.95E-121	NP_510603.1	88	437.573	269	239	hypothetical protein F59F4.1
Locus_15294_Transcript_1/1_Conf_1.000	356	4	3.29E-13	XP_001895370.1	64	78.1814	116	75	hypothetical protein Bm1_19575
Locus_15295_Transcript_1/1_Conf_1.000	218	0							
Locus_15296_Transcript_1/1_Conf_1.000	147	0							
Locus_15297_Transcript_1/1_Conf_1.000	139	0							
Locus_15298_Transcript_1/1_Conf_1.000	367	20	9.98E-47	NP_001023627.1	89	189.504	119	106	Na/H eXchanger family member (nhx-9)
Locus_15299_Transcript_1/1_Conf_1.000	183	0							
Locus_153_Transcript_1/3_Conf_0.333	166	0							
Locus_153_Transcript_2/3_Conf_0.833	411	20	2.59E-15	NP_508612.1	68	81.6481	80	55	VITellogenin structural genes (yolk protein genes) family member (vit-4)
Locus_153_Transcript_3/3_Conf_0.833	402	20	5.75E-15	NP_508612.1	69	80.4925	78	54	VITellogenin structural genes (yolk protein genes) family member (vit-4)
Locus_1530_Transcript_1/1_Conf_1.000	509	5	2.94E-36	NP_496819.1	65	154.836	159	104	hypothetical protein Y48C3A.20
Locus_15300_Transcript_1/1_Conf_1.000	252	20	2.65E-26	XP_002629711.1	79	121.709	83	66	C. briggsae CBR-RHY-1 protein
Locus_15301_Transcript_1/1_Conf_1.000	226	0							
Locus_15302_Transcript_1/1_Conf_1.000	304	0							
Locus_15303_Transcript_1/1_Conf_1.000	203	20	1.48E-13	NP_001022166.1	79	79.337	59	47	Temporarily Assigned Gene name family member (tag-169)
Locus_15304_Transcript_1/1_Conf_1.000	157	0							
Locus_15305_Transcript_1/1_Conf_1.000	575	20	3.46E-30	XP_002631433.1	64	135.191	153	99	C. briggsae CBR-REV-1 protein
Locus_15306_Transcript_1/1_Conf_1.000	153	20	2.16E-20	XP_002829638.1	100	102.064	51	51	PREDICTED: prostate tumor-overexpressed gene 1 protein-like
Locus_15307_Transcript_1/1_Conf_1.000	154	3	8.79E-06	XP_002641552.1	68	53.5286	47	32	C. briggsae CBR-RBC-2 protein

Locus_15308_Transcript_1/1_Conf_1.000	342	0							
Locus_15309_Transcript_1/1_Conf_1.000	136	0							
Locus_1531_Transcript_1/3_Conf_0.714	691	0							
Locus_1531_Transcript_2/3_Conf_0.714	1342	4	3.80E-18	NP_872051.1	50	97.4413	213	107	hypothetical protein Y17G7B.20
Locus_1531_Transcript_3/3_Conf_0.714	615	0							
Locus_15310_Transcript_1/1_Conf_1.000	439	20	3.67E-41	NP_498122.2	80	171.014	134	108	abnormal GROwth rate family member (gro-1)
Locus_15311_Transcript_1/1_Conf_1.000	280	20	8.51E-30	XP_002634229.1	80	133.265	90	72	C. briggsae CBR-UNC-26 protein
Locus_15312_Transcript_1/1_Conf_1.000	142	0							
Locus_15313_Transcript_1/1_Conf_1.000	145	1	1.28E-04	XP_002638613.1	86	49.6766	43	37	C. briggsae CBR-PGP-9 protein
Locus_15314_Transcript_1/1_Conf_1.000	533	20	4.76E-46	NP_502386.1	73	187.578	171	126	hypothetical protein T04A11.2
Locus_15315_Transcript_1/1_Conf_1.000	395	20	8.21E-20	NP_494781.1	74	100.138	86	64	hypothetical protein ZK430.7
Locus_15316_Transcript_1/1_Conf_1.000	342	0							
Locus_15317_Transcript_1/1_Conf_1.000	384	0							
Locus_15318_Transcript_1/1_Conf_1.000	797	20	1.60E-45	EFO17307.1	59	187.193	278	165	hypothetical protein LOAG_11192
Locus_15319_Transcript_1/1_Conf_1.000	395	2	3.45E-18	NP_500196.2	77	94.7449	72	56	hypothetical protein Y38F2AR.3
Locus_1532_Transcript_1/1_Conf_1.000	755	20	1.09E-37	CAB71314.1	70	160.999	136	96	galectin
Locus_15320_Transcript_1/1_Conf_1.000	198	0							

Locus_15321_Transcript_1/1_Conf_1.000	263	19	8.75E-06	XP_002934628.1	52	53.5286	71	37	PREDICTED: regenerating islet-derived protein 4-like
Locus_15322_Transcript_1/1_Conf_1.000	383	20	1.28E-41	XP_002636935.1	84	172.555	126	106	C. briggsae CBR-UIG-1 protein
Locus_15323_Transcript_1/1_Conf_1.000	226	0							
Locus_15324_Transcript_1/1_Conf_1.000	390	8	5.72E-18	NP_001021405.1	82	93.9745	114	94	asparagiNyl tRNA Synthetase family member (nrs-1)
Locus_15325_Transcript_1/1_Conf_1.000	271	5	2.20E-09	EFO23808.1	57	65.4698	91	52	hypothetical protein LOAG_04674
Locus_15326_Transcript_1/1_Conf_1.000	165	0							
Locus_15327_Transcript_1/1_Conf_1.000	556	3	1.75E-28	NP_506256.3	72	129.413	177	128	CaDHerin family member (cdh-6)
Locus_15328_Transcript_1/1_Conf_1.000	200	0							
Locus_15329_Transcript_1/1_Conf_1.000	529	20	1.04E-29	XP_002640799.1	65	133.265	155	101	Hypothetical protein CBG15679
Locus_1533_Transcript_1/3_Conf_0.333	409	0							
Locus_1533_Transcript_3/3_Conf_0.667	418	0							
Locus_15330_Transcript_1/1_Conf_1.000	370	0							
Locus_15331_Transcript_1/1_Conf_1.000	609	20	2.54E-40	NP_495248.1	80	169.088	131	106	hypothetical protein T24H7.3
Locus_15332_Transcript_1/1_Conf_1.000	313	20	4.67E-23	EFO18094.1	82	110.923	64	53	hypothetical protein LOAG_10404
Locus_15333_Transcript_1/1_Conf_1.000	194	0							
Locus_15334_Transcript_1/1_Conf_1.000	296	20	7.07E-40	XP_002644104.1	90	166.777	97	88	C. briggsae CBR-PLC-1 protein
Locus_15335_Transcript_1/1_Conf_1.000	558	20	3.29E-19	XP_392522.2	49	98.5969	199	98	PREDICTED: similar to CG3894-PA, isoform A
Locus_15336_Transcript_1/1_Conf_1.000	213	0							
Locus_15337_Transcript_1/1_Conf_1.000	279	4	3.03E-19	NP_492839.4	78	98.2117	71	56	Leucine-rich repeats, Ras-like domain, Kinase family member (lrk-1)
Locus_15338_Transcript_1/1_Conf_1.000	385	20	1.01E-30	EFO16233.1	78	136.346	124	97	variant SH3 domain-containing protein
Locus_15339_Transcript_1/1_Conf_1.000	340	20	1.72E-14	AAN10061.1	72	82.4185	54	39	Kunitz-like protease inhibitor precursor
Locus_1534_Transcript_1/1_Conf_1.000	253	0							

Locus_15340_Transcript_1/1_Conf_1.000	291	20	8.14E-28	NP_500084.2	79	126.716	97	77	hypothetical protein Y77E11A.2
Locus_15341_Transcript_1/1_Conf_1.000	1280	3	4.49E-05	EFO24673.1	58	53.9138	84	49	hypothetical protein LOAG_03814
Locus_15342_Transcript_1/1_Conf_1.000	169	3	4.01E-11		75	71.2478	56	42	myoblast city protein homolog
Locus_15343_Transcript_1/1_Conf_1.000	539	0							
Locus_15344_Transcript_1/1_Conf_1.000	151	0							
Locus_15345_Transcript_1/1_Conf_1.000	443	0							
Locus_15346_Transcript_1/1_Conf_1.000	427	20	2.52E-21	NP_001022683.1	67	105.145	123	83	hypothetical protein M01A8.2
Locus_15347_Transcript_1/1_Conf_1.000	247	0							
Locus_15348_Transcript_1/1_Conf_1.000	142	0							
Locus_15349_Transcript_1/1_Conf_1.000	418	0							
Locus_1535_Transcript_1/1_Conf_1.000	1998	20	0	EFO18359.1	78	710.294	534	421	hypothetical protein LOAG_10137
Locus_15350_Transcript_1/1_Conf_1.000	298	0							
Locus_15351_Transcript_1/1_Conf_1.000	179	0							
Locus_15352_Transcript_1/1_Conf_1.000	195	20	5.09E-30	EAX09318.1	100	134.035	64	64	collagen, type VI, alpha 2, isoform CRA_c
Locus_15353_Transcript_1/1_Conf_1.000	267	0							
Locus_15354_Transcript_1/1_Conf_1.000	369	0							
Locus_15355_Transcript_1/1_Conf_1.000	517	0							
Locus_15356_Transcript_1/1_Conf_1.000	150	0							
Locus_15357_Transcript_1/1_Conf_1.000	364	6	1.31E-30	XP_002631359.1	74	135.961	118	88	Hypothetical protein CBG03194
Locus_15358_Transcript_1/1_Conf_1.000	179	0							
Locus_15359_Transcript_1/1_Conf_1.000	245	0							
Locus_1536_Transcript_1/1_Conf_1.000	279	0							

Locus_15360_Transcript_1/1_Conf_1.000	237	0							
Locus_15361_Transcript_1/1_Conf_1.000	169	0							
Locus_15362_Transcript_1/1_Conf_1.000	552	20	5.67E-56	XP_002923059.1	100	220.705	106	106	PREDICTED: LOW QUALITY PROTEIN: cellular retinoic acid-binding protein 1-like
Locus_15363_Transcript_1/1_Conf_1.000	1027	0							
Locus_15364_Transcript_1/1_Conf_1.000	1141	20	2.52E-33	XP_002647599.1	54	147.517	381	206	C. briggsae CBR-EEA-1 protein
Locus_15365_Transcript_1/1_Conf_1.000	217	0							
Locus_15366_Transcript_1/1_Conf_1.000	286	0							
Locus_15367_Transcript_1/1_Conf_1.000	439	20	6.94E-32	XP_002639196.1	64	140.198	137	89	Hypothetical protein CBG03739
Locus_15368_Transcript_1/1_Conf_1.000	812	20	2.08E-32	XP_001900821.1	57	143.665	236	135	hypothetical protein Bm1_46790
Locus_15369_Transcript_1/1_Conf_1.000	148	0							
Locus_1537_Transcript_1/1_Conf_1.000	322	0							
Locus_15370_Transcript_1/1_Conf_1.000	405	0							
Locus_15371_Transcript_1/1_Conf_1.000	234	0							
Locus_15372_Transcript_1/1_Conf_1.000	412	20	3.30E-16	XP_002712017.1	60	77.0258	92	56	PREDICTED: thiamin pyrophosphokinase 1-like
Locus_15373_Transcript_1/1_Conf_1.000	180	20	3.49E-10	CAG04255.1	71	68.1662	56	40	unnamed protein product
Locus_15374_Transcript_1/1_Conf_1.000	842	4	6.53E-08	XP_002644385.1	53	62.3882	91	49	Hypothetical protein CBG14225
Locus_15375_Transcript_1/1_Conf_1.000	148	0							
Locus_15376_Transcript_1/1_Conf_1.000	238	0							
Locus_15377_Transcript_1/1_Conf_1.000	210	2	1.24E-04	NP_502000.1	62	49.6766	69	43	hypothetical protein C06G8.1

Locus_15378_Transcript_1/1_Conf_1.000	631	20	2.07E-80	XP_002632140.1	86	302.368	192	167	C. briggsae CBR-SPTL-1 protein
Locus_15379_Transcript_1/1_Conf_1.000	484	20	5.97E-71	XP_002914026.1	100	270.011	161	161	PREDICTED: polyadenylate-binding protein 1-like
Locus_1538_Transcript_1/1_Conf_1.000	1115	0							
Locus_15380_Transcript_1/1_Conf_1.000	420	1	2.16E-04	NP_497921.1	42	48.9062	123	52	hypothetical protein M88.3
Locus_15381_Transcript_1/1_Conf_1.000	515	20	2.09E-13	EFO16274.1	49	78.9518	148	73	hypothetical protein LOAG_12234
Locus_15382_Transcript_1/1_Conf_1.000	259	0							
Locus_15383_Transcript_1/1_Conf_1.000	191	0							
Locus_15384_Transcript_1/1_Conf_1.000	195	0							
Locus_15385_Transcript_1/1_Conf_1.000	492	5	1.29E-17	NP_508573.1	60	92.8189	147	89	Discoidin Domain Receptor family member (ddr-2)
Locus_15386_Transcript_1/1_Conf_1.000	928	9	7.42E-51	NP_492132.1	56	205.297	331	186	Enhancer of Glp-One (glp-1) family member (ego-1)
Locus_15387_Transcript_1/1_Conf_1.000	285	0							
Locus_15388_Transcript_1/1_Conf_1.000	506	20	3.41E-21	Q17678.6	71	104.76	102	73	UPF0632 protein C05G5.5

Locus_15389_Transcript_1/1_Conf_1.000	212	20	5.56E-13	3LTV	100	77.411	37	37	Mouse-Human Sod1 Chimera
Locus_1539_Transcript_1/1_Conf_1.000	501	20	4.01E-67	XP_002634908.1	83	257.299	161	135	Hypothetical protein CBG22506
Locus_15390_Transcript_1/1_Conf_1.000	326	20	1.98E-58	XP_002831943.1	100	228.409	108	108	PREDICTED: 60S ribosomal protein L36a-like isoform 1
Locus_15391_Transcript_1/1_Conf_1.000	830	20	9.86E-102	P34288.4	83	374.015	275	230	GTPase-activating protein pac-1
Locus_15392_Transcript_1/1_Conf_1.000	539	20	4.23E-50	NP_506859.2	79	201.06	177	140	hypothetical protein C06B8.7
Locus_15393_Transcript_1/1_Conf_1.000	615	20	1.47E-67	EFO23641.1	76	259.61	210	161	hypothetical protein LOAG_04841
Locus_15394_Transcript_1/1_Conf_1.000	329	0							

Locus_15395_Transcript_1/1_Conf_1.000	481	20	1.81E-64	XP_002630872.1	92	248.44	140	129	Hypothetical protein CBG02589
Locus_15396_Transcript_1/1_Conf_1.000	365	20	4.69E-20	EFO25500.1	78	100.908	80	63	STE/STE20/TAO protein kinase
Locus_15397_Transcript_1/1_Conf_1.000	150	0							
Locus_15398_Transcript_1/1_Conf_1.000	303	6	1.24E-12	CAA10033.1	67	76.2554	100	67	DYS-1 protein
Locus_15399_Transcript_1/1_Conf_1.000	312	20	1.90E-24	NP_506256.3	66	115.546	104	69	CaDHerin family member (cdh-6)
Locus_154_Transcript_1/1_Conf_1.000	366	20	1.07E-32	XP_001897933.1	77	142.895	115	89	RE01069p
Locus_1540_Transcript_1/1_Conf_1.000	534	0							

Locus_15400_Transcript_1/1_Conf_1.000	669	20	9.29E-101	CAR63641.1	97	370.163	206	200	putative 26S proteasome regulatory chain 4
Locus_15401_Transcript_1/1_Conf_1.000	401	0							
Locus_15402_Transcript_1/1_Conf_1.000	1057	20	7.41E-69	NP_493723.3	85	265.388	199	170	hypothetical protein C03H5.2
Locus_15403_Transcript_1/1_Conf_1.000	217	0							
Locus_15404_Transcript_1/1_Conf_1.000	194	0							
Locus_15405_Transcript_1/1_Conf_1.000	273	0							
Locus_15406_Transcript_1/1_Conf_1.000	105	0							
Locus_15407_Transcript_1/1_Conf_1.000	617	0							
Locus_15408_Transcript_1/1_Conf_1.000	214	20	6.55E-14	EFO25803.1	84	80.4925	53	45	enoyl-CoA hydratase/isomerase
Locus_15409_Transcript_1/1_Conf_1.000	313	20	1.78E-06	XP_002940157.1	56	55.8398	83	47	PREDICTED: PI-PLC X domain-containing protein 2-like
Locus_1541_Transcript_1/1_Conf_1.000	4728	20	0	NP_494819.3	57	843.958	1579	910	abnormal DYe Filling family member (dyf-14)
Locus_15410_Transcript_1/1_Conf_1.000	336	0							
Locus_15411_Transcript_1/1_Conf_1.000	250	0							
Locus_15412_Transcript_1/1_Conf_1.000	668	20	6.68E-51	NP_001041018.1	72	204.527	200	144	hypothetical protein Y11D7A.3
Locus_15413_Transcript_1/1_Conf_1.000	315	20	5.32E-19	NP_498593.1	74	97.4413	103	77	hypothetical protein R151.10
Locus_15414_Transcript_1/1_Conf_1.000	205	0							
Locus_15415_Transcript_1/2_Conf_1.000	201	1	5.63E-05	XP_002638777.1	65	50.8322	38	25	C. briggsae CBR-NAS-30 protein
Locus_15415_Transcript_2/2_Conf_1.000	336	5	5.92E-23	XP_002638777.1	71	110.538	107	76	C. briggsae CBR-NAS-30 protein

Locus_15416_Transcript_1/1_Conf_1.000	280	4	2.32E-19	CBM41243.1	68	98.5969	89	61	C. elegans protein Y39B6A.43c, partially confirmed by transcript evidence
Locus_15417_Transcript_1/1_Conf_1.000	452	0							
Locus_15418_Transcript_1/1_Conf_1.000	286	20	7.45E-13	XP_002637159.1	78	77.0258	82	64	C. briggsae CBR-AQP-6 protein
Locus_15419_Transcript_1/1_Conf_1.000	179	0							
Locus_1542_Transcript_1/3_Conf_0.556	533	20	3.37E-84	XP_002638552.1	94	314.309	170	161	C. briggsae CBR-RPL-2 protein
Locus_1542_Transcript_2/3_Conf_0.778	633	20	3.02E-87	XP_002638552.1	94	325.094	193	182	C. briggsae CBR-RPL-2 protein
Locus_1542_Transcript_3/3_Conf_0.667	633	20	3.02E-87	XP_002638552.1	94	325.094	193	182	C. briggsae CBR-RPL-2 protein
Locus_15420_Transcript_1/1_Conf_1.000	264	0							
Locus_15421_Transcript_1/1_Conf_1.000	420	0							
Locus_15422_Transcript_1/1_Conf_1.000	457	0							
Locus_15423_Transcript_1/1_Conf_1.000	151	0							
Locus_15424_Transcript_1/1_Conf_1.000	131	20	2.13E-12	XP_002641501.1	93	75.485	43	40	Hypothetical protein CBG09795
Locus_15425_Transcript_1/1_Conf_1.000	312	0							
Locus_15426_Transcript_1/1_Conf_1.000	251	3	2.03E-23	XP_002642237.1	80	112.079	83	67	Hypothetical protein CBG18219
Locus_15427_Transcript_1/1_Conf_1.000	379	0							
Locus_15428_Transcript_1/1_Conf_1.000	167	0							
Locus_15429_Transcript_1/1_Conf_1.000	310	0							
Locus_1543_Transcript_1/1_Conf_1.000	1050	20	2.03E-119	XP_002642557.1	78	433.335	343	268	Hypothetical protein CBG20194
Locus_15430_Transcript_1/1_Conf_1.000	449	10	1.58E-31	CBK55579.1	68	139.043	132	91	C. elegans protein C25G4.3b, confirmed by transcript evidence

Locus_15431_Transcript_1/1_Conf_1.000	515	19	5.14E-20	XP_002639725.1	63	100.908	146	92	Hypothetical protein CBG12452
Locus_15432_Transcript_1/1_Conf_1.000	284	20	4.66E-31	EFO15717.1	84	137.502	93	79	hypothetical protein LOAG_12793
Locus_15433_Transcript_1/1_Conf_1.000	270	3	5.23E-19	NP_501219.1	69	97.4413	81	56	hypothetical protein R05G6.1
Locus_15434_Transcript_1/1_Conf_1.000	311	20	1.18E-39	XP_002641970.1	91	166.007	92	84	Hypothetical protein CBG16677
Locus_15435_Transcript_1/2_Conf_1.000	1069	3	4.90E-60	NP_509393.3	89	236.113	157	140	hypothetical protein M60.6
Locus_15435_Transcript_2/2_Conf_1.000	239	3	3.07E-19	NP_509393.3	86	98.2117	66	57	hypothetical protein M60.6
Locus_15436_Transcript_1/1_Conf_1.000	155	0							
Locus_15437_Transcript_1/1_Conf_1.000	215	0							
Locus_15438_Transcript_1/1_Conf_1.000	807	0							
Locus_15439_Transcript_1/2_Conf_1.000	550	20	5.35E-75	NP_741437.1	88	283.878	182	161	DEnse Body family member (deb-1)
Locus_15439_Transcript_2/2_Conf_1.000	555	20	3.25E-75	NP_741437.1	88	284.648	184	162	DEnse Body family member (deb-1)
Locus_1544_Transcript_1/1_Conf_1.000	310	0							
Locus_15440_Transcript_1/1_Conf_1.000	185	0							
Locus_15441_Transcript_1/1_Conf_1.000	425	20	1.25E-44	XP_002645045.1	78	182.57	132	104	C. briggsae CBR-MEK-1 protein
Locus_15442_Transcript_1/1_Conf_1.000	150	0							
Locus_15443_Transcript_1/1_Conf_1.000	322	20	1.26E-12	NP_001024271.1	70	76.2554	71	50	CHeckpoint Kinase family member (chk-2)
Locus_15444_Transcript_1/1_Conf_1.000	138	20	5.92E-15	ADD20480.1	95	83.9593	45	43	hypothetical conserved protein
Locus_15445_Transcript_1/1_Conf_1.000	320	20	9.02E-27	NP_506082.2	75	123.25	104	79	hypothetical protein F55C5.7

Locus_15446_Transcript_1/1_Conf_1.000	664	20	2.10E-81	EAX09318.1	100	305.834	166	166	collagen, type VI, alpha 2, isoform CRA_c
Locus_15447_Transcript_1/2_Conf_1.000	328	0							
Locus_15447_Transcript_2/2_Conf_1.000	328	0							
Locus_15448_Transcript_1/1_Conf_1.000	203	20	2.69E-15	XP_002643273.1	86	85.1149	67	58	C. briggsae CBR-MRP-1 protein
Locus_15449_Transcript_1/1_Conf_1.000	497	20	6.33E-33	XP_001896024.1	68	143.665	150	102	DNA ligase III
Locus_1545_Transcript_1/1_Conf_1.000	865	20	1.18E-116	XP_002637027.1	84	423.705	257	218	Hypothetical protein CBG09520
Locus_15450_Transcript_1/1_Conf_1.000	355	0							
Locus_15451_Transcript_1/2_Conf_1.000	424	20	7.63E-10	XP_001892560.1	66	67.0106	69	46	GPI transamidase subunit PIG-U family protein
Locus_15451_Transcript_2/2_Conf_1.000	409	20	5.78E-10	XP_001892560.1	66	67.3958	69	46	GPI transamidase subunit PIG-U family protein
Locus_15452_Transcript_1/1_Conf_1.000	883	20	4.00E-27	XP_002636475.1	60	126.331	192	117	Hypothetical protein CBG23146
Locus_15453_Transcript_1/1_Conf_1.000	281	0							
Locus_15454_Transcript_1/1_Conf_1.000	157	0							
Locus_15455_Transcript_1/1_Conf_1.000	268	0							
Locus_15456_Transcript_1/1_Conf_1.000	577	20	2.78E-27	XP_002641517.1	86	125.561	79	68	Hypothetical protein CBG09813
Locus_15457_Transcript_1/1_Conf_1.000	342	20	8.42E-49	XP_002634599.1	89	196.438	112	100	Hypothetical protein CBG08414

Locus_15458_Transcript_1/1_Conf_1.000	365	20	3.92E-59	ABM84473.1	100	230.72	121	121	cathepsin D (lysosomal aspartyl peptidase)
Locus_15459_Transcript_1/1_Conf_1.000	134	0							
Locus_1546_Transcript_1/1_Conf_1.000	961	6	1.92E-49	NP_492029.2	93	200.675	117	109	hypothetical protein M05B5.2
Locus_15460_Transcript_1/1_Conf_1.000	292	0							
Locus_15461_Transcript_1/1_Conf_1.000	305	20	1.33E-22	ACO15791.1	73	109.383	100	73	Hypothetical protein Y71F9B.9b
Locus_15462_Transcript_1/1_Conf_1.000	141	0							
Locus_15463_Transcript_1/1_Conf_1.000	260	2	1.49E-29	NP_500538.2	93	132.494	86	80	Ligand-Gated ion Channel family member (lgc-22)
Locus_15464_Transcript_1/1_Conf_1.000	286	0							
Locus_15465_Transcript_1/1_Conf_1.000	194	0							
Locus_15466_Transcript_1/2_Conf_1.000	409	9	1.24E-28	NP_506123.2	74	129.413	99	74	hypothetical protein C54D10.10
Locus_15466_Transcript_2/2_Conf_1.000	416	9	1.23E-28	NP_506123.2	74	129.413	99	74	hypothetical protein C54D10.10
Locus_15467_Transcript_1/1_Conf_1.000	381	20	7.07E-16	NP_001023850.1	79	87.0409	98	78	LEThal family member (let-413)

Locus_15468_Transcript_1/1_Conf_1.000	141	20	3.24E-13	XP_002925604.1	100	78.1814	36	36	PREDICTED: receptor-type tyrosine-protein phosphatase F-like isoform 2
Locus_15469_Transcript_1/1_Conf_1.000	485	0							
Locus_1547_Transcript_1/1_Conf_1.000	550	2	1.26E-07	XP_002644421.1	64	60.077	74	48	C. briggsae CBR-NLP-1 protein
Locus_15470_Transcript_1/1_Conf_1.000	166	0							
Locus_15471_Transcript_1/1_Conf_1.000	220	0							
Locus_15472_Transcript_1/1_Conf_1.000	171	0							
Locus_15473_Transcript_1/1_Conf_1.000	224	0							
Locus_15474_Transcript_1/1_Conf_1.000	595	20	1.93E-50	NP_506382.1	93	202.601	141	132	LETM1 (Leucine zipper, EF-hand, TransMembrane mitochondrial protein) homolog family member (letm-1)
Locus_15475_Transcript_1/1_Conf_1.000	278	0							
Locus_15476_Transcript_1/1_Conf_1.000	594	1	3.11E-08	XP_002813353.1	55	62.3882	83	46	PREDICTED: hypothetical protein LOC100439541
Locus_15477_Transcript_1/1_Conf_1.000	187	2	6.53E-09	NP_504708.1	80	63.929	57	46	hypothetical protein T25F10.3
Locus_15478_Transcript_1/1_Conf_1.000	325	1	7.52E-04	AAB61392.1	59	45.4394	54	32	transposase
Locus_15479_Transcript_1/1_Conf_1.000	249	0							
Locus_1548_Transcript_1/1_Conf_1.000	1383	20	6.32E-141	NP_510669.1	86	505.368	322	277	hypothetical protein F38E9.5
Locus_15480_Transcript_1/1_Conf_1.000	265	0							
Locus_15481_Transcript_1/1_Conf_1.000	267	0							
Locus_15482_Transcript_1/1_Conf_1.000	338	3	2.66E-15	NP_497943.2	61	85.1149	116	71	hypothetical protein F10F2.4

Locus_15483_Transcript_1/1_Conf_1.000	291	20	1.06E-43	NP_499783.1	96	179.489	96	93	Cyclin-Dependent Kinase family member (cdk-5)
Locus_15484_Transcript_1/1_Conf_1.000	348	3	7.86E-31	NP_500393.2	75	136.732	115	87	hypothetical protein Y37E11AL.5
Locus_15485_Transcript_1/1_Conf_1.000	145	2	1.62E-07	XP_002642776.1	80	59.3066	46	37	C. briggsae CBR-WRS-2 protein
Locus_15486_Transcript_1/1_Conf_1.000	409	0							
Locus_15487_Transcript_1/1_Conf_1.000	1319	20	1.15E-144	XP_002636212.1	74	517.694	438	327	Hypothetical protein CBG12133
Locus_15488_Transcript_1/1_Conf_1.000	251	5	4.52E-15	XP_002629829.1	68	84.3445	83	57	C. briggsae CBR-PLC-3 protein
Locus_15489_Transcript_1/2_Conf_1.000	751	20	3.50E-68	NP_499676.1	82	262.307	177	146	hypothetical protein Y37D8A.10

Locus_15489_Transcript_2/2_Conf_1.000	573	20	1.88E-68	NP_499676.1	82	262.307	177	146	hypothetical protein Y37D8A.10
Locus_1549_Transcript_1/2_Conf_1.000	1206	20	5.20E-141	XP_002631017.1	81	505.368	402	326	Hypothetical protein CBG02769
Locus_1549_Transcript_2/2_Conf_1.000	1206	20	5.20E-141	XP_002631017.1	80	505.368	402	324	Hypothetical protein CBG02769
Locus_15490_Transcript_1/1_Conf_1.000	266	0							
Locus_15491_Transcript_1/1_Conf_1.000	302	0							
Locus_15492_Transcript_1/1_Conf_1.000	247	0							
Locus_15493_Transcript_1/1_Conf_1.000	314	0							
Locus_15494_Transcript_1/1_Conf_1.000	284	16	7.21E-24	XP_002646276.1	74	113.62	85	63	C. briggsae CBR-ABF-2 protein
Locus_15495_Transcript_1/1_Conf_1.000	1353	20	0	NP_740900.1	86	639.802	450	389	hypothetical protein T08G11.1
Locus_15496_Transcript_1/1_Conf_1.000	378	20	2.88E-25	NP_498264.1	80	118.242	82	66	Dipeptidyl Peptidase Four (IV) family member (dpf-4)
Locus_15497_Transcript_1/1_Conf_1.000	158	0							
Locus_15498_Transcript_1/1_Conf_1.000	140	20	5.92E-15	XP_001098677.2	100	83.9593	38	38	PREDICTED: serine incorporator 2
Locus_15499_Transcript_1/1_Conf_1.000	372	0							

Locus_155_Transcript_1/1_Conf_1.000	842	20	6.83E-82	XP_002636957.1	96	308.145	150	145	C. briggsae CBR-EAT-6 protein
Locus_1550_Transcript_1/1_Conf_1.000	301	15	8.94E-11	XP_002634040.1	66	70.0922	104	69	C. briggsae CBR-VIT-6 protein
Locus_15500_Transcript_1/1_Conf_1.000	419	5	1.82E-27	ACT20210.1	67	125.561	139	94	Hypothetical protein Y34B4A.8b
Locus_15501_Transcript_1/2_Conf_1.000	509	0							
Locus_15501_Transcript_2/2_Conf_1.000	509	0							
Locus_15502_Transcript_1/1_Conf_1.000	300	20	2.19E-25	XP_001891853.1	78	118.627	97	76	Patched family protein
Locus_15503_Transcript_1/1_Conf_1.000	438	20	4.50E-31	NP_001032972.1	76	137.502	98	75	hypothetical protein C36B1.14
Locus_15504_Transcript_1/1_Conf_1.000	647	0							
Locus_15505_Transcript_1/1_Conf_1.000	940	20	6.54E-103	NP_492779.1	92	378.252	240	223	hypothetical protein B0511.6

Locus_15506_Transcript_1/1_Conf_1.000	191	20	1.03E-30	CAX12872.1	100	136.346	63	63	major histocompatibility complex, class I, F
Locus_15507_Transcript_1/1_Conf_1.000	278	0							
Locus_15508_Transcript_1/1_Conf_1.000	254								
Locus_15509_Transcript_1/2_Conf_1.000	235	6	2.28E-22	EFO24879.1	76	108.612	78	60	hypothetical protein LOAG_03607
Locus_15509_Transcript_2/2_Conf_1.000	235	6	2.28E-22	EFO24879.1	76	108.612	78	60	hypothetical protein LOAG_03607
Locus_1551_Transcript_1/1_Conf_1.000	689	2	3.27E-11	XP_002637606.1	53	72.7886	116	62	Hypothetical protein CBG19344
Locus_15510_Transcript_1/1_Conf_1.000	150	0							
Locus_15511_Transcript_1/1_Conf_1.000	326	0							
Locus_15512_Transcript_1/1_Conf_1.000	371	1	1.31E-09	NP_001022291.1	58	66.2402	102	60	hypothetical protein T01B7.5
Locus_15513_Transcript_1/1_Conf_1.000	454	0							
Locus_15514_Transcript_1/1_Conf_1.000	528	20	1.50E-44	NP_493617.2	86	182.57	119	103	hypothetical protein F33H2.6
Locus_15515_Transcript_1/1_Conf_1.000	667	20	7.79E-92	BAB32114.1	92	340.502	200	185	unnamed protein product
Locus_15516_Transcript_1/1_Conf_1.000	135	0							
Locus_15517_Transcript_1/1_Conf_1.000	439	2	9.45E-05	AAX33674.1	39	50.0618	113	45	plus agglutinin
Locus_15518_Transcript_1/1_Conf_1.000	552	20	9.39E-43	NP_497829.1	84	176.792	118	100	hypothetical protein C16C10.8

Locus_15519_Transcript_1/2_Conf_1.000	702	20	7.80E-64	NP_492861.1	76	247.669	238	183	hypothetical protein Y52B11A.10
Locus_15519_Transcript_2/2_Conf_1.000	702	20	7.80E-64	NP_492861.1	76	247.669	238	183	hypothetical protein Y52B11A.10
Locus_1552_Transcript_1/1_Conf_1.000	415	0							
Locus_15520_Transcript_1/1_Conf_1.000	332	0							
Locus_15521_Transcript_1/1_Conf_1.000	671	0							
Locus_15522_Transcript_1/1_Conf_1.000	551	0							
Locus_15523_Transcript_1/1_Conf_1.000	269	6	3.39E-26	NP_502119.2	86	121.324	79	68	hypothetical protein F54D1.6
Locus_15524_Transcript_1/1_Conf_1.000	324	20	6.42E-25	NP_491660.1	79	117.087	94	75	hypothetical protein F55F8.9
Locus_15525_Transcript_1/1_Conf_1.000	138	0							
Locus_15526_Transcript_1/1_Conf_1.000	271	0							
Locus_15527_Transcript_1/1_Conf_1.000	501	0							
Locus_15528_Transcript_1/1_Conf_1.000	284	0							
Locus_15529_Transcript_1/1_Conf_1.000	391	0							
Locus_1553_Transcript_1/1_Conf_1.000	2756	20	0	NP_741743.1	93	922.924	532	495	Propionyl Coenzyme A Carboxylase Beta subunit family member (pccb-1)
Locus_15530_Transcript_1/1_Conf_1.000	285	0							
Locus_15531_Transcript_1/1_Conf_1.000	381	20	1.24E-44	XP_002640754.1	84	182.57	123	104	Hypothetical protein CBG24191
Locus_15532_Transcript_1/1_Conf_1.000	252	0							
Locus_15533_Transcript_1/1_Conf_1.000	278	20	5.18E-27	XP_002635871.1	86	124.02	88	76	Hypothetical protein CBG01087
Locus_15534_Transcript_1/1_Conf_1.000	273	0							
Locus_15535_Transcript_1/1_Conf_1.000	361	0							
Locus_15536_Transcript_1/1_Conf_1.000	220	0							

Locus_15537_Transcript_1/1_Conf_1.000	129	20	2.78E-12	EFO25124.1	90	75.0998	42	38	bromodomain containing protein
Locus_15538_Transcript_1/1_Conf_1.000	411	20	1.19E-31	XP_002631305.1	67	139.428	139	94	C. briggsae CBR-DNA-2 protein
Locus_15539_Transcript_1/1_Conf_1.000	135	0							
Locus_1554_Transcript_1/1_Conf_1.000	1072	3	5.95E-98	NP_499903.3	70	362.073	357	252	Defecation Suppressor of Clk-1 family member (dsc-4)
Locus_15540_Transcript_1/1_Conf_1.000	216	0							
Locus_15541_Transcript_1/1_Conf_1.000	636	20	1.59E-51	NP_508877.1	73	206.453	176	130	hypothetical protein T03G11.4
Locus_15542_Transcript_1/1_Conf_1.000	131	0							
Locus_15543_Transcript_1/1_Conf_1.000	151	7	5.70E-13	XP_001900069.1	85	77.411	49	42	protein C18H9.7
Locus_15544_Transcript_1/1_Conf_1.000	394	0							
Locus_15545_Transcript_1/1_Conf_1.000	479	6	1.67E-17	CBM41243.1	60	92.4337	120	72	C. elegans protein Y39B6A.43c, partially confirmed by transcript evidence
Locus_15546_Transcript_1/2_Conf_1.000	363	20	2.82E-49	NP_498923.1	93	197.978	108	101	hypothetical protein B0303.15

Locus_15546_Transcript_2/2_Conf_1.000	345	20	2.61E-50	NP_498923.1	92	201.445	113	104	hypothetical protein B0303.15
Locus_15547_Transcript_1/1_Conf_1.000	138	0							
Locus_15548_Transcript_1/1_Conf_1.000	342	0							
Locus_15549_Transcript_1/1_Conf_1.000	665	20	8.05E-57	NP_741241.1	67	224.172	221	150	Dipeptidyl Peptidase Four (IV) family member (dpf-6)
Locus_1555_Transcript_1/1_Conf_1.000	237	20	5.78E-26	NP_491399.1	85	120.553	78	67	Ribosomal Protein, Large subunit family member (rpl-24.1)
Locus_15550_Transcript_1/1_Conf_1.000	249	20	3.23E-29	NP_509693.1	85	131.339	81	69	hypothetical protein W07E11.1
Locus_15551_Transcript_1/1_Conf_1.000	669	0							
Locus_15552_Transcript_1/1_Conf_1.000	186	20	2.73E-23	NP_497696.2	91	111.694	62	57	Pim (mammalian oncogene) Related Kinase family member (prk-2)
Locus_15553_Transcript_1/1_Conf_1.000	464	20	1.05E-67	NP_505493.1	90	259.225	154	140	SULfate Permease family member (sulp-8)
Locus_15554_Transcript_1/1_Conf_1.000	149	0							
Locus_15555_Transcript_1/1_Conf_1.000	852	20	8.57E-88	EFO26794.1	75	327.791	280	211	galactoside-binding lectin family protein
Locus_15556_Transcript_1/1_Conf_1.000	405	0							
Locus_15557_Transcript_1/1_Conf_1.000	597	20	7.64E-71	NP_496968.1	82	270.396	188	155	hypothetical protein Y48B6A.12

Locus_15558_Transcript_1/2_Conf_1.000	267	0							
Locus_15558_Transcript_2/2_Conf_1.000	290	0							
Locus_15559_Transcript_1/1_Conf_1.000	741	5	5.18E-08	XP_001897464.1	51	62.3882	107	55	hypothetical protein Bm1_30125
Locus_1556_Transcript_1/1_Conf_1.000	1175	20	3.30E-68	NP_504349.1	79	263.462	216	172	hypothetical protein K11D12.5
Locus_15560_Transcript_1/1_Conf_1.000	534	20	3.76E-35	EFO27810.1	70	151.369	144	101	plasmid Maintenance protein containing protein
Locus_15561_Transcript_1/1_Conf_1.000	501	0							
Locus_15562_Transcript_1/1_Conf_1.000	289	20	3.80E-25	XP_002632959.1	77	117.857	93	72	C. briggsae CBR-RAD-26 protein
Locus_15563_Transcript_1/1_Conf_1.000	414	0							
Locus_15564_Transcript_1/1_Conf_1.000	718	20	1.74E-66	NP_001021021.1	80	256.529	189	152	hypothetical protein C32F10.8
Locus_15565_Transcript_1/1_Conf_1.000	179	0							
Locus_15566_Transcript_1/1_Conf_1.000	164	20	1.21E-15	XP_001900591.1	88	86.2705	53	47	Blistered cuticle protein 3
Locus_15567_Transcript_1/1_Conf_1.000	582	20	2.07E-09	XP_001895583.1	73	66.2402	49	36	Surfeit locus protein 4 homolog
Locus_15568_Transcript_1/1_Conf_1.000	614								

Locus_15569_Transcript_1/1_Conf_1.000	294	0							
Locus_1557_Transcript_1/1_Conf_1.000	1009	0							
Locus_15570_Transcript_1/1_Conf_1.000	195	3	3.93E-06	NP_504274.2	82	54.6842	39	32	UDP-GlucuronosylTransferase family member (ugt-61)
Locus_15571_Transcript_1/1_Conf_1.000	1578	20	1.67E-140	EFO23974.1	71	504.212	471	337	hypothetical protein LOAG_04507
Locus_15572_Transcript_1/1_Conf_1.000	338	10	5.52E-29	NP_001021303.1	69	130.568	108	75	Nuclear Hormone Receptor family member (nhr-105)
Locus_15573_Transcript_1/1_Conf_1.000	328	20	8.58E-46	XP_001111129.1	100	186.422	103	103	PREDICTED: CD63 antigen isoform 1
Locus_15574_Transcript_1/1_Conf_1.000	204	20	7.07E-16	NP_508272.1	88	87.0409	52	46	human SEDL (spondyloepiphyseal dysplasia tarda) related family member (sedl-1)
Locus_15575_Transcript_1/1_Conf_1.000	768	20	4.71E-92	NP_507487.1	84	341.658	252	214	P-GlycoProtein related family member (pgp-9)
Locus_15576_Transcript_1/1_Conf_1.000	402	20	1.09E-32	XP_002632873.1	69	142.895	132	92	Hypothetical protein CBG15077
Locus_15577_Transcript_1/1_Conf_1.000	557	6	6.25E-10	CAD44516.1	55	67.781	184	102	VAB-10B protein
Locus_15578_Transcript_1/1_Conf_1.000	167	0							
Locus_15579_Transcript_1/1_Conf_1.000	353	0							
Locus_1558_Transcript_1/1_Conf_1.000	3022	17	1.53E-21	EFO26551.1	60	110.153	157	95	hypothetical protein LOAG_01926
Locus_15580_Transcript_1/1_Conf_1.000	197	0							
Locus_15581_Transcript_1/1_Conf_1.000	160	0							
Locus_15582_Transcript_1/1_Conf_1.000	696	20	4.08E-41	XP_002640039.1	76	172.17	170	130	Hypothetical protein CBG12511
Locus_15583_Transcript_1/1_Conf_1.000	207	0							
Locus_15584_Transcript_1/1_Conf_1.000	426	0							
Locus_15585_Transcript_1/1_Conf_1.000	135	3	1.28E-09	NP_001041140.1	84	66.2402	44	37	hypothetical protein F58H1.7
Locus_15586_Transcript_1/1_Conf_1.000	302	0							

Locus_15587_Transcript_1/1_Conf_1.000	290	20	1.76E-22	XP_001897819.1	88	108.997	79	70	Surfeit locus protein 5 containing protein
Locus_15588_Transcript_1/1_Conf_1.000	270	2	9.05E-39	CAH93159.1	100	135.961	67	67	hypothetical protein
Locus_15589_Transcript_1/1_Conf_1.000	235	0							
Locus_1559_Transcript_1/1_Conf_1.000	2882	20	0	EFO24169.1	70	836.639	887	627	hypothetical protein LOAG_04317
Locus_15590_Transcript_1/1_Conf_1.000	172	0							
Locus_15591_Transcript_1/1_Conf_1.000	133	0							
Locus_15592_Transcript_1/1_Conf_1.000	222	20	6.50E-25	NP_494991.1	92	117.087	69	64	Phosphoethanolamine MethyTransferase family member (pmt-1)
Locus_15593_Transcript_1/1_Conf_1.000	196	0							
Locus_15594_Transcript_1/1_Conf_1.000	265	0							
Locus_15595_Transcript_1/1_Conf_1.000	491	20	1.56E-55	XP_002633256.1	80	218.779	155	125	Hypothetical protein CBG05981
Locus_15596_Transcript_1/1_Conf_1.000	487	0							
Locus_15597_Transcript_1/1_Conf_1.000	300	0							
Locus_15598_Transcript_1/1_Conf_1.000	638	20	1.02E-82	XP_002630211.1	86	310.071	213	184	C. briggsae CBR-FRS-2 protein
Locus_15599_Transcript_1/1_Conf_1.000	500	0							
Locus_156_Transcript_1/2_Conf_1.000	391	0							
Locus_156_Transcript_2/2_Conf_1.000	366	0							
Locus_1560_Transcript_1/1_Conf_1.000	331	0							

Locus_15600_Transcript_1/1_Conf_1.000	327	20	3.16E-40	EFO23513.1	85	167.933	108	92	CMGC/CDK/CRK7 protein kinase
Locus_15601_Transcript_1/1_Conf_1.000	173	0							
Locus_15602_Transcript_1/1_Conf_1.000	378	0							
Locus_15603_Transcript_1/1_Conf_1.000	312	0							
Locus_15604_Transcript_1/1_Conf_1.000	301	0							
Locus_15605_Transcript_1/1_Conf_1.000	184	0							
Locus_15606_Transcript_1/1_Conf_1.000	379	20	1.73E-46	P51535.1	90	188.734	113	102	Myoglobin
Locus_15607_Transcript_1/1_Conf_1.000	396	0							
Locus_15608_Transcript_1/1_Conf_1.000	509	20	1.20E-13	XP_001897610.1	67	79.7221	87	59	SNARE-associated protein Snapin
Locus_15609_Transcript_1/1_Conf_1.000	438	2	1.61E-04	XP_002067139.1	52	49.2914	110	58	GK24176
Locus_1561_Transcript_1/1_Conf_1.000	1253	20	3.52E-71	NP_495686.2	72	273.478	266	194	hypothetical protein T05H10.1
Locus_15610_Transcript_1/1_Conf_1.000	188	0							
Locus_15611_Transcript_1/1_Conf_1.000	232	20	5.83E-18	NP_499865.1	75	93.9745	79	60	hypothetical protein F29C4.6
Locus_15612_Transcript_1/1_Conf_1.000	140	0							
Locus_15613_Transcript_1/1_Conf_1.000	229	0							
Locus_15614_Transcript_1/1_Conf_1.000	398	20	4.17E-40	XP_002632119.1	77	167.548	134	104	Hypothetical protein CBG06974
Locus_15615_Transcript_1/1_Conf_1.000	921	20	1.96E-112	NP_490973.2	90	409.838	255	231	hypothetical protein F23C8.5
Locus_15616_Transcript_1/1_Conf_1.000	135	0							
Locus_15617_Transcript_1/1_Conf_1.000	343	0							
Locus_15618_Transcript_1/1_Conf_1.000	391	2	1.66E-33	NP_496432.2	69	145.591	123	86	hypothetical protein C05D12.1
Locus_15619_Transcript_1/1_Conf_1.000	553	20	1.50E-48	XP_002635580.1	70	196.052	151	106	C. briggsae CBR-PPN-1 protein

Locus_1562_Transcript_1/1_Conf_1.000	359	0							
Locus_15620_Transcript_1/1_Conf_1.000	839	0							
Locus_15621_Transcript_1/1_Conf_1.000	278	0							
Locus_15622_Transcript_1/1_Conf_1.000	282	0							
Locus_15623_Transcript_1/1_Conf_1.000	473	20	4.26E-37	XP_001894688.1	66	157.532	155	103	Protein-tyrosine phosphatase containing protein
Locus_15624_Transcript_1/1_Conf_1.000	347	20	3.29E-53	NP_001122975.1	98	211.075	114	112	hypothetical protein K10C8.3
Locus_15625_Transcript_1/1_Conf_1.000	326	0							
Locus_15626_Transcript_1/1_Conf_1.000	277	0							
Locus_15627_Transcript_1/1_Conf_1.000	558	0							
Locus_15628_Transcript_1/1_Conf_1.000	715								
Locus_15629_Transcript_1/1_Conf_1.000	245	0							
Locus_1563_Transcript_1/2_Conf_1.000	3044	20	1.65E-148		56	531.946	842	475	hypothetical protein H15N14.1a - Caenorhabditis elegans
Locus_1563_Transcript_2/2_Conf_1.000	3038	20	4.94E-153		56	546.969	842	474	hypothetical protein H15N14.1a - Caenorhabditis elegans
Locus_15630_Transcript_1/2_Conf_1.000	280	0							
Locus_15630_Transcript_2/2_Conf_1.000	280	0							
Locus_15631_Transcript_1/1_Conf_1.000	242	0							
Locus_15632_Transcript_1/2_Conf_1.000	834	20	8.20E-96	XP_002631134.1	86	354.369	229	199	Hypothetical protein CBG02918
Locus_15632_Transcript_2/2_Conf_1.000	232	20	7.60E-26	NP_496427.1	74	120.168	95	71	hypothetical protein B0491.7
Locus_15633_Transcript_1/1_Conf_1.000	145	20	2.58E-13	NP_499028.1	85	78.5666	48	41	NHL (ring finger b-box coiled coil) domain containing family member (nhl-1)
Locus_15634_Transcript_1/1_Conf_1.000	282	0							
Locus_15635_Transcript_1/1_Conf_1.000	410	0							
Locus_15636_Transcript_1/2_Conf_1.000	695	20	4.12E-94	NP_493832.1	84	348.206	231	196	Acyl CoA DeHydrogenase family member (acdh-9)
Locus_15636_Transcript_2/2_Conf_1.000	695	20	1.41E-94	NP_493832.1	84	349.747	231	196	Acyl CoA DeHydrogenase family member (acdh-9)
Locus_15637_Transcript_1/1_Conf_1.000	385	20	1.42E-24	NP_001122663.1	76	115.931	91	70	hypothetical protein Y53F4B.39
Locus_15638_Transcript_1/1_Conf_1.000	309	0							
Locus_15639_Transcript_1/1_Conf_1.000	542	0							

Locus_1564_Transcript_1/1_Conf_1.000	785	20	5.12E-57	XP_001899636.1	71	225.328	207	147	Chain A, Two Seven-Bladed Beta-Propeller Domains Revealed By The Structure Of A C. Elegans Homologue Of Yeast Actin Interacting Protein 1, putative
Locus_15640_Transcript_1/1_Conf_1.000	266	0							
Locus_15641_Transcript_1/1_Conf_1.000	279	0							
Locus_15642_Transcript_1/1_Conf_1.000	426	20	2.94E-62	XP_001896500.1	87	241.121	139	122	leucyl-tRNA synthetase
Locus_15643_Transcript_1/1_Conf_1.000	319	20	6.63E-54	EFO21255.1	97	213.386	106	103	hypothetical protein LOAG_07233
Locus_15644_Transcript_1/1_Conf_1.000	618	20	1.35E-44	NP_497787.1	88	183.341	109	97	Paralysed Arrest at Two-fold family member (pat-3)
Locus_15645_Transcript_1/1_Conf_1.000	527	0							
Locus_15646_Transcript_1/1_Conf_1.000	266	0							
Locus_15647_Transcript_1/1_Conf_1.000	332	8	2.78E-04	NP_001174833.1	59	48.521	54	32	Os06g0534900
Locus_15648_Transcript_1/1_Conf_1.000	290	0							
Locus_15649_Transcript_1/1_Conf_1.000	495	20	5.74E-26	XP_002646337.1	55	120.553	170	95	Hypothetical protein CBG12050
Locus_1565_Transcript_1/1_Conf_1.000	2446	20	8.87E-25	XP_001464299.1	41	120.553	806	333	kinesin K39
Locus_15650_Transcript_1/1_Conf_1.000	849	3	1.93E-23	NP_001022400.1	45	114.005	284	130	Polarity and Osmotic sensitivity Defect family member (pod-2)
Locus_15651_Transcript_1/1_Conf_1.000	568	20	8.14E-69	NP_001129905.1	80	263.462	190	152	hypothetical protein T03D8.6
Locus_15652_Transcript_1/1_Conf_1.000	200	0							
Locus_15653_Transcript_1/1_Conf_1.000	209	0							
Locus_15654_Transcript_1/1_Conf_1.000	784	20	2.91E-52	XP_002639833.1	64	209.534	219	141	C. briggsae CBR-MET-1 protein
Locus_15655_Transcript_1/1_Conf_1.000	159	0							

Locus_15656_Transcript_1/2_Conf_1.000	592	20	1.22E-73	NP_499759.1	78	279.641	198	156	DNaJ domain (prokaryotic heat shock protein) family member (dnj-17)
Locus_15656_Transcript_2/2_Conf_1.000	744	20	2.53E-95	NP_499759.1	81	352.443	248	201	DNaJ domain (prokaryotic heat shock protein) family member (dnj-17)
Locus_15657_Transcript_1/1_Conf_1.000	428	20	9.86E-34	XP_001901272.1	73	146.362	143	105	DEAD
Locus_15658_Transcript_1/1_Conf_1.000	214	0							
Locus_15659_Transcript_1/1_Conf_1.000	188	0							
Locus_1566_Transcript_1/2_Conf_1.000	979	0							
Locus_1566_Transcript_2/2_Conf_1.000	1193	0							
Locus_15660_Transcript_1/1_Conf_1.000	446	2	5.29E-11	XP_001902408.1	50	70.8626	162	81	hypothetical protein Bm1_54750
Locus_15661_Transcript_1/1_Conf_1.000	678	20	7.40E-77	XP_001892908.1	86	290.812	195	169	K+ channel tetramerisation domain containing protein
Locus_15662_Transcript_1/1_Conf_1.000	444	20	3.18E-40	XP_001899240.1	76	167.933	131	100	Tetraspanin family protein
Locus_15663_Transcript_1/1_Conf_1.000	152	20	4.82E-20	XP_002927000.1	100	100.908	50	50	PREDICTED: LOW QUALITY PROTEIN: lamin-A/C-like
Locus_15664_Transcript_1/1_Conf_1.000	515	0							
Locus_15665_Transcript_1/1_Conf_1.000	440	0							
Locus_15666_Transcript_1/1_Conf_1.000	329	0							

Locus_15667_Transcript_1/1_Conf_1.000	144	20	5.93E-18	XP_002687731.1	100	93.9745	47	47	PREDICTED: myosin, heavy chain 9, non-muscle
Locus_15668_Transcript_1/1_Conf_1.000	504	20	3.38E-53	XP_002645216.1	87	211.075	143	125	Hypothetical protein CBG00074
Locus_15669_Transcript_1/1_Conf_1.000	155	0							
Locus_1567_Transcript_1/1_Conf_1.000	255	20	2.47E-24	CAG25499.1	76	115.161	85	65	heat shock protein 20
Locus_15670_Transcript_1/1_Conf_1.000	383	6	1.13E-13	XP_002644887.1	61	79.7221	92	57	C. briggsae CBR-OPT-2 protein
Locus_15671_Transcript_1/1_Conf_1.000	167	0							
Locus_15672_Transcript_1/1_Conf_1.000	174	20	5.73E-26	NP_502576.1	100	120.553	58	58	RAB family member (rab-19)

Locus_15673_Transcript_1/1_Conf_1.000	265	20	1.26E-12	EFO23269.1	83	76.2554	53	44	vacuolar protein sorting-associated protein 45
Locus_15674_Transcript_1/1_Conf_1.000	134	0							
Locus_15675_Transcript_1/1_Conf_1.000	285	0							
Locus_15676_Transcript_1/1_Conf_1.000	735	15	4.99E-72	XP_002631027.1	78	275.018	230	181	Hypothetical protein CBG02784
Locus_15677_Transcript_1/1_Conf_1.000	183	20	1.12E-08	2G64	87	63.1586	39	34	Structure Of Caenorhabditis Elegans 6-Pyruvoyl Tetrahydropterin Synthase
Locus_15678_Transcript_1/1_Conf_1.000	421	0							
Locus_15679_Transcript_1/1_Conf_1.000	436	0							
Locus_1568_Transcript_1/1_Conf_1.000	1301	20	5.29E-94	NP_498963.1	79	349.362	254	202	Temporarily Assigned Gene name family member (tag-256)
Locus_15680_Transcript_1/1_Conf_1.000	310	0							
Locus_15681_Transcript_1/1_Conf_1.000	168	0							
Locus_15682_Transcript_1/1_Conf_1.000	381	20	1.19E-55	XP_002630466.1	92	219.164	126	116	Hypothetical protein CBG11199

Locus_15683_Transcript_1/1_Conf_1.000	253	20	1.50E-29	AAV83778.1	100	132.494	83	83	HSD48
Locus_15684_Transcript_1/1_Conf_1.000	289	2	1.60E-07	XP_002630551.1	75	59.3066	49	37	Hypothetical protein CBG12993
Locus_15685_Transcript_1/1_Conf_1.000	420	20	4.60E-47	XP_002629647.1	95	190.66	103	98	C. briggsae CBR-VHA-9 protein
Locus_15686_Transcript_1/1_Conf_1.000	149	0							
Locus_15687_Transcript_1/1_Conf_1.000	655	0							
Locus_15688_Transcript_1/1_Conf_1.000	183	0							
Locus_15689_Transcript_1/1_Conf_1.000	302	20	6.83E-19	NP_741553.1	71	97.0561	100	71	ALdehyde deHydrogenase family member (alh-4)
Locus_1569_Transcript_1/1_Conf_1.000	478	0							
Locus_15690_Transcript_1/1_Conf_1.000	339	0							
Locus_15691_Transcript_1/1_Conf_1.000	1207	14	3.37E-31	NP_504556.3	45	140.584	279	128	Chondroitin ProteoGlycan family member (cpg-4)
Locus_15692_Transcript_1/1_Conf_1.000	172	0							
Locus_15693_Transcript_1/1_Conf_1.000	800	20	1.11E-70	XP_001900427.1	70	270.781	251	176	Histone acetyltransferase type B catalytic subunit
Locus_15694_Transcript_1/1_Conf_1.000	465	5	2.62E-18	XP_001902197.1	61	95.1301	117	72	hypothetical protein Bm1_53660
Locus_15695_Transcript_1/1_Conf_1.000	203	0							
Locus_15696_Transcript_1/1_Conf_1.000	646	20	1.96E-28	NP_509836.1	56	129.798	208	117	VEGF (vascular endothelial growth factor) Receptor family member (ver-3)
Locus_15697_Transcript_1/1_Conf_1.000	843								
Locus_15698_Transcript_1/1_Conf_1.000	279	0							
Locus_15699_Transcript_1/1_Conf_1.000	295	20	8.13E-20	XP_001895480.1	65	100.138	96	63	Immunoglobulin I-set domain containing protein

Locus_157_Transcript_1/1_Conf_1.000	1611	20	2.46E-163	XP_002642099.1	88	580.096	383	339	Hypothetical protein CBG18040
Locus_1570_Transcript_1/1_Conf_1.000	574	20	1.07E-55	ACO56244.1	74	219.935	169	126	putative DEAD-box RNA helicase
Locus_15700_Transcript_1/1_Conf_1.000	198	0							
Locus_15701_Transcript_1/1_Conf_1.000	382	20	2.86E-25	XP_002638481.1	76	118.242	126	96	Hypothetical protein CBG12909
Locus_15702_Transcript_1/1_Conf_1.000	494	20	3.56E-76	BAC56579.1	100	287.345	144	144	similar to ribosomal protein S14
Locus_15703_Transcript_1/1_Conf_1.000	476	20	3.50E-07	EFA75185.1	45	58.151	91	41	Scar1
Locus_15704_Transcript_1/1_Conf_1.000	484	5	4.21E-08	XP_002737158.1	72	61.2326	69	50	PREDICTED: intracisternal A particle-promoted polypeptide-like

Locus_15705_Transcript_1/1_Conf_1.000	752	20	3.40E-55	ADI61822.1	62	219.164	240	151	endonuclease-reverse transcriptase
Locus_15706_Transcript_1/1_Conf_1.000	301	3	1.25E-12	EFO20394.1	73	76.2554	60	44	hypothetical protein LOAG_08094
Locus_15707_Transcript_1/1_Conf_1.000	230	0							
Locus_15708_Transcript_1/1_Conf_1.000	263	20	2.54E-13	NP_001123686.1	62	78.5666	79	49	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein
Locus_15709_Transcript_1/1_Conf_1.000	297	20	5.60E-29	XP_001892618.1	76	130.568	98	75	Acyltransferase family protein
Locus_1571_Transcript_1/1_Conf_1.000	542	20	2.87E-70	XP_001072155.2	99	268.085	140	139	PREDICTED: histone cluster 2, H3c2-like
Locus_15710_Transcript_1/1_Conf_1.000	587	0							
Locus_15711_Transcript_1/1_Conf_1.000	266	0							
Locus_15712_Transcript_1/1_Conf_1.000	230	20	6.72E-06	AAN10061.1	65	52.373	38	25	Kunitz-like protease inhibitor precursor

Locus_15713_Transcript_1/2_Conf_1.000	372	2	3.33E-05	CAE17836.3	64	51.6026	51	33	C. elegans protein F46F2.5, partially confirmed by transcript evidence
Locus_15713_Transcript_2/2_Conf_1.000	385	0							
Locus_15714_Transcript_1/1_Conf_1.000	370	12	1.50E-13	NP_001023075.1	59	79.337	96	57	inorganic PYroPhosphatase family member (pyp-1)
Locus_15715_Transcript_1/1_Conf_1.000	841	0							
Locus_15716_Transcript_1/1_Conf_1.000	138	20	1.61E-12	EFO19409.1	94	75.8702	39	37	hypothetical protein LOAG_09084
Locus_15717_Transcript_1/1_Conf_1.000	715	20	1.28E-61	CBL87054.2	68	240.35	245	169	C. elegans protein F54E4.1, partially confirmed by transcript evidence
Locus_15718_Transcript_1/1_Conf_1.000	610	20	1.71E-28	EFO24963.1	70	129.798	121	85	hypothetical protein LOAG_03520
Locus_15719_Transcript_1/1_Conf_1.000	752	0							
Locus_1572_Transcript_1/1_Conf_1.000	784	20	4.75E-87	NP_495701.2	73	325.094	265	195	IRE1 kinase related family member (ire-1)
Locus_15720_Transcript_1/1_Conf_1.000	500	20	7.43E-42	NP_495514.1	95	173.326	92	88	LSM Sm-like protein family member (lsm-4)
Locus_15721_Transcript_1/1_Conf_1.000	706	0							

Locus_15722_Transcript_1/1_Conf_1.000	206	3	1.02E-06	NP_496984.1	87	56.6102	39	34	hypothetical protein R06A4.8
Locus_15723_Transcript_1/1_Conf_1.000	464	6	2.31E-14	EFO19081.1	76	82.0333	56	43	hypothetical protein LOAG_09412
Locus_15724_Transcript_1/1_Conf_1.000	186	0							
Locus_15725_Transcript_1/1_Conf_1.000	667	0							
Locus_15726_Transcript_1/1_Conf_1.000	360	0							
Locus_15727_Transcript_1/1_Conf_1.000	704	20	3.89E-47	XP_002635830.1	53	192.2	228	123	Hypothetical protein CBG10495
Locus_15728_Transcript_1/2_Conf_1.000	1048	20	1.38E-51	XP_002738625.1	66	207.994	227	150	PREDICTED: 5-nucleotidase domain containing 2-like
Locus_15728_Transcript_2/2_Conf_1.000	584	20	7.53E-44	NP_499552.1	88	180.644	108	96	hypothetical protein Y56A3A.18
Locus_15729_Transcript_1/1_Conf_1.000	188	0							
Locus_1573_Transcript_1/1_Conf_1.000	648	3	1.37E-45	NP_505986.1	59	186.808	222	132	hypothetical protein R13H4.5
Locus_15730_Transcript_1/1_Conf_1.000	448	20	5.62E-21	XP_002634599.1	86	103.99	59	51	Hypothetical protein CBG08414
Locus_15731_Transcript_1/1_Conf_1.000	333	1	8.33E-09	NP_741828.1	69	63.5438	65	45	hypothetical protein C54D1.7
Locus_15732_Transcript_1/1_Conf_1.000	150	20	2.39E-19	XP_002831109.1	100	98.5969	49	49	PREDICTED: LOW QUALITY PROTEIN: myosin 9-like
Locus_15733_Transcript_1/1_Conf_1.000	549	0							

Locus_15734_Transcript_1/1_Conf_1.000	724	20	8.53E-53	XP_002633447.1	66	211.075	209	140	Hypothetical protein CBG06215
Locus_15735_Transcript_1/1_Conf_1.000	395	1	7.97E-07	EFO23365.1	56	56.9954	105	59	hypothetical protein LOAG_05120
Locus_15736_Transcript_1/1_Conf_1.000	340	0							
Locus_15737_Transcript_1/1_Conf_1.000	240	0							
Locus_15738_Transcript_1/1_Conf_1.000	567	0							
Locus_15739_Transcript_1/1_Conf_1.000	176	0							
Locus_1574_Transcript_1/2_Conf_1.000	981	20	1.41E-111	CAR63577.1	85	407.142	266	227	putative Thyroglobulin type-1 repeat family protein
Locus_1574_Transcript_2/2_Conf_1.000	529	1	2.49E-23	CAR63577.1	78	112.079	111	87	putative Thyroglobulin type-1 repeat family protein
Locus_15740_Transcript_1/1_Conf_1.000	418	13	9.05E-27	NP_501395.1	67	123.25	138	93	hypothetical protein K07H8.1
Locus_15741_Transcript_1/1_Conf_1.000	255	8	7.21E-08	CAR63553.1	55	60.4622	79	44	putative major allergen
Locus_15742_Transcript_1/1_Conf_1.000	233	0							
Locus_15743_Transcript_1/1_Conf_1.000	384	20	2.12E-20	NP_001041018.1	78	102.064	70	55	hypothetical protein Y11D7A.3
Locus_15744_Transcript_1/2_Conf_1.000	862	20	1.36E-56	XP_001897063.1	64	224.172	269	174	Bromodomain containing protein
Locus_15744_Transcript_2/2_Conf_1.000	553	20	2.65E-37	XP_001897063.1	63	158.688	184	117	Bromodomain containing protein
Locus_15745_Transcript_1/1_Conf_1.000	504	20	3.29E-32	XP_002922306.1	100	141.354	70	70	PREDICTED: triosephosphate isomerase-like, partial
Locus_15746_Transcript_1/1_Conf_1.000	545	20	7.55E-26	XP_001920862.2	62	120.553	159	99	PREDICTED: zgc:172302
Locus_15747_Transcript_1/1_Conf_1.000	235	0							
Locus_15748_Transcript_1/1_Conf_1.000	356	0							

Locus_15749_Transcript_1/1_Conf_1.000	318	3	3.93E-14	XP_002635581.1	76	81.2629	56	43	Hypothetical protein CBG20567
Locus_1575_Transcript_1/1_Conf_1.000	399	20	8.43E-17	NP_500284.2	97	90.1225	43	42	Enhancer of EfL-1 mutant phenotype family member (eel-1)
Locus_15750_Transcript_1/1_Conf_1.000	231	20	9.61E-21	XP_002923753.1	100	103.219	50	50	PREDICTED: rRNA 2'-O-methyltransferase fibrillarin-like
Locus_15751_Transcript_1/1_Conf_1.000	901	5	2.29E-09	XP_001896365.1	44	67.3958	227	100	hypothetical protein Bm1_24535
Locus_15752_Transcript_1/1_Conf_1.000	188	0							
Locus_15753_Transcript_1/1_Conf_1.000	469	0							
Locus_15754_Transcript_1/1_Conf_1.000	379	20	4.59E-23	XP_001898623.1	70	110.923	96	68	Piwi domain containing protein
Locus_15755_Transcript_1/2_Conf_1.000	583	20	7.01E-58	NP_495708.1	75	227.254	180	135	hypothetical protein F10B5.2
Locus_15755_Transcript_2/2_Conf_1.000	532	20	2.69E-57	NP_495708.1	78	224.942	162	127	hypothetical protein F10B5.2
Locus_15756_Transcript_1/1_Conf_1.000	167	0							
Locus_15757_Transcript_1/2_Conf_1.000	391	20	5.90E-23	NP_504643.1	86	110.538	69	60	ACyLtransferase-like family member (acl-8)
Locus_15757_Transcript_2/2_Conf_1.000	388	20	1.27E-41	NP_504643.1	88	172.555	104	92	ACyLtransferase-like family member (acl-8)
Locus_15758_Transcript_1/1_Conf_1.000	289	0							
Locus_15759_Transcript_1/1_Conf_1.000	134	0							
Locus_1576_Transcript_1/1_Conf_1.000	936	0							
Locus_15760_Transcript_1/1_Conf_1.000	174	0							
Locus_15761_Transcript_1/2_Conf_1.000	1313	18	6.06E-21	NP_499234.1	54	106.686	243	133	Enhancer of Ksr-1 Lethality family member (ekl-6)
Locus_15761_Transcript_2/2_Conf_1.000	222	0							
Locus_15762_Transcript_1/1_Conf_1.000	305	2	7.29E-13	XP_002649028.1	67	77.0258	65	44	Hypothetical protein CBG21482
Locus_15763_Transcript_1/1_Conf_1.000	186	0							
Locus_15764_Transcript_1/1_Conf_1.000	554	20	3.53E-74	NP_001021681.1	85	281.182	183	156	hypothetical protein Y105E8A.10
Locus_15765_Transcript_1/1_Conf_1.000	209	0							
Locus_15766_Transcript_1/1_Conf_1.000	412	20	3.24E-37	XP_002641220.1	82	157.918	120	99	Hypothetical protein CBG09084
Locus_15767_Transcript_1/1_Conf_1.000	266	0							
Locus_15768_Transcript_1/2_Conf_1.000	515	0							
Locus_15768_Transcript_2/2_Conf_1.000	464	0							

Locus_15769_Transcript_1/1_Conf_1.000	483	20	1.67E-89	XP_002818294.1	100	331.643	161	161	PREDICTED: collagen alpha-2(I) chain-like
Locus_1577_Transcript_1/4_Conf_0.786	2137	20	4.05E-10	XP_001660048.1	57	71.633	100	57	hypothetical protein AaeL_AAEL009430
Locus_1577_Transcript_2/4_Conf_0.786	2121	20	1.29E-08	XP_001660048.1	55	66.6254	102	57	hypothetical protein AaeL_AAEL009430
Locus_1577_Transcript_3/4_Conf_0.214	397	20	2.64E-10	EFO16022.1	61	68.5514	80	49	hypothetical protein LOAG_12486
Locus_1577_Transcript_4/4_Conf_0.786	2115	20	4.00E-10	XP_001660048.1	57	71.633	100	57	hypothetical protein AaeL_AAEL009430
Locus_15770_Transcript_1/1_Conf_1.000	431	0							
Locus_15771_Transcript_1/1_Conf_1.000	172	7	3.74E-09	NP_491336.2	80	64.6994	50	40	NuDiX family member (ndx-7)
Locus_15772_Transcript_1/1_Conf_1.000	265	20	1.06E-11	XP_002638233.1	65	73.1738	87	57	Hypothetical protein CBG15892
Locus_15773_Transcript_1/1_Conf_1.000	183	2	1.01E-17	NP_492177.2	81	93.2041	55	45	hypothetical protein R11A5.7
Locus_15774_Transcript_1/1_Conf_1.000	570	20	2.14E-16	EFO22249.1	72	89.3521	72	52	hypothetical protein LOAG_06236
Locus_15775_Transcript_1/1_Conf_1.000	136	0							

Locus_15776_Transcript_1/1_Conf_1.000	439	20	6.31E-17	XP_002108517.1	69	90.5077	83	58	hypothetical protein TRIADDRAFT_51503
Locus_15777_Transcript_1/1_Conf_1.000	270	0							
Locus_15778_Transcript_1/1_Conf_1.000	189	0							
Locus_15779_Transcript_1/1_Conf_1.000	458	20	9.72E-42	NP_077275.1	100	172.94	91	91	pancreatic progenitor cell differentiation and proliferation factor
Locus_1578_Transcript_1/1_Conf_1.000	1339	20	1.62E-69	EFO20046.1	86	268.085	159	138	hypothetical protein LOAG_08445
Locus_15780_Transcript_1/1_Conf_1.000	163	20	4.03E-19	EFO17870.1	100	97.8265	48	48	calmodulin-like protein
Locus_15781_Transcript_1/1_Conf_1.000	212	20	2.57E-34	XP_001142642.1	100	148.288	70	70	PREDICTED: Tu translation elongation factor, mitochondrial isoform 1
Locus_15782_Transcript_1/1_Conf_1.000	467	0							
Locus_15783_Transcript_1/1_Conf_1.000	292	20	1.58E-47	BAG60492.1	100	192.2	92	92	unnamed protein product
Locus_15784_Transcript_1/1_Conf_1.000	383	20	2.25E-46	XP_002631604.1	96	188.348	96	93	Hypothetical protein CBG20785
Locus_15785_Transcript_1/1_Conf_1.000	336	20	5.16E-35	XP_002630326.1	83	150.599	104	87	Hypothetical protein CBG04253
Locus_15786_Transcript_1/1_Conf_1.000	555	20	2.35E-41	NP_001024131.1	64	172.17	187	121	Peroxisomal Membrane Protein related family member (pmp-5)
Locus_15787_Transcript_1/1_Conf_1.000	141	0							
Locus_15788_Transcript_1/1_Conf_1.000	130	20	2.87E-17	3BJ5	100	91.6633	43	43	Alternative Conformations OfThe X Region Of Human Protein Disulphide-Isomerase Modulate Exposure OfThe Substrate Binding B' Domain

Locus_15789_Transcript_1/1_Conf_1.000	637	20	3.77E-61	XP_002631214.1	86	238.424	157	136	C. briggsae CBR-MPZ-1 protein
Locus_1579_Transcript_1/1_Conf_1.000	970	20	1.49E-57	XP_002646929.1	91	227.639	129	118	Hypothetical protein CBG19634
Locus_15790_Transcript_1/1_Conf_1.000	300	20	6.15E-36	XP_002641343.1	88	153.68	99	88	C. briggsae CBR-DPY-18 protein
Locus_15791_Transcript_1/1_Conf_1.000	505	20	1.69E-20	XP_002735371.1	55	102.449	165	91	PREDICTED: hypothetical protein
Locus_15792_Transcript_1/1_Conf_1.000	279	0							
Locus_15793_Transcript_1/1_Conf_1.000	498	2	9.44E-21	XP_002632353.1	54	103.219	180	98	Hypothetical protein CBG00367
Locus_15794_Transcript_1/1_Conf_1.000	496	3	2.12E-04	XP_001639273.1	45	48.9062	70	32	predicted protein
Locus_15795_Transcript_1/1_Conf_1.000	231	0							
Locus_15796_Transcript_1/1_Conf_1.000	702	20	2.91E-18	XP_001902854.1	52	96.2857	192	100	cytoplasmic intermediate filament protein
Locus_15797_Transcript_1/1_Conf_1.000	368	20	3.09E-56	CAB05601.2	96	221.09	122	118	C. elegans protein R11A5.1b, partially confirmed by transcript evidence
Locus_15798_Transcript_1/1_Conf_1.000	147	0							
Locus_15799_Transcript_1/1_Conf_1.000	233	0							
Locus_158_Transcript_1/3_Conf_0.727	486	20	5.46E-16	XP_002641290.1	47	87.4261	147	70	Hypothetical protein CBG05204
Locus_158_Transcript_2/3_Conf_0.636	476	20	5.96E-15	XP_002641290.1	46	83.9593	147	69	Hypothetical protein CBG05204
Locus_158_Transcript_3/3_Conf_0.818	500	20	5.36E-16	XP_002641290.1	47	87.4261	147	70	Hypothetical protein CBG05204
Locus_1580_Transcript_1/2_Conf_1.000	1109	0							
Locus_1580_Transcript_2/2_Conf_1.000	1115	0							

Locus_15800_Transcript_1/2_Conf_1.000	842	20	5.85E-41	CAX51676.1	62	172.17	222	139	C. elegans protein F56A8.9, confirmed by transcript evidence
Locus_15800_Transcript_2/2_Conf_1.000	700	20	3.38E-35	CAX51676.1	68	152.525	161	110	C. elegans protein F56A8.9, confirmed by transcript evidence
Locus_15801_Transcript_1/1_Conf_1.000	256	2	9.75E-05	XP_002639508.1	58	50.0618	67	39	Hypothetical protein CBG04113
Locus_15802_Transcript_1/1_Conf_1.000	149	3	2.33E-06	AAG12204.1	68	55.4546	41	28	AF287482_5Orf122
Locus_15803_Transcript_1/1_Conf_1.000	251	0							
Locus_15804_Transcript_1/1_Conf_1.000	215	0							
Locus_15805_Transcript_1/1_Conf_1.000	139	0							
Locus_15806_Transcript_1/1_Conf_1.000	164	20	4.45E-18	Q8I0P7.3	94	94.3597	50	47	Probable 3'
Locus_15807_Transcript_1/1_Conf_1.000	329	15	1.69E-09	XP_002641343.1	67	65.855	67	45	C. briggsae CBR-DPY-18 protein
Locus_15808_Transcript_1/1_Conf_1.000	287	20	6.91E-43	ADD13547.1	96	176.792	93	90	Inositol triphosphate receptor protein 1, isoform h
Locus_15809_Transcript_1/1_Conf_1.000	238	1	1.80E-11	CAB07859.3	94	72.4034	36	34	C. elegans protein W09D10.2, partially confirmed by transcript evidence
Locus_1581_Transcript_1/1_Conf_1.000	1270	20	2.83E-177	EFO21688.1	87	625.935	422	369	phosphatidylinositol 3
Locus_15810_Transcript_1/1_Conf_1.000	815	20	9.58E-78	XP_002636833.1	72	294.278	273	197	C. briggsae CBR-PST-1 protein
Locus_15811_Transcript_1/1_Conf_1.000	239	0							

Locus_15812_Transcript_1/1_Conf_1.000	352	20	2.80E-12	XP_002812714.1	100	75.0998	35	35	PREDICTED: collagen alpha-1(III) chain-like isoform 2
Locus_15813_Transcript_1/1_Conf_1.000	355	0							
Locus_15814_Transcript_1/1_Conf_1.000	532	0							
Locus_15815_Transcript_1/1_Conf_1.000	497	20	3.36E-34	XP_002631025.1	72	147.902	122	89	Hypothetical protein CBG02782
Locus_15816_Transcript_1/1_Conf_1.000	279	0							
Locus_15817_Transcript_1/2_Conf_1.000	258	0							
Locus_15817_Transcript_2/2_Conf_1.000	252	0							
Locus_15818_Transcript_1/1_Conf_1.000	292	2	4.96E-09	NP_001032977.1	72	64.3142	50	36	hypothetical protein K02A11.4
Locus_15819_Transcript_1/1_Conf_1.000	491	20	4.01E-27	EFO20863.1	65	124.405	166	109	hypothetical protein LOAG_07626
Locus_1582_Transcript_1/1_Conf_1.000	407	0							
Locus_15820_Transcript_1/1_Conf_1.000	416	0							
Locus_15821_Transcript_1/1_Conf_1.000	474	20	1.99E-10	XP_001900444.1	45	68.9366	130	59	Calponin homology
Locus_15822_Transcript_1/1_Conf_1.000	443	20	2.81E-28	EFO20355.1	69	128.257	143	100	aminotransferase
Locus_15823_Transcript_1/2_Conf_1.000	398	20	5.61E-53	NP_493832.1	90	210.305	132	120	Acyl CoA DeHydrogenase family member (acdh-9)
Locus_15823_Transcript_2/2_Conf_1.000	398	20	5.61E-53	NP_493832.1	90	210.305	132	120	Acyl CoA DeHydrogenase family member (acdh-9)

Locus_15824_Transcript_1/1_Conf_1.000	448	20	2.66E-71	XP_002638706.1	97	271.166	144	140	Hypothetical protein CBG00285
Locus_15825_Transcript_1/1_Conf_1.000	567	0							
Locus_15826_Transcript_1/1_Conf_1.000	532	0							
Locus_15827_Transcript_1/1_Conf_1.000	381	20	1.33E-30	CAB03414.3	69	135.961	132	92	Hypothetical protein T23G11.5a
Locus_15828_Transcript_1/1_Conf_1.000	521	5	3.06E-15	XP_002636819.1	81	85.1149	55	45	C. briggsae CBR-DHS-17 protein
Locus_15829_Transcript_1/1_Conf_1.000	265	20	7.55E-42	XP_002813776.1	100	173.326	82	82	PREDICTED: guanine nucleotide-binding protein G(i) subunit alpha-2-like
Locus_1583_Transcript_1/1_Conf_1.000	398	0							
Locus_15830_Transcript_1/1_Conf_1.000	283	0							
Locus_15831_Transcript_1/1_Conf_1.000	535	0							
Locus_15832_Transcript_1/1_Conf_1.000	473	20	4.89E-25	XP_002646472.1	74	117.472	127	95	C. briggsae CBR-NSF-1 protein
Locus_15833_Transcript_1/1_Conf_1.000	178	0							
Locus_15834_Transcript_1/1_Conf_1.000	131	0							
Locus_15835_Transcript_1/1_Conf_1.000	263	11	9.35E-08	XP_002633270.1	71	60.077	74	53	C. briggsae CBR-TTR-17 protein
Locus_15836_Transcript_1/1_Conf_1.000	773	20	5.10E-78	XP_001893993.1	83	295.049	213	177	Flavoprotein
Locus_15837_Transcript_1/1_Conf_1.000	329	0							
Locus_15838_Transcript_1/1_Conf_1.000	314	20	7.68E-34	NP_492127.1	89	146.747	98	88	Low-density lipoprotein Receptor Related family member (lrp-1)
Locus_15839_Transcript_1/1_Conf_1.000	800	20	3.22E-62	XP_001900232.1	67	242.662	268	181	transportin-SR

Locus_1584_Transcript_1/1_Conf_1.000	625	0							
Locus_15840_Transcript_1/1_Conf_1.000	503	0							
Locus_15841_Transcript_1/1_Conf_1.000	196	0							
Locus_15842_Transcript_1/1_Conf_1.000	392	14	9.10E-24	EFO22879.1	67	113.235	118	80	hypothetical protein LOAG_05602
Locus_15843_Transcript_1/1_Conf_1.000	297	0							
Locus_15844_Transcript_1/1_Conf_1.000	687	20	2.38E-70	AAF81283.1	81	269.24	190	155	glutathione S-transferase
Locus_15845_Transcript_1/1_Conf_1.000	136	0							
Locus_15846_Transcript_1/1_Conf_1.000	557	4	1.47E-51	XP_002641427.1	77	206.068	188	145	Hypothetical protein CBG13296
Locus_15847_Transcript_1/1_Conf_1.000	441	20	1.94E-37	XP_002750116.1	100	158.688	93	93	PREDICTED: vimentin-like isoform 2
Locus_15848_Transcript_1/1_Conf_1.000	411	0							
Locus_15849_Transcript_1/1_Conf_1.000	187	20	3.96E-14	3KM6	100	81.2629	39	39	CrystalStructure OfThe Human Gst Pi C47sY108V DOUBLE Mutant In Complex WithThe Ethacrynic Acid-Glutathione Conjugate
Locus_1585_Transcript_1/1_Conf_1.000	2712	20	0	NP_495269.1	75	837.795	712	541	hypothetical protein C32D5.3
Locus_15850_Transcript_1/1_Conf_1.000	267	0							
Locus_15851_Transcript_1/1_Conf_1.000	112	0							
Locus_15852_Transcript_1/1_Conf_1.000	181	0							
Locus_15853_Transcript_1/1_Conf_1.000	142	0							
Locus_15854_Transcript_1/1_Conf_1.000	447	13	1.29E-41	NP_499880.3	80	172.555	136	110	hypothetical protein R02D3.3
Locus_15855_Transcript_1/1_Conf_1.000	215	0							
Locus_15856_Transcript_1/1_Conf_1.000	397	0							
Locus_15857_Transcript_1/2_Conf_1.000	167	0							
Locus_15857_Transcript_2/2_Conf_1.000	205	0							
Locus_15858_Transcript_1/1_Conf_1.000	1007	20	1.45E-151	XP_002638687.1	88	540.036	328	290	Hypothetical protein CBG11882
Locus_15859_Transcript_1/1_Conf_1.000	261	0							

Locus_1586_Transcript_1/1_Conf_1.000	453	12	2.12E-20	NP_495986.3	68	102.064	110	75	EATing: abnormal pharyngeal pumping family member (eat-3)
Locus_15860_Transcript_1/1_Conf_1.000	358	20	2.60E-10	XP_001895583.1	75	68.5514	49	37	Surfeit locus protein 4 homolog
Locus_15861_Transcript_1/1_Conf_1.000	467	20	4.00E-59	XP_002631703.1	93	230.72	125	117	Hypothetical protein CBG20902
Locus_15862_Transcript_1/1_Conf_1.000	351	0							
Locus_15863_Transcript_1/2_Conf_1.000	346	0							
Locus_15863_Transcript_2/2_Conf_1.000	343	0							
Locus_15864_Transcript_1/1_Conf_1.000	1083	20	1.82E-110	NP_504268.1	75	403.675	354	269	PeRoXisome assembly factor family member (prx-6)
Locus_15865_Transcript_1/1_Conf_1.000	145	20	4.25E-16	NP_497837.1	91	87.8113	48	44	Leucyl tRNA Synthetase family member (lrs-1)

Locus_15866_Transcript_1/1_Conf_1.000	614	20	1.19E-61	XP_001891579.1	73	239.965	205	151	ImpB/MucB/SamB family protein
Locus_15867_Transcript_1/1_Conf_1.000	194	5	3.22E-08	AAF43009.1	70	61.6178	57	40	DNAse II homolog F09G8.2
Locus_15868_Transcript_1/1_Conf_1.000	173	0							
Locus_15869_Transcript_1/1_Conf_1.000	213	20	5.01E-14	XP_002643380.1	75	80.8777	65	49	Hypothetical protein CBG15993
Locus_1587_Transcript_1/1_Conf_1.000	657	20	2.01E-100	XP_002643349.1	91	369.007	217	198	Hypothetical protein CBG15946
Locus_15870_Transcript_1/1_Conf_1.000	580	0							
Locus_15871_Transcript_1/1_Conf_1.000	334	0							
Locus_15872_Transcript_1/2_Conf_1.000	571	0							
Locus_15872_Transcript_2/2_Conf_1.000	567	0							
Locus_15873_Transcript_1/1_Conf_1.000	130	0							
Locus_15874_Transcript_1/2_Conf_1.000	366	0							
Locus_15874_Transcript_2/2_Conf_1.000	427	0							
Locus_15875_Transcript_1/1_Conf_1.000	391	20	2.48E-21	EFO22018.1	65	105.145	129	84	hypothetical protein LOAG_06465
Locus_15876_Transcript_1/1_Conf_1.000	325	3	5.11E-06	XP_002639283.1	51	54.299	111	57	C. briggsae CBR-NAS-5 protein
Locus_15877_Transcript_1/1_Conf_1.000	271	20	2.35E-11	NP_491197.2	67	72.0182	85	57	SeMaPhorin related family member (smp-2)
Locus_15878_Transcript_1/1_Conf_1.000	753	20	2.50E-58	XP_002645084.1	75	229.565	186	141	Hypothetical protein CBG16758
Locus_15879_Transcript_1/1_Conf_1.000	1170	0							
Locus_1588_Transcript_1/2_Conf_1.000	1627	20	2.40E-65	EFO13989.1	74	254.603	229	170	hypothetical protein LOAG_14538
Locus_1588_Transcript_2/2_Conf_1.000	1612	20	2.37E-65	EFO13989.1	74	254.603	229	170	hypothetical protein LOAG_14538
Locus_15880_Transcript_1/1_Conf_1.000	331	4	2.97E-14		61	81.6481	105	65	myoblast city protein homolog
Locus_15881_Transcript_1/1_Conf_1.000	200	0							

Locus_15882_Transcript_1/1_Conf_1.000	157	10	2.23E-09	XP_001902320.1	68	65.4698	50	34	Protein-tyrosine phosphatase containing protein
Locus_15883_Transcript_1/1_Conf_1.000	419	20	3.89E-62	XP_001897890.1	86	240.736	139	120	Serine/threonine protein phosphatase PP1-alpha catalytic subunit
Locus_15884_Transcript_1/1_Conf_1.000	369	20	1.59E-39	NP_497814.3	72	165.622	122	89	UNCoordinated family member (unc-79)
Locus_15885_Transcript_1/1_Conf_1.000	147	0							
Locus_15886_Transcript_1/1_Conf_1.000	368	20	2.91E-38	EFO25550.1	80	161.384	114	92	nucleolar protein 10
Locus_15887_Transcript_1/1_Conf_1.000	214	20	3.24E-21	ABJ99064.1	83	104.76	71	59	Hypothetical protein W03A3.2
Locus_15888_Transcript_1/1_Conf_1.000	328	2	1.21E-15	XP_002648567.1	58	86.2705	103	60	Hypothetical protein CBG24887
Locus_15889_Transcript_1/1_Conf_1.000	330	0							
Locus_1589_Transcript_1/1_Conf_1.000	1848	8	1.74E-06	XP_002647483.1	41	59.3066	388	161	Hypothetical protein CBG06557
Locus_15890_Transcript_1/1_Conf_1.000	3179	20	0	XP_002646198.1	64	877.085	1095	710	Hypothetical protein CBG04359
Locus_15891_Transcript_1/2_Conf_1.000	309	0							
Locus_15891_Transcript_2/2_Conf_1.000	309	0							
Locus_15892_Transcript_1/1_Conf_1.000	616	20	2.86E-71	XP_002629988.1	80	271.937	206	166	C. briggsae CBR-NRF-6 protein
Locus_15893_Transcript_1/1_Conf_1.000	171	0							
Locus_15894_Transcript_1/1_Conf_1.000	280	20	1.05E-11	CBW48338.1	61	73.1738	93	57	Hypothetical protein C27A7.1d
Locus_15895_Transcript_1/1_Conf_1.000	161	0							
Locus_15896_Transcript_1/1_Conf_1.000	799	20	5.56E-22	BAB68205.1	68	108.997	117	80	keratin-like protein
Locus_15897_Transcript_1/1_Conf_1.000	145	0							
Locus_15898_Transcript_1/1_Conf_1.000	141	0							
Locus_15899_Transcript_1/1_Conf_1.000	239	0							

Locus_159_Transcript_1/1_Conf_1.000	1797	20	0	XP_002641211.1	91	829.706	538	493	C. briggsae CBR-CCT-6 protein
Locus_1590_Transcript_1/1_Conf_1.000	826	20	9.23E-76	NP_492339.1	88	287.73	184	163	CalPoNin family member (cpn-1)
Locus_15900_Transcript_1/1_Conf_1.000	450	0							
Locus_15901_Transcript_1/1_Conf_1.000	250	20	2.24E-22	XP_001892089.1	81	108.612	79	64	S-antigen protein precursor
Locus_15902_Transcript_1/1_Conf_1.000	458	20	7.39E-66	ACI49151.1	90	253.062	151	137	hypothetical protein Cbre_JD20.006
Locus_15903_Transcript_1/1_Conf_1.000	300	20	1.52E-18	NP_493981.1	77	95.9005	70	54	hypothetical protein H17B01.1
Locus_15904_Transcript_1/1_Conf_1.000	135	0							
Locus_15905_Transcript_1/1_Conf_1.000	381	0							
Locus_15906_Transcript_1/1_Conf_1.000	150	0							
Locus_15907_Transcript_1/1_Conf_1.000	461	0							
Locus_15908_Transcript_1/1_Conf_1.000	420	2	4.06E-11	NP_491994.2	70	71.2478	62	44	hypothetical protein H06O01.2
Locus_15909_Transcript_1/1_Conf_1.000	559	20	8.26E-71	NP_499212.1	89	270.011	183	164	Masculinisation Of Germline family member (mog-1)
Locus_1591_Transcript_1/1_Conf_1.000	628	20	1.33E-55	XP_002630918.1	89	219.935	155	138	Hypothetical protein CBG02643

Locus_15910_Transcript_1/1_Conf_1.000	278	20	2.49E-29	XP_001892891.1	82	131.724	92	76	cullin homolog 3
Locus_15911_Transcript_1/1_Conf_1.000	224	20	2.10E-07	XP_539278.2	74	58.9214	50	37	PREDICTED: similar to 2-aminoadipic 6-semialdehyde dehydrogenase isoform 1
Locus_15912_Transcript_1/1_Conf_1.000	182	4	1.37E-22	NP_503059.2	93	109.383	60	56	hypothetical protein ZK550.3
Locus_15913_Transcript_1/1_Conf_1.000	392	20	1.34E-59	EFO27533.1	90	232.261	130	117	hypothetical protein LOAG_00947
Locus_15914_Transcript_1/1_Conf_1.000	222	20	2.46E-32	XP_002634980.1	97	141.739	74	72	C. briggsae CBR-ARK-1 protein
Locus_15915_Transcript_1/1_Conf_1.000	310	20	5.17E-19	NP_497751.1	69	97.4413	102	71	hypothetical protein C14B1.10
Locus_15916_Transcript_1/1_Conf_1.000	561	20	1.22E-53	XP_002640778.1	85	213.001	171	147	C. briggsae CBR-FRL-1 protein

Locus_15917_Transcript_1/1_Conf_1.000	551	20	2.13E-31	AAO63576.1	58	139.043	179	105	secreted protein 4 precursor
Locus_15918_Transcript_1/1_Conf_1.000	138	20	1.97E-10	NP_505688.1	82	68.9366	46	38	Cdc-42 Related Protein family member (crp-1)
Locus_15919_Transcript_1/1_Conf_1.000	782	4	9.06E-22	NP_001022206.1	48	108.227	251	122	hypothetical protein F56D1.2
Locus_1592_Transcript_1/1_Conf_1.000	716	20	1.72E-74	XP_002649016.1	82	283.108	207	171	Hypothetical protein CBG21464
Locus_15920_Transcript_1/1_Conf_1.000	303	12	4.14E-08	BAB68205.1	69	61.2326	66	46	keratin-like protein
Locus_15921_Transcript_1/1_Conf_1.000	177	0							
Locus_15922_Transcript_1/1_Conf_1.000	139	0							
Locus_15923_Transcript_1/1_Conf_1.000	253	0							
Locus_15924_Transcript_1/1_Conf_1.000	151	4	2.17E-04	XP_002755675.1	98	48.9062	50	49	PREDICTED: uncharacterized protein C11orf24-like
Locus_15925_Transcript_1/1_Conf_1.000	305	0							
Locus_15926_Transcript_1/1_Conf_1.000	453	0							
Locus_15927_Transcript_1/1_Conf_1.000	1028	20	5.36E-16	XP_002158612.1	53	89.7373	137	73	PREDICTED: hypothetical protein, partial
Locus_15928_Transcript_1/1_Conf_1.000	287	2	3.57E-15	XP_001897687.1	68	84.7297	85	58	Zinc finger, C2H2 type family protein
Locus_15929_Transcript_1/1_Conf_1.000	312	0							
Locus_1593_Transcript_1/1_Conf_1.000	261	0							
Locus_15930_Transcript_1/1_Conf_1.000	502	3	4.50E-18	NP_497077.2	85	94.3597	69	59	hypothetical protein R05H10.2
Locus_15931_Transcript_1/1_Conf_1.000	192	5	3.80E-17	XP_002636415.1	81	91.2781	60	49	Hypothetical protein CBG23068
Locus_15932_Transcript_1/1_Conf_1.000	361	20	7.46E-42	NP_491219.1	89	173.326	119	106	hypothetical protein C32E8.3
Locus_15933_Transcript_1/1_Conf_1.000	262	4	6.05E-15	XP_002646198.1	80	83.9593	67	54	Hypothetical protein CBG04359
Locus_15934_Transcript_1/1_Conf_1.000	452	20	3.48E-47	NP_498398.1	77	191.045	150	116	LEThal family member (let-716)

Locus_15935_Transcript_1/1_Conf_1.000	587	3	8.25E-14	XP_002640845.1	48	80.8777	211	103	C. briggsae CBR-CDH-1 protein
Locus_15936_Transcript_1/1_Conf_1.000	233	0							
Locus_15937_Transcript_1/1_Conf_1.000	135	0							
Locus_15938_Transcript_1/1_Conf_1.000	443	0							
Locus_15939_Transcript_1/1_Conf_1.000	217	0							
Locus_1594_Transcript_1/2_Conf_1.000	812	20	6.55E-95	NP_741371.2	92	351.288	234	217	Ribosomal Protein, Large subunit family member (rpl-7A)
Locus_1594_Transcript_2/2_Conf_1.000	812	20	6.55E-95	NP_741371.2	92	351.288	234	217	Ribosomal Protein, Large subunit family member (rpl-7A)
Locus_15940_Transcript_1/2_Conf_1.000	587	3	2.24E-27	NP_508028.2	89	125.946	69	62	hypothetical protein F31D4.9
Locus_15940_Transcript_2/2_Conf_1.000	587	3	2.24E-27	NP_508028.2	89	125.946	69	62	hypothetical protein F31D4.9
Locus_15941_Transcript_1/1_Conf_1.000	363	0							
Locus_15942_Transcript_1/1_Conf_1.000	160	20	3.54E-15	EFO21962.1	87	84.7297	48	42	TK/EGFR protein kinase
Locus_15943_Transcript_1/1_Conf_1.000	421	2	2.55E-13	NP_491418.1	75	78.5666	66	50	hypothetical protein B0041.5
Locus_15944_Transcript_1/1_Conf_1.000	1391	20	1.05E-127	XP_002647378.1	96	461.455	300	288	C. briggsae CBR-TTB-1 protein
Locus_15945_Transcript_1/1_Conf_1.000	459	20	1.14E-50	XP_002643561.1	83	202.601	156	131	Hypothetical protein CBG16259
Locus_15946_Transcript_1/1_Conf_1.000	235	0							

Locus_15947_Transcript_1/1_Conf_1.000	421	20	4.92E-41	NP_491082.2	92	170.629	96	89	hypothetical protein Y71F9AR.2
Locus_15948_Transcript_1/1_Conf_1.000	784	0							
Locus_15949_Transcript_1/1_Conf_1.000	623	20	3.00E-52	EFO17715.1	72	208.764	193	140	oxidoreductase
Locus_1595_Transcript_1/2_Conf_1.000	1643	20	1.37E-76	XP_002636911.1	61	291.967	345	213	Hypothetical protein CBG09375
Locus_1595_Transcript_2/2_Conf_1.000	1583	20	1.26E-79	NP_504461.1	67	301.982	325	218	hypothetical protein C24G6.8
Locus_15950_Transcript_1/1_Conf_1.000	371	0							
Locus_15951_Transcript_1/1_Conf_1.000	635	20	4.08E-92	XP_002642342.1	91	341.273	210	192	Hypothetical protein CBG18338
Locus_15952_Transcript_1/1_Conf_1.000	321	2	1.18E-18	NP_504827.2	64	96.2857	102	66	hypothetical protein F09G2.1
Locus_15953_Transcript_1/1_Conf_1.000	196	0							
Locus_15954_Transcript_1/1_Conf_1.000	410	0							
Locus_15955_Transcript_1/1_Conf_1.000	150	0							
Locus_15956_Transcript_1/1_Conf_1.000	421	0							
Locus_15957_Transcript_1/1_Conf_1.000	289	20	5.44E-48	XP_002816866.1	100	193.741	96	96	PREDICTED: 60S ribosomal protein L10a-like
Locus_15958_Transcript_1/1_Conf_1.000	171	0							
Locus_15959_Transcript_1/1_Conf_1.000	482	6	3.24E-13	XP_001900333.1	53	78.1814	145	77	Anaphase promoting complex subunit 8 / cdc23 family protein
Locus_1596_Transcript_1/1_Conf_1.000	3277	20	0	NP_509658.1	75	1268.06	1107	841	Multidrug Resistance Protein family member (mrp-4)

Locus_15960_Transcript_1/1_Conf_1.000	308	2	1.37E-11	XP_001899300.1	62	72.7886	83	52	Negative elongation factor B homolog
Locus_15961_Transcript_1/1_Conf_1.000	151	0							
Locus_15962_Transcript_1/1_Conf_1.000	431	20	6.57E-38	XP_002636980.1	78	160.229	119	93	Hypothetical protein CBG09463
Locus_15963_Transcript_1/1_Conf_1.000	301	0							
Locus_15964_Transcript_1/1_Conf_1.000	224	20	3.03E-06	XP_001635789.1	60	55.0694	70	42	predicted protein
Locus_15965_Transcript_1/1_Conf_1.000	567	3	1.16E-06	XP_002642235.1	51	56.9954	74	38	C. briggsae CBR-BRD-1 protein
Locus_15966_Transcript_1/1_Conf_1.000	352	0							
Locus_15967_Transcript_1/1_Conf_1.000	569	20	9.07E-44	EFO17782.1	72	180.259	128	93	hypothetical protein LOAG_10716
Locus_15968_Transcript_1/1_Conf_1.000	241	0							
Locus_15969_Transcript_1/1_Conf_1.000	656	20	3.47E-20	NP_001123073.1	50	102.449	204	104	hypothetical protein ZC250.5
Locus_1597_Transcript_1/1_Conf_1.000	227	20	5.87E-18	NP_491756.2	76	93.9745	72	55	hypothetical protein ZK484.6
Locus_15970_Transcript_1/1_Conf_1.000	370	20	1.48E-61	XP_002634817.1	95	238.81	123	118	C. briggsae CBR-CLP-7 protein
Locus_15971_Transcript_1/1_Conf_1.000	144	0							
Locus_15972_Transcript_1/1_Conf_1.000	150	0							

Locus_15973_Transcript_1/1_Conf_1.000	186	20	7.68E-26	NP_001132929.1	100	120.168	62	62	B-cell receptor-associated protein 31 isoform a
Locus_15974_Transcript_1/1_Conf_1.000	370	0							
Locus_15975_Transcript_1/1_Conf_1.000	213	0							
Locus_15976_Transcript_1/1_Conf_1.000	243	0							
Locus_15977_Transcript_1/1_Conf_1.000	170	0							
Locus_15978_Transcript_1/1_Conf_1.000	150	0							
Locus_15979_Transcript_1/1_Conf_1.000	199	0							
Locus_1598_Transcript_1/1_Conf_1.000	1524	20	4.39E-122	XP_002639175.1	78	442.965	385	303	C. briggsae CBR-ILE-1 protein
Locus_15980_Transcript_1/1_Conf_1.000	379	20	2.51E-37	XP_002632404.1	78	158.303	125	98	Hypothetical protein CBG00428
Locus_15981_Transcript_1/1_Conf_1.000	181	0							
Locus_15982_Transcript_1/1_Conf_1.000	379	20	8.54E-70	XP_002927427.1	100	266.159	126	126	PREDICTED: transcription elongation factor SPT5-like isoform 2

Locus_15983_Transcript_1/1_Conf_1.000	170	20	1.68E-25	XP_002811271.1	100	119.013	56	56	PREDICTED: nuclear migration protein nudC-like
Locus_15984_Transcript_1/1_Conf_1.000	194	0							
Locus_15985_Transcript_1/2_Conf_1.000	611	0							
Locus_15985_Transcript_2/2_Conf_1.000	592	0							
Locus_15986_Transcript_1/1_Conf_1.000	995	11	1.86E-18	NP_492646.1	51	97.8265	180	93	Feminization Of Germline family member (fog-3)
Locus_15987_Transcript_1/1_Conf_1.000	280	0							
Locus_15988_Transcript_1/1_Conf_1.000	214	0							
Locus_15989_Transcript_1/1_Conf_1.000	152	0							
Locus_1599_Transcript_1/1_Conf_1.000	1238	20	1.47E-146	EFO21722.1	75	523.857	413	312	A-macroglobulin complement component family protein
Locus_15990_Transcript_1/1_Conf_1.000	238	20	8.93E-19	XP_002637127.1	85	96.6709	78	67	Hypothetical protein CBG09629
Locus_15991_Transcript_1/1_Conf_1.000	171	20	2.87E-09	NP_497334.1	71	65.0846	56	40	INverted Formin/formin Three-related family member (inft-1)
Locus_15992_Transcript_1/1_Conf_1.000	210	0							
Locus_15993_Transcript_1/1_Conf_1.000	303	2	2.05E-15	EFO18627.1	77	85.5001	88	68	hypothetical protein LOAG_09870
Locus_15994_Transcript_1/1_Conf_1.000	171	0							
Locus_15995_Transcript_1/1_Conf_1.000	562	0							
Locus_15996_Transcript_1/1_Conf_1.000	256	20	1.88E-32	NP_493778.1	83	142.124	85	71	hypothetical protein K07E8.7
Locus_15997_Transcript_1/1_Conf_1.000	288	0							
Locus_15998_Transcript_1/1_Conf_1.000	294	0							
Locus_15999_Transcript_1/1_Conf_1.000	514	4	2.32E-04	XP_002647225.1	43	48.9062	162	71	Hypothetical protein CBG23815
Locus_16_Transcript_1/2_Conf_1.000	549	2	4.94E-04	AAD13339.1	52	48.1358	65	34	ancylostoma-secreted protein 1 precursor
Locus_16_Transcript_2/2_Conf_1.000	225	2	6.30E-04	AAN11402.1	55	47.3654	54	30	secreted-protein 1 precursor
Locus_160_Transcript_1/5_Conf_0.133	609	20	4.80E-31	NP_001122684.1	96	138.272	95	92	UNCoordinated family member (unc-103)
Locus_160_Transcript_2/5_Conf_0.467	537	20	3.36E-31	AAO63577.1	60	138.272	160	97	secreted protein 5 precursor
Locus_160_Transcript_3/5_Conf_0.600	740	20	8.11E-38	AAO63577.1	59	161.384	192	115	secreted protein 5 precursor

Locus_160_Transcript_4/5_Conf_0.733	791	20	2.43E-38	AAO63577.1	60	163.31	192	116	secreted protein 5 precursor
Locus_160_Transcript_5/5_Conf_0.733	740	20	2.79E-38	AAO63577.1	59	162.925	192	115	secreted protein 5 precursor
Locus_1600_Transcript_1/1_Conf_1.000	2966	20	4.13E-96	NP_490758.1	46	357.836	921	431	Synthetic secondary siRNA-deficient ArGOnaute mutant family member (sago-2)
Locus_16000_Transcript_1/1_Conf_1.000	326	0							
Locus_16001_Transcript_1/1_Conf_1.000	239	20	1.05E-27	NP_501689.1	82	126.331	79	65	fatty acid ELOngation family member (elo-1)
Locus_16002_Transcript_1/1_Conf_1.000	342	0							
Locus_16003_Transcript_1/1_Conf_1.000	350	0							
Locus_16004_Transcript_1/1_Conf_1.000	561	20	9.00E-65	AAN11401.1	78	249.98	184	145	metalloprotease 1 precursor
Locus_16005_Transcript_1/1_Conf_1.000	128	0							
Locus_16006_Transcript_1/1_Conf_1.000	1297	20	0	NP_506128.1	95	787.719	412	393	AcTiniN family member (atn-1)

Locus_16007_Transcript_1/1_Conf_1.000	511	20	2.95E-12	XP_001182427.1	54	75.0998	111	60	PREDICTED: similar to mannose receptor, partial
Locus_16008_Transcript_1/1_Conf_1.000	287	0							
Locus_16009_Transcript_1/1_Conf_1.000	145	0							
Locus_1601_Transcript_1/1_Conf_1.000	1644	5	4.07E-20	XP_002640451.1	45	104.375	320	144	Hypothetical protein CBG08508
Locus_16010_Transcript_1/1_Conf_1.000	695	5	1.11E-14	EFO21657.1	52	84.3445	161	85	hypothetical protein LOAG_06828
Locus_16011_Transcript_1/1_Conf_1.000	211	20	1.24E-20	NP_497751.1	81	102.834	70	57	hypothetical protein C14B1.10
Locus_16012_Transcript_1/1_Conf_1.000	269	20	5.96E-39	EFO21248.1	93	163.696	89	83	CMGC/CDK/CDK5 protein kinase
Locus_16013_Transcript_1/1_Conf_1.000	330	20	1.33E-06	XP_001764884.1	57	56.225	92	53	predicted protein
Locus_16014_Transcript_1/1_Conf_1.000	598	20	1.62E-12	XP_001896971.1	64	76.6406	102	66	hypothetical protein Bm1_27600
Locus_16015_Transcript_1/1_Conf_1.000	515	20	3.43E-40	NP_509417.2	81	167.933	118	96	hypothetical protein F40B5.2
Locus_16016_Transcript_1/1_Conf_1.000	734	20	1.36E-29	CAB07368.3	53	134.035	258	138	C. elegans protein F22G12.4, confirmed by transcript evidence

Locus_16017_Transcript_1/1_Conf_1.000	750	20	5.17E-104	NP_492752.1	93	381.333	218	203	hypothetical protein F59C6.5
Locus_16018_Transcript_1/1_Conf_1.000	1576	4	1.12E-27	XP_002641592.1	52	129.413	288	151	Hypothetical protein CBG09896
Locus_16019_Transcript_1/1_Conf_1.000	173	0							
Locus_1602_Transcript_1/1_Conf_1.000	580	20	5.34E-26	XP_001899692.1	62	121.324	135	85	WW domain containing protein
Locus_16020_Transcript_1/1_Conf_1.000	287	20	2.82E-28	NP_001022571.1	94	128.257	69	65	NeuroFibroMatosis homolog family member (nfm-1)
Locus_16021_Transcript_1/1_Conf_1.000	478	0							
Locus_16022_Transcript_1/1_Conf_1.000	485	20	3.08E-51	XP_002633387.1	81	204.527	149	121	C. briggsae CBR-TWK-25 protein
Locus_16023_Transcript_1/1_Conf_1.000	147	0							
Locus_16024_Transcript_1/1_Conf_1.000	586	0							
Locus_16025_Transcript_1/1_Conf_1.000	590	20	1.39E-29	NP_001122554.1	61	133.265	198	121	hypothetical protein Y71G12A.2
Locus_16026_Transcript_1/1_Conf_1.000	423	12	1.22E-07	XP_001744572.1	48	59.6918	117	57	hypothetical protein
Locus_16027_Transcript_1/1_Conf_1.000	187	2	2.84E-04	EFO23538.1	63	48.521	60	38	hypothetical protein LOAG_04945
Locus_16028_Transcript_1/1_Conf_1.000	317	5	8.21E-20	XP_002643599.1	65	100.138	113	74	C. briggsae CBR-HDA-4 protein
Locus_16029_Transcript_1/1_Conf_1.000	379	0							
Locus_1603_Transcript_1/1_Conf_1.000	656	20	1.78E-16	XP_002634226.1	53	90.1225	143	77	Hypothetical protein CBG01796
Locus_16030_Transcript_1/1_Conf_1.000	225	0							
Locus_16031_Transcript_1/1_Conf_1.000	670	20	2.03E-55	NP_001024971.1	74	219.55	224	167	abnormal cell MIGration family member (mig-15)
Locus_16032_Transcript_1/1_Conf_1.000	277	2	1.92E-05	EFO19241.1	52	52.373	88	46	hypothetical protein LOAG_09252
Locus_16033_Transcript_1/1_Conf_1.000	411	4	1.97E-18	XP_002633725.1	53	95.5153	142	76	Hypothetical protein CBG03410
Locus_16034_Transcript_1/1_Conf_1.000	270	0							

Locus_16035_Transcript_1/1_Conf_1.000	136	20	6.15E-12	EFO13686.1	86	73.9442	44	38	CAMK/TSSK protein kinase
Locus_16036_Transcript_1/1_Conf_1.000	258	20	2.22E-25	XP_001902207.1	92	118.627	76	70	Hypothetical GTP-binding protein C02F5.3 in chromosome III, putative
Locus_16037_Transcript_1/1_Conf_1.000	860	0							
Locus_16038_Transcript_1/1_Conf_1.000	476	20	9.52E-13	CAA84693.3	64	76.6406	88	57	C. elegans protein D2045.2, partially confirmed by transcript evidence
Locus_16039_Transcript_1/1_Conf_1.000	1002	20	5.14E-141	XP_002629752.1	90	504.982	334	302	Hypothetical protein CBG00986
Locus_1604_Transcript_1/1_Conf_1.000	350	20	3.51E-47	XP_002630779.1	88	191.045	113	100	Hypothetical protein CBG02475
Locus_16040_Transcript_1/1_Conf_1.000	130	0							
Locus_16041_Transcript_1/1_Conf_1.000	417	20	4.49E-26	NP_508948.2	83	120.939	96	80	hypothetical protein T21F4.1
Locus_16042_Transcript_1/1_Conf_1.000	295	1	1.44E-08	CAL22705.2	62	62.7734	93	58	C. elegans protein K03H1.13, partially confirmed by transcript evidence
Locus_16043_Transcript_1/1_Conf_1.000	479	0							
Locus_16044_Transcript_1/1_Conf_1.000	560	0							
Locus_16045_Transcript_1/1_Conf_1.000	291	20	1.09E-48	XP_001110023.2	100	196.052	97	97	PREDICTED: sentrin-specific protease 3-like isoform 3
Locus_16046_Transcript_1/1_Conf_1.000	247	10	4.38E-26	XP_002633733.1	87	120.939	78	68	Hypothetical protein CBG03418
Locus_16047_Transcript_1/2_Conf_1.000	643	6	1.58E-38	NP_509272.1	66	163.31	204	136	hypothetical protein F46C8.3
Locus_16047_Transcript_2/2_Conf_1.000	788	6	1.91E-35	NP_509272.1	68	153.68	175	120	hypothetical protein F46C8.3
Locus_16048_Transcript_1/1_Conf_1.000	545	17	4.60E-07	XP_396560.3	50	58.151	106	53	PREDICTED: similar to CG1402-PA
Locus_16049_Transcript_1/1_Conf_1.000	168	0							

Locus_1605_Transcript_1/1_Conf_1.000	719	20	2.44E-44	NP_494841.3	63	182.956	174	111	hypothetical protein F10G7.10
Locus_16050_Transcript_1/1_Conf_1.000	783	20	2.39E-38	NP_001022548.1	58	163.31	210	123	hypothetical protein F25B5.6
Locus_16051_Transcript_1/2_Conf_1.000	759	20	6.87E-88	ACY39993.1	76	327.791	252	192	C. elegans FLN-2 protein, isoform a, partially confirmed by transcript evidence
Locus_16051_Transcript_2/2_Conf_1.000	443	20	7.37E-37	ACY39994.1	90	156.762	92	83	C. elegans FLN-2 protein, isoform d
Locus_16052_Transcript_1/1_Conf_1.000	291	0							
Locus_16053_Transcript_1/1_Conf_1.000	396	0							
Locus_16054_Transcript_1/1_Conf_1.000	469	20	9.14E-72	NP_000032.1	100	272.707	137	137	apolipoprotein E precursor
Locus_16055_Transcript_1/1_Conf_1.000	310	19	1.32E-22	XP_002646997.1	72	109.383	97	70	Hypothetical protein CBG22453
Locus_16056_Transcript_1/1_Conf_1.000	456	3	2.26E-06	XP_001893605.1	43	55.4546	150	65	Trypsin family protein
Locus_16057_Transcript_1/1_Conf_1.000	281	0							
Locus_16058_Transcript_1/1_Conf_1.000	312	20	2.25E-09	NP_500767.1	55	65.4698	95	53	hypothetical protein F36H12.3
Locus_16059_Transcript_1/1_Conf_1.000	365	0							
Locus_1606_Transcript_1/2_Conf_1.000	1071	20	3.18E-67	XP_002640805.1	65	259.996	264	173	Hypothetical protein CBG15687

Locus_1606_Transcript_2/2_Conf_1.000	987	20	5.46E-71	NP_497690.1	68	272.322	263	180	hypothetical protein Y53G8AR.9
Locus_16060_Transcript_1/1_Conf_1.000	1121	20	4.50E-152	XP_002639404.1	85	541.962	370	317	Hypothetical protein CBG03992
Locus_16061_Transcript_1/1_Conf_1.000	199	0							
Locus_16062_Transcript_1/1_Conf_1.000	174	0							
Locus_16063_Transcript_1/1_Conf_1.000	253	0							
Locus_16064_Transcript_1/1_Conf_1.000	382	2	5.80E-10	NP_491209.3	89	67.3958	39	35	LARP (RNA binding La related protein) homolog family member (larp-5)
Locus_16065_Transcript_1/1_Conf_1.000	212	0							
Locus_16066_Transcript_1/1_Conf_1.000	220	4	1.23E-07	NP_509283.1	82	59.6918	41	34	APYrase family member (apy-1)
Locus_16067_Transcript_1/1_Conf_1.000	220	0							
Locus_16068_Transcript_1/1_Conf_1.000	212	0							
Locus_16069_Transcript_1/1_Conf_1.000	316	0							
Locus_1607_Transcript_1/3_Conf_0.714	3501	20	1.99E-145	NP_001022562.1	50	521.931	1152	585	Suppressor/Enhancer of Lin-12 family member (sel-5)
Locus_1607_Transcript_2/3_Conf_0.714	3411	20	1.58E-147	NP_001022562.1	50	528.865	1145	578	Suppressor/Enhancer of Lin-12 family member (sel-5)
Locus_1607_Transcript_3/3_Conf_0.714	3417	20	6.03E-147	NP_001022562.1	50	526.939	1147	580	Suppressor/Enhancer of Lin-12 family member (sel-5)
Locus_16070_Transcript_1/1_Conf_1.000	217	20	1.83E-24	NP_005006.3	100	115.546	72	72	mitochondrial inner membrane protein OXA1L
Locus_16071_Transcript_1/1_Conf_1.000	147	0							
Locus_16072_Transcript_1/1_Conf_1.000	287	0							
Locus_16073_Transcript_1/1_Conf_1.000	247	20	1.61E-28	AAL06641.1	100	129.028	82	82	serine-threonine protein kinase

Locus_16074_Transcript_1/1_Conf_1.000	197	2	5.85E-10	NP_506090.1	97	67.3958	38	37	hypothetical protein R04F11.2
Locus_16075_Transcript_1/1_Conf_1.000	268	20	3.40E-18	XP_002636870.1	80	94.7449	71	57	Hypothetical protein CBG09328
Locus_16076_Transcript_1/1_Conf_1.000	1189	20	1.49E-108	EDL03932.1	97	397.512	206	200	mCG15678, isoform CRA_c
Locus_16077_Transcript_1/1_Conf_1.000	598	20	5.88E-55	XP_002639150.1	78	217.624	188	147	C. briggsae CBR-ROM-5 protein
Locus_16078_Transcript_1/1_Conf_1.000	317	3	4.96E-33	XP_002645845.1	82	144.05	104	86	Hypothetical protein CBG07579
Locus_16079_Transcript_1/1_Conf_1.000	511	2	4.71E-10	NP_505787.1	65	67.781	101	66	hypothetical protein F58B4.4
Locus_1608_Transcript_1/1_Conf_1.000	350	3	2.30E-06	NP_491341.1	63	55.4546	63	40	MUS (Drosophila mutagen sensitive) related family member (mus-81)
Locus_16080_Transcript_1/1_Conf_1.000	483	20	1.34E-46	NP_001020956.1	86	189.119	124	107	related to yeast Vacuolar Protein Sorting factor family member (vps-34)
Locus_16081_Transcript_1/1_Conf_1.000	254	0							
Locus_16082_Transcript_1/1_Conf_1.000	236	0							
Locus_16083_Transcript_1/1_Conf_1.000	267	20	2.52E-21	CAA72916.2	73	105.145	88	65	serine protease inhibitor-like protein

Locus_16084_Transcript_1/1_Conf_1.000	215	5	1.24E-04	EFN81442.1	65	49.6766	44	29	Protein TRS85-like protein
Locus_16085_Transcript_1/1_Conf_1.000	186	0							
Locus_16086_Transcript_1/1_Conf_1.000	730	0							
Locus_16087_Transcript_1/1_Conf_1.000	533	20	3.89E-56	NP_510385.1	77	221.09	176	137	hypothetical protein C11H1.3
Locus_16088_Transcript_1/1_Conf_1.000	320	0							
Locus_16089_Transcript_1/1_Conf_1.000	226	6	1.60E-07	EFO26306.1	80	59.3066	40	32	hypothetical protein LOAG_02178
Locus_1609_Transcript_1/1_Conf_1.000	1841	20	3.46E-39	EFO23299.1	58	167.933	225	132	hypothetical protein LOAG_05186
Locus_16090_Transcript_1/1_Conf_1.000	231	20	6.44E-17	XP_002632463.1	91	90.5077	71	65	Hypothetical protein CBG13687
Locus_16091_Transcript_1/1_Conf_1.000	159	0							
Locus_16092_Transcript_1/1_Conf_1.000	253	0							
Locus_16093_Transcript_1/1_Conf_1.000	325	0							
Locus_16094_Transcript_1/1_Conf_1.000	227	0							
Locus_16095_Transcript_1/1_Conf_1.000	149	0							
Locus_16096_Transcript_1/1_Conf_1.000	359	3	4.57E-15	NP_501984.1	60	84.3445	120	73	Na/Ca eXchangers family member (ncx-3)
Locus_16097_Transcript_1/1_Conf_1.000	605	20	7.06E-96	XP_002645162.1	85	353.599	205	176	Hypothetical protein CBG16872
Locus_16098_Transcript_1/1_Conf_1.000	406	2	7.09E-08	NP_501059.1	86	60.4622	36	31	hypothetical protein T05A12.3
Locus_16099_Transcript_1/1_Conf_1.000	150	0							
Locus_161_Transcript_1/1_Conf_1.000	941	0							
Locus_1610_Transcript_1/2_Conf_1.000	901	20	1.73E-41	NP_498985.3	57	174.096	273	158	hypothetical protein R08D7.4
Locus_1610_Transcript_2/2_Conf_1.000	854	20	9.61E-39	NP_498985.3	57	164.851	264	152	hypothetical protein R08D7.4
Locus_16100_Transcript_1/1_Conf_1.000	150	20	7.96E-15	XP_002634817.1	89	83.5741	48	43	C. briggsae CBR-CLP-7 protein
Locus_16101_Transcript_1/1_Conf_1.000	466	0							
Locus_16102_Transcript_1/1_Conf_1.000	529	0							
Locus_16103_Transcript_1/1_Conf_1.000	214	0							

Locus_16104_Transcript_1/1_Conf_1.000	528	20	1.30E-88	XP_002638687.1	96	328.946	175	168	Hypothetical protein CBG11882
Locus_16105_Transcript_1/1_Conf_1.000	335	20	3.59E-36	XP_002636068.1	76	154.451	111	85	Hypothetical protein CBG01308
Locus_16106_Transcript_1/1_Conf_1.000	235	0							
Locus_16107_Transcript_1/1_Conf_1.000	301	10	2.11E-36	CAR63539.1	78	155.221	97	76	hypothetical protein
Locus_16108_Transcript_1/1_Conf_1.000	523	20	8.45E-37	XP_001894795.1	77	156.762	119	92	Aspartyl aminopeptidase
Locus_16109_Transcript_1/1_Conf_1.000	152	8	6.51E-17	NP_495365.1	92	90.5077	50	46	RaPsYn family member (rpy-1)
Locus_1611_Transcript_1/1_Conf_1.000	884	20	2.24E-62	P0C5E6.2	70	243.432	244	171	Mediator of RNA polymerase II transcription subunit 8
Locus_16110_Transcript_1/1_Conf_1.000	354	20	2.36E-11	XP_001112673.1	71	72.0182	56	40	PREDICTED: UPF0587 protein C1orf123-like isoform 3

Locus_16111_Transcript_1/1_Conf_1.000	549	16	1.73E-57	NP_497035.3	83	225.713	169	141	Trehalose 6-Phosphate Synthase family member (tps-2)
Locus_16112_Transcript_1/1_Conf_1.000	801	20	1.30E-10	XP_002802251.1	43	71.2478	303	132	PREDICTED: rootletin-like
Locus_16113_Transcript_1/1_Conf_1.000	334	0							
Locus_16114_Transcript_1/1_Conf_1.000	189	20	2.72E-23	XP_002822850.1	100	111.694	62	62	PREDICTED: CD9 antigen-like
Locus_16115_Transcript_1/1_Conf_1.000	258	20	2.80E-36	NP_497814.3	94	154.836	85	80	UNCoordinated family member (unc-79)
Locus_16116_Transcript_1/1_Conf_1.000	194	20	6.94E-11	XP_001422216.1	67	70.4774	64	43	predicted protein
Locus_16117_Transcript_1/1_Conf_1.000	593	20	2.64E-60	NP_493583.1	85	235.343	168	143	SeMaPhorin related family member (smp-1)
Locus_16118_Transcript_1/1_Conf_1.000	155	0							
Locus_16119_Transcript_1/1_Conf_1.000	480	20	6.09E-28	XP_640893.1	61	127.102	159	97	hypothetical protein DDB_G0281219

Locus_1612_Transcript_1/1_Conf_1.000	282	20	6.29E-36	NP_001041183.1	85	153.68	95	81	Na/Ca eXchangers family member (ncx-1)
Locus_16120_Transcript_1/1_Conf_1.000	370	20	4.08E-11	XP_001983598.1	79	71.2478	49	39	GH15492
Locus_16121_Transcript_1/1_Conf_1.000	177	20	7.97E-28	EAW98190.1	100	126.716	59	59	cytochrome c oxidase subunit VIa polypeptide 1, isoform CRA_a
Locus_16122_Transcript_1/1_Conf_1.000	434	0							
Locus_16123_Transcript_1/1_Conf_1.000	137	1	4.72E-04	NP_494220.2	69	47.7506	43	30	hypothetical protein F54A3.1
Locus_16124_Transcript_1/1_Conf_1.000	331	0							
Locus_16125_Transcript_1/2_Conf_1.000	293	0							
Locus_16125_Transcript_2/2_Conf_1.000	293	0							
Locus_16126_Transcript_1/1_Conf_1.000	284	0							
Locus_16127_Transcript_1/1_Conf_1.000	627	20	2.97E-63	XP_002635377.1	78	245.358	210	165	Hypothetical protein CBG00768
Locus_16128_Transcript_1/2_Conf_1.000	817	20	2.90E-82	ADG63133.1	71	309.301	269	193	calcium-dependent apyrase
Locus_16128_Transcript_2/2_Conf_1.000	817	20	3.79E-82	ADG63133.1	71	308.916	269	193	calcium-dependent apyrase
Locus_16129_Transcript_1/1_Conf_1.000	220	2	3.04E-06	XP_001900855.1	61	55.0694	67	41	hypothetical protein Bm1_46970
Locus_1613_Transcript_1/1_Conf_1.000	301	6	2.60E-18	AAT02162.1	97	95.1301	43	42	hypothetical protein L3ni51
Locus_16130_Transcript_1/1_Conf_1.000	505	2	8.72E-09	XP_002640245.1	61	63.5438	123	76	Hypothetical protein CBG12763

Locus_16131_Transcript_1/1_Conf_1.000	287	20	2.81E-44	EFO21966.1	97	181.415	94	92	pre-mRNA splicing factor ATP-dependent RNA helicase
Locus_16132_Transcript_1/1_Conf_1.000	496	4	9.51E-13	XP_002639360.1	58	76.6406	167	97	Hypothetical protein CBG03940
Locus_16133_Transcript_1/1_Conf_1.000	218	4	1.07E-24	CAR63710.1	88	116.316	71	63	putative C2 domain containing protein
Locus_16134_Transcript_1/1_Conf_1.000	257	0							
Locus_16135_Transcript_1/1_Conf_1.000	261	0							
Locus_16136_Transcript_1/1_Conf_1.000	936	20	2.39E-97	XP_002639541.1	79	359.762	284	227	Hypothetical protein CBG04170
Locus_16137_Transcript_1/1_Conf_1.000	228	0							
Locus_16138_Transcript_1/1_Conf_1.000	515	20	5.27E-49	NP_498761.1	79	197.208	174	138	DiCer Related family member (dcr-1)
Locus_16139_Transcript_1/1_Conf_1.000	158	0							
Locus_1614_Transcript_1/1_Conf_1.000	2487	20	0	XP_002639688.1	91	1379.39	828	761	C. briggsae CBR-FASN-1 protein

Locus_16140_Transcript_1/1_Conf_1.000	499	20	3.94E-43	CAD24794.1	93	177.563	94	88	HOM-C transcription factor
Locus_16141_Transcript_1/1_Conf_1.000	461	20	5.46E-61	XP_002634990.1	86	236.884	152	131	Hypothetical protein CBG13530
Locus_16142_Transcript_1/1_Conf_1.000	324	20	4.04E-11	AAD49436.1	64	71.2478	109	70	AF083642_1P-glycoprotein
Locus_16143_Transcript_1/1_Conf_1.000	302	0							
Locus_16144_Transcript_1/1_Conf_1.000	170	0							
Locus_16145_Transcript_1/1_Conf_1.000	368	20	6.72E-27	NP_497575.2	69	123.635	121	84	Homeobox family member (ceh-44)
Locus_16146_Transcript_1/1_Conf_1.000	201	0							
Locus_16147_Transcript_1/1_Conf_1.000	257	0							
Locus_16148_Transcript_1/1_Conf_1.000	591	2	8.30E-30	XP_002638587.1	61	134.035	201	123	Hypothetical protein CBG05635
Locus_16149_Transcript_1/1_Conf_1.000	359	0							
Locus_1615_Transcript_1/1_Conf_1.000	937	20	2.65E-88	XP_002647046.1	72	329.717	309	225	Hypothetical protein CBG03564
Locus_16150_Transcript_1/1_Conf_1.000	302	0							
Locus_16151_Transcript_1/1_Conf_1.000	260	20	4.18E-32	XP_001902960.1	96	140.969	86	83	Rap/ran-GAP family protein
Locus_16152_Transcript_1/1_Conf_1.000	270	19	3.67E-23	YP_173415.1	100	77.411	36	36	hypothetical protein NitaMp073
Locus_16153_Transcript_1/1_Conf_1.000	375	7	9.02E-11	NP_001021225.1	48	70.0922	154	74	CEll Death abnormality family member (ced-7)
Locus_16154_Transcript_1/1_Conf_1.000	174	0							
Locus_16155_Transcript_1/1_Conf_1.000	328	7	3.19E-08	XP_001897687.1	60	61.6178	84	51	Zinc finger, C2H2 type family protein
Locus_16156_Transcript_1/1_Conf_1.000	147	0							

Locus_16157_Transcript_1/1_Conf_1.000	225	20	6.28E-12	XP_002612934.1	78	73.9442	60	47	hypothetical protein BRAFLDRAFT_278667
Locus_16158_Transcript_1/1_Conf_1.000	175	0							
Locus_16159_Transcript_1/1_Conf_1.000	137	0							
Locus_1616_Transcript_1/1_Conf_1.000	480	20	2.02E-31	NP_001041137.1	67	138.658	156	105	Alpha MANnosidase family member (aman-2)
Locus_16160_Transcript_1/1_Conf_1.000	350	6	2.53E-21	XP_002641319.1	73	105.145	113	83	Hypothetical protein CBG24620
Locus_16161_Transcript_1/1_Conf_1.000	152	0							
Locus_16162_Transcript_1/1_Conf_1.000	259	0							
Locus_16163_Transcript_1/1_Conf_1.000	160	0							
Locus_16164_Transcript_1/1_Conf_1.000	166	0							
Locus_16165_Transcript_1/1_Conf_1.000	369	3	6.10E-07	NP_496477.2	57	57.3806	103	59	hypothetical protein D1043.1
Locus_16166_Transcript_1/1_Conf_1.000	249	20	1.67E-09	CAA22110.2	62	65.855	82	51	C. elegans protein Y75B8A.26, partially confirmed by transcript evidence
Locus_16167_Transcript_1/1_Conf_1.000	223	4	1.50E-13	NP_493592.1	69	79.337	72	50	hypothetical protein F32A7.4
Locus_16168_Transcript_1/1_Conf_1.000	133	20	5.05E-14	NP_492007.1	93	80.8777	44	41	NADH Ubiquinone oxidoreductase Fe-S protein family member (nduf-6)
Locus_16169_Transcript_1/1_Conf_1.000	493	0							
Locus_1617_Transcript_1/1_Conf_1.000	675	20	1.81E-67	CAN99708.2	93	259.61	176	164	C. elegans protein Y54G11A.10a, confirmed by transcript evidence
Locus_16170_Transcript_1/1_Conf_1.000	967	20	1.55E-131	CAA60046.1	96	473.396	261	251	cytoplasmic intermediate filament protein
Locus_16171_Transcript_1/1_Conf_1.000	196	20	3.00E-14	NP_491127.1	76	81.6481	65	50	hypothetical protein Y54E10A.3
Locus_16172_Transcript_1/1_Conf_1.000	209	0							
Locus_16173_Transcript_1/1_Conf_1.000	380	4	1.42E-40	NP_505267.1	88	169.088	127	112	Regulator of Presynaptic Morphology family member (rpm-1)
Locus_16174_Transcript_1/1_Conf_1.000	334	0							
Locus_16175_Transcript_1/1_Conf_1.000	143	0							

Locus_16176_Transcript_1/1_Conf_1.000	734	20	7.93E-54	AAA68328.2	66	214.542	239	158	Hypothetical protein F35D2.4
Locus_16177_Transcript_1/1_Conf_1.000	453	20	3.03E-51	XP_002638651.1	84	204.527	132	112	Hypothetical protein CBG23705
Locus_16178_Transcript_1/1_Conf_1.000	157	0							
Locus_16179_Transcript_1/1_Conf_1.000	258	20	8.45E-25	EFO26733.1	77	116.701	83	64	GTP1/OBG family protein
Locus_1618_Transcript_1/2_Conf_1.000	731	2	1.15E-04	XP_002642452.1	76	51.2174	38	29	Hypothetical protein CBG06862
Locus_1618_Transcript_2/2_Conf_1.000	731	2	1.15E-04	XP_002642452.1	76	51.2174	38	29	Hypothetical protein CBG06862
Locus_16180_Transcript_1/2_Conf_1.000	608	0							
Locus_16180_Transcript_2/2_Conf_1.000	562	0							
Locus_16181_Transcript_1/1_Conf_1.000	221	0							
Locus_16182_Transcript_1/1_Conf_1.000	596	4	2.64E-07	EFO21213.1	49	59.3066	161	80	hypothetical protein LOAG_07275
Locus_16183_Transcript_1/1_Conf_1.000	394	16	4.65E-23	XP_001900825.1	64	110.923	113	73	CG3579-PA
Locus_16184_Transcript_1/1_Conf_1.000	442	0							
Locus_16185_Transcript_1/1_Conf_1.000	388	0							
Locus_16186_Transcript_1/1_Conf_1.000	272	4	9.23E-16	NP_495925.1	63	86.6557	90	57	hypothetical protein F44G4.8
Locus_16187_Transcript_1/1_Conf_1.000	544	20	2.04E-55	XP_002646278.1	72	218.779	177	128	Hypothetical protein CBG11983
Locus_16188_Transcript_1/1_Conf_1.000	240	1	2.46E-05	XP_002764298.1	69	46.595	39	27	PREDICTED: hypothetical protein LOC100405620, partial
Locus_16189_Transcript_1/1_Conf_1.000	473	0							
Locus_1619_Transcript_1/4_Conf_0.571	2187	20	0	XP_002640691.1	82	891.338	676	561	Hypothetical protein CBG19756
Locus_1619_Transcript_2/4_Conf_0.571	2176	20	0	XP_002640691.1	82	891.338	676	561	Hypothetical protein CBG19756
Locus_1619_Transcript_3/4_Conf_0.571	2264	20	0	XP_002640691.1	81	893.264	701	571	Hypothetical protein CBG19756

Locus_1619_Transcript_4/4_Conf_0.571	2176	20	0	XP_002640691.1	82	891.338	676	561	Hypothetical protein CBG19756
Locus_16190_Transcript_1/1_Conf_1.000	199	3	1.70E-09	CAA22108.2	98	65.855	50	49	C. elegans protein Y75B8A.24, partially confirmed by transcript evidence
Locus_16191_Transcript_1/1_Conf_1.000	254	20	8.53E-17		74	90.1225	74	55	myoblast city protein homolog
Locus_16192_Transcript_1/1_Conf_1.000	460	0							
Locus_16193_Transcript_1/1_Conf_1.000	147	0							
Locus_16194_Transcript_1/1_Conf_1.000	300	0							
Locus_16195_Transcript_1/1_Conf_1.000	232	0							
Locus_16196_Transcript_1/1_Conf_1.000	138	0							
Locus_16197_Transcript_1/1_Conf_1.000	906	8	1.07E-22	XP_002636857.1	49	111.694	239	118	Hypothetical protein CBG09313
Locus_16198_Transcript_1/1_Conf_1.000	207	20	8.30E-25	XP_002643153.1	97	116.701	68	66	C. briggsae CBR-RHA-2 protein
Locus_16199_Transcript_1/1_Conf_1.000	189	0							
Locus_162_Transcript_1/8_Conf_0.083	303	0							
Locus_162_Transcript_2/8_Conf_0.083	261	0							
Locus_162_Transcript_3/8_Conf_0.333	1458	20	9.49E-10	XP_001753823.1	32	69.707	359	117	predicted protein
Locus_162_Transcript_4/8_Conf_0.333	1500	20	9.87E-10	XP_001753823.1	32	69.707	359	117	predicted protein
Locus_162_Transcript_5/8_Conf_0.292	1567	6	3.13E-06	XP_001753823.1	31	58.151	370	115	predicted protein
Locus_162_Transcript_6/8_Conf_0.292	1567	6	3.13E-06	XP_001753823.1	31	58.151	370	115	predicted protein
Locus_162_Transcript_7/8_Conf_0.333	1488	6	2.94E-06	XP_001753823.1	31	58.151	370	115	predicted protein
Locus_162_Transcript_8/8_Conf_0.333	1446	6	2.82E-06	XP_001753823.1	31	58.151	370	115	predicted protein
Locus_1620_Transcript_1/3_Conf_0.333	245	6	1.85E-08	ACF74367.1	64	62.3882	82	53	Hypothetical protein R13F6.4d
Locus_1620_Transcript_2/3_Conf_0.667	2034	20	1.01E-95	XP_002641869.1	55	355.91	628	349	C. briggsae CBR-TEN-1 protein
Locus_1620_Transcript_3/3_Conf_0.667	2034	20	1.01E-95	XP_002641869.1	55	355.91	628	349	C. briggsae CBR-TEN-1 protein
Locus_16200_Transcript_1/1_Conf_1.000	316	20	5.49E-24	XP_002732970.1	75	114.005	101	76	PREDICTED: Cell-death-Related Nuclease family member (crn-2)-like

Locus_16201_Transcript_1/2_Conf_1.000	313	4	1.27E-12	NP_498871.2	57	76.2554	102	59	hypothetical protein F42H10.5
Locus_16201_Transcript_2/2_Conf_1.000	313	4	1.27E-12	NP_498871.2	57	76.2554	102	59	hypothetical protein F42H10.5
Locus_16202_Transcript_1/1_Conf_1.000	134	0							
Locus_16203_Transcript_1/1_Conf_1.000	1426	20	1.81E-82	EFO22071.1	61	311.227	479	295	hypothetical protein LOAG_06415
Locus_16204_Transcript_1/1_Conf_1.000	253	0							
Locus_16205_Transcript_1/1_Conf_1.000	144	0							
Locus_16206_Transcript_1/1_Conf_1.000	202	0							
Locus_16207_Transcript_1/1_Conf_1.000	378	20	6.65E-14	EFO28351.1	80	80.4925	51	41	2Fe-2S iron-sulfur cluster binding domain-containing protein
Locus_16208_Transcript_1/1_Conf_1.000	469	20	1.22E-07	XP_001892000.1	76	59.6918	47	36	linker histone H1 and H5 family protein
Locus_16209_Transcript_1/1_Conf_1.000	481	0							
Locus_1621_Transcript_1/2_Conf_1.000	985	20	1.15E-12	XP_001897369.1	82	78.5666	52	43	Protein kinase domain containing protein
Locus_1621_Transcript_2/2_Conf_1.000	435	20	3.68E-49	XP_001897369.1	79	197.593	142	113	Protein kinase domain containing protein
Locus_16210_Transcript_1/1_Conf_1.000	303	20	5.38E-24	XP_002632297.1	73	114.005	87	64	C. briggsae CBR-NOL-6 protein
Locus_16211_Transcript_1/1_Conf_1.000	533	20	3.79E-27	XP_002640768.1	69	124.79	136	95	C. briggsae CBR-HYL-1 protein

Locus_16212_Transcript_1/1_Conf_1.000	603	11	9.44E-16	EFO22836.1	47	87.4261	189	90	hypothetical protein LOAG_05647
Locus_16213_Transcript_1/1_Conf_1.000	2075	20	9.21E-44	EFO25547.1	50	183.341	352	176	hypothetical protein LOAG_02935
Locus_16214_Transcript_1/1_Conf_1.000	380	20	1.25E-20	NP_502406.1	77	102.834	77	60	Heat Shock factor Binding protein family member (hsb-1)
Locus_16215_Transcript_1/1_Conf_1.000	523	20	2.10E-11	NP_001123062.1	48	72.4034	101	49	hypothetical protein Y69H2.3
Locus_16216_Transcript_1/1_Conf_1.000	827	0							
Locus_16217_Transcript_1/1_Conf_1.000	272	0							
Locus_16218_Transcript_1/1_Conf_1.000	198	1	3.66E-04	ACI49251.1	72	48.1358	44	32	hypothetical protein Csp3_JD07.001
Locus_16219_Transcript_1/1_Conf_1.000	149	0							
Locus_1622_Transcript_1/1_Conf_1.000	508	20	3.10E-86	AAH00553.2	100	320.857	154	154	PLD3 protein

Locus_16220_Transcript_1/1_Conf_1.000	358	20	2.59E-18	AAB23867.2	80	95.1301	77	62	UNC-5
Locus_16221_Transcript_1/1_Conf_1.000	406	0							
Locus_16222_Transcript_1/1_Conf_1.000	968	20	1.94E-166	NP_492476.1	92	589.341	322	299	hypothetical protein F14B4.3
Locus_16223_Transcript_1/1_Conf_1.000	1019	20	3.23E-98	NP_502432.1	77	362.844	339	262	RBD (RNA binding domain) protein family member (rbd-1)
Locus_16224_Transcript_1/1_Conf_1.000	192	8	4.33E-21	CAR63588.1	82	104.375	63	52	hypothetical protein
Locus_16225_Transcript_1/1_Conf_1.000	239	0							
Locus_16226_Transcript_1/1_Conf_1.000	149	0							
Locus_16227_Transcript_1/1_Conf_1.000	147	5	6.78E-06	XP_001898552.1	71	53.9138	49	35	hypothetical protein Bm1_35525
Locus_16228_Transcript_1/1_Conf_1.000	1087	20	2.99E-137	XP_002637530.1	89	492.656	312	278	C. briggsae CBR-UCP-4 protein
Locus_16229_Transcript_1/1_Conf_1.000	141	0							
Locus_1623_Transcript_1/1_Conf_1.000	722	20	6.00E-83	XP_002644219.1	88	311.227	177	157	Hypothetical protein CBG17217
Locus_16230_Transcript_1/1_Conf_1.000	210	20	7.76E-15	NP_496490.2	72	83.5741	69	50	NEPrilysin metallopeptidase family member (nep-1)
Locus_16231_Transcript_1/1_Conf_1.000	185	20	1.72E-25	AAA03517.1	98	119.013	61	60	kinesin-related protein
Locus_16232_Transcript_1/1_Conf_1.000	400	0							
Locus_16233_Transcript_1/1_Conf_1.000	225	0							
Locus_16234_Transcript_1/1_Conf_1.000	332	0							
Locus_16235_Transcript_1/1_Conf_1.000	236	0							

Locus_16236_Transcript_1/1_Conf_1.000	440	0							
Locus_16237_Transcript_1/1_Conf_1.000	188	0							
Locus_16238_Transcript_1/1_Conf_1.000	215	5	3.59E-20	AAD01960.1	88	101.293	70	62	UNC-45
Locus_16239_Transcript_1/1_Conf_1.000	303	2	7.31E-05	AAB63465.1	74	50.447	35	26	O-linked GlcNAc transferase
Locus_1624_Transcript_1/1_Conf_1.000	623	3	1.11E-14	NP_492344.2	93	83.9593	44	41	FMRF-Like Peptide family member (flp-22)
Locus_16240_Transcript_1/1_Conf_1.000	293	20	3.79E-17	NP_491902.3	69	91.2781	94	65	hypothetical protein D2092.5
Locus_16241_Transcript_1/1_Conf_1.000	142	0							
Locus_16242_Transcript_1/1_Conf_1.000	129	0							
Locus_16243_Transcript_1/1_Conf_1.000	423	0							
Locus_16244_Transcript_1/1_Conf_1.000	510	20	3.22E-59	ACI49130.1	82	231.106	173	142	hypothetical protein Cbre_JD16.002
Locus_16245_Transcript_1/2_Conf_1.000	1365	20	2.45E-129	XP_002631212.1	77	466.848	386	298	C. briggsae CBR-ECH-4 protein
Locus_16245_Transcript_2/2_Conf_1.000	1428	20	2.59E-129	XP_002631212.1	77	466.848	386	298	C. briggsae CBR-ECH-4 protein
Locus_16246_Transcript_1/1_Conf_1.000	129	0							
Locus_16247_Transcript_1/1_Conf_1.000	178	1	1.12E-05	CBA11992.1	79	53.1434	44	35	endonuclease-reverse transcriptase HmRTE-e01

Locus_16248_Transcript_1/1_Conf_1.000	231	20	1.81E-19	3HOF	97	98.9821	48	47	Structure Of Macrophage Migration Inhibitory Factor (Mif) With Caffeic Acid At 1.9a Resolution
Locus_16249_Transcript_1/1_Conf_1.000	148	0							
Locus_1625_Transcript_1/1_Conf_1.000	321	20	5.63E-29	XP_001901345.1	79	130.568	104	83	Beta-tubulin cofactor D family protein
Locus_16250_Transcript_1/1_Conf_1.000	566	20	3.64E-29	XP_002634284.1	88	131.724	81	72	Hypothetical protein CBG17617
Locus_16251_Transcript_1/1_Conf_1.000	407	20	2.76E-36	NP_495979.1	74	154.836	135	100	hypothetical protein C01G6.7
Locus_16252_Transcript_1/2_Conf_1.000	517	20	5.36E-50	XP_002632657.1	82	162.925	109	90	C. briggsae CBR-TRA-3 protein
Locus_16252_Transcript_2/2_Conf_1.000	419	20	3.20E-48	XP_002632657.1	79	194.512	139	111	C. briggsae CBR-TRA-3 protein
Locus_16253_Transcript_1/1_Conf_1.000	152	0							
Locus_16254_Transcript_1/1_Conf_1.000	202	0							
Locus_16255_Transcript_1/2_Conf_1.000	332	0							
Locus_16255_Transcript_2/2_Conf_1.000	332	0							

Locus_16256_Transcript_1/1_Conf_1.000	247	20	2.75E-20	NP_001040934.1	73	101.679	78	57	hypothetical protein F13E9.13
Locus_16257_Transcript_1/1_Conf_1.000	624	1	1.06E-04	NP_497287.2	42	50.8322	126	54	hypothetical protein F23H11.2
Locus_16258_Transcript_1/1_Conf_1.000	477	4	1.65E-49	NP_506653.1	84	198.749	158	134	hypothetical protein W06A7.2
Locus_16259_Transcript_1/1_Conf_1.000	132	0							
Locus_1626_Transcript_1/1_Conf_1.000	249	20	7.71E-15	AAD51334.1	86	83.5741	50	43	Kunitz type serine protease inhibitor
Locus_16260_Transcript_1/1_Conf_1.000	129	0							
Locus_16261_Transcript_1/1_Conf_1.000	163	0							
Locus_16262_Transcript_1/1_Conf_1.000	372	3	1.22E-07	ABS19466.2	59	59.6918	91	54	Hypothetical protein F49D11.10
Locus_16263_Transcript_1/1_Conf_1.000	437	15	9.80E-10	AAN11402.1	51	66.6254	105	54	secreted-protein 1 precursor
Locus_16264_Transcript_1/1_Conf_1.000	280	0							
Locus_16265_Transcript_1/1_Conf_1.000	207	20	6.81E-19	XP_002634252.1	83	97.0561	65	54	Hypothetical protein CBG01823
Locus_16266_Transcript_1/1_Conf_1.000	391	0							
Locus_16267_Transcript_1/1_Conf_1.000	337	20	2.94E-22	XP_002647284.1	70	108.227	114	80	Hypothetical protein CBG06324
Locus_16268_Transcript_1/1_Conf_1.000	276	0							
Locus_16269_Transcript_1/1_Conf_1.000	147	0							
Locus_1627_Transcript_1/1_Conf_1.000	421	20	7.41E-13	NP_497719.1	63	77.0258	98	62	GLYcosylation related family member (gly-14)
Locus_16270_Transcript_1/1_Conf_1.000	187	3	2.17E-12	ACI49212.1	74	75.485	62	46	hypothetical protein Csp3_JD04.011
Locus_16271_Transcript_1/1_Conf_1.000	412	20	2.31E-51	NP_497659.1	82	204.912	136	112	hypothetical protein Y53G8B.2
Locus_16272_Transcript_1/1_Conf_1.000	135	0							
Locus_16273_Transcript_1/1_Conf_1.000	192	20	1.03E-14	BAG59226.1	100	83.1889	63	63	unnamed protein product
Locus_16274_Transcript_1/1_Conf_1.000	198	20	1.94E-05	XP_001121729.1	66	52.373	53	35	PREDICTED: similar to CG10979-PA
Locus_16275_Transcript_1/1_Conf_1.000	185	20	7.47E-21	XP_002630326.1	90	103.605	61	55	Hypothetical protein CBG04253
Locus_16276_Transcript_1/1_Conf_1.000	205	0							

Locus_16277_Transcript_1/1_Conf_1.000	297	20	1.98E-50	XP_002643622.1	94	201.83	98	93	C. briggsae CBR-NAS-39 protein
Locus_16278_Transcript_1/1_Conf_1.000	159	0							
Locus_16279_Transcript_1/1_Conf_1.000	294	20	3.63E-36	NP_001022234.1	86	154.451	99	86	hypothetical protein K05F1.6
Locus_1628_Transcript_1/2_Conf_1.000	375	0							
Locus_1628_Transcript_2/2_Conf_1.000	262	0							
Locus_16280_Transcript_1/1_Conf_1.000	657	20	2.39E-85	XP_002643273.1	85	318.931	218	187	C. briggsae CBR-MRP-1 protein
Locus_16281_Transcript_1/1_Conf_1.000	287	0							
Locus_16282_Transcript_1/2_Conf_1.000	328	20	5.04E-38	XP_001891848.1	81	160.614	99	81	cytoplasmic polyadenylation element binding protein 3
Locus_16282_Transcript_2/2_Conf_1.000	328	20	5.04E-38	XP_001891848.1	81	160.614	99	81	cytoplasmic polyadenylation element binding protein 3
Locus_16283_Transcript_1/1_Conf_1.000	554	3	5.87E-53	NP_497506.3	72	210.69	193	139	hypothetical protein Y48G9A.3
Locus_16284_Transcript_1/1_Conf_1.000	225	0							
Locus_16285_Transcript_1/1_Conf_1.000	404	20	8.62E-38	XP_002633240.1	92	159.844	99	92	C. briggsae CBR-LSM-7 protein
Locus_16286_Transcript_1/1_Conf_1.000	421	20	6.84E-59	XP_002635072.1	92	229.95	140	130	C. briggsae CBR-TMD-2 protein
Locus_16287_Transcript_1/1_Conf_1.000	167	0							
Locus_16288_Transcript_1/1_Conf_1.000	156	3	3.01E-06	NP_499405.4	68	55.0694	47	32	2 (Zwei) IG-domain protein family member (zig-5)
Locus_16289_Transcript_1/1_Conf_1.000	195	1	6.27E-04	XP_001896346.1	62	47.3654	53	33	laminin alpha chain

Locus_1629_Transcript_1/1_Conf_1.000	1366	20	4.49E-107	XP_001895824.1	67	392.889	419	282	SH2 domain containing protein
Locus_16290_Transcript_1/1_Conf_1.000	168	10	6.40E-09	NP_508180.1	81	63.929	49	40	hypothetical protein F35H12.1
Locus_16291_Transcript_1/1_Conf_1.000	242	20	5.74E-34	XP_001368223.1	100	147.132	72	72	PREDICTED: similar to ribosomal protein S21
Locus_16292_Transcript_1/1_Conf_1.000	362	0							
Locus_16293_Transcript_1/1_Conf_1.000	326	20	8.06E-44	XP_002633498.1	88	179.874	108	96	Hypothetical protein CBG06270
Locus_16294_Transcript_1/1_Conf_1.000	141	0							
Locus_16295_Transcript_1/1_Conf_1.000	500	0							
Locus_16296_Transcript_1/1_Conf_1.000	991	20	2.79E-99	EFO27969.1	81	366.311	323	263	hypothetical protein LOAG_00509
Locus_16297_Transcript_1/1_Conf_1.000	230	0							
Locus_16298_Transcript_1/1_Conf_1.000	162	2	4.62E-07	NP_505112.1	68	57.7658	54	37	hypothetical protein F20D6.11
Locus_16299_Transcript_1/1_Conf_1.000	339	0							
Locus_163_Transcript_1/1_Conf_1.000	3210	20	0	NP_495343.1	68	718.768	770	525	hypothetical protein C56C10.12
Locus_1630_Transcript_1/2_Conf_1.000	1919	20	4.83E-108	XP_001898078.1	57	396.741	647	374	Ubiquitin carboxyl-terminal hydrolase family protein
Locus_1630_Transcript_2/2_Conf_1.000	1898	20	1.38E-107	XP_001898078.1	57	395.201	647	370	Ubiquitin carboxyl-terminal hydrolase family protein
Locus_16300_Transcript_1/1_Conf_1.000	382	4	6.38E-25	NP_497649.1	73	117.087	106	78	hypothetical protein Y55D5A.4
Locus_16301_Transcript_1/1_Conf_1.000	502	20	4.48E-34	EFO18114.1	61	147.517	164	101	hypothetical protein LOAG_10384

Locus_16302_Transcript_1/2_Conf_1.000	546	20	5.17E-14	NP_501018.1	67	81.2629	78	53	Dicer Related Helicase family member (drh-1)
Locus_16302_Transcript_2/2_Conf_1.000	487	20	7.33E-37	XP_002633533.1	63	156.762	161	103	C. briggsae CBR-DRH-1 protein
Locus_16303_Transcript_1/1_Conf_1.000	270	20	2.12E-20	NP_496477.2	75	102.064	86	65	hypothetical protein D1043.1
Locus_16304_Transcript_1/1_Conf_1.000	572	6	1.94E-17	XP_002638739.1	58	92.8189	129	76	Hypothetical protein CBG18539
Locus_16305_Transcript_1/1_Conf_1.000	264	0							
Locus_16306_Transcript_1/1_Conf_1.000	129	0							
Locus_16307_Transcript_1/1_Conf_1.000	254	0							
Locus_16308_Transcript_1/2_Conf_1.000	723	20	5.34E-55	NP_491590.1	75	218.394	182	138	hypothetical protein F27C1.6
Locus_16308_Transcript_2/2_Conf_1.000	726	20	1.42E-55	NP_491590.1	75	220.32	182	138	hypothetical protein F27C1.6
Locus_16309_Transcript_1/1_Conf_1.000	577	0							
Locus_1631_Transcript_1/1_Conf_1.000	1308	20	4.49E-125	NP_495181.2	72	452.595	374	271	Ceramide Glucosyl Transferase family member (cgt-3)
Locus_16310_Transcript_1/1_Conf_1.000	289	5	1.31E-17	NP_498650.2	68	92.8189	92	63	CLocK (biological timing) abnormality family member (clk-2)

Locus_16311_Transcript_1/1_Conf_1.000	323	20	8.97E-35	NP_503027.1	92	149.828	82	76	Small Nuclear Ribonucleoprotein family member (snr-1)
Locus_16312_Transcript_1/1_Conf_1.000	253	0							
Locus_16313_Transcript_1/1_Conf_1.000	131	20	1.29E-09	ADN00780.1	83	66.2402	43	36	class 3 lipase protein
Locus_16314_Transcript_1/1_Conf_1.000	174	0							
Locus_16315_Transcript_1/1_Conf_1.000	356	20	2.05E-39	ACT20206.1	84	165.236	109	92	Hypothetical protein F55F1.5
Locus_16316_Transcript_1/1_Conf_1.000	199	0							
Locus_16317_Transcript_1/1_Conf_1.000	731	20	2.09E-22	XP_002641983.1	48	110.153	218	105	Hypothetical protein CBG09205
Locus_16318_Transcript_1/1_Conf_1.000	197	20	6.03E-23	EFO18009.1	87	110.538	64	56	hypothetical protein LOAG_10489
Locus_16319_Transcript_1/1_Conf_1.000	1397	20	0	NP_491859.1	91	656.366	394	360	Acyl CoA DeHydrogenase family member (acdh-3)

Locus_1632_Transcript_1/1_Conf_1.000	447	20	3.51E-31	NP_491662.1	85	137.887	94	80	DNaJ domain (prokaryotic heat shock protein) family member (dnj-21)
Locus_16320_Transcript_1/1_Conf_1.000	1301	20	1.81E-118	XP_002634047.1	85	430.639	363	312	Hypothetical protein CBG01586
Locus_16321_Transcript_1/1_Conf_1.000	813	20	8.13E-69	NP_502174.2	69	264.618	245	170	hypothetical protein M04B2.2
Locus_16322_Transcript_1/1_Conf_1.000	174	0							
Locus_16323_Transcript_1/1_Conf_1.000	173	2	2.27E-06	NP_506118.1	75	55.4546	45	34	hypothetical protein C54D10.5
Locus_16324_Transcript_1/1_Conf_1.000	541	20	1.99E-71	2JG8	100	271.937	132	132	CrystallographicStructure Of Human C1q Globular Heads Complexed To Phosphatidyl-Serine
Locus_16325_Transcript_1/1_Conf_1.000	159	20	6.04E-15	NP_504512.1	88	83.9593	52	46	hypothetical protein F44E7.2
Locus_16326_Transcript_1/1_Conf_1.000	465	0							
Locus_16327_Transcript_1/1_Conf_1.000	201	0							
Locus_16328_Transcript_1/1_Conf_1.000	255	0							
Locus_16329_Transcript_1/1_Conf_1.000	429	2	6.18E-20	NP_500393.2	65	100.523	114	75	hypothetical protein Y37E11AL.5
Locus_1633_Transcript_1/1_Conf_1.000	250	0							
Locus_16330_Transcript_1/1_Conf_1.000	1137	20	2.54E-25	XP_001900089.1	49	120.939	305	150	hypothetical protein Bm1_43135
Locus_16331_Transcript_1/1_Conf_1.000	518	20	3.75E-34	XP_001901404.1	71	147.902	129	92	ribonuclease P protein subunit p29

Locus_16332_Transcript_1/1_Conf_1.000	1073	20	9.37E-27	EFO25858.1	50	125.561	234	119	low-density lipoprotein receptor repeat class B containing protein
Locus_16333_Transcript_1/1_Conf_1.000	141	20	1.08E-16	XP_001896000.1	95	89.7373	46	44	hypothetical protein
Locus_16334_Transcript_1/2_Conf_1.000	487	20	3.91E-14	EFO25573.1	58	81.2629	93	54	RING finger protein 20

Locus_16334_Transcript_2/2_Conf_1.000	487	20	3.91E-14	EFO25573.1	58	81.2629	93	54	RING finger protein 20
Locus_16335_Transcript_1/1_Conf_1.000	206	20	9.25E-08	CBN79121.1	63	60.077	65	41	conserved unknown protein
Locus_16336_Transcript_1/1_Conf_1.000	202	0							
Locus_16337_Transcript_1/1_Conf_1.000	336	20	1.66E-33	XP_001899441.1	83	145.591	112	93	Xeroderma Pigmentosum Group E Complementing protein
Locus_16338_Transcript_1/1_Conf_1.000	389	20	2.17E-41	NP_001024707.1	79	171.785	121	96	UNCoordinated family member (unc-84)

Locus_16339_Transcript_1/1_Conf_1.000	633	20	6.18E-40	AAL34093.1	69	167.933	164	114	SKR-1
Locus_1634_Transcript_1/2_Conf_1.000	1756	20	2.51E-165	NP_491749.2	88	491.5	280	247	ARI (ubiquitin ligase Ariadne) homolog family member (ari-1)
Locus_1634_Transcript_2/2_Conf_1.000	1752	20	4.98E-173	NP_491749.2	83	612.453	385	320	ARI (ubiquitin ligase Ariadne) homolog family member (ari-1)
Locus_16340_Transcript_1/1_Conf_1.000	170	0							
Locus_16341_Transcript_1/1_Conf_1.000	347	0							
Locus_16342_Transcript_1/1_Conf_1.000	159	0							
Locus_16343_Transcript_1/1_Conf_1.000	560	11	9.94E-08	YP_002478296.1	47	60.4622	180	86	Transposase and inactivated derivatives-like protein
Locus_16344_Transcript_1/1_Conf_1.000	292	0							
Locus_16345_Transcript_1/1_Conf_1.000	505	20	2.97E-41	EFO24017.1	73	171.4	168	123	hypothetical protein LOAG_04469
Locus_16346_Transcript_1/2_Conf_1.000	758	20	2.30E-27	EFO16973.1	59	126.716	238	141	calpain
Locus_16346_Transcript_2/2_Conf_1.000	2555	20	0	EFO16973.1	77	950.658	795	618	calpain
Locus_16347_Transcript_1/1_Conf_1.000	354	0							
Locus_16348_Transcript_1/1_Conf_1.000	333	0							
Locus_16349_Transcript_1/1_Conf_1.000	542	2	3.57E-12	NP_740830.2	47	75.0998	219	104	hypothetical protein Y47G6A.29
Locus_1635_Transcript_1/1_Conf_1.000	1696	20	8.02E-11	NP_038835.2	46	73.559	212	98	serine/threonine-protein kinase PLK3
Locus_16350_Transcript_1/1_Conf_1.000	595	20	1.44E-29	CAZ65501.2	58	133.265	200	117	C. elegans protein F46C3.3c, partially confirmed by transcript evidence

Locus_16351_Transcript_1/1_Conf_1.000	187	5	3.83E-09	XP_001896129.1	70	64.6994	62	44	Hypothetical 216.3 kDa protein R06F6.8 in chromosome II, putative
Locus_16352_Transcript_1/1_Conf_1.000	198	0							
Locus_16353_Transcript_1/1_Conf_1.000	799	2	5.04E-15	NP_510529.1	44	85.8853	284	126	hypothetical protein F39B1.1
Locus_16354_Transcript_1/1_Conf_1.000	180	0							
Locus_16355_Transcript_1/1_Conf_1.000	198	20	1.17E-26	XP_001898798.1	92	122.865	65	60	glucose-6-phosphate dehydrogenase
Locus_16356_Transcript_1/2_Conf_1.000	545	20	2.42E-40	NP_506573.1	80	168.703	165	132	hypothetical protein C15H11.9
Locus_16356_Transcript_2/2_Conf_1.000	544	20	2.42E-40	NP_506573.1	80	168.703	165	132	hypothetical protein C15H11.9
Locus_16357_Transcript_1/1_Conf_1.000	472	20	1.96E-66	NP_495840.1	91	254.988	147	134	hypothetical protein D2085.6
Locus_16358_Transcript_1/1_Conf_1.000	212	0							
Locus_16359_Transcript_1/1_Conf_1.000	961	20	6.58E-66	XP_002636770.1	66	255.373	289	193	Hypothetical protein CBG23501
Locus_1636_Transcript_1/1_Conf_1.000	2059	20	0	XP_002642663.1	82	752.281	518	425	C. briggsae CBR-NCL-1 protein
Locus_16360_Transcript_1/2_Conf_1.000	873	20	3.81E-46	NP_495437.2	78	189.504	151	118	hypothetical protein C52E12.4
Locus_16360_Transcript_2/2_Conf_1.000	896	20	1.55E-50	NP_495437.2	79	204.142	158	126	hypothetical protein C52E12.4

Locus_16361_Transcript_1/1_Conf_1.000	283	20	3.13E-27	XP_001900557.1	86	124.79	94	81	Bromodomain containing protein
Locus_16362_Transcript_1/1_Conf_1.000	197	0							
Locus_16363_Transcript_1/1_Conf_1.000	477	2	1.42E-08	XP_002631345.1	80	62.7734	41	33	Hypothetical protein CBG03175
Locus_16364_Transcript_1/1_Conf_1.000	146	0							
Locus_16365_Transcript_1/1_Conf_1.000	158	0							
Locus_16366_Transcript_1/1_Conf_1.000	373	20	1.75E-46	XP_002630247.1	86	188.734	124	107	Hypothetical protein CBG00666
Locus_16367_Transcript_1/1_Conf_1.000	524	20	8.37E-69	NP_001041257.1	90	263.077	171	155	Regulator of G protein Signaling family member (rgs-7)
Locus_16368_Transcript_1/1_Conf_1.000	496	0							
Locus_16369_Transcript_1/1_Conf_1.000	739	20	2.74E-94	NP_500379.1	82	348.977	245	201	hypothetical protein Y37E11B.5
Locus_1637_Transcript_1/1_Conf_1.000	132	0							
Locus_16370_Transcript_1/1_Conf_1.000	298	0							
Locus_16371_Transcript_1/1_Conf_1.000	363	20	3.34E-34	XP_002636220.1	78	147.902	107	84	Hypothetical protein CBG12141
Locus_16372_Transcript_1/1_Conf_1.000	189	0							
Locus_16373_Transcript_1/1_Conf_1.000	913	7	4.95E-76	CBK19481.1	79	288.886	210	167	C. elegans protein Y105C5A.15a, partially confirmed by transcript evidence
Locus_16374_Transcript_1/1_Conf_1.000	298	3	3.90E-06	NP_495170.1	51	54.6842	77	40	Temporarily Assigned Gene name family member (tag-234)
Locus_16375_Transcript_1/1_Conf_1.000	171	16	5.06E-06	NP_502508.1	69	54.299	39	27	SCP-Like extracellular protein family member (scl-6)
Locus_16376_Transcript_1/1_Conf_1.000	517	20	5.45E-17	XP_002638473.1	56	90.8929	175	98	Hypothetical protein CBG12901
Locus_16377_Transcript_1/1_Conf_1.000	267	1	4.77E-04	NP_001021551.1	66	47.7506	48	32	hypothetical protein K07A1.15
Locus_16378_Transcript_1/1_Conf_1.000	226	0							
Locus_16379_Transcript_1/1_Conf_1.000	162	2	1.10E-08	XP_002645729.1	92	63.1586	53	49	Hypothetical protein CBG07396
Locus_1638_Transcript_1/1_Conf_1.000	2637	20	2.90E-170	XP_001893842.1	62	603.979	675	419	hypothetical protein
Locus_16380_Transcript_1/1_Conf_1.000	196	20	2.01E-18	NP_501419.2	76	95.5153	65	50	hypothetical protein D2096.3

Locus_16381_Transcript_1/1_Conf_1.000	380	20	1.42E-40	NP_508799.1	86	169.088	111	96	hypothetical protein F16H11.1
Locus_16382_Transcript_1/1_Conf_1.000	545	0							
Locus_16383_Transcript_1/1_Conf_1.000	523	20	1.22E-27	NP_493278.2	78	126.331	98	77	Neuropeptide-Like Protein family member (nlp-15)
Locus_16384_Transcript_1/1_Conf_1.000	255	0							
Locus_16385_Transcript_1/1_Conf_1.000	383	20	7.82E-15	XP_002312307.1	65	83.5741	84	55	predicted protein
Locus_16386_Transcript_1/1_Conf_1.000	281	20	3.35E-18	NP_498265.1	68	94.7449	94	64	hypothetical protein F01F1.9
Locus_16387_Transcript_1/1_Conf_1.000	568	20	2.70E-80	XP_001896559.1	84	301.597	191	161	hypothetical protein
Locus_16388_Transcript_1/1_Conf_1.000	617	5	9.05E-09	NP_495641.1	49	64.3142	139	69	CKI family (Cyclin-dependent Kinase Inhibitor) family member (cki-1)
Locus_16389_Transcript_1/1_Conf_1.000	176	0							
Locus_1639_Transcript_1/2_Conf_1.000	537	20	4.22E-58	XP_002631526.1	75	227.639	177	133	C. briggsae CBR-MIG-14 protein
Locus_1639_Transcript_2/2_Conf_1.000	537	20	8.49E-59	XP_002631526.1	75	229.95	177	134	C. briggsae CBR-MIG-14 protein
Locus_16390_Transcript_1/1_Conf_1.000	392	0							
Locus_16391_Transcript_1/1_Conf_1.000	505	20	1.21E-34	XP_002645124.1	68	149.443	164	113	Hypothetical protein CBG16818

Locus_16392_Transcript_1/2_Conf_1.000	1400	20	3.91E-98	NP_741868.1	59	363.229	475	282	Apical Junction Molecule family member (ajm-1)
Locus_16392_Transcript_2/2_Conf_1.000	1435	20	4.34E-92	XP_002645282.1	58	343.199	484	282	C. briggsae CBR-AJM-1 protein
Locus_16393_Transcript_1/1_Conf_1.000	366	20	9.13E-08	ACI49172.1	51	60.077	124	64	hypothetical protein Csp3_JD01.004
Locus_16394_Transcript_1/1_Conf_1.000	471	20	5.41E-24	XP_002425539.1	90	114.005	55	50	Early growth response protein, putative
Locus_16395_Transcript_1/1_Conf_1.000	516	20	1.09E-33	NP_492769.1	65	146.362	167	109	RTEL (mammalian Regulator of TELomere length) homolog family member (rtel-1)
Locus_16396_Transcript_1/1_Conf_1.000	283	0							
Locus_16397_Transcript_1/1_Conf_1.000	280	0							
Locus_16398_Transcript_1/1_Conf_1.000	525	0							
Locus_16399_Transcript_1/1_Conf_1.000	467	20	5.84E-18	XP_001897531.1	55	93.9745	154	86	WW domain containing protein
Locus_164_Transcript_1/2_Conf_1.000	1686	20	7.35E-57	NP_499083.2	48	226.483	496	241	hypothetical protein B0464.6
Locus_164_Transcript_2/2_Conf_1.000	1686	20	2.14E-56	NP_499083.2	51	224.942	428	220	hypothetical protein B0464.6
Locus_1640_Transcript_1/1_Conf_1.000	441	20	8.46E-17	XP_002641151.1	52	90.1225	144	75	Hypothetical protein CBG09003
Locus_16400_Transcript_1/1_Conf_1.000	545	3	3.52E-07	XP_002636981.1	86	58.5362	36	31	C. briggsae CBR-LIN-33 protein
Locus_16401_Transcript_1/1_Conf_1.000	237	0							
Locus_16402_Transcript_1/1_Conf_1.000	231	3	2.89E-25	XP_002641969.1	81	118.242	76	62	Hypothetical protein CBG16676
Locus_16403_Transcript_1/1_Conf_1.000	688	2	5.76E-16	XP_002635026.1	63	88.5817	136	87	Hypothetical protein CBG13570

Locus_16404_Transcript_1/1_Conf_1.000	348	0							
Locus_16405_Transcript_1/1_Conf_1.000	198	7	1.76E-06	XP_002642555.1	54	55.8398	77	42	C. briggsae CBR-UNC-103.2 protein
Locus_16406_Transcript_1/1_Conf_1.000	274	0							
Locus_16407_Transcript_1/1_Conf_1.000	302	0							
Locus_16408_Transcript_1/1_Conf_1.000	290	20	1.95E-29	XP_001902375.1	80	132.109	95	76	Protein kinase domain containing protein
Locus_16409_Transcript_1/1_Conf_1.000	653	0							
Locus_1641_Transcript_1/1_Conf_1.000	1954	20	0	XP_002642110.1	94	876.315	538	509	C. briggsae CBR-CCT-5 protein
Locus_16410_Transcript_1/1_Conf_1.000	291	0							
Locus_16411_Transcript_1/1_Conf_1.000	269	0							
Locus_16412_Transcript_1/1_Conf_1.000	245	4	1.85E-16	NP_509518.1	77	88.9669	70	54	hypothetical protein C24A3.2
Locus_16413_Transcript_1/1_Conf_1.000	340	20	2.99E-59	ACJ65168.1	99	231.106	113	112	Uncoordinated protein 68, isoform b, partially confirmed by transcript evidence
Locus_16414_Transcript_1/1_Conf_1.000	617	3	2.00E-40	EFO25429.1	58	169.474	206	120	hypothetical protein LOAG_03053
Locus_16415_Transcript_1/1_Conf_1.000	467	20	5.61E-45	NP_491182.2	75	183.726	160	120	LiPid Depleted family member (lpd-3)
Locus_16416_Transcript_1/1_Conf_1.000	236	9	1.53E-10	NP_493057.1	70	69.3218	79	56	RNA-dependent RNA polymerase Family family member (rrf-2)
Locus_16417_Transcript_1/1_Conf_1.000	538	6	1.15E-39	XP_002647538.1	71	166.392	130	93	Hypothetical protein CBG06620
Locus_16418_Transcript_1/1_Conf_1.000	155	0							
Locus_16419_Transcript_1/1_Conf_1.000	227	0							

Locus_1642_Transcript_1/1_Conf_1.000	454	20	4.82E-57	XP_002647797.1	90	223.787	125	113	Hypothetical protein CBG23568
Locus_16420_Transcript_1/1_Conf_1.000	222	0							
Locus_16421_Transcript_1/1_Conf_1.000	268	0							
Locus_16422_Transcript_1/1_Conf_1.000	356	3	4.45E-10	NP_508551.1	64	67.781	104	67	hypothetical protein F28B4.3
Locus_16423_Transcript_1/1_Conf_1.000	389	20	7.84E-34	XP_002828455.1	89	136.346	76	68	PREDICTED: LOW QUALITY PROTEIN: ornithine decarboxylase antizyme 1-like
Locus_16424_Transcript_1/1_Conf_1.000	241	0							
Locus_16425_Transcript_1/1_Conf_1.000	387	0							
Locus_16426_Transcript_1/1_Conf_1.000	458	20	2.83E-41	EFO23504.1	77	171.4	157	121	TK protein kinase
Locus_16427_Transcript_1/1_Conf_1.000	220	0							
Locus_16428_Transcript_1/1_Conf_1.000	230	1	4.81E-04	XP_002898487.1	66	47.7506	53	35	microtubule -associated protein EB1
Locus_16429_Transcript_1/1_Conf_1.000	222	0							
Locus_1643_Transcript_1/1_Conf_1.000	629	5	2.81E-21	NP_001022775.1	88	105.916	85	75	hypothetical protein T20G5.14
Locus_16430_Transcript_1/2_Conf_1.000	792	0							
Locus_16430_Transcript_2/2_Conf_1.000	299	0							
Locus_16431_Transcript_1/1_Conf_1.000	180	0							
Locus_16432_Transcript_1/1_Conf_1.000	563	20	2.55E-35	XP_002426892.1	60	152.14	193	116	myst histone acetyltransferase, putative
Locus_16433_Transcript_1/1_Conf_1.000	275	20	3.85E-30	XP_002646095.1	83	134.42	90	75	C. briggsae CBR-HMR-1 protein
Locus_16434_Transcript_1/1_Conf_1.000	393	20	1.40E-11	P48460.4	70	72.7886	64	45	Putative serine/threonine-protein phosphatase C27B7.6
Locus_16435_Transcript_1/1_Conf_1.000	240	0							
Locus_16436_Transcript_1/1_Conf_1.000	550	0							
Locus_16437_Transcript_1/1_Conf_1.000	161	0							

Locus_16438_Transcript_1/2_Conf_1.000	1275	20	1.68E-36	EFO20862.1	50	158.303	289	147	zinc finger protein
Locus_16438_Transcript_2/2_Conf_1.000	1268	20	5.72E-37	EFO20862.1	46	159.844	365	169	zinc finger protein
Locus_16439_Transcript_1/1_Conf_1.000	309	20	1.27E-33	NP_497786.2	89	145.976	100	89	MethylMalonylCoA Mutase homolog family member (mmcm-1)
Locus_1644_Transcript_1/3_Conf_0.556	972	20	1.18E-86	XP_002644841.1	74	324.324	240	178	C. briggsae CBR-HSP-43 protein
Locus_1644_Transcript_3/3_Conf_0.444	941	20	1.12E-86	XP_002644841.1	74	324.324	240	178	C. briggsae CBR-HSP-43 protein
Locus_16440_Transcript_1/1_Conf_1.000	176	0							
Locus_16441_Transcript_1/1_Conf_1.000	312	0							
Locus_16442_Transcript_1/1_Conf_1.000	516	0							
Locus_16443_Transcript_1/1_Conf_1.000	476	0							
Locus_16444_Transcript_1/2_Conf_1.000	603	5	1.04E-38	XP_001895905.1	64	163.696	201	130	Fanconi anemia complementation group D2 protein, isoform 2, putative
Locus_16444_Transcript_2/2_Conf_1.000	399	5	7.37E-21	EFO26102.1	64	103.605	113	73	hypothetical protein LOAG_02385

Locus_16445_Transcript_1/1_Conf_1.000	621	20	3.54E-53	XP_001891594.1	88	211.846	140	124	MH1 domain containing protein
Locus_16446_Transcript_1/1_Conf_1.000	352	0							
Locus_16447_Transcript_1/1_Conf_1.000	523	20	2.52E-65	XP_002645826.1	81	251.521	174	142	Hypothetical protein CBG07557
Locus_16448_Transcript_1/1_Conf_1.000	134	20	6.17E-12	NP_493554.1	86	73.9442	44	38	hypothetical protein Y54E5A.6
Locus_16449_Transcript_1/1_Conf_1.000	358	2	2.68E-15	NP_495433.1	67	85.1149	74	50	hypothetical protein C15F1.2
Locus_1645_Transcript_1/2_Conf_1.000	890	20	2.71E-31	XP_002630755.1	54	140.198	224	122	C. briggsae CBR-LYS-8 protein
Locus_1645_Transcript_2/2_Conf_1.000	890	20	2.71E-31	XP_002630755.1	54	140.198	224	122	C. briggsae CBR-LYS-8 protein
Locus_16450_Transcript_1/1_Conf_1.000	232	0							
Locus_16451_Transcript_1/1_Conf_1.000	246	0							
Locus_16452_Transcript_1/1_Conf_1.000	234	0							
Locus_16453_Transcript_1/1_Conf_1.000	135	0							
Locus_16454_Transcript_1/1_Conf_1.000	712	0							
Locus_16455_Transcript_1/1_Conf_1.000	250	0							
Locus_16456_Transcript_1/1_Conf_1.000	799	20	7.92E-69	NP_495441.1	87	264.618	178	155	hypothetical protein ZK1127.6
Locus_16457_Transcript_1/1_Conf_1.000	138	0							
Locus_16458_Transcript_1/1_Conf_1.000	135	0							
Locus_16459_Transcript_1/1_Conf_1.000	145	0							

Locus_1646_Transcript_1/1_Conf_1.000	1004	20	3.83E-120	NP_504638.1	86	435.647	274	237	hypothetical protein T05H4.5
Locus_16460_Transcript_1/1_Conf_1.000	154	0							
Locus_16461_Transcript_1/1_Conf_1.000	321	0							
Locus_16462_Transcript_1/1_Conf_1.000	840	20	5.20E-106	XP_002637794.1	84	388.267	264	224	C. briggsae CBR-PES-9 protein
Locus_16463_Transcript_1/1_Conf_1.000	450	3	2.32E-59	XP_002634053.1	84	231.491	150	127	Hypothetical protein CBG01593
Locus_16464_Transcript_1/1_Conf_1.000	1058	20	3.19E-96	XP_002639898.1	78	356.295	296	233	Hypothetical protein CBG08220
Locus_16465_Transcript_1/1_Conf_1.000	332	0							
Locus_16466_Transcript_1/1_Conf_1.000	172	20	1.51E-26	XP_001091804.2	100	122.479	57	57	PREDICTED: hypothetical protein LOC703501
Locus_16467_Transcript_1/1_Conf_1.000	474	2	1.80E-11	XP_002647749.1	72	72.4034	47	34	C. briggsae CBR-NLP-42 protein
Locus_16468_Transcript_1/1_Conf_1.000	238	0							
Locus_16469_Transcript_1/1_Conf_1.000	1098	20	8.99E-81	NP_507118.1	57	305.064	365	209	O-ACyltransferase homolog family member (oac-6)
Locus_1647_Transcript_1/2_Conf_1.000	882	20	7.20E-69	NP_501459.1	77	265.003	195	151	Homolog of Yeast Longevity gene family member (hyl-1)

Locus_1647_Transcript_2/2_Conf_1.000	803	20	1.15E-62	NP_501459.1	89	216.083	126	113	Homolog of Yeast Longevity gene family member (hyl-1)
Locus_16470_Transcript_1/1_Conf_1.000	552	20	1.16E-08	XP_001896107.1	46	63.5438	144	67	hypothetical protein Bm1_23250
Locus_16471_Transcript_1/1_Conf_1.000	215	0							
Locus_16472_Transcript_1/1_Conf_1.000	208	2	5.75E-26	XP_002636221.1	95	120.553	68	65	Hypothetical protein CBG12142
Locus_16473_Transcript_1/1_Conf_1.000	775	20	1.85E-35	NP_001040994.1	70	153.68	131	92	WaRThog (hedgehog-like family) family member (wrt-5)
Locus_16474_Transcript_1/1_Conf_1.000	193	19	1.54E-26	XP_002645128.1	92	122.479	64	59	C. briggsae CBR-NSY-4 protein
Locus_16475_Transcript_1/1_Conf_1.000	135	0							
Locus_16476_Transcript_1/1_Conf_1.000	865	20	5.44E-138	XP_002646763.1	90	494.582	278	252	C. briggsae CBR-GSY-1 protein
Locus_16477_Transcript_1/1_Conf_1.000	268	8	2.89E-09	XP_001895179.1	88	65.0846	35	31	Suppressor of forked protein
Locus_16478_Transcript_1/1_Conf_1.000	664	0							
Locus_16479_Transcript_1/1_Conf_1.000	181	0							
Locus_1648_Transcript_1/1_Conf_1.000	1218	20	1.05E-72	NP_499022.1	61	278.485	357	220	hypothetical protein ZK512.5
Locus_16480_Transcript_1/1_Conf_1.000	412	20	3.94E-51	NP_499895.2	86	204.142	137	119	hypothetical protein T21D12.9
Locus_16481_Transcript_1/1_Conf_1.000	301	20	2.11E-36	XP_001895201.1	89	155.221	99	89	protein phosphatase 1 regulatory inhibitor subunit 16A, putative
Locus_16482_Transcript_1/1_Conf_1.000	308	3	1.67E-09	XP_001896335.1	50	65.855	108	55	helix-turn-helix, Psq domain containing protein
Locus_16483_Transcript_1/1_Conf_1.000	189	20	6.71E-22	XP_002630112.1	88	107.071	63	56	Hypothetical protein CBG00513

Locus_16484_Transcript_1/1_Conf_1.000	334	20	6.57E-22	NP_001021889.1	67	107.071	102	69	hypothetical protein B0252.3
Locus_16485_Transcript_1/1_Conf_1.000	167	20	2.70E-07	XP_002648412.1	66	58.5362	53	35	C. briggsae CBR-PQE-1 protein
Locus_16486_Transcript_1/1_Conf_1.000	314	0							
Locus_16487_Transcript_1/1_Conf_1.000	516	1	2.37E-04	NP_506662.1	43	48.9062	142	62	hypothetical protein ZC412.3
Locus_16488_Transcript_1/1_Conf_1.000	537	0							
Locus_16489_Transcript_1/1_Conf_1.000	626	0							
Locus_1649_Transcript_1/1_Conf_1.000	2463	20	3.08E-17	XP_509666.2	37	95.5153	498	189	PREDICTED: similar to KIAA0853 protein
Locus_16490_Transcript_1/1_Conf_1.000	310	2	4.53E-15	NP_502613.2	72	84.3445	93	67	QUInine non-avoider family member (qui-1)
Locus_16491_Transcript_1/1_Conf_1.000	362	20	4.09E-40	XP_001902741.1	75	167.548	120	90	DNA topoisomerase III
Locus_16492_Transcript_1/1_Conf_1.000	205	0							
Locus_16493_Transcript_1/1_Conf_1.000	246	0							
Locus_16494_Transcript_1/1_Conf_1.000	398	5	5.86E-18	NP_494916.1	65	93.9745	133	87	SHC (Src Homology domain C-terminal) adaptor homolog family member (shc-2)
Locus_16495_Transcript_1/1_Conf_1.000	325	0							
Locus_16496_Transcript_1/1_Conf_1.000	631	20	4.68E-32	NP_503727.1	52	141.739	198	104	hypothetical protein W02G9.4
Locus_16497_Transcript_1/1_Conf_1.000	232	0							
Locus_16498_Transcript_1/1_Conf_1.000	300	20	2.19E-25	O96650.1	82	118.627	87	72	Thymidylate synthase

Locus_16499_Transcript_1/1_Conf_1.000	518	20	1.05E-52	NP_509229.1	75	209.534	174	132	SUppressor of activated let-60 Ras family member (sur-5)
Locus_165_Transcript_1/1_Conf_1.000	3162	20	0	NP_496136.1	81	1140.56	915	743	hypothetical protein C08H9.2
Locus_1650_Transcript_1/1_Conf_1.000	845	20	3.08E-90	NP_497876.2	78	335.88	277	218	Heparan Sulfate-glucuronic acid-5-Epimerase family member (hse-5)
Locus_16500_Transcript_1/1_Conf_1.000	330	0							
Locus_16501_Transcript_1/1_Conf_1.000	963	20	3.78E-45	CAA84693.3	56	186.422	312	175	C. elegans protein D2045.2, partially confirmed by transcript evidence
Locus_16502_Transcript_1/1_Conf_1.000	442	0							
Locus_16503_Transcript_1/1_Conf_1.000	307	0							
Locus_16504_Transcript_1/1_Conf_1.000	392	8	9.44E-13	NP_001076703.1	68	76.6406	117	80	hypothetical protein T11G6.2
Locus_16505_Transcript_1/1_Conf_1.000	284	0							
Locus_16506_Transcript_1/1_Conf_1.000	753	20	5.60E-42	XP_002645124.1	66	175.252	162	107	Hypothetical protein CBG16818
Locus_16507_Transcript_1/1_Conf_1.000	273	0							
Locus_16508_Transcript_1/1_Conf_1.000	219	1	1.56E-10	EFO25846.1	69	69.3218	71	49	hypothetical protein LOAG_02637
Locus_16509_Transcript_1/1_Conf_1.000	158	0							

Locus_1651_Transcript_1/2_Conf_1.000	544	0							
Locus_1651_Transcript_2/2_Conf_1.000	550	0							
Locus_16510_Transcript_1/1_Conf_1.000	241	20	6.59E-22	XP_002644770.1	84	107.071	78	66	C. briggsae CBR-ACS-17 protein
Locus_16511_Transcript_1/1_Conf_1.000	748	20	2.33E-64	AAK68292.3	70	249.595	261	184	U28943_4Clc-type chloride channel protein 3, isoform b, confirmed by transcript evidence
Locus_16512_Transcript_1/1_Conf_1.000	218	0							
Locus_16513_Transcript_1/1_Conf_1.000	255	20	3.22E-24	NP_494384.2	75	114.775	85	64	PaTChed family member (ptc-3)
Locus_16514_Transcript_1/1_Conf_1.000	450	20	1.42E-32	EFO16233.1	67	142.51	140	94	variant SH3 domain-containing protein
Locus_16515_Transcript_1/1_Conf_1.000	273	20	6.56E-30	XP_002753198.1	96	133.65	87	84	PREDICTED: poly(rC)-binding protein 2-like isoform 2
Locus_16516_Transcript_1/1_Conf_1.000	148	0							
Locus_16517_Transcript_1/1_Conf_1.000	803	0							
Locus_16518_Transcript_1/1_Conf_1.000	288	0							
Locus_16519_Transcript_1/1_Conf_1.000	540	20	6.20E-65	XP_002640715.1	83	250.366	178	149	C. briggsae CBR-VPS-28 protein
Locus_1652_Transcript_1/1_Conf_1.000	1166	20	2.22E-133	XP_002633423.1	77	479.945	335	260	C. briggsae CBR-FAT-6 protein
Locus_16520_Transcript_1/1_Conf_1.000	906	20	5.97E-82	EFO25806.1	74	308.531	299	223	hypothetical protein LOAG_02677
Locus_16521_Transcript_1/1_Conf_1.000	597	0							
Locus_16522_Transcript_1/1_Conf_1.000	279	0							

Locus_16523_Transcript_1/1_Conf_1.000	411	5	4.09E-40	NP_506132.1	72	167.548	123	89	hypothetical protein W04D2.4
Locus_16524_Transcript_1/1_Conf_1.000	138	0							
Locus_16525_Transcript_1/1_Conf_1.000	347	20	4.59E-55	EFO25295.1	95	217.238	115	110	STE/STE20/KHS protein kinase
Locus_16526_Transcript_1/1_Conf_1.000	801	20	5.24E-28	XP_001900507.1	49	129.028	241	120	Protein set-2.
Locus_16527_Transcript_1/1_Conf_1.000	261	18	1.39E-11	AAS91567.1	82	72.7886	45	37	transformer-1
Locus_16528_Transcript_1/1_Conf_1.000	148	2	3.36E-05	EFO19039.1	84	51.6026	46	39	Tln1 protein
Locus_16529_Transcript_1/1_Conf_1.000	696	20	1.67E-26	NP_497348.3	78	123.635	94	74	hypothetical protein Y119D3B.12
Locus_1653_Transcript_1/1_Conf_1.000	1106	20	4.52E-64	CAZ65529.1	68	249.595	317	216	C. elegans protein T28C6.7b, partially confirmed by transcript evidence
Locus_16530_Transcript_1/1_Conf_1.000	482	8	5.65E-58	XP_002637142.1	88	226.868	137	121	Hypothetical protein CBG09644
Locus_16531_Transcript_1/1_Conf_1.000	626	20	3.82E-71	NP_491354.1	78	271.552	188	148	AcetylCholine Receptor family member (acr-6)
Locus_16532_Transcript_1/2_Conf_1.000	448	2	4.18E-08	XP_002631722.1	49	61.2326	145	72	C. briggsae CBR-SINH-1 protein
Locus_16532_Transcript_2/2_Conf_1.000	412	1	6.16E-04	XP_002631722.1	54	47.3654	97	53	C. briggsae CBR-SINH-1 protein
Locus_16533_Transcript_1/1_Conf_1.000	377	0							
Locus_16534_Transcript_1/1_Conf_1.000	334	20	3.95E-51	XP_002758725.1	100	204.142	107	107	PREDICTED: dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1-like isoform 2
Locus_16535_Transcript_1/1_Conf_1.000	327	0							
Locus_16536_Transcript_1/1_Conf_1.000	168	0							
Locus_16537_Transcript_1/1_Conf_1.000	148	2	8.26E-12	NP_001022051.1	80	73.559	47	38	SREBP Cleavage activating Protein (SCAP) homolog family member (scp-1)

Locus_16538_Transcript_1/1_Conf_1.000	246	2	2.50E-05	XP_002634825.1	63	51.9878	61	39	Hypothetical protein CBG13933
Locus_16539_Transcript_1/1_Conf_1.000	262	0							
Locus_1654_Transcript_1/1_Conf_1.000	262	0							
Locus_16540_Transcript_1/1_Conf_1.000	177	0							
Locus_16541_Transcript_1/1_Conf_1.000	539	20	2.03E-52	NP_506007.1	83	208.764	143	119	CYclin L family member (cyl-1)
Locus_16542_Transcript_1/1_Conf_1.000	341	6	7.22E-13	EFO19489.1	56	77.0258	113	64	IQ calmodulin-binding domain-containing protein
Locus_16543_Transcript_1/1_Conf_1.000	464	11	1.75E-38	NP_001122650.1	67	162.155	159	107	PaTChed family member (ptc-3)
Locus_16544_Transcript_1/1_Conf_1.000	146	2	2.50E-08	CAD19995.2	82	62.003	39	32	metalloprotease III
Locus_16545_Transcript_1/1_Conf_1.000	278	0							
Locus_16546_Transcript_1/1_Conf_1.000	140	0							
Locus_16547_Transcript_1/1_Conf_1.000	136	4	5.04E-06	XP_001895407.1	79	54.299	43	34	Phospholipase D. Active site motif family protein
Locus_16548_Transcript_1/1_Conf_1.000	225	4	4.66E-07	NP_495463.2	61	57.7658	73	45	hypothetical protein T02G5.2
Locus_16549_Transcript_1/1_Conf_1.000	283	0							
Locus_1655_Transcript_1/1_Conf_1.000	248	0							
Locus_16550_Transcript_1/1_Conf_1.000	343	0							
Locus_16551_Transcript_1/1_Conf_1.000	247	3	2.84E-17	CAO72177.1	69	91.6633	83	58	hexosaminidase
Locus_16552_Transcript_1/1_Conf_1.000	273	0							
Locus_16553_Transcript_1/1_Conf_1.000	243	4	1.57E-07	EFO27452.1	77	59.3066	81	63	hypothetical protein LOAG_01023
Locus_16554_Transcript_1/1_Conf_1.000	348	20	2.68E-55	NP_740906.1	98	218.009	115	113	hypothetical protein F26E4.7
Locus_16555_Transcript_1/2_Conf_1.000	383	0							
Locus_16555_Transcript_2/2_Conf_1.000	393	0							
Locus_16556_Transcript_1/1_Conf_1.000	187	2	1.27E-12	NP_507767.2	88	76.2554	60	53	hypothetical protein C14B4.2

Locus_16557_Transcript_1/1_Conf_1.000	213	20	2.75E-20	NP_491664.1	81	101.679	70	57	UNCoordinated family member (unc-40)
Locus_16558_Transcript_1/1_Conf_1.000	489	0							
Locus_16559_Transcript_1/1_Conf_1.000	396	0							
Locus_1656_Transcript_1/1_Conf_1.000	488	0							
Locus_16560_Transcript_1/1_Conf_1.000	364	0							
Locus_16561_Transcript_1/1_Conf_1.000	230	0							
Locus_16562_Transcript_1/1_Conf_1.000	131	0							
Locus_16563_Transcript_1/1_Conf_1.000	238	20	5.06E-22	P10253.3	100	107.457	52	52	Lysosomal alpha-glucosidase
Locus_16564_Transcript_1/1_Conf_1.000	190	0							
Locus_16565_Transcript_1/1_Conf_1.000	626	20	2.35E-20	XP_002636128.1	79	102.834	88	70	Hypothetical protein CBG01378
Locus_16566_Transcript_1/1_Conf_1.000	792	20	7.54E-72	XP_002637669.1	76	274.633	208	159	Hypothetical protein CBG19425
Locus_16567_Transcript_1/1_Conf_1.000	233	0							

Locus_16568_Transcript_1/1_Conf_1.000	486	20	2.00E-26	XP_002639142.1	55	122.094	168	94	Hypothetical protein CBG14966
Locus_16569_Transcript_1/1_Conf_1.000	267	0							
Locus_1657_Transcript_1/1_Conf_1.000	261	0							
Locus_16570_Transcript_1/1_Conf_1.000	385	20	5.91E-47	NP_505312.1	85	190.274	128	110	hypothetical protein T19A5.1
Locus_16571_Transcript_1/1_Conf_1.000	198	0							
Locus_16572_Transcript_1/1_Conf_1.000	568	20	3.24E-25	EFO22800.1	54	118.627	182	100	hypothetical protein LOAG_05685
Locus_16573_Transcript_1/1_Conf_1.000	170	0							
Locus_16574_Transcript_1/1_Conf_1.000	158	0							
Locus_16575_Transcript_1/1_Conf_1.000	192	0							
Locus_16576_Transcript_1/1_Conf_1.000	457	0							
Locus_16577_Transcript_1/1_Conf_1.000	615	2	2.46E-06	XP_001899613.1	62	56.225	70	44	hypothetical protein Bm1_40770
Locus_16578_Transcript_1/1_Conf_1.000	182	0							
Locus_16579_Transcript_1/1_Conf_1.000	453	20	6.50E-62	AAH62437.1	100	239.965	115	115	Cytochrome c oxidase subunit IV isoform 1
Locus_1658_Transcript_1/1_Conf_1.000	172	0							
Locus_16580_Transcript_1/1_Conf_1.000	282	0							
Locus_16581_Transcript_1/1_Conf_1.000	166	0							
Locus_16582_Transcript_1/1_Conf_1.000	359	20	2.50E-21	NP_491427.1	75	105.145	99	75	hypothetical protein W09C3.4
Locus_16583_Transcript_1/1_Conf_1.000	532	20	8.35E-67	NP_502120.1	80	256.529	177	142	hypothetical protein B0035.16
Locus_16584_Transcript_1/1_Conf_1.000	454	10	9.81E-26	XP_002638736.1	66	119.783	130	87	C. briggsae CBR-EGO-1 protein
Locus_16585_Transcript_1/1_Conf_1.000	502	20	5.47E-32	EFO21215.1	64	140.584	157	101	AMP-binding enzyme family protein

Locus_16586_Transcript_1/1_Conf_1.000	168	20	9.83E-26	XP_002807155.1	100	119.783	55	55	PREDICTED: LOW QUALITY PROTEIN: poly(rC)-binding protein 2-like
Locus_16587_Transcript_1/1_Conf_1.000	177	20	3.03E-27	XP_002760341.1	100	124.79	58	58	PREDICTED: glutamine synthetase
Locus_16588_Transcript_1/1_Conf_1.000	443	0							
Locus_16589_Transcript_1/1_Conf_1.000	293	20	1.87E-40	NP_491513.2	93	168.703	96	90	Formin HOmology Domain family member (fhod-1)
Locus_1659_Transcript_1/1_Conf_1.000	296	0							
Locus_16590_Transcript_1/1_Conf_1.000	277	0							
Locus_16591_Transcript_1/1_Conf_1.000	216	4	2.65E-15	XP_002633968.1	83	85.1149	56	47	C. briggsae CBR-MCA-1 protein
Locus_16592_Transcript_1/1_Conf_1.000	154	0							
Locus_16593_Transcript_1/1_Conf_1.000	546	20	7.66E-42	XP_001190458.1	69	173.711	178	123	PREDICTED: similar to ATP-binding cassette, sub-family C (CFTR/MRP), member 4
Locus_16594_Transcript_1/1_Conf_1.000	134	0							
Locus_16595_Transcript_1/1_Conf_1.000	249	0							
Locus_16596_Transcript_1/1_Conf_1.000	220	0							
Locus_16597_Transcript_1/1_Conf_1.000	267	20	2.27E-30	NP_740900.1	84	135.191	88	74	hypothetical protein T08G11.1
Locus_16598_Transcript_1/1_Conf_1.000	217	0							
Locus_16599_Transcript_1/1_Conf_1.000	226	0							
Locus_166_Transcript_1/1_Conf_1.000	1411	20	4.24E-92	XP_002645826.1	58	343.199	425	250	Hypothetical protein CBG07557
Locus_1660_Transcript_1/3_Conf_0.400	1995	20	0	XP_002638688.1	83	749.969	514	431	Hypothetical protein CBG11883

Locus_1660_Transcript_2/3_Conf_0.600	2103	20	0	XP_002638688.1	83	749.969	514	431	Hypothetical protein CBG11883
Locus_1660_Transcript_3/3_Conf_0.400	1696	20	5.39E-116	BAI79333.1	62	422.935	548	343	mitochondrial elongation factor G2
Locus_16600_Transcript_1/1_Conf_1.000	142	2	5.35E-08	XP_002638375.1	85	60.8474	34	29	Hypothetical protein CBG18580
Locus_16601_Transcript_1/1_Conf_1.000	549	0							
Locus_16602_Transcript_1/1_Conf_1.000	263	0							
Locus_16603_Transcript_1/1_Conf_1.000	294	20	5.83E-18	EFN72462.1	82	93.9745	73	60	Copper homeostasis protein cutC-like protein
Locus_16604_Transcript_1/2_Conf_1.000	825	4	2.99E-50	XP_002631532.1	78	202.986	193	152	Hypothetical protein CBG20698
Locus_16604_Transcript_2/2_Conf_1.000	825	4	6.02E-51	XP_002631532.1	79	205.297	193	153	Hypothetical protein CBG20698
Locus_16605_Transcript_1/2_Conf_1.000	528	0							
Locus_16605_Transcript_2/2_Conf_1.000	542	0							
Locus_16606_Transcript_1/1_Conf_1.000	687	20	6.75E-41	NP_502212.1	60	171.4	225	137	hypothetical protein ZK792.5
Locus_16607_Transcript_1/1_Conf_1.000	450	20	4.01E-19	NP_495338.1	56	97.8265	151	85	hypothetical protein C56C10.9
Locus_16608_Transcript_1/1_Conf_1.000	253	0							
Locus_16609_Transcript_1/2_Conf_1.000	637	0							
Locus_16609_Transcript_2/2_Conf_1.000	637	0							
Locus_1661_Transcript_1/1_Conf_1.000	286	0							
Locus_16610_Transcript_1/1_Conf_1.000	286	0							
Locus_16611_Transcript_1/1_Conf_1.000	285	0							
Locus_16612_Transcript_1/1_Conf_1.000	388	20	3.24E-37	NP_490840.2	76	157.918	130	99	DAP (Death-Associated Protein) Kinase homolog family member (dapk-1)
Locus_16613_Transcript_1/1_Conf_1.000	361	20	1.98E-18	XP_002647178.1	63	95.5153	119	75	Hypothetical protein CBG22337

Locus_16614_Transcript_1/1_Conf_1.000	382	20	2.19E-33	NP_741467.1	81	145.206	94	77	hypothetical protein C09G4.2
Locus_16615_Transcript_1/1_Conf_1.000	368	20	4.81E-33	EFO27702.1	79	144.05	124	98	roadblock/LC7 domain-containing protein
Locus_16616_Transcript_1/1_Conf_1.000	142	0							
Locus_16617_Transcript_1/1_Conf_1.000	314	20	2.63E-50	XP_002927596.1	100	201.445	96	96	PREDICTED: myosin regulatory light polypeptide 9-like
Locus_16618_Transcript_1/1_Conf_1.000	322	0							
Locus_16619_Transcript_1/1_Conf_1.000	133	0							
Locus_1662_Transcript_1/1_Conf_1.000	701	20	3.48E-48	XP_002632763.1	85	195.667	140	119	Hypothetical protein CBG11654
Locus_16620_Transcript_1/1_Conf_1.000	396	0							
Locus_16621_Transcript_1/1_Conf_1.000	381	4	3.74E-25	NP_496802.2	63	117.857	128	81	BTAF (TBP-associated factor) homolog family member (btf-1)
Locus_16622_Transcript_1/1_Conf_1.000	441	20	4.45E-50	EFO26644.1	78	200.675	143	112	hypothetical protein LOAG_01839
Locus_16623_Transcript_1/1_Conf_1.000	821	1	9.29E-04	XP_002635323.1	45	48.521	231	104	Hypothetical protein CBG01490

Locus_16624_Transcript_1/1_Conf_1.000	144	20	1.20E-10	XP_002601536.1	80	69.707	42	34	hypothetical protein BRAFLDRAFT_230606
Locus_16625_Transcript_1/1_Conf_1.000	423	3	1.76E-06	EFO22932.1	47	55.8398	120	57	hypothetical protein LOAG_05551
Locus_16626_Transcript_1/1_Conf_1.000	431	9	5.78E-18	A8X9H4.2	56	93.9745	120	68	Chondroitin proteoglycan 4
Locus_16627_Transcript_1/1_Conf_1.000	156	0							
Locus_16628_Transcript_1/1_Conf_1.000	164	0							
Locus_16629_Transcript_1/1_Conf_1.000	145	0							
Locus_1663_Transcript_1/1_Conf_1.000	2720	20	0	XP_002645952.1	96	1395.56	758	733	C. briggsae CBR-DYN-1 protein
Locus_16630_Transcript_1/1_Conf_1.000	659	20	1.27E-78	NP_508515.2	79	296.59	214	170	AQuaPorin or aquaglyceroporin related family member (aqp-7)
Locus_16631_Transcript_1/1_Conf_1.000	145	0							
Locus_16632_Transcript_1/1_Conf_1.000	519	5	2.68E-11	NP_503141.1	63	72.0182	101	64	hypothetical protein W03F9.10

Locus_16633_Transcript_1/1_Conf_1.000	638	20	2.86E-85	NP_501266.1	89	318.546	201	180	hypothetical protein C50F7.4
Locus_16634_Transcript_1/1_Conf_1.000	226	0							
Locus_16635_Transcript_1/1_Conf_1.000	1290	6	2.91E-52	XP_002631435.1	64	210.69	223	143	Hypothetical protein CBG03297
Locus_16636_Transcript_1/1_Conf_1.000	535	0							
Locus_16637_Transcript_1/1_Conf_1.000	245	0							
Locus_16638_Transcript_1/1_Conf_1.000	315	0							
Locus_16639_Transcript_1/1_Conf_1.000	141	18	2.94E-06	EFO23788.1	76	55.0694	42	32	hypothetical protein LOAG_04700
Locus_1664_Transcript_1/7_Conf_0.167	335	0							
Locus_1664_Transcript_2/7_Conf_0.667	1320	20	8.55E-132	NP_501877.2	80	474.937	362	290	hypothetical protein F01G10.7
Locus_1664_Transcript_3/7_Conf_0.667	1333	20	1.93E-131	NP_501877.2	80	473.781	362	290	hypothetical protein F01G10.7
Locus_1664_Transcript_4/7_Conf_0.556	1048	20	1.11E-125	NP_501877.2	79	454.136	353	282	hypothetical protein F01G10.7
Locus_1664_Transcript_5/7_Conf_0.556	1333	20	2.98E-132	NP_501877.2	80	476.478	362	290	hypothetical protein F01G10.7

Locus_1664_Transcript_6/7_Conf_0.611	1333	20	1.02E-132	NP_501877.2	80	478.019	362	291	hypothetical protein F01G10.7
Locus_1664_Transcript_7/7_Conf_0.667	1333	20	8.67E-132	NP_501877.2	80	474.937	362	290	hypothetical protein F01G10.7
Locus_16640_Transcript_1/1_Conf_1.000	475	20	4.07E-64	XP_002633392.1	85	247.284	158	135	C. briggsae CBR-WHT-2 protein
Locus_16641_Transcript_1/1_Conf_1.000	245	0							
Locus_16642_Transcript_1/1_Conf_1.000	617	2	1.99E-56	NP_001024385.1	77	222.631	192	148	hypothetical protein C09F12.3
Locus_16643_Transcript_1/1_Conf_1.000	345	20	1.18E-18	NP_740939.1	81	96.2857	72	59	hypothetical protein Y105E8A.11
Locus_16644_Transcript_1/1_Conf_1.000	270	2	2.69E-07	XP_002646257.1	58	58.5362	91	53	Hypothetical protein CBG11961
Locus_16645_Transcript_1/2_Conf_1.000	368	1	5.00E-14	CAR63617.1	79	80.8777	64	51	hypothetical protein
Locus_16645_Transcript_2/2_Conf_1.000	368	1	5.00E-14	CAR63617.1	79	80.8777	64	51	hypothetical protein
Locus_16646_Transcript_1/1_Conf_1.000	507	20	5.06E-12	EFO27069.1	65	74.3294	70	46	Ulp1 protease
Locus_16647_Transcript_1/1_Conf_1.000	216	20	5.34E-16	XP_002639908.1	72	87.4261	66	48	Hypothetical protein CBG08236
Locus_16648_Transcript_1/1_Conf_1.000	484	20	5.81E-50	NP_001129769.1	76	200.29	156	120	DAP (Death Associated Protein kinase) Like Kinase family member (dlk-1)

Locus_16649_Transcript_1/1_Conf_1.000	550	20	8.09E-31	XP_001897975.1	59	137.117	176	104	SOH1 family protein
Locus_1665_Transcript_1/1_Conf_1.000	545	4	2.10E-68	XP_002631447.1	86	261.922	160	139	Hypothetical protein CBG03309
Locus_16650_Transcript_1/1_Conf_1.000	271	0							
Locus_16651_Transcript_1/1_Conf_1.000	1146	20	1.43E-52	NP_509671.3	59	211.46	300	178	hypothetical protein ZC506.1
Locus_16652_Transcript_1/1_Conf_1.000	329	4	1.79E-43	NP_001022254.1	88	178.718	104	92	hypothetical protein M05D6.9
Locus_16653_Transcript_1/1_Conf_1.000	246	20	1.23E-28	XP_002634963.1	89	129.413	73	65	C. briggsae CBR-DIS-3 protein
Locus_16654_Transcript_1/1_Conf_1.000	445	0							
Locus_16655_Transcript_1/1_Conf_1.000	647	20	6.70E-45	XP_002661818.1	64	184.496	212	137	PREDICTED: Gap-Pol polyprotein-like
Locus_16656_Transcript_1/1_Conf_1.000	491	0							
Locus_16657_Transcript_1/1_Conf_1.000	269	20	4.02E-19	XP_002636816.1	61	97.8265	86	53	Hypothetical protein CBG09260
Locus_16658_Transcript_1/1_Conf_1.000	213	0							
Locus_16659_Transcript_1/1_Conf_1.000	142	0							
Locus_1666_Transcript_1/1_Conf_1.000	280	20	1.56E-15	XP_002634963.1	64	85.8853	93	60	C. briggsae CBR-DIS-3 protein
Locus_16660_Transcript_1/1_Conf_1.000	372	20	7.39E-21	NP_509237.1	69	103.605	102	71	SaPosin-like Protein family member (spp-4)
Locus_16661_Transcript_1/1_Conf_1.000	270	0							
Locus_16662_Transcript_1/1_Conf_1.000	301	0							
Locus_16663_Transcript_1/1_Conf_1.000	162	0							
Locus_16664_Transcript_1/1_Conf_1.000	155	2	8.79E-06	EFO27087.1	74	53.5286	51	38	hypothetical protein LOAG_01392
Locus_16665_Transcript_1/1_Conf_1.000	139	6	3.36E-10	NP_498641.1	83	68.1662	42	35	hypothetical protein H14A12.3
Locus_16666_Transcript_1/1_Conf_1.000	175	0							

Locus_16667_Transcript_1/1_Conf_1.000	504	20	8.23E-92	2I07	100	339.347	159	159	Human Complement Component C3b
Locus_16668_Transcript_1/1_Conf_1.000	575	20	9.63E-65	NP_504498.2	76	249.98	193	148	hypothetical protein F25B4.7
Locus_16669_Transcript_1/1_Conf_1.000	152	20	6.29E-20	NP_871645.1	98	100.523	50	49	hypothetical protein C28H8.11
Locus_1667_Transcript_1/1_Conf_1.000	1874	20	3.31E-154	XP_002643742.1	70	550.051	582	409	Hypothetical protein CBG01937
Locus_16670_Transcript_1/1_Conf_1.000	575	0							
Locus_16671_Transcript_1/1_Conf_1.000	590	5	1.30E-27	CAB04569.3	60	126.716	182	110	C. elegans protein K05C4.5, confirmed by transcript evidence
Locus_16672_Transcript_1/1_Conf_1.000	560	20	1.73E-52	NP_490726.1	77	209.149	179	139	hypothetical protein R119.3

Locus_16673_Transcript_1/1_Conf_1.000	260	0							
Locus_16674_Transcript_1/1_Conf_1.000	426	20	3.37E-50	XP_001897105.1	81	201.06	133	109	protein phosphatase 2A, regulatory subunit B'
Locus_16675_Transcript_1/1_Conf_1.000	140	6	2.49E-05	EFO25333.1	62	51.9878	48	30	hypothetical protein LOAG_03154
Locus_16676_Transcript_1/1_Conf_1.000	409	0							
Locus_16677_Transcript_1/1_Conf_1.000	221	13	5.91E-18	ACV31107.1	85	93.9745	67	57	Hypothetical protein F22D3.2b
Locus_16678_Transcript_1/2_Conf_1.000	546	20	1.35E-46	EFO28378.1	78	189.504	137	107	mediator complex subunit 31
Locus_16678_Transcript_2/2_Conf_1.000	545	20	1.01E-46	EFO28378.1	78	189.889	137	107	mediator complex subunit 31
Locus_16679_Transcript_1/1_Conf_1.000	923	10	1.19E-101	EFO20752.1	75	374.015	292	219	AMOP domain-containing protein
Locus_1668_Transcript_1/2_Conf_1.000	1303	20	9.77E-64	NP_492076.1	68	248.825	302	207	hypothetical protein F52A8.6
Locus_1668_Transcript_2/2_Conf_1.000	1116	20	5.62E-62	NP_001040668.1	81	242.662	200	163	hypothetical protein F52A8.6
Locus_16680_Transcript_1/1_Conf_1.000	230	20	9.29E-32	NP_502751.1	89	139.813	76	68	TRAnsformer : XX animals transformed into males family member (tra-3)
Locus_16681_Transcript_1/1_Conf_1.000	650	0							

Locus_16682_Transcript_1/1_Conf_1.000	197	0							
Locus_16683_Transcript_1/1_Conf_1.000	275	20	8.53E-46	XP_002834824.1	100	186.422	91	91	PREDICTED: LOW QUALITY PROTEIN: guanine nucleotide-binding protein subunit beta-2-like 1-like
Locus_16684_Transcript_1/1_Conf_1.000	284	20	9.72E-29	EFO16325.1	69	129.798	100	69	hypothetical protein LOAG_12180
Locus_16685_Transcript_1/1_Conf_1.000	507	20	3.05E-33	EFO21515.1	64	144.821	170	109	guanylate kinase
Locus_16686_Transcript_1/1_Conf_1.000	206	2	1.29E-09	NP_495911.3	63	66.2402	66	42	hypothetical protein C18E9.5
Locus_16687_Transcript_1/1_Conf_1.000	286	0							
Locus_16688_Transcript_1/1_Conf_1.000	1233	20	9.46E-37	XP_001892593.1	54	159.073	340	185	KH domain containing protein
Locus_16689_Transcript_1/1_Conf_1.000	429	0							
Locus_1669_Transcript_1/2_Conf_1.000	1412	20	9.12E-95	NP_497100.1	63	352.058	419	264	human Activating Signal Cointegrator homolog family member (asc-1)
Locus_1669_Transcript_2/2_Conf_1.000	1412	20	9.12E-95	NP_497100.1	63	352.058	419	264	human Activating Signal Cointegrator homolog family member (asc-1)
Locus_16690_Transcript_1/1_Conf_1.000	210	20	2.85E-17	XP_002645317.1	75	91.6633	69	52	C. briggsae CBR-TRK-1 protein
Locus_16691_Transcript_1/1_Conf_1.000	346	20	4.31E-45	CAR63665.1	92	184.111	98	91	hypothetical protein
Locus_16692_Transcript_1/1_Conf_1.000	132	20	2.87E-09	A8XJL7.2	88	65.0846	43	38	Serine/threonine-protein kinase sax-1
Locus_16693_Transcript_1/1_Conf_1.000	181	0							
Locus_16694_Transcript_1/1_Conf_1.000	375	0							
Locus_16695_Transcript_1/1_Conf_1.000	568	20	5.69E-38	EFO25439.1	70	160.999	161	113	srpr protein
Locus_16696_Transcript_1/1_Conf_1.000	246	0							
Locus_16697_Transcript_1/1_Conf_1.000	291	0							
Locus_16698_Transcript_1/1_Conf_1.000	280	0							

Locus_16699_Transcript_1/1_Conf_1.000	301	20	3.99E-35	EFO21757.1	85	150.984	99	85	hypothetical protein LOAG_06731
Locus_167_Transcript_1/1_Conf_1.000	243	0							
Locus_1670_Transcript_1/1_Conf_1.000	195	13	2.15E-12	NP_493741.1	71	75.485	59	42	hypothetical protein W10D9.5
Locus_16700_Transcript_1/1_Conf_1.000	235	0							
Locus_16701_Transcript_1/1_Conf_1.000	146	20	6.35E-12	NP_510249.2	91	73.9442	36	33	TREhalase family member (tre-4)
Locus_16702_Transcript_1/1_Conf_1.000	255	0							
Locus_16703_Transcript_1/2_Conf_1.000	264	0							
Locus_16703_Transcript_2/2_Conf_1.000	131	0							
Locus_16704_Transcript_1/1_Conf_1.000	220	20	3.12E-35	ACC44768.1	100	151.369	72	72	APA-2
Locus_16705_Transcript_1/1_Conf_1.000	343	3	1.55E-10	NP_001021445.1	60	69.3218	106	64	DAP (Death Associated Protein kinase) Like Kinase family member (dlk-1)
Locus_16706_Transcript_1/1_Conf_1.000	284	0							
Locus_16707_Transcript_1/1_Conf_1.000	197	0							
Locus_16708_Transcript_1/1_Conf_1.000	330	20	1.16E-34	NP_496959.1	89	149.443	107	96	EATing: abnormal pharyngeal pumping family member (eat-2)

Locus_16709_Transcript_1/1_Conf_1.000	533	6	7.18E-10	NP_001021054.1	50	67.3958	174	87	Suppressor with Morphological effect on Genitalia family member (smg-1)
Locus_1671_Transcript_1/1_Conf_1.000	215	1	1.24E-04	XP_002405836.1	64	49.6766	34	22	conserved hypothetical protein
Locus_16710_Transcript_1/1_Conf_1.000	148	0							
Locus_16711_Transcript_1/1_Conf_1.000	727	2	5.20E-66	XP_002639917.1	73	254.988	241	176	C. briggsae CBR-SMGL-1 protein
Locus_16712_Transcript_1/1_Conf_1.000	160	5	2.80E-12	EFO19924.1	79	75.0998	53	42	hypothetical protein LOAG_08567
Locus_16713_Transcript_1/1_Conf_1.000	303	0							
Locus_16714_Transcript_1/1_Conf_1.000	151	0							
Locus_16715_Transcript_1/1_Conf_1.000	354	0							
Locus_16716_Transcript_1/1_Conf_1.000	337	20	1.45E-37	NP_492905.1	97	159.073	88	86	hypothetical protein H25P06.1
Locus_16717_Transcript_1/1_Conf_1.000	302	20	1.57E-31	XP_001152859.1	98	139.043	67	66	PREDICTED: hypothetical protein
Locus_16718_Transcript_1/1_Conf_1.000	495	0							
Locus_16719_Transcript_1/1_Conf_1.000	147	20	5.92E-10	XP_001896664.1	81	67.3958	48	39	Protein kinase domain containing protein
Locus_1672_Transcript_1/1_Conf_1.000	490	0							
Locus_16720_Transcript_1/1_Conf_1.000	134	0							
Locus_16721_Transcript_1/1_Conf_1.000	396	20	1.82E-27	EFO21962.1	58	125.561	130	76	TK/EGFR protein kinase
Locus_16722_Transcript_1/1_Conf_1.000	174	0							
Locus_16723_Transcript_1/1_Conf_1.000	396	20	3.18E-56	AAA36105.1	97	221.09	106	103	gamma-interferon-inducible protein precursor
Locus_16724_Transcript_1/1_Conf_1.000	137	0							
Locus_16725_Transcript_1/1_Conf_1.000	166	0							
Locus_16726_Transcript_1/1_Conf_1.000	384	20	3.84E-38	NP_507509.3	79	160.999	126	100	hypothetical protein C06H5.6
Locus_16727_Transcript_1/1_Conf_1.000	482	0							
Locus_16728_Transcript_1/1_Conf_1.000	235	4	1.64E-12	NP_872065.1	82	75.8702	45	37	hypothetical protein F35C11.7

Locus_16729_Transcript_1/1_Conf_1.000	495	20	2.50E-21	NP_493658.2	70	105.145	131	93	hypothetical protein C50D2.8
Locus_1673_Transcript_1/1_Conf_1.000	907	0							
Locus_16730_Transcript_1/1_Conf_1.000	690	0							
Locus_16731_Transcript_1/1_Conf_1.000	178	0							
Locus_16732_Transcript_1/1_Conf_1.000	460	20	6.55E-06	XP_392160.2	48	53.9138	134	65	PREDICTED: similar to ubiquitin specific protease 3
Locus_16733_Transcript_1/1_Conf_1.000	341	20	3.00E-51	XP_001509789.1	100	204.527	112	112	PREDICTED: hypothetical protein, partial
Locus_16734_Transcript_1/1_Conf_1.000	237	0							
Locus_16735_Transcript_1/1_Conf_1.000	262	4	1.44E-16	NP_001122565.1	60	89.3521	107	65	Variable ABnormal morphology family member (vab-10)
Locus_16736_Transcript_1/2_Conf_1.000	619	3	2.17E-26	NP_491462.2	71	122.865	92	66	C-type LECtin family member (clec-90)
Locus_16736_Transcript_2/2_Conf_1.000	619	3	4.84E-26	NP_491462.2	71	121.709	92	66	C-type LECtin family member (clec-90)
Locus_16737_Transcript_1/1_Conf_1.000	309	0							
Locus_16738_Transcript_1/1_Conf_1.000	332	0							
Locus_16739_Transcript_1/1_Conf_1.000	1007	3	1.19E-28	NP_492325.2	49	131.724	308	153	hypothetical protein R05D11.6
Locus_1674_Transcript_1/1_Conf_1.000	843	0							
Locus_16740_Transcript_1/1_Conf_1.000	177	2	1.16E-10	NP_495620.1	75	69.707	58	44	hypothetical protein B0495.9
Locus_16741_Transcript_1/1_Conf_1.000	152	0							
Locus_16742_Transcript_1/1_Conf_1.000	250	0							
Locus_16743_Transcript_1/1_Conf_1.000	168	0							
Locus_16744_Transcript_1/1_Conf_1.000	322	20	1.30E-25	XP_001894170.1	66	119.398	106	70	Ribonucleases P/MRP protein subunit POP1 containing protein
Locus_16745_Transcript_1/1_Conf_1.000	174	0							

Locus_16746_Transcript_1/1_Conf_1.000	258	20	8.70E-38	XP_001898882.1	92	159.844	85	79	casein kinase 1, delta
Locus_16747_Transcript_1/1_Conf_1.000	1057	20	2.17E-153	XP_001901272.1	91	546.199	352	322	DEAD
Locus_16748_Transcript_1/1_Conf_1.000	240	20	7.82E-07	EFN81401.1	65	56.9954	61	40	Putative AC transposase
Locus_16749_Transcript_1/1_Conf_1.000	264	0							
Locus_1675_Transcript_1/1_Conf_1.000	230	1	1.49E-05	ACV86995.1	74	52.7582	39	29	gut-associated larval antigen-1
Locus_16750_Transcript_1/1_Conf_1.000	191	0							
Locus_16751_Transcript_1/1_Conf_1.000	293	0							
Locus_16752_Transcript_1/1_Conf_1.000	145	0							
Locus_16753_Transcript_1/1_Conf_1.000	364	20	1.15E-26	NP_506077.1	70	122.865	121	85	hypothetical protein F55C5.2
Locus_16754_Transcript_1/1_Conf_1.000	192	0							
Locus_16755_Transcript_1/1_Conf_1.000	150	0							
Locus_16756_Transcript_1/1_Conf_1.000	518	3	6.24E-05	ZP_07577412.1	48	50.8322	131	64	chromosome segregation protein SMC
Locus_16757_Transcript_1/1_Conf_1.000	138	20	1.36E-19	XP_002812342.1	100	99.3673	45	45	PREDICTED: ornithine decarboxylase-like
Locus_16758_Transcript_1/1_Conf_1.000	173	0							
Locus_16759_Transcript_1/1_Conf_1.000	1278	20	2.29E-17	NP_492467.1	55	94.7449	219	122	mammalian ASPM (Abnormal SPindles and primary Microcephaly) homolog family member (aspm-1)
Locus_1676_Transcript_1/1_Conf_1.000	1539	20	0	NP_491363.1	88	835.869	513	455	Dynein Heavy Chain family member (dhc-1)
Locus_16760_Transcript_1/1_Conf_1.000	174	0							

Locus_16761_Transcript_1/1_Conf_1.000	704	20	2.18E-82	XP_002645723.1	81	309.301	222	180	C. briggsae CBR-GCK-4 protein
Locus_16762_Transcript_1/1_Conf_1.000	300	6	1.37E-27	XP_541499.2	89	125.946	75	67	PREDICTED: similar to Orphan sodium- and chloride-dependent neurotransmitter transporter NTT5 (Solute carrier family 6 member 16)
Locus_16763_Transcript_1/1_Conf_1.000	188	0							
Locus_16764_Transcript_1/1_Conf_1.000	226	4	2.92E-09	XP_001899164.1	67	65.0846	62	42	Leucine Rich Repeat family protein
Locus_16765_Transcript_1/1_Conf_1.000	311	0							
Locus_16766_Transcript_1/1_Conf_1.000	1066	20	1.13E-149	XP_002641970.1	87	533.872	354	309	Hypothetical protein CBG16677
Locus_16767_Transcript_1/1_Conf_1.000	465	20	2.62E-18	EFO24621.1	66	95.1301	101	67	DNA repair protein Rad4 containing protein
Locus_16768_Transcript_1/1_Conf_1.000	540	20	2.30E-27	XP_002633766.1	70	125.561	151	106	Hypothetical protein CBG03455
Locus_16769_Transcript_1/1_Conf_1.000	263	2	1.49E-05	EFO27866.1	52	52.7582	89	47	GTPase activating protein and VPS9 domains 1
Locus_1677_Transcript_1/1_Conf_1.000	935	0							
Locus_16770_Transcript_1/1_Conf_1.000	145	20	6.33E-20	XP_522295.2	100	100.523	48	48	PREDICTED: T-cell, immune regulator 1
Locus_16771_Transcript_1/1_Conf_1.000	2206	11	2.15E-06	EDV09471.1	33	59.3066	520	173	conserved hypothetical protein
Locus_16772_Transcript_1/1_Conf_1.000	165	0							
Locus_16773_Transcript_1/1_Conf_1.000	971	0							
Locus_16774_Transcript_1/1_Conf_1.000	463	0							

Locus_16775_Transcript_1/1_Conf_1.000	197	20	3.30E-29	CAG33263.1	100	131.339	65	65	PSMB10
Locus_16776_Transcript_1/1_Conf_1.000	400	0							
Locus_16777_Transcript_1/1_Conf_1.000	147	20	3.96E-14	NP_495614.3	87	81.2629	49	43	Na/H eXchanger family member (nhx-2)
Locus_16778_Transcript_1/1_Conf_1.000	286	0							
Locus_16779_Transcript_1/1_Conf_1.000	368	0							
Locus_1678_Transcript_1/1_Conf_1.000	372	20	8.73E-22	XP_001901465.1	65	106.686	123	80	steroid hormone receptor
Locus_16780_Transcript_1/1_Conf_1.000	160	0							
Locus_16781_Transcript_1/1_Conf_1.000	309	1	2.76E-04	XP_001648563.1	58	48.521	72	42	bone morphogenetic protein receptor type II, putative
Locus_16782_Transcript_1/1_Conf_1.000	353	2	1.34E-06	XP_001894613.1	53	56.225	95	51	hypothetical protein
Locus_16783_Transcript_1/1_Conf_1.000	456	0							
Locus_16784_Transcript_1/1_Conf_1.000	478	0							
Locus_16785_Transcript_1/1_Conf_1.000	232	0							
Locus_16786_Transcript_1/1_Conf_1.000	196	0							
Locus_16787_Transcript_1/1_Conf_1.000	339	0							

Locus_16788_Transcript_1/1_Conf_1.000	717	20	2.08E-19	NP_001024724.2	49	100.138	202	99	EGg Laying defective family member (egl-15)
Locus_16789_Transcript_1/1_Conf_1.000	407	0							
Locus_1679_Transcript_1/2_Conf_1.000	1523	0							
Locus_1679_Transcript_2/2_Conf_1.000	1286	0							
Locus_16790_Transcript_1/1_Conf_1.000	295	20	2.71E-15	CBA11612.1	53	85.1149	104	56	C. elegans protein F54F3.1b, partially confirmed by transcript evidence
Locus_16791_Transcript_1/1_Conf_1.000	305	2	9.16E-32	NP_499205.1	73	139.813	101	74	hypothetical protein K03H1.5

Locus_16792_Transcript_1/1_Conf_1.000	256	0							
Locus_16793_Transcript_1/1_Conf_1.000	156	20	1.40E-11	CBL43465.1	88	72.7886	51	45	C. elegans protein Y55D9A.1d, confirmed by transcript evidence
Locus_16794_Transcript_1/1_Conf_1.000	333	0							
Locus_16795_Transcript_1/1_Conf_1.000	228	11	1.11E-08	NP_001024812.1	76	63.1586	38	29	hypothetical protein M163.8
Locus_16796_Transcript_1/1_Conf_1.000	369	20	8.72E-38	NP_741200.1	78	159.844	123	97	DIsplaced Gonad family member (dig-1)
Locus_16797_Transcript_1/1_Conf_1.000	188	20	1.40E-27	XP_002945331.1	100	125.946	62	62	PREDICTED: heat shock cognate 71 kDa protein-like, partial
Locus_16798_Transcript_1/1_Conf_1.000	175	0							
Locus_16799_Transcript_1/1_Conf_1.000	311	20	4.36E-34	XP_001897050.1	80	147.517	103	83	Endonuclease III-like protein 1
Locus_168_Transcript_1/3_Conf_0.273	427	0							
Locus_168_Transcript_2/3_Conf_0.364	569	0							
Locus_168_Transcript_3/3_Conf_0.818	764	7	8.08E-12	XP_001895031.1	71	75.0998	57	41	hypothetical protein Bm1_17870
Locus_1680_Transcript_1/1_Conf_1.000	1281	20	5.50E-120	XP_002646302.1	68	435.647	416	284	Hypothetical protein CBG12009
Locus_16800_Transcript_1/1_Conf_1.000	283	0							
Locus_16801_Transcript_1/1_Conf_1.000	144	0							
Locus_16802_Transcript_1/1_Conf_1.000	420	20	3.21E-16	ADI61822.1	58	88.1965	92	54	endonuclease-reverse transcriptase
Locus_16803_Transcript_1/1_Conf_1.000	252	0							
Locus_16804_Transcript_1/1_Conf_1.000	267	20	2.96E-38	XP_002632657.1	90	161.384	86	78	C. briggsae CBR-TRA-3 protein
Locus_16805_Transcript_1/1_Conf_1.000	322	20	1.26E-12	EFO18611.1	71	76.2554	71	51	hypothetical protein LOAG_09883
Locus_16806_Transcript_1/1_Conf_1.000	156	0							
Locus_16807_Transcript_1/1_Conf_1.000	184	1	6.35E-04	XP_002636985.1	61	47.3654	52	32	Hypothetical protein CBG09473
Locus_16808_Transcript_1/1_Conf_1.000	555	5	2.69E-45	XP_002645672.1	71	185.267	184	132	Hypothetical protein CBG07319
Locus_16809_Transcript_1/1_Conf_1.000	310	0							
Locus_1681_Transcript_1/1_Conf_1.000	140	2	7.75E-07	XP_002630428.1	75	56.9954	41	31	Hypothetical protein CBG11154

Locus_16810_Transcript_1/1_Conf_1.000	301	2	9.58E-05	NP_498634.1	51	50.0618	97	50	hypothetical protein T20B12.3
Locus_16811_Transcript_1/1_Conf_1.000	129	0							
Locus_16812_Transcript_1/1_Conf_1.000	851	5	2.07E-17	XP_001893623.1	48	93.9745	283	137	hypothetical protein Bm1_10755
Locus_16813_Transcript_1/1_Conf_1.000	363	0							
Locus_16814_Transcript_1/1_Conf_1.000	655	19	1.01E-27	NP_495774.1	51	127.487	199	103	hypothetical protein F14E5.4
Locus_16815_Transcript_1/1_Conf_1.000	249	20	1.45E-29	AAV40104.1	89	132.494	82	73	immunoglobulin mu heavy chain
Locus_16816_Transcript_1/1_Conf_1.000	136	0							
Locus_16817_Transcript_1/1_Conf_1.000	166	0							
Locus_16818_Transcript_1/1_Conf_1.000	171	19	1.29E-09	NP_504227.3	82	66.2402	40	33	hypothetical protein Y47D7A.14
Locus_16819_Transcript_1/1_Conf_1.000	173	20	3.61E-20	NP_498777.2	92	101.293	57	53	hypothetical protein C14B9.8
Locus_1682_Transcript_1/1_Conf_1.000	1194	3	4.08E-05	XP_001953944.1	37	53.9138	312	118	GF18021
Locus_16820_Transcript_1/1_Conf_1.000	404	6	3.91E-06	XP_002639968.1	51	54.6842	106	55	Hypothetical protein CBG10792
Locus_16821_Transcript_1/1_Conf_1.000	235	0							
Locus_16822_Transcript_1/1_Conf_1.000	407	2	1.02E-06	NP_505659.1	59	56.6102	54	32	hypothetical protein K07C5.3
Locus_16823_Transcript_1/1_Conf_1.000	272	0							
Locus_16824_Transcript_1/1_Conf_1.000	591	4	4.14E-13	EFO18237.1	51	78.5666	198	101	hypothetical protein LOAG_10257
Locus_16825_Transcript_1/1_Conf_1.000	301	0							
Locus_16826_Transcript_1/1_Conf_1.000	188	20	2.40E-11	ZP_04173150.1	65	72.0182	60	39	LPXTG-motif cell wall anchor domain protein
Locus_16827_Transcript_1/1_Conf_1.000	310	0							
Locus_16828_Transcript_1/1_Conf_1.000	642	0							
Locus_16829_Transcript_1/1_Conf_1.000	501	3	2.24E-09	NP_490949.3	79	65.4698	54	43	ABC Transporter family member (abt-2)

Locus_1683_Transcript_1/1_Conf_1.000	642	20	5.27E-26	NP_499343.2	80	121.709	88	71	hypothetical protein Y39A1A.8
Locus_16830_Transcript_1/1_Conf_1.000	371	1	6.44E-49	AAG23172.1	100	196.823	103	103	AF269289_1unknown
Locus_16831_Transcript_1/1_Conf_1.000	381	20	1.11E-69	BAG58223.1	100	265.774	126	126	unnamed protein product
Locus_16832_Transcript_1/2_Conf_1.000	327	0							
Locus_16832_Transcript_2/2_Conf_1.000	281	0							
Locus_16833_Transcript_1/1_Conf_1.000	567	2	5.74E-06	EFO22036.1	45	54.6842	140	64	hypothetical protein LOAG_06451
Locus_16834_Transcript_1/1_Conf_1.000	154	0							
Locus_16835_Transcript_1/1_Conf_1.000	237	0							
Locus_16836_Transcript_1/1_Conf_1.000	272	0							
Locus_16837_Transcript_1/1_Conf_1.000	174	0							
Locus_16838_Transcript_1/1_Conf_1.000	318	20	1.22E-23	NP_001122601.1	79	112.849	92	73	Multiple PDZ domain protein family member (mpz-1)
Locus_16839_Transcript_1/1_Conf_1.000	165	20	6.00E-15	CBL43465.1	90	83.9593	54	49	C. elegans protein Y55D9A.1d, confirmed by transcript evidence
Locus_1684_Transcript_1/1_Conf_1.000	482	0							

Locus_16840_Transcript_1/1_Conf_1.000	270	5	1.09E-08	XP_002630534.1	62	63.1586	82	51	Hypothetical protein CBG12974
Locus_16841_Transcript_1/1_Conf_1.000	246	0							
Locus_16842_Transcript_1/1_Conf_1.000	242	0							
Locus_16843_Transcript_1/1_Conf_1.000	668	20	8.94E-80	NP_490949.3	84	300.442	216	182	ABC Transporter family member (abt-2)
Locus_16844_Transcript_1/2_Conf_1.000	791	20	2.44E-101	NP_491572.2	92	227.254	128	118	AdaPtin, Mu/medium chain (clathrin associated complex) family member (apm-1)
Locus_16844_Transcript_2/2_Conf_1.000	763	20	3.30E-106	NP_491572.2	92	388.652	227	210	AdaPtin, Mu/medium chain (clathrin associated complex) family member (apm-1)
Locus_16845_Transcript_1/1_Conf_1.000	128	0							
Locus_16846_Transcript_1/1_Conf_1.000	372	20	2.69E-47	NP_001122835.1	90	191.43	124	112	UNCoordinated family member (unc-22)
Locus_16847_Transcript_1/1_Conf_1.000	136	0							
Locus_16848_Transcript_1/1_Conf_1.000	281	0							
Locus_16849_Transcript_1/1_Conf_1.000	398	20	5.85E-26	NP_505052.2	69	120.553	114	79	hypothetical protein F26D11.1
Locus_1685_Transcript_1/1_Conf_1.000	239	0							
Locus_16850_Transcript_1/1_Conf_1.000	405	11	4.43E-18	NP_499495.1	66	94.3597	124	82	hypothetical protein Y66D12A.7
Locus_16851_Transcript_1/1_Conf_1.000	180	0							
Locus_16852_Transcript_1/1_Conf_1.000	228	2	1.03E-06	XP_002639895.1	74	56.6102	47	35	Hypothetical protein CBG08217

Locus_16853_Transcript_1/1_Conf_1.000	330	20	3.36E-42	NP_508504.2	87	174.481	113	99	Non-muscle MYosin family member (nmy-1)
Locus_16854_Transcript_1/1_Conf_1.000	668	20	1.78E-128	CAI40836.1	100	462.225	222	222	prosaposin
Locus_16855_Transcript_1/1_Conf_1.000	132	0							
Locus_16856_Transcript_1/1_Conf_1.000	311	0							
Locus_16857_Transcript_1/1_Conf_1.000	356	20	5.07E-22	NP_496542.1	64	107.457	117	76	hypothetical protein ZK930.1
Locus_16858_Transcript_1/1_Conf_1.000	176	0							
Locus_16859_Transcript_1/1_Conf_1.000	734	20	1.01E-32	NP_503501.1	85	144.436	99	85	DeHydrogenases, Short chain family member (dhs-13)
Locus_1686_Transcript_1/1_Conf_1.000	572	0							
Locus_16860_Transcript_1/1_Conf_1.000	267	20	2.14E-12	EFN74509.1	61	75.485	83	51	hypothetical protein EAG_13603

Locus_16861_Transcript_1/1_Conf_1.000	354	20	3.16E-40	NP_493945.1	83	167.933	116	97	hypothetical protein Y57G7A.10
Locus_16862_Transcript_1/1_Conf_1.000	145	0							
Locus_16863_Transcript_1/1_Conf_1.000	290	0							
Locus_16864_Transcript_1/1_Conf_1.000	233	0							
Locus_16865_Transcript_1/1_Conf_1.000	137	0							
Locus_16866_Transcript_1/1_Conf_1.000	677	4	1.15E-13	XP_001897722.1	50	80.8777	153	78	hypothetical protein Bm1_31385
Locus_16867_Transcript_1/1_Conf_1.000	143	1	7.98E-12	AAK21295.1	100	73.559	35	35	NM-4
Locus_16868_Transcript_1/1_Conf_1.000	392	0							
Locus_16869_Transcript_1/1_Conf_1.000	426	0							
Locus_1687_Transcript_1/1_Conf_1.000	173	0							
Locus_16870_Transcript_1/1_Conf_1.000	207	0							
Locus_16871_Transcript_1/1_Conf_1.000	828	20	4.30E-89	XP_002645934.1	76	332.028	277	212	Hypothetical protein CBG07699
Locus_16872_Transcript_1/1_Conf_1.000	425	20	8.91E-51	XP_002633498.1	89	202.986	126	113	Hypothetical protein CBG06270
Locus_16873_Transcript_1/1_Conf_1.000	244	0							
Locus_16874_Transcript_1/1_Conf_1.000	1032	9	9.19E-32	NP_001023892.1	50	142.124	258	130	HIF (hypoxia inducible factor) homolog family member (hif-1)
Locus_16875_Transcript_1/1_Conf_1.000	1322	20	1.40E-49	EFO24754.1	56	201.83	334	190	hypothetical protein LOAG_03725
Locus_16876_Transcript_1/2_Conf_1.000	406	20	3.86E-38	CBK19479.1	88	160.999	96	85	C. elegans protein W08D2.5b, confirmed by transcript evidence
Locus_16876_Transcript_2/2_Conf_1.000	360	20	3.83E-38	CBK19479.1	88	160.999	96	85	C. elegans protein W08D2.5b, confirmed by transcript evidence
Locus_16877_Transcript_1/1_Conf_1.000	201	0							
Locus_16878_Transcript_1/1_Conf_1.000	154	0							
Locus_16879_Transcript_1/1_Conf_1.000	332	20	7.52E-26	XP_002629741.1	78	120.168	71	56	Hypothetical protein CBG00975
Locus_1688_Transcript_1/2_Conf_1.000	690	0							
Locus_1688_Transcript_2/2_Conf_1.000	684	0							

Locus_16880_Transcript_1/3_Conf_0.600	412	3	2.50E-13	XP_002647980.1	75	78.5666	60	45	C. briggsae CBR-PUS-1 protein
Locus_16880_Transcript_2/3_Conf_0.400	433	3	2.50E-13	XP_002647980.1	75	78.5666	60	45	C. briggsae CBR-PUS-1 protein
Locus_16880_Transcript_3/3_Conf_0.600	503	3	2.55E-13	XP_002647980.1	75	78.5666	60	45	C. briggsae CBR-PUS-1 protein
Locus_16881_Transcript_1/1_Conf_1.000	285	20	8.49E-25	ACO14988.1	86	116.701	69	60	Transcription elongation factor B polypeptide 1
Locus_16882_Transcript_1/1_Conf_1.000	577	20	5.40E-47	NP_495087.1	70	191.045	171	121	hypothetical protein C17G10.2
Locus_16883_Transcript_1/1_Conf_1.000	220	6	4.84E-12	NP_492113.2	75	74.3294	54	41	CHitin Synthase family member (chs-1)
Locus_16884_Transcript_1/1_Conf_1.000	527	3	4.94E-08	XP_001900523.1	53	61.2326	104	56	RWD domain containing protein
Locus_16885_Transcript_1/1_Conf_1.000	498	20	1.04E-35	NP_501024.1	69	152.91	168	116	hypothetical protein C01B10.8
Locus_16886_Transcript_1/1_Conf_1.000	622	4	1.90E-14	XP_001893304.1	66	83.1889	99	66	hypothetical protein
Locus_16887_Transcript_1/1_Conf_1.000	417	3	2.56E-13	XP_002639547.1	57	78.5666	142	82	Hypothetical protein CBG04176
Locus_16888_Transcript_1/1_Conf_1.000	980	20	7.08E-39	XP_001900253.1	63	165.622	218	138	hypothetical protein Bm1_43955
Locus_16889_Transcript_1/1_Conf_1.000	233	0							
Locus_1689_Transcript_1/1_Conf_1.000	1518	20	0	XP_002642074.1	85	679.863	455	389	Hypothetical protein CBG18013
Locus_16890_Transcript_1/1_Conf_1.000	649	20	1.97E-44	XP_001891895.1	64	182.956	190	123	metallo-beta-lactamase superfamily protein
Locus_16891_Transcript_1/1_Conf_1.000	665	0							
Locus_16892_Transcript_1/1_Conf_1.000	159	0							
Locus_16893_Transcript_1/1_Conf_1.000	246	2	6.57E-06	NP_001076772.1	75	53.9138	45	34	GEX Interacting protein family member (gei-3)
Locus_16894_Transcript_1/1_Conf_1.000	178	0							

Locus_16895_Transcript_1/1_Conf_1.000	244	0								
Locus_16896_Transcript_1/1_Conf_1.000	1169	20	0	ACT34056.1		91	648.277	389	356	glutamate dehydrogenase
Locus_16897_Transcript_1/1_Conf_1.000	182	0								
Locus_16898_Transcript_1/1_Conf_1.000	300	20	4.27E-29	ACI49079.1		89	130.954	84	75	hypothetical protein Cbre_JD11.003
Locus_16899_Transcript_1/1_Conf_1.000	761	8	6.79E-11	NP_494977.1		66	72.0182	68	45	hypothetical protein C34F11.1
Locus_169_Transcript_1/2_Conf_1.000	749	20	1.78E-64	CAD20464.1		91	249.98	177	162	putative ES protein F7
Locus_169_Transcript_2/2_Conf_1.000	579	20	4.64E-46	CAD20464.1		92	187.963	139	128	putative ES protein F7

Locus_1690_Transcript_1/1_Conf_1.000	1454	20	0	XP_001895390.1	96	643.269	330	317	Serine/threonine protein phosphatase F56C9.1 in chromosomeIII, putative
Locus_16900_Transcript_1/1_Conf_1.000	267	2	1.25E-12	NP_001021809.1	63	76.2554	88	56	Branching AbnorMal family member (bam-2)
Locus_16901_Transcript_1/1_Conf_1.000	378	0							
Locus_16902_Transcript_1/1_Conf_1.000	980	20	5.89E-102	EFO18398.1	74	375.17	313	233	Prp18 domain-containing protein
Locus_16903_Transcript_1/1_Conf_1.000	515	20	6.62E-68	NP_001023148.1	84	259.996	173	146	ForKHead transcription factor family member (fkh-7)
Locus_16904_Transcript_1/1_Conf_1.000	474	0							
Locus_16905_Transcript_1/1_Conf_1.000	1429	20	1.74E-55		57	192.971	277	158	hypothetical protein F13H8.5 - Caenorhabditis elegans
Locus_16906_Transcript_1/1_Conf_1.000	140	0							
Locus_16907_Transcript_1/1_Conf_1.000	230	20	5.64E-29	XP_002637520.1	86	130.568	76	66	Hypothetical protein CBG19243
Locus_16908_Transcript_1/1_Conf_1.000	220	1	1.51E-05	XP_002639022.1	48	52.7582	74	36	Hypothetical protein CBG22271
Locus_16909_Transcript_1/1_Conf_1.000	171	0							
Locus_1691_Transcript_1/2_Conf_1.000	1782	20	0	NP_497043.2	73	662.144	596	436	Amino acid Transporter GlycoProtein subunit family member (atgp-2)
Locus_1691_Transcript_2/2_Conf_1.000	2014	20	0	NP_497043.2	72	739.184	661	482	Amino acid Transporter GlycoProtein subunit family member (atgp-2)

Locus_16910_Transcript_1/1_Conf_1.000	255	20	1.22E-23	XP_001901338.1	78	112.849	84	66	Bloom's syndrome protein homolog
Locus_16911_Transcript_1/1_Conf_1.000	130	20	5.41E-16	XP_002747286.1	100	87.4261	42	42	PREDICTED: endoplasmic reticulum-Golgi intermediate compartment protein 3 isoform 2
Locus_16912_Transcript_1/2_Conf_1.000	249	0							
Locus_16912_Transcript_2/2_Conf_1.000	249	0							
Locus_16913_Transcript_1/1_Conf_1.000	398	20	7.94E-07	NP_001021756.1	55	56.9954	79	44	UDP-GlucuronosylTransferase family member (ugt-31)
Locus_16914_Transcript_1/1_Conf_1.000	165	0							
Locus_16915_Transcript_1/1_Conf_1.000	479	0							
Locus_16916_Transcript_1/1_Conf_1.000	326	20	3.52E-23	XP_002630450.1	73	111.309	87	64	C. briggsae CBR-ASM-1 protein
Locus_16917_Transcript_1/1_Conf_1.000	222	4	2.47E-16	XP_002642663.1	76	88.5817	73	56	C. briggsae CBR-NCL-1 protein
Locus_16918_Transcript_1/1_Conf_1.000	502	0							
Locus_16919_Transcript_1/1_Conf_1.000	175	0							

Locus_1692_Transcript_1/1_Conf_1.000	975	20	5.35E-71	NP_001022317.1	72	272.322	329	238	abnormal cell MIGration family member (mig-5)
Locus_16920_Transcript_1/1_Conf_1.000	174	20	7.52E-10	XP_002640523.1	77	67.0106	45	35	Hypothetical protein CBG18685
Locus_16921_Transcript_1/1_Conf_1.000	143	20	1.11E-13	EAW56733.1	92	79.7221	40	37	similar to zinc finger protein 569, isoform CRA_a
Locus_16922_Transcript_1/1_Conf_1.000	133	0							
Locus_16923_Transcript_1/1_Conf_1.000	184	0							
Locus_16924_Transcript_1/1_Conf_1.000	426	0							
Locus_16925_Transcript_1/1_Conf_1.000	236	1	5.42E-24	XP_002343485.1	100	114.005	48	48	PREDICTED: hypothetical protein XP_002343485
Locus_16926_Transcript_1/1_Conf_1.000	296	0							
Locus_16927_Transcript_1/1_Conf_1.000	398	2	1.60E-15	NP_492266.2	56	85.8853	117	66	hypothetical protein C34B7.2
Locus_16928_Transcript_1/1_Conf_1.000	295	4	5.11E-14	XP_002637429.1	65	80.8777	95	62	Hypothetical protein CBG19140
Locus_16929_Transcript_1/1_Conf_1.000	405	2	7.84E-07	EFO23509.1	64	56.9954	71	46	STAT protein
Locus_1693_Transcript_1/1_Conf_1.000	2313	20	1.67E-41	XP_001657404.1	56	176.022	266	151	ubiquitin-conjugating enzyme E2-230k
Locus_16930_Transcript_1/1_Conf_1.000	1595	20	1.68E-39	XP_002647371.1	56	168.703	294	166	Hypothetical protein CBG06428
Locus_16931_Transcript_1/1_Conf_1.000	144	0							

Locus_16932_Transcript_1/1_Conf_1.000	435	20	3.33E-50	NP_507912.2	77	201.06	146	113	MoLTing defective family member (mlt-4)
Locus_16933_Transcript_1/1_Conf_1.000	287	3	1.40E-19	NP_491915.2	80	99.3673	78	63	hypothetical protein ZC581.9
Locus_16934_Transcript_1/1_Conf_1.000	265	0							
Locus_16935_Transcript_1/2_Conf_1.000	625	20	3.98E-36	NP_491579.1	62	155.221	205	128	hypothetical protein F55A12.1
Locus_16935_Transcript_2/2_Conf_1.000	625	20	3.98E-36	NP_491579.1	62	155.221	205	128	hypothetical protein F55A12.1
Locus_16936_Transcript_1/1_Conf_1.000	324	0							
Locus_16937_Transcript_1/1_Conf_1.000	419	20	1.94E-45	NP_495666.3	79	185.267	138	110	Temporarily Assigned Gene name family member (tag-341)
Locus_16938_Transcript_1/1_Conf_1.000	665	20	2.05E-52	NP_497324.3	68	209.534	209	143	hypothetical protein BE0003N10.1
Locus_16939_Transcript_1/1_Conf_1.000	268	0							
Locus_1694_Transcript_1/1_Conf_1.000	156	0							
Locus_16940_Transcript_1/1_Conf_1.000	468	20	9.24E-32	NP_491891.1	64	139.813	155	100	XPG (Xeroderma Pigmentosum group G) DNA repair gene homolog family member (xpg-1)
Locus_16941_Transcript_1/1_Conf_1.000	416	17	3.84E-06	XP_002629756.1	65	54.6842	55	36	Hypothetical protein CBG00991
Locus_16942_Transcript_1/1_Conf_1.000	426	20	2.42E-48	CAX65056.1	83	194.897	140	117	C. elegans protein F25C8.3d, partially confirmed by transcript evidence
Locus_16943_Transcript_1/1_Conf_1.000	164	0							
Locus_16944_Transcript_1/1_Conf_1.000	267	19	5.10E-06	CAR63735.1	66	54.299	36	24	hypothetical protein
Locus_16945_Transcript_1/1_Conf_1.000	951	0							
Locus_16946_Transcript_1/1_Conf_1.000	183	0							
Locus_16947_Transcript_1/1_Conf_1.000	338	20	1.89E-45	NP_501399.1	91	185.267	111	102	Vacuolar H ATPase family member (vha-5)
Locus_16948_Transcript_1/1_Conf_1.000	185	0							
Locus_16949_Transcript_1/1_Conf_1.000	239	0							
Locus_1695_Transcript_1/1_Conf_1.000	403	0							

Locus_16950_Transcript_1/1_Conf_1.000	536	20	1.51E-76	AAF66614.1	87	288.886	177	155	AF142441_1H+/oligopeptide symporter OPT-3
Locus_16951_Transcript_1/1_Conf_1.000	725	13	2.75E-43	NP_001040915.1	62	179.489	236	147	hypothetical protein C27D8.3
Locus_16952_Transcript_1/1_Conf_1.000	417	0							
Locus_16953_Transcript_1/1_Conf_1.000	157	0							
Locus_16954_Transcript_1/1_Conf_1.000	273	0							
Locus_16955_Transcript_1/1_Conf_1.000	228	0							
Locus_16956_Transcript_1/1_Conf_1.000	359	0							
Locus_16957_Transcript_1/1_Conf_1.000	230	20	4.80E-12	XP_002642125.1	68	74.3294	76	52	Hypothetical protein CBG18072
Locus_16958_Transcript_1/1_Conf_1.000	434	14	8.33E-09	NP_510664.1	78	63.5438	144	113	LEThal family member (let-2)
Locus_16959_Transcript_1/1_Conf_1.000	317	0							
Locus_1696_Transcript_1/1_Conf_1.000	661	20	3.44E-68	NP_509342.1	90	261.922	154	140	SEx Muscle abnormal family member (sem-5)
Locus_16960_Transcript_1/3_Conf_0.667	641	0							
Locus_16960_Transcript_2/3_Conf_0.667	681	0							
Locus_16960_Transcript_3/3_Conf_0.667	681	0							
Locus_16961_Transcript_1/1_Conf_1.000	353	0							
Locus_16962_Transcript_1/1_Conf_1.000	203	0							
Locus_16963_Transcript_1/1_Conf_1.000	135	0							
Locus_16964_Transcript_1/1_Conf_1.000	306	0							
Locus_16965_Transcript_1/1_Conf_1.000	128	20	2.21E-09	ABU48855.1	78	65.4698	42	33	heparan sulfate 3-O sulfotransferase isoform a
Locus_16966_Transcript_1/1_Conf_1.000	144	0							
Locus_16967_Transcript_1/1_Conf_1.000	169	0							
Locus_16968_Transcript_1/1_Conf_1.000	618	20	1.24E-13	AAG24090.4	46	80.4925	187	87	Hypothetical protein F31F4.11
Locus_16969_Transcript_1/1_Conf_1.000	627	0							
Locus_1697_Transcript_1/2_Conf_1.000	538	1	9.22E-05	XP_001899906.1	56	50.447	66	37	MOZ/SAS family protein

Locus_1697_Transcript_2/2_Conf_1.000	998	20	3.77E-19	XP_002639480.1	50	100.138	150	76	Hypothetical protein CBG04078
Locus_16970_Transcript_1/1_Conf_1.000	234	0							
Locus_16971_Transcript_1/1_Conf_1.000	271	20	4.25E-45	XP_002810085.1	100	184.111	89	89	PREDICTED: lamin-A/C-like
Locus_16972_Transcript_1/1_Conf_1.000	631	7	3.73E-05	EER44235.1	49	52.373	134	66	calmodulin-binding coil-coil protein
Locus_16973_Transcript_1/1_Conf_1.000	221	20	1.15E-29	CAZ39159.1	94	132.88	72	68	C. elegans protein C01C7.1b, partially confirmed by transcript evidence
Locus_16974_Transcript_1/1_Conf_1.000	638	3	1.63E-64	XP_002634053.1	77	249.595	212	165	Hypothetical protein CBG01593

Locus_16975_Transcript_1/1_Conf_1.000	755	20	3.70E-86	ADK47995.1	100	322.013	158	158	c-myc promoter-binding protein 1
Locus_16976_Transcript_1/1_Conf_1.000	156	0							
Locus_16977_Transcript_1/1_Conf_1.000	620	20	8.43E-71	XP_002632331.1	83	270.396	200	166	C. briggsae CBR-ROM-4 protein
Locus_16978_Transcript_1/1_Conf_1.000	165	0							
Locus_16979_Transcript_1/1_Conf_1.000	374	2	7.65E-18	NP_498388.1	66	93.5893	83	55	hypothetical protein C56G2.3
Locus_1698_Transcript_1/1_Conf_1.000	341	0							
Locus_16980_Transcript_1/1_Conf_1.000	733	20	1.27E-43	XP_002641461.1	77	180.644	157	121	C. briggsae CBR-WAH-1 protein
Locus_16981_Transcript_1/1_Conf_1.000	203	1	3.47E-11	AAC06295.1	84	60.8474	45	38	hypothetical protein jmo23
Locus_16982_Transcript_1/1_Conf_1.000	248	0							
Locus_16983_Transcript_1/1_Conf_1.000	253	0							
Locus_16984_Transcript_1/1_Conf_1.000	601	7	9.59E-29	ACY39994.1	58	130.568	202	118	C. elegans FLN-2 protein, isoform d
Locus_16985_Transcript_1/1_Conf_1.000	859	20	1.10E-90	NP_496170.1	89	337.421	191	170	LEThal family member (let-268)
Locus_16986_Transcript_1/1_Conf_1.000	696	20	5.15E-44	NP_001040927.1	65	181.8	217	143	hypothetical protein C47A4.2
Locus_16987_Transcript_1/1_Conf_1.000	180	0							
Locus_16988_Transcript_1/1_Conf_1.000	547	0							
Locus_16989_Transcript_1/1_Conf_1.000	373	20	7.32E-53	NP_501979.3	89	209.92	124	111	hypothetical protein R102.4

Locus_1699_Transcript_1/1_Conf_1.000	1480	20	0	XP_002636638.1	97	818.92	435	423	C. briggsae CBR-RPT-1 protein
Locus_16990_Transcript_1/1_Conf_1.000	460	0							
Locus_16991_Transcript_1/1_Conf_1.000	605	2	4.84E-20	NP_496323.1	51	101.679	158	82	SET (trithorax/polycomb) domain containing family member (set-14)
Locus_16992_Transcript_1/1_Conf_1.000	240	0							
Locus_16993_Transcript_1/1_Conf_1.000	447	20	7.09E-24	NP_001022170.1	72	113.62	95	69	UNCoordinated family member (unc-53)
Locus_16994_Transcript_1/1_Conf_1.000	164	6	6.67E-06	XP_002643836.1	67	53.9138	55	37	Hypothetical protein CBG02060
Locus_16995_Transcript_1/1_Conf_1.000	355	20	9.28E-08	XP_002158963.1	50	60.077	91	46	PREDICTED: similar to Rps2e protein

Locus_16996_Transcript_1/1_Conf_1.000	246	20	3.45E-39	AAP88768.1	100	164.466	78	78	cytochrome c oxidase subunit VIIb
Locus_16997_Transcript_1/1_Conf_1.000	279	0							
Locus_16998_Transcript_1/1_Conf_1.000	271	0							
Locus_16999_Transcript_1/1_Conf_1.000	296	0							
Locus_17_Transcript_17/30_Conf_1.000	270	20	3.60E-44	ACR36970.1	96	181.03	89	86	unknown
Locus_17_Transcript_18/30_Conf_1.000	263	1	9.35E-08	XP_002467304.1	77	60.077	44	34	hypothetical protein SORBIDRAFT_01g024221
Locus_17_Transcript_19/30_Conf_1.000	263	1	3.21E-08	XP_002467304.1	75	61.6178	48	36	hypothetical protein SORBIDRAFT_01g024221
Locus_17_Transcript_20/30_Conf_1.000	270	20	3.60E-44	ACR36970.1	96	181.03	89	86	unknown
Locus_17_Transcript_21/30_Conf_0.019	363	11	2.48E-29	BAB33421.1	92	131.724	68	63	putative senescence-associated protein
Locus_17_Transcript_22/30_Conf_0.287	1283	20	1.46E-80	BAB33421.1	71	304.679	260	185	putative senescence-associated protein
Locus_17_Transcript_23/30_Conf_0.065	426	13	1.61E-12	XP_002638702.1	63	60.8474	61	39	Hypothetical protein CBG11901
Locus_17_Transcript_24/30_Conf_0.315	1384	20	1.07E-63	XP_001028745.1	67	248.825	246	167	hypothetical protein TTHERM_02141640
Locus_17_Transcript_25/30_Conf_0.361	1485	20	4.31E-58	XP_001028745.1	67	230.335	224	152	hypothetical protein TTHERM_02141640
Locus_17_Transcript_26/30_Conf_0.361	1527	20	7.64E-58	XP_001028745.1	67	229.565	222	150	hypothetical protein TTHERM_02141640
Locus_17_Transcript_27/30_Conf_0.296	1059	20	2.65E-58	XP_001028745.1	67	230.335	224	152	hypothetical protein TTHERM_02141640
Locus_17_Transcript_28/30_Conf_0.056	300	1	1.54E-12	XP_002638702.1	63	60.8474	61	39	Hypothetical protein CBG11901
Locus_17_Transcript_29/30_Conf_0.343	1387	20	3.94E-58	XP_001028745.1	67	230.335	224	152	hypothetical protein TTHERM_02141640
Locus_17_Transcript_30/30_Conf_0.565	2123	20	6.76E-58	XP_001028745.1	67	230.335	224	152	hypothetical protein TTHERM_02141640
Locus_170_Transcript_1/1_Conf_1.000	530	9	1.03E-69	AAR25200.1	90	266.159	162	147	surface-associated antigen 1
Locus_1700_Transcript_1/3_Conf_0.600	1828	20	2.03E-124	NP_741191.1	78	451.055	346	270	hypothetical protein C56G2.1
Locus_1700_Transcript_2/3_Conf_0.600	2035	20	1.03E-132	NP_741190.1	70	478.789	430	305	hypothetical protein C56G2.1
Locus_1700_Transcript_3/3_Conf_0.600	1832	20	2.03E-124	NP_741191.1	78	451.055	346	270	hypothetical protein C56G2.1
Locus_17000_Transcript_1/1_Conf_1.000	404	20	2.13E-20	ACI48997.1	62	102.064	136	85	hypothetical protein Cbre_JD01.004
Locus_17001_Transcript_1/1_Conf_1.000	175	0							
Locus_17002_Transcript_1/1_Conf_1.000	589	20	2.08E-25	NP_499759.1	75	119.398	109	82	DNaJ domain (prokaryotic heat shock protein) family member (dnj-17)

Locus_17003_Transcript_1/1_Conf_1.000	681	20	3.67E-116	NP_492127.1	93	421.394	226	211	Low-density lipoprotein Receptor Related family member (lrp-1)
Locus_17004_Transcript_1/1_Conf_1.000	214	0							
Locus_17005_Transcript_1/1_Conf_1.000	622	20	1.15E-19	NP_001040945.1	54	100.523	200	108	human HnRNP A1 homolog family member (hrp-1)
Locus_17006_Transcript_1/1_Conf_1.000	208	0							
Locus_17007_Transcript_1/1_Conf_1.000	345	0							
Locus_17008_Transcript_1/1_Conf_1.000	241	0							
Locus_17009_Transcript_1/1_Conf_1.000	415	20	4.54E-07	XP_002189413.1	59	57.7658	62	37	PREDICTED: putative U5 snRNP-specific 40 kDa protein, partial
Locus_1701_Transcript_1/1_Conf_1.000	502	0							
Locus_17010_Transcript_1/1_Conf_1.000	674	0							
Locus_17011_Transcript_1/1_Conf_1.000	245	4	2.68E-07	NP_495342.2	61	58.5362	81	50	related to yeast Vacuolar Protein Sorting factor family member (vps-33.2)
Locus_17012_Transcript_1/2_Conf_1.000	396	0							
Locus_17012_Transcript_2/2_Conf_1.000	481	0							
Locus_17013_Transcript_1/2_Conf_1.000	733	20	3.06E-114	XP_862070.1	99	415.231	202	201	PREDICTED: similar to Tubulin alpha-6 chain (Alpha-tubulin 6) (Alpha-tubulin isotype M-alpha-6) isoform 6
Locus_17013_Transcript_2/2_Conf_1.000	835	20	3.92E-114	XP_862070.1	99	415.231	202	201	PREDICTED: similar to Tubulin alpha-6 chain (Alpha-tubulin 6) (Alpha-tubulin isotype M-alpha-6) isoform 6
Locus_17014_Transcript_1/1_Conf_1.000	316	0							

Locus_17015_Transcript_1/1_Conf_1.000	287	20	3.57E-23	EFO16535.1	76	111.309	94	72	hypothetical protein LOAG_11971
Locus_17016_Transcript_1/1_Conf_1.000	451	0							
Locus_17017_Transcript_1/1_Conf_1.000	415	0							
Locus_17018_Transcript_1/1_Conf_1.000	320	0							
Locus_17019_Transcript_1/1_Conf_1.000	276	0							
Locus_1702_Transcript_1/1_Conf_1.000	1029	0							
Locus_17020_Transcript_1/1_Conf_1.000	171	0							
Locus_17021_Transcript_1/1_Conf_1.000	239	2	2.79E-04	NP_492616.1	52	48.521	82	43	Nematode AStacin protease family member (nas-5)
Locus_17022_Transcript_1/1_Conf_1.000	279	20	9.05E-48	XP_002763564.1	100	192.971	92	92	PREDICTED: transmembrane emp24 domain-containing protein 9-like
Locus_17023_Transcript_1/1_Conf_1.000	470	20	1.03E-14	EFO28126.1	60	83.1889	135	82	hypothetical protein LOAG_00360
Locus_17024_Transcript_1/1_Conf_1.000	311	20	5.17E-19	NP_740774.1	81	97.4413	77	63	hypothetical protein Y48G1A.4
Locus_17025_Transcript_1/1_Conf_1.000	362	20	1.24E-20	ACI49149.1	63	102.834	121	77	hypothetical protein Cbre_JD20.004
Locus_17026_Transcript_1/1_Conf_1.000	213	0							
Locus_17027_Transcript_1/1_Conf_1.000	455	20	3.27E-21	XP_002199753.1	57	104.76	119	69	PREDICTED: similar to FLJ14007
Locus_17028_Transcript_1/1_Conf_1.000	177	11	7.73E-15	XP_001901295.1	80	83.5741	56	45	Nematode astacin protease protein 30
Locus_17029_Transcript_1/2_Conf_1.000	752	0							

Locus_17029_Transcript_2/2_Conf_1.000	752	0							
Locus_1703_Transcript_1/1_Conf_1.000	468	20	1.62E-60	XP_002645153.1	91	235.343	156	143	C. briggsae CBR-SFXN-2 protein
Locus_17030_Transcript_1/1_Conf_1.000	387	20	2.66E-23	NP_491806.2	78	111.694	89	70	LiPid Depleted family member (lpd-2)
Locus_17031_Transcript_1/1_Conf_1.000	146	1	8.31E-04	XP_001893741.1	63	46.9802	49	31	LIM domain containing protein
Locus_17032_Transcript_1/1_Conf_1.000	552	0							
Locus_17033_Transcript_1/1_Conf_1.000	148	20	6.33E-12	XP_002823973.1	100	73.9442	34	34	PREDICTED: ADP-ribosylation factor-like protein 6-interacting protein 4-like isoform 5
Locus_17034_Transcript_1/1_Conf_1.000	150	0							
Locus_17035_Transcript_1/1_Conf_1.000	584	20	1.53E-20	NP_491574.1	64	103.219	135	87	hypothetical protein F55A12.8
Locus_17036_Transcript_1/1_Conf_1.000	158	20	3.92E-22	BAF83756.1	100	107.842	52	52	unnamed protein product
Locus_17037_Transcript_1/1_Conf_1.000	158	0							
Locus_17038_Transcript_1/1_Conf_1.000	267	20	1.06E-11	XP_002641218.1	64	73.1738	77	50	Hypothetical protein CBG09082
Locus_17039_Transcript_1/1_Conf_1.000	330	20	2.66E-47	NP_001122450.1	90	191.43	110	100	hypothetical protein F10G8.8
Locus_1704_Transcript_1/1_Conf_1.000	555	2	3.53E-29	NP_001022723.2	59	131.724	156	93	TENeurin family member (ten-1)
Locus_17040_Transcript_1/1_Conf_1.000	406	20	4.26E-37	EFO28414.1	71	157.532	133	95	hypothetical protein LOAG_00060
Locus_17041_Transcript_1/1_Conf_1.000	256	3	1.11E-24	AAC39119.1	73	116.316	78	57	low-affinity peptide transporter
Locus_17042_Transcript_1/1_Conf_1.000	166	0							
Locus_17043_Transcript_1/1_Conf_1.000	443	0							

Locus_17044_Transcript_1/1_Conf_1.000	308	20	3.70E-41	XP_002630183.1	91	171.014	102	93	C. briggsae CBR-FLI-1 protein
Locus_17045_Transcript_1/2_Conf_1.000	594	0							
Locus_17045_Transcript_2/2_Conf_1.000	594	0							
Locus_17046_Transcript_1/1_Conf_1.000	486	20	1.13E-45	CAA30855.1	91	186.037	137	125	myosin heavy chain 2
Locus_17047_Transcript_1/1_Conf_1.000	235	0							
Locus_17048_Transcript_1/1_Conf_1.000	176	0							
Locus_17049_Transcript_1/2_Conf_1.000	464	2	3.69E-04	NP_495257.3	46	48.1358	111	52	Biotin Protein Ligase family member (bpl-1)
Locus_17049_Transcript_2/2_Conf_1.000	464	2	3.69E-04	NP_495257.3	46	48.1358	111	52	Biotin Protein Ligase family member (bpl-1)
Locus_1705_Transcript_1/1_Conf_1.000	496	0							
Locus_17050_Transcript_1/1_Conf_1.000	354	20	7.32E-21	XP_002634722.1	67	103.605	101	68	Hypothetical protein CBG24065
Locus_17051_Transcript_1/1_Conf_1.000	132	20	1.98E-18	NP_001087890.2	100	95.5153	43	43	LIM domain only 4, gene 1
Locus_17052_Transcript_1/1_Conf_1.000	401	20	9.21E-56	XP_002645894.1	90	219.55	133	121	Hypothetical protein CBG07647
Locus_17053_Transcript_1/1_Conf_1.000	351	20	4.93E-17	NP_496909.1	67	90.8929	101	68	ING (mammalian INhibitor of Growth) homolog family member (ing-3)
Locus_17054_Transcript_1/1_Conf_1.000	1012	20	6.94E-77	XP_002637110.1	76	291.967	257	197	Hypothetical protein CBG09610
Locus_17055_Transcript_1/1_Conf_1.000	175	0							
Locus_17056_Transcript_1/1_Conf_1.000	224	0							
Locus_17057_Transcript_1/1_Conf_1.000	404	0							
Locus_17058_Transcript_1/1_Conf_1.000	502	20	4.51E-10	XP_975003.1	49	67.781	163	80	PREDICTED: similar to CG31751 CG31751-PA
Locus_17059_Transcript_1/1_Conf_1.000	233	0							

Locus_1706_Transcript_1/2_Conf_1.000	1467	20	1.87E-122	XP_002633783.1	72	444.121	425	309	Hypothetical protein CBG03474
Locus_1706_Transcript_2/2_Conf_1.000	1453	20	2.96E-115	XP_002633783.1	69	330.102	347	242	Hypothetical protein CBG03474
Locus_17060_Transcript_1/1_Conf_1.000	430	3	1.93E-05	XP_002644943.1	44	52.373	142	63	Hypothetical protein CBG10898
Locus_17061_Transcript_1/1_Conf_1.000	849	4	3.20E-10	NP_493646.1	56	70.0922	144	82	hypothetical protein F23F1.9
Locus_17062_Transcript_1/1_Conf_1.000	243	20	1.01E-22	NP_501127.2	96	109.768	57	55	RNA Polymerase, Class III (C) family member (rpc-1)
Locus_17063_Transcript_1/1_Conf_1.000	524	13	3.52E-67	XP_002640548.1	93	257.684	174	163	Hypothetical protein CBG15812
Locus_17064_Transcript_1/1_Conf_1.000	230	20	6.05E-15	XP_002647188.1	79	83.9593	59	47	Hypothetical protein CBG22355
Locus_17065_Transcript_1/1_Conf_1.000	665	4	5.10E-19	NP_001040707.1	60	98.5969	211	128	CDT (S. pombe CDC10 Dependent Transcript) homolog family member (cdt-1)
Locus_17066_Transcript_1/1_Conf_1.000	367	0							
Locus_17067_Transcript_1/1_Conf_1.000	432	0							
Locus_17068_Transcript_1/1_Conf_1.000	183	20	6.34E-12	XP_002634144.1	76	73.9442	60	46	Hypothetical protein CBG01705
Locus_17069_Transcript_1/1_Conf_1.000	193	0							

Locus_1707_Transcript_1/1_Conf_1.000	415	20	3.44E-39	NP_499099.1	74	164.466	136	101	hypothetical protein ZK1098.7
Locus_17070_Transcript_1/1_Conf_1.000	149	0							
Locus_17071_Transcript_1/1_Conf_1.000	339	2	1.61E-04	EFO20756.1	49	49.2914	104	51	nucleolar RNA-associated protein alpha
Locus_17072_Transcript_1/1_Conf_1.000	179	20	2.11E-12	XP_002637265.1	76	75.485	59	45	C. briggsae CBR-CPT-6 protein
Locus_17073_Transcript_1/1_Conf_1.000	255	0							
Locus_17074_Transcript_1/1_Conf_1.000	252	4	6.33E-12	NP_509145.2	68	73.9442	76	52	AuTophaGy (yeast Atg homolog) family member (atg-2)
Locus_17075_Transcript_1/1_Conf_1.000	370	0							
Locus_17076_Transcript_1/1_Conf_1.000	302	20	6.83E-19	XP_002640837.1	78	97.0561	64	50	Hypothetical protein CBG15725
Locus_17077_Transcript_1/1_Conf_1.000	268	20	8.06E-36	XP_001891652.1	97	153.295	79	77	myosin heavy chain, nonmuscle type 1
Locus_17078_Transcript_1/1_Conf_1.000	321	0							
Locus_17079_Transcript_1/1_Conf_1.000	157	4	1.49E-13	EFO21662.1	82	79.337	51	42	hypothetical protein LOAG_06825
Locus_1708_Transcript_1/1_Conf_1.000	460	0							
Locus_17080_Transcript_1/1_Conf_1.000	306	20	2.48E-37	NP_497182.2	88	158.303	101	89	hypothetical protein Y50D7A.2
Locus_17081_Transcript_1/1_Conf_1.000	188	0							
Locus_17082_Transcript_1/1_Conf_1.000	317	4	1.11E-24	XP_002644860.1	71	116.316	113	81	Hypothetical protein CBG05033
Locus_17083_Transcript_1/1_Conf_1.000	168	0							
Locus_17084_Transcript_1/1_Conf_1.000	736	20	3.75E-27	EFO22480.1	54	125.946	235	127	BSD domain-containing protein
Locus_17085_Transcript_1/1_Conf_1.000	256	0							
Locus_17086_Transcript_1/1_Conf_1.000	147	0							
Locus_17087_Transcript_1/1_Conf_1.000	149	0							
Locus_17088_Transcript_1/1_Conf_1.000	294	0							
Locus_17089_Transcript_1/1_Conf_1.000	286	0							
Locus_1709_Transcript_1/1_Conf_1.000	824	0							
Locus_17090_Transcript_1/1_Conf_1.000	485	0							
Locus_17091_Transcript_1/1_Conf_1.000	207	0							
Locus_17092_Transcript_1/1_Conf_1.000	214	0							
Locus_17093_Transcript_1/1_Conf_1.000	244	8	8.85E-27	XP_002636220.1	79	123.25	73	58	Hypothetical protein CBG12141
Locus_17094_Transcript_1/1_Conf_1.000	243	0							
Locus_17095_Transcript_1/1_Conf_1.000	195	0							
Locus_17096_Transcript_1/1_Conf_1.000	327	0							
Locus_17097_Transcript_1/1_Conf_1.000	155	0							

Locus_17098_Transcript_1/4_Conf_0.333	587	20	2.99E-64	XP_001892307.1	77	248.44	191	148	ATP-dependent DNA helicase, RecQ family protein
Locus_17098_Transcript_2/4_Conf_0.444	1113	20	7.48E-99	XP_002642560.1	72	365.155	315	227	C. briggsae CBR-RCQ-5 protein
Locus_17098_Transcript_3/4_Conf_0.444	1113	20	7.48E-99	XP_002642560.1	72	365.155	315	227	C. briggsae CBR-RCQ-5 protein
Locus_17098_Transcript_4/4_Conf_0.333	587	20	2.99E-64	XP_001892307.1	77	248.44	191	148	ATP-dependent DNA helicase, RecQ family protein
Locus_17099_Transcript_1/1_Conf_1.000	941	20	6.97E-113	XP_002641585.1	81	411.379	302	245	Hypothetical protein CBG09887
Locus_171_Transcript_1/1_Conf_1.000	677	20	3.67E-36	XP_001896629.1	57	155.606	229	131	U-box domain containing protein
Locus_1710_Transcript_1/1_Conf_1.000	271	20	8.37E-09	XP_001899631.1	57	63.5438	90	52	WD-repeat protein 26
Locus_17100_Transcript_1/1_Conf_1.000	157	0							
Locus_17101_Transcript_1/1_Conf_1.000	515	20	2.54E-35	NP_001021671.2	68	151.754	168	115	hypothetical protein W09G3.7
Locus_17102_Transcript_1/1_Conf_1.000	517	20	1.39E-12	XP_002049622.1	47	76.2554	166	79	GJ21697
Locus_17103_Transcript_1/1_Conf_1.000	280	0							
Locus_17104_Transcript_1/1_Conf_1.000	777	20	3.48E-66	CBL87054.2	69	255.758	262	181	C. elegans protein F54E4.1, partially confirmed by transcript evidence
Locus_17105_Transcript_1/1_Conf_1.000	232	0							

Locus_17106_Transcript_1/1_Conf_1.000	714	20	1.83E-76	XP_001893036.1	83	289.656	210	176	SMC family, C-terminal domain containing protein
Locus_17107_Transcript_1/1_Conf_1.000	287	20	1.66E-20	ADI61822.1	67	102.449	90	61	endonuclease-reverse transcriptase
Locus_17108_Transcript_1/1_Conf_1.000	280	4	1.84E-08	XP_001895740.1	68	62.3882	73	50	hypothetical protein Bm1_21430
Locus_17109_Transcript_1/1_Conf_1.000	465	20	2.62E-26	XP_001149667.1	72	121.709	115	83	PREDICTED: transcription factor AP-2 beta (activating enhancer binding protein 2 beta) isoform 1
Locus_1711_Transcript_1/1_Conf_1.000	878	20	5.15E-144	EFO23330.1	94	514.612	287	270	GTP-binding regulatory protein alpha chain
Locus_17110_Transcript_1/1_Conf_1.000	536	1	5.86E-04	NP_001022760.1	62	47.7506	54	34	hypothetical protein T16G12.9
Locus_17111_Transcript_1/1_Conf_1.000	680	20	3.02E-62	XP_002630829.1	76	242.276	227	174	C. briggsae CBR-VPS-35 protein
Locus_17112_Transcript_1/2_Conf_1.000	347	0							
Locus_17112_Transcript_2/2_Conf_1.000	345	0							
Locus_17113_Transcript_1/1_Conf_1.000	157	20	2.09E-07	XP_002157644.1	78	58.9214	51	40	PREDICTED: similar to predicted protein, partial
Locus_17114_Transcript_1/1_Conf_1.000	239	3	1.17E-10	NP_491138.2	63	69.707	79	50	SULfate Permease family member (sulp-6)
Locus_17115_Transcript_1/1_Conf_1.000	1047	20	9.30E-40	NP_001022032.1	54	168.703	333	181	TRRAP-like (transcription/transformation domain-associated protein) family member (trr-1)
Locus_17116_Transcript_1/1_Conf_1.000	143	3	1.61E-04	XP_002631235.1	66	49.2914	54	36	C. briggsae CBR-PTB-1 protein
Locus_17117_Transcript_1/1_Conf_1.000	157	0							

Locus_17118_Transcript_1/1_Conf_1.000	206	20	7.78E-31	XP_002762172.1	100	136.732	68	68	PREDICTED: 26S protease regulatory subunit 6B
Locus_17119_Transcript_1/1_Conf_1.000	1297	13	1.05E-25	XP_001895099.1	47	122.479	350	165	hypothetical protein Bm1_18210
Locus_1712_Transcript_1/1_Conf_1.000	1375	20	1.69E-61	EFO21998.1	50	241.506	385	194	RWD domain-containing protein
Locus_17120_Transcript_1/1_Conf_1.000	350	9	9.26E-40	XP_002635876.1	80	166.392	116	93	C. briggsae CBR-PTR-16 protein
Locus_17121_Transcript_1/1_Conf_1.000	279	4	1.90E-29	XP_002642450.1	79	132.109	92	73	Hypothetical protein CBG06858
Locus_17122_Transcript_1/1_Conf_1.000	391	20	5.92E-15	ADI61811.1	58	83.9593	111	65	endonuclease-reverse transcriptase
Locus_17123_Transcript_1/1_Conf_1.000	577	20	1.06E-18	NP_495324.2	80	97.0561	63	51	human WRN (Werner's syndrome) related family member (wrn-1)
Locus_17124_Transcript_1/1_Conf_1.000	530	20	4.20E-63	NP_496444.1	78	244.202	175	138	Alanyl tRNA Synthetase family member (ars-1)
Locus_17125_Transcript_1/1_Conf_1.000	223	0							
Locus_17126_Transcript_1/1_Conf_1.000	961	0							
Locus_17127_Transcript_1/1_Conf_1.000	461	0							
Locus_17128_Transcript_1/1_Conf_1.000	476	0							
Locus_17129_Transcript_1/1_Conf_1.000	360	0							

Locus_1713_Transcript_1/1_Conf_1.000	2758	20	0	XP_002646632.1	84	1382.47	926	783	C. briggsae CBR-UNC-52 protein
Locus_17130_Transcript_1/1_Conf_1.000	200	20	2.89E-17	XP_002636925.1	83	91.6633	68	57	C. briggsae CBR-RHR-1 protein
Locus_17131_Transcript_1/1_Conf_1.000	198	0							
Locus_17132_Transcript_1/1_Conf_1.000	503	4	3.44E-18	XP_002630955.1	59	94.7449	166	98	C. briggsae CBR-WRN-1 protein
Locus_17133_Transcript_1/3_Conf_0.333	483	2	4.66E-07	AAO63576.1	40	57.7658	154	62	secreted protein 4 precursor
Locus_17133_Transcript_2/3_Conf_0.667	687	4	1.29E-07	ABB53347.1	41	60.8474	214	89	secreted protein 5 precursor
Locus_17133_Transcript_3/3_Conf_0.500	175	0							
Locus_17134_Transcript_1/1_Conf_1.000	162	0							
Locus_17135_Transcript_1/1_Conf_1.000	196	5	3.54E-15	XP_002638527.1	76	84.7297	65	50	C. briggsae CBR-UNC-80 protein
Locus_17136_Transcript_1/1_Conf_1.000	255	2	1.04E-06	XP_002643159.1	63	56.6102	65	41	C. briggsae CBR-VPS-33.1 protein
Locus_17137_Transcript_1/2_Conf_1.000	260	8	2.90E-25	EFO25373.1	76	118.242	89	68	laterally symmetric protein 2
Locus_17137_Transcript_2/2_Conf_1.000	270	8	3.06E-27	EFO25373.1	77	124.79	92	71	laterally symmetric protein 2
Locus_17138_Transcript_1/1_Conf_1.000	382	8	3.87E-22	EFO20275.1	64	107.842	126	81	hypothetical protein LOAG_08213

Locus_17139_Transcript_1/1_Conf_1.000	1633	20	1.05E-60	XP_001893645.1	67	239.195	238	161	MGC79624 protein
Locus_1714_Transcript_1/1_Conf_1.000	1104	20	1.32E-63	NP_496151.1	74	248.054	213	158	hypothetical protein R53.2
Locus_17140_Transcript_1/1_Conf_1.000	640	0							
Locus_17141_Transcript_1/1_Conf_1.000	278	0							
Locus_17142_Transcript_1/1_Conf_1.000	400	20	1.34E-22	XP_002641332.1	60	109.383	138	84	Hypothetical protein CBG13180
Locus_17143_Transcript_1/1_Conf_1.000	821								
Locus_17144_Transcript_1/1_Conf_1.000	297	2	8.40E-09	XP_002636395.1	53	63.5438	97	52	Hypothetical protein CBG08700
Locus_17145_Transcript_1/1_Conf_1.000	413	20	1.57E-07	EFN69864.1	56	59.3066	89	50	Serine/threonine-protein kinase grp
Locus_17146_Transcript_1/1_Conf_1.000	402	1	2.80E-04	NP_508445.1	76	48.521	34	26	hypothetical protein T07D1.3
Locus_17147_Transcript_1/1_Conf_1.000	162	0							
Locus_17148_Transcript_1/1_Conf_1.000	143	0							
Locus_17149_Transcript_1/1_Conf_1.000	219	4	4.10E-11	NP_495673.2	94	71.2478	36	34	hypothetical protein DH11.4

Locus_1715_Transcript_1/1_Conf_1.000	936	20	2.38E-113	NP_505736.2	77	412.92	311	242	yeast MRE recombination/repair homolog family member (mre-11)
Locus_17150_Transcript_1/1_Conf_1.000	379	0							
Locus_17151_Transcript_1/1_Conf_1.000	390	3	1.18E-39	NP_001021158.1	86	166.007	104	90	UDP-GlucuronosylTransferase family member (ugt-60)
Locus_17152_Transcript_1/1_Conf_1.000	188	0							
Locus_17153_Transcript_1/1_Conf_1.000	249	20	1.19E-15	NP_495614.3	84	86.2705	58	49	Na/H eXchanger family member (nhx-2)
Locus_17154_Transcript_1/1_Conf_1.000	822	20	2.12E-64	EFO21353.1	70	249.98	269	190	oxidoreductase
Locus_17155_Transcript_1/1_Conf_1.000	250	0							
Locus_17156_Transcript_1/1_Conf_1.000	406	20	1.28E-33	NP_503029.2	80	145.976	117	94	hypothetical protein Y116A8C.27
Locus_17157_Transcript_1/1_Conf_1.000	133	0							

Locus_17158_Transcript_1/1_Conf_1.000	331	20	9.83E-26	XP_002634557.1	87	119.783	95	83	C. briggsae CBR-TAX-6 protein
Locus_17159_Transcript_1/1_Conf_1.000	260	0							
Locus_1716_Transcript_1/1_Conf_1.000	931	20	2.18E-42	XP_001897236.1	62	177.178	200	124	Zinc finger, C2H2 type family protein
Locus_17160_Transcript_1/1_Conf_1.000	351	2	2.43E-32	NP_506678.2	74	141.739	116	86	hypothetical protein W09D12.1
Locus_17161_Transcript_1/1_Conf_1.000	276	2	2.26E-06	XP_002639005.1	49	55.4546	91	45	Hypothetical protein CBG22251
Locus_17162_Transcript_1/1_Conf_1.000	349	0							
Locus_17163_Transcript_1/1_Conf_1.000	126	0							
Locus_17164_Transcript_1/2_Conf_1.000	596	20	2.79E-41	NP_499333.1	63	172.17	198	126	hypothetical protein Y45F3A.9
Locus_17164_Transcript_2/2_Conf_1.000	406	20	1.52E-26	NP_499333.1	65	122.479	135	89	hypothetical protein Y45F3A.9

Locus_17165_Transcript_1/1_Conf_1.000	211	20	1.15E-34	XP_002928912.1	100	149.443	70	70	PREDICTED: tubulin beta chain-like
Locus_17166_Transcript_1/1_Conf_1.000	158	0							
Locus_17167_Transcript_1/1_Conf_1.000	381	0							
Locus_17168_Transcript_1/1_Conf_1.000	272	4	4.59E-07	XP_001894916.1	55	57.7658	70	39	Zinc finger, C2H2 type family protein
Locus_17169_Transcript_1/1_Conf_1.000	148	0							
Locus_1717_Transcript_1/1_Conf_1.000	545	20	8.81E-67	NP_496402.1	82	256.529	175	144	hypothetical protein T06D8.5
Locus_17170_Transcript_1/1_Conf_1.000	128	20	1.43E-16	NP_001024858.2	95	89.3521	42	40	Sensory AXon guidance family member (sax-1)
Locus_17171_Transcript_1/2_Conf_1.000	313	20	4.66E-31	NP_500367.1	76	137.502	104	80	hypothetical protein M57.2

Locus_17171_Transcript_2/2_Conf_1.000	329	20	1.86E-32	NP_500367.1	76	142.124	110	84	hypothetical protein M57.2
Locus_17172_Transcript_1/1_Conf_1.000	448	20	9.83E-50	NP_499387.1	74	199.519	149	111	hypothetical protein R17.3
Locus_17173_Transcript_1/1_Conf_1.000	216	20	1.71E-22	NP_498418.2	88	108.997	69	61	hypothetical protein T26A5.5
Locus_17174_Transcript_1/1_Conf_1.000	525	20	4.04E-10	NP_001022699.1	52	68.1662	186	98	Ring Finger Protein, UBC associated family member (rfp-1)
Locus_17175_Transcript_1/1_Conf_1.000	204	0							
Locus_17176_Transcript_1/1_Conf_1.000	522	20	4.22E-12	XP_001273939.1	48	74.7146	166	81	sulfur metabolism regulator SkpA, putative
Locus_17177_Transcript_1/1_Conf_1.000	460	20	3.34E-26	XP_002632532.1	88	121.324	104	92	C. briggsae CBR-DPY-4 protein
Locus_17178_Transcript_1/1_Conf_1.000	516	20	1.16E-67	NP_498121.1	82	259.225	168	138	yeast HAP (HydroxylAminoPurine sensitivity) related family member (hap-1)
Locus_17179_Transcript_1/1_Conf_1.000	553	0							
Locus_1718_Transcript_1/2_Conf_1.000	867	20	5.97E-68	XP_001898186.1	75	261.922	188	142	AMME syndrome candidate gene 1 protein homolog
Locus_1718_Transcript_2/2_Conf_1.000	312	0							
Locus_17180_Transcript_1/1_Conf_1.000	541	0							
Locus_17181_Transcript_1/1_Conf_1.000	206	1	4.75E-04	XP_002631426.1	63	47.7506	49	31	Hypothetical protein CBG03282

Locus_17182_Transcript_1/1_Conf_1.000	168	20	2.13E-12	NP_001021239.1	74	75.485	54	40	Endo-b-N-acetylGlucosaminidase family member (eng-1)
Locus_17183_Transcript_1/1_Conf_1.000	360	0							
Locus_17184_Transcript_1/1_Conf_1.000	999	20	4.77E-30	XP_002636702.1	52	136.346	333	175	C. briggsae CBR-RAD-50 protein
Locus_17185_Transcript_1/1_Conf_1.000	129	0							
Locus_17186_Transcript_1/1_Conf_1.000	197	0							
Locus_17187_Transcript_1/1_Conf_1.000	405	0							
Locus_17188_Transcript_1/1_Conf_1.000	368	20	6.04E-52	XP_860709.1	93	206.838	118	110	PREDICTED: hypothetical protein XP_855616 isoform 2
Locus_17189_Transcript_1/1_Conf_1.000	430	20	2.27E-22	XP_002635357.1	72	108.612	92	67	C. briggsae CBR-CLN-3.3 protein
Locus_1719_Transcript_1/1_Conf_1.000	722	20	5.92E-14	EFO20048.1	51	82.0333	201	103	hypothetical protein LOAG_08441
Locus_17190_Transcript_1/1_Conf_1.000	135	0							
Locus_17191_Transcript_1/1_Conf_1.000	212	1	1.67E-09	EDL85946.1	71	65.855	53	38	rCG37353, isoform CRA_a
Locus_17192_Transcript_1/1_Conf_1.000	250	0							
Locus_17193_Transcript_1/1_Conf_1.000	309	0							
Locus_17194_Transcript_1/1_Conf_1.000	146	0							
Locus_17195_Transcript_1/1_Conf_1.000	659	20	1.32E-51	NP_498494.2	65	206.838	221	145	Central Region Assembly in meiosis abnormal family member (cra-1)
Locus_17196_Transcript_1/1_Conf_1.000	353	0							

Locus_17197_Transcript_1/1_Conf_1.000	510	20	1.27E-47	NP_505616.2	85	192.586	132	113	CULlin family member (cul-5)
Locus_17198_Transcript_1/1_Conf_1.000	419	0							
Locus_17199_Transcript_1/1_Conf_1.000	647	0							
Locus_172_Transcript_1/1_Conf_1.000	1053	5	5.84E-66	NP_497742.2	56	255.758	316	177	hypothetical protein C46F11.5
Locus_1720_Transcript_1/1_Conf_1.000	1258	20	5.42E-72	NP_496786.2	61	276.174	351	217	hypothetical protein F29C12.3
Locus_17200_Transcript_1/1_Conf_1.000	146	0							
Locus_17201_Transcript_1/1_Conf_1.000	351	0							
Locus_17202_Transcript_1/1_Conf_1.000	158	1	4.81E-04	NP_505683.1	70	47.7506	41	29	Poly-A Polymerase family member (pap-1)
Locus_17203_Transcript_1/1_Conf_1.000	794	20	4.67E-70	XP_002629667.1	73	163.31	140	103	C. briggsae CBR-TAG-165 protein
Locus_17204_Transcript_1/1_Conf_1.000	640	20	3.59E-43	AAO39166.1	92	178.718	98	91	nuclear receptor NHR-1
Locus_17205_Transcript_1/1_Conf_1.000	155	20	2.82E-12	XP_001895196.1	95	75.0998	47	45	Nematode cuticle collagen N-terminal domain containing protein

Locus_17206_Transcript_1/1_Conf_1.000	590	20	4.02E-61	BAG65301.1	100	238.039	106	106	unnamed protein product
Locus_17207_Transcript_1/1_Conf_1.000	232	0							
Locus_17208_Transcript_1/1_Conf_1.000	258	0							
Locus_17209_Transcript_1/1_Conf_1.000	415	2	5.55E-05	XP_002634505.1	62	50.8322	72	45	Hypothetical protein CBG08295
Locus_1721_Transcript_1/1_Conf_1.000	819	20	1.12E-41	AAK31453.4	64	174.481	209	135	Hypothetical protein C25H3.8
Locus_17210_Transcript_1/1_Conf_1.000	235	0							
Locus_17211_Transcript_1/1_Conf_1.000	354	20	6.19E-20	AAN34967.1	69	100.523	98	68	thioredoxin 2
Locus_17212_Transcript_1/1_Conf_1.000	275	0							
Locus_17213_Transcript_1/2_Conf_1.000	1049	2	2.56E-05	XP_843163.1	36	54.299	302	109	proteophosphoglycan 5
Locus_17213_Transcript_2/2_Conf_1.000	1049	2	2.56E-05	XP_843163.1	36	54.299	302	109	proteophosphoglycan 5
Locus_17214_Transcript_1/1_Conf_1.000	200	2	1.26E-04	NP_492157.2	56	49.6766	53	30	hypothetical protein D2005.6
Locus_17215_Transcript_1/1_Conf_1.000	559	4	2.52E-27	XP_002640034.1	61	125.561	180	111	C. briggsae CBR-EDC-3 protein
Locus_17216_Transcript_1/1_Conf_1.000	567	12	1.03E-71	NP_496205.2	83	273.092	188	157	PhosphoLipase C family member (plc-3)
Locus_17217_Transcript_1/1_Conf_1.000	249	20	1.00E-30	NP_508993.2	91	136.346	82	75	fatty Acid CoA Synthetase family member (acs-17)

Locus_17218_Transcript_1/1_Conf_1.000	187	4	1.61E-15	XP_002629798.1	83	85.8853	62	52	Hypothetical protein CBG01041
Locus_17219_Transcript_1/1_Conf_1.000	193	0							
Locus_1722_Transcript_1/2_Conf_1.000	1358	20	1.03E-79	EFO27010.1	79	301.982	215	170	uracil-DNA glycosylase
Locus_1722_Transcript_2/2_Conf_1.000	1148	20	8.07E-80	EFO27010.1	79	301.982	215	170	uracil-DNA glycosylase
Locus_17220_Transcript_1/1_Conf_1.000	134	0							
Locus_17221_Transcript_1/1_Conf_1.000	505	20	2.98E-25	EFO28229.1	83	118.242	72	60	hypothetical protein LOAG_00257
Locus_17222_Transcript_1/1_Conf_1.000	339	0							
Locus_17223_Transcript_1/1_Conf_1.000	154	6	3.81E-09	NP_509110.1	94	64.6994	36	34	TransThyretin-Related family domain family member (ttr-6)
Locus_17224_Transcript_1/1_Conf_1.000	172	0							
Locus_17225_Transcript_1/1_Conf_1.000	313	20	4.36E-29	XP_002640716.1	75	130.954	104	78	Hypothetical protein CBG19783
Locus_17226_Transcript_1/1_Conf_1.000	460	20	2.29E-59	NP_001022488.1	85	231.491	127	109	UNCoordinated family member (unc-52)
Locus_17227_Transcript_1/1_Conf_1.000	172	0							
Locus_17228_Transcript_1/1_Conf_1.000	188	0							
Locus_17229_Transcript_1/1_Conf_1.000	303	20	1.20E-23	XP_002636715.1	76	112.849	97	74	Hypothetical protein CBG23434
Locus_1723_Transcript_1/1_Conf_1.000	1662	20	2.87E-122	NP_500364.2	72	443.736	424	307	Tumor Susceptibility Gene homolog family member (tsg-101)
Locus_17230_Transcript_1/1_Conf_1.000	299	20	4.90E-25	NP_496829.1	73	117.472	94	69	hypothetical protein Y48E1C.2

Locus_17231_Transcript_1/1_Conf_1.000	163	20	1.02E-22	XP_002925888.1	100	109.768	54	54	PREDICTED: eukaryotic translation initiation factor 3 subunit K-like
Locus_17232_Transcript_1/1_Conf_1.000	628	20	1.91E-94	NP_505734.2	93	348.977	193	181	Protein PHosphatase family member (pph-1)
Locus_17233_Transcript_1/1_Conf_1.000	197	0							
Locus_17234_Transcript_1/1_Conf_1.000	309	20	2.55E-42	CAX65056.1	91	174.866	102	93	C. elegans protein F25C8.3d, partially confirmed by transcript evidence
Locus_17235_Transcript_1/1_Conf_1.000	149	0							
Locus_17236_Transcript_1/1_Conf_1.000	229	0							
Locus_17237_Transcript_1/1_Conf_1.000	1166	20	1.00E-101	XP_001898107.1	67	374.785	378	257	PDZ-domain protein scribble
Locus_17238_Transcript_1/1_Conf_1.000	349	0							
Locus_17239_Transcript_1/1_Conf_1.000	375	0							

Locus_1724_Transcript_1/1_Conf_1.000	3328	20	0	XP_002640935.1	73	919.842	830	607	C. briggsae CBR-SSL-1 protein
Locus_17240_Transcript_1/1_Conf_1.000	167	0							
Locus_17241_Transcript_1/1_Conf_1.000	154	14	2.23E-17	XP_002642067.1	92	92.0485	51	47	Hypothetical protein CBG18006
Locus_17242_Transcript_1/1_Conf_1.000	451	0							
Locus_17243_Transcript_1/1_Conf_1.000	322	7	6.25E-12	XP_002630536.1	57	73.9442	107	62	Hypothetical protein CBG12976
Locus_17244_Transcript_1/1_Conf_1.000	1201	20	4.64E-49	NP_491336.2	62	199.904	240	151	NuDiX family member (ndx-7)
Locus_17245_Transcript_1/1_Conf_1.000	431	0							
Locus_17246_Transcript_1/1_Conf_1.000	262	0							
Locus_17247_Transcript_1/1_Conf_1.000	224	20	3.45E-18	NP_491222.2	74	94.7449	74	55	hypothetical protein C32E8.9
Locus_17248_Transcript_1/1_Conf_1.000	506	2	2.89E-12	NP_509145.2	53	75.0998	129	69	AuTophaGy (yeast Atg homolog) family member (atg-2)
Locus_17249_Transcript_1/1_Conf_1.000	460	0							
Locus_1725_Transcript_1/2_Conf_1.000	2486	20	3.22E-139	XP_002639606.1	60	500.745	690	414	C. briggsae CBR-FRM-4 protein

Locus_1725_Transcript_2/2_Conf_1.000	2435	20	3.25E-136	XP_002639606.1	61	490.73	667	410	C. briggsae CBR-FRM-4 protein
Locus_17250_Transcript_1/1_Conf_1.000	477	0							
Locus_17251_Transcript_1/1_Conf_1.000	332	3	7.82E-07	NP_495954.1	62	56.9954	102	64	Regulator of HYpoxia-inducible factor (hif-1) family member (rhy-1)
Locus_17252_Transcript_1/1_Conf_1.000	495	20	1.36E-35	NP_505508.1	74	152.525	136	101	hypothetical protein F40F9.6
Locus_17253_Transcript_1/1_Conf_1.000	443	20	1.71E-17	NP_509794.2	100	92.4337	45	45	honeybee MBlk-1 Related factor family member (mbr-1)
Locus_17254_Transcript_1/1_Conf_1.000	320	2	1.11E-08	XP_002633778.1	60	63.1586	96	58	Hypothetical protein CBG03469
Locus_17255_Transcript_1/1_Conf_1.000	465	5	1.18E-10	XP_001900440.1	63	69.707	87	55	hypothetical protein Bm1_44890
Locus_17256_Transcript_1/1_Conf_1.000	164	3	2.29E-14	NP_493603.1	86	82.0333	52	45	PaTched Related family member (ptr-23)
Locus_17257_Transcript_1/1_Conf_1.000	716	0							
Locus_17258_Transcript_1/1_Conf_1.000	169	6	4.00E-19	XP_001899075.1	92	97.8265	55	51	hypothetical protein Bm1_38110
Locus_17259_Transcript_1/1_Conf_1.000	418	20	3.67E-36	NP_740853.2	77	154.451	122	95	TOMosyn synaptic protein family member (tom-1)
Locus_1726_Transcript_1/1_Conf_1.000	1901	20	0	NP_508550.1	87	830.091	544	476	Ral GDS-Like family member (rgl-1)

Locus_17260_Transcript_1/1_Conf_1.000	217	0							
Locus_17261_Transcript_1/1_Conf_1.000	476	20	1.42E-16	XP_002641832.1	55	89.3521	158	88	Hypothetical protein CBG16501
Locus_17262_Transcript_1/1_Conf_1.000	308	20	4.37E-42	EFN83153.1	100	174.096	90	90	Histone H3.3
Locus_17263_Transcript_1/1_Conf_1.000	203	20	1.47E-29	XP_002762066.1	100	132.494	64	64	PREDICTED: transmembrane protein 147-like
Locus_17264_Transcript_1/1_Conf_1.000	374	20	2.44E-48	XP_002642870.1	88	194.897	120	106	Hypothetical protein CBG15140
Locus_17265_Transcript_1/1_Conf_1.000	161	20	1.39E-11	NP_886553.3	100	72.7886	34	34	eukaryotic translation initiation factor 4 gamma 1 isoform 1
Locus_17266_Transcript_1/2_Conf_1.000	384	0							
Locus_17266_Transcript_2/2_Conf_1.000	380	0							
Locus_17267_Transcript_1/1_Conf_1.000	305	1	6.19E-04	XP_002637243.1	64	47.3654	59	38	Hypothetical protein CBG18919
Locus_17268_Transcript_1/1_Conf_1.000	220	0							
Locus_17269_Transcript_1/1_Conf_1.000	130	0							
Locus_1727_Transcript_1/1_Conf_1.000	761	20	2.48E-37	XP_002631715.1	63	159.844	181	115	Hypothetical protein CBG20916
Locus_17270_Transcript_1/1_Conf_1.000	233	0							
Locus_17271_Transcript_1/1_Conf_1.000	372	20	1.75E-30	AAN11401.1	68	135.576	122	84	metalloprotease 1 precursor

Locus_17272_Transcript_1/1_Conf_1.000	238	20	2.34E-35	XP_002634104.1	100	151.754	78	78	Hypothetical protein CBG01656
Locus_17273_Transcript_1/1_Conf_1.000	293	3	6.28E-04	ZP_04116816.1	59	47.3654	54	32	Collagen triple helix repeat domain protein
Locus_17274_Transcript_1/1_Conf_1.000	207	20	1.08E-24	NP_612634.3	100	116.316	57	57	synaptotagmin-8
Locus_17275_Transcript_1/1_Conf_1.000	154	4	4.22E-08	EFO20018.1	68	61.2326	50	34	negative elongation factor C/D
Locus_17276_Transcript_1/1_Conf_1.000	241	20	7.26E-29	XP_002637169.1	93	130.183	77	72	C. briggsae CBR-MRE-11 protein

Locus_17277_Transcript_1/1_Conf_1.000	604	20	8.40E-73	XP_002646357.1	80	276.944	186	149	Hypothetical protein CBG12071
Locus_17278_Transcript_1/1_Conf_1.000	225	20	1.07E-27	NP_502964.2	87	126.331	74	65	hypothetical protein Y51H4A.7
Locus_17279_Transcript_1/1_Conf_1.000	285	1	2.84E-04	XP_002638582.1	58	48.521	79	46	Hypothetical protein CBG05629
Locus_1728_Transcript_1/1_Conf_1.000	230	2	5.85E-18	AAQ18782.1	94	93.9745	51	48	GATA transcription factor
Locus_17280_Transcript_1/1_Conf_1.000	186	0							
Locus_17281_Transcript_1/1_Conf_1.000	130	0							
Locus_17282_Transcript_1/1_Conf_1.000	547	0							
Locus_17283_Transcript_1/1_Conf_1.000	714	20	3.81E-90	NP_501853.1	87	335.109	248	216	TetraSPanin family member (tsp-12)
Locus_17284_Transcript_1/1_Conf_1.000	309	6	3.58E-28	XP_002633574.1	71	127.872	103	74	Hypothetical protein CBG05448
Locus_17285_Transcript_1/1_Conf_1.000	348	20	5.09E-30	NP_495375.3	84	134.035	94	79	hypothetical protein T14B4.1
Locus_17286_Transcript_1/1_Conf_1.000	429	2	2.69E-07	NP_493320.1	50	58.5362	102	51	hypothetical protein ZK1053.2
Locus_17287_Transcript_1/1_Conf_1.000	400	0							
Locus_17288_Transcript_1/1_Conf_1.000	480	0							
Locus_17289_Transcript_1/1_Conf_1.000	169	20	1.28E-25	XP_002801133.1	100	119.398	55	55	PREDICTED: lysosomal alpha-mannosidase-like
Locus_1729_Transcript_1/1_Conf_1.000	428	0							
Locus_17290_Transcript_1/1_Conf_1.000	141	1	3.59E-04	XP_002634634.1	63	48.1358	44	28	Hypothetical protein CBG18497
Locus_17291_Transcript_1/1_Conf_1.000	217	0							
Locus_17292_Transcript_1/1_Conf_1.000	548	20	6.44E-65	EFO19031.1	83	250.366	176	147	hypothetical protein LOAG_09464
Locus_17293_Transcript_1/1_Conf_1.000	214	0							
Locus_17294_Transcript_1/1_Conf_1.000	294	20	4.43E-42	EFO26082.1	91	174.096	98	90	hypothetical protein LOAG_02394
Locus_17295_Transcript_1/1_Conf_1.000	311	20	1.01E-22	NP_491887.1	70	109.768	98	69	hypothetical protein F57B10.8
Locus_17296_Transcript_1/1_Conf_1.000	152	0							

Locus_17297_Transcript_1/1_Conf_1.000	159	20	4.17E-24	XP_002816748.1	100	114.39	53	53	PREDICTED: LOW QUALITY PROTEIN: large proline-rich protein BAT2-like
Locus_17298_Transcript_1/1_Conf_1.000	362	0							
Locus_17299_Transcript_1/1_Conf_1.000	238	0							
Locus_173_Transcript_1/2_Conf_1.000	2157	7	3.84E-08	XP_002632964.1	40	65.0846	151	61	Hypothetical protein CBG21722
Locus_173_Transcript_2/2_Conf_1.000	1791	4	2.04E-12	XP_002632964.1	35	78.9518	261	92	Hypothetical protein CBG21722
Locus_1730_Transcript_1/1_Conf_1.000	1908	20	0	XP_002629713.1	83	681.404	564	473	Hypothetical protein CBG00943
Locus_17300_Transcript_1/2_Conf_1.000	1008	20	1.53E-84	XP_002633358.1	76	317.39	244	187	C. briggsae CBR-ACL-3 protein

Locus_17300_Transcript_2/2_Conf_1.000	1005	20	1.53E-84	XP_002633358.1	76	317.39	244	187	C. briggsae CBR-ACL-3 protein
Locus_17301_Transcript_1/1_Conf_1.000	258	0							
Locus_17302_Transcript_1/1_Conf_1.000	153	0							
Locus_17303_Transcript_1/1_Conf_1.000	397	20	7.62E-34	EFO23539.1	74	146.747	131	97	hypothetical protein LOAG_04946
Locus_17304_Transcript_1/1_Conf_1.000	332	20	2.75E-44	XP_001896744.1	83	181.415	110	92	Trehalase family protein
Locus_17305_Transcript_1/1_Conf_1.000	153	0							
Locus_17306_Transcript_1/1_Conf_1.000	447	8	1.09E-48	XP_002644403.1	84	196.052	148	125	Hypothetical protein CBG14248
Locus_17307_Transcript_1/1_Conf_1.000	375	4	9.59E-29	NP_491019.1	67	129.798	124	84	hypothetical protein F40E3.5
Locus_17308_Transcript_1/1_Conf_1.000	543	0							
Locus_17309_Transcript_1/1_Conf_1.000	150	20	7.98E-07	XP_002640915.1	71	56.9954	49	35	Hypothetical protein CBG00476
Locus_1731_Transcript_1/1_Conf_1.000	1129	20	1.57E-35	XP_002640023.1	65	154.836	206	135	Hypothetical protein CBG12495
Locus_17310_Transcript_1/1_Conf_1.000	171	20	1.52E-18	XP_002643095.1	85	95.9005	56	48	C. briggsae CBR-GLY-11 protein

Locus_17311_Transcript_1/1_Conf_1.000	190	20	1.83E-19	BAF83766.1	100	98.9821	60	60	unnamed protein product
Locus_17312_Transcript_1/1_Conf_1.000	414	20	5.89E-31	XP_002647605.1	75	137.117	105	79	Hypothetical protein CBG06696
Locus_17313_Transcript_1/1_Conf_1.000	469	20	8.67E-22	XP_002640707.1	68	106.686	112	77	Hypothetical protein CBG19773
Locus_17314_Transcript_1/1_Conf_1.000	265	4	1.10E-16	CBI63237.1	63	89.7373	104	66	C. elegans protein Y111B2A.4a, partially confirmed by transcript evidence
Locus_17315_Transcript_1/1_Conf_1.000	287	20	4.51E-18	EFO23906.1	69	94.3597	85	59	hypothetical protein LOAG_04576
Locus_17316_Transcript_1/1_Conf_1.000	437	2	3.49E-07	XP_002636583.1	51	58.151	146	75	Hypothetical protein CBG23277
Locus_17317_Transcript_1/1_Conf_1.000	160	0							
Locus_17318_Transcript_1/1_Conf_1.000	245	0							
Locus_17319_Transcript_1/1_Conf_1.000	199	0							
Locus_1732_Transcript_1/1_Conf_1.000	2295	20	5.32E-165	NP_501339.2	60	586.26	740	447	neuRonal IGCAM family member (rig-4)
Locus_17320_Transcript_1/1_Conf_1.000	383	0							
Locus_17321_Transcript_1/1_Conf_1.000	400	0							
Locus_17322_Transcript_1/1_Conf_1.000	160	10	1.35E-06	XP_001902385.1	72	56.225	48	35	Patched family protein
Locus_17323_Transcript_1/1_Conf_1.000	153	0							
Locus_17324_Transcript_1/1_Conf_1.000	345	20	1.22E-23	NP_502129.1	85	112.849	70	60	hypothetical protein B0035.5
Locus_17325_Transcript_1/1_Conf_1.000	137	0							
Locus_17326_Transcript_1/1_Conf_1.000	656	20	1.04E-40	EFO23575.1	89	170.629	104	93	proteasome regulatory particle
Locus_17327_Transcript_1/1_Conf_1.000	307	0							

Locus_17328_Transcript_1/1_Conf_1.000	291	5	3.01E-06	AAX47336.1	65	55.0694	52	34	beta-catenin
Locus_17329_Transcript_1/1_Conf_1.000	294	0							
Locus_1733_Transcript_1/1_Conf_1.000	406	0							
Locus_17330_Transcript_1/1_Conf_1.000	155								
Locus_17331_Transcript_1/1_Conf_1.000	281	20	1.19E-15	EFO20952.1	70	86.2705	68	48	endonuclease/Exonuclease/phosphatase
Locus_17332_Transcript_1/2_Conf_1.000	435	0							
Locus_17332_Transcript_2/2_Conf_1.000	444	0							
Locus_17333_Transcript_1/1_Conf_1.000	251	20	2.31E-27	CAR63587.1	87	125.176	79	69	putative BolA-like family protein
Locus_17334_Transcript_1/1_Conf_1.000	480	20	3.67E-49	XP_002634049.1	75	197.593	158	120	Hypothetical protein CBG01588
Locus_17335_Transcript_1/1_Conf_1.000	199	20	2.07E-07	ACI49169.1	65	58.9214	64	42	hypothetical protein Csp3_JD01.001
Locus_17336_Transcript_1/1_Conf_1.000	185	0							
Locus_17337_Transcript_1/1_Conf_1.000	441	0							
Locus_17338_Transcript_1/1_Conf_1.000	538	20	1.56E-28	EFO23663.1	60	129.413	181	110	myosin xviiia
Locus_17339_Transcript_1/1_Conf_1.000	245	0							
Locus_1734_Transcript_1/2_Conf_1.000	262	0							
Locus_1734_Transcript_2/2_Conf_1.000	181	0							
Locus_17340_Transcript_1/1_Conf_1.000	155	0							
Locus_17341_Transcript_1/1_Conf_1.000	175	20	3.73E-09	XP_002633845.1	77	64.6994	48	37	C. briggsae CBR-BEC-1 protein
Locus_17342_Transcript_1/1_Conf_1.000	749	20	2.92E-91	XP_002630786.1	85	338.961	227	195	Hypothetical protein CBG02483
Locus_17343_Transcript_1/1_Conf_1.000	258	20	2.63E-18	BAD88409.1	66	95.1301	87	58	multidrug resistance-associated protein

Locus_17344_Transcript_1/1_Conf_1.000	387	20	7.76E-15	XP_001626861.1	67	83.5741	84	57	predicted protein
Locus_17345_Transcript_1/1_Conf_1.000	337	20	3.71E-25	CBA11992.1	70	117.857	111	78	endonuclease-reverse transcriptase HmRTE-e01
Locus_17346_Transcript_1/1_Conf_1.000	859	20	3.05E-125	XP_002643856.1	90	452.21	286	260	C. briggsae CBR-AAT-3 protein
Locus_17347_Transcript_1/1_Conf_1.000	145	1	1.56E-18	EAW60095.1	100	95.9005	44	44	hCG2041804
Locus_17348_Transcript_1/1_Conf_1.000	306	0							
Locus_17349_Transcript_1/1_Conf_1.000	189	2	1.00E-09	XP_002635377.1	91	66.6254	34	31	Hypothetical protein CBG00768
Locus_1735_Transcript_1/3_Conf_0.400	1343	20	0	NP_492790.1	84	675.241	448	377	hypothetical protein B0511.12
Locus_1735_Transcript_2/3_Conf_0.400	606	20	8.07E-31	XP_002640257.1	74	137.502	109	81	Hypothetical protein CBG12782
Locus_1735_Transcript_3/3_Conf_0.600	2986	20	0	NP_492790.1	74	1149.04	994	736	hypothetical protein B0511.12
Locus_17350_Transcript_1/1_Conf_1.000	185	0							
Locus_17351_Transcript_1/1_Conf_1.000	303	20	1.37E-27	NP_492590.1	69	125.946	101	70	hypothetical protein K02A11.3
Locus_17352_Transcript_1/1_Conf_1.000	479	20	2.09E-44	XP_002640631.1	73	181.8	165	121	Hypothetical protein CBG08749
Locus_17353_Transcript_1/1_Conf_1.000	252	20	1.45E-16	NP_496282.2	69	89.3521	83	58	hypothetical protein C14A4.3
Locus_17354_Transcript_1/1_Conf_1.000	251	0							
Locus_17355_Transcript_1/1_Conf_1.000	739	20	1.38E-45	EFO17241.1	58	187.193	234	138	hypothetical protein LOAG_11260
Locus_17356_Transcript_1/1_Conf_1.000	518	7	1.74E-31	XP_002647546.1	58	139.043	171	100	C. briggsae CBR-PME-5 protein
Locus_17357_Transcript_1/1_Conf_1.000	586	0							
Locus_17358_Transcript_1/1_Conf_1.000	535	7	4.18E-18	CAA84693.3	55	94.7449	177	98	C. elegans protein D2045.2, partially confirmed by transcript evidence
Locus_17359_Transcript_1/1_Conf_1.000	513	0							

Locus_1736_Transcript_1/1_Conf_1.000	774	20	1.67E-36	EFO16781.1	55	157.147	252	140	bone morphogenic protein 6
Locus_17360_Transcript_1/1_Conf_1.000	187	1	9.76E-05	ABD39382.1	75	50.0618	61	46	putative galectin protein 140
Locus_17361_Transcript_1/1_Conf_1.000	282	0							
Locus_17362_Transcript_1/1_Conf_1.000	168	0							
Locus_17363_Transcript_1/1_Conf_1.000	173	0							
Locus_17364_Transcript_1/1_Conf_1.000	224	0							
Locus_17365_Transcript_1/1_Conf_1.000	279	20	2.48E-29	XP_002646489.1	86	131.724	97	84	Hypothetical protein CBG19471
Locus_17366_Transcript_1/1_Conf_1.000	390	20	5.54E-13	NP_001022669.1	72	77.411	74	54	hypothetical protein K08E3.10
Locus_17367_Transcript_1/1_Conf_1.000	486	0							
Locus_17368_Transcript_1/1_Conf_1.000	441	20	3.41E-42	NP_508216.1	78	174.481	146	115	Sorting NeXin family member (snx-1)
Locus_17369_Transcript_1/1_Conf_1.000	274	20	2.18E-25	XP_002634480.1	73	118.627	90	66	Hypothetical protein CBG10739
Locus_1737_Transcript_1/5_Conf_0.333	911	20	2.81E-51	CAT00091.1	99	198.749	104	103	translationally controlled tumor protein
Locus_1737_Transcript_2/5_Conf_0.167	658	0							

Locus_1737_Transcript_3/5_Conf_0.417	859	20	4.31E-87	CAT00091.1	98	325.479	181	178	translationally controlled tumor protein
Locus_1737_Transcript_4/5_Conf_0.500	1311	20	8.29E-87	CAT00091.1	98	325.479	181	178	translationally controlled tumor protein
Locus_1737_Transcript_5/5_Conf_0.333	875	20	7.75E-132	XP_002639809.1	97	474.167	264	257	C. briggsae CBR-RPA-0 protein
Locus_17370_Transcript_1/1_Conf_1.000	750	5	7.55E-63	NP_495112.1	69	244.588	263	182	hypothetical protein C25H3.11
Locus_17371_Transcript_1/1_Conf_1.000	193	0							
Locus_17372_Transcript_1/1_Conf_1.000	135	0							
Locus_17373_Transcript_1/1_Conf_1.000	315	15	2.73E-15	XP_002646997.1	60	85.1149	104	63	Hypothetical protein CBG22453
Locus_17374_Transcript_1/1_Conf_1.000	527	20	4.80E-104	XP_001101364.2	100	380.178	175	175	PREDICTED: SPARC
Locus_17375_Transcript_1/1_Conf_1.000	221	0							
Locus_17376_Transcript_1/2_Conf_1.000	890	20	2.35E-67	XP_002633534.1	82	259.996	223	183	Hypothetical protein CBG05401
Locus_17376_Transcript_2/2_Conf_1.000	890	20	2.35E-67	XP_002633534.1	82	259.996	223	183	Hypothetical protein CBG05401
Locus_17377_Transcript_1/1_Conf_1.000	293	20	6.23E-28	XP_002630862.1	77	127.102	98	76	C. briggsae CBR-RRT-2 protein
Locus_17378_Transcript_1/1_Conf_1.000	486	20	1.87E-32	NP_499394.2	68	142.124	159	109	hypothetical protein C44B9.1

Locus_17379_Transcript_1/1_Conf_1.000	213	20	4.10E-16	NP_504274.2	77	87.8113	70	54	UDP-GlucuronosylTransferase family member (ugt-61)
Locus_1738_Transcript_1/1_Conf_1.000	1269	20	0	XP_002638687.1	96	796.964	422	409	Hypothetical protein CBG11882
Locus_17380_Transcript_1/1_Conf_1.000	1266	20	5.97E-10	XP_001602928.1	45	70.0922	328	148	PREDICTED: similar to GA21383-PA
Locus_17381_Transcript_1/1_Conf_1.000	243	0							
Locus_17382_Transcript_1/1_Conf_1.000	374	8	3.80E-09	XP_002631036.1	55	64.6994	114	63	Hypothetical protein CBG02793
Locus_17383_Transcript_1/1_Conf_1.000	356	0							
Locus_17384_Transcript_1/1_Conf_1.000	483	20	5.85E-26	EFO25878.1	70	120.553	140	98	RDD family protein
Locus_17385_Transcript_1/1_Conf_1.000	155	0							
Locus_17386_Transcript_1/1_Conf_1.000	356	0							
Locus_17387_Transcript_1/1_Conf_1.000	226								
Locus_17388_Transcript_1/2_Conf_1.000	631	0							
Locus_17388_Transcript_2/2_Conf_1.000	617	0							
Locus_17389_Transcript_1/1_Conf_1.000	178	0							
Locus_1739_Transcript_1/1_Conf_1.000	586	20	5.84E-52	NP_501020.2	93	207.608	115	107	hypothetical protein C01B10.3
Locus_17390_Transcript_1/1_Conf_1.000	222	0							
Locus_17391_Transcript_1/1_Conf_1.000	184	0							
Locus_17392_Transcript_1/1_Conf_1.000	302	2	1.02E-06	XP_002645841.1	64	56.6102	62	40	Hypothetical protein CBG07574

Locus_17393_Transcript_1/1_Conf_1.000	464	20	1.26E-69	A8X3A7.2	89	259.225	142	127	Integrin alpha pat-2
Locus_17394_Transcript_1/1_Conf_1.000	908	20	2.75E-111	XP_002631326.1	74	405.986	303	227	C. briggsae CBR-FUT-1 protein
Locus_17395_Transcript_1/1_Conf_1.000	416	6	3.22E-37	Q20548.2	76	157.918	138	106	Probable RING finger protein 207 homolog
Locus_17396_Transcript_1/1_Conf_1.000	791	1	3.66E-10	EFO16945.1	46	69.707	215	101	hypothetical protein LOAG_11558
Locus_17397_Transcript_1/1_Conf_1.000	452	20	9.12E-64	NP_492483.1	85	246.128	150	128	hypothetical protein F26H9.5
Locus_17398_Transcript_1/1_Conf_1.000	594	0							
Locus_17399_Transcript_1/1_Conf_1.000	333	4	8.33E-09	NP_496398.2	66	63.5438	65	43	hypothetical protein T06D8.1
Locus_174_Transcript_1/8_Conf_0.600	1809	20	7.07E-29	XP_002631180.1	56	133.65	253	142	C. briggsae CBR-NASP-1 protein
Locus_174_Transcript_2/8_Conf_0.560	1797	20	7.00E-29	XP_002631180.1	56	133.65	253	142	C. briggsae CBR-NASP-1 protein
Locus_174_Transcript_3/8_Conf_0.400	935	17	6.01E-08	NP_506298.1	58	62.7734	95	56	NASP (human Nuclear Autoantigenic Sperm Protein) homolog family member (nasp-2)
Locus_174_Transcript_4/8_Conf_0.560	1809	20	1.21E-28	XP_002631180.1	55	132.88	253	141	C. briggsae CBR-NASP-1 protein
Locus_174_Transcript_5/8_Conf_0.560	1816	20	7.10E-29	XP_002631180.1	56	133.65	253	142	C. briggsae CBR-NASP-1 protein
Locus_174_Transcript_6/8_Conf_0.360	935	17	6.01E-08	NP_506298.1	58	62.7734	95	56	NASP (human Nuclear Autoantigenic Sperm Protein) homolog family member (nasp-2)

Locus_174_Transcript_7/8_Conf_0.200	445	20	7.64E-10	NP_506298.1	60	67.0106	98	59	NASP (human Nuclear Autoantigenic Sperm Protein) homolog family member (nasp-2)
Locus_174_Transcript_8/8_Conf_0.560	1809	20	7.07E-29	XP_002631180.1	56	133.65	253	142	C. briggsae CBR-NASP-1 protein
Locus_1740_Transcript_1/1_Conf_1.000	759	20	9.04E-56	XP_002637954.1	68	221.09	238	164	Hypothetical protein CBG04771
Locus_17400_Transcript_1/1_Conf_1.000	262	20	5.26E-35	ACJ65168.1	94	150.599	87	82	Uncoordinated protein 68, isoform b, partially confirmed by transcript evidence
Locus_17401_Transcript_1/1_Conf_1.000	244	2	9.83E-10	XP_002642848.1	72	66.6254	76	55	Hypothetical protein CBG15114
Locus_17402_Transcript_1/1_Conf_1.000	220	20	3.03E-22	XP_002648832.1	82	108.227	73	60	Hypothetical protein CBG16947

Locus_17403_Transcript_1/1_Conf_1.000	281	20	6.73E-35	NP_495838.2	84	150.214	93	79	PYRimidine biosynthesis family member (pyr-1)
Locus_17404_Transcript_1/1_Conf_1.000	935	20	2.62E-112	XP_002646922.1	78	409.453	311	245	Hypothetical protein CBG19625
Locus_17405_Transcript_1/1_Conf_1.000	345	20	7.12E-40	NP_497319.1	85	166.777	114	97	hypothetical protein Y46E12BL.2
Locus_17406_Transcript_1/1_Conf_1.000	920	20	3.39E-40	XP_002633792.1	89	169.859	86	77	Hypothetical protein CBG03484
Locus_17407_Transcript_1/1_Conf_1.000	151	0							
Locus_17408_Transcript_1/1_Conf_1.000	167	20	7.59E-10	EFN89993.1	67	67.0106	53	36	Probable cytochrome P450 6a13
Locus_17409_Transcript_1/1_Conf_1.000	446	2	1.03E-22	XP_002631708.1	82	109.768	87	72	Hypothetical protein CBG20908
Locus_1741_Transcript_1/1_Conf_1.000	1858	20	0	XP_002630288.1	92	828.55	547	507	C. briggsae CBR-CCT-1 protein
Locus_17410_Transcript_1/1_Conf_1.000	239	0							

Locus_17411_Transcript_1/1_Conf_1.000	227	5	5.70E-05	NP_001021268.1	72	50.8322	40	29	UNCoordinated family member (unc-44)
Locus_17412_Transcript_1/1_Conf_1.000	423	20	1.58E-23	NP_001041046.1	61	112.464	120	74	hypothetical protein Y57G11C.22
Locus_17413_Transcript_1/1_Conf_1.000	130	0							
Locus_17414_Transcript_1/1_Conf_1.000	437	0							
Locus_17415_Transcript_1/1_Conf_1.000	221	0							
Locus_17416_Transcript_1/1_Conf_1.000	393	9	1.19E-18	CAB60377.4	59	96.2857	134	80	C. elegans protein Y46G5A.29, partially confirmed by transcript evidence
Locus_17417_Transcript_1/1_Conf_1.000	529	0							
Locus_17418_Transcript_1/1_Conf_1.000	205	0							
Locus_17419_Transcript_1/1_Conf_1.000	446	20	1.16E-58	XP_002642359.1	85	229.18	148	127	Hypothetical protein CBG18356
Locus_1742_Transcript_1/1_Conf_1.000	452	1	2.79E-04	XP_002648823.1	42	48.521	85	36	Hypothetical protein CBG16936
Locus_17420_Transcript_1/1_Conf_1.000	205	0							
Locus_17421_Transcript_1/1_Conf_1.000	206	2	1.25E-04	EFO26312.1	65	49.6766	41	27	hypothetical protein LOAG_02167
Locus_17422_Transcript_1/1_Conf_1.000	149	20	7.98E-15	NP_001129924.1	81	83.5741	49	40	SLOwpoke potassium channel family member (slo-2)
Locus_17423_Transcript_1/1_Conf_1.000	269	0							

Locus_17424_Transcript_1/1_Conf_1.000	146	20	3.71E-20	XP_002832350.1	100	101.293	48	48	PREDICTED: LOW QUALITY PROTEIN: filamin-A-like
Locus_17425_Transcript_1/1_Conf_1.000	411	13	3.23E-45	XP_002639996.1	78	184.496	136	107	Hypothetical protein CBG10826
Locus_17426_Transcript_1/1_Conf_1.000	345	20	5.28E-35	NP_001023496.1	75	150.599	114	86	L1 CAM ADhesion molecule homolog family member (lad-2)
Locus_17427_Transcript_1/1_Conf_1.000	649	4	1.99E-12	XP_002640451.1	68	76.6406	63	43	Hypothetical protein CBG08508
Locus_17428_Transcript_1/1_Conf_1.000	274	0							
Locus_17429_Transcript_1/2_Conf_1.000	322	0							
Locus_17429_Transcript_2/2_Conf_1.000	349	0							
Locus_1743_Transcript_1/1_Conf_1.000	1269	5	3.85E-33	NP_740830.2	55	147.132	246	137	hypothetical protein Y47G6A.29
Locus_17430_Transcript_1/1_Conf_1.000	219	20	5.70E-29	XP_002638487.1	95	130.568	73	70	Hypothetical protein CBG12917

Locus_17431_Transcript_1/1_Conf_1.000	143	20	5.34E-16	NP_501984.1	93	87.4261	47	44	Na/Ca eXchangers family member (ncx-3)
Locus_17432_Transcript_1/1_Conf_1.000	193	20	5.30E-19	XP_002405101.1	87	97.4413	62	54	protein 4.1G, putative
Locus_17433_Transcript_1/1_Conf_1.000	814	20	2.23E-42	NP_740987.2	55	176.792	268	149	hypothetical protein C27D6.4
Locus_17434_Transcript_1/1_Conf_1.000	216	0							
Locus_17435_Transcript_1/1_Conf_1.000	613	0							
Locus_17436_Transcript_1/1_Conf_1.000	390	4	1.04E-35	NP_504440.2	65	152.91	147	97	hypothetical protein F08F3.1
Locus_17437_Transcript_1/1_Conf_1.000	142	0							
Locus_17438_Transcript_1/1_Conf_1.000	130	0							
Locus_17439_Transcript_1/1_Conf_1.000	176	0							
Locus_1744_Transcript_1/1_Conf_1.000	1178	20	3.00E-61	EFO16596.1	65	240.35	279	183	hypothetical protein LOAG_11909
Locus_17440_Transcript_1/1_Conf_1.000	1197	20	6.74E-133	XP_002637705.1	86	478.404	312	271	Hypothetical protein CBG11570
Locus_17441_Transcript_1/1_Conf_1.000	196	20	1.21E-23	XP_002828959.1	93	112.849	62	58	PREDICTED: hypothetical protein LOC100434366
Locus_17442_Transcript_1/1_Conf_1.000	967	20	7.93E-152	XP_001900845.1	92	540.806	322	297	Beta-centractin

Locus_17443_Transcript_1/1_Conf_1.000	150	20	3.57E-15	XP_002821493.1	100	84.7297	39	39	PREDICTED: LOW QUALITY PROTEIN: serine/threonine-protein phosphatase PP1-alpha catalytic subunit-like
Locus_17444_Transcript_1/1_Conf_1.000	195	0							
Locus_17445_Transcript_1/1_Conf_1.000	404	20	3.19E-16	EFO22662.1	68	88.1965	82	56	exostosin family protein
Locus_17446_Transcript_1/1_Conf_1.000	154	4	1.83E-11	XP_002646726.1	74	72.4034	50	37	Hypothetical protein CBG13109
Locus_17447_Transcript_1/1_Conf_1.000	133	20	2.77E-12	NP_001040856.1	90	75.0998	43	39	PAPS (adenosine 3'-phosphate 5'-phosphosulfate) Transporter family member (pst-2)
Locus_17448_Transcript_1/1_Conf_1.000	189	0							
Locus_17449_Transcript_1/1_Conf_1.000	595	0							
Locus_1745_Transcript_1/1_Conf_1.000	371	0							
Locus_17450_Transcript_1/1_Conf_1.000	602	3	6.17E-52	XP_002643880.1	67	207.608	200	134	Hypothetical protein CBG02118
Locus_17451_Transcript_1/1_Conf_1.000	893	0							
Locus_17452_Transcript_1/1_Conf_1.000	455	0							
Locus_17453_Transcript_1/1_Conf_1.000	168	0							
Locus_17454_Transcript_1/1_Conf_1.000	531	1	3.21E-26	CAR63592.1	65	121.709	141	93	hypothetical protein
Locus_17455_Transcript_1/1_Conf_1.000	367	20	4.34E-42	XP_002630208.1	83	174.096	117	98	C. briggsae CBR-LACT-4 protein
Locus_17456_Transcript_1/1_Conf_1.000	195	6	7.37E-21	NP_001021988.1	79	103.605	63	50	Epithelial Fusion Failure family member (eff-1)
Locus_17457_Transcript_1/1_Conf_1.000	230	0							
Locus_17458_Transcript_1/1_Conf_1.000	217	4	1.04E-27	NP_492127.1	93	126.331	72	67	Low-density lipoprotein Receptor Related family member (lrp-1)
Locus_17459_Transcript_1/1_Conf_1.000	128	2	2.98E-06	AAV28323.2	70	55.0694	40	28	Hypothetical protein T15B7.1
Locus_1746_Transcript_1/1_Conf_1.000	488	1	8.18E-04	NP_001024088.1	46	46.9802	116	54	hypothetical protein T01C3.11

Locus_17460_Transcript_1/1_Conf_1.000	769	20	2.62E-42	XP_002639655.1	80	176.407	118	95	Hypothetical protein CBG12371
Locus_17461_Transcript_1/1_Conf_1.000	203	15	3.08E-19	XP_002641899.1	79	98.2117	68	54	C. briggsae CBR-NHR-10 protein
Locus_17462_Transcript_1/1_Conf_1.000	209	20	5.78E-10	NP_497641.2	67	67.3958	68	46	CaDHerin family member (cdh-1)
Locus_17463_Transcript_1/1_Conf_1.000	134	20	7.29E-13	NP_495437.2	90	77.0258	44	40	hypothetical protein C52E12.4
Locus_17464_Transcript_1/1_Conf_1.000	290	20	1.26E-20	XP_002645050.1	79	102.834	96	76	Hypothetical protein CBG16703
Locus_17465_Transcript_1/1_Conf_1.000	199	4	7.87E-15	XP_002644812.1	72	83.5741	65	47	Hypothetical protein CBG14830
Locus_17466_Transcript_1/1_Conf_1.000	1242	20	4.24E-85	XP_002640804.1	88	319.701	197	174	C. briggsae CBR-RAL-1 protein
Locus_17467_Transcript_1/1_Conf_1.000	499	20	6.32E-25	XP_002631305.1	74	117.087	108	80	C. briggsae CBR-DNA-2 protein
Locus_17468_Transcript_1/2_Conf_1.000	367	20	1.35E-35	CAA72915.1	79	152.525	116	92	serine protease inhibitor-like protein

Locus_17468_Transcript_2/2_Conf_1.000	366	20	8.76E-35	CAA72915.1	79	149.828	116	92	serine protease inhibitor-like protein
Locus_17469_Transcript_1/1_Conf_1.000	247	0							
Locus_1747_Transcript_1/1_Conf_1.000	1175	20	1.04E-122	XP_002637936.1	80	444.506	333	267	Hypothetical protein CBG04748
Locus_17470_Transcript_1/1_Conf_1.000	192	0							
Locus_17471_Transcript_1/1_Conf_1.000	249	5	8.26E-09		66	63.5438	63	42	myoblast city protein homolog
Locus_17472_Transcript_1/1_Conf_1.000	339	0							
Locus_17473_Transcript_1/1_Conf_1.000	283	20	7.69E-34	NP_500460.1	80	146.747	93	75	hypothetical protein W02C12.1
Locus_17474_Transcript_1/1_Conf_1.000	177	0							
Locus_17475_Transcript_1/1_Conf_1.000	281	2	1.97E-10	XP_002632596.1	64	68.9366	64	41	Hypothetical protein CBG23720
Locus_17476_Transcript_1/1_Conf_1.000	361	20	1.72E-30	NP_498089.2	76	135.576	115	88	hypothetical protein Y54H5A.2
Locus_17477_Transcript_1/1_Conf_1.000	756	20	4.13E-85	NP_509008.2	80	318.546	230	186	Inositol Polyphosphate 5-Phosphatase family member (ipp-5)
Locus_17478_Transcript_1/1_Conf_1.000	149	20	1.90E-16	NP_509898.1	91	88.9669	49	45	ACOnitase family member (aco-1)
Locus_17479_Transcript_1/1_Conf_1.000	178	0							
Locus_1748_Transcript_1/1_Conf_1.000	1113	20	2.16E-05	XP_001897183.1	64	54.6842	62	40	HMG box family protein
Locus_17480_Transcript_1/1_Conf_1.000	407	3	2.28E-06	NP_001123076.1	48	55.4546	129	62	hypothetical protein ZC455.1
Locus_17481_Transcript_1/1_Conf_1.000	132	0							
Locus_17482_Transcript_1/1_Conf_1.000	260	0							
Locus_17483_Transcript_1/1_Conf_1.000	320	0							
Locus_17484_Transcript_1/1_Conf_1.000	452	6	1.48E-05	AAA74035.1	58	52.7582	70	41	CV-FLP-1A

Locus_17485_Transcript_1/1_Conf_1.000	429	20	4.67E-60	NP_493778.1	85	233.802	142	121	hypothetical protein K07E8.7
Locus_17486_Transcript_1/1_Conf_1.000	361	20	1.41E-24	NP_001033391.1	64	115.931	125	81	GLutaRedoXin family member (glrx-22)
Locus_17487_Transcript_1/1_Conf_1.000	514	20	2.90E-39	XP_002647238.1	71	164.851	171	123	Hypothetical protein CBG24582
Locus_17488_Transcript_1/1_Conf_1.000	144	0							
Locus_17489_Transcript_1/1_Conf_1.000	188	0							
Locus_1749_Transcript_1/2_Conf_1.000	1200	20	3.19E-74	XP_001894031.1	64	283.493	318	205	Protein kinase domain containing protein
Locus_1749_Transcript_2/2_Conf_1.000	1200	20	3.19E-74	XP_001894031.1	64	283.493	318	205	Protein kinase domain containing protein
Locus_17490_Transcript_1/1_Conf_1.000	664	0							
Locus_17491_Transcript_1/1_Conf_1.000	189	0							
Locus_17492_Transcript_1/1_Conf_1.000	448	20	2.60E-26	A8XZU0.2	63	121.709	147	93	Probable cytosolic Fe-S cluster assembly factor oxy-4
Locus_17493_Transcript_1/1_Conf_1.000	179	1	3.60E-04	NP_496205.2	61	48.1358	54	33	PhosphoLipase C family member (plc-3)
Locus_17494_Transcript_1/1_Conf_1.000	395	20	3.01E-22	NP_741496.2	71	108.227	97	69	hypothetical protein Y10G11A.1
Locus_17495_Transcript_1/1_Conf_1.000	396	6	4.34E-21	XP_002634643.1	61	104.375	129	79	C. briggsae CBR-GEI-9 protein
Locus_17496_Transcript_1/1_Conf_1.000	308	0							
Locus_17497_Transcript_1/1_Conf_1.000	286	20	9.43E-08	AAI24420.1	58	60.077	79	46	Dgcr8 protein
Locus_17498_Transcript_1/1_Conf_1.000	789	20	5.98E-37	NP_505460.1	67	158.688	161	109	hypothetical protein C50F4.12
Locus_17499_Transcript_1/1_Conf_1.000	427	3	1.74E-38	XP_002645893.1	76	162.155	142	108	Hypothetical protein CBG07646

Locus_175_Transcript_1/2_Conf_1.000	2404	20	4.16E-51	XP_002642145.1	41	207.994	898	370	C. briggsae CBR-EVL-14 protein
Locus_175_Transcript_2/2_Conf_1.000	2404	20	2.70E-50	XP_002642145.1	41	205.297	898	369	C. briggsae CBR-EVL-14 protein
Locus_1750_Transcript_1/1_Conf_1.000	1086	20	7.74E-77	NP_498713.3	71	291.967	271	195	hypothetical protein ZK688.9
Locus_17500_Transcript_1/1_Conf_1.000	137	0							
Locus_17501_Transcript_1/1_Conf_1.000	395	20	1.60E-23	EFO22018.1	82	112.464	74	61	hypothetical protein LOAG_06465
Locus_17502_Transcript_1/1_Conf_1.000	422	4	1.40E-11	XP_002632757.1	66	72.7886	72	48	C. briggsae CBR-EOR-1 protein
Locus_17503_Transcript_1/1_Conf_1.000	647	20	4.46E-65	XP_002646632.1	74	251.521	216	160	C. briggsae CBR-UNC-52 protein
Locus_17504_Transcript_1/1_Conf_1.000	238	0							
Locus_17505_Transcript_1/1_Conf_1.000	194	0							
Locus_17506_Transcript_1/1_Conf_1.000	306	0							
Locus_17507_Transcript_1/1_Conf_1.000	178	2	3.48E-07	NP_504750.2	81	58.151	58	47	hypothetical protein K11C4.2
Locus_17508_Transcript_1/1_Conf_1.000	236	0							
Locus_17509_Transcript_1/1_Conf_1.000	176	0							
Locus_1751_Transcript_1/1_Conf_1.000	1317	7	5.52E-22	CAB07693.3	65	110.153	119	78	C. elegans protein Y48E1B.7, partially confirmed by transcript evidence
Locus_17510_Transcript_1/1_Conf_1.000	315	4	7.93E-23	NP_505399.1	71	110.153	104	74	hypothetical protein ZK682.2
Locus_17511_Transcript_1/1_Conf_1.000	163	0							
Locus_17512_Transcript_1/1_Conf_1.000	256	20	9.10E-11	XP_001122011.1	57	70.0922	89	51	PREDICTED: similar to easter CG4920-PA
Locus_17513_Transcript_1/1_Conf_1.000	248	0							
Locus_17514_Transcript_1/1_Conf_1.000	191	0							
Locus_17515_Transcript_1/1_Conf_1.000	397	0							
Locus_17516_Transcript_1/1_Conf_1.000	250	0							
Locus_17517_Transcript_1/1_Conf_1.000	357	20	1.28E-25	XP_002630721.1	66	119.398	133	88	C. briggsae CBR-CLR-1 protein
Locus_17518_Transcript_1/1_Conf_1.000	480	0							

Locus_17519_Transcript_1/1_Conf_1.000	1301	2	6.61E-20	NP_505209.2	48	103.219	428	206	hypothetical protein F25G6.9
Locus_1752_Transcript_1/1_Conf_1.000	761	20	1.87E-93	CBW44400.1	74	346.28	280	208	C. elegans protein Y59A8B.22a, confirmed by transcript evidence
Locus_17520_Transcript_1/1_Conf_1.000	301								
Locus_17521_Transcript_1/1_Conf_1.000	394	0							
Locus_17522_Transcript_1/1_Conf_1.000	265	0							
Locus_17523_Transcript_1/1_Conf_1.000	131	0							
Locus_17524_Transcript_1/1_Conf_1.000	336	0							
Locus_17525_Transcript_1/1_Conf_1.000	518	3	1.39E-04	EEQ88268.1	42	49.6766	155	66	hypothetical protein BDCG_03388
Locus_17526_Transcript_1/1_Conf_1.000	1007	20	3.31E-63	EFO15384.1	68	246.514	240	165	hypothetical protein LOAG_13128
Locus_17527_Transcript_1/1_Conf_1.000	169	3	4.58E-15	NP_001033381.1	84	84.3445	52	44	hypothetical protein Y71H2AM.15
Locus_17528_Transcript_1/1_Conf_1.000	293	1	8.20E-04	NP_509315.1	72	46.9802	37	27	hypothetical protein ZK154.4
Locus_17529_Transcript_1/1_Conf_1.000	538	20	1.79E-16	NP_001022401.1	70	89.3521	98	69	Polarity and Osmotic sensitivity Defect family member (pod-2)
Locus_1753_Transcript_1/1_Conf_1.000	288	6	4.36E-05	XP_002433635.1	68	51.2174	45	31	protein tyrosine phosphatase, putative
Locus_17530_Transcript_1/1_Conf_1.000	563	0							
Locus_17531_Transcript_1/1_Conf_1.000	354	20	1.52E-26	XP_002631704.1	73	122.479	101	74	Hypothetical protein CBG20903
Locus_17532_Transcript_1/1_Conf_1.000	179	5	1.23E-20	EFO22429.1	93	102.834	59	55	hypothetical protein LOAG_06054
Locus_17533_Transcript_1/1_Conf_1.000	480	0							
Locus_17534_Transcript_1/1_Conf_1.000	403	3	8.71E-06	ACI49231.1	66	53.5286	50	33	hypothetical protein Csp3_JD05.016
Locus_17535_Transcript_1/1_Conf_1.000	829	20	9.66E-57	CAA91288.2	60	224.557	255	155	C. elegans protein K08F8.5b, partially confirmed by transcript evidence

Locus_17536_Transcript_1/1_Conf_1.000	266	20	1.29E-25	NP_502170.3	75	119.398	86	65	TWiK family of potassium channels family member (twk-25)
Locus_17537_Transcript_1/1_Conf_1.000	331	0							
Locus_17538_Transcript_1/1_Conf_1.000	143	0							
Locus_17539_Transcript_1/1_Conf_1.000	250	20	1.65E-41	CAV31771.1	96	172.17	83	80	C. elegans protein F25D7.3b, partially confirmed by transcript evidence
Locus_1754_Transcript_1/2_Conf_1.000	2556	20	0	NP_740776.1	87	1202.96	713	627	WW domain Protein (E3 ubiquitin ligase) family member (wwp-1)
Locus_1754_Transcript_2/2_Conf_1.000	2589	20	0	NP_740776.1	84	1228.39	800	677	WW domain Protein (E3 ubiquitin ligase) family member (wwp-1)
Locus_17540_Transcript_1/1_Conf_1.000	270	0							
Locus_17541_Transcript_1/1_Conf_1.000	427	0							
Locus_17542_Transcript_1/1_Conf_1.000	768	5	2.12E-76	CAR63603.1	95	289.656	169	161	putative somatostatin receptor
Locus_17543_Transcript_1/1_Conf_1.000	163	0							
Locus_17544_Transcript_1/1_Conf_1.000	134	20	2.77E-12	NP_741757.1	92	75.0998	42	39	Endophilin-Related Protein family member (erp-1)
Locus_17545_Transcript_1/1_Conf_1.000	324	0							
Locus_17546_Transcript_1/1_Conf_1.000	392	20	1.55E-23	XP_002637289.1	75	112.464	89	67	Hypothetical protein CBG18976
Locus_17547_Transcript_1/1_Conf_1.000	165	0							
Locus_17548_Transcript_1/1_Conf_1.000	308	20	1.96E-34	NP_491390.2	85	148.673	100	85	hypothetical protein D1007.15

Locus_17549_Transcript_1/1_Conf_1.000	493	20	1.55E-71	XP_002642701.1	92	271.937	162	150	C. briggsae CBR-GLY-3 protein
Locus_1755_Transcript_1/1_Conf_1.000	1189	20	4.53E-81	NP_495808.2	85	306.22	200	171	STCH (truncated HSP) family member (stc-1)
Locus_17550_Transcript_1/1_Conf_1.000	630	6	1.45E-49	NP_001021494.1	69	199.904	196	136	hypothetical protein F55A12.2
Locus_17551_Transcript_1/1_Conf_1.000	228	0							
Locus_17552_Transcript_1/1_Conf_1.000	241	15	2.19E-17	NP_001122650.1	69	92.0485	79	55	PaTChed family member (ptc-3)
Locus_17553_Transcript_1/1_Conf_1.000	432	20	3.05E-27	NP_001041274.2	69	124.79	134	93	hypothetical protein K11G12.6
Locus_17554_Transcript_1/1_Conf_1.000	184	20	2.83E-28	ABW22635.1	100	128.257	61	61	GABA receptor subunit
Locus_17555_Transcript_1/1_Conf_1.000	155	0							
Locus_17556_Transcript_1/1_Conf_1.000	308	0							
Locus_17557_Transcript_1/1_Conf_1.000	193	0							
Locus_17558_Transcript_1/1_Conf_1.000	371	0							
Locus_17559_Transcript_1/1_Conf_1.000	345	4	6.94E-11	NP_001122607.1	65	70.4774	79	52	NURF (nucleosome remodeling factor) complex homolog family member (nurf-1)
Locus_1756_Transcript_1/1_Conf_1.000	1250	20	9.00E-160	NP_493742.1	78	567.77	447	350	NucleOLar protein family member (nol-1)

Locus_17560_Transcript_1/1_Conf_1.000	267	2	3.77E-09	NP_491354.1	61	64.6994	97	60	AcetylCholine Receptor family member (acr-6)
Locus_17561_Transcript_1/1_Conf_1.000	414	13	1.27E-25	CAA21686.2	67	119.398	135	91	C. elegans protein Y54E2A.4, partially confirmed by transcript evidence
Locus_17562_Transcript_1/1_Conf_1.000	173	0							
Locus_17563_Transcript_1/1_Conf_1.000	156	0							
Locus_17564_Transcript_1/1_Conf_1.000	157	2	6.71E-06	NP_498385.2	64	53.9138	51	33	hypothetical protein C56G2.4
Locus_17565_Transcript_1/1_Conf_1.000	444	20	2.87E-49	XP_002643809.1	78	197.978	147	115	Hypothetical protein CBG02021
Locus_17566_Transcript_1/1_Conf_1.000	220	5	3.03E-14	NP_510542.2	72	81.6481	66	48	Temporarily Assigned Gene name family member (tag-97)
Locus_17567_Transcript_1/1_Conf_1.000	291	5	3.56E-07	XP_001895488.1	59	58.151	92	55	hypothetical protein
Locus_17568_Transcript_1/1_Conf_1.000	584	0							
Locus_17569_Transcript_1/1_Conf_1.000	326	0							
Locus_1757_Transcript_1/6_Conf_0.167	656	20	1.19E-36	AAV28323.2	58	157.147	173	102	Hypothetical protein T15B7.1
Locus_1757_Transcript_2/6_Conf_0.500	2537	20	0	NP_497786.2	91	1217.99	729	670	MethylMalonylCoA Mutase homolog family member (mmcm-1)
Locus_1757_Transcript_3/6_Conf_0.583	2181	20	0	XP_002647077.1	92	905.205	521	480	C. briggsae CBR-MMCM-1 protein
Locus_1757_Transcript_4/6_Conf_0.417	2523	20	0	NP_497786.2	91	1223.38	748	682	MethylMalonylCoA Mutase homolog family member (mmcm-1)
Locus_1757_Transcript_5/6_Conf_0.583	3076	20	0	NP_497786.2	91	1215.68	729	669	MethylMalonylCoA Mutase homolog family member (mmcm-1)
Locus_1757_Transcript_6/6_Conf_0.583	3076	20	0	NP_497786.2	91	1217.99	729	670	MethylMalonylCoA Mutase homolog family member (mmcm-1)

Locus_17570_Transcript_1/1_Conf_1.000	496	20	1.66E-41	NP_741237.1	89	172.17	105	94	CaLPain family member (clp-1)
Locus_17571_Transcript_1/1_Conf_1.000	212	0							
Locus_17572_Transcript_1/1_Conf_1.000	420	20	2.15E-20	XP_002640915.1	69	102.064	103	72	Hypothetical protein CBG00476
Locus_17573_Transcript_1/1_Conf_1.000	243	0							
Locus_17574_Transcript_1/1_Conf_1.000	165	20	6.86E-11	NP_510625.2	80	70.4774	50	40	hypothetical protein T27A8.1
Locus_17575_Transcript_1/1_Conf_1.000	214	0							
Locus_17576_Transcript_1/1_Conf_1.000	149	0							
Locus_17577_Transcript_1/1_Conf_1.000	212	0							
Locus_17578_Transcript_1/1_Conf_1.000	543	0							
Locus_17579_Transcript_1/1_Conf_1.000	313	0							
Locus_1758_Transcript_1/1_Conf_1.000	616	20	1.25E-50	EFO16392.1	86	203.371	123	107	VCP protein
Locus_17580_Transcript_1/1_Conf_1.000	197	20	2.81E-12	EFO28029.1	95	75.0998	43	41	AP-1 complex subunit mu-1
Locus_17581_Transcript_1/1_Conf_1.000	169	20	1.85E-24	ABS45067.1	96	115.546	56	54	latrophilin-like protein 2
Locus_17582_Transcript_1/1_Conf_1.000	171	3	1.73E-14	NP_498952.1	76	82.4185	56	43	hypothetical protein F44E2.4

Locus_17583_Transcript_1/1_Conf_1.000	191	20	8.74E-30	ADK36640.1	100	133.265	63	63	L-lactate dehydrogenase B chain
Locus_17584_Transcript_1/1_Conf_1.000	429	20	2.66E-47	CAQ48388.2	86	191.43	143	123	C. elegans protein C26H9A.1b, confirmed by transcript evidence
Locus_17585_Transcript_1/1_Conf_1.000	196	0							
Locus_17586_Transcript_1/1_Conf_1.000	281	20	3.84E-14	NP_494219.3	59	81.2629	114	68	hypothetical protein F54A3.2
Locus_17587_Transcript_1/1_Conf_1.000	933	20	1.61E-69	XP_002631319.1	64	267.314	328	213	Hypothetical protein CBG03141
Locus_17588_Transcript_1/1_Conf_1.000	1091	20	8.47E-124	XP_002632173.1	88	447.973	296	262	Hypothetical protein CBG07032
Locus_17589_Transcript_1/1_Conf_1.000	292	0							
Locus_1759_Transcript_1/3_Conf_0.400	362	20	8.27E-33	NP_498590.4	87	143.28	105	92	hypothetical protein R151.6
Locus_1759_Transcript_2/3_Conf_0.600	573	20	1.27E-32	NP_498590.4	87	143.28	105	92	hypothetical protein R151.6
Locus_1759_Transcript_3/3_Conf_0.600	802	20	2.68E-32	NP_498590.4	87	143.28	105	92	hypothetical protein R151.6
Locus_17590_Transcript_1/1_Conf_1.000	184	0							
Locus_17591_Transcript_1/1_Conf_1.000	316	0							

Locus_17592_Transcript_1/1_Conf_1.000	137	0							
Locus_17593_Transcript_1/1_Conf_1.000	353	0							
Locus_17594_Transcript_1/1_Conf_1.000	255	0							
Locus_17595_Transcript_1/1_Conf_1.000	147	0							
Locus_17596_Transcript_1/1_Conf_1.000	156	0							
Locus_17597_Transcript_1/1_Conf_1.000	325	20	3.42E-10	XP_001636049.1	64	68.1662	98	63	predicted protein
Locus_17598_Transcript_1/1_Conf_1.000	142	20	5.35E-08	YP_001328864.1	80	60.8474	46	37	tRNA modification GTPase TrmE
Locus_17599_Transcript_1/1_Conf_1.000	132	20	2.12E-12	XP_002641552.1	86	75.485	44	38	C. briggsae CBR-RBC-2 protein
Locus_176_Transcript_1/1_Conf_1.000	1563	20	1.49E-141	XP_002642495.1	75	507.679	460	345	C. briggsae CBR-MIG-22 protein
Locus_1760_Transcript_1/1_Conf_1.000	1196	20	2.70E-49	EFO26991.1	60	200.675	261	159	hypothetical protein LOAG_01487
Locus_17600_Transcript_1/1_Conf_1.000	151	0							
Locus_17601_Transcript_1/1_Conf_1.000	267	2	3.40E-18	NP_492624.2	82	94.7449	69	57	hypothetical protein F52F12.7
Locus_17602_Transcript_1/1_Conf_1.000	245	2	1.79E-11	XP_002641411.1	65	72.4034	83	54	Hypothetical protein CBG13276
Locus_17603_Transcript_1/1_Conf_1.000	990	20	3.49E-25	NP_508831.3	56	120.168	168	95	hypothetical protein T07F12.2
Locus_17604_Transcript_1/1_Conf_1.000	212	0							
Locus_17605_Transcript_1/1_Conf_1.000	222	0							

Locus_17606_Transcript_1/1_Conf_1.000	150	6	4.37E-13	NP_001033327.1	84	77.7962	45	38	CAN cell Migration defective family member (cam-1)
Locus_17607_Transcript_1/1_Conf_1.000	489	20	4.61E-07	NP_492328.1	51	57.7658	122	63	yeast Enhancer of DeCapping homolog family member (edc-3)
Locus_17608_Transcript_1/1_Conf_1.000	400	20	1.47E-61	NP_506145.1	94	238.81	131	124	hypothetical protein E02A10.1
Locus_17609_Transcript_1/1_Conf_1.000	245	0							
Locus_1761_Transcript_1/1_Conf_1.000	781	0							
Locus_17610_Transcript_1/1_Conf_1.000	292	0							
Locus_17611_Transcript_1/1_Conf_1.000	286	0							
Locus_17612_Transcript_1/1_Conf_1.000	558								
Locus_17613_Transcript_1/1_Conf_1.000	340	20	2.74E-20	CAA91288.2	62	101.679	101	63	C. elegans protein K08F8.5b, partially confirmed by transcript evidence
Locus_17614_Transcript_1/1_Conf_1.000	265	1	6.24E-12	CAR63599.1	69	73.9442	65	45	hypothetical protein
Locus_17615_Transcript_1/1_Conf_1.000	132	0							
Locus_17616_Transcript_1/1_Conf_1.000	178	0							
Locus_17617_Transcript_1/1_Conf_1.000	278	0							
Locus_17618_Transcript_1/1_Conf_1.000	184	0							
Locus_17619_Transcript_1/1_Conf_1.000	467	1	8.46E-09	XP_002635121.1	42	63.5438	173	74	Hypothetical protein CBG11345
Locus_1762_Transcript_1/4_Conf_0.700	1967	1	2.36E-09	XP_002640249.1	35	68.9366	403	145	C. briggsae CBR-PQN-20 protein
Locus_1762_Transcript_2/4_Conf_0.700	1943	1	2.33E-09	XP_002640249.1	35	68.9366	403	145	C. briggsae CBR-PQN-20 protein
Locus_1762_Transcript_3/4_Conf_0.700	1943	1	2.33E-09	XP_002640249.1	35	68.9366	403	145	C. briggsae CBR-PQN-20 protein
Locus_1762_Transcript_4/4_Conf_0.700	1943	1	2.33E-09	XP_002640249.1	35	68.9366	403	145	C. briggsae CBR-PQN-20 protein
Locus_17620_Transcript_1/1_Conf_1.000	528	20	7.43E-52	AAN61521.1	70	206.838	175	124	301KDa_2 protein

Locus_17621_Transcript_1/1_Conf_1.000	140	20	8.83E-19	XP_002832350.1	100	96.6709	46	46	PREDICTED: LOW QUALITY PROTEIN: filamin-A-like
Locus_17622_Transcript_1/1_Conf_1.000	336	20	2.92E-38	NP_494753.3	87	161.384	97	85	hypothetical protein C01F1.6
Locus_17623_Transcript_1/1_Conf_1.000	216	0							
Locus_17624_Transcript_1/1_Conf_1.000	415	20	8.78E-35	AAN11401.1	71	149.828	127	91	metalloprotease 1 precursor
Locus_17625_Transcript_1/1_Conf_1.000	474	20	2.41E-32	XP_002634336.1	64	141.739	154	99	C. briggsae CBR-KLP-10 protein
Locus_17626_Transcript_1/1_Conf_1.000	168	2	4.01E-11	XP_002636973.1	72	71.2478	55	40	Hypothetical protein CBG09454

Locus_17627_Transcript_1/1_Conf_1.000	298	20	2.06E-31	EFO21606.1	81	138.658	99	81	PDZ-domain-containing protein scribble
Locus_17628_Transcript_1/1_Conf_1.000	345	0							
Locus_17629_Transcript_1/1_Conf_1.000	153	0							
Locus_1763_Transcript_1/1_Conf_1.000	844	4	1.37E-21	NP_508166.1	49	107.842	259	129	ImmunoGlobulin-like Cell adhesion Molecule family member (igcm-1)
Locus_17630_Transcript_1/1_Conf_1.000	400	20	1.21E-23	XP_002637712.1	63	112.849	133	84	C. briggsae CBR-RAP-2 protein
Locus_17631_Transcript_1/1_Conf_1.000	154	0							
Locus_17632_Transcript_1/1_Conf_1.000	301	20	7.06E-24	NP_001122600.1	84	113.62	76	64	Multiple PDZ domain protein family member (mpz-1)
Locus_17633_Transcript_1/1_Conf_1.000	655	0							
Locus_17634_Transcript_1/1_Conf_1.000	241	20	4.42E-18	NP_499704.1	73	94.3597	80	59	CYtochrome P450 family member (cyp-13A11)
Locus_17635_Transcript_1/1_Conf_1.000	262	0							

Locus_17636_Transcript_1/1_Conf_1.000	275	20	4.86E-33	NP_492476.1	85	144.05	91	78	hypothetical protein F14B4.3
Locus_17637_Transcript_1/1_Conf_1.000	141	0							
Locus_17638_Transcript_1/1_Conf_1.000	150	0							
Locus_17639_Transcript_1/1_Conf_1.000	454	4	2.59E-18	EFO26050.1	59	95.1301	131	78	PEK/PEK protein kinase
Locus_1764_Transcript_1/1_Conf_1.000	1018	20	3.49E-60	XP_002642911.1	66	236.498	317	211	Hypothetical protein CBG15186
Locus_17640_Transcript_1/1_Conf_1.000	189	20	2.46E-24	XP_001896329.1	96	115.161	62	60	calcium ATPase
Locus_17641_Transcript_1/1_Conf_1.000	172	20	2.27E-14	P00736.2	100	82.0333	36	36	Complement C1r subcomponent
Locus_17642_Transcript_1/1_Conf_1.000	681	6	1.26E-15	CAN99691.2	49	87.4261	206	101	C. elegans protein F54B3.1b, partially confirmed by transcript evidence
Locus_17643_Transcript_1/1_Conf_1.000	193	2	7.18E-08	NP_495415.2	72	60.4622	44	32	Acid SphingoMyelinase family member (asm-1)
Locus_17644_Transcript_1/1_Conf_1.000	324	20	4.44E-26	XP_002639976.1	73	120.939	109	80	C. briggsae CBR-KIN-32 protein
Locus_17645_Transcript_1/1_Conf_1.000	150	3	3.02E-14	CAA86821.1	87	81.6481	49	43	excretory/secretory antigen
Locus_17646_Transcript_1/1_Conf_1.000	129	8	8.63E-14	NP_001020988.1	93	80.1073	43	40	UNCoordinated family member (unc-89)
Locus_17647_Transcript_1/1_Conf_1.000	163	4	2.71E-07	XP_002640991.1	84	58.5362	53	45	Hypothetical protein CBG11740
Locus_17648_Transcript_1/1_Conf_1.000	153	0							
Locus_17649_Transcript_1/1_Conf_1.000	229	0							
Locus_1765_Transcript_1/1_Conf_1.000	375	20	2.89E-17	NP_001094784.1	100	91.6633	65	65	transmembrane protein 176B isoform b
Locus_17650_Transcript_1/1_Conf_1.000	239	0							
Locus_17651_Transcript_1/1_Conf_1.000	423	7	6.24E-12	EFO21962.1	63	73.9442	91	58	TK/EGFR protein kinase

Locus_17652_Transcript_1/1_Conf_1.000	159	20	1.14E-21	XP_001118006.2	100	106.301	52	52	PREDICTED: elongation factor 2
Locus_17653_Transcript_1/1_Conf_1.000	520	3	1.19E-51	NP_501400.1	90	206.068	174	158	hypothetical protein F35H10.10
Locus_17654_Transcript_1/1_Conf_1.000	131	0							
Locus_17655_Transcript_1/1_Conf_1.000	391	0							
Locus_17656_Transcript_1/1_Conf_1.000	373	20	3.65E-36	XP_002634229.1	77	154.451	123	95	C. briggsae CBR-UNC-26 protein
Locus_17657_Transcript_1/1_Conf_1.000	720	20	1.25E-88	XP_002636978.1	88	330.102	238	211	Hypothetical protein CBG09461
Locus_17658_Transcript_1/1_Conf_1.000	361	0							
Locus_17659_Transcript_1/1_Conf_1.000	830	20	1.30E-61	XP_002631397.1	70	240.736	249	176	C. briggsae CBR-DEP-1 protein
Locus_1766_Transcript_1/1_Conf_1.000	435	2	1.84E-24	NP_499357.2	73	115.546	94	69	hypothetical protein Y39A1A.20
Locus_17660_Transcript_1/1_Conf_1.000	427	0							
Locus_17661_Transcript_1/1_Conf_1.000	140	0							
Locus_17662_Transcript_1/1_Conf_1.000	220	0							
Locus_17663_Transcript_1/1_Conf_1.000	321	0							
Locus_17664_Transcript_1/1_Conf_1.000	778	20	1.32E-73	XP_002647977.1	69	280.411	265	183	Hypothetical protein CBG23894
Locus_17665_Transcript_1/1_Conf_1.000	596	20	2.85E-86	XP_002641537.1	92	321.627	182	169	Hypothetical protein CBG09836
Locus_17666_Transcript_1/1_Conf_1.000	1766	1	3.42E-04	YP_003834.1	57	51.6026	88	51	unknown
Locus_17667_Transcript_1/1_Conf_1.000	191	1	8.78E-14	NP_494276.2	78	80.1073	64	50	Variable ABnormal morphology family member (vab-19)

Locus_17668_Transcript_1/1_Conf_1.000	293	11	8.43E-25	EFO27980.1	76	116.701	97	74	hypothetical protein LOAG_00505
Locus_17669_Transcript_1/1_Conf_1.000	209	20	2.12E-20	XP_002630579.1	91	102.064	69	63	C. briggsae CBR-NHX-2 protein
Locus_1767_Transcript_1/2_Conf_1.000	1257	20	1.88E-40	XP_001366252.1	64	171.4	207	134	PREDICTED: similar to Ubiquitin specific peptidase 3
Locus_1767_Transcript_2/2_Conf_1.000	1018	20	8.62E-51	XP_002110506.1	62	205.297	258	161	hypothetical protein TRIADDRAFT_22897
Locus_17670_Transcript_1/1_Conf_1.000	214	0							
Locus_17671_Transcript_1/1_Conf_1.000	260	0							
Locus_17672_Transcript_1/2_Conf_1.000	565	20	9.83E-51	EFO22315.1	75	203.371	176	133	hypothetical protein LOAG_06169
Locus_17672_Transcript_2/2_Conf_1.000	402	20	1.99E-34	XP_002639921.1	71	148.673	131	94	Hypothetical protein CBG08253
Locus_17673_Transcript_1/1_Conf_1.000	438	0							
Locus_17674_Transcript_1/1_Conf_1.000	333	20	3.24E-45	EFO17249.1	92	184.496	106	98	RNA polymerase II

Locus_17675_Transcript_1/1_Conf_1.000	604	20	8.31E-113	XP_002639744.1	91	409.838	199	183	C. briggsae CBR-LAM-3 protein
Locus_17676_Transcript_1/1_Conf_1.000	742	20	5.57E-103	NP_491257.1	88	377.867	241	214	FK506-Binding protein family member (fkb-5)
Locus_17677_Transcript_1/1_Conf_1.000	177	20	1.19E-23	AAC27893.1	93	112.849	58	54	ornithine decarboxylase
Locus_17678_Transcript_1/1_Conf_1.000	170	20	3.74E-25	XP_002922306.1	100	117.857	56	56	PREDICTED: triosephosphate isomerase-like, partial
Locus_17679_Transcript_1/1_Conf_1.000	461	20	1.19E-15	XP_869306.2	73	86.2705	76	56	PREDICTED: hypothetical protein isoform 1
Locus_1768_Transcript_10/12_Conf_0.588	1767	20	3.07E-154	XP_001897032.1	99	550.051	288	286	polyubiquitin precursor
Locus_1768_Transcript_11/12_Conf_0.559	1767	20	3.07E-154	XP_001897032.1	99	550.051	288	286	polyubiquitin precursor
Locus_1768_Transcript_12/12_Conf_0.588	1767	20	3.07E-154	XP_001897032.1	99	550.051	288	286	polyubiquitin precursor

Locus_1768_Transcript_3/12_Conf_0.353	957	20	1.29E-154	XP_001897032.1	99	550.051	288	286	polyubiquitin precursor
Locus_1768_Transcript_4/12_Conf_0.324	915	20	3.86E-153	XP_001897032.1	99	545.043	285	283	polyubiquitin precursor
Locus_1768_Transcript_5/12_Conf_0.471	1298	20	3.73E-140	XP_001897032.1	99	502.671	264	262	polyubiquitin precursor
Locus_1768_Transcript_6/12_Conf_0.500	1343	20	2.14E-154	XP_001897032.1	99	550.051	288	286	polyubiquitin precursor
Locus_1768_Transcript_7/12_Conf_0.500	1343	20	3.92E-140	XP_001897032.1	99	502.671	264	262	polyubiquitin precursor
Locus_1768_Transcript_8/12_Conf_0.235	818	20	2.50E-134	XP_001897032.1	99	482.256	253	251	polyubiquitin precursor
Locus_1768_Transcript_9/12_Conf_0.088	349	20	1.29E-57	EFO21508.1	100	225.713	116	116	ubiquitin C II
Locus_17680_Transcript_1/1_Conf_1.000	298	20	2.06E-23	XP_002633309.1	76	112.079	98	75	Hypothetical protein CBG06044
Locus_17681_Transcript_1/1_Conf_1.000	241	0							

Locus_17682_Transcript_1/1_Conf_1.000	371	20	7.20E-08	XP_002818294.1	98	60.4622	75	74	PREDICTED: collagen alpha-2(I) chain-like
Locus_17683_Transcript_1/1_Conf_1.000	887	4	2.13E-36	XP_001901821.1	52	157.147	310	163	hypothetical protein Bm1_51765
Locus_17684_Transcript_1/2_Conf_1.000	526	2	9.18E-55	XP_002633375.1	71	216.468	172	123	Hypothetical protein CBG06123
Locus_17684_Transcript_2/2_Conf_1.000	357	2	1.46E-37	XP_002633375.1	74	159.073	116	86	Hypothetical protein CBG06123
Locus_17685_Transcript_1/1_Conf_1.000	214	20	1.41E-24	XP_002631304.1	91	115.931	71	65	Hypothetical protein CBG03118
Locus_17686_Transcript_1/1_Conf_1.000	615	0							
Locus_17687_Transcript_1/1_Conf_1.000	249	1	1.19E-15	AAT07449.1	78	86.2705	61	48	putative protein
Locus_17688_Transcript_1/1_Conf_1.000	396	0							
Locus_17689_Transcript_1/1_Conf_1.000	313	20	3.45E-26	XP_002637058.1	74	121.324	104	77	C. briggsae CBR-TTR-19 protein
Locus_1769_Transcript_1/2_Conf_1.000	231	0							
Locus_1769_Transcript_2/2_Conf_1.000	257	0							
Locus_17690_Transcript_1/1_Conf_1.000	223	0							
Locus_17691_Transcript_1/2_Conf_1.000	249	0							
Locus_17691_Transcript_2/2_Conf_1.000	250	0							
Locus_17692_Transcript_1/1_Conf_1.000	550	20	2.19E-44	XP_002637648.1	64	182.185	182	118	C. briggsae CBR-FSHR-1 protein
Locus_17693_Transcript_1/1_Conf_1.000	156	0							
Locus_17694_Transcript_1/1_Conf_1.000	832	20	8.14E-96	XP_002634173.1	79	354.369	275	219	C. briggsae CBR-HOE-1 protein
Locus_17695_Transcript_1/1_Conf_1.000	853	20	1.40E-130	NP_497814.3	88	469.929	281	250	UNCoordinated family member (unc-79)
Locus_17696_Transcript_1/1_Conf_1.000	291	2	4.06E-11	EFO26621.1	51	71.2478	96	49	AIDA-1b
Locus_17697_Transcript_1/1_Conf_1.000	159	20	3.55E-07	XP_002414302.1	82	58.151	40	33	multidrug resistance protein, putative
Locus_17698_Transcript_1/1_Conf_1.000	137	0							

Locus_17699_Transcript_1/1_Conf_1.000	965	20	3.60E-96	NP_001021501.1	77	355.91	292	227	UNCoordinated family member (unc-73)
Locus_177_Transcript_1/1_Conf_1.000	1587	20	4.84E-180	NP_506706.1	80	635.565	490	394	yeast MCM (licensing factor) related family member (mcm-3)
Locus_1770_Transcript_1/1_Conf_1.000	3320	20	0	NP_494782.1	64	870.537	1102	716	hypothetical protein ZK430.1
Locus_17700_Transcript_1/1_Conf_1.000	189	0							
Locus_17701_Transcript_1/1_Conf_1.000	189	20	2.38E-27	XP_002638537.1	96	125.176	62	60	Hypothetical protein CBG05572
Locus_17702_Transcript_1/1_Conf_1.000	408	1	2.51E-05	XP_002639683.1	71	51.9878	38	27	C. briggsae CBR-GEI-11 protein
Locus_17703_Transcript_1/1_Conf_1.000	329	0							
Locus_17704_Transcript_1/1_Conf_1.000	377	9	6.20E-36	XP_002638473.1	80	153.68	124	100	Hypothetical protein CBG12901
Locus_17705_Transcript_1/1_Conf_1.000	562	3	6.32E-18	NP_510840.2	74	94.3597	79	59	hypothetical protein F31A3.5
Locus_17706_Transcript_1/1_Conf_1.000	237	0							
Locus_17707_Transcript_1/1_Conf_1.000	426	0							
Locus_17708_Transcript_1/1_Conf_1.000	172	20	1.16E-26	XP_002834627.1	100	122.865	57	57	PREDICTED: collagen alpha-2(VI) chain-like, partial
Locus_17709_Transcript_1/1_Conf_1.000	661	20	1.06E-101	XP_002647328.1	91	373.244	219	200	C. briggsae CBR-EGL-8 protein

Locus_1771_Transcript_1/1_Conf_1.000	329	0							
Locus_17710_Transcript_1/2_Conf_1.000	356	20	1.58E-15	ADD13547.1	77	85.8853	67	52	Inositol triphosphate receptor protein 1, isoform h
Locus_17710_Transcript_2/2_Conf_1.000	250	0							
Locus_17711_Transcript_1/1_Conf_1.000	151	3	3.83E-09	XP_002637315.1	84	64.6994	50	42	Hypothetical protein CBG19004
Locus_17712_Transcript_1/2_Conf_1.000	553	2	1.57E-05	XP_002642641.1	46	53.1434	158	74	C. briggsae CBR-LIN-13 protein
Locus_17712_Transcript_2/2_Conf_1.000	547	2	1.51E-05	XP_002642641.1	46	53.1434	158	74	C. briggsae CBR-LIN-13 protein
Locus_17713_Transcript_1/1_Conf_1.000	204	20	5.41E-16	ZP_03131362.1	91	87.4261	46	42	protein of unknown function DUF255
Locus_17714_Transcript_1/1_Conf_1.000	771	20	1.25E-100	XP_002631092.1	83	370.163	253	210	Hypothetical protein CBG02865
Locus_17715_Transcript_1/1_Conf_1.000	223	0							
Locus_17716_Transcript_1/1_Conf_1.000	510	20	1.54E-77	XP_001897606.1	89	291.967	169	151	Adaptin or adaptin-related protein protein 7
Locus_17717_Transcript_1/1_Conf_1.000	200	0							

Locus_17718_Transcript_1/1_Conf_1.000	159	0							
Locus_17719_Transcript_1/1_Conf_1.000	269	16	2.88E-17	XP_002634836.1	65	91.6633	89	58	C. briggsae CBR-JTR-1 protein
Locus_1772_Transcript_1/1_Conf_1.000	1975	20	1.59E-138	XP_002643974.1	71	498.049	481	344	Hypothetical protein CBG17350
Locus_17720_Transcript_1/1_Conf_1.000	246	20	5.00E-30	EFO23722.1	92	134.035	81	75	hypothetical protein LOAG_04763
Locus_17721_Transcript_1/1_Conf_1.000	442	20	2.20E-65	XP_002643286.1	84	251.521	146	124	Hypothetical protein CBG08162
Locus_17722_Transcript_1/1_Conf_1.000	319	0							
Locus_17723_Transcript_1/1_Conf_1.000	186	0							
Locus_17724_Transcript_1/1_Conf_1.000	234	20	2.68E-39	ACZ64268.1	93	164.851	77	72	astacin metalloprotease a
Locus_17725_Transcript_1/1_Conf_1.000	280	0							
Locus_17726_Transcript_1/1_Conf_1.000	423	4	4.92E-25	NP_501044.1	81	117.472	69	56	hypothetical protein C17H12.11
Locus_17727_Transcript_1/1_Conf_1.000	167	0							
Locus_17728_Transcript_1/1_Conf_1.000	1300	5	6.73E-73	XP_001901141.1	57	279.256	375	216	hypothetical protein Bm1_48395
Locus_17729_Transcript_1/1_Conf_1.000	492	20	1.20E-23	AAK31527.3	67	112.849	139	94	Neuronal symmetry protein 1, partially confirmed by transcript evidence
Locus_1773_Transcript_1/1_Conf_1.000	771	20	5.51E-40	NP_001122441.1	60	168.703	230	138	hypothetical protein F02E9.10
Locus_17730_Transcript_1/1_Conf_1.000	540	20	2.16E-17	XP_002631113.1	55	92.4337	158	88	C. briggsae CBR-ARS-1 protein
Locus_17731_Transcript_1/1_Conf_1.000	330	5	1.86E-16	NP_001122928.1	90	88.9669	54	49	hypothetical protein F23H12.3
Locus_17732_Transcript_1/1_Conf_1.000	153	0							
Locus_17733_Transcript_1/1_Conf_1.000	216	0							
Locus_17734_Transcript_1/1_Conf_1.000	272	20	4.01E-19	XP_001897385.1	70	97.8265	91	64	hypothetical protein Bm1_29715
Locus_17735_Transcript_1/1_Conf_1.000	160	1	4.79E-04	XP_001893275.1	70	47.7506	48	34	LMBR1-like conserved region family protein
Locus_17736_Transcript_1/1_Conf_1.000	258	0							
Locus_17737_Transcript_1/1_Conf_1.000	359	0							
Locus_17738_Transcript_1/1_Conf_1.000	374	0							
Locus_17739_Transcript_1/1_Conf_1.000	145	0							
Locus_1774_Transcript_1/1_Conf_1.000	988	20	3.94E-45	ADN00783.1	100	186.422	96	96	collagen protein

Locus_17740_Transcript_1/1_Conf_1.000	506	20	3.40E-29	NP_492763.1	62	131.339	136	85	hypothetical protein F25H2.7
Locus_17741_Transcript_1/1_Conf_1.000	447	20	3.09E-11	XP_002600120.1	54	71.633	147	80	hypothetical protein BRAFLDRAFT_118238
Locus_17742_Transcript_1/1_Conf_1.000	194	0							
Locus_17743_Transcript_1/1_Conf_1.000	254	20	4.37E-21	NP_001129835.1	96	104.375	78	75	Novel Channel type/putative Nematode CAlcium channel family member (nca-2)
Locus_17744_Transcript_1/1_Conf_1.000	234	0							
Locus_17745_Transcript_1/1_Conf_1.000	150	0							
Locus_17746_Transcript_1/1_Conf_1.000	381								
Locus_17747_Transcript_1/1_Conf_1.000	256	20	1.83E-19	NP_001024053.1	86	98.9821	60	52	UNCoordinated family member (unc-70)
Locus_17748_Transcript_1/1_Conf_1.000	310	20	4.54E-07	YP_001701724.1	51	57.7658	101	52	hypothetical protein MAB_0978
Locus_17749_Transcript_1/1_Conf_1.000	220	0							
Locus_1775_Transcript_1/1_Conf_1.000	1334	20	1.49E-115	XP_002641312.1	85	421.009	288	245	C. briggsae CBR-UNC-50 protein
Locus_17750_Transcript_1/1_Conf_1.000	343	0							
Locus_17751_Transcript_1/1_Conf_1.000	180	0							

Locus_17752_Transcript_1/1_Conf_1.000	331	20	1.02E-14	AAC28140.1	59	59.6918	69	41	mariner transposase
Locus_17753_Transcript_1/1_Conf_1.000	307	2	6.59E-06	NP_499757.2	71	53.9138	38	27	hypothetical protein T03F6.4
Locus_17754_Transcript_1/1_Conf_1.000	194	0							
Locus_17755_Transcript_1/1_Conf_1.000	301	0							
Locus_17756_Transcript_1/1_Conf_1.000	219	2	5.16E-22	NP_001024385.1	85	107.457	68	58	hypothetical protein C09F12.3
Locus_17757_Transcript_1/1_Conf_1.000	576	0							
Locus_17758_Transcript_1/1_Conf_1.000	369	20	3.56E-23	XP_002634520.1	66	111.309	99	66	Hypothetical protein CBG08313
Locus_17759_Transcript_1/1_Conf_1.000	270	0							
Locus_1776_Transcript_1/1_Conf_1.000	532	1	5.89E-04	NP_999656.1	61	47.7506	65	40	kinesin-like protein KIF15
Locus_17760_Transcript_1/1_Conf_1.000	449	5	7.12E-08	ABB53347.1	52	60.4622	97	51	secreted protein 5 precursor
Locus_17761_Transcript_1/1_Conf_1.000	249	0							
Locus_17762_Transcript_1/1_Conf_1.000	402	20	3.99E-51	XP_002914026.1	100	204.142	117	117	PREDICTED: polyadenylate-binding protein 1-like
Locus_17763_Transcript_1/1_Conf_1.000	287	0							
Locus_17764_Transcript_1/1_Conf_1.000	441	20	2.53E-37	NP_505424.2	82	158.303	102	84	TransThyretin-Related family domain family member (ttr-40)
Locus_17765_Transcript_1/1_Conf_1.000	239	2	8.67E-06	ADM53755.1	55	53.5286	74	41	Hypothetical protein ZK1127.13

Locus_17766_Transcript_1/1_Conf_1.000	550	20	2.50E-48	ACD47109.1	93	195.282	126	118	profilin
Locus_17767_Transcript_1/2_Conf_1.000	415	20	7.41E-42	ACK57928.1	78	173.326	133	105	microsomal aminopeptidase H11
Locus_17767_Transcript_2/2_Conf_1.000	546	20	1.81E-59	AAV68383.1	81	232.261	181	148	antigen h11
Locus_17768_Transcript_1/1_Conf_1.000	307	20	4.36E-50	XP_002825166.1	100	200.675	100	100	PREDICTED: cytoplasmic dynein 1 heavy chain 1-like, partial
Locus_17769_Transcript_1/1_Conf_1.000	175	0							
Locus_1777_Transcript_1/2_Conf_1.000	1187	20	2.61E-121	NP_497799.1	94	439.884	242	228	MuSashI (fly neural) family member (msi-1)
Locus_1777_Transcript_2/2_Conf_1.000	1188	20	2.62E-121	NP_497799.1	94	439.884	242	228	MuSashI (fly neural) family member (msi-1)
Locus_17770_Transcript_1/1_Conf_1.000	141	0							
Locus_17771_Transcript_1/1_Conf_1.000	712	0							
Locus_17772_Transcript_1/1_Conf_1.000	633	3	2.99E-10	XP_002637670.1	65	69.3218	67	44	C. briggsae CBR-RDE-1 protein
Locus_17773_Transcript_1/1_Conf_1.000	1214	4	1.10E-106	NP_501362.2	76	391.349	357	272	hypothetical protein F42G8.5

Locus_17774_Transcript_1/1_Conf_1.000	213	3	1.56E-07	NP_491050.3	56	59.3066	74	42	InTestinal Neurexin-like family member (itx-1)
Locus_17775_Transcript_1/1_Conf_1.000	159	0							
Locus_17776_Transcript_1/1_Conf_1.000	188	20	8.21E-28	NP_496814.1	98	126.716	62	61	Member of AAA family binding CED-4 family member (mac-1)
Locus_17777_Transcript_1/1_Conf_1.000	621	20	3.77E-63	XP_002644784.1	73	244.973	194	142	Hypothetical protein CBG14799
Locus_17778_Transcript_1/1_Conf_1.000	445	1	8.19E-04	XP_002635917.1	56	46.9802	69	39	Hypothetical protein CBG01142
Locus_17779_Transcript_1/1_Conf_1.000	391	0							
Locus_1778_Transcript_1/1_Conf_1.000	524	20	2.62E-38	EFO22634.1	91	161.77	95	87	fibronectin type III domain-containing protein
Locus_17780_Transcript_1/1_Conf_1.000	205	0							
Locus_17781_Transcript_1/1_Conf_1.000	173	0							
Locus_17782_Transcript_1/1_Conf_1.000	924	14	2.38E-33	NP_500590.2	53	147.132	291	155	hypothetical protein F28E10.4
Locus_17783_Transcript_1/1_Conf_1.000	636	20	3.75E-77	NP_490992.2	79	291.582	211	168	hypothetical protein Y23H5B.4
Locus_17784_Transcript_1/1_Conf_1.000	691	20	4.08E-86	XP_002644575.1	85	321.627	204	175	Hypothetical protein CBG14518
Locus_17785_Transcript_1/1_Conf_1.000	483	20	5.10E-38	XP_001896380.1	76	160.614	164	125	XAP5 protein
Locus_17786_Transcript_1/1_Conf_1.000	200	0							
Locus_17787_Transcript_1/1_Conf_1.000	308	0							
Locus_17788_Transcript_1/1_Conf_1.000	277	4	1.37E-11	XP_001900186.1	62	72.7886	94	59	hypothetical protein
Locus_17789_Transcript_1/1_Conf_1.000	238	0							
Locus_1779_Transcript_1/1_Conf_1.000	274	4	8.91E-11	NP_492777.1	70	70.0922	71	50	hypothetical protein C43H8.2
Locus_17790_Transcript_1/1_Conf_1.000	166	0							
Locus_17791_Transcript_1/1_Conf_1.000	444	20	1.17E-26	XP_002640105.1	63	122.865	149	95	C. briggsae CBR-MUT-2 protein
Locus_17792_Transcript_1/1_Conf_1.000	340	20	2.91E-38	NP_497918.1	81	161.384	112	91	UDP-GlucuronosylTransferase family member (ugt-62)
Locus_17793_Transcript_1/1_Conf_1.000	488	20	4.44E-42	NP_502445.1	71	174.096	160	114	hypothetical protein M02B1.3

Locus_17794_Transcript_1/1_Conf_1.000	310	20	3.80E-46	XP_002643972.1	95	187.578	103	98	C. briggsae CBR-SLO-2 protein
Locus_17795_Transcript_1/1_Conf_1.000	178	20	5.53E-21	NP_502367.2	89	103.99	59	53	hypothetical protein F28D1.9
Locus_17796_Transcript_1/1_Conf_1.000	213	1	5.03E-06	NP_505001.1	64	54.299	64	41	hypothetical protein T05B11.1
Locus_17797_Transcript_1/1_Conf_1.000	469	20	9.28E-16	XP_002129449.1	50	86.6557	160	80	PREDICTED: hypothetical protein
Locus_17798_Transcript_1/1_Conf_1.000	399	20	1.02E-46	NP_497261.2	88	189.504	114	101	SyNapTotagmin family member (snt-2)
Locus_17799_Transcript_1/1_Conf_1.000	289	9	2.82E-12	EFO27735.1	58	75.0998	97	57	leucine Rich Repeat family protein
Locus_178_Transcript_1/2_Conf_1.000	1557	20	0	NP_491955.1	94	790.801	437	414	hypothetical protein K02F2.2

Locus_178_Transcript_2/2_Conf_1.000	1557	20	0	NP_491955.1	94	790.801	437	414	hypothetical protein K02F2.2
Locus_1780_Transcript_1/1_Conf_1.000	1590	20	3.63E-26	XP_002130953.1	44	124.405	547	241	PREDICTED: similar to chromosome 10 open reading frame 119
Locus_17800_Transcript_1/1_Conf_1.000	240	0							
Locus_17801_Transcript_1/1_Conf_1.000	247	9	3.25E-21	NP_871810.1	92	104.76	56	52	HAlF transporter (PGP related) family member (haf-9)
Locus_17802_Transcript_1/1_Conf_1.000	170	0							
Locus_17803_Transcript_1/1_Conf_1.000	419	14	1.45E-16	NP_510686.4	61	89.3521	112	69	hypothetical protein F59C12.3
Locus_17804_Transcript_1/1_Conf_1.000	341	20	4.32E-58	XP_002760341.1	100	227.254	110	110	PREDICTED: glutamine synthetase
Locus_17805_Transcript_1/1_Conf_1.000	353	5	8.68E-22	XP_002631039.1	73	106.686	82	60	Hypothetical protein CBG02799
Locus_17806_Transcript_1/2_Conf_1.000	334	20	5.19E-27	AAN11401.1	69	124.02	108	75	metalloprotease 1 precursor
Locus_17806_Transcript_2/2_Conf_1.000	352	20	1.25E-28	AAN11401.1	68	129.413	114	78	metalloprotease 1 precursor
Locus_17807_Transcript_1/1_Conf_1.000	691	0							
Locus_17808_Transcript_1/1_Conf_1.000	912	2	1.97E-32	CAR63629.1	57	144.05	259	150	hypothetical protein
Locus_17809_Transcript_1/1_Conf_1.000	426	20	2.87E-25	NP_872207.1	61	118.242	150	92	hypothetical protein Y69H2.14
Locus_1781_Transcript_1/1_Conf_1.000	230	0							

Locus_17810_Transcript_1/1_Conf_1.000	323	20	1.29E-41	EFO20030.1	89	172.555	107	96	toll and interleukin 1 receptor domain-containing protein isoform f
Locus_17811_Transcript_1/2_Conf_1.000	327	20	5.23E-27	XP_002640811.1	71	124.02	108	77	Hypothetical protein CBG15695
Locus_17811_Transcript_2/2_Conf_1.000	327	20	5.23E-27	XP_002640811.1	71	124.02	108	77	Hypothetical protein CBG15695
Locus_17812_Transcript_1/1_Conf_1.000	137	0							
Locus_17813_Transcript_1/1_Conf_1.000	162	0							
Locus_17814_Transcript_1/1_Conf_1.000	224	0							
Locus_17815_Transcript_1/1_Conf_1.000	318	0							
Locus_17816_Transcript_1/1_Conf_1.000	527	0							
Locus_17817_Transcript_1/1_Conf_1.000	304	0							
Locus_17818_Transcript_1/1_Conf_1.000	238	0							
Locus_17819_Transcript_1/1_Conf_1.000	239	0							
Locus_1782_Transcript_1/1_Conf_1.000	404	20	1.15E-74	AAH86899.1	100	282.337	133	133	Ribosomal protein S8
Locus_17820_Transcript_1/1_Conf_1.000	352	20	2.61E-26	NP_502060.1	73	121.709	108	79	TransThyretin-Related family domain family member (ttr-16)
Locus_17821_Transcript_1/1_Conf_1.000	376	0							
Locus_17822_Transcript_1/1_Conf_1.000	402	20	8.04E-52	NP_510711.2	86	206.453	135	117	AMP-Activated Kinase family member (aak-2)
Locus_17823_Transcript_1/1_Conf_1.000	265	0							
Locus_17824_Transcript_1/1_Conf_1.000	142	0							
Locus_17825_Transcript_1/1_Conf_1.000	191	0							
Locus_17826_Transcript_1/1_Conf_1.000	755	4	1.18E-15	NP_509620.2	48	87.8113	175	84	hypothetical protein C11E4.6
Locus_17827_Transcript_1/1_Conf_1.000	412	1	2.66E-23	NP_502795.2	72	111.694	90	65	Homolog of Hedgehog AcylTransferase family member (hhat-2)
Locus_17828_Transcript_1/1_Conf_1.000	181	0							
Locus_17829_Transcript_1/1_Conf_1.000	361	20	2.19E-09	EFN83858.1	75	65.4698	52	39	Histone-lysine N-methyltransferase SETMAR
Locus_1783_Transcript_1/1_Conf_1.000	1706	20	0	NP_001022078.1	91	894.419	524	479	ALdehyde deHydrogenase family member (alh-8)
Locus_17830_Transcript_1/1_Conf_1.000	559	20	3.87E-36	EFO24024.1	97	154.836	81	79	CMGC/DYRK/HIPK protein kinase
Locus_17831_Transcript_1/1_Conf_1.000	202	0							

Locus_17832_Transcript_1/1_Conf_1.000	171	20	6.58E-22	XP_002823622.1	100	107.071	48	48	PREDICTED: decorin-like isoform 1
Locus_17833_Transcript_1/1_Conf_1.000	171	0							
Locus_17834_Transcript_1/1_Conf_1.000	144	20	1.46E-08	BAA95178.1	71	62.7734	49	35	hgPTPR2Ab
Locus_17835_Transcript_1/1_Conf_1.000	547	20	3.21E-48	NP_490889.1	82	194.897	140	115	hypothetical protein Y71G12B.10
Locus_17836_Transcript_1/1_Conf_1.000	156	0							
Locus_17837_Transcript_1/1_Conf_1.000	155	2	1.89E-08	NP_495090.1	82	62.3882	50	41	hypothetical protein C17G10.7
Locus_17838_Transcript_1/1_Conf_1.000	466	20	4.04E-27	NP_001021801.1	87	124.405	74	65	hypothetical protein Y6B3B.5

Locus_17839_Transcript_1/1_Conf_1.000	1289	20	2.39E-147	NP_740931.2	79	526.554	433	345	hypothetical protein Y105E8A.3
Locus_1784_Transcript_1/1_Conf_1.000	2433	20	0	XP_002647083.1	86	1048.88	678	584	Hypothetical protein CBG03613
Locus_17840_Transcript_1/1_Conf_1.000	158	0							
Locus_17841_Transcript_1/1_Conf_1.000	342	20	1.07E-19	XP_001649524.1	70	99.7525	103	73	multiple ankyrin repeats single kh domain protein
Locus_17842_Transcript_1/1_Conf_1.000	670	20	5.32E-64	NP_001041144.1	83	248.054	171	143	hypothetical protein H27A22.1
Locus_17843_Transcript_1/1_Conf_1.000	383	20	1.97E-42	NP_492423.2	81	175.252	127	103	FCP1 (yeast TFIIF-interacting CTD phosphatase subunit) homolog family member (fcp-1)
Locus_17844_Transcript_1/1_Conf_1.000	199	20	1.26E-12	NP_008817.1	100	76.2554	38	38	ATP synthase subunit epsilon, mitochondrial
Locus_17845_Transcript_1/1_Conf_1.000	502	20	1.71E-09	XP_001635605.1	55	65.855	108	60	predicted protein
Locus_17846_Transcript_1/1_Conf_1.000	152	0							

Locus_17847_Transcript_1/1_Conf_1.000	258	20	2.23E-17	EAW98190.1	100	92.0485	38	38	cytochrome c oxidase subunit VIa polypeptide 1, isoform CRA_a
Locus_17848_Transcript_1/1_Conf_1.000	351	20	1.05E-43	XP_002640379.1	87	179.489	116	102	C. briggsae CBR-OPT-3 protein
Locus_17849_Transcript_1/1_Conf_1.000	277	0							
Locus_1785_Transcript_1/1_Conf_1.000	162	2	1.34E-06	NP_500107.1	70	56.225	54	38	hypothetical protein Y41D4B.11
Locus_17850_Transcript_1/1_Conf_1.000	785	20	1.28E-124	CBW48341.1	91	449.899	261	239	Hypothetical protein C27H6.1c
Locus_17851_Transcript_1/1_Conf_1.000	329	20	2.77E-28	XP_002640543.1	77	128.257	94	73	C. briggsae CBR-SCRM-1 protein
Locus_17852_Transcript_1/1_Conf_1.000	683	20	5.81E-29	NP_501200.1	53	131.724	226	121	ROD (Drosophila RoughDeal) homolog family member (rod-1)
Locus_17853_Transcript_1/1_Conf_1.000	542	5	3.01E-19	Q9NA80.3	54	98.5969	186	101	Stress-activated map kinase-interacting protein 1 homolog
Locus_17854_Transcript_1/1_Conf_1.000	329	20	3.51E-23	NP_001041035.1	70	111.309	90	63	Temporarily Assigned Gene name family member (tag-208)
Locus_17855_Transcript_1/1_Conf_1.000	310	0							
Locus_17856_Transcript_1/1_Conf_1.000	317	4	5.32E-19	NP_492775.2	65	97.4413	105	69	LAMinin related. See also lmb- family member (lam-3)
Locus_17857_Transcript_1/1_Conf_1.000	562	20	2.75E-13	EFO20139.1	88	78.9518	42	37	peripheral plasma membrane protein CASK
Locus_17858_Transcript_1/1_Conf_1.000	646	4	4.05E-58	CAR63536.1	71	228.409	185	132	hypothetical protein
Locus_17859_Transcript_1/1_Conf_1.000	241	20	2.86E-17	EFO20687.1	83	91.6633	60	50	hypothetical protein LOAG_07803
Locus_1786_Transcript_1/2_Conf_1.000	507	20	1.20E-13	EFO25573.1	62	79.7221	150	94	RING finger protein 20
Locus_1786_Transcript_2/2_Conf_1.000	507	20	1.20E-13	EFO25573.1	62	79.7221	150	94	RING finger protein 20
Locus_17860_Transcript_1/1_Conf_1.000	178	5	1.37E-11	NP_510744.1	75	72.7886	60	45	hypothetical protein F52G3.1

Locus_17861_Transcript_1/1_Conf_1.000	284	16	2.11E-07	XP_002643990.1	54	58.9214	95	52	C. briggsae CBR-VHL-1 protein
Locus_17862_Transcript_1/1_Conf_1.000	168	0							
Locus_17863_Transcript_1/1_Conf_1.000	242	2	3.62E-12	NP_490776.2	75	74.7146	58	44	hypothetical protein Y18H1A.9
Locus_17864_Transcript_1/1_Conf_1.000	435	20	2.22E-70	XP_002631669.1	95	268.085	144	137	C. briggsae CBR-MOG-4 protein
Locus_17865_Transcript_1/1_Conf_1.000	155	0							
Locus_17866_Transcript_1/1_Conf_1.000	153	0							
Locus_17867_Transcript_1/1_Conf_1.000	303	0							
Locus_17868_Transcript_1/1_Conf_1.000	671	0							
Locus_17869_Transcript_1/1_Conf_1.000	273	2	5.05E-14	NP_502337.1	95	80.8777	42	40	hypothetical protein C42C1.10
Locus_1787_Transcript_1/1_Conf_1.000	1162	20	5.07E-29	XP_001898268.1	53	133.265	214	114	Eukaryotic-type carbonic anhydrase family protein
Locus_17870_Transcript_1/1_Conf_1.000	444	20	8.97E-35	XP_001902632.1	80	149.828	130	104	Arid4a protein
Locus_17871_Transcript_1/1_Conf_1.000	365	0							
Locus_17872_Transcript_1/1_Conf_1.000	260	0							
Locus_17873_Transcript_1/1_Conf_1.000	160	0							
Locus_17874_Transcript_1/1_Conf_1.000	253	0							
Locus_17875_Transcript_1/1_Conf_1.000	342	20	4.98E-17	XP_002640122.1	75	90.8929	100	75	C. briggsae CBR-NCBP-1 protein
Locus_17876_Transcript_1/1_Conf_1.000	1007	20	5.07E-88	CAA16382.5	63	328.946	360	228	C. elegans protein Y45F10D.7, partially confirmed by transcript evidence
Locus_17877_Transcript_1/1_Conf_1.000	265	0							

Locus_17878_Transcript_1/1_Conf_1.000	201	20	1.63E-20	XP_002834351.1	100	102.449	43	43	PREDICTED: hypothetical protein LOC100438152
Locus_17879_Transcript_1/2_Conf_1.000	521	0							
Locus_17879_Transcript_2/2_Conf_1.000	521	0							
Locus_1788_Transcript_1/1_Conf_1.000	962	20	2.24E-106	EFO22691.1	83	389.808	291	244	hypothetical protein LOAG_05796
Locus_17880_Transcript_1/1_Conf_1.000	494	4	2.75E-44	CAR63586.1	90	181.415	102	92	hypothetical protein
Locus_17881_Transcript_1/1_Conf_1.000	702	4	3.20E-33	XP_002645822.1	56	145.976	235	133	Hypothetical protein CBG07553
Locus_17882_Transcript_1/1_Conf_1.000	247	0							
Locus_17883_Transcript_1/1_Conf_1.000	433	20	4.85E-33	XP_002639673.1	76	144.05	145	111	Hypothetical protein CBG12391
Locus_17884_Transcript_1/1_Conf_1.000	316	20	7.63E-42	NP_501792.2	89	173.326	99	89	abnormal GONad development family member (gon-1)

Locus_17885_Transcript_1/1_Conf_1.000	431	20	1.68E-25	XP_001901813.1	64	119.013	117	75	rad50 family protein
Locus_17886_Transcript_1/1_Conf_1.000	226	20	1.70E-33	NP_001021324.1	97	145.591	74	72	hypothetical protein C10G6.1
Locus_17887_Transcript_1/1_Conf_1.000	402	0							
Locus_17888_Transcript_1/1_Conf_1.000	291	20	2.61E-34	XP_001895873.1	80	148.288	96	77	hypothetical protein
Locus_17889_Transcript_1/1_Conf_1.000	471	3	2.05E-31	NP_741656.2	63	138.658	156	99	hypothetical protein Y39B6A.41
Locus_1789_Transcript_1/1_Conf_1.000	468	20	2.44E-24	XP_002631600.1	58	115.161	153	89	Hypothetical protein CBG20781
Locus_17890_Transcript_1/1_Conf_1.000	204	2	4.59E-07	XP_002634011.1	60	57.7658	65	39	Hypothetical protein CBG01544
Locus_17891_Transcript_1/1_Conf_1.000	274	5	1.98E-26	NP_001024333.1	81	122.094	87	71	Olfactory LeaRNing defective family member (olrn-1)
Locus_17892_Transcript_1/1_Conf_1.000	300	0							
Locus_17893_Transcript_1/1_Conf_1.000	253	0							
Locus_17894_Transcript_1/2_Conf_1.000	323	0							
Locus_17894_Transcript_2/2_Conf_1.000	204	0							
Locus_17895_Transcript_1/1_Conf_1.000	302	0							
Locus_17896_Transcript_1/1_Conf_1.000	706	20	3.62E-45	CAA21636.3	91	185.652	124	113	C. elegans protein Y38F1A.3, partially confirmed by transcript evidence
Locus_17897_Transcript_1/1_Conf_1.000	216	0							
Locus_17898_Transcript_1/1_Conf_1.000	360	0							
Locus_17899_Transcript_1/1_Conf_1.000	319	20	2.30E-22	NP_492340.1	69	108.612	94	65	hypothetical protein F43G9.10

Locus_179_Transcript_1/2_Conf_1.000	421	20	1.06E-43	Q07160.1	81	179.489	119	97	Heat shock protein homolog
Locus_179_Transcript_2/2_Conf_1.000	182	20	1.90E-24	CAG25499.1	95	115.546	60	57	heat shock protein 20
Locus_1790_Transcript_1/6_Conf_0.350	442	20	2.01E-18	AAD51334.1	70	95.5153	74	52	Kunitz type serine protease inhibitor
Locus_1790_Transcript_2/6_Conf_0.350	400	20	2.01E-18	AAD51334.1	70	95.5153	74	52	Kunitz type serine protease inhibitor
Locus_1790_Transcript_3/6_Conf_0.200	676	20	4.51E-18	AAD51334.1	70	95.5153	74	52	Kunitz type serine protease inhibitor
Locus_1790_Transcript_4/6_Conf_0.200	676	20	4.51E-18	AAD51334.1	70	95.5153	74	52	Kunitz type serine protease inhibitor
Locus_1790_Transcript_5/6_Conf_0.400	556	20	2.80E-18	AAD51334.1	70	95.5153	74	52	Kunitz type serine protease inhibitor

Locus_1790_Transcript_6/6_Conf_0.400	556	20	2.80E-18	AAD51334.1	70	95.5153	74	52	Kunitz type serine protease inhibitor
Locus_17900_Transcript_1/1_Conf_1.000	566	2	4.77E-13	XP_002640628.1	73	78.1814	57	42	C. briggsae CBR-EAT-18 protein
Locus_17901_Transcript_1/1_Conf_1.000	157	1	3.33E-05	XP_002637780.1	68	51.6026	50	34	Hypothetical protein CBG04563
Locus_17902_Transcript_1/1_Conf_1.000	368	14	4.09E-16	XP_002415665.1	61	87.8113	118	72	conserved hypothetical protein
Locus_17903_Transcript_1/1_Conf_1.000	370	5	3.68E-20	NP_492775.2	75	101.293	84	63	LAMinin related. See also lmb- family member (lam-3)
Locus_17904_Transcript_1/1_Conf_1.000	832	20	2.92E-69	XP_002632892.1	70	266.159	297	208	Hypothetical protein CBG15100
Locus_17905_Transcript_1/1_Conf_1.000	169	20	1.16E-18	XP_002743627.1	87	96.2857	56	49	PREDICTED: hypothetical protein LOC100405423
Locus_17906_Transcript_1/1_Conf_1.000	310	1	1.91E-05	EFO26102.1	46	52.373	101	47	hypothetical protein LOAG_02385
Locus_17907_Transcript_1/1_Conf_1.000	274	0							
Locus_17908_Transcript_1/1_Conf_1.000	565	20	2.36E-28	XP_002642471.1	67	129.028	136	92	Hypothetical protein CBG06887
Locus_17909_Transcript_1/1_Conf_1.000	135	0							
Locus_1791_Transcript_1/1_Conf_1.000	290	20	2.39E-11	NP_001122454.1	77	72.0182	48	37	abnormal ThermoTaXis family member (ttx-7)
Locus_17910_Transcript_1/1_Conf_1.000	935	20	4.02E-129	XP_002634971.1	89	465.307	284	255	Hypothetical protein CBG13507
Locus_17911_Transcript_1/1_Conf_1.000	229	0							
Locus_17912_Transcript_1/1_Conf_1.000	214	0							
Locus_17913_Transcript_1/1_Conf_1.000	597	0							
Locus_17914_Transcript_1/4_Conf_0.625	490	0							
Locus_17914_Transcript_2/4_Conf_0.625	490	0							
Locus_17914_Transcript_3/4_Conf_0.625	497	0							
Locus_17914_Transcript_4/4_Conf_0.625	497	0							

Locus_17915_Transcript_1/1_Conf_1.000	377	3	2.54E-05	EFO27305.1	45	51.9878	127	58	hypothetical protein LOAG_01169
Locus_17916_Transcript_1/1_Conf_1.000	899	20	6.13E-39	ABD39382.1	86	165.622	133	115	putative galectin protein 140
Locus_17917_Transcript_1/1_Conf_1.000	242	0							
Locus_17918_Transcript_1/1_Conf_1.000	559	20	1.23E-74	XP_002630326.1	84	282.722	186	158	Hypothetical protein CBG04253
Locus_17919_Transcript_1/1_Conf_1.000	252	20	1.97E-13	XP_002634749.1	67	78.9518	81	55	Hypothetical protein CBG21079
Locus_1792_Transcript_1/1_Conf_1.000	1361	5	6.18E-16	XP_001896257.1	51	90.1225	193	100	hypothetical protein Bm1_24000
Locus_17920_Transcript_1/1_Conf_1.000	143	0							
Locus_17921_Transcript_1/1_Conf_1.000	159	3	7.90E-07	XP_002637600.1	77	56.9954	53	41	C. briggsae CBR-SULP-8 protein
Locus_17922_Transcript_1/1_Conf_1.000	145	1	1.67E-04	XP_001897983.1	68	49.2914	48	33	RIKEN cDNA 2700097O09
Locus_17923_Transcript_1/1_Conf_1.000	358	0							
Locus_17924_Transcript_1/1_Conf_1.000	183	0							
Locus_17925_Transcript_1/1_Conf_1.000	136	0							
Locus_17926_Transcript_1/1_Conf_1.000	142	0							
Locus_17927_Transcript_1/1_Conf_1.000	156	2	3.68E-04	XP_001512989.1	57	48.1358	52	30	PREDICTED: similar to protocadherin 19
Locus_17928_Transcript_1/1_Conf_1.000	775	20	1.78E-54	EFO21392.1	69	216.853	230	159	hypothetical protein LOAG_07098
Locus_17929_Transcript_1/2_Conf_1.000	332	20	1.09E-16	EFO13838.1	90	89.7373	64	58	hypothetical protein LOAG_14688
Locus_17929_Transcript_2/2_Conf_1.000	332	20	1.09E-16	EFO13838.1	90	89.7373	64	58	hypothetical protein LOAG_14688
Locus_1793_Transcript_1/1_Conf_1.000	341	0							
Locus_17930_Transcript_1/1_Conf_1.000	150	18	2.74E-15	NP_502587.2	89	85.1149	49	44	Pelle/IL-1 receptor associated Kinase (IRAK) family member (pik-1)
Locus_17931_Transcript_1/1_Conf_1.000	505	15	3.77E-20	EFO23262.1	60	101.293	116	70	hypothetical protein LOAG_05225

Locus_17932_Transcript_1/1_Conf_1.000	282	0							
Locus_17933_Transcript_1/1_Conf_1.000	445	20	2.18E-73	XP_002638687.1	92	278.1	148	137	Hypothetical protein CBG11882
Locus_17934_Transcript_1/1_Conf_1.000	429	20	4.37E-66	NP_001040875.1	91	253.832	143	131	hypothetical protein T23G5.2
Locus_17935_Transcript_1/1_Conf_1.000	134	0							
Locus_17936_Transcript_1/1_Conf_1.000	263	1	5.12E-14	XP_001166450.1	84	80.8777	66	56	PREDICTED: hypothetical protein
Locus_17937_Transcript_1/1_Conf_1.000	276	0							
Locus_17938_Transcript_1/1_Conf_1.000	148	0							
Locus_17939_Transcript_1/1_Conf_1.000	260	5	6.71E-14	CAA84706.3	63	80.4925	87	55	C. elegans protein C38H2.1, partially confirmed by transcript evidence
Locus_1794_Transcript_1/1_Conf_1.000	1468	20	4.89E-22	AAN05752.1	64	110.538	128	83	heat shock protein 20
Locus_17940_Transcript_1/1_Conf_1.000	591	0							
Locus_17941_Transcript_1/1_Conf_1.000	470	0							
Locus_17942_Transcript_1/1_Conf_1.000	158	0							
Locus_17943_Transcript_1/1_Conf_1.000	259	20	4.04E-35	AAB37835.2	94	150.984	86	81	Dnaj domain (prokaryotic heat shock protein) protein 9, partially confirmed by transcript evidence
Locus_17944_Transcript_1/1_Conf_1.000	665	20	3.18E-37	XP_002639077.1	59	159.073	208	124	Hypothetical protein CBG14895
Locus_17945_Transcript_1/1_Conf_1.000	316	3	1.40E-27	NP_507767.2	79	125.946	107	85	hypothetical protein C14B4.2
Locus_17946_Transcript_1/1_Conf_1.000	374	20	5.46E-32	NP_001076652.1	94	140.584	74	70	NOT-Like (yeast CCR4/NOT complex component) family member (ntl-3)
Locus_17947_Transcript_1/1_Conf_1.000	276	5	1.79E-11	XP_002630778.1	79	72.4034	44	35	Hypothetical protein CBG02473
Locus_17948_Transcript_1/1_Conf_1.000	200	0							
Locus_17949_Transcript_1/1_Conf_1.000	128	0							
Locus_1795_Transcript_1/1_Conf_1.000	799	20	6.53E-47	EFO24294.1	62	191.815	253	157	hypothetical protein LOAG_04191
Locus_17950_Transcript_1/1_Conf_1.000	283	0							
Locus_17951_Transcript_1/1_Conf_1.000	636	0							

Locus_17952_Transcript_1/1_Conf_1.000	456	20	5.51E-45	NP_491087.1	85	183.726	151	129	MAP kinase kinase or Erk Kinase family member (mek-2)
Locus_17953_Transcript_1/1_Conf_1.000	351	20	3.39E-42	NP_491246.4	80	174.481	113	91	COenzyme Q (ubiquinone) biosynthesis family member (coq-4)
Locus_17954_Transcript_1/1_Conf_1.000	599	20	2.71E-84	XP_002643253.1	87	315.079	199	175	C. briggsae CBR-AEX-3 protein
Locus_17955_Transcript_1/1_Conf_1.000	147	0							
Locus_17956_Transcript_1/1_Conf_1.000	237	20	3.63E-12	NP_493027.1	71	74.7146	82	59	hypothetical protein R06C1.2
Locus_17957_Transcript_1/1_Conf_1.000	138	0							
Locus_17958_Transcript_1/1_Conf_1.000	192	0							
Locus_17959_Transcript_1/1_Conf_1.000	143	0							
Locus_1796_Transcript_1/2_Conf_1.000	2501	20	0	XP_002642411.1	73	819.305	754	553	C. briggsae CBR-INA-1 protein

Locus_1796_Transcript_2/2_Conf_1.000	2501	20	0	XP_002642411.1	73	819.305	754	553	C. briggsae CBR-INA-1 protein
Locus_17960_Transcript_1/1_Conf_1.000	309	20	9.16E-08	XP_002129690.1	49	60.077	73	36	PREDICTED: similar to C-type lectin domain family 4 member F (C-type lectin superfamily member 13) (C-type lectin 13) (Kupffer cell receptor)
Locus_17961_Transcript_1/1_Conf_1.000	343	0							
Locus_17962_Transcript_1/1_Conf_1.000	230	3	1.03E-14	XP_002638987.1	73	83.1889	76	56	Hypothetical protein CBG22233
Locus_17963_Transcript_1/1_Conf_1.000	274	20	7.47E-42	XP_002641621.1	90	173.326	91	82	Hypothetical protein CBG09941
Locus_17964_Transcript_1/1_Conf_1.000	249	0							
Locus_17965_Transcript_1/1_Conf_1.000	271	0							
Locus_17966_Transcript_1/1_Conf_1.000	259	20	8.45E-25	XP_002647748.1	80	116.701	86	69	C. briggsae CBR-WRS-1 protein
Locus_17967_Transcript_1/1_Conf_1.000	678	20	4.12E-27	NP_492329.1	62	125.561	142	89	hypothetical protein F43G9.13
Locus_17968_Transcript_1/1_Conf_1.000	179	20	9.76E-18	XP_002633968.1	87	93.2041	57	50	C. briggsae CBR-MCA-1 protein
Locus_17969_Transcript_1/1_Conf_1.000	146	20	8.86E-14	EFO20394.1	87	80.1073	48	42	hypothetical protein LOAG_08094
Locus_1797_Transcript_1/1_Conf_1.000	986	20	2.35E-82	XP_002636883.1	73	310.071	275	202	Hypothetical protein CBG09344
Locus_17970_Transcript_1/1_Conf_1.000	460	0							
Locus_17971_Transcript_1/1_Conf_1.000	135	0							

Locus_17972_Transcript_1/1_Conf_1.000	318	6	5.10E-38	XP_002636221.1	80	160.614	106	85	Hypothetical protein CBG12142
Locus_17973_Transcript_1/1_Conf_1.000	249	7	2.10E-20	EFO19192.1	74	102.064	83	62	MYND finger family protein
Locus_17974_Transcript_1/1_Conf_1.000	231	0							
Locus_17975_Transcript_1/1_Conf_1.000	157	0							
Locus_17976_Transcript_1/1_Conf_1.000	367	20	1.84E-16	NP_490726.1	76	88.9669	69	53	hypothetical protein R119.3
Locus_17977_Transcript_1/1_Conf_1.000	150	20	6.29E-20	P01023.3	100	100.523	49	49	Alpha-2-macroglobulin
Locus_17978_Transcript_1/1_Conf_1.000	171	1	4.28E-05	EFO22577.1	69	51.2174	55	38	hypothetical protein LOAG_05911
Locus_17979_Transcript_1/1_Conf_1.000	245	20	2.11E-28	XP_001897997.1	89	128.642	79	71	anion exchange protein

Locus_1798_Transcript_1/3_Conf_0.750	1313	20	2.79E-42	ADK91433.1	68	177.563	173	118	c-type lectin 1
Locus_1798_Transcript_2/3_Conf_0.750	1469	20	4.26E-42	ADK91433.1	68	177.178	173	119	c-type lectin 1

Locus_1798_Transcript_3/3_Conf_0.750	1469	20	1.12E-42	ADK91433.1	68	179.104	173	119	c-type lectin 1
Locus_17980_Transcript_1/1_Conf_1.000	180	0							
Locus_17981_Transcript_1/1_Conf_1.000	243	1	9.52E-05	XP_001895050.1	57	50.0618	54	31	hypothetical protein Bm1_17960
Locus_17982_Transcript_1/1_Conf_1.000	250	3	6.13E-04	XP_002634125.1	58	47.3654	62	36	C. briggsae CBR-MSH-5 protein
Locus_17983_Transcript_1/1_Conf_1.000	460	0							
Locus_17984_Transcript_1/1_Conf_1.000	185	4	4.24E-16	XP_002633677.1	80	87.8113	60	48	C. briggsae CBR-LAD-2 protein
Locus_17985_Transcript_1/1_Conf_1.000	426	20	1.75E-14	ACN62126.1	54	82.4185	142	78	tryptophan decarboxylase
Locus_17986_Transcript_1/1_Conf_1.000	156	20	1.10E-16	XP_002635876.1	94	89.7373	51	48	C. briggsae CBR-PTR-16 protein
Locus_17987_Transcript_1/1_Conf_1.000	143	0							
Locus_17988_Transcript_1/1_Conf_1.000	377	20	1.94E-21	NP_497480.2	65	105.531	127	83	POLH (DNA polymerase eta) homolog family member (polh-1)

Locus_17989_Transcript_1/1_Conf_1.000	374	20	3.41E-42	NP_001123000.1	77	174.481	124	96	hypothetical protein T05C3.6
Locus_1799_Transcript_1/1_Conf_1.000	489	20	1.92E-45	XP_001901624.1	73	185.267	148	109	valyl-tRNA synthetase family protein
Locus_17990_Transcript_1/1_Conf_1.000	263	0							
Locus_17991_Transcript_1/1_Conf_1.000	270	20	1.74E-14	XP_002131575.1	68	82.4185	88	60	PREDICTED: mitogen-activated protein kinase kinase
Locus_17992_Transcript_1/1_Conf_1.000	242	0							
Locus_17993_Transcript_1/1_Conf_1.000	360	5	7.28E-13	ADI24623.1	54	77.0258	113	62	Copine domain protein, atypical protein 2, isoform c, partially confirmed by transcript evidence
Locus_17994_Transcript_1/1_Conf_1.000	324	0							
Locus_17995_Transcript_1/1_Conf_1.000	327	0							
Locus_17996_Transcript_1/1_Conf_1.000	671	0							
Locus_17997_Transcript_1/1_Conf_1.000	251	0							
Locus_17998_Transcript_1/1_Conf_1.000	478	2	5.38E-08	XP_002631107.1	50	60.8474	122	62	Hypothetical protein CBG02882
Locus_17999_Transcript_1/1_Conf_1.000	180	20	1.41E-27	XP_002922896.1	100	125.946	60	60	PREDICTED: macrophage-capping protein-like
Locus_18_Transcript_1/1_Conf_1.000	1840	20	0	NP_492114.2	87	783.482	513	450	hypothetical protein T25G3.3
Locus_180_Transcript_1/6_Conf_0.111	1363	20	3.42E-115	XP_002640295.1	90	419.853	252	228	Hypothetical protein CBG12821

Locus_180_Transcript_2/6_Conf_0.111	1363	20	3.42E-115	XP_002640295.1	90	419.853	252	228	Hypothetical protein CBG12821
Locus_180_Transcript_3/6_Conf_0.278	738	12	5.45E-26	CAJ45481.1	68	122.094	122	84	legumain
Locus_180_Transcript_4/6_Conf_0.278	780	8	6.70E-25	CAJ45481.1	67	118.627	122	82	legumain
Locus_180_Transcript_5/6_Conf_0.389	2216	20	1.60E-134	CAJ45481.1	72	484.952	404	294	legumain
Locus_180_Transcript_6/6_Conf_0.389	2174	20	1.41E-135	CAJ45481.1	73	488.419	404	296	legumain
Locus_1800_Transcript_1/1_Conf_1.000	424	5	8.44E-09	XP_002631731.1	94	63.5438	52	49	Hypothetical protein CBG20933
Locus_18000_Transcript_1/1_Conf_1.000	589	20	8.19E-22	NP_491362.1	55	107.457	187	104	hypothetical protein ZK973.1
Locus_18001_Transcript_1/1_Conf_1.000	414	20	2.23E-38	NP_497589.3	81	161.77	138	113	hypothetical protein Y71H2B.5

Locus_18002_Transcript_1/1_Conf_1.000	303	20	6.16E-20	XP_001899247.1	81	100.523	100	81	Probable nucleolar GTP-binding protein 1.
Locus_18003_Transcript_1/1_Conf_1.000	128	0							
Locus_18004_Transcript_1/1_Conf_1.000	153	7	5.32E-11	XP_001897512.1	87	70.8626	41	36	Patched family protein
Locus_18005_Transcript_1/2_Conf_1.000	400	3	7.91E-07	CBX25202.1	46	56.9954	110	51	Hypothetical protein Y17G7B.23a
Locus_18005_Transcript_2/2_Conf_1.000	400	3	7.91E-07	CBX25202.1	46	56.9954	110	51	Hypothetical protein Y17G7B.23a
Locus_18006_Transcript_1/1_Conf_1.000	135	4	4.26E-13	XP_002637318.1	82	77.7962	45	37	Hypothetical protein CBG19009
Locus_18007_Transcript_1/1_Conf_1.000	596	20	7.36E-34	XP_002640693.1	58	147.517	204	119	Hypothetical protein CBG19758
Locus_18008_Transcript_1/1_Conf_1.000	377	20	5.24E-43	XP_002646355.1	88	177.178	109	96	Hypothetical protein CBG12069
Locus_18009_Transcript_1/1_Conf_1.000	441	6	1.60E-15	NP_497868.1	56	85.8853	138	78	Temporarily Assigned Gene name family member (tag-131)
Locus_1801_Transcript_1/1_Conf_1.000	700	20	2.76E-45	EFO22561.1	73	186.037	169	124	hypothetical protein LOAG_05921
Locus_18010_Transcript_1/1_Conf_1.000	621	20	1.17E-64	NP_495666.3	80	249.98	212	170	Temporarily Assigned Gene name family member (tag-341)
Locus_18011_Transcript_1/1_Conf_1.000	441	0							
Locus_18012_Transcript_1/1_Conf_1.000	1068	5	1.65E-15	NP_001022123.1	46	88.1965	273	126	hypothetical protein F28C6.4
Locus_18013_Transcript_1/1_Conf_1.000	169	20	6.17E-20	XP_002641994.1	96	100.523	56	54	Hypothetical protein CBG09217
Locus_18014_Transcript_1/1_Conf_1.000	151	2	3.35E-05	NP_508866.1	75	51.6026	53	40	Unidentified Vitellogenin-linked Transcript family member (uvt-3)
Locus_18015_Transcript_1/1_Conf_1.000	226	0							

Locus_18016_Transcript_1/1_Conf_1.000	632	20	2.95E-10	BAF47075.1	53	69.3218	136	73	AP2 homolog
Locus_18017_Transcript_1/1_Conf_1.000	469	20	1.09E-40	EFO20767.1	73	169.474	156	114	Smad1
Locus_18018_Transcript_1/1_Conf_1.000	285	0							
Locus_18019_Transcript_1/1_Conf_1.000	662	5	7.05E-13	XP_002639135.1	50	78.1814	216	109	C. briggsae CBR-SEP-1 protein
Locus_1802_Transcript_1/1_Conf_1.000	145	0							

Locus_18020_Transcript_1/1_Conf_1.000	205	20	4.42E-26	XP_002832350.1	100	120.939	68	68	PREDICTED: LOW QUALITY PROTEIN: filamin-A-like
Locus_18021_Transcript_1/1_Conf_1.000	412	20	8.25E-33	NP_505116.1	66	143.28	137	91	hypothetical protein K07C11.7
Locus_18022_Transcript_1/1_Conf_1.000	269	20	1.95E-16	NP_001122749.1	70	83.1889	80	56	hypothetical protein ZK643.3
Locus_18023_Transcript_1/1_Conf_1.000	176	2	1.28E-09	XP_002637557.1	75	66.2402	56	42	Hypothetical protein CBG19289
Locus_18024_Transcript_1/1_Conf_1.000	168	20	7.08E-08	XP_002643075.1	79	60.4622	44	35	Hypothetical protein CBG22995
Locus_18025_Transcript_1/1_Conf_1.000	231	0							
Locus_18026_Transcript_1/1_Conf_1.000	222	20	3.01E-30	BAE90469.1	90	134.806	72	65	unnamed protein product
Locus_18027_Transcript_1/1_Conf_1.000	1774	20	0	NP_508475.2	79	697.582	587	468	Inner Membrane of MiTochondria protein homolog family member (immt-1)
Locus_18028_Transcript_1/1_Conf_1.000	378	0							
Locus_18029_Transcript_1/1_Conf_1.000	177	7	1.97E-10	AAN61521.1	70	68.9366	58	41	301KDa_2 protein
Locus_1803_Transcript_1/1_Conf_1.000	922	20	9.02E-25	XP_002639695.1	72	118.627	108	78	C. briggsae CBR-FCP-1 protein
Locus_18030_Transcript_1/1_Conf_1.000	130	0							
Locus_18031_Transcript_1/1_Conf_1.000	135	0							
Locus_18032_Transcript_1/1_Conf_1.000	131	0							
Locus_18033_Transcript_1/1_Conf_1.000	265	0							
Locus_18034_Transcript_1/1_Conf_1.000	384	0							
Locus_18035_Transcript_1/1_Conf_1.000	185	0							
Locus_18036_Transcript_1/1_Conf_1.000	259	0							

Locus_18037_Transcript_1/1_Conf_1.000	168	0							
Locus_18038_Transcript_1/1_Conf_1.000	276	0							
Locus_18039_Transcript_1/1_Conf_1.000	432	2	2.27E-06	NP_495102.1	59	55.4546	74	44	hypothetical protein F59E12.11
Locus_1804_Transcript_1/6_Conf_0.762	1122	0							
Locus_1804_Transcript_2/6_Conf_0.762	1119	0							
Locus_1804_Transcript_3/6_Conf_0.762	1140	0							
Locus_1804_Transcript_4/6_Conf_0.762	1161	0							
Locus_1804_Transcript_5/6_Conf_0.762	1119	0							
Locus_1804_Transcript_6/6_Conf_0.762	1128	0							
Locus_18040_Transcript_1/1_Conf_1.000	369	0							
Locus_18041_Transcript_1/1_Conf_1.000	243	0							
Locus_18042_Transcript_1/1_Conf_1.000	256	0							
Locus_18043_Transcript_1/1_Conf_1.000	368	20	4.82E-25	3N9L	66	117.472	117	78	Cekdm7a From C.Elegans
Locus_18044_Transcript_1/1_Conf_1.000	285	0							
Locus_18045_Transcript_1/1_Conf_1.000	549	20	2.42E-51	NP_492132.1	73	205.297	178	131	Enhancer of Glp-One (glp-1) family member (ego-1)
Locus_18046_Transcript_1/1_Conf_1.000	424	20	1.43E-40	XP_002634303.1	76	169.088	141	108	C. briggsae CBR-NCX-3 protein
Locus_18047_Transcript_1/1_Conf_1.000	548	20	1.87E-64	NP_493426.2	87	248.825	183	160	TAF (TBP-associated transcription factor) family member (taf-1)
Locus_18048_Transcript_1/1_Conf_1.000	818	20	1.36E-39	CBW48397.1	72	167.548	157	114	Hypothetical protein F54C8.7e
Locus_18049_Transcript_1/1_Conf_1.000	702	20	2.98E-47	XP_002640651.1	65	192.586	231	152	Hypothetical protein CBG19709

Locus_1805_Transcript_1/1_Conf_1.000	1075	20	1.21E-90	EFO19288.1	96	337.806	179	173	RAB14 protein
Locus_18050_Transcript_1/1_Conf_1.000	451	4	3.07E-19	XP_002634268.1	55	98.2117	148	82	Hypothetical protein CBG01840
Locus_18051_Transcript_1/1_Conf_1.000	551	20	2.29E-17	XP_002123175.1	69	92.4337	92	64	PREDICTED: similar to predicted protein
Locus_18052_Transcript_1/1_Conf_1.000	244	0							
Locus_18053_Transcript_1/1_Conf_1.000	488	0							
Locus_18054_Transcript_1/1_Conf_1.000	265	0							
Locus_18055_Transcript_1/1_Conf_1.000	285	0							
Locus_18056_Transcript_1/2_Conf_1.000	457	20	1.33E-06	EFA09420.1	50	56.225	120	60	hypothetical protein TcasGA2_TC005222

Locus_18056_Transcript_2/2_Conf_1.000	457	20	1.33E-06	EFA09420.1	50	56.225	120	60	hypothetical protein TcasGA2_TC005222
Locus_18057_Transcript_1/1_Conf_1.000	347	20	3.54E-31	XP_001900176.1	89	137.887	82	73	LIM domain containing protein
Locus_18058_Transcript_1/1_Conf_1.000	182	0							
Locus_18059_Transcript_1/1_Conf_1.000	287	20	2.09E-23	NP_498250.3	74	112.079	95	71	POLQ (DNA polymerase theta) homolog family member (polq-1)
Locus_1806_Transcript_1/1_Conf_1.000	896	0							
Locus_18060_Transcript_1/1_Conf_1.000	153	18	1.50E-05	CBL43432.1	68	52.7582	47	32	C. elegans protein F01D4.1b, partially confirmed by transcript evidence
Locus_18061_Transcript_1/1_Conf_1.000	610	2	1.71E-12	NP_506085.2	45	76.6406	217	99	FERM domain (protein4.1-ezrin-radixin-moesin) family member (frm-7)
Locus_18062_Transcript_1/1_Conf_1.000	220	20	2.92E-33	XP_519230.2	100	144.821	72	72	PREDICTED: actin related protein 2/3 complex subunit 1B
Locus_18063_Transcript_1/1_Conf_1.000	525	20	1.47E-44	XP_002638481.1	70	182.57	175	123	Hypothetical protein CBG12909
Locus_18064_Transcript_1/1_Conf_1.000	306	0							
Locus_18065_Transcript_1/1_Conf_1.000	227	4	1.07E-11	NP_492746.2	94	73.1738	38	36	Temporarily Assigned Gene name family member (tag-68)
Locus_18066_Transcript_1/1_Conf_1.000	289	0							
Locus_18067_Transcript_1/1_Conf_1.000	732	0							
Locus_18068_Transcript_1/1_Conf_1.000	288	1	4.50E-10	NP_490992.2	79	67.781	48	38	hypothetical protein Y23H5B.4
Locus_18069_Transcript_1/1_Conf_1.000	246	0							

Locus_1807_Transcript_1/1_Conf_1.000	1724	20	0	XP_002634023.1	77	666.381	563	434	Hypothetical protein CBG01556
Locus_18070_Transcript_1/2_Conf_1.000	760	20	6.47E-62	NP_495796.1	74	241.506	225	168	RNase H family member (rnh-2)
Locus_18070_Transcript_2/2_Conf_1.000	760	20	4.95E-62	NP_495796.1	74	241.891	225	168	RNase H family member (rnh-2)
Locus_18071_Transcript_1/1_Conf_1.000	335	0							
Locus_18072_Transcript_1/1_Conf_1.000	174	20	1.85E-08	XP_002761583.1	93	62.3882	46	43	PREDICTED: 40S ribosomal protein S15-like
Locus_18073_Transcript_1/1_Conf_1.000	167	0							
Locus_18074_Transcript_1/1_Conf_1.000	320	2	1.26E-12	XP_002642676.1	57	76.2554	105	60	Hypothetical protein CBG12260
Locus_18075_Transcript_1/1_Conf_1.000	144	20	9.16E-11	AAL11454.1	88	70.0922	36	32	Skp1
Locus_18076_Transcript_1/1_Conf_1.000	165	0							
Locus_18077_Transcript_1/1_Conf_1.000	320	20	1.64E-28	XP_001894370.1	69	129.028	105	73	Immunoglobulin I-set domain containing protein
Locus_18078_Transcript_1/1_Conf_1.000	208	0							

Locus_18079_Transcript_1/1_Conf_1.000	178	20	4.39E-10	XP_002831205.1	100	67.781	34	34	PREDICTED: cyclic AMP-dependent transcription factor ATF-4-like
Locus_1808_Transcript_1/1_Conf_1.000	598	20	2.75E-20	XP_002638769.1	56	102.449	180	101	Hypothetical protein CBG05113
Locus_18080_Transcript_1/2_Conf_1.000	273	0							
Locus_18080_Transcript_2/2_Conf_1.000	252	0							
Locus_18081_Transcript_1/1_Conf_1.000	389	20	3.56E-52	XP_002648958.1	82	207.608	127	105	Hypothetical protein CBG21275
Locus_18082_Transcript_1/1_Conf_1.000	164	0							
Locus_18083_Transcript_1/1_Conf_1.000	310	0							
Locus_18084_Transcript_1/1_Conf_1.000	246	0							
Locus_18085_Transcript_1/1_Conf_1.000	156	0							
Locus_18086_Transcript_1/1_Conf_1.000	277	4	1.79E-19	NP_509455.3	73	98.9821	75	55	hypothetical protein F18E9.3
Locus_18087_Transcript_1/1_Conf_1.000	297	20	1.57E-39	XP_002639744.1	87	165.622	86	75	C. briggsae CBR-LAM-3 protein
Locus_18088_Transcript_1/1_Conf_1.000	146	0							
Locus_18089_Transcript_1/1_Conf_1.000	839	20	1.01E-93	XP_002634766.1	73	347.436	286	209	Hypothetical protein CBG05362
Locus_1809_Transcript_1/1_Conf_1.000	459	20	5.31E-40	XP_001898512.1	84	167.162	105	89	Protein kinase domain containing protein
Locus_18090_Transcript_1/1_Conf_1.000	187	0							
Locus_18091_Transcript_1/1_Conf_1.000	321	0							
Locus_18092_Transcript_1/1_Conf_1.000	1377	0							
Locus_18093_Transcript_1/2_Conf_1.000	732	20	8.83E-29	XP_968473.1	58	131.339	179	104	PREDICTED: similar to CG10343 CG10343-PA
Locus_18093_Transcript_2/2_Conf_1.000	720	20	8.51E-29	XP_968473.1	58	131.339	179	104	PREDICTED: similar to CG10343 CG10343-PA
Locus_18094_Transcript_1/1_Conf_1.000	237	20	3.51E-15	XP_002636807.1	74	84.7297	71	53	Hypothetical protein CBG09249
Locus_18095_Transcript_1/1_Conf_1.000	495	1	7.05E-08	NP_491118.2	46	60.4622	132	62	hypothetical protein Y54E10A.11
Locus_18096_Transcript_1/1_Conf_1.000	141	20	6.11E-12	XP_001998550.1	79	73.9442	44	35	GI23574

Locus_18097_Transcript_1/1_Conf_1.000	316	20	9.02E-43	XP_002638878.1	90	176.407	105	95	C. briggsae CBR-CSN-2 protein
Locus_18098_Transcript_1/1_Conf_1.000	521	0							
Locus_18099_Transcript_1/1_Conf_1.000	289	0							
Locus_181_Transcript_1/1_Conf_1.000	513	20	3.01E-20	NP_500698.1	79	101.679	81	64	Sperm-Specific family, class Q family member (ssq-2)
Locus_1810_Transcript_1/1_Conf_1.000	305	15	2.18E-33	NP_498273.1	85	145.206	90	77	hypothetical protein F01F1.2
Locus_18100_Transcript_1/1_Conf_1.000	234	0							
Locus_18101_Transcript_1/1_Conf_1.000	290	0							
Locus_18102_Transcript_1/1_Conf_1.000	269	20	3.90E-06	XP_002739735.1	49	54.6842	89	44	PREDICTED: UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase 1-like
Locus_18103_Transcript_1/1_Conf_1.000	249	20	6.30E-25	EFO27053.1	79	117.087	82	65	glutaminase
Locus_18104_Transcript_1/1_Conf_1.000	502	3	7.81E-71	CAR63658.1	83	269.626	165	138	hypothetical protein
Locus_18105_Transcript_1/1_Conf_1.000	265	4	2.29E-14	NP_492775.2	75	82.0333	69	52	LAMinin related. See also lmb- family member (lam-3)
Locus_18106_Transcript_1/1_Conf_1.000	548	8	1.00E-33	NP_500822.2	57	146.747	194	112	UNCoordinated family member (unc-5)
Locus_18107_Transcript_1/1_Conf_1.000	547	20	1.50E-21	NP_741042.1	98	106.301	53	52	human PTB (hnRNP) homolog family member (ptb-1)
Locus_18108_Transcript_1/1_Conf_1.000	203	0							
Locus_18109_Transcript_1/1_Conf_1.000	229	20	9.34E-16	NP_001041296.1	80	86.6557	47	38	COLlagen family member (col-181)

Locus_1811_Transcript_1/1_Conf_1.000	1312	20	6.88E-41	NP_491745.1	45	172.94	452	206	hypothetical protein C27A12.2
Locus_18110_Transcript_1/1_Conf_1.000	230	4	4.20E-08	EFO25668.1	64	61.2326	71	46	hypothetical protein LOAG_02820
Locus_18111_Transcript_1/1_Conf_1.000	252	20	6.55E-09	NP_499664.2	60	63.929	83	50	hypothetical protein BE10.2
Locus_18112_Transcript_1/1_Conf_1.000	203	0							
Locus_18113_Transcript_1/1_Conf_1.000	555	0							
Locus_18114_Transcript_1/1_Conf_1.000	158	0							
Locus_18115_Transcript_1/1_Conf_1.000	194	0							
Locus_18116_Transcript_1/1_Conf_1.000	401	20	6.89E-19	EFO28349.1	60	97.0561	105	63	major sperm protein
Locus_18117_Transcript_1/1_Conf_1.000	184	20	1.36E-14	NP_499749.1	87	82.8037	55	48	Aspergillus NUclear Division related family member (nud-1)
Locus_18118_Transcript_1/1_Conf_1.000	453	20	7.48E-42	XP_002640831.1	81	173.326	137	111	Hypothetical protein CBG15718
Locus_18119_Transcript_1/1_Conf_1.000	231	7	8.71E-14	XP_002630536.1	71	80.1073	70	50	Hypothetical protein CBG12976
Locus_1812_Transcript_1/1_Conf_1.000	161	0							
Locus_18120_Transcript_1/1_Conf_1.000	1040	17	5.98E-15	NP_499886.1	49	86.2705	135	67	hypothetical protein R02D3.7

Locus_18121_Transcript_1/1_Conf_1.000	758	20	2.03E-07	XP_002735551.1	44	60.4622	249	111	PREDICTED: janus kinase and microtubule interacting protein 1-like
Locus_18122_Transcript_1/1_Conf_1.000	243	0							
Locus_18123_Transcript_1/2_Conf_1.000	404	11	3.04E-67	ACZ64266.1	91	257.684	134	122	serine protease inhibitor
Locus_18123_Transcript_2/2_Conf_1.000	404	11	3.04E-67	ACZ64266.1	91	257.684	134	122	serine protease inhibitor
Locus_18124_Transcript_1/1_Conf_1.000	171	0							
Locus_18125_Transcript_1/1_Conf_1.000	216	0							
Locus_18126_Transcript_1/1_Conf_1.000	131	0							
Locus_18127_Transcript_1/1_Conf_1.000	372	2	3.92E-22	NP_501557.2	79	107.842	82	65	hypothetical protein C53B4.3
Locus_18128_Transcript_1/1_Conf_1.000	144	0							
Locus_18129_Transcript_1/1_Conf_1.000	136	0							
Locus_1813_Transcript_1/1_Conf_1.000	1352	0							
Locus_18130_Transcript_1/1_Conf_1.000	168	0							
Locus_18131_Transcript_1/2_Conf_0.333	152	0							
Locus_18131_Transcript_2/2_Conf_0.667	151	0							
Locus_18132_Transcript_1/1_Conf_1.000	191	20	3.33E-21	YP_002725716.1	88	104.76	63	56	NADH dehydrogenase subunit 1
Locus_18133_Transcript_1/1_Conf_1.000	271	0							
Locus_18134_Transcript_1/1_Conf_1.000	282	0							
Locus_18135_Transcript_1/1_Conf_1.000	232	0							
Locus_18136_Transcript_1/1_Conf_1.000	375	0							
Locus_18137_Transcript_1/1_Conf_1.000	351	0							

Locus_18138_Transcript_1/1_Conf_1.000	218	20	2.65E-15	XP_002635166.1	72	85.1149	72	52	Hypothetical protein CBG11402
Locus_18139_Transcript_1/1_Conf_1.000	162	0							
Locus_1814_Transcript_1/1_Conf_1.000	635	20	2.93E-74	NP_492761.1	92	281.952	153	141	hypothetical protein F25H2.5
Locus_18140_Transcript_1/1_Conf_1.000	153	5	7.67E-18	XP_002634716.1	91	93.5893	49	45	C. briggsae CBR-EXC-5 protein
Locus_18141_Transcript_1/1_Conf_1.000	1032	20	8.76E-83	AAX34423.1	67	311.612	336	228	anion transporter SULP-5
Locus_18142_Transcript_1/1_Conf_1.000	211	20	6.14E-20	XP_002645743.1	80	100.523	70	56	C. briggsae CBR-UNC-84 protein
Locus_18143_Transcript_1/1_Conf_1.000	140	0							
Locus_18144_Transcript_1/1_Conf_1.000	505	20	2.34E-62	NP_509572.1	84	241.506	156	132	AdaPtin, Alpha chain (clathrin associated complex) family member (apa-2)
Locus_18145_Transcript_1/1_Conf_1.000	146	0							

Locus_18146_Transcript_1/1_Conf_1.000	363	20	4.21E-45	NP_507972.1	84	184.111	122	103	hypothetical protein F26F2.7
Locus_18147_Transcript_1/1_Conf_1.000	721	20	3.18E-92	CBL43435.1	89	342.043	212	189	C. elegans protein F32F2.1e, partially confirmed by transcript evidence
Locus_18148_Transcript_1/1_Conf_1.000	494	20	2.05E-31	XP_002639518.1	61	138.658	153	94	Hypothetical protein CBG04124
Locus_18149_Transcript_1/1_Conf_1.000	147	2	3.84E-09	NP_505266.1	80	64.6994	47	38	hypothetical protein C01B7.5
Locus_1815_Transcript_1/1_Conf_1.000	1411	20	4.72E-67	XP_002630353.1	67	259.996	267	179	Hypothetical protein CBG04283
Locus_18150_Transcript_1/1_Conf_1.000	673	0							
Locus_18151_Transcript_1/1_Conf_1.000	217	0							
Locus_18152_Transcript_1/1_Conf_1.000	437	0							
Locus_18153_Transcript_1/1_Conf_1.000	145	0							
Locus_18154_Transcript_1/1_Conf_1.000	171	2	2.12E-12	XP_002342418.1	100	75.485	50	50	PREDICTED: hypothetical protein XP_002342418
Locus_18155_Transcript_1/1_Conf_1.000	395	20	7.63E-42	EFO26003.1	72	173.326	132	96	SPRY domain-containing protein
Locus_18156_Transcript_1/1_Conf_1.000	566	20	5.94E-64	NP_505071.1	77	247.284	188	145	hypothetical protein ZC513.5
Locus_18157_Transcript_1/1_Conf_1.000	860	20	1.77E-40	XP_002639601.1	66	170.629	247	165	Hypothetical protein CBG12310
Locus_18158_Transcript_1/1_Conf_1.000	227	0							
Locus_18159_Transcript_1/1_Conf_1.000	176	0							
Locus_1816_Transcript_1/1_Conf_1.000	1544	20	1.64E-92	EFO22955.1	58	344.739	470	273	MIZ zinc finger family protein
Locus_18160_Transcript_1/1_Conf_1.000	420	20	4.16E-48	XP_001900297.1	82	194.126	138	114	Importin-beta N-terminal domain containing protein

Locus_18161_Transcript_1/1_Conf_1.000	610	20	6.65E-57	AAC35506.1	81	224.172	158	129	putative actin-binding protein UNC-115
Locus_18162_Transcript_1/1_Conf_1.000	301	0							
Locus_18163_Transcript_1/1_Conf_1.000	201	0							
Locus_18164_Transcript_1/1_Conf_1.000	347	2	4.50E-10	XP_002636871.1	55	67.781	96	53	Hypothetical protein CBG09330
Locus_18165_Transcript_1/1_Conf_1.000	255	3	4.52E-10	XP_002633836.1	75	67.781	83	63	Hypothetical protein CBG19874
Locus_18166_Transcript_1/1_Conf_1.000	427	0							
Locus_18167_Transcript_1/1_Conf_1.000	167	0							
Locus_18168_Transcript_1/1_Conf_1.000	341	7	9.71E-26	CAX65089.1	78	119.783	91	71	C. elegans protein Y54G11A.17, confirmed by transcript evidence
Locus_18169_Transcript_1/1_Conf_1.000	184	0							
Locus_1817_Transcript_1/2_Conf_1.000	475	0							
Locus_1817_Transcript_2/2_Conf_1.000	478	0							
Locus_18170_Transcript_1/1_Conf_1.000	299	20	9.23E-32	NP_502747.1	78	139.813	99	78	hypothetical protein F55B11.1
Locus_18171_Transcript_1/1_Conf_1.000	961	20	1.79E-71	XP_002638881.1	64	273.863	319	205	C. briggsae CBR-VPS-34 protein
Locus_18172_Transcript_1/1_Conf_1.000	150	0							
Locus_18173_Transcript_1/1_Conf_1.000	413	20	7.67E-55	AAT76298.1	94	216.468	115	109	FMRFamide-related peptide FLP-18 precursor
Locus_18174_Transcript_1/1_Conf_1.000	169	0							
Locus_18175_Transcript_1/1_Conf_1.000	336	20	2.03E-31	NP_496483.1	79	138.658	110	87	hypothetical protein F07A11.5
Locus_18176_Transcript_1/1_Conf_1.000	144	0							
Locus_18177_Transcript_1/1_Conf_1.000	186	20	2.17E-12	XP_002635781.1	78	75.485	61	48	Hypothetical protein CBG10437
Locus_18178_Transcript_1/1_Conf_1.000	190	0							

Locus_18179_Transcript_1/1_Conf_1.000	289	20	9.08E-11	XP_001898051.1	61	70.0922	94	58	Ran-binding protein 7
Locus_1818_Transcript_1/1_Conf_1.000	3002	20	0	AAO85274.1	86	983.4	658	570	chondroitin disaccharide polymerase
Locus_18180_Transcript_1/1_Conf_1.000	192	0							
Locus_18181_Transcript_1/1_Conf_1.000	128	2	1.13E-05	NP_498470.1	76	53.1434	42	32	hypothetical protein F37A4.5
Locus_18182_Transcript_1/1_Conf_1.000	314	0							
Locus_18183_Transcript_1/1_Conf_1.000	157	0							
Locus_18184_Transcript_1/1_Conf_1.000	340	0							
Locus_18185_Transcript_1/1_Conf_1.000	152	0							
Locus_18186_Transcript_1/1_Conf_1.000	278	0							
Locus_18187_Transcript_1/1_Conf_1.000	460	2	5.73E-10	XP_002642255.1	71	67.3958	56	40	C. briggsae CBR-FLP-15 protein
Locus_18188_Transcript_1/1_Conf_1.000	132	0							
Locus_18189_Transcript_1/1_Conf_1.000	428	20	5.06E-30	NP_506393.1	66	134.035	145	96	hypothetical protein T01D3.5
Locus_1819_Transcript_1/1_Conf_1.000	3580	20	0	NP_508280.1	87	1718.75	1112	972	hypothetical protein D1005.1
Locus_18190_Transcript_1/1_Conf_1.000	155	0							
Locus_18191_Transcript_1/1_Conf_1.000	157	0							
Locus_18192_Transcript_1/1_Conf_1.000	336	0							

Locus_18193_Transcript_1/1_Conf_1.000	251	20	1.90E-13	XP_002635372.1	84	78.9518	52	44	C. briggsae CBR-RPM-1 protein
Locus_18194_Transcript_1/1_Conf_1.000	229	4	3.93E-06	EFO14601.1	72	54.6842	47	34	hypothetical protein LOAG_13915
Locus_18195_Transcript_1/1_Conf_1.000	151	0							
Locus_18196_Transcript_1/1_Conf_1.000	232	7	7.61E-18	CAX65068.1	73	93.5893	76	56	C. elegans protein K08C7.3d, confirmed by transcript evidence
Locus_18197_Transcript_1/1_Conf_1.000	246	4	8.82E-27	XP_002647365.1	85	123.25	82	70	C. briggsae CBR-SNT-5 protein
Locus_18198_Transcript_1/1_Conf_1.000	722	1	3.72E-08	NP_494776.2	54	62.7734	113	62	hypothetical protein B0286.1
Locus_18199_Transcript_1/1_Conf_1.000	308	0							
Locus_182_Transcript_1/1_Conf_1.000	498	20	1.25E-73	XP_002634875.1	88	278.87	166	147	Hypothetical protein CBG10541
Locus_1820_Transcript_1/1_Conf_1.000	603	20	3.10E-59	NP_492480.1	76	231.876	195	149	hypothetical protein F26H9.4
Locus_18200_Transcript_1/1_Conf_1.000	314	1	1.28E-04	XP_002642931.1	60	49.6766	70	42	C. briggsae CBR-ALH-11 protein
Locus_18201_Transcript_1/1_Conf_1.000	201	20	5.42E-24	NP_004533.1	100	114.005	50	50	NADH dehydrogenase ubiquinone 1 alpha subcomplex subunit 3
Locus_18202_Transcript_1/1_Conf_1.000	162	0							

Locus_18203_Transcript_1/1_Conf_1.000	243	20	1.41E-32	NP_001023645.1	92	142.51	80	74	AKT kinase family member (akt-1)
Locus_18204_Transcript_1/1_Conf_1.000	488	20	1.81E-43	XP_001896664.1	75	178.718	162	122	Protein kinase domain containing protein
Locus_18205_Transcript_1/1_Conf_1.000	272	0							
Locus_18206_Transcript_1/1_Conf_1.000	164	0							
Locus_18207_Transcript_1/1_Conf_1.000	853	20	6.05E-25	NP_510852.1	62	119.013	156	97	hypothetical protein T23E7.2
Locus_18208_Transcript_1/1_Conf_1.000	1381	0							
Locus_18209_Transcript_1/1_Conf_1.000	148	0							
Locus_1821_Transcript_1/1_Conf_1.000	1478	9	1.05E-48	NP_493601.2	46	199.134	515	238	FERM domain (protein4.1-ezrin-radixin-moesin) family member (frm-1)
Locus_18210_Transcript_1/1_Conf_1.000	237	20	7.82E-15	NP_491437.1	69	83.5741	79	55	UDP-GlucuronosylTransferase family member (ugt-28)
Locus_18211_Transcript_1/1_Conf_1.000	136	0							
Locus_18212_Transcript_1/1_Conf_1.000	420	20	6.47E-17	AAD13339.1	50	90.5077	126	63	ancylostoma-secreted protein 1 precursor
Locus_18213_Transcript_1/1_Conf_1.000	483	20	9.27E-48	XP_001897051.1	73	192.971	160	118	RNA polymerase Rpb1, domain 1 family protein
Locus_18214_Transcript_1/1_Conf_1.000	184	0							
Locus_18215_Transcript_1/1_Conf_1.000	135	0							
Locus_18216_Transcript_1/1_Conf_1.000	144	0							

Locus_18217_Transcript_1/1_Conf_1.000	425	20	2.85E-65	NP_502218.1	96	251.136	141	136	hypothetical protein T22B3.2
Locus_18218_Transcript_1/1_Conf_1.000	377	20	2.98E-30	XP_002641557.1	79	134.806	93	74	C. briggsae CBR-PRK-2 protein
Locus_18219_Transcript_1/1_Conf_1.000	503	20	5.41E-72	XP_002646621.1	89	273.478	160	143	Hypothetical protein CBG20508
Locus_1822_Transcript_1/1_Conf_1.000	777	20	5.22E-54	XP_001896728.1	71	215.312	224	160	Rhomboid family protein
Locus_18220_Transcript_1/1_Conf_1.000	228	0							
Locus_18221_Transcript_1/1_Conf_1.000	191	0							
Locus_18222_Transcript_1/1_Conf_1.000	435	3	3.15E-16	XP_002634303.1	62	88.1965	135	85	C. briggsae CBR-NCX-3 protein
Locus_18223_Transcript_1/1_Conf_1.000	166	0							
Locus_18224_Transcript_1/1_Conf_1.000	323	20	1.94E-21	XP_002633194.1	71	105.531	100	71	Hypothetical protein CBG05911
Locus_18225_Transcript_1/1_Conf_1.000	165	20	2.69E-15	NP_506520.1	82	85.1149	52	43	hypothetical protein T16A9.4
Locus_18226_Transcript_1/1_Conf_1.000	158	20	1.88E-24	XP_002930821.1	100	115.546	52	52	PREDICTED: splicing factor U2AF 35 kDa subunit-like
Locus_18227_Transcript_1/1_Conf_1.000	234	0							
Locus_18228_Transcript_1/2_Conf_1.000	835	20	1.12E-68	XP_783119.1	74	264.233	281	208	PREDICTED: similar to mFLJ00229 protein

Locus_18228_Transcript_2/2_Conf_1.000	835	20	1.12E-68	XP_783119.1	74	264.233	281	208	PREDICTED: similar to mFLJ00229 protein
Locus_18229_Transcript_1/1_Conf_1.000	386	0							
Locus_1823_Transcript_1/1_Conf_1.000	593	4	6.35E-30	XP_002640094.1	60	134.42	180	108	Hypothetical protein CBG12581
Locus_18230_Transcript_1/1_Conf_1.000	203	0							
Locus_18231_Transcript_1/1_Conf_1.000	288	0							
Locus_18232_Transcript_1/1_Conf_1.000	268	20	5.99E-23	NP_502118.4	71	110.538	89	64	Gon-Two Like (TRP subfamily) family member (gtl-2)
Locus_18233_Transcript_1/1_Conf_1.000	418	0							
Locus_18234_Transcript_1/1_Conf_1.000	233	20	7.09E-32	CBA11613.1	93	140.198	77	72	C. elegans protein F54F3.1c, partially confirmed by transcript evidence
Locus_18235_Transcript_1/1_Conf_1.000	380	5	2.34E-51	NP_001123175.1	87	204.912	120	105	ImmunoGlobulin-like Cell adhesion Molecule family member (igcm-3)
Locus_18236_Transcript_1/1_Conf_1.000	324	4	9.29E-16	EFO17810.1	71	86.6557	108	77	hypothetical protein LOAG_10687
Locus_18237_Transcript_1/1_Conf_1.000	146	2	1.67E-04	AAC31568.1	60	49.2914	48	29	putative zinc metallopeptidase
Locus_18238_Transcript_1/1_Conf_1.000	492	20	3.72E-41	NP_494918.2	66	171.014	168	111	hypothetical protein T27F7.3
Locus_18239_Transcript_1/1_Conf_1.000	203	20	9.87E-26	EDL12480.1	96	119.783	63	61	eukaryotic translation initiation factor 5A, isoform CRA_d
Locus_1824_Transcript_1/2_Conf_1.000	343	0							

Locus_1824_Transcript_2/2_Conf_1.000	341	0							
Locus_18240_Transcript_1/1_Conf_1.000	734	5	1.32E-24	NP_505973.1	46	117.472	263	123	hypothetical protein F55A11.7
Locus_18241_Transcript_1/1_Conf_1.000	199	0							
Locus_18242_Transcript_1/1_Conf_1.000	339	20	1.27E-17	XP_002632168.1	66	92.8189	112	74	C. briggsae CBR-PQN-85 protein
Locus_18243_Transcript_1/1_Conf_1.000	171	20	3.17E-08	XP_002633325.1	94	61.6178	35	33	Hypothetical protein CBG06062
Locus_18244_Transcript_1/1_Conf_1.000	312	0							
Locus_18245_Transcript_1/1_Conf_1.000	136	0							
Locus_18246_Transcript_1/1_Conf_1.000	480	5	7.00E-08	EFO27664.1	42	60.4622	137	58	BUB protein kinase
Locus_18247_Transcript_1/1_Conf_1.000	323	3	2.71E-23	NP_507767.2	71	111.694	105	75	hypothetical protein C14B4.2
Locus_18248_Transcript_1/1_Conf_1.000	176	20	3.16E-08	EFO19751.1	79	61.6178	48	38	prefoldin subunit 4
Locus_18249_Transcript_1/1_Conf_1.000	275	1	1.25E-04	XP_001901066.1	72	49.6766	40	29	Alpha-catulin
Locus_1825_Transcript_1/1_Conf_1.000	393	20	5.47E-40	ADD10740.1	100	167.162	81	81	ribosomal protein S26

Locus_18250_Transcript_1/1_Conf_1.000	137	0							
Locus_18251_Transcript_1/1_Conf_1.000	102	0							
Locus_18252_Transcript_1/1_Conf_1.000	455	20	1.16E-34	XP_001950864.1	72	149.443	152	110	PREDICTED: similar to werner syndrome helicase
Locus_18253_Transcript_1/1_Conf_1.000	632	2	1.98E-06	NP_506680.1	86	56.6102	37	32	HIstone H1 Like family member (hil-1)
Locus_18254_Transcript_1/1_Conf_1.000	391	2	2.25E-06	XP_002641416.1	53	55.4546	92	49	C. briggsae CBR-SBP-1 protein
Locus_18255_Transcript_1/1_Conf_1.000	305	20	2.48E-45	NP_509268.1	93	184.882	101	94	hypothetical protein F48E3.3
Locus_18256_Transcript_1/1_Conf_1.000	174	0							
Locus_18257_Transcript_1/1_Conf_1.000	211	0							
Locus_18258_Transcript_1/1_Conf_1.000	421	20	1.10E-40	NP_491776.1	85	169.474	119	102	hypothetical protein T09B4.7
Locus_18259_Transcript_1/1_Conf_1.000	692	20	2.68E-45	NP_500997.1	64	186.037	234	150	hypothetical protein C01G5.8
Locus_1826_Transcript_1/1_Conf_1.000	366	20	3.10E-48	CAA21573.2	96	194.512	106	102	C. elegans protein Y106G6H.3, confirmed by transcript evidence
Locus_18260_Transcript_1/1_Conf_1.000	318	0							
Locus_18261_Transcript_1/1_Conf_1.000	612	20	2.74E-50	XP_001891673.1	69	202.216	207	143	hypothetical protein Bm1_00760
Locus_18262_Transcript_1/1_Conf_1.000	514	2	3.24E-06	NP_001021459.2	46	55.0694	135	63	hypothetical protein F36H2.3
Locus_18263_Transcript_1/1_Conf_1.000	616	0							
Locus_18264_Transcript_1/1_Conf_1.000	177	0							
Locus_18265_Transcript_1/1_Conf_1.000	206	20	7.28E-29	EFO28029.1	95	130.183	68	65	AP-1 complex subunit mu-1
Locus_18266_Transcript_1/1_Conf_1.000	293	20	2.54E-21	NP_497959.1	78	105.145	95	75	hypothetical protein T04A8.6
Locus_18267_Transcript_1/1_Conf_1.000	189	0							
Locus_18268_Transcript_1/1_Conf_1.000	299	0							
Locus_18269_Transcript_1/1_Conf_1.000	694	20	3.75E-71	A8XYX2.2	74	271.937	223	166	Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 1A

Locus_1827_Transcript_1/1_Conf_1.000	1883	20	0	NP_499065.1	83	726.087	483	404	hypothetical protein C38C10.2
Locus_18270_Transcript_1/1_Conf_1.000	176	0							
Locus_18271_Transcript_1/1_Conf_1.000	1567	10	2.31E-25	XP_002632478.1	51	121.709	267	137	Hypothetical protein CBG13713
Locus_18272_Transcript_1/1_Conf_1.000	316	0							
Locus_18273_Transcript_1/1_Conf_1.000	397	0							
Locus_18274_Transcript_1/1_Conf_1.000	379	4	6.65E-14	NP_498113.1	73	80.4925	64	47	hypothetical protein C34E10.11
Locus_18275_Transcript_1/1_Conf_1.000	162	20	8.99E-11	XP_002634244.1	98	70.0922	54	53	C. briggsae CBR-LEV-1 protein
Locus_18276_Transcript_1/1_Conf_1.000	219	20	8.21E-36	CAR63550.1	97	153.295	72	70	putative Mediator of RNA polymerase II transcription subunit 6
Locus_18277_Transcript_1/1_Conf_1.000	296	20	4.63E-07	EFO20608.1	66	57.7658	72	48	ran-binding protein 7

Locus_18278_Transcript_1/1_Conf_1.000	201	20	3.39E-26	XP_002633097.1	95	121.324	66	63	C. briggsae CBR-RPC-1 protein
Locus_18279_Transcript_1/1_Conf_1.000	302	0							
Locus_1828_Transcript_1/1_Conf_1.000	1144	20	8.91E-71	NP_491332.1	66	271.937	355	237	NeurABin family member (nab-1)
Locus_18280_Transcript_1/1_Conf_1.000	297	0							
Locus_18281_Transcript_1/1_Conf_1.000	241	5	1.74E-06	XP_001900528.1	71	55.8398	60	43	GRIP domain containing protein
Locus_18282_Transcript_1/1_Conf_1.000	208	1	1.16E-10	NP_492417.2	72	69.707	54	39	Fatty Acid SyNthase family member (fasn-1)
Locus_18283_Transcript_1/1_Conf_1.000	318	20	2.99E-38	XP_002632600.1	87	161.384	105	92	Hypothetical protein CBG21499
Locus_18284_Transcript_1/1_Conf_1.000	129	0							
Locus_18285_Transcript_1/1_Conf_1.000	144	20	1.37E-14	XP_625155.1	82	82.8037	47	39	PREDICTED: similar to WD repeat domain 19, partial
Locus_18286_Transcript_1/2_Conf_1.000	868	20	3.63E-57	XP_002645108.1	76	226.098	165	126	Hypothetical protein CBG16797
Locus_18286_Transcript_2/2_Conf_1.000	725	20	2.56E-57	XP_002645108.1	76	226.098	165	126	Hypothetical protein CBG16797
Locus_18287_Transcript_1/1_Conf_1.000	141	0							
Locus_18288_Transcript_1/1_Conf_1.000	171	0							
Locus_18289_Transcript_1/1_Conf_1.000	243	0							
Locus_1829_Transcript_1/1_Conf_1.000	244	20	3.85E-14	NP_001033569.1	66	81.2629	81	54	SULfate Permease family member (sulp-7)
Locus_18290_Transcript_1/1_Conf_1.000	402	2	8.41E-09	EFO20920.1	52	63.5438	113	59	hypothetical protein LOAG_07566
Locus_18291_Transcript_1/1_Conf_1.000	993	20	1.49E-108	XP_002634112.1	76	397.127	317	244	C. briggsae CBR-COGC-8 protein
Locus_18292_Transcript_1/1_Conf_1.000	609	20	6.90E-46	XP_002646253.1	66	187.578	201	133	C. briggsae CBR-PRG-1 protein
Locus_18293_Transcript_1/1_Conf_1.000	345	0							
Locus_18294_Transcript_1/1_Conf_1.000	394	0							
Locus_18295_Transcript_1/1_Conf_1.000	154	0							
Locus_18296_Transcript_1/1_Conf_1.000	189	0							
Locus_18297_Transcript_1/1_Conf_1.000	460	20	9.35E-45	XP_002635106.1	78	182.956	136	107	C. briggsae CBR-TAG-225 protein
Locus_18298_Transcript_1/1_Conf_1.000	252	20	3.82E-25	EFO16377.1	76	117.857	82	63	hypothetical protein LOAG_12131
Locus_18299_Transcript_1/1_Conf_1.000	266	0							

Locus_183_Transcript_1/1_Conf_1.000	441	20	1.18E-26		70	122.865	148	104	hypothetical protein C52B9.7 - Caenorhabditis elegans
Locus_1830_Transcript_1/1_Conf_1.000	1067	4	2.00E-29	NP_491642.2	52	134.42	235	123	hypothetical protein F46F11.9
Locus_18300_Transcript_1/1_Conf_1.000	337	20	6.54E-22	AAG15121.1	66	107.071	108	72	nuclear receptor NHR-22
Locus_18301_Transcript_1/1_Conf_1.000	201	0							
Locus_18302_Transcript_1/1_Conf_1.000	389	0							
Locus_18303_Transcript_1/1_Conf_1.000	603	20	8.76E-46	XP_002644506.1	61	187.193	200	122	Hypothetical protein CBG14396
Locus_18304_Transcript_1/1_Conf_1.000	163	0							
Locus_18305_Transcript_1/1_Conf_1.000	219	0							
Locus_18306_Transcript_1/1_Conf_1.000	705	20	1.43E-33	XP_002639559.1	78	147.132	114	90	C. briggsae CBR-MEK-2 protein
Locus_18307_Transcript_1/1_Conf_1.000	263	0							
Locus_18308_Transcript_1/1_Conf_1.000	692	8	2.07E-13	XP_002636857.1	51	80.1073	201	103	Hypothetical protein CBG09313
Locus_18309_Transcript_1/1_Conf_1.000	283	0							
Locus_1831_Transcript_1/1_Conf_1.000	664	0							
Locus_18310_Transcript_1/1_Conf_1.000	239	3	6.01E-07	NP_741458.2	61	57.3806	60	37	P38 Map Kinase family member (pmk-2)
Locus_18311_Transcript_1/1_Conf_1.000	290	0							
Locus_18312_Transcript_1/1_Conf_1.000	365	20	8.86E-11	XP_002611624.1	63	70.0922	76	48	hypothetical protein BRAFLDRAFT_117138
Locus_18313_Transcript_1/1_Conf_1.000	427	20	1.91E-61	AAK62032.1	85	238.424	141	121	metalloprotease 1 precursor

Locus_18314_Transcript_1/1_Conf_1.000	339	20	8.55E-06	YP_001805161.1	59	53.5286	84	50	hypothetical protein cce_3747
Locus_18315_Transcript_1/1_Conf_1.000	447	20	2.14E-12	NP_495978.1	72	75.485	68	49	Temporarily Assigned Gene name family member (tag-165)
Locus_18316_Transcript_1/1_Conf_1.000	669	20	7.45E-58	NP_502862.1	73	227.639	197	144	hypothetical protein Y73F8A.26
Locus_18317_Transcript_1/2_Conf_1.000	431	20	8.58E-38	NP_505382.2	69	159.844	143	99	hypothetical protein C24B5.4
Locus_18317_Transcript_2/2_Conf_1.000	431	20	1.01E-38	XP_002637502.1	68	162.925	143	98	Hypothetical protein CBG19223
Locus_18318_Transcript_1/1_Conf_1.000	319	20	4.96E-17	NP_497641.2	67	90.8929	92	62	CaDHerin family member (cdh-1)
Locus_18319_Transcript_1/1_Conf_1.000	247	0							
Locus_1832_Transcript_1/1_Conf_1.000	225	1	5.70E-05	XP_002156800.1	71	50.8322	38	27	PREDICTED: similar to tyrosyl-DNA phodphodiesterase 1
Locus_18320_Transcript_1/1_Conf_1.000	231	0							
Locus_18321_Transcript_1/1_Conf_1.000	1602	7	3.02E-12	XP_002640169.1	35	78.1814	452	162	Hypothetical protein CBG12671

Locus_18322_Transcript_1/1_Conf_1.000	197	20	2.45E-16	XP_002631921.1	97	88.5817	46	45	Hypothetical protein CBG07909
Locus_18323_Transcript_1/1_Conf_1.000	378	20	1.16E-42	NP_001022488.1	92	176.022	103	95	UNCoordinated family member (unc-52)
Locus_18324_Transcript_1/1_Conf_1.000	146	0							
Locus_18325_Transcript_1/1_Conf_1.000	255	0							
Locus_18326_Transcript_1/1_Conf_1.000	139	2	9.48E-05	CAD20812.1	63	50.0618	44	28	SXC2 protein
Locus_18327_Transcript_1/1_Conf_1.000	400	20	2.01E-18	XP_001900715.1	67	95.5153	121	82	hypothetical protein
Locus_18328_Transcript_1/1_Conf_1.000	174	20	8.56E-22	XP_002919926.1	100	106.686	50	50	PREDICTED: hypothetical protein LOC100478075
Locus_18329_Transcript_1/1_Conf_1.000	128	0							
Locus_1833_Transcript_1/1_Conf_1.000	1541	4	6.63E-09	NP_491929.1	41	67.0106	275	115	Suppressor with Morphological effect on Genitalia family member (smg-5)
Locus_18330_Transcript_1/1_Conf_1.000	380	20	5.59E-37	XP_002629723.1	78	157.147	118	93	C. briggsae CBR-UGT-58 protein
Locus_18331_Transcript_1/1_Conf_1.000	195	8	1.44E-08	NP_492568.1	72	62.7734	50	36	Nuclear Pore complex Protein family member (npp-14)
Locus_18332_Transcript_1/1_Conf_1.000	330	20	2.84E-49	P01023.3	100	197.978	99	99	Alpha-2-macroglobulin
Locus_18333_Transcript_1/1_Conf_1.000	334	0							
Locus_18334_Transcript_1/1_Conf_1.000	794	0							
Locus_18335_Transcript_1/1_Conf_1.000	155	0							
Locus_18336_Transcript_1/1_Conf_1.000	241	20	3.60E-36	BAI46776.1	100	154.451	80	80	keratin 8
Locus_18337_Transcript_1/1_Conf_1.000	590	0							

Locus_18338_Transcript_1/1_Conf_1.000	436	20	6.97E-32	NP_500551.2	64	140.198	148	96	hypothetical protein F55F10.1
Locus_18339_Transcript_1/1_Conf_1.000	228	20	1.18E-10	NP_500215.2	63	69.707	71	45	hypothetical protein Y69A2AR.17
Locus_1834_Transcript_1/1_Conf_1.000	254	0							
Locus_18340_Transcript_1/1_Conf_1.000	208	1	1.98E-18	XP_001142623.1	100	95.5153	43	43	PREDICTED: similar to lysyl hydroxylase isoform 5
Locus_18341_Transcript_1/1_Conf_1.000	271	0							
Locus_18342_Transcript_1/1_Conf_1.000	167	0							
Locus_18343_Transcript_1/1_Conf_1.000	229	0							
Locus_18344_Transcript_1/1_Conf_1.000	155	0							
Locus_18345_Transcript_1/1_Conf_1.000	250	0							
Locus_18346_Transcript_1/1_Conf_1.000	237	0							
Locus_18347_Transcript_1/1_Conf_1.000	328	0							
Locus_18348_Transcript_1/1_Conf_1.000	354	0							
Locus_18349_Transcript_1/1_Conf_1.000	260	0							
Locus_1835_Transcript_1/3_Conf_0.714	1177	20	7.73E-25	XP_001892966.1	64	119.398	155	100	KH domain containing protein
Locus_1835_Transcript_2/3_Conf_0.714	1342	20	2.08E-24	XP_001892966.1	69	118.242	135	94	KH domain containing protein

Locus_1835_Transcript_3/3_Conf_0.714	1336	20	9.28E-25	XP_001892966.1	64	119.398	155	100	KH domain containing protein
Locus_18350_Transcript_1/1_Conf_1.000	171	20	6.35E-25	XP_002801692.1	98	117.087	56	55	PREDICTED: hypothetical protein LOC100430805
Locus_18351_Transcript_1/1_Conf_1.000	268	20	2.61E-18	NP_507972.1	63	95.1301	93	59	hypothetical protein F26F2.7
Locus_18352_Transcript_1/1_Conf_1.000	134	0							
Locus_18353_Transcript_1/1_Conf_1.000	249	20	2.16E-33	XP_002630855.1	92	145.206	83	77	Hypothetical protein CBG02570
Locus_18354_Transcript_1/1_Conf_1.000	693	20	9.47E-99	BAA08309.1	91	363.614	231	212	ryanodine receptor
Locus_18355_Transcript_1/1_Conf_1.000	163	20	1.03E-14	NP_508515.2	87	83.1889	47	41	AQuaPorin or aquaglyceroporin related family member (aqp-7)
Locus_18356_Transcript_1/1_Conf_1.000	375	20	1.06E-35	XP_001899245.1	98	152.91	76	75	Dumpy : shorter than wild-type protein 23, isoform b
Locus_18357_Transcript_1/1_Conf_1.000	158	0							
Locus_18358_Transcript_1/1_Conf_1.000	272	0							

Locus_18359_Transcript_1/1_Conf_1.000	238	20	7.04E-32	XP_002189607.1	93	140.198	78	73	PREDICTED: similar to cytochrome b5 reductase 3
Locus_1836_Transcript_1/1_Conf_1.000	950	20	2.40E-52	EFO25070.1	61	210.305	281	172	protein-L-isoaspartate O-methyltransferase domain-containing protein 2
Locus_18360_Transcript_1/1_Conf_1.000	523	7	7.33E-65	ABO36652.1	84	249.98	177	149	latrophilin-like protein 2
Locus_18361_Transcript_1/2_Conf_1.000	442	4	2.23E-09	XP_002631099.1	59	65.4698	82	49	C. briggsae CBR-OOC-3 protein
Locus_18361_Transcript_2/2_Conf_1.000	442	4	2.92E-09	XP_002631099.1	59	65.0846	82	49	C. briggsae CBR-OOC-3 protein
Locus_18362_Transcript_1/1_Conf_1.000	169	0							
Locus_18363_Transcript_1/1_Conf_1.000	157	0							
Locus_18364_Transcript_1/1_Conf_1.000	284	0							
Locus_18365_Transcript_1/1_Conf_1.000	348	20	8.13E-28	XP_002633875.1	66	126.716	113	75	C. briggsae CBR-FEM-1 protein
Locus_18366_Transcript_1/1_Conf_1.000	204	0							
Locus_18367_Transcript_1/1_Conf_1.000	632	20	1.45E-49	NP_001021522.1	74	199.904	161	120	hypothetical protein F59C6.12
Locus_18368_Transcript_1/1_Conf_1.000	534	5	6.05E-09	NP_505360.3	49	64.3142	177	87	hypothetical protein F21C10.9
Locus_18369_Transcript_1/1_Conf_1.000	188	5	1.04E-06	NP_496976.2	59	56.6102	62	37	hypothetical protein Y54G11A.7
Locus_1837_Transcript_1/2_Conf_1.000	2063	20	1.46E-158	NP_505864.1	72	564.688	475	344	GLYcosylation related family member (gly-20)
Locus_1837_Transcript_2/2_Conf_1.000	2063	20	1.46E-158	NP_505864.1	72	564.688	475	344	GLYcosylation related family member (gly-20)

Locus_18370_Transcript_1/1_Conf_1.000	406	20	3.70E-65	NP_495706.2	92	250.751	135	125	hypothetical protein F10B5.8
Locus_18371_Transcript_1/1_Conf_1.000	276	11	8.01E-20	ADD13547.1	78	100.138	93	73	Inositol triphosphate receptor protein 1, isoform h
Locus_18372_Transcript_1/1_Conf_1.000	484	20	7.85E-47	NP_502633.1	74	189.889	155	115	UDP-GlucuronosylTransferase family member (ugt-22)
Locus_18373_Transcript_1/1_Conf_1.000	154	20	6.70E-22	DAA31575.1	100	107.071	51	51	cold shock domain containing E1, RNA-binding
Locus_18374_Transcript_1/1_Conf_1.000	396	0							
Locus_18375_Transcript_1/1_Conf_1.000	234	20	1.21E-15	EFO20381.1	70	86.2705	74	52	ZIP Zinc transporter
Locus_18376_Transcript_1/1_Conf_1.000	169	2	1.43E-08	NP_494782.1	76	62.7734	52	40	hypothetical protein ZK430.1
Locus_18377_Transcript_1/1_Conf_1.000	151	0							
Locus_18378_Transcript_1/1_Conf_1.000	137	0							
Locus_18379_Transcript_1/1_Conf_1.000	242	20	5.56E-29	XP_002640509.1	92	130.568	79	73	C. briggsae CBR-RGA-2 protein
Locus_1838_Transcript_1/1_Conf_1.000	490	20	7.83E-23	XP_002643840.1	77	110.153	105	81	Hypothetical protein CBG02064
Locus_18380_Transcript_1/2_Conf_1.000	329	0							
Locus_18380_Transcript_2/2_Conf_1.000	345	0							
Locus_18381_Transcript_1/1_Conf_1.000	189	0							
Locus_18382_Transcript_1/1_Conf_1.000	491	20	9.51E-45	NP_508165.2	72	182.956	160	116	hypothetical protein F39H12.3
Locus_18383_Transcript_1/1_Conf_1.000	316	20	2.22E-49	XP_001166832.1	100	198.364	98	98	PREDICTED: similar to interferon-gamma isoform 2
Locus_18384_Transcript_1/1_Conf_1.000	375	1	1.30E-09	EFO24319.1	63	66.2402	74	47	hypothetical protein LOAG_04165

Locus_18385_Transcript_1/1_Conf_1.000	425	20	5.07E-38	XP_002633709.1	71	160.614	138	98	Hypothetical protein CBG03392
Locus_18386_Transcript_1/1_Conf_1.000	313	0							
Locus_18387_Transcript_1/1_Conf_1.000	149	0							
Locus_18388_Transcript_1/1_Conf_1.000	491	0							
Locus_18389_Transcript_1/1_Conf_1.000	194	0							
Locus_1839_Transcript_1/1_Conf_1.000	791	20	1.50E-80	NP_001122411.1	82	303.523	234	194	SCP(Small C-terminal domain Phosphatase)-Like phosphatase family member (scpl-1)
Locus_18390_Transcript_1/1_Conf_1.000	320	0							
Locus_18391_Transcript_1/1_Conf_1.000	708	20	7.46E-123	NP_501709.2	97	443.736	235	230	Membrane Calcium ATPase family member (mca-1)
Locus_18392_Transcript_1/1_Conf_1.000	206	0							
Locus_18393_Transcript_1/1_Conf_1.000	548	8	6.68E-54	NP_499047.1	96	213.772	105	101	FOrm-homology and ZInc finger domains family member (fozi-1)
Locus_18394_Transcript_1/1_Conf_1.000	214	20	8.25E-25	NP_510672.2	88	116.701	71	63	Nematode AStacin protease family member (nas-39)
Locus_18395_Transcript_1/1_Conf_1.000	128	0							
Locus_18396_Transcript_1/1_Conf_1.000	139	0							
Locus_18397_Transcript_1/1_Conf_1.000	252	6	3.04E-06	XP_002634634.1	54	55.0694	70	38	Hypothetical protein CBG18497
Locus_18398_Transcript_1/1_Conf_1.000	265	4	4.94E-09	XP_002639468.1	80	64.3142	46	37	Hypothetical protein CBG04063
Locus_18399_Transcript_1/1_Conf_1.000	148	20	7.99E-15	NP_498248.2	91	83.5741	47	43	hypothetical protein Y37B11A.2

Locus_184_Transcript_1/2_Conf_1.000	2838	20	0	NP_500815.2	55	671.774	916	506	Receptor Mediated Endocytosis family member (rme-2)
Locus_184_Transcript_2/2_Conf_1.000	2784	20	0	NP_500815.2	54	676.781	924	508	Receptor Mediated Endocytosis family member (rme-2)
Locus_1840_Transcript_1/1_Conf_1.000	1042	20	1.55E-79	XP_002646388.1	81	300.827	243	198	Hypothetical protein CBG15355
Locus_18400_Transcript_1/1_Conf_1.000	236	0							
Locus_18401_Transcript_1/1_Conf_1.000	236	20	2.53E-13	NP_506352.1	61	78.5666	77	47	TransThyretin-Related family domain family member (ttr-44)
Locus_18402_Transcript_1/1_Conf_1.000	387	0							
Locus_18403_Transcript_1/1_Conf_1.000	133	17	1.02E-06	NP_001024294.1	79	56.6102	44	35	hypothetical protein Y97E10AR.2
Locus_18404_Transcript_1/1_Conf_1.000	215	0							
Locus_18405_Transcript_1/3_Conf_0.625	370	0							
Locus_18405_Transcript_2/3_Conf_0.250	547	4	3.04E-06	XP_392462.3	58	55.4546	129	76	PREDICTED: similar to Stretchin-Mlck CG18255-PA, isoform A
Locus_18405_Transcript_3/3_Conf_0.625	502	20	1.45E-08	XP_392462.3	54	62.7734	164	90	PREDICTED: similar to Stretchin-Mlck CG18255-PA, isoform A
Locus_18406_Transcript_1/1_Conf_1.000	142	1	1.61E-04	AAO63576.1	67	49.2914	46	31	secreted protein 4 precursor
Locus_18407_Transcript_1/1_Conf_1.000	343	0							
Locus_18408_Transcript_1/1_Conf_1.000	435	5	8.24E-33	NP_501257.1	90	143.28	99	90	hypothetical protein F33D4.5

Locus_18409_Transcript_1/1_Conf_1.000	327	4	8.94E-19	NP_492524.2	72	96.6709	79	57	hypothetical protein F30A10.10
Locus_1841_Transcript_1/1_Conf_1.000	909	20	3.90E-73	AAV38629.1	100	279.256	138	138	cellular retinoic acid binding protein 2
Locus_18410_Transcript_1/1_Conf_1.000	203	0							
Locus_18411_Transcript_1/1_Conf_1.000	393	0							
Locus_18412_Transcript_1/1_Conf_1.000	130	20	1.57E-15	XP_575592.2	100	85.8853	43	43	PREDICTED: poly(rC) binding protein 1-like
Locus_18413_Transcript_1/1_Conf_1.000	360	3	8.61E-06	CBW44362.1	51	53.5286	129	67	C. elegans protein C33A11.4b, partially confirmed by transcript evidence
Locus_18414_Transcript_1/1_Conf_1.000	257	0							
Locus_18415_Transcript_1/1_Conf_1.000	230	0							
Locus_18416_Transcript_1/1_Conf_1.000	376	3	4.45E-34	NP_499680.1	83	147.517	98	82	UNCoordinated family member (unc-71)
Locus_18417_Transcript_1/1_Conf_1.000	638	0							
Locus_18418_Transcript_1/1_Conf_1.000	511	20	3.23E-43	XP_001901812.1	66	177.948	177	118	RNase3 domain containing protein
Locus_18419_Transcript_1/1_Conf_1.000	712	8	2.86E-05	XP_002169885.1	42	53.1434	202	85	PREDICTED: similar to cytosolic beta-N-acetylglucosaminidase
Locus_1842_Transcript_1/2_Conf_1.000	1016	20	7.76E-52	NP_491159.2	72	208.764	172	125	hypothetical protein K03E5.1
Locus_1842_Transcript_2/2_Conf_1.000	1553	20	8.45E-105	NP_491159.2	72	385.571	320	231	hypothetical protein K03E5.1

Locus_18420_Transcript_1/1_Conf_1.000	344	20	2.89E-49	EFO18549.1	82	197.978	113	93	hypothetical protein LOAG_09946
Locus_18421_Transcript_1/1_Conf_1.000	473	0							
Locus_18422_Transcript_1/1_Conf_1.000	616	20	1.03E-36	EFO23679.1	73	157.147	186	137	hypothetical protein LOAG_04806
Locus_18423_Transcript_1/1_Conf_1.000	764								
Locus_18424_Transcript_1/1_Conf_1.000	305	6	7.01E-32	NP_500982.2	83	140.198	95	79	hypothetical protein Y73B6BL.24
Locus_18425_Transcript_1/1_Conf_1.000	298	0							
Locus_18426_Transcript_1/1_Conf_1.000	693	20	2.00E-48	XP_002631178.1	60	196.438	246	149	C. briggsae CBR-MAT-2 protein
Locus_18427_Transcript_1/1_Conf_1.000	254	0							
Locus_18428_Transcript_1/1_Conf_1.000	1002	20	1.47E-71	CAA22108.2	64	274.248	335	217	C. elegans protein Y75B8A.24, partially confirmed by transcript evidence
Locus_18429_Transcript_1/1_Conf_1.000	409	2	1.33E-06	XP_002632194.1	61	56.225	70	43	Hypothetical protein CBG07060
Locus_1843_Transcript_1/1_Conf_1.000	159	0							
Locus_18430_Transcript_1/1_Conf_1.000	375	2	1.76E-06	NP_497334.1	50	55.8398	114	57	INverted Formin/formin Three-related family member (inft-1)
Locus_18431_Transcript_1/1_Conf_1.000	387	0							
Locus_18432_Transcript_1/1_Conf_1.000	148	0							
Locus_18433_Transcript_1/1_Conf_1.000	233	0							
Locus_18434_Transcript_1/1_Conf_1.000	211	2	2.77E-04	XP_001892872.1	53	48.521	62	33	hypothetical protein Bm1_07015
Locus_18435_Transcript_1/1_Conf_1.000	444	20	1.33E-54	NP_495436.1	88	215.698	144	127	SQuashed Vulva family member (sqv-7)
Locus_18436_Transcript_1/1_Conf_1.000	132	0							

Locus_18437_Transcript_1/1_Conf_1.000	342	20	5.13E-30	AAP36875.1	100	134.035	83	83	Homo sapiens apolipoprotein C-I
Locus_18438_Transcript_1/1_Conf_1.000	439	0							
Locus_18439_Transcript_1/1_Conf_1.000	432	6	1.62E-12		53	75.8702	142	76	hypothetical protein T28B8.4
Locus_1844_Transcript_1/1_Conf_1.000	530	6	1.88E-63	ABS50363.1	90	245.358	175	159	LIM domain protein variant
Locus_18440_Transcript_1/1_Conf_1.000	211	3	8.31E-09	XP_001901164.1	63	63.5438	69	44	hypothetical protein Bm1_48510
Locus_18441_Transcript_1/1_Conf_1.000	158	0							
Locus_18442_Transcript_1/1_Conf_1.000	177	0							
Locus_18443_Transcript_1/1_Conf_1.000	167	0							
Locus_18444_Transcript_1/1_Conf_1.000	493	0							
Locus_18445_Transcript_1/1_Conf_1.000	196	20	1.82E-19	EFO20545.1	94	98.9821	52	49	beta-centractin
Locus_18446_Transcript_1/1_Conf_1.000	288	20	1.34E-38	XP_002640011.1	90	162.54	95	86	Hypothetical protein CBG12481
Locus_18447_Transcript_1/1_Conf_1.000	237	0							
Locus_18448_Transcript_1/1_Conf_1.000	288	20	4.06E-27	XP_002646691.1	85	124.405	87	74	Hypothetical protein CBG13068
Locus_18449_Transcript_1/1_Conf_1.000	155	0							
Locus_1845_Transcript_1/1_Conf_1.000	1282	20	1.08E-99	NP_499274.3	67	368.237	386	259	Connector/eNhancer of KSR family member (cnk-1)
Locus_18450_Transcript_1/1_Conf_1.000	272	5	6.38E-25	NP_504292.2	84	117.087	88	74	hypothetical protein C37H5.5
Locus_18451_Transcript_1/1_Conf_1.000	298	4	7.34E-13	XP_002631639.1	67	77.0258	58	39	Hypothetical protein CBG20828
Locus_18452_Transcript_1/1_Conf_1.000	136	20	1.73E-06	XP_786652.1	77	55.8398	44	34	PREDICTED: similar to ENSANGP00000028235
Locus_18453_Transcript_1/1_Conf_1.000	147	0							

Locus_18454_Transcript_1/1_Conf_1.000	345	0							
Locus_18455_Transcript_1/1_Conf_1.000	584	2	7.58E-20	EFO20351.1	56	100.908	179	102	phosphatidylinositol 3
Locus_18456_Transcript_1/1_Conf_1.000	800	20	9.75E-43	NP_498636.2	66	177.948	248	165	hypothetical protein T20B12.1
Locus_18457_Transcript_1/1_Conf_1.000	245	0							
Locus_18458_Transcript_1/1_Conf_1.000	143	20	1.19E-07	NP_491930.1	77	59.6918	48	37	DiHydroOrotate Dehydrogenas family member (dhod-1)
Locus_18459_Transcript_1/1_Conf_1.000	328	20	1.34E-14	NP_498936.1	95	82.8037	42	40	hypothetical protein K02D10.1
Locus_1846_Transcript_1/1_Conf_1.000	1645	20	3.33E-139	NP_508777.1	73	499.975	438	324	hypothetical protein C07A12.7
Locus_18460_Transcript_1/1_Conf_1.000	149	0							
Locus_18461_Transcript_1/1_Conf_1.000	283	2	4.25E-08	NP_001022400.1	56	61.2326	81	46	Polarity and Osmotic sensitivity Defect family member (pod-2)
Locus_18462_Transcript_1/1_Conf_1.000	397	20	8.98E-43	XP_002636807.1	76	176.407	131	100	Hypothetical protein CBG09249
Locus_18463_Transcript_1/1_Conf_1.000	306	0							
Locus_18464_Transcript_1/1_Conf_1.000	434	20	2.50E-13	CAR63705.1	100	78.5666	38	38	putative CREB Homolog family member
Locus_18465_Transcript_1/1_Conf_1.000	551	20	3.07E-38	XP_002631239.1	71	161.77	179	128	C. briggsae CBR-LACT-3 protein
Locus_18466_Transcript_1/1_Conf_1.000	200	4	3.31E-05	CBL87058.1	57	51.6026	61	35	C. elegans protein T23F1.7c, partially confirmed by transcript evidence
Locus_18467_Transcript_1/1_Conf_1.000	155	0							

Locus_18468_Transcript_1/1_Conf_1.000	576	20	4.26E-60	CAA72916.2	77	234.572	188	145	serine protease inhibitor-like protein
Locus_18469_Transcript_1/1_Conf_1.000	162	20	7.61E-10	EFO26418.1	78	67.0106	50	39	hypothetical protein LOAG_02063
Locus_1847_Transcript_10/11_Conf_0.481	1586	20	0	BAG64279.1	94	862.448	480	453	unnamed protein product
Locus_1847_Transcript_11/11_Conf_0.556	1275	20	0	BAG62883.1	97	729.169	381	373	unnamed protein product
Locus_1847_Transcript_2/11_Conf_0.444	1251	20	0	AAB21181.1	97	701.049	372	364	immunoglobulin heavy chain
Locus_1847_Transcript_3/11_Conf_0.296	521	20	4.05E-76	AAO17822.1	91	287.345	173	159	anti-rabies SOJB immunoglobulin heavy chain
Locus_1847_Transcript_4/11_Conf_0.259	801	20	4.02E-129	ACN59874.1	99	464.922	222	221	chimeric anti-human type VII collagen immunoglobulin G1
Locus_1847_Transcript_5/11_Conf_0.556	1297	20	0	BAG62883.1	97	729.169	381	373	unnamed protein product
Locus_1847_Transcript_6/11_Conf_0.074	355	20	6.33E-57	ABI74358.1	91	223.402	121	111	immunoglobulin heavy chain variable region
Locus_1847_Transcript_7/11_Conf_0.074	316	20	3.20E-48	AAM75843.1	91	194.512	109	100	immunoglobulin heavy chain variable region

Locus_1847_Transcript_8/11_Conf_0.481	1266	20	0	BAG62883.1	95	691.804	381	362	unnamed protein product
Locus_1847_Transcript_9/11_Conf_0.481	1263	20	0	BAG62883.1	92	649.432	381	353	unnamed protein product
Locus_18470_Transcript_1/1_Conf_1.000	170	0							
Locus_18471_Transcript_1/1_Conf_1.000	306	0							
Locus_18472_Transcript_1/1_Conf_1.000	600	18	2.71E-07	XP_002631917.1	82	59.3066	46	38	Hypothetical protein CBG07905
Locus_18473_Transcript_1/1_Conf_1.000	312	0							
Locus_18474_Transcript_1/1_Conf_1.000	268	2	1.64E-04	NP_491537.1	55	49.2914	76	42	HoloCentric chromosome binding Protein family member (hcp-6)
Locus_18475_Transcript_1/1_Conf_1.000	189	0							
Locus_18476_Transcript_1/1_Conf_1.000	227	0							
Locus_18477_Transcript_1/1_Conf_1.000	1197	20	1.96E-124	NP_001129829.1	74	450.284	367	275	hypothetical protein Y46G5A.19
Locus_18478_Transcript_1/1_Conf_1.000	146	0							
Locus_18479_Transcript_1/1_Conf_1.000	431	0							
Locus_1848_Transcript_1/1_Conf_1.000	1393	20	1.12E-121	NP_490872.1	70	441.425	393	277	BT (Bacillus thuringiensis) toxin REsistant family member (bre-4)
Locus_18480_Transcript_1/1_Conf_1.000	350	20	6.87E-35	BAD88409.1	81	150.214	116	94	multidrug resistance-associated protein
Locus_18481_Transcript_1/1_Conf_1.000	159	20	7.12E-24	XP_001113553.2	100	113.62	52	52	PREDICTED: complement factor B isoform 1
Locus_18482_Transcript_1/1_Conf_1.000	410	1	9.20E-16	CAR63626.1	67	86.6557	77	52	hypothetical protein
Locus_18483_Transcript_1/1_Conf_1.000	1244	20	1.74E-163	NP_001122531.1	80	580.096	415	334	hypothetical protein Y105E8A.23

Locus_18484_Transcript_1/1_Conf_1.000	153	1	6.30E-04	XP_002634303.1	71	47.3654	52	37	C. briggsae CBR-NCX-3 protein
Locus_18485_Transcript_1/1_Conf_1.000	470	20	2.68E-39	NP_499652.1	76	164.851	131	100	hypothetical protein Y111B2A.20
Locus_18486_Transcript_1/1_Conf_1.000	271	3	1.58E-07	XP_002640845.1	55	59.3066	80	44	C. briggsae CBR-CDH-1 protein
Locus_18487_Transcript_1/1_Conf_1.000	128	0							
Locus_18488_Transcript_1/1_Conf_1.000	422	0							
Locus_18489_Transcript_1/1_Conf_1.000	234	20	2.88E-25	NP_494775.1	86	118.242	67	58	ForKHead transcription factor family member (fkh-6)
Locus_1849_Transcript_1/1_Conf_1.000	273	20	3.48E-31	XP_002412610.1	80	137.887	90	72	sorbitol dehydrogenase, putative

Locus_18490_Transcript_1/1_Conf_1.000	342	20	4.49E-34	XP_002641355.1	78	147.517	114	89	C. briggsae CBR-GLY-9 protein
Locus_18491_Transcript_1/1_Conf_1.000	491	20	2.25E-70	NP_496487.1	85	268.085	163	139	hypothetical protein ZK20.4
Locus_18492_Transcript_1/1_Conf_1.000	195	0							
Locus_18493_Transcript_1/1_Conf_1.000	317	7	2.82E-20	XP_002633023.1	78	101.679	74	58	Hypothetical protein CBG21797
Locus_18494_Transcript_1/2_Conf_1.000	416	0							
Locus_18494_Transcript_2/2_Conf_1.000	412	0							
Locus_18495_Transcript_1/1_Conf_1.000	243	0							
Locus_18496_Transcript_1/1_Conf_1.000	402	9	5.63E-13	NP_509538.1	75	77.411	66	50	Apical Junction Molecule family member (ajm-1)
Locus_18497_Transcript_1/1_Conf_1.000	254	0							
Locus_18498_Transcript_1/1_Conf_1.000	334	20	5.35E-40	XP_001894893.1	82	167.162	111	92	MiaB-like tRNA modifying enzyme, archaeal-type family protein
Locus_18499_Transcript_1/1_Conf_1.000	171	0							
Locus_185_Transcript_1/1_Conf_1.000	326	20	1.30E-17	XP_002645122.1	82	92.8189	74	61	Hypothetical protein CBG16816
Locus_1850_Transcript_1/1_Conf_1.000	773	20	6.28E-52	NP_505642.1	59	208.379	250	148	LYSozyme family member (lys-1)
Locus_18500_Transcript_1/1_Conf_1.000	204	0							
Locus_18501_Transcript_1/1_Conf_1.000	367	0							
Locus_18502_Transcript_1/1_Conf_1.000	452	20	7.75E-47	XP_002631100.1	85	189.889	124	106	Hypothetical protein CBG02874
Locus_18503_Transcript_1/1_Conf_1.000	229	0							
Locus_18504_Transcript_1/1_Conf_1.000	442	18	5.46E-32	NP_001023978.1	85	140.584	101	86	hypothetical protein F55C10.5
Locus_18505_Transcript_1/1_Conf_1.000	640	8	3.10E-87	NP_509030.2	95	325.094	169	161	hypothetical protein Y72A10A.1
Locus_18506_Transcript_1/1_Conf_1.000	203	3	4.60E-15	NP_001022279.1	88	84.3445	67	59	Serpentine Receptor, class AB (class A-like) family member (srab-14)

Locus_18507_Transcript_1/1_Conf_1.000	467	20	1.70E-17	XP_002629686.1	61	92.4337	129	79	Hypothetical protein CBG00906
Locus_18508_Transcript_1/1_Conf_1.000	783	20	1.18E-45	NP_506271.1	56	187.578	265	151	C-type LECtin family member (clec-41)
Locus_18509_Transcript_1/1_Conf_1.000	234	0							
Locus_1851_Transcript_1/1_Conf_1.000	2707	20	2.62E-166	XP_002639375.1	59	590.882	908	543	C. briggsae CBR-LET-502 protein
Locus_18510_Transcript_1/1_Conf_1.000	659	6	8.94E-16	EFO27431.1	48	87.8113	235	115	hypothetical protein LOAG_01051
Locus_18511_Transcript_1/1_Conf_1.000	506	20	2.75E-79	XP_002634766.1	87	297.745	170	149	Hypothetical protein CBG05362
Locus_18512_Transcript_1/1_Conf_1.000	148	0							
Locus_18513_Transcript_1/1_Conf_1.000	275	0							
Locus_18514_Transcript_1/1_Conf_1.000	165	20	8.39E-09	EFO16065.1	70	63.5438	51	36	asparagine synthase
Locus_18515_Transcript_1/1_Conf_1.000	765	20	3.01E-115	AAK31527.3	90	418.698	237	214	Neuronal symmetry protein 1, partially confirmed by transcript evidence
Locus_18516_Transcript_1/1_Conf_1.000	370	20	1.64E-52	NP_741809.1	87	208.764	123	108	Beta Carbonic Anhydrase family member (bca-1)
Locus_18517_Transcript_1/1_Conf_1.000	253	0							
Locus_18518_Transcript_1/1_Conf_1.000	171	20	1.73E-22	XP_002634622.1	94	108.997	57	54	Hypothetical protein CBG18478
Locus_18519_Transcript_1/1_Conf_1.000	172	0							
Locus_1852_Transcript_1/1_Conf_1.000	1393	20	0	NP_501804.1	88	647.121	395	350	Seryl tRNA Synthetase family member (srs-2)

Locus_18520_Transcript_1/1_Conf_1.000	203	20	2.36E-11	BAD92295.1	100	72.0182	52	52	HLA-DPA1 protein variant
Locus_18521_Transcript_1/1_Conf_1.000	344	20	4.34E-37	NP_495793.2	78	157.532	113	89	Gamma Butyrobetaine Hydroxylase family member (gbh-2)
Locus_18522_Transcript_1/1_Conf_1.000	275	20	3.05E-27	CAB05601.2	94	124.79	71	67	C. elegans protein R11A5.1b, partially confirmed by transcript evidence
Locus_18523_Transcript_1/1_Conf_1.000	269	20	5.60E-29	AAK62032.1	78	130.568	89	70	metalloprotease 1 precursor
Locus_18524_Transcript_1/1_Conf_1.000	255	20	3.01E-30	NP_741217.1	90	134.806	84	76	EXOSome (multiexonuclease complex) component family member (exos-9)
Locus_18525_Transcript_1/1_Conf_1.000	452	20	1.21E-07	1N0R	48	59.6918	126	61	Designed Ankyrin Repeat Protein With Four Identical Consensus Repeats
Locus_18526_Transcript_1/1_Conf_1.000	228	0							
Locus_18527_Transcript_1/1_Conf_1.000	225	0							
Locus_18528_Transcript_1/1_Conf_1.000	294	0							
Locus_18529_Transcript_1/1_Conf_1.000	525	20	2.06E-22	XP_001898275.1	51	108.997	199	102	GRIP domain containing protein
Locus_1853_Transcript_1/1_Conf_1.000	1125	20	1.04E-63	XP_001897956.1	62	248.44	311	195	UBA/TS-N domain containing protein

Locus_18530_Transcript_1/1_Conf_1.000	743	20	1.92E-87	NP_001021798.2	80	326.25	245	198	Arf-1 Guanine nucleotide Exchange Factor homolog family member (agef-1)
Locus_18531_Transcript_1/1_Conf_1.000	344	0							
Locus_18532_Transcript_1/1_Conf_1.000	695	4	7.66E-24	XP_002641244.1	53	114.775	222	119	Hypothetical protein CBG09112
Locus_18533_Transcript_1/1_Conf_1.000	469	2	9.63E-05	XP_002643723.1	62	50.0618	64	40	Hypothetical protein CBG01914
Locus_18534_Transcript_1/1_Conf_1.000	321	20	7.12E-24	NP_499704.1	66	113.62	105	70	CYtochrome P450 family member (cyp-13A11)
Locus_18535_Transcript_1/1_Conf_1.000	223	0							
Locus_18536_Transcript_1/1_Conf_1.000	889	20	2.55E-13	AAD31839.1	46	80.4925	171	80	AF132291_1ancylostoma-secreted protein 1 precursor
Locus_18537_Transcript_1/1_Conf_1.000	431	0							
Locus_18538_Transcript_1/1_Conf_1.000	403	20	1.62E-52	AAS99337.1	100	208.764	103	103	putative calmodulin isoform a
Locus_18539_Transcript_1/1_Conf_1.000	254	20	4.22E-24	CAM25761.1	100	114.39	72	72	major histocompatibility complex, class II, DP alpha 1
Locus_1854_Transcript_1/1_Conf_1.000	764	0							
Locus_18540_Transcript_1/1_Conf_1.000	292	20	3.79E-17	EFO14797.1	80	91.2781	67	54	hypothetical protein LOAG_13718
Locus_18541_Transcript_1/1_Conf_1.000	346	0							
Locus_18542_Transcript_1/1_Conf_1.000	169	20	2.87E-17	NP_001022911.1	92	91.6633	56	52	HELicase family member (hel-308)
Locus_18543_Transcript_1/1_Conf_1.000	262	20	3.00E-22	NP_499515.1	77	108.227	87	67	hypothetical protein Y41C4A.8

Locus_18544_Transcript_1/2_Conf_1.000	450	20	1.78E-51	EFO23808.1	78	205.297	151	118	hypothetical protein LOAG_04674
Locus_18544_Transcript_2/2_Conf_1.000	450	20	1.78E-51	EFO23808.1	78	205.297	151	118	hypothetical protein LOAG_04674
Locus_18545_Transcript_1/1_Conf_1.000	141	20	5.00E-14	EFO26621.1	91	80.8777	45	41	AIDA-1b

Locus_18546_Transcript_1/1_Conf_1.000	205	17	4.01E-11	CAA93884.2	64	71.2478	68	44	C. elegans protein ZK1067.2, partially confirmed by transcript evidence
Locus_18547_Transcript_1/1_Conf_1.000	179	0							
Locus_18548_Transcript_1/1_Conf_1.000	213	0							
Locus_18549_Transcript_1/1_Conf_1.000	256	0							
Locus_1855_Transcript_1/2_Conf_1.000	1479	1	1.00E-06	XP_002631725.1	42	59.6918	194	83	Hypothetical protein CBG20927
Locus_1855_Transcript_2/2_Conf_1.000	1479	1	1.00E-06	XP_002631725.1	42	59.6918	194	83	Hypothetical protein CBG20927
Locus_18550_Transcript_1/1_Conf_1.000	286	20	9.38E-24	NP_498534.2	84	113.235	70	59	ectopic membrane RuFfLes in embryo family member (rfl-1)
Locus_18551_Transcript_1/1_Conf_1.000	254	1	3.72E-04	XP_002649031.1	64	48.1358	64	41	Hypothetical protein CBG21486
Locus_18552_Transcript_1/2_Conf_1.000	242	0							
Locus_18552_Transcript_2/2_Conf_1.000	242	0							
Locus_18553_Transcript_1/1_Conf_1.000	148	0							
Locus_18554_Transcript_1/1_Conf_1.000	347	20	6.93E-19	NP_491099.1	83	97.0561	68	57	ARp2/3 compleX component family member (arx-7)
Locus_18555_Transcript_1/1_Conf_1.000	360	20	5.55E-29	EFO20693.1	71	130.568	119	85	hypothetical protein LOAG_07794
Locus_18556_Transcript_1/1_Conf_1.000	327	20	3.05E-43	XP_002798643.1	100	177.948	108	108	PREDICTED: keratin, type II cytoskeletal 8 isoform 3
Locus_18557_Transcript_1/1_Conf_1.000	418	20	7.82E-71	XP_002646356.1	96	269.626	139	134	Hypothetical protein CBG12070
Locus_18558_Transcript_1/1_Conf_1.000	131	20	1.86E-16	XP_002640864.1	100	88.9669	43	43	C. briggsae CBR-UNC-25 protein

Locus_18559_Transcript_1/1_Conf_1.000	160	0							
Locus_1856_Transcript_1/3_Conf_0.714	2144	20	0	XP_002639673.1	82	907.131	699	580	Hypothetical protein CBG12391
Locus_1856_Transcript_2/3_Conf_0.714	2144	20	0	XP_002639673.1	82	907.131	699	580	Hypothetical protein CBG12391
Locus_1856_Transcript_3/3_Conf_0.714	2144	20	0	XP_002639673.1	82	907.131	699	580	Hypothetical protein CBG12391
Locus_18560_Transcript_1/1_Conf_1.000	361	0							
Locus_18561_Transcript_1/1_Conf_1.000	811								
Locus_18562_Transcript_1/1_Conf_1.000	313	20	4.68E-15	AAD51334.1	66	84.3445	80	53	Kunitz type serine protease inhibitor
Locus_18563_Transcript_1/1_Conf_1.000	457	0							
Locus_18564_Transcript_1/1_Conf_1.000	139	2	8.57E-06	XP_002632655.1	78	53.5286	38	30	Hypothetical protein CBG21578
Locus_18565_Transcript_1/1_Conf_1.000	471	2	5.07E-14	NP_499928.1	51	80.8777	127	66	hypothetical protein Y66H1A.5
Locus_18566_Transcript_1/1_Conf_1.000	273	0							
Locus_18567_Transcript_1/1_Conf_1.000	193	2	3.11E-11	XP_002631732.1	65	71.633	64	42	Hypothetical protein CBG20934
Locus_18568_Transcript_1/1_Conf_1.000	219	5	1.55E-26	XP_002641766.1	88	122.479	71	63	Hypothetical protein CBG10108
Locus_18569_Transcript_1/1_Conf_1.000	266	0							
Locus_1857_Transcript_1/1_Conf_1.000	306	20	1.85E-16	NP_498551.3	63	88.9669	86	55	Chondroitin ProteoGlycan family member (cpg-2)
Locus_18570_Transcript_1/1_Conf_1.000	302	20	2.12E-20	XP_002635231.1	69	102.064	98	68	Hypothetical protein CBG11474
Locus_18571_Transcript_1/1_Conf_1.000	210	10	1.73E-22	NP_001129927.1	90	108.997	66	60	PhosphoLipase C family member (plc-1)
Locus_18572_Transcript_1/1_Conf_1.000	460	2	2.11E-04	NP_497502.2	50	48.9062	118	59	hypothetical protein Y48G9A.11
Locus_18573_Transcript_1/1_Conf_1.000	296	20	1.30E-25	NP_490949.3	75	119.398	94	71	ABC Transporter family member (abt-2)
Locus_18574_Transcript_1/1_Conf_1.000	257	0							
Locus_18575_Transcript_1/1_Conf_1.000	193	0							

Locus_18576_Transcript_1/1_Conf_1.000	989	20	1.40E-50	NP_503359.2	54	204.527	333	183	SQuashed Vulva family member (sqv-6)
Locus_18577_Transcript_1/1_Conf_1.000	244	0							
Locus_18578_Transcript_1/1_Conf_1.000	234	0							
Locus_18579_Transcript_1/1_Conf_1.000	752	0							
Locus_1858_Transcript_1/1_Conf_1.000	1420	20	3.88E-85	NP_496416.1	58	320.087	488	285	hypothetical protein T24F1.2
Locus_18580_Transcript_1/1_Conf_1.000	172	9	1.79E-19	CAA21636.3	94	98.9821	57	54	C. elegans protein Y38F1A.3, partially confirmed by transcript evidence
Locus_18581_Transcript_1/1_Conf_1.000	294	20	3.18E-32	NP_499664.2	79	141.354	96	76	hypothetical protein BE10.2
Locus_18582_Transcript_1/1_Conf_1.000	173	20	2.87E-09	NP_494824.1	75	65.0846	57	43	hypothetical protein T05A7.6
Locus_18583_Transcript_1/2_Conf_1.000	660	20	8.05E-17	NP_498219.1	58	91.2781	113	66	hypothetical protein F54E7.9
Locus_18583_Transcript_2/2_Conf_1.000	660	20	3.49E-20	NP_498219.1	58	102.449	113	66	hypothetical protein F54E7.9
Locus_18584_Transcript_1/1_Conf_1.000	341	20	6.96E-24	XP_002636068.1	72	113.62	98	71	Hypothetical protein CBG01308
Locus_18585_Transcript_1/1_Conf_1.000	537	0							
Locus_18586_Transcript_1/1_Conf_1.000	298	20	2.14E-12	AAM22023.2	75	75.485	60	45	L15188_2Hypothetical protein C14B9.10
Locus_18587_Transcript_1/1_Conf_1.000	1050	20	1.16E-114	XP_002645256.1	83	417.542	294	245	Hypothetical protein CBG00135
Locus_18588_Transcript_1/1_Conf_1.000	135	4	8.88E-11	XP_002643942.1	84	70.0922	45	38	C. briggsae CBR-LEV-8 protein
Locus_18589_Transcript_1/1_Conf_1.000	224	0							

Locus_1859_Transcript_1/1_Conf_1.000	1479	20	0	XP_002644843.1	90	682.559	409	369	Hypothetical protein CBG05011
Locus_18590_Transcript_1/5_Conf_0.400	203	0							
Locus_18590_Transcript_2/5_Conf_0.400	254	0							
Locus_18590_Transcript_4/5_Conf_0.600	380	0							
Locus_18590_Transcript_5/5_Conf_0.467	245	0							
Locus_18591_Transcript_1/1_Conf_1.000	132	0							
Locus_18592_Transcript_1/1_Conf_1.000	557	20	6.46E-15	XP_001989392.1	55	84.3445	126	70	GH11701
Locus_18593_Transcript_1/1_Conf_1.000	361	20	4.28E-05	NP_741539.2	50	51.2174	120	60	hypothetical protein C18C4.5
Locus_18594_Transcript_1/1_Conf_1.000	182	2	5.04E-09	AAM45145.1	86	64.3142	43	37	AF278680_1L3B25
Locus_18595_Transcript_1/1_Conf_1.000	141	3	6.76E-11	NP_510494.2	84	70.4774	44	37	hypothetical protein C18B12.6
Locus_18596_Transcript_1/1_Conf_1.000	232	0							
Locus_18597_Transcript_1/1_Conf_1.000	130	20	8.34E-17	XP_001114147.2	100	90.1225	43	43	PREDICTED: uncharacterized protein C1orf43-like isoform 3
Locus_18598_Transcript_1/1_Conf_1.000	319	20	4.34E-21	NP_001022673.1	74	104.375	105	78	NADC (Na+-coupled dicarboxylate transporter) family member (nac-3)
Locus_18599_Transcript_1/1_Conf_1.000	229	0							
Locus_186_Transcript_1/3_Conf_0.500	738	0							
Locus_186_Transcript_2/3_Conf_0.600	930	0							
Locus_186_Transcript_3/3_Conf_0.700	806	0							

Locus_1860_Transcript_1/1_Conf_1.000	647	20	4.35E-36	XP_001899156.1	75	155.221	150	113	Nuclear hormone receptor family member nhr-41
Locus_18600_Transcript_1/1_Conf_1.000	222	0							
Locus_18601_Transcript_1/1_Conf_1.000	278	2	4.27E-05	XP_002642236.1	60	51.2174	68	41	Hypothetical protein CBG18218
Locus_18602_Transcript_1/1_Conf_1.000	196	0							
Locus_18603_Transcript_1/1_Conf_1.000	213	20	1.90E-29	NP_493755.1	97	132.109	70	68	MoLTing defective family member (mlt-10)
Locus_18604_Transcript_1/1_Conf_1.000	157	20	1.26E-12	EAW97458.1	100	76.2554	36	36	decorin, isoform CRA_g
Locus_18605_Transcript_1/2_Conf_1.000	444	0							
Locus_18605_Transcript_2/2_Conf_1.000	444	0							
Locus_18606_Transcript_1/1_Conf_1.000	158	1	1.27E-04	XP_002632108.1	78	49.6766	52	41	C. briggsae CBR-PTR-3 protein
Locus_18607_Transcript_1/1_Conf_1.000	387	20	1.27E-33	XP_002630605.1	89	145.976	122	109	Hypothetical protein CBG02267
Locus_18608_Transcript_1/1_Conf_1.000	169	0							
Locus_18609_Transcript_1/1_Conf_1.000	247	0							

Locus_1861_Transcript_1/1_Conf_1.000	450	20	4.69E-52	EFO22655.1	79	207.223	134	106	hypothetical protein LOAG_05826
Locus_18610_Transcript_1/1_Conf_1.000	1013	20	1.75E-112	NP_505849.2	79	410.223	297	236	hypothetical protein T19B10.3
Locus_18611_Transcript_1/1_Conf_1.000	165	0							
Locus_18612_Transcript_1/1_Conf_1.000	224	20	2.64E-18	XP_002639616.1	86	95.1301	60	52	C. briggsae CBR-APM-1 protein
Locus_18613_Transcript_1/1_Conf_1.000	466	5	3.19E-32	XP_002634225.1	66	141.354	150	99	Hypothetical protein CBG01795
Locus_18614_Transcript_1/1_Conf_1.000	172	0							
Locus_18615_Transcript_1/1_Conf_1.000	182	0							
Locus_18616_Transcript_1/1_Conf_1.000	443	5	9.39E-08	NP_510705.1	80	60.077	40	32	hypothetical protein C10E2.6
Locus_18617_Transcript_1/1_Conf_1.000	702	20	2.95E-79	NP_001023875.1	93	298.901	175	163	hypothetical protein F32D8.14
Locus_18618_Transcript_1/2_Conf_1.000	405	0							
Locus_18618_Transcript_2/2_Conf_1.000	428	0							
Locus_18619_Transcript_1/1_Conf_1.000	340	20	1.96E-18	XP_002631544.1	54	95.5153	109	59	Hypothetical protein CBG20713
Locus_1862_Transcript_1/1_Conf_1.000	650	20	1.74E-16	XP_002608187.1	55	90.1225	157	87	hypothetical protein BRAFLDRAFT_125861
Locus_18620_Transcript_1/1_Conf_1.000	239	0							
Locus_18621_Transcript_1/1_Conf_1.000	136	0							
Locus_18622_Transcript_1/1_Conf_1.000	273	0							
Locus_18623_Transcript_1/1_Conf_1.000	146	0							
Locus_18624_Transcript_1/1_Conf_1.000	274	20	5.20E-27	NP_499949.2	90	124.02	90	81	Gut on EXterior family member (gex-2)

Locus_18625_Transcript_1/1_Conf_1.000	224	0							
Locus_18626_Transcript_1/1_Conf_1.000	138	4	5.02E-14	NP_492772.1	93	80.8777	45	42	SET (trithorax/polycomb) domain containing family member (set-18)
Locus_18627_Transcript_1/1_Conf_1.000	369	20	2.08E-39	NP_499603.1	83	165.236	115	96	Protein PHosphatase family member (pph-4.1)
Locus_18628_Transcript_1/1_Conf_1.000	464	20	1.64E-44	NP_496483.1	73	182.185	154	113	hypothetical protein F07A11.5
Locus_18629_Transcript_1/1_Conf_1.000	189	0							
Locus_1863_Transcript_1/1_Conf_1.000	1423	20	2.56E-36	XP_001891682.1	50	157.918	392	198	MRG family protein
Locus_18630_Transcript_1/1_Conf_1.000	143	0							
Locus_18631_Transcript_1/1_Conf_1.000	330	20	1.25E-12	EFA06146.1	59	76.2554	96	57	hypothetical protein TcasGA2_TC008990
Locus_18632_Transcript_1/1_Conf_1.000	319	2	2.81E-20	NP_001024902.1	68	101.679	95	65	hypothetical protein T10B10.4
Locus_18633_Transcript_1/1_Conf_1.000	529	20	1.00E-48	NP_492169.2	72	196.438	161	117	TAF (TBP-associated transcription factor) family member (taf-5)
Locus_18634_Transcript_1/1_Conf_1.000	244	0							
Locus_18635_Transcript_1/1_Conf_1.000	144	20	1.12E-16	NP_492775.2	85	89.7373	47	40	LAMinin related. See also lmb- family member (lam-3)
Locus_18636_Transcript_1/1_Conf_1.000	136	0							
Locus_18637_Transcript_1/1_Conf_1.000	130	0							
Locus_18638_Transcript_1/1_Conf_1.000	134	0							
Locus_18639_Transcript_1/1_Conf_1.000	227	0							

Locus_1864_Transcript_1/1_Conf_1.000	1321	20	8.83E-20	XP_002639715.1	61	102.834	129	79	Hypothetical protein CBG12437
Locus_18640_Transcript_1/1_Conf_1.000	304	20	1.37E-35	NP_510447.1	87	152.525	100	87	hypothetical protein C05G5.1
Locus_18641_Transcript_1/1_Conf_1.000	318	7	3.53E-39	XP_002645055.1	80	164.466	106	85	Hypothetical protein CBG16715
Locus_18642_Transcript_1/1_Conf_1.000	130	0							
Locus_18643_Transcript_1/1_Conf_1.000	341	20	2.09E-36	NP_506047.5	79	155.221	113	90	abnormal CHEmotaxis family member (che-11)
Locus_18644_Transcript_1/1_Conf_1.000	171	0							
Locus_18645_Transcript_1/1_Conf_1.000	427	0							
Locus_18646_Transcript_1/1_Conf_1.000	874	0							
Locus_18647_Transcript_1/1_Conf_1.000	473	20	1.12E-37	EFO25106.1	66	159.458	156	104	hypothetical protein LOAG_03373
Locus_18648_Transcript_1/1_Conf_1.000	123	0							
Locus_18649_Transcript_1/1_Conf_1.000	233	0							
Locus_1865_Transcript_1/2_Conf_0.500	1726	20	1.21E-38	CAR63549.1	86	166.007	99	86	hypothetical protein
Locus_1865_Transcript_2/2_Conf_0.750	2307	20	6.91E-88	CAR63549.1	80	330.102	231	185	hypothetical protein
Locus_18650_Transcript_1/1_Conf_1.000	162	0							
Locus_18651_Transcript_1/1_Conf_1.000	143	0							
Locus_18652_Transcript_1/1_Conf_1.000	492	20	4.40E-42	NP_495617.1	73	174.096	156	114	hypothetical protein B0495.2
Locus_18653_Transcript_1/1_Conf_1.000	244	0							
Locus_18654_Transcript_1/1_Conf_1.000	342	2	4.98E-17	XP_002633839.1	61	90.8929	106	65	Hypothetical protein CBG19878
Locus_18655_Transcript_1/1_Conf_1.000	930	20	3.13E-49	EFO16234.1	60	199.904	303	183	pold2-prov protein
Locus_18656_Transcript_1/1_Conf_1.000	252	20	2.74E-15	AAV88076.1	69	85.1149	78	54	putative retrotransposon polyprotein
Locus_18657_Transcript_1/1_Conf_1.000	258	1	1.15E-05	XP_002646401.1	59	53.1434	86	51	C. briggsae CBR-DYS-1 protein
Locus_18658_Transcript_1/1_Conf_1.000	206	4	3.64E-04	XP_002636748.1	73	48.1358	46	34	Hypothetical protein CBG23475
Locus_18659_Transcript_1/1_Conf_1.000	142	0							

Locus_1866_Transcript_1/2_Conf_1.000	1271	3	1.25E-07	AAO33571.1	50	62.3882	109	55	Thr-Ser protein
Locus_1866_Transcript_2/2_Conf_1.000	1208	3	1.17E-07	AAO33571.1	50	62.3882	109	55	Thr-Ser protein
Locus_18660_Transcript_1/1_Conf_1.000	360	20	1.20E-15	NP_491604.3	56	86.2705	119	67	hypothetical protein T05E8.3
Locus_18661_Transcript_1/1_Conf_1.000	425	0							
Locus_18662_Transcript_1/1_Conf_1.000	190	20	9.36E-24	CAB55030.2	91	113.235	61	56	C. elegans protein Y57A10A.10, partially confirmed by transcript evidence
Locus_18663_Transcript_1/1_Conf_1.000	254	0							
Locus_18664_Transcript_1/1_Conf_1.000	522	4	5.33E-15	NP_001041216.1	59	84.3445	104	62	hypothetical protein C05D9.9
Locus_18665_Transcript_1/1_Conf_1.000	129	0							
Locus_18666_Transcript_1/1_Conf_1.000	219	0							
Locus_18667_Transcript_1/1_Conf_1.000	571	5	5.95E-59	NP_001122951.1	85	230.72	157	135	Rod-like lethal, DYe-filling defective family member (rdy-2)
Locus_18668_Transcript_1/1_Conf_1.000	146	0							
Locus_18669_Transcript_1/1_Conf_1.000	479	20	5.51E-45	XP_002637016.1	75	183.726	141	107	C. briggsae CBR-TTR-27 protein
Locus_1867_Transcript_1/2_Conf_1.000	304	2	2.05E-07	XP_002645104.1	58	58.9214	55	32	Hypothetical protein CBG16791
Locus_1867_Transcript_2/2_Conf_1.000	482	2	2.03E-15	XP_002645104.1	67	85.5001	100	67	Hypothetical protein CBG16791
Locus_18670_Transcript_1/1_Conf_1.000	487	5	3.66E-12	NP_741607.1	51	74.7146	140	72	hypothetical protein T07C12.12
Locus_18671_Transcript_1/1_Conf_1.000	155	11	3.56E-15	XP_002631133.1	84	84.7297	50	42	C. briggsae CBR-CLH-2 protein
Locus_18672_Transcript_1/1_Conf_1.000	217	0							
Locus_18673_Transcript_1/1_Conf_1.000	160	0							
Locus_18674_Transcript_1/1_Conf_1.000	488	1	6.26E-04	XP_001551642.1	47	47.3654	109	52	predicted protein
Locus_18675_Transcript_1/1_Conf_1.000	129	4	2.28E-06	NP_506824.1	76	55.4546	39	30	hypothetical protein T06E6.1
Locus_18676_Transcript_1/1_Conf_1.000	312	20	3.68E-36	XP_002634196.1	87	154.451	99	87	Hypothetical protein CBG01765
Locus_18677_Transcript_1/1_Conf_1.000	416	20	7.38E-58	XP_002641543.1	85	226.483	138	118	Hypothetical protein CBG09842
Locus_18678_Transcript_1/1_Conf_1.000	231	0							
Locus_18679_Transcript_1/1_Conf_1.000	549	0							

Locus_1868_Transcript_1/2_Conf_1.000	1785	20	4.00E-85	CAC42336.2	65	320.472	360	234	C. elegans protein T06E6.2b, confirmed by transcript evidence
Locus_1868_Transcript_2/2_Conf_1.000	1785	20	4.01E-85	CAC42336.2	65	320.472	360	234	C. elegans protein T06E6.2b, confirmed by transcript evidence
Locus_18680_Transcript_1/1_Conf_1.000	476	0							
Locus_18681_Transcript_1/1_Conf_1.000	235	2	2.98E-22	XP_002632209.1	91	108.227	61	56	Hypothetical protein CBG07076
Locus_18682_Transcript_1/1_Conf_1.000	1030	20	1.48E-90	NP_505918.2	72	337.421	309	224	Tubulin Tyrosine Ligase Like family member (ttll-5)
Locus_18683_Transcript_1/1_Conf_1.000	463	3	1.19E-10	EFO18993.1	63	69.707	103	65	hypothetical protein LOAG_09502
Locus_18684_Transcript_1/1_Conf_1.000	241	20	1.79E-27	XP_001901477.1	85	125.561	78	67	Homeobox domain containing protein
Locus_18685_Transcript_1/1_Conf_1.000	226	0							
Locus_18686_Transcript_1/1_Conf_1.000	257	0							
Locus_18687_Transcript_1/1_Conf_1.000	277	0							
Locus_18688_Transcript_1/1_Conf_1.000	166	20	1.25E-20	EFO23546.1	98	102.834	52	51	PDZ domain-containing protein
Locus_18689_Transcript_1/1_Conf_1.000	321	0							
Locus_1869_Transcript_1/2_Conf_1.000	1835	20	2.71E-52	AAC72298.1	51	211.46	479	245	reverse transcriptase
Locus_1869_Transcript_2/2_Conf_1.000	292	1	7.69E-11	ZP_06734949.1	88	63.929	54	48	hypothetical protein NEIELOOT_01783
Locus_18690_Transcript_1/1_Conf_1.000	168	0							
Locus_18691_Transcript_1/1_Conf_1.000	499	20	1.78E-19	EFN65839.1	57	98.9821	149	85	Craniofacial development protein 2
Locus_18692_Transcript_1/1_Conf_1.000	341	0							
Locus_18693_Transcript_1/1_Conf_1.000	172	0							

Locus_18694_Transcript_1/1_Conf_1.000	137	20	1.01E-14	BAB33325.1	82	83.1889	45	37	KIAA1655 protein
Locus_18695_Transcript_1/1_Conf_1.000	201	2	9.61E-05	XP_002630279.1	61	50.0618	62	38	Hypothetical protein CBG00710
Locus_18696_Transcript_1/1_Conf_1.000	547	20	3.56E-39	XP_001902364.1	65	164.851	182	120	Myotubularin-related family protein
Locus_18697_Transcript_1/1_Conf_1.000	446	20	1.75E-30	XP_002631488.1	63	135.576	152	97	C. briggsae CBR-PTR-8 protein
Locus_18698_Transcript_1/1_Conf_1.000	174	0							
Locus_18699_Transcript_1/1_Conf_1.000	262	0							
Locus_187_Transcript_1/1_Conf_1.000	1760	20	1.83E-66	XP_002638761.1	86	258.455	207	180	C. briggsae CBR-MEX-3 protein
Locus_1870_Transcript_1/1_Conf_1.000	289	20	1.44E-32	NP_741546.3	86	142.51	94	81	PAPS (adenosine 3'-phosphate 5'-phosphosulfate) Transporter family member (pst-1)
Locus_18700_Transcript_1/1_Conf_1.000	256	9	4.51E-18	NP_498134.1	72	94.3597	83	60	hypothetical protein F52C9.7

Locus_18701_Transcript_1/1_Conf_1.000	197	20	1.17E-34	3MQL	100	149.443	65	65	CrystalStructure OfThe Fibronectin 6fni1-2fnii7fni Fragment
Locus_18702_Transcript_1/1_Conf_1.000	215	0							
Locus_18703_Transcript_1/1_Conf_1.000	129	0							
Locus_18704_Transcript_1/1_Conf_1.000	604	20	1.41E-11	NP_001121593.1	47	73.559	184	87	sinc finger protein Ci-ZF(C2H2)-148
Locus_18705_Transcript_1/1_Conf_1.000	410	20	1.05E-27	XP_002635372.1	66	126.331	137	91	C. briggsae CBR-RPM-1 protein
Locus_18706_Transcript_1/1_Conf_1.000	539	0							
Locus_18707_Transcript_1/1_Conf_1.000	619	20	4.07E-49	AAF98588.2	67	198.364	167	112	Trehalase protein 2, confirmed by transcript evidence
Locus_18708_Transcript_1/1_Conf_1.000	217	20	2.93E-14	XP_002640651.1	83	81.6481	60	50	Hypothetical protein CBG19709
Locus_18709_Transcript_1/1_Conf_1.000	374	0							
Locus_1871_Transcript_1/1_Conf_1.000	1713	20	0	NP_510705.1	78	666.766	563	441	hypothetical protein C10E2.6
Locus_18710_Transcript_1/1_Conf_1.000	415	20	7.16E-45	XP_002633760.1	82	183.341	121	100	C. briggsae CBR-GON-1 protein
Locus_18711_Transcript_1/1_Conf_1.000	326	4	2.06E-31	XP_002640784.1	76	138.658	101	77	Hypothetical protein CBG15659
Locus_18712_Transcript_1/1_Conf_1.000	191	20	2.02E-18	NP_504228.2	88	95.5153	53	47	human GoNadotropin-Releasing hormone Receptor (GnRHR) related family member (gnrr-5)

Locus_18713_Transcript_1/1_Conf_1.000	923	20	1.15E-96	XP_002641314.1	78	357.451	292	230	Hypothetical protein CBG24614
Locus_18714_Transcript_1/1_Conf_1.000	154	0							
Locus_18715_Transcript_1/1_Conf_1.000	139	0							
Locus_18716_Transcript_1/1_Conf_1.000	218	0							
Locus_18717_Transcript_1/1_Conf_1.000	317	20	2.47E-24	NP_509760.2	73	115.161	105	77	Temporarily Assigned Gene name family member (tag-289)
Locus_18718_Transcript_1/1_Conf_1.000	148	2	1.37E-06	XP_002640681.1	70	56.225	48	34	Hypothetical protein CBG19743
Locus_18719_Transcript_1/1_Conf_1.000	134	1	1.52E-10	EAW50568.1	100	69.3218	44	44	hCG1990620
Locus_1872_Transcript_1/1_Conf_1.000	795	20	3.24E-22	XP_001900476.1	70	109.768	104	73	DNA / pantothenate metabolism flavoprotein
Locus_18720_Transcript_1/1_Conf_1.000	184	5	4.68E-23	CAB04449.3	90	110.923	61	55	C. elegans protein F53A2.1, partially confirmed by transcript evidence
Locus_18721_Transcript_1/1_Conf_1.000	177	0							
Locus_18722_Transcript_1/1_Conf_1.000	249	2	1.51E-10	XP_001892617.1	62	69.3218	81	51	Protein kinase domain containing protein
Locus_18723_Transcript_1/1_Conf_1.000	766	9	2.80E-12	NP_499886.1	46	76.6406	187	87	hypothetical protein R02D3.7
Locus_18724_Transcript_1/1_Conf_1.000	154	20	1.65E-20	XP_002799187.1	100	102.449	51	51	PREDICTED: protein disulfide-isomerase A6 isoform 2
Locus_18725_Transcript_1/1_Conf_1.000	214	20	7.72E-23	XP_001891673.1	87	110.153	71	62	hypothetical protein Bm1_00760
Locus_18726_Transcript_1/1_Conf_1.000	158	0							

Locus_18727_Transcript_1/1_Conf_1.000	230	2	2.82E-04	XP_002641697.1	66	48.521	42	28	C. briggsae CBR-PRI-1 protein
Locus_18728_Transcript_1/1_Conf_1.000	149	0							
Locus_18729_Transcript_1/1_Conf_1.000	379	0							
Locus_1873_Transcript_1/2_Conf_1.000	1373	0							
Locus_1873_Transcript_2/2_Conf_1.000	1385	0							
Locus_18730_Transcript_1/1_Conf_1.000	176	0							
Locus_18731_Transcript_1/1_Conf_1.000	488	0							
Locus_18732_Transcript_1/1_Conf_1.000	281	0							
Locus_18733_Transcript_1/1_Conf_1.000	296	3	6.20E-36	CAR63525.1	84	153.68	98	83	hypothetical protein
Locus_18734_Transcript_1/1_Conf_1.000	1167	20	2.35E-58	NP_498041.1	57	230.72	313	181	SET (trithorax/polycomb) domain containing family member (set-2)
Locus_18735_Transcript_1/1_Conf_1.000	298	20	5.95E-47	NP_509871.2	92	190.274	98	91	Heparan SulphoTransferase family member (hst-2)
Locus_18736_Transcript_1/1_Conf_1.000	508	0							
Locus_18737_Transcript_1/1_Conf_1.000	208	20	1.47E-21	AAB65324.3	83	105.916	65	54	Hypothetical protein F40A3.5
Locus_18738_Transcript_1/1_Conf_1.000	305	20	3.86E-22	XP_002635372.1	67	107.842	106	72	C. briggsae CBR-RPM-1 protein
Locus_18739_Transcript_1/1_Conf_1.000	393	20	8.19E-28	NP_001040743.1	68	126.716	130	89	hypothetical protein C17C3.1
Locus_1874_Transcript_1/1_Conf_1.000	985	3	2.65E-17	NP_001122695.1	44	93.9745	327	146	hypothetical protein F34D10.9
Locus_18740_Transcript_1/1_Conf_1.000	172	20	2.95E-22	NP_503409.1	92	108.227	57	53	SyNapTotagmin family member (snt-5)

Locus_18741_Transcript_1/1_Conf_1.000	302	20	1.33E-30	NP_001021871.1	77	135.961	105	81	UNCoordinated family member (unc-13)
Locus_18742_Transcript_1/1_Conf_1.000	547	20	3.95E-22	NP_501018.1	62	108.227	130	81	Dicer Related Helicase family member (drh-1)
Locus_18743_Transcript_1/1_Conf_1.000	305	3	4.58E-07	NP_505360.3	54	57.7658	102	56	hypothetical protein F21C10.9
Locus_18744_Transcript_1/1_Conf_1.000	518	0							
Locus_18745_Transcript_1/1_Conf_1.000	226	0							
Locus_18746_Transcript_1/1_Conf_1.000	363	0							
Locus_18747_Transcript_1/1_Conf_1.000	242	20	6.15E-28	NP_498711.1	85	127.102	80	68	TYRosinase family member (tyr-1)
Locus_18748_Transcript_1/1_Conf_1.000	374	0							
Locus_18749_Transcript_1/1_Conf_1.000	462	20	3.67E-28	NP_491439.1	68	127.872	135	92	hypothetical protein C10H11.8
Locus_1875_Transcript_1/1_Conf_1.000	1225	20	6.90E-165	AAK28335.1	88	584.719	365	324	glycogen synthase
Locus_18750_Transcript_1/1_Conf_1.000	164	0							
Locus_18751_Transcript_1/1_Conf_1.000	194	0							
Locus_18752_Transcript_1/1_Conf_1.000	268	7	6.66E-06	XP_002644661.1	55	53.9138	88	49	Hypothetical protein CBG14642
Locus_18753_Transcript_1/1_Conf_1.000	174	0							
Locus_18754_Transcript_1/1_Conf_1.000	155	20	4.50E-18	CBI70492.1	98	94.3597	51	50	vacuolar ATPase a subunit
Locus_18755_Transcript_1/1_Conf_1.000	336	0							

Locus_18756_Transcript_1/1_Conf_1.000	497	20	2.73E-60	NP_001122508.1	85	234.572	165	141	DeHydrogenases, Short chain family member (dhs-3)
Locus_18757_Transcript_1/1_Conf_1.000	692	20	2.17E-79	XP_002633915.1	74	299.286	225	167	Hypothetical protein CBG19981
Locus_18758_Transcript_1/1_Conf_1.000	207	2	6.39E-09	XP_002645082.1	83	63.929	48	40	C. briggsae CBR-DHS-29 protein
Locus_18759_Transcript_1/1_Conf_1.000	290	2	8.23E-04	NP_001122656.1	58	46.9802	96	56	hypothetical protein Y46G5A.18
Locus_1876_Transcript_1/1_Conf_1.000	323	0							
Locus_18760_Transcript_1/1_Conf_1.000	200	16	1.48E-13	NP_490834.1	75	79.337	65	49	hypothetical protein Y48G8AL.1
Locus_18761_Transcript_1/1_Conf_1.000	595	4	1.54E-23	XP_002639320.1	60	113.235	136	82	C. briggsae CBR-DCT-9 protein
Locus_18762_Transcript_1/1_Conf_1.000	270	0							
Locus_18763_Transcript_1/1_Conf_1.000	1067	20	0	ACJ65168.1	94	653.284	354	336	Uncoordinated protein 68, isoform b, partially confirmed by transcript evidence
Locus_18764_Transcript_1/1_Conf_1.000	400	20	9.96E-18	XP_002640827.1	70	93.2041	93	66	Hypothetical protein CBG15714
Locus_18765_Transcript_1/1_Conf_1.000	224	0							
Locus_18766_Transcript_1/1_Conf_1.000	301	9	1.92E-21	NP_492082.2	69	105.531	100	69	hypothetical protein F07A5.4
Locus_18767_Transcript_1/1_Conf_1.000	288	0							
Locus_18768_Transcript_1/1_Conf_1.000	157	0							
Locus_18769_Transcript_1/1_Conf_1.000	169	0							
Locus_1877_Transcript_1/1_Conf_1.000	1054	20	4.77E-76	NP_501805.1	68	289.271	321	221	hypothetical protein F44D12.1
Locus_18770_Transcript_1/1_Conf_1.000	318	0							
Locus_18771_Transcript_1/1_Conf_1.000	157	0							
Locus_18772_Transcript_1/1_Conf_1.000	185	0							

Locus_18773_Transcript_1/1_Conf_1.000	903	20	1.04E-102	XP_002640962.1	75	377.481	294	222	Hypothetical protein CBG11705
Locus_18774_Transcript_1/1_Conf_1.000	128	4	7.35E-05	ABI52804.1	76	50.447	38	29	mitochondrial associated endoribonuclease MAR1-isochorismatase superfamily
Locus_18775_Transcript_1/1_Conf_1.000	246	2	4.26E-05	XP_002631065.1	75	51.2174	69	52	C. briggsae CBR-SFXN-1.4 protein
Locus_18776_Transcript_1/1_Conf_1.000	581	0							
Locus_18777_Transcript_1/1_Conf_1.000	204	1	8.11E-04	XP_002634811.1	52	46.9802	55	29	Hypothetical protein CBG13916
Locus_18778_Transcript_1/1_Conf_1.000	155	13	2.02E-10	AAS47831.1	78	68.9366	46	36	metalloprotease IV
Locus_18779_Transcript_1/1_Conf_1.000	315	0							
Locus_1878_Transcript_1/2_Conf_1.000	401	20	5.24E-43	XP_002637058.1	80	177.178	128	103	C. briggsae CBR-TTR-19 protein
Locus_1878_Transcript_2/2_Conf_1.000	469	20	8.05E-44	XP_002637058.1	80	179.874	130	105	C. briggsae CBR-TTR-19 protein
Locus_18780_Transcript_1/1_Conf_1.000	294	20	1.30E-17	XP_002642870.1	66	92.8189	78	52	Hypothetical protein CBG15140
Locus_18781_Transcript_1/1_Conf_1.000	144	0							
Locus_18782_Transcript_1/1_Conf_1.000	306	0							
Locus_18783_Transcript_1/1_Conf_1.000	169	20	1.09E-16	NP_510342.1	80	89.7373	56	45	hypothetical protein C33G3.4
Locus_18784_Transcript_1/1_Conf_1.000	509	20	7.77E-29	XP_002629716.1	59	130.183	170	101	Hypothetical protein CBG00946
Locus_18785_Transcript_1/1_Conf_1.000	566	20	8.95E-28	P0C5E7.1	55	127.102	195	109	Phosphatidylinositol 3-kinase age-1

Locus_18786_Transcript_1/1_Conf_1.000	373	20	1.77E-06	XP_001661184.1	73	55.8398	41	30	beta-1,3-n-acetylglucosaminyltransferase radical fringe (o-fucosylpeptide 3-beta-n-acetylglucosaminyltransferase)
Locus_18787_Transcript_1/1_Conf_1.000	180	20	5.37E-19	ACJ65168.1	100	97.4413	59	59	Uncoordinated protein 68, isoform b, partially confirmed by transcript evidence
Locus_18788_Transcript_1/1_Conf_1.000	133	20	2.19E-17	EFO20074.1	97	92.0485	43	42	KIN protein
Locus_18789_Transcript_1/1_Conf_1.000	457	3	3.03E-35	NP_496398.2	71	151.369	133	95	hypothetical protein T06D8.1
Locus_1879_Transcript_1/1_Conf_1.000	946	6	2.09E-56	XP_002636983.1	68	223.787	257	176	C. briggsae CBR-PQN-22 protein
Locus_18790_Transcript_1/1_Conf_1.000	245	0							
Locus_18791_Transcript_1/1_Conf_1.000	610	20	1.50E-24	XP_001900249.1	67	116.701	127	86	Ctr copper transporter family protein
Locus_18792_Transcript_1/1_Conf_1.000	223	0							
Locus_18793_Transcript_1/1_Conf_1.000	297	4	6.01E-15	EFO26610.1	68	83.9593	77	53	hypothetical protein LOAG_01866

Locus_18794_Transcript_1/1_Conf_1.000	369	20	6.91E-35	3O47	100	150.214	72	72	CrystalStructure Of Arfgap1-Arf1 Fusion Protein
Locus_18795_Transcript_1/1_Conf_1.000	130	0							
Locus_18796_Transcript_1/1_Conf_1.000	546	0							
Locus_18797_Transcript_1/1_Conf_1.000	181	20	7.75E-18	AAD00776.1	88	93.5893	53	47	2,5 dihydroxyphenylacetate oxidase
Locus_18798_Transcript_1/1_Conf_1.000	724	7	4.09E-55	CBA11611.1	74	218.779	246	184	C. elegans protein F53B7.2b, partially confirmed by transcript evidence
Locus_18799_Transcript_1/1_Conf_1.000	245	20	9.14E-32	EFO18852.1	93	139.813	81	76	RNA polymerase III 128kD subunit-PA
Locus_188_Transcript_1/1_Conf_1.000	311	0							
Locus_1880_Transcript_1/1_Conf_1.000	519	0							
Locus_18800_Transcript_1/1_Conf_1.000	314	4	3.14E-11	EFO28277.1	69	71.633	59	41	piwi domain-containing protein
Locus_18801_Transcript_1/1_Conf_1.000	273	20	7.29E-13	XP_002647311.1	72	77.0258	75	54	Hypothetical protein CBG06352
Locus_18802_Transcript_1/1_Conf_1.000	128	0							
Locus_18803_Transcript_1/1_Conf_1.000	205	0							
Locus_18804_Transcript_1/1_Conf_1.000	129	6	2.43E-08	NP_001076639.1	97	62.003	39	38	TWiK family of potassium channels family member (twk-39)

Locus_18805_Transcript_1/1_Conf_1.000	199	6	3.00E-06	NP_508151.1	62	55.0694	62	39	Intracellular LEctin family member (ile-2)
Locus_18806_Transcript_1/1_Conf_1.000	412	0							
Locus_18807_Transcript_1/1_Conf_1.000	843	4	1.01E-24	NP_001040707.1	59	118.242	197	118	CDT (S. pombe CDC10 Dependent Transcript) homolog family member (cdt-1)
Locus_18808_Transcript_1/1_Conf_1.000	222	20	1.54E-34	3O78	100	149.058	73	73	TheStructure Of Ca2+ Sensor (Case-12)
Locus_18809_Transcript_1/1_Conf_1.000	222	5	9.11E-11	XP_002641407.1	65	70.0922	69	45	C. briggsae CBR-SUCH-1 protein
Locus_1881_Transcript_1/2_Conf_0.750	133	0							
Locus_1881_Transcript_2/2_Conf_0.958	166	5	1.13E-05	XP_001348421.2	67	53.1434	55	37	conserved Plasmodium protein, unknown function
Locus_18810_Transcript_1/1_Conf_1.000	155	0							
Locus_18811_Transcript_1/1_Conf_1.000	361	20	1.78E-27	NP_502580.2	85	125.561	92	79	hypothetical protein Y62E10A.13
Locus_18812_Transcript_1/1_Conf_1.000	323	0							
Locus_18813_Transcript_1/1_Conf_1.000	365	20	1.76E-59	ABD77505.1	98	231.876	120	118	60S ribosomal protein L34-like protein
Locus_18814_Transcript_1/1_Conf_1.000	327	0							

Locus_18815_Transcript_1/1_Conf_1.000	375	0							
Locus_18816_Transcript_1/1_Conf_1.000	300	0							
Locus_18817_Transcript_1/1_Conf_1.000	472	20	4.40E-42	NP_497903.1	82	174.096	128	105	anNEXin family member (nex-3)
Locus_18818_Transcript_1/1_Conf_1.000	168	0							
Locus_18819_Transcript_1/1_Conf_1.000	140	0							
Locus_1882_Transcript_1/1_Conf_1.000	250	0							
Locus_18820_Transcript_1/1_Conf_1.000	164	0							
Locus_18821_Transcript_1/1_Conf_1.000	210	0							
Locus_18822_Transcript_1/1_Conf_1.000	230	8	2.63E-10	NP_502123.1	71	68.5514	60	43	hypothetical protein B0035.13
Locus_18823_Transcript_1/1_Conf_1.000	135	0							
Locus_18824_Transcript_1/1_Conf_1.000	178	0							
Locus_18825_Transcript_1/1_Conf_1.000	140	0							
Locus_18826_Transcript_1/1_Conf_1.000	189	20	3.68E-20	3ICH	100	101.293	63	63	CrystalStructure Of Cyclophilin B At 1.2 A Resolution
Locus_18827_Transcript_1/1_Conf_1.000	143	3	8.00E-04	AAB42328.2	81	46.9802	38	31	Hypothetical protein C32E8.11
Locus_18828_Transcript_1/1_Conf_1.000	768	4	3.70E-04	XP_002099137.1	41	49.6766	181	75	GE23539
Locus_18829_Transcript_1/1_Conf_1.000	378	20	7.05E-40	XP_002642051.1	74	166.777	126	94	Hypothetical protein CBG17988
Locus_1883_Transcript_1/2_Conf_1.000	2056	20	3.03E-156	NP_501180.1	70	556.984	531	375	hypothetical protein C48A7.2

Locus_1883_Transcript_2/2_Conf_1.000	1981	20	1.93E-160	NP_501180.1	74	570.852	506	375	hypothetical protein C48A7.2
Locus_18830_Transcript_1/1_Conf_1.000	154	0							
Locus_18831_Transcript_1/1_Conf_1.000	168	0							
Locus_18832_Transcript_1/1_Conf_1.000	334	0							
Locus_18833_Transcript_1/1_Conf_1.000	258	0							
Locus_18834_Transcript_1/1_Conf_1.000	180	0							
Locus_18835_Transcript_1/1_Conf_1.000	627	0							
Locus_18836_Transcript_1/1_Conf_1.000	190	0							
Locus_18837_Transcript_1/2_Conf_1.000	370	0							
Locus_18837_Transcript_2/2_Conf_1.000	369	0							
Locus_18838_Transcript_1/1_Conf_1.000	167	0							
Locus_18839_Transcript_1/1_Conf_1.000	423	0							
Locus_1884_Transcript_1/1_Conf_1.000	1248	20	1.37E-83	XP_002634010.1	57	314.694	433	248	C. briggsae CBR-RABS-5 protein
Locus_18840_Transcript_1/1_Conf_1.000	176	0							
Locus_18841_Transcript_1/1_Conf_1.000	577	20	1.04E-74	NP_491574.1	85	283.108	195	167	hypothetical protein F55A12.8
Locus_18842_Transcript_1/1_Conf_1.000	432	6	4.28E-05	AAD13339.1	52	51.2174	76	40	ancylostoma-secreted protein 1 precursor
Locus_18843_Transcript_1/1_Conf_1.000	261	6	1.60E-07	XP_002630534.1	69	59.3066	66	46	Hypothetical protein CBG12974
Locus_18844_Transcript_1/1_Conf_1.000	146	20	1.08E-11	NP_500458.1	81	73.1738	48	39	hypothetical protein F47C12.1
Locus_18845_Transcript_1/1_Conf_1.000	625	2	1.33E-15	XP_001892397.1	49	87.0409	187	93	hypothetical protein Bm1_04595
Locus_18846_Transcript_1/1_Conf_1.000	210	0							
Locus_18847_Transcript_1/1_Conf_1.000	129	0							
Locus_18848_Transcript_1/1_Conf_1.000	128	0							
Locus_18849_Transcript_1/1_Conf_1.000	148	20	1.41E-11	NP_502513.1	93	72.7886	43	40	hypothetical protein C39E9.10
Locus_1885_Transcript_1/1_Conf_1.000	626	20	3.49E-32	XP_001895135.1	62	142.124	180	112	replication factor A 73 kDa subunit
Locus_18850_Transcript_1/1_Conf_1.000	130	0							
Locus_18851_Transcript_1/1_Conf_1.000	419	20	4.17E-56	XP_001894250.1	87	220.705	139	122	Low-density lipoprotein receptor-related protein
Locus_18852_Transcript_1/1_Conf_1.000	305	4	2.05E-23	NP_001021638.1	71	112.079	101	72	hypothetical protein T23G11.6
Locus_18853_Transcript_1/1_Conf_1.000	353	0							

Locus_18854_Transcript_1/1_Conf_1.000	128	16	3.52E-07	NP_501934.3	69	58.151	42	29	hypothetical protein F01D4.3
Locus_18855_Transcript_1/1_Conf_1.000	640	20	1.09E-108	NP_491193.2	98	396.356	215	211	Calcium Channel, Beta subunit family member (ccb-1)
Locus_18856_Transcript_1/1_Conf_1.000	451	20	2.59E-26	NP_501549.1	98	121.709	65	64	RAP homolog (vertebrate Rap GTPase family) family member (rap-1)
Locus_18857_Transcript_1/1_Conf_1.000	212	10	1.33E-06	CAN86632.2	63	56.225	69	44	C. elegans protein Y48C3A.18b, confirmed by transcript evidence
Locus_18858_Transcript_1/1_Conf_1.000	437	0							
Locus_18859_Transcript_1/1_Conf_1.000	338	20	4.49E-55	AAL06640.1	95	217.238	112	107	serine-threonine protein kinase
Locus_1886_Transcript_1/1_Conf_1.000	1882	20	0	XP_002647048.1	89	956.822	596	534	Hypothetical protein CBG03566
Locus_18860_Transcript_1/1_Conf_1.000	196	4	2.72E-07	NP_001021444.1	59	58.5362	59	35	DAP (Death Associated Protein kinase) Like Kinase family member (dlk-1)
Locus_18861_Transcript_1/1_Conf_1.000	255	5	5.89E-18	NP_510539.1	80	93.9745	62	50	hypothetical protein Y15E3A.4
Locus_18862_Transcript_1/1_Conf_1.000	172	0							
Locus_18863_Transcript_1/1_Conf_1.000	349	0							

Locus_18864_Transcript_1/1_Conf_1.000	803	20	9.24E-25	XP_421314.2	51	118.242	230	118	PREDICTED: hypothetical protein
Locus_18865_Transcript_1/1_Conf_1.000	209	0							
Locus_18866_Transcript_1/2_Conf_1.000	261	0							
Locus_18866_Transcript_2/2_Conf_1.000	520	0							
Locus_18867_Transcript_1/1_Conf_1.000	390	0							
Locus_18868_Transcript_1/1_Conf_1.000	271	0							
Locus_18869_Transcript_1/1_Conf_1.000	217	0							
Locus_1887_Transcript_1/1_Conf_1.000	553	20	5.48E-59	XP_002632482.1	82	230.72	160	132	Hypothetical protein CBG13717
Locus_18870_Transcript_1/1_Conf_1.000	442	20	2.29E-38	XP_002630861.1	73	161.77	139	102	Hypothetical protein CBG02576
Locus_18871_Transcript_1/1_Conf_1.000	141	0							
Locus_18872_Transcript_1/1_Conf_1.000	265	6	8.15E-12	XP_001899774.1	76	73.559	71	54	Guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif family protein
Locus_18873_Transcript_1/1_Conf_1.000	198	0							
Locus_18874_Transcript_1/1_Conf_1.000	178	0							
Locus_18875_Transcript_1/1_Conf_1.000	163	4	7.61E-10	NP_499922.1	75	67.0106	53	40	Kinase, GLH-Binding family member (kgb-1)
Locus_18876_Transcript_1/1_Conf_1.000	450	20	1.33E-38	NP_495410.4	75	162.54	149	112	hypothetical protein C44B7.11
Locus_18877_Transcript_1/1_Conf_1.000	206	0							
Locus_18878_Transcript_1/1_Conf_1.000	253	20	3.96E-14	ACI49197.1	61	81.2629	80	49	hypothetical protein Csp3_JD03.006
Locus_18879_Transcript_1/1_Conf_1.000	180	0							
Locus_1888_Transcript_1/3_Conf_0.667	522	0							
Locus_1888_Transcript_2/3_Conf_0.667	493	0							
Locus_1888_Transcript_3/3_Conf_0.667	514	0							
Locus_18880_Transcript_1/1_Conf_1.000	361	2	3.27E-05	XP_001898007.1	69	51.6026	53	37	Origin recognition complex subunit 5
Locus_18881_Transcript_1/1_Conf_1.000	391	20	8.52E-22	XP_001898421.1	63	106.686	132	84	NG,NG-dimethylarginine dimethylaminohydrolase 1
Locus_18882_Transcript_1/1_Conf_1.000	208	0							
Locus_18883_Transcript_1/1_Conf_1.000	143	0							
Locus_18884_Transcript_1/1_Conf_1.000	228	20	6.66E-30	XP_001154014.1	97	133.65	69	67	PREDICTED: similar to COX4I1 protein isoform 1
Locus_18885_Transcript_1/1_Conf_1.000	446	2	6.25E-12	XP_002640218.1	59	73.9442	98	58	C. briggsae CBR-ZTF-4 protein

Locus_18886_Transcript_1/1_Conf_1.000	134	0							
Locus_18887_Transcript_1/1_Conf_1.000	206	0							
Locus_18888_Transcript_1/1_Conf_1.000	151	0							
Locus_18889_Transcript_1/1_Conf_1.000	283	20	5.71E-21	XP_002647214.1	71	103.99	94	67	Hypothetical protein CBG22398
Locus_1889_Transcript_1/2_Conf_1.000	1149	20	3.44E-163	XP_002643004.1	91	578.941	359	329	Hypothetical protein CBG24278
Locus_1889_Transcript_2/2_Conf_1.000	1149	20	1.70E-162	XP_002643004.1	91	576.63	359	328	Hypothetical protein CBG24278
Locus_18890_Transcript_1/1_Conf_1.000	416	20	1.27E-25	XP_002631207.1	74	119.398	123	92	Hypothetical protein CBG03003
Locus_18891_Transcript_1/1_Conf_1.000	164	5	3.19E-16	NP_496398.2	77	88.1965	54	42	hypothetical protein T06D8.1
Locus_18892_Transcript_1/1_Conf_1.000	194	0							
Locus_18893_Transcript_1/1_Conf_1.000	207	1	5.38E-24	AAQ15253.1	100	114.005	68	68	AF370417_1PP13850
Locus_18894_Transcript_1/1_Conf_1.000	275	0							
Locus_18895_Transcript_1/1_Conf_1.000	146	0							
Locus_18896_Transcript_1/1_Conf_1.000	395	5	1.23E-07	ABB53347.1	53	59.6918	86	46	secreted protein 5 precursor
Locus_18897_Transcript_1/1_Conf_1.000	264	0							
Locus_18898_Transcript_1/1_Conf_1.000	785	20	1.97E-16	NP_494956.1	49	90.5077	256	127	Serpentine Receptor, class B (beta) family member (srb-16)
Locus_18899_Transcript_1/1_Conf_1.000	192	20	4.19E-24	NP_001122009.1	85	114.39	63	54	host cell factor C1b
Locus_189_Transcript_1/3_Conf_0.750	1516	20	1.56E-95	XP_002636254.1	58	354.755	462	272	C. briggsae CBR-EGG-1 protein
Locus_189_Transcript_2/3_Conf_0.750	1748	20	1.86E-95	XP_002636254.1	58	354.755	462	272	C. briggsae CBR-EGG-1 protein
Locus_189_Transcript_3/3_Conf_0.750	1516	20	1.56E-95	XP_002636254.1	58	354.755	462	272	C. briggsae CBR-EGG-1 protein
Locus_1890_Transcript_1/1_Conf_1.000	1332	20	2.26E-156	XP_002643220.1	84	556.599	405	343	C. briggsae CBR-ARR-1 protein

Locus_18900_Transcript_1/1_Conf_1.000	290	20	3.66E-36	NP_509087.1	84	154.451	97	82	OligoPeptide Transporter family member (opt-2)
Locus_18901_Transcript_1/1_Conf_1.000	256	0							
Locus_18902_Transcript_1/1_Conf_1.000	477	20	4.23E-37	NP_495010.2	76	157.532	151	115	hypothetical protein F09E5.2
Locus_18903_Transcript_1/1_Conf_1.000	175	0							
Locus_18904_Transcript_1/1_Conf_1.000	311	20	4.68E-20	XP_002630767.1	78	100.908	83	65	C. briggsae CBR-ZYG-1 protein
Locus_18905_Transcript_1/1_Conf_1.000	296	16	1.75E-14		60	82.4185	92	56	hypothetical protein Y105C5B.d
Locus_18906_Transcript_1/1_Conf_1.000	456	0							
Locus_18907_Transcript_1/1_Conf_1.000	255	0							
Locus_18908_Transcript_1/2_Conf_1.000	966	0							
Locus_18908_Transcript_2/2_Conf_1.000	966	0							
Locus_18909_Transcript_1/1_Conf_1.000	259	1	8.22E-04	AAZ67106.1	68	46.9802	47	32	transposase
Locus_1891_Transcript_1/2_Conf_1.000	741	0							
Locus_1891_Transcript_2/2_Conf_1.000	664	0							
Locus_18910_Transcript_1/1_Conf_1.000	521	20	3.94E-63	NP_493371.1	81	244.202	170	139	hypothetical protein Y48G10A.1
Locus_18911_Transcript_1/1_Conf_1.000	208	0							
Locus_18912_Transcript_1/1_Conf_1.000	535	0							
Locus_18913_Transcript_1/1_Conf_1.000	289	0							
Locus_18914_Transcript_1/1_Conf_1.000	738	20	2.68E-57	XP_001473804.1	71	226.098	199	142	PREDICTED: similar to B cell antigen receptor Ig beta associated protein 1
Locus_18915_Transcript_1/1_Conf_1.000	162	0							
Locus_18916_Transcript_1/1_Conf_1.000	180	20	1.98E-13	Q8MNV0.2	74	78.9518	59	44	Probable spastin homolog spas-1

Locus_18917_Transcript_1/1_Conf_1.000	272	20	4.11E-48	XP_002804983.1	100	194.126	90	90	PREDICTED: isocitrate dehydrogenase
Locus_18918_Transcript_1/1_Conf_1.000	192	5	3.33E-05	EFO24938.1	62	51.6026	61	38	hypothetical protein LOAG_03545
Locus_18919_Transcript_1/1_Conf_1.000	1537	20	0	NP_495285.1	83	665.611	456	381	abnormal cell LINeage family member (lin-23)

Locus_1892_Transcript_1/1_Conf_1.000	1204	20	3.45E-52	AAC47238.1	63	210.305	323	204	non-muscle myosin heavy chain II
Locus_18920_Transcript_1/1_Conf_1.000	313	0							
Locus_18921_Transcript_1/1_Conf_1.000	131	3	1.86E-08	XP_002809210.1	80	62.3882	35	28	PREDICTED: myosin regulatory light chain 12B-like
Locus_18922_Transcript_1/1_Conf_1.000	474	3	3.63E-04	XP_001202730.1	51	48.1358	107	55	PREDICTED: similar to zinc finger protein, partial
Locus_18923_Transcript_1/1_Conf_1.000	221	0							
Locus_18924_Transcript_1/1_Conf_1.000	193	0							
Locus_18925_Transcript_1/1_Conf_1.000	222	0							
Locus_18926_Transcript_1/1_Conf_1.000	541	20	9.05E-24	NP_500084.2	83	113.62	79	66	hypothetical protein Y77E11A.2
Locus_18927_Transcript_1/1_Conf_1.000	303	0							
Locus_18928_Transcript_1/1_Conf_1.000	356	0							
Locus_18929_Transcript_1/1_Conf_1.000	447	2	1.22E-07	EFO20888.1	79	59.6918	44	35	hypothetical protein LOAG_07599
Locus_1893_Transcript_1/1_Conf_1.000	308	0							
Locus_18930_Transcript_1/1_Conf_1.000	438	0							
Locus_18931_Transcript_1/1_Conf_1.000	129	0							
Locus_18932_Transcript_1/1_Conf_1.000	274	0							
Locus_18933_Transcript_1/1_Conf_1.000	787	20	2.90E-92	NP_492031.1	82	342.428	263	217	hypothetical protein M05B5.6
Locus_18934_Transcript_1/1_Conf_1.000	280	0							

Locus_18935_Transcript_1/1_Conf_1.000	252	20	4.23E-16	CAA06162.1	82	87.8113	62	51	CB-CYP-4
Locus_18936_Transcript_1/1_Conf_1.000	136	0							
Locus_18937_Transcript_1/1_Conf_1.000	183	0							
Locus_18938_Transcript_1/1_Conf_1.000	205	5	1.92E-21	NP_506678.2	85	105.531	67	57	hypothetical protein W09D12.1
Locus_18939_Transcript_1/1_Conf_1.000	135	0							
Locus_1894_Transcript_1/1_Conf_1.000	1168	20	2.41E-95	NP_508455.2	93	353.599	197	184	hypothetical protein K02E10.1
Locus_18940_Transcript_1/1_Conf_1.000	254	9	6.98E-19	NP_493701.1	78	97.0561	60	47	hypothetical protein K01A2.5
Locus_18941_Transcript_1/1_Conf_1.000	204	0							
Locus_18942_Transcript_1/1_Conf_1.000	1232	20	9.30E-85	ABU49430.1	67	318.546	376	254	PRO-2
Locus_18943_Transcript_1/1_Conf_1.000	201	7	4.76E-12	EFO19031.1	87	74.3294	49	43	hypothetical protein LOAG_09464
Locus_18944_Transcript_1/1_Conf_1.000	578	20	2.51E-44	XP_002644494.1	67	182.185	196	133	Hypothetical protein CBG14382
Locus_18945_Transcript_1/1_Conf_1.000	690	20	3.88E-36	XP_002646140.1	76	155.606	121	92	Hypothetical protein CBG08020
Locus_18946_Transcript_1/1_Conf_1.000	329	5	2.50E-37	NP_493560.1	84	158.303	111	94	hypothetical protein K05C4.11
Locus_18947_Transcript_1/1_Conf_1.000	272	6	2.43E-16	NP_494828.1	75	88.5817	72	54	hypothetical protein T05A7.1
Locus_18948_Transcript_1/1_Conf_1.000	280	20	1.19E-15	NP_001123161.1	58	86.2705	87	51	hypothetical protein K03A11.6

Locus_18949_Transcript_1/1_Conf_1.000	331	20	2.33E-35	XP_002641709.1	80	151.754	110	88	C. briggsae CBR-CED-7 protein
Locus_1895_Transcript_1/1_Conf_1.000	623	20	3.37E-104	AAR07614.1	98	381.333	191	189	UNC-18
Locus_18950_Transcript_1/1_Conf_1.000	304	20	7.01E-32	NP_509110.1	89	140.198	76	68	TransThyretin-Related family domain family member (ttr-6)
Locus_18951_Transcript_1/1_Conf_1.000	230	17	1.77E-06	NP_001122780.1	56	55.8398	75	42	hypothetical protein F41H10.6
Locus_18952_Transcript_1/1_Conf_1.000	399	0							
Locus_18953_Transcript_1/1_Conf_1.000	155	0							
Locus_18954_Transcript_1/1_Conf_1.000	217	8	1.04E-27	CAR81372.1	91	126.331	70	64	C. elegans protein F57B7.2b, partially confirmed by transcript evidence
Locus_18955_Transcript_1/1_Conf_1.000	258	20	5.11E-30	NP_872081.1	88	134.035	84	74	Acyl CoA DeHydrogenase family member (acdh-13)
Locus_18956_Transcript_1/1_Conf_1.000	134	15	1.47E-13	NP_500715.1	88	79.337	43	38	hypothetical protein R13H9.5
Locus_18957_Transcript_1/1_Conf_1.000	549	20	3.76E-28	NP_501123.1	74	128.257	152	113	COLlagen family member (col-113)

Locus_18958_Transcript_1/1_Conf_1.000	153	20	1.15E-13	NP_001122771.1	80	79.7221	50	40	hypothetical protein F13H10.4
Locus_18959_Transcript_1/1_Conf_1.000	146	0							
Locus_1896_Transcript_1/1_Conf_1.000	793	20	3.27E-75	NP_507513.2	70	285.804	272	193	hypothetical protein E01B7.1
Locus_18960_Transcript_1/1_Conf_1.000	742	20	6.47E-43	NP_497604.2	59	178.333	254	150	SET (trithorax/polycomb) domain containing family member (set-27)
Locus_18961_Transcript_1/1_Conf_1.000	211	0							
Locus_18962_Transcript_1/1_Conf_1.000	158	0							
Locus_18963_Transcript_1/1_Conf_1.000	329	20	6.19E-20	XP_002633531.1	76	100.523	98	75	Hypothetical protein CBG05398
Locus_18964_Transcript_1/1_Conf_1.000	251	0							
Locus_18965_Transcript_1/1_Conf_1.000	173	0							
Locus_18966_Transcript_1/1_Conf_1.000	384	6	3.36E-34	ABH10656.1	92	147.902	83	77	FMRFamide-related peptide FLP-11 precursor
Locus_18967_Transcript_1/1_Conf_1.000	158	20	7.66E-10	XP_002633316.1	75	67.0106	52	39	C. briggsae CBR-GTL-2 protein
Locus_18968_Transcript_1/1_Conf_1.000	159	0							
Locus_18969_Transcript_1/1_Conf_1.000	187	0							
Locus_1897_Transcript_1/1_Conf_1.000	428	0							
Locus_18970_Transcript_1/1_Conf_1.000	480	20	3.92E-51	NP_497319.1	78	204.142	157	124	hypothetical protein Y46E12BL.2
Locus_18971_Transcript_1/1_Conf_1.000	310	0							
Locus_18972_Transcript_1/1_Conf_1.000	460	20	1.88E-61	XP_002753304.1	100	238.424	153	153	PREDICTED: 60S ribosomal protein L4-like

Locus_18973_Transcript_1/1_Conf_1.000	368	20	1.07E-32	ADK09905.1	100	142.895	122	122	non-muscle myosin IIA
Locus_18974_Transcript_1/1_Conf_1.000	289	0							
Locus_18975_Transcript_1/1_Conf_1.000	217	0							
Locus_18976_Transcript_1/1_Conf_1.000	198	0							
Locus_18977_Transcript_1/1_Conf_1.000	258	20	7.14E-32	NP_504498.2	91	140.198	81	74	hypothetical protein F25B4.7
Locus_18978_Transcript_1/1_Conf_1.000	226	0							
Locus_18979_Transcript_1/1_Conf_1.000	526	20	3.13E-79	NP_493549.1	84	297.745	175	148	hypothetical protein Y54E5A.1
Locus_1898_Transcript_1/1_Conf_1.000	1979	20	2.90E-140	NP_493982.1	75	503.827	436	327	hypothetical protein H17B01.1
Locus_18980_Transcript_1/1_Conf_1.000	132	0							
Locus_18981_Transcript_1/1_Conf_1.000	157	0							
Locus_18982_Transcript_1/1_Conf_1.000	273	0							

Locus_18983_Transcript_1/1_Conf_1.000	382	20	3.35E-66	XP_002630298.1	96	254.218	127	123	C. briggsae CBR-LTD-1 protein
Locus_18984_Transcript_1/1_Conf_1.000	153	0							
Locus_18985_Transcript_1/1_Conf_1.000	233	0							
Locus_18986_Transcript_1/1_Conf_1.000	238	2	1.02E-06	NP_506256.3	57	56.6102	77	44	CaDHerin family member (cdh-6)
Locus_18987_Transcript_1/1_Conf_1.000	129	0							
Locus_18988_Transcript_1/1_Conf_1.000	231	0							
Locus_18989_Transcript_1/1_Conf_1.000	136	20	5.56E-13	NP_501214.1	95	77.411	40	38	hypothetical protein R05G6.4
Locus_1899_Transcript_1/1_Conf_1.000	292	0							
Locus_18990_Transcript_1/1_Conf_1.000	453	20	1.46E-37	NP_508493.1	70	159.073	151	106	protein KINase family member (kin-29)
Locus_18991_Transcript_1/1_Conf_1.000	268	0							
Locus_18992_Transcript_1/1_Conf_1.000	311	0							
Locus_18993_Transcript_1/1_Conf_1.000	137	0							
Locus_18994_Transcript_1/1_Conf_1.000	196	0							
Locus_18995_Transcript_1/1_Conf_1.000	141	0							
Locus_18996_Transcript_1/1_Conf_1.000	371	7	3.23E-16	XP_002646731.1	56	88.1965	127	72	C. briggsae CBR-ADA-2 protein
Locus_18997_Transcript_1/1_Conf_1.000	365	0							
Locus_18998_Transcript_1/1_Conf_1.000	252	0							
Locus_18999_Transcript_1/1_Conf_1.000	139	0							
Locus_19_Transcript_1/1_Conf_1.000	1371	20	0	NP_498775.2	85	668.692	442	377	hypothetical protein C14B9.2
Locus_190_Transcript_1/1_Conf_1.000	356	0							
Locus_1900_Transcript_1/6_Conf_0.467	1098	20	1.17E-88	CBW38507.1	75	331.257	283	213	calcium-activated apyrase
Locus_1900_Transcript_2/6_Conf_0.600	1098	20	2.79E-90	CBW38507.1	75	336.65	283	215	calcium-activated apyrase

Locus_1900_Transcript_3/6_Conf_0.600	908	20	1.73E-89	CBW38507.1	75	333.569	283	213	calcium-activated apyrase
Locus_1900_Transcript_4/6_Conf_0.667	1098	20	2.36E-89	CBW38507.1	75	333.569	283	214	calcium-activated apyrase
Locus_1900_Transcript_5/6_Conf_0.467	1098	20	8.96E-89	CBW38507.1	75	331.643	283	213	calcium-activated apyrase
Locus_1900_Transcript_6/6_Conf_0.667	1098	20	2.36E-89	CBW38507.1	75	333.569	283	214	calcium-activated apyrase
Locus_19000_Transcript_1/1_Conf_1.000	165	20	1.34E-14	XP_002758248.1	100	82.8037	38	38	PREDICTED: calcium-regulated heat stable protein 1-like
Locus_19001_Transcript_1/1_Conf_1.000	450	20	1.29E-25	XP_002638288.1	60	119.398	149	90	Hypothetical protein CBG22835
Locus_19002_Transcript_1/1_Conf_1.000	141	0							
Locus_19003_Transcript_1/1_Conf_1.000	409	4	1.36E-43	XP_002638941.1	87	179.104	135	118	Hypothetical protein CBG22168
Locus_19004_Transcript_1/1_Conf_1.000	602	0							
Locus_19005_Transcript_1/1_Conf_1.000	283	20	3.96E-22	XP_002639142.1	77	107.842	94	73	Hypothetical protein CBG14966
Locus_19006_Transcript_1/1_Conf_1.000	158	20	1.59E-15	XP_002632333.1	94	85.8853	52	49	Hypothetical protein CBG00341

Locus_19007_Transcript_1/1_Conf_1.000	183	18	3.37E-05	YP_001854253.1	77	51.6026	35	27	heat shock protein DnaJ family protein
Locus_19008_Transcript_1/1_Conf_1.000	163	20	1.69E-17	NP_495675.1	85	92.4337	54	46	hypothetical protein DH11.1
Locus_19009_Transcript_1/1_Conf_1.000	168	0							
Locus_1901_Transcript_1/1_Conf_1.000	1440	20	0	XP_002647082.1	94	657.522	375	355	C. briggsae CBR-RPL-3 protein
Locus_19010_Transcript_1/1_Conf_1.000	742	20	1.59E-41	XP_001892576.1	84	173.711	125	105	Voltage-gated calcium channel, T-type, alpha subunit. C. elegans cca-1 ortholog
Locus_19011_Transcript_1/1_Conf_1.000	177	20	5.34E-24	NP_001021973.1	98	114.005	58	57	RAB family member (rab-3)

Locus_19012_Transcript_1/1_Conf_1.000	477	20	1.35E-51	EFO24598.1	81	205.682	144	117	hypothetical protein LOAG_03887
Locus_19013_Transcript_1/1_Conf_1.000	169	20	1.09E-16	XP_002642806.1	91	89.7373	48	44	C. briggsae CBR-CDK-5 protein
Locus_19014_Transcript_1/1_Conf_1.000	333	2	1.61E-28	NP_492185.2	78	129.028	97	76	SMG-associated and Lethal family member (smgl-1)
Locus_19015_Transcript_1/1_Conf_1.000	170	0							
Locus_19016_Transcript_1/1_Conf_1.000	453	20	5.00E-46	XP_002640189.1	72	187.193	148	107	Hypothetical protein CBG12692
Locus_19017_Transcript_1/3_Conf_0.600	1013	0							
Locus_19017_Transcript_2/3_Conf_0.600	455	0							
Locus_19017_Transcript_3/3_Conf_0.600	1037	0							
Locus_19018_Transcript_1/1_Conf_1.000	335	11	1.73E-22	EFO13548.1	73	108.997	98	72	hypothetical protein LOAG_14980
Locus_19019_Transcript_1/1_Conf_1.000	362	3	1.08E-32	XP_001892606.1	83	142.895	108	90	hypothetical protein Bm1_05665
Locus_1902_Transcript_1/3_Conf_0.714	1454	20	1.45E-26	NP_498156.1	51	125.561	235	122	hypothetical protein W03A5.4

Locus_1902_Transcript_2/3_Conf_0.714	1475	20	8.67E-27	XP_002641265.1	50	126.331	251	128	Hypothetical protein CBG05177
Locus_1902_Transcript_3/3_Conf_0.714	1448	20	1.44E-26	NP_498156.1	51	125.561	235	122	hypothetical protein W03A5.4
Locus_19020_Transcript_1/1_Conf_1.000	141	0							
Locus_19021_Transcript_1/1_Conf_1.000	325	0							
Locus_19022_Transcript_1/1_Conf_1.000	255	20	4.67E-07	ACX53644.1	55	57.7658	79	44	polyprotein
Locus_19023_Transcript_1/1_Conf_1.000	243	0							
Locus_19024_Transcript_1/1_Conf_1.000	1185	20	7.73E-65	EFO16078.1	63	252.292	349	220	hypothetical protein LOAG_12430
Locus_19025_Transcript_1/1_Conf_1.000	427	2	4.01E-27	XP_002636178.1	81	124.405	92	75	Hypothetical protein CBG01435
Locus_19026_Transcript_1/1_Conf_1.000	224	0							
Locus_19027_Transcript_1/1_Conf_1.000	639	4	2.19E-16	XP_002632958.1	74	89.7373	74	55	Hypothetical protein CBG21714
Locus_19028_Transcript_1/1_Conf_1.000	419	0							
Locus_19029_Transcript_1/1_Conf_1.000	513	20	1.49E-35	XP_002631317.1	77	152.525	112	87	Hypothetical protein CBG03139
Locus_1903_Transcript_1/1_Conf_1.000	1542	20	5.35E-160	XP_002630721.1	69	568.926	533	373	C. briggsae CBR-CLR-1 protein
Locus_19030_Transcript_1/1_Conf_1.000	302	0							
Locus_19031_Transcript_1/1_Conf_1.000	314	20	1.96E-21	XP_394116.3	68	105.531	104	71	PREDICTED: similar to Aromatic-L-amino-acid decarboxylase (AADC) (DOPA decarboxylase) (DDC)
Locus_19032_Transcript_1/1_Conf_1.000	212	0							
Locus_19033_Transcript_1/1_Conf_1.000	355	1	8.13E-04	XP_001897852.1	45	46.9802	126	57	notch-like transmembrane receptor
Locus_19034_Transcript_1/1_Conf_1.000	153	9	7.19E-08	XP_002646475.1	72	60.4622	50	36	Hypothetical protein CBG19448
Locus_19035_Transcript_1/1_Conf_1.000	188	0							
Locus_19036_Transcript_1/1_Conf_1.000	311	20	2.84E-17	NP_508551.1	59	91.6633	107	64	hypothetical protein F28B4.3

Locus_19037_Transcript_1/1_Conf_1.000	176	19	6.57E-14	XP_002811165.1	100	80.4925	38	38	PREDICTED: MARCKS-related protein-like
Locus_19038_Transcript_1/1_Conf_1.000	368	20	2.81E-41	XP_002638487.1	91	171.4	121	111	Hypothetical protein CBG12917
Locus_19039_Transcript_1/1_Conf_1.000	330	3	3.27E-21	NP_497897.1	82	104.76	91	75	PDCD (mammalian ProgrammeD Cell Death protein) homolog family member (pdcd-2)
Locus_1904_Transcript_1/1_Conf_1.000	806	20	4.33E-14	NP_507645.2	38	82.8037	248	96	hypothetical protein Y69H2.3
Locus_19040_Transcript_1/1_Conf_1.000	212	2	1.73E-06	XP_002637606.1	65	55.8398	52	34	Hypothetical protein CBG19344
Locus_19041_Transcript_1/1_Conf_1.000	511	20	1.84E-30	NP_498290.1	74	135.576	135	100	hypothetical protein F25B5.5
Locus_19042_Transcript_1/1_Conf_1.000	496	5	2.25E-38	NP_001022759.1	78	161.77	126	99	hypothetical protein T12D8.9
Locus_19043_Transcript_1/1_Conf_1.000	240	20	5.93E-39	XP_001084827.2	100	163.696	80	80	PREDICTED: serpin H1
Locus_19044_Transcript_1/1_Conf_1.000	318	20	4.04E-35	NP_498808.2	96	150.984	75	72	hypothetical protein C02F5.3

Locus_19045_Transcript_1/1_Conf_1.000	464	20	1.00E-17	XP_002648990.1	77	93.2041	72	56	Hypothetical protein CBG21322
Locus_19046_Transcript_1/1_Conf_1.000	276	20	5.93E-23	EFO22951.1	73	110.538	91	67	hypothetical protein LOAG_05534
Locus_19047_Transcript_1/1_Conf_1.000	338	13	1.36E-35	CBK19475.1	86	152.525	106	92	C. elegans protein T12G3.2e, confirmed by transcript evidence
Locus_19048_Transcript_1/1_Conf_1.000	250	0							
Locus_19049_Transcript_1/1_Conf_1.000	203	0							
Locus_1905_Transcript_1/1_Conf_1.000	495	0							
Locus_19050_Transcript_1/1_Conf_1.000	540	20	1.98E-87	NP_508184.2	92	325.094	180	166	AdaPtin, Mu/medium chain (clathrin associated complex) family member (apm-3)
Locus_19051_Transcript_1/1_Conf_1.000	323	20	4.48E-10	ABG23688.1	53	67.781	106	57	RNA-dependent RNA polymerase
Locus_19052_Transcript_1/1_Conf_1.000	890	20	7.51E-82	NP_492524.2	71	308.145	297	211	hypothetical protein F30A10.10
Locus_19053_Transcript_1/1_Conf_1.000	435	4	3.02E-43	NP_503059.2	85	177.948	111	95	hypothetical protein ZK550.3
Locus_19054_Transcript_1/2_Conf_1.000	375	0							
Locus_19054_Transcript_2/2_Conf_1.000	296	0							
Locus_19055_Transcript_1/1_Conf_1.000	162	6	1.58E-23	XP_530140.2	96	112.464	54	52	PREDICTED: hypothetical protein
Locus_19056_Transcript_1/1_Conf_1.000	483	0							
Locus_19057_Transcript_1/1_Conf_1.000	317	20	4.97E-25	NP_497482.1	78	117.472	89	70	hypothetical protein F53A3.7
Locus_19058_Transcript_1/1_Conf_1.000	171	0							
Locus_19059_Transcript_1/1_Conf_1.000	230	0							
Locus_1906_Transcript_1/1_Conf_1.000	712	20	2.23E-66	EFO22922.1	91	256.144	147	135	eukaryotic translation initiation factor 2 subunit 2
Locus_19060_Transcript_1/1_Conf_1.000	317	20	2.73E-15	EFO22683.1	68	85.1149	82	56	STE/STE11/MEKK2 protein kinase
Locus_19061_Transcript_1/1_Conf_1.000	136	0							
Locus_19062_Transcript_1/1_Conf_1.000	727	20	2.59E-49	NP_507155.1	57	199.519	224	129	hypothetical protein F26D2.13
Locus_19063_Transcript_1/1_Conf_1.000	197	0							

Locus_19064_Transcript_1/1_Conf_1.000	275	20	5.04E-22	NP_491855.1	84	107.457	66	56	Nuclear Pore complex Protein family member (npp-12)
Locus_19065_Transcript_1/1_Conf_1.000	717	20	5.02E-90	XP_002643890.1	81	334.724	243	198	Hypothetical protein CBG02142
Locus_19066_Transcript_1/1_Conf_1.000	273	20	3.38E-18	XP_002642446.1	74	94.7449	86	64	Hypothetical protein CBG06851
Locus_19067_Transcript_1/1_Conf_1.000	260	0							
Locus_19068_Transcript_1/1_Conf_1.000	149	0							
Locus_19069_Transcript_1/1_Conf_1.000	141	0							
Locus_1907_Transcript_1/5_Conf_0.308	747	20	6.15E-49	XP_001892438.1	82	198.364	137	113	60S ribosomal protein L23a
Locus_1907_Transcript_2/5_Conf_0.538	751	20	6.20E-49	XP_001892438.1	82	198.364	137	113	60S ribosomal protein L23a
Locus_1907_Transcript_3/5_Conf_0.462	751	20	6.20E-49	XP_001892438.1	82	198.364	137	113	60S ribosomal protein L23a

Locus_1907_Transcript_4/5_Conf_0.462	747	20	6.15E-49	XP_001892438.1	82	198.364	137	113	60S ribosomal protein L23a
Locus_1907_Transcript_5/5_Conf_0.308	543	20	2.85E-49	XP_001892438.1	82	198.364	137	113	60S ribosomal protein L23a
Locus_19070_Transcript_1/1_Conf_1.000	278	20	1.19E-47	EFO25348.1	100	192.586	92	92	rab family protein 3
Locus_19071_Transcript_1/1_Conf_1.000	308	0							
Locus_19072_Transcript_1/1_Conf_1.000	144	6	7.26E-08	XP_002639125.1	78	60.4622	47	37	C. briggsae CBR-FER-1 protein
Locus_19073_Transcript_1/1_Conf_1.000	653	20	2.08E-17	XP_001894228.1	61	93.2041	180	110	hypothetical protein
Locus_19074_Transcript_1/1_Conf_1.000	632	0							
Locus_19075_Transcript_1/1_Conf_1.000	492	20	1.61E-52	NP_001021681.1	73	208.764	172	126	hypothetical protein Y105E8A.10
Locus_19076_Transcript_1/1_Conf_1.000	238	8	1.74E-30	XP_002638768.1	90	135.576	76	69	Hypothetical protein CBG05111
Locus_19077_Transcript_1/1_Conf_1.000	188	0							
Locus_19078_Transcript_1/1_Conf_1.000	151	0							
Locus_19079_Transcript_1/1_Conf_1.000	294	20	1.75E-30	XP_002648619.1	78	135.576	98	77	Hypothetical protein CBG24962

Locus_1908_Transcript_1/2_Conf_1.000	1127	20	5.63E-102	AAM82155.1	69	375.555	324	224	cysteine proteinase
Locus_1908_Transcript_2/2_Conf_1.000	928	20	1.76E-60	AAM82155.1	67	237.269	209	141	cysteine proteinase
Locus_19080_Transcript_1/1_Conf_1.000	256	0							
Locus_19081_Transcript_1/1_Conf_1.000	134	0							
Locus_19082_Transcript_1/1_Conf_1.000	960	7	5.85E-14	XP_002640822.1	41	82.8037	286	119	Hypothetical protein CBG15709
Locus_19083_Transcript_1/1_Conf_1.000	429	5	2.60E-10	XP_002639923.1	85	68.5514	42	36	C. briggsae CBR-JPH-1 protein
Locus_19084_Transcript_1/1_Conf_1.000	230	0							
Locus_19085_Transcript_1/1_Conf_1.000	337	0							
Locus_19086_Transcript_1/1_Conf_1.000	193	20	4.96E-17	EAW84750.1	100	90.8929	63	63	coatomer protein complex, subunit epsilon, isoform CRA_c
Locus_19087_Transcript_1/1_Conf_1.000	200	20	4.60E-23	XP_001900213.1	90	110.923	66	60	Hypothetical oxidoreductase F56D1.5
Locus_19088_Transcript_1/1_Conf_1.000	235	1	2.07E-07	EFO24426.1	62	58.9214	67	42	hypothetical protein LOAG_04062
Locus_19089_Transcript_1/1_Conf_1.000	137	0							
Locus_1909_Transcript_1/1_Conf_1.000	317	4	1.11E-24	XP_002638813.1	71	116.316	106	76	C. briggsae CBR-ATM-1 protein
Locus_19090_Transcript_1/1_Conf_1.000	175	0							
Locus_19091_Transcript_1/1_Conf_1.000	209	0							
Locus_19092_Transcript_1/1_Conf_1.000	183	20	3.57E-31	EAW65357.1	100	137.887	60	60	filamin B, beta (actin binding protein 278), isoform CRA_e
Locus_19093_Transcript_1/1_Conf_1.000	525	20	4.70E-59	NP_496910.1	78	230.72	174	137	Histone DeAcetylase family member (hda-6)

Locus_19094_Transcript_1/1_Conf_1.000	275	20	1.52E-18	XP_786833.2	83	95.9005	68	57	PREDICTED: similar to MGC89020 protein
Locus_19095_Transcript_1/1_Conf_1.000	641	4	4.52E-54	NP_510177.1	69	214.927	213	148	hypothetical protein F17H10.1
Locus_19096_Transcript_1/1_Conf_1.000	1051	20	1.37E-91	XP_002633254.1	78	340.887	275	217	C. briggsae CBR-NDX-9 protein
Locus_19097_Transcript_1/1_Conf_1.000	137	0							
Locus_19098_Transcript_1/1_Conf_1.000	902	20	4.41E-45	EFO20748.1	58	186.037	269	157	MBOAT family protein
Locus_19099_Transcript_1/1_Conf_1.000	378	20	8.92E-35	XP_002640827.1	78	149.828	126	99	Hypothetical protein CBG15714
Locus_191_Transcript_1/1_Conf_1.000	1799	20	1.91E-26	AAO63577.1	48	125.561	266	129	secreted protein 5 precursor
Locus_1910_Transcript_1/3_Conf_0.286	308	15	2.67E-07	EFO20587.1	54	58.5362	96	52	groucho protein GRG1-S
Locus_1910_Transcript_2/3_Conf_0.714	1611	6	2.49E-06	EFO20587.1	54	58.5362	96	52	groucho protein GRG1-S
Locus_1910_Transcript_3/3_Conf_0.714	1611	6	2.49E-06	EFO20587.1	54	58.5362	96	52	groucho protein GRG1-S

Locus_19100_Transcript_1/1_Conf_1.000	207	20	1.05E-19	NP_510290.1	80	99.7525	68	55	Germinal Center Kinase family member (gck-4)
Locus_19101_Transcript_1/1_Conf_1.000	153	0							
Locus_19102_Transcript_1/1_Conf_1.000	131	0							
Locus_19103_Transcript_1/1_Conf_1.000	271	0							
Locus_19104_Transcript_1/1_Conf_1.000	144	0							
Locus_19105_Transcript_1/1_Conf_1.000	379	20	4.29E-29	NP_506019.2	81	130.954	90	73	aspartyl(D) tRNA Synthetase family member (drs-2)
Locus_19106_Transcript_1/1_Conf_1.000	210	0							
Locus_19107_Transcript_1/1_Conf_1.000	232	0							
Locus_19108_Transcript_1/1_Conf_1.000	213	2	1.73E-06	XP_002631789.1	60	55.8398	73	44	Hypothetical protein CBG21003
Locus_19109_Transcript_1/1_Conf_1.000	255	4	3.22E-24	XP_001898469.1	93	114.775	59	55	Zinc knuckle family protein
Locus_1911_Transcript_1/1_Conf_1.000	261	20	7.92E-07	XP_001495113.2	52	56.9954	85	45	PREDICTED: BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)
Locus_19110_Transcript_1/1_Conf_1.000	321	15	7.39E-13	CAA73142.1	67	77.0258	100	67	VPS34 homologue

Locus_19111_Transcript_1/1_Conf_1.000	387	10	6.54E-30	Q93890.5	82	133.65	103	85	UDP-galactose/UDP-N-acetylglucosamine transporter srf-3
Locus_19112_Transcript_1/1_Conf_1.000	379	2	2.14E-04	EFO63420.1	47	48.9062	117	56	Hypothetical protein GLP15_3736
Locus_19113_Transcript_1/1_Conf_1.000	285	0							
Locus_19114_Transcript_1/1_Conf_1.000	697	20	7.13E-78	XP_002634797.1	88	294.278	230	203	Hypothetical protein CBG13900
Locus_19115_Transcript_1/1_Conf_1.000	201	0							
Locus_19116_Transcript_1/1_Conf_1.000	322	0							
Locus_19117_Transcript_1/1_Conf_1.000	395	0							
Locus_19118_Transcript_1/1_Conf_1.000	158	0							
Locus_19119_Transcript_1/1_Conf_1.000	229	0							
Locus_1912_Transcript_1/2_Conf_1.000	416	3	2.94E-06	NP_740842.1	62	55.0694	77	48	protein KINase family member (kin-32)
Locus_1912_Transcript_2/2_Conf_1.000	1501	20	2.53E-106	NP_740842.1	64	390.578	470	303	protein KINase family member (kin-32)
Locus_19120_Transcript_1/1_Conf_1.000	329	20	2.98E-14	XP_002642974.1	79	81.6481	58	46	Hypothetical protein CBG15258
Locus_19121_Transcript_1/1_Conf_1.000	297	0							
Locus_19122_Transcript_1/1_Conf_1.000	214	0							
Locus_19123_Transcript_1/1_Conf_1.000	387	0							
Locus_19124_Transcript_1/1_Conf_1.000	366	0							
Locus_19125_Transcript_1/1_Conf_1.000	466	20	8.99E-27	NP_508866.1	54	123.25	153	83	Unidentified Vitellogenin-linked Transcript family member (uvt-3)

Locus_19126_Transcript_1/1_Conf_1.000	236	20	2.20E-33	XP_002639036.1	96	145.206	78	75	C. briggsae CBR-DYB-1 protein
Locus_19127_Transcript_1/1_Conf_1.000	292	1	7.66E-10	EFO25846.1	54	67.0106	96	52	hypothetical protein LOAG_02637
Locus_19128_Transcript_1/1_Conf_1.000	895	2	4.10E-27	XP_002640906.1	78	126.331	84	66	Hypothetical protein CBG00463
Locus_19129_Transcript_1/1_Conf_1.000	422	20	8.77E-06	ABK42176.1	53	53.5286	98	52	Chk2
Locus_1913_Transcript_1/2_Conf_1.000	590	0							
Locus_1913_Transcript_2/2_Conf_1.000	379	0							
Locus_19130_Transcript_1/1_Conf_1.000	433	4	2.58E-18	NP_497051.1	76	95.1301	72	55	hypothetical protein K02B7.3
Locus_19131_Transcript_1/1_Conf_1.000	339	0							
Locus_19132_Transcript_1/1_Conf_1.000	186	2	7.48E-05	XP_002639088.1	72	50.447	40	29	C. briggsae CBR-TAG-83 protein
Locus_19133_Transcript_1/1_Conf_1.000	244	0							
Locus_19134_Transcript_1/1_Conf_1.000	324	3	3.78E-09	XP_002633677.1	76	64.6994	65	50	C. briggsae CBR-LAD-2 protein
Locus_19135_Transcript_1/1_Conf_1.000	135	0							
Locus_19136_Transcript_1/1_Conf_1.000	219	0							
Locus_19137_Transcript_1/1_Conf_1.000	532	0							
Locus_19138_Transcript_1/1_Conf_1.000	533	4	3.40E-52	NP_499313.2	80	207.994	177	142	hypothetical protein F43D9.1

Locus_19139_Transcript_1/1_Conf_1.000	367	20	4.99E-22	XP_002637375.1	60	107.457	120	72	C. briggsae CBR-MYS-1 protein
Locus_1914_Transcript_1/1_Conf_1.000	494	0							
Locus_19140_Transcript_1/1_Conf_1.000	149	0							
Locus_19141_Transcript_1/1_Conf_1.000	420	20	3.91E-30	NP_001033350.1	68	134.42	132	90	hypothetical protein C23G10.7
Locus_19142_Transcript_1/1_Conf_1.000	151	0							
Locus_19143_Transcript_1/1_Conf_1.000	528	2	1.24E-06	XP_001901497.1	53	56.6102	104	56	Zinc finger, C2H2 type family protein
Locus_19144_Transcript_1/1_Conf_1.000	407	2	3.75E-17	EFO18996.1	60	91.2781	126	76	hypothetical protein LOAG_09500
Locus_19145_Transcript_1/1_Conf_1.000	243	0							
Locus_19146_Transcript_1/1_Conf_1.000	209	4	6.61E-06	NP_001129925.1	85	53.9138	35	30	High Incidence of Males (increased X chromosome loss) family member (him-4)
Locus_19147_Transcript_1/1_Conf_1.000	211	0							
Locus_19148_Transcript_1/1_Conf_1.000	218	20	6.96E-24	EFO28414.1	86	113.62	72	62	hypothetical protein LOAG_00060
Locus_19149_Transcript_1/1_Conf_1.000	434	0							

Locus_1915_Transcript_1/1_Conf_1.000	244	20	2.75E-28	CAV31817.1	87	128.257	79	69	C. elegans protein Y54G9A.3b, partially confirmed by transcript evidence
Locus_19150_Transcript_1/1_Conf_1.000	196	20	1.70E-17	XP_002719350.1	100	92.4337	48	48	PREDICTED: prohibitin
Locus_19151_Transcript_1/1_Conf_1.000	201	0							
Locus_19152_Transcript_1/1_Conf_1.000	151	2	1.90E-08	NP_492763.1	69	62.3882	49	34	hypothetical protein F25H2.7
Locus_19153_Transcript_1/1_Conf_1.000	129	0							
Locus_19154_Transcript_1/2_Conf_1.000	1470	20	6.22E-126	NP_508552.1	62	455.677	501	314	hypothetical protein F40F4.6
Locus_19154_Transcript_2/2_Conf_1.000	1470	20	3.65E-126	NP_508552.1	62	456.447	501	314	hypothetical protein F40F4.6
Locus_19155_Transcript_1/1_Conf_1.000	446	20	6.84E-51	XP_002638900.1	87	203.371	148	129	Hypothetical protein CBG22126

Locus_19156_Transcript_1/1_Conf_1.000	219	20	1.72E-25	XP_002645154.1	86	119.013	69	60	C. briggsae CBR-SEM-5 protein
Locus_19157_Transcript_1/1_Conf_1.000	820	20	2.46E-97	NP_509408.1	74	359.377	275	205	hypothetical protein R09F10.1
Locus_19158_Transcript_1/1_Conf_1.000	217	0							
Locus_19159_Transcript_1/2_Conf_1.000	403	1	6.24E-04	NP_505787.1	52	47.3654	103	54	hypothetical protein F58B4.4
Locus_19159_Transcript_2/2_Conf_1.000	403	0							
Locus_1916_Transcript_1/1_Conf_1.000	2977	20	0	XP_002630360.1	84	1172.53	880	743	C. briggsae CBR-TSN-1 protein
Locus_19160_Transcript_1/1_Conf_1.000	355	0							
Locus_19161_Transcript_1/1_Conf_1.000	151	0							
Locus_19162_Transcript_1/1_Conf_1.000	153	0							
Locus_19163_Transcript_1/1_Conf_1.000	397	20	4.03E-43	NP_506047.5	83	177.563	132	110	abnormal CHEmotaxis family member (che-11)
Locus_19164_Transcript_1/1_Conf_1.000	340	4	9.74E-18	XP_002636415.1	84	93.2041	113	96	Hypothetical protein CBG23068
Locus_19165_Transcript_1/1_Conf_1.000	371	20	2.22E-41	CAX65065.1	85	171.785	111	95	C. elegans protein K01A6.2c, partially confirmed by transcript evidence
Locus_19166_Transcript_1/1_Conf_1.000	640	20	4.49E-78	ADD13547.1	80	294.664	222	179	Inositol triphosphate receptor protein 1, isoform h

Locus_19167_Transcript_1/1_Conf_1.000	213	2	1.01E-14	XP_002632364.1	83	83.1889	53	44	Hypothetical protein CBG00382
Locus_19168_Transcript_1/1_Conf_1.000	348	3	1.03E-22	XP_002647656.1	62	109.768	117	73	Hypothetical protein CBG06763
Locus_19169_Transcript_1/1_Conf_1.000	251	0							
Locus_1917_Transcript_1/1_Conf_1.000	2068	20	0	XP_002637841.1	96	1114.37	603	581	C. briggsae CBR-VHA-13 protein
Locus_19170_Transcript_1/1_Conf_1.000	242	0							
Locus_19171_Transcript_1/1_Conf_1.000	791	20	1.54E-117	NP_493910.2	87	426.402	263	230	Sodium:Neurotransmitter symporter Family family member (snf-3)
Locus_19172_Transcript_1/1_Conf_1.000	213	0							
Locus_19173_Transcript_1/1_Conf_1.000	266	3	9.32E-08	XP_002636556.1	67	60.077	58	39	Hypothetical protein CBG23246
Locus_19174_Transcript_1/1_Conf_1.000	311	0							
Locus_19175_Transcript_1/1_Conf_1.000	174	0							
Locus_19176_Transcript_1/1_Conf_1.000	217	0							
Locus_19177_Transcript_1/2_Conf_1.000	596	4	1.49E-18	NP_490990.2	65	96.6709	155	102	hypothetical protein Y23H5B.5
Locus_19177_Transcript_2/2_Conf_1.000	437	3	1.28E-09	NP_490990.2	64	66.2402	85	55	hypothetical protein Y23H5B.5
Locus_19178_Transcript_1/1_Conf_1.000	295	20	6.88E-19	XP_001895786.1	85	97.0561	61	52	Fringe-like family protein
Locus_19179_Transcript_1/1_Conf_1.000	182	20	9.81E-13	NP_493967.1	83	76.6406	55	46	Conserved Oligomeric Golgi (COG) Component family member (cogc-4)
Locus_1918_Transcript_1/1_Conf_1.000	2006	20	0	NP_001022876.1	73	734.947	587	429	GLYcosylation related family member (gly-9)
Locus_19180_Transcript_1/1_Conf_1.000	298	0							
Locus_19181_Transcript_1/1_Conf_1.000	364	0							
Locus_19182_Transcript_1/1_Conf_1.000	341	0							
Locus_19183_Transcript_1/1_Conf_1.000	158	0							
Locus_19184_Transcript_1/1_Conf_1.000	192	2	1.35E-06	XP_002643956.1	57	56.225	61	35	Hypothetical protein CBG17315
Locus_19185_Transcript_1/1_Conf_1.000	168	0							

Locus_19186_Transcript_1/1_Conf_1.000	135	10	1.91E-13	XP_002637401.1	95	78.9518	43	41	C. briggsae CBR-FKB-3 protein
Locus_19187_Transcript_1/1_Conf_1.000	650	20	6.26E-91	NP_510336.2	85	337.421	215	184	TBC (Tre-2/Bub2/Cdc16) domain family member (tbc-19)
Locus_19188_Transcript_1/1_Conf_1.000	565	20	2.49E-62	XP_002634543.1	76	241.891	188	143	C. briggsae CBR-CED-5 protein
Locus_19189_Transcript_1/1_Conf_1.000	134	0							
Locus_1919_Transcript_1/1_Conf_1.000	1198	20	1.57E-97	XP_001901770.1	85	360.918	220	189	translation initiation factor 4E
Locus_19190_Transcript_1/1_Conf_1.000	228	0							
Locus_19191_Transcript_1/1_Conf_1.000	380	20	2.98E-22	NP_497538.1	63	108.227	130	82	hypothetical protein Y54F10BM.13
Locus_19192_Transcript_1/1_Conf_1.000	227	0							
Locus_19193_Transcript_1/1_Conf_1.000	361	2	9.14E-32	XP_001899472.1	70	139.813	128	90	Patatin-like phospholipase family protein
Locus_19194_Transcript_1/1_Conf_1.000	387	20	3.32E-66	XP_002630534.1	97	254.218	128	125	Hypothetical protein CBG12974
Locus_19195_Transcript_1/1_Conf_1.000	358	20	8.04E-28	NP_507683.2	83	126.716	80	67	tryptophanyl (W) tRNA Synthetase family member (wrs-1)
Locus_19196_Transcript_1/1_Conf_1.000	260	0							
Locus_19197_Transcript_1/1_Conf_1.000	179	0							
Locus_19198_Transcript_1/1_Conf_1.000	426	20	8.96E-19	XP_394116.3	65	96.6709	113	74	PREDICTED: similar to Aromatic-L-amino-acid decarboxylase (AADC) (DOPA decarboxylase) (DDC)
Locus_19199_Transcript_1/1_Conf_1.000	153	20	2.55E-13	NP_510672.2	90	78.5666	50	45	Nematode AStacin protease family member (nas-39)
Locus_192_Transcript_1/1_Conf_1.000	1244	20	2.85E-73	NP_494789.1	60	280.411	379	228	hypothetical protein W06B4.2
Locus_1920_Transcript_1/1_Conf_1.000	559	4	1.69E-23	XP_001899166.1	68	112.849	106	73	GTP-ase activating protein for Arf containing protein
Locus_19200_Transcript_1/1_Conf_1.000	133	0							

Locus_19201_Transcript_1/1_Conf_1.000	237	6	1.75E-06	XP_002644145.1	71	55.8398	53	38	C. briggsae CBR-DAF-12 protein
Locus_19202_Transcript_1/1_Conf_1.000	303	4	2.87E-09	XP_002641939.1	60	65.0846	95	57	C. briggsae CBR-MIG-10 protein
Locus_19203_Transcript_1/1_Conf_1.000	321	0							
Locus_19204_Transcript_1/1_Conf_1.000	182	0							
Locus_19205_Transcript_1/1_Conf_1.000	692	0							
Locus_19206_Transcript_1/1_Conf_1.000	822	20	4.73E-56	XP_001902208.1	71	222.246	177	127	TM2 domain containing protein
Locus_19207_Transcript_1/1_Conf_1.000	167	0							
Locus_19208_Transcript_1/1_Conf_1.000	142	0							
Locus_19209_Transcript_1/1_Conf_1.000	188	20	1.96E-21	XP_002113675.1	93	105.531	62	58	hypothetical protein TRIADDRAFT_50388
Locus_1921_Transcript_1/2_Conf_1.000	672	20	4.54E-79	NP_502655.1	87	298.13	187	164	Ribosomal Protein, Large subunit family member (rpl-18)
Locus_1921_Transcript_2/2_Conf_1.000	672	20	1.01E-78	NP_502655.1	87	296.975	187	164	Ribosomal Protein, Large subunit family member (rpl-18)
Locus_19210_Transcript_1/1_Conf_1.000	234	0							
Locus_19211_Transcript_1/1_Conf_1.000	387	20	3.36E-26	NP_502803.3	95	121.324	63	60	EPS (human endocytosis) related family member (eps-8)
Locus_19212_Transcript_1/1_Conf_1.000	298	3	3.90E-06	XP_002643075.1	60	54.6842	65	39	Hypothetical protein CBG22995
Locus_19213_Transcript_1/1_Conf_1.000	694	19	2.30E-36	EFO26231.1	67	156.377	165	111	hypothetical protein LOAG_02257

Locus_19214_Transcript_1/1_Conf_1.000	422	20	2.89E-33	XP_002645074.1	65	144.821	138	91	Hypothetical protein CBG16737
Locus_19215_Transcript_1/1_Conf_1.000	227	20	3.68E-12	CAR63556.1	68	74.7146	64	44	putative Lin-5 (Five) Interacting protein
Locus_19216_Transcript_1/1_Conf_1.000	214	20	3.59E-12	XP_002633609.1	71	74.7146	69	49	Hypothetical protein CBG05491
Locus_19217_Transcript_1/1_Conf_1.000	216	20	4.84E-09	XP_002594167.1	59	64.3142	66	39	hypothetical protein BRAFLDRAFT_195549
Locus_19218_Transcript_1/1_Conf_1.000	194	3	7.90E-23	NP_492730.2	90	110.153	64	58	hypothetical protein Y106G6H.5
Locus_19219_Transcript_1/1_Conf_1.000	227	20	1.22E-31	NP_499205.1	94	139.428	75	71	hypothetical protein K03H1.5
Locus_1922_Transcript_1/1_Conf_1.000	1067	20	2.66E-82	XP_001895586.1	63	310.071	377	238	N terminus of Rad21 / Rec8 like protein
Locus_19220_Transcript_1/1_Conf_1.000	183	20	3.57E-31	BAG60662.1	100	137.887	60	60	unnamed protein product
Locus_19221_Transcript_1/1_Conf_1.000	709	20	5.90E-11	ABB53347.1	45	72.0182	170	78	secreted protein 5 precursor
Locus_19222_Transcript_1/1_Conf_1.000	282	0							
Locus_19223_Transcript_1/1_Conf_1.000	317	20	3.33E-29	NP_497990.1	76	131.339	106	81	hypothetical protein C38D4.9
Locus_19224_Transcript_1/1_Conf_1.000	497	0							
Locus_19225_Transcript_1/1_Conf_1.000	148	17	1.01E-09	XP_002638772.1	81	66.6254	48	39	C. briggsae CBR-PTR-21 protein
Locus_19226_Transcript_1/1_Conf_1.000	310	20	3.72E-09	XP_002631206.1	90	64.6994	41	37	Hypothetical protein CBG03002
Locus_19227_Transcript_1/1_Conf_1.000	150	0							
Locus_19228_Transcript_1/1_Conf_1.000	222	20	4.50E-26	NP_492127.1	87	120.939	74	65	Low-density lipoprotein Receptor Related family member (lrp-1)
Locus_19229_Transcript_1/1_Conf_1.000	215	2	3.47E-15	NP_495787.1	74	84.7297	70	52	hypothetical protein M05D6.2
Locus_1923_Transcript_1/3_Conf_0.400	790	0							

Locus_1923_Transcript_2/3_Conf_0.600	2129	20	9.49E-52	EFO20470.1	64	209.92	300	192	hypothetical protein LOAG_08019
Locus_1923_Transcript_3/3_Conf_0.400	1559	20	8.29E-76	EFO20470.1	65	289.271	375	245	hypothetical protein LOAG_08019
Locus_19230_Transcript_1/1_Conf_1.000	186	0							
Locus_19231_Transcript_1/1_Conf_1.000	143	20	2.83E-17	ABW80082.1	95	91.6633	47	45	immunoglobulin heavy chain variable region
Locus_19232_Transcript_1/1_Conf_1.000	187	0							
Locus_19233_Transcript_1/1_Conf_1.000	213	0							
Locus_19234_Transcript_1/1_Conf_1.000	181	0							
Locus_19235_Transcript_1/1_Conf_1.000	200	0							
Locus_19236_Transcript_1/1_Conf_1.000	140	20	4.11E-08	XP_002644355.1	78	61.2326	46	36	C. briggsae CBR-DDR-2 protein
Locus_19237_Transcript_1/1_Conf_1.000	157	0							
Locus_19238_Transcript_1/1_Conf_1.000	229	0							
Locus_19239_Transcript_1/1_Conf_1.000	164	0							
Locus_1924_Transcript_1/1_Conf_1.000	280	20	4.51E-31	NP_502553.2	93	137.502	83	78	Cleavage and Polyadenylation Specificity Factor family member (cpsf-3)
Locus_19240_Transcript_1/1_Conf_1.000	254	0							

Locus_19241_Transcript_1/2_Conf_1.000	315	20	1.49E-37	XP_001175663.1	100	159.073	79	79	PREDICTED: similar to H4 histone protein
Locus_19241_Transcript_2/2_Conf_1.000	378	20	1.20E-39	XP_001175663.1	100	166.007	83	83	PREDICTED: similar to H4 histone protein
Locus_19242_Transcript_1/1_Conf_1.000	153	0							
Locus_19243_Transcript_1/1_Conf_1.000	284	20	1.23E-31	XP_513264.2	100	139.428	94	94	PREDICTED: similar to KIAA0085
Locus_19244_Transcript_1/1_Conf_1.000	190	2	2.17E-04	XP_002634109.1	62	48.9062	64	40	C. briggsae CBR-CSN-3 protein
Locus_19245_Transcript_1/1_Conf_1.000	156	0							
Locus_19246_Transcript_1/1_Conf_1.000	218	0							
Locus_19247_Transcript_1/1_Conf_1.000	322	2	3.31E-21	NP_499330.2	80	104.76	63	51	hypothetical protein Y45F3A.4
Locus_19248_Transcript_1/1_Conf_1.000	423	0							
Locus_19249_Transcript_1/1_Conf_1.000	213	20	7.44E-34	3GQY	100	146.747	70	70	Activator-BoundStructure Of Human Pyruvate Kinase M2

Locus_1925_Transcript_1/1_Conf_1.000	243	4	1.47E-05	NP_872245.2	65	52.7582	58	38	protein KINase family member (kin-25)
Locus_19250_Transcript_1/1_Conf_1.000	164	20	2.14E-12	CAA30855.1	97	75.485	41	40	myosin heavy chain 2
Locus_19251_Transcript_1/1_Conf_1.000	200	0							
Locus_19252_Transcript_1/1_Conf_1.000	273	20	1.16E-26	NP_510130.2	82	122.865	90	74	hypothetical protein F22E10.5
Locus_19253_Transcript_1/1_Conf_1.000	214	0							
Locus_19254_Transcript_1/1_Conf_1.000	292	6	8.16E-20	XP_001896152.1	73	100.138	73	54	hypothetical protein Bm1_23475
Locus_19255_Transcript_1/1_Conf_1.000	769	0							
Locus_19256_Transcript_1/1_Conf_1.000	231	20	2.01E-10	XP_002639913.1	70	68.9366	60	42	Hypothetical protein CBG08243
Locus_19257_Transcript_1/1_Conf_1.000	141	0							

Locus_19258_Transcript_1/1_Conf_1.000	265	20	1.30E-17	XP_001096144.2	100	92.8189	42	42	PREDICTED: hypothetical protein LOC707717
Locus_19259_Transcript_1/1_Conf_1.000	492	0							
Locus_1926_Transcript_1/2_Conf_1.000	2083	20	0	NP_001122877.1	82	909.442	642	531	hypothetical protein C39F7.2
Locus_1926_Transcript_2/2_Conf_1.000	2083	20	0	NP_001122877.1	82	909.442	642	531	hypothetical protein C39F7.2
Locus_19260_Transcript_1/1_Conf_1.000	206	0							
Locus_19261_Transcript_1/1_Conf_1.000	162	20	8.13E-12	NP_506047.5	79	73.559	53	42	abnormal CHEmotaxis family member (che-11)
Locus_19262_Transcript_1/1_Conf_1.000	138	0							

Locus_19263_Transcript_1/1_Conf_1.000	213	20	5.52E-29	NP_001040912.1	94	130.568	70	66	hypothetical protein C08F8.2
Locus_19264_Transcript_1/1_Conf_1.000	261	1	1.54E-10	NP_503410.3	62	69.3218	74	46	hypothetical protein R12A1.3
Locus_19265_Transcript_1/1_Conf_1.000	328	10	1.16E-34	NP_509899.3	77	149.443	110	85	Organic Cation Transporter family member (oct-2)
Locus_19266_Transcript_1/1_Conf_1.000	525	0							
Locus_19267_Transcript_1/1_Conf_1.000	289	20	5.65E-37	NP_509002.2	82	157.147	96	79	INneXin family member (inx-3)
Locus_19268_Transcript_1/1_Conf_1.000	353	0							
Locus_19269_Transcript_1/1_Conf_1.000	287	20	1.40E-19	XP_002647861.1	72	99.3673	95	69	Hypothetical protein CBG23659
Locus_1927_Transcript_1/1_Conf_1.000	832	13	1.40E-71	CBL43423.1	69	273.863	275	190	C. elegans protein C53A5.13b, partially confirmed by transcript evidence
Locus_19270_Transcript_1/1_Conf_1.000	432	0							
Locus_19271_Transcript_1/1_Conf_1.000	578	20	3.83E-77	NP_001022641.1	83	291.197	192	161	LEThal family member (let-805)
Locus_19272_Transcript_1/1_Conf_1.000	712	4	1.11E-57	XP_002645171.1	65	227.254	240	156	Hypothetical protein CBG16891
Locus_19273_Transcript_1/1_Conf_1.000	134	5	3.74E-09	XP_002630796.1	86	64.6994	38	33	Hypothetical protein CBG02494
Locus_19274_Transcript_1/1_Conf_1.000	958	20	1.52E-46	XP_002641058.1	61	191.045	320	196	Hypothetical protein CBG22469
Locus_19275_Transcript_1/1_Conf_1.000	139	0							
Locus_19276_Transcript_1/1_Conf_1.000	128	0							
Locus_19277_Transcript_1/1_Conf_1.000	133	0							
Locus_19278_Transcript_1/1_Conf_1.000	365	0							
Locus_19279_Transcript_1/1_Conf_1.000	470	20	1.99E-34	ACI49192.1	69	148.673	160	111	hypothetical protein Csp3_JD03.001
Locus_1928_Transcript_1/1_Conf_1.000	818	20	4.25E-25	XP_001897581.1	53	119.398	279	150	hypothetical protein Bm1_30710

Locus_19280_Transcript_1/1_Conf_1.000	139	3	5.03E-06	XP_002647772.1	83	54.299	36	30	Hypothetical protein CBG20529
Locus_19281_Transcript_1/1_Conf_1.000	128	0							
Locus_19282_Transcript_1/1_Conf_1.000	259	20	7.61E-42	XP_002920355.1	100	173.326	85	85	PREDICTED: proteasome subunit alpha type-7-like
Locus_19283_Transcript_1/1_Conf_1.000	372	11	1.49E-29	AAK31453.4	71	132.494	123	88	Hypothetical protein C25H3.8
Locus_19284_Transcript_1/1_Conf_1.000	372	20	9.06E-11	XP_001032930.1	70	70.0922	51	36	DHHC zinc finger domain containing protein
Locus_19285_Transcript_1/1_Conf_1.000	192	0							
Locus_19286_Transcript_1/1_Conf_1.000	237	0							
Locus_19287_Transcript_1/1_Conf_1.000	182	0							
Locus_19288_Transcript_1/1_Conf_1.000	158	0							
Locus_19289_Transcript_1/1_Conf_1.000	216	0							
Locus_1929_Transcript_1/1_Conf_1.000	491	20	1.16E-58	XP_002639025.1	83	229.18	150	125	C. briggsae CBR-RPS-10 protein
Locus_19290_Transcript_1/1_Conf_1.000	266	0							
Locus_19291_Transcript_1/1_Conf_1.000	332	0							
Locus_19292_Transcript_1/1_Conf_1.000	223	0							
Locus_19293_Transcript_1/1_Conf_1.000	216	0							
Locus_19294_Transcript_1/1_Conf_1.000	842	0							
Locus_19295_Transcript_1/1_Conf_1.000	525	20	3.48E-62	NP_001022870.1	79	241.121	169	134	hypothetical protein Y43F4A.1
Locus_19296_Transcript_1/1_Conf_1.000	132	0							
Locus_19297_Transcript_1/1_Conf_1.000	259	3	3.93E-22	XP_002642486.1	83	107.842	86	72	Hypothetical protein CBG06905
Locus_19298_Transcript_1/1_Conf_1.000	752	20	1.81E-32	EFO22295.1	88	143.665	123	109	hypothetical protein LOAG_06193
Locus_19299_Transcript_1/1_Conf_1.000	220	0							
Locus_193_Transcript_1/2_Conf_1.000	1078	20	1.95E-64	CAR63652.1	95	250.751	135	129	hypothetical protein
Locus_193_Transcript_2/2_Conf_1.000	2045	20	5.69E-139	NP_497804.2	69	499.59	441	306	PleXin Domain containing family member (pxd-1)

Locus_1930_Transcript_1/1_Conf_1.000	572	20	1.69E-21	NP_492370.1	96	106.301	56	54	Transport to INner mitochondrial membrane (yeast TIM) family member (tin-13)
Locus_19300_Transcript_1/1_Conf_1.000	155	0							
Locus_19301_Transcript_1/1_Conf_1.000	411	0							
Locus_19302_Transcript_1/1_Conf_1.000	722	20	1.50E-33	NP_510576.2	57	147.132	242	139	hypothetical protein K09E9.1
Locus_19303_Transcript_1/1_Conf_1.000	227	0							
Locus_19304_Transcript_1/1_Conf_1.000	209	20	3.99E-19	NP_497420.1	89	97.8265	69	62	hypothetical protein Y67D2.6
Locus_19305_Transcript_1/1_Conf_1.000	150	0							
Locus_19306_Transcript_1/1_Conf_1.000	332	20	4.25E-37	XP_001899111.1	88	157.532	96	85	Mitochondrial carrier protein
Locus_19307_Transcript_1/1_Conf_1.000	377	20	4.01E-43	XP_002636973.1	76	177.563	125	95	Hypothetical protein CBG09454
Locus_19308_Transcript_1/2_Conf_1.000	884	20	8.20E-81	CAA22108.2	74	304.679	295	219	C. elegans protein Y75B8A.24, partially confirmed by transcript evidence
Locus_19308_Transcript_2/2_Conf_1.000	578	20	7.26E-60	CAA22108.2	74	233.802	204	152	C. elegans protein Y75B8A.24, partially confirmed by transcript evidence
Locus_19309_Transcript_1/1_Conf_1.000	355	20	1.51E-50	AAF59456.4	91	202.216	118	108	Smg-associated and lethal protein 2, partially confirmed by transcript evidence
Locus_1931_Transcript_1/1_Conf_1.000	1692	20	6.40E-93	ACV31107.1	66	346.28	413	273	Hypothetical protein F22D3.2b
Locus_19310_Transcript_1/1_Conf_1.000	334	20	1.37E-11	NP_505133.1	58	72.7886	80	47	ASpartyl Protease family member (asp-6)
Locus_19311_Transcript_1/1_Conf_1.000	281	0							

Locus_19312_Transcript_1/2_Conf_1.000	588	20	4.20E-26	XP_002640523.1	83	121.709	80	67	Hypothetical protein CBG18685
Locus_19312_Transcript_2/2_Conf_1.000	588	20	4.20E-26	XP_002640523.1	83	121.709	80	67	Hypothetical protein CBG18685
Locus_19313_Transcript_1/1_Conf_1.000	290	0							
Locus_19314_Transcript_1/1_Conf_1.000	353	20	2.27E-38	XP_002632772.1	83	161.77	117	98	C. briggsae CBR-TAT-2 protein
Locus_19315_Transcript_1/1_Conf_1.000	157	0							
Locus_19316_Transcript_1/1_Conf_1.000	212	20	5.19E-19	NP_504373.2	72	97.4413	70	51	hypothetical protein F14F9.5
Locus_19317_Transcript_1/1_Conf_1.000	191	20	1.60E-23	ACJ65180.1	90	112.464	63	57	Gaba b receptor subunit protein 2, confirmed by transcript evidence
Locus_19318_Transcript_1/1_Conf_1.000	278	0							
Locus_19319_Transcript_1/1_Conf_1.000	211	0							
Locus_1932_Transcript_1/1_Conf_1.000	543	20	7.93E-84	BAG52420.1	100	313.153	180	180	unnamed protein product
Locus_19320_Transcript_1/1_Conf_1.000	423	0							
Locus_19321_Transcript_1/1_Conf_1.000	178	0							
Locus_19322_Transcript_1/1_Conf_1.000	152	0							
Locus_19323_Transcript_1/1_Conf_1.000	138	3	4.71E-04	CAX12927.1	68	47.7506	45	31	novel protein similar to human major facilitator superfamily domain containing 5 (MFSD5, zgc:91807)
Locus_19324_Transcript_1/1_Conf_1.000	131	0							
Locus_19325_Transcript_1/1_Conf_1.000	184	20	1.78E-14	XP_002630326.1	75	82.4185	58	44	Hypothetical protein CBG04253
Locus_19326_Transcript_1/1_Conf_1.000	150	0							

Locus_19327_Transcript_1/1_Conf_1.000	614	20	6.55E-44	XP_002648449.1	63	181.03	204	129	Hypothetical protein CBG24724
Locus_19328_Transcript_1/1_Conf_1.000	165	20	3.28E-21	XP_002927427.1	100	104.76	53	53	PREDICTED: transcription elongation factor SPT5-like isoform 2
Locus_19329_Transcript_1/1_Conf_1.000	484	4	1.69E-41	AAQ11020.1	69	172.17	172	120	mesocentin
Locus_1933_Transcript_1/1_Conf_1.000	2006	20	0	XP_002646154.1	82	826.624	627	516	C. briggsae CBR-CYN-15 protein
Locus_19330_Transcript_1/1_Conf_1.000	222	20	3.56E-23	NP_508805.3	94	111.309	53	50	hypothetical protein K02G10.1
Locus_19331_Transcript_1/1_Conf_1.000	423								
Locus_19332_Transcript_1/1_Conf_1.000	130	20	4.15E-08	XP_002600688.1	88	61.2326	34	30	hypothetical protein BRAFLDRAFT_118551
Locus_19333_Transcript_1/1_Conf_1.000	447	20	7.86E-15	NP_505516.1	55	83.5741	129	71	hypothetical protein F58E6.5
Locus_19334_Transcript_1/1_Conf_1.000	357	0							
Locus_19335_Transcript_1/1_Conf_1.000	254	20	8.51E-25	XP_002645934.1	83	116.701	83	69	Hypothetical protein CBG07699
Locus_19336_Transcript_1/1_Conf_1.000	397	20	1.64E-44	NP_492590.1	83	182.185	123	103	hypothetical protein K02A11.3

Locus_19337_Transcript_1/1_Conf_1.000	130	1	7.55E-18	XP_001171837.1	95	93.5893	43	41	PREDICTED: DnaJ (Hsp40) homolog, subfamily B, member 1 isoform 1
Locus_19338_Transcript_1/1_Conf_1.000	637	2	9.67E-33	NP_509416.2	72	144.05	178	129	hypothetical protein F55E10.7
Locus_19339_Transcript_1/1_Conf_1.000	291	20	7.57E-50	XP_002928507.1	100	199.904	97	97	PREDICTED: elongation factor 2-like
Locus_1934_Transcript_1/1_Conf_1.000	650	0							
Locus_19340_Transcript_1/1_Conf_1.000	618	20	7.42E-51	NP_505595.2	68	204.142	203	139	UDP-GlucuronosylTransferase family member (ugt-47)
Locus_19341_Transcript_1/1_Conf_1.000	205	0							
Locus_19342_Transcript_1/1_Conf_1.000	740	20	4.14E-58	NP_492244.1	66	228.794	226	150	hypothetical protein ZK265.3
Locus_19343_Transcript_1/1_Conf_1.000	213	0							
Locus_19344_Transcript_1/1_Conf_1.000	310	0							
Locus_19345_Transcript_1/1_Conf_1.000	1214	20	2.23E-99	EFO22512.1	66	367.081	415	274	hypothetical protein LOAG_05973
Locus_19346_Transcript_1/1_Conf_1.000	439	0							
Locus_19347_Transcript_1/1_Conf_1.000	280	0							
Locus_19348_Transcript_1/1_Conf_1.000	218	3	4.24E-05	NP_500978.1	62	51.2174	56	35	EXOSome (multiexonuclease complex) component family member (exos-2)
Locus_19349_Transcript_1/1_Conf_1.000	194	0							
Locus_1935_Transcript_1/4_Conf_0.556	1543	2	1.02E-09	XP_001902753.1	54	69.707	126	69	RhoGAP domain containing protein
Locus_1935_Transcript_2/4_Conf_0.444	1429	2	7.05E-10	XP_001902753.1	50	70.0922	161	81	RhoGAP domain containing protein
Locus_1935_Transcript_3/4_Conf_0.333	1480	2	7.41E-10	XP_001902753.1	50	70.0922	161	81	RhoGAP domain containing protein
Locus_1935_Transcript_4/4_Conf_0.556	1594	2	8.15E-10	XP_001902753.1	50	70.0922	161	81	RhoGAP domain containing protein
Locus_19350_Transcript_1/1_Conf_1.000	335	0							
Locus_19351_Transcript_1/1_Conf_1.000	494	20	1.01E-38	EFO17779.1	66	162.925	159	105	hypothetical protein LOAG_10719
Locus_19352_Transcript_1/1_Conf_1.000	142	0							
Locus_19353_Transcript_1/1_Conf_1.000	234	1	1.17E-10	NP_001129775.1	79	69.707	54	43	GLoBin family member (glb-18)
Locus_19354_Transcript_1/1_Conf_1.000	208	0							

Locus_19355_Transcript_1/1_Conf_1.000	158	20	8.17E-20	XP_002647071.1	90	100.138	52	47	C. briggsae CBR-NIT-1 protein
Locus_19356_Transcript_1/1_Conf_1.000	141	0							
Locus_19357_Transcript_1/1_Conf_1.000	452	20	9.22E-24	NP_001041088.1	60	113.235	146	89	hypothetical protein C27A7.3
Locus_19358_Transcript_1/1_Conf_1.000	669	0							
Locus_19359_Transcript_1/1_Conf_1.000	488	17	7.38E-13	XP_001898480.1	62	77.0258	122	76	integrin cytoplasmic domain-associated protein 1, isoform 1, putative
Locus_1936_Transcript_1/4_Conf_0.444	473	20	4.39E-50	EFO20496.1	72	200.675	157	114	hypothetical protein LOAG_07994
Locus_1936_Transcript_2/4_Conf_0.667	1144	20	3.60E-88	EFO20496.1	56	329.717	432	245	hypothetical protein LOAG_07994
Locus_1936_Transcript_3/4_Conf_0.222	498	8	2.25E-14	XP_001893982.1	47	82.0333	190	91	Mitotic control protein dis3
Locus_1936_Transcript_4/4_Conf_0.444	473	20	7.49E-50	EFO20496.1	72	199.904	157	114	hypothetical protein LOAG_07994
Locus_19360_Transcript_1/1_Conf_1.000	172	5	2.19E-09	CBL43415.1	68	65.4698	54	37	C. elegans protein C32C4.2b, partially confirmed by transcript evidence
Locus_19361_Transcript_1/1_Conf_1.000	1228	20	5.24E-96	NP_001022767.1	72	355.91	345	251	protein KINase family member (kin-18)
Locus_19362_Transcript_1/1_Conf_1.000	274	0							

Locus_19363_Transcript_1/1_Conf_1.000	505	20	1.58E-26	NP_495701.2	75	122.479	97	73	IRE1 kinase related family member (ire-1)
Locus_19364_Transcript_1/1_Conf_1.000	267	20	8.65E-22	XP_001742234.1	74	106.686	89	66	hypothetical protein
Locus_19365_Transcript_1/1_Conf_1.000	255	0							
Locus_19366_Transcript_1/1_Conf_1.000	495	20	5.52E-45	EFO23518.1	72	183.726	160	116	serine/threonine protein kinase
Locus_19367_Transcript_1/1_Conf_1.000	465	2	1.03E-06	XP_001900574.1	47	56.6102	121	58	hypothetical protein Bm1_45555
Locus_19368_Transcript_1/1_Conf_1.000	168	3	1.43E-08	NP_496184.2	79	62.7734	49	39	Location Of Vulva defective family member (lov-1)
Locus_19369_Transcript_1/1_Conf_1.000	133	20	1.24E-12	NP_504553.1	95	76.2554	42	40	Adenylyl CYclase family member (acy-2)
Locus_1937_Transcript_1/1_Conf_1.000	565	0							
Locus_19370_Transcript_1/1_Conf_1.000	182	0							
Locus_19371_Transcript_1/1_Conf_1.000	145	0							
Locus_19372_Transcript_1/1_Conf_1.000	218	0							
Locus_19373_Transcript_1/1_Conf_1.000	201	3	5.42E-24	XP_002641473.1	88	114.005	67	59	Hypothetical protein CBG09762
Locus_19374_Transcript_1/1_Conf_1.000	141	0							
Locus_19375_Transcript_1/1_Conf_1.000	490	4	8.03E-52	NP_871810.1	80	206.453	164	132	HAlF transporter (PGP related) family member (haf-9)

Locus_19376_Transcript_1/1_Conf_1.000	382	20	6.56E-46	XP_002647328.1	88	186.808	106	94	C. briggsae CBR-EGL-8 protein
Locus_19377_Transcript_1/1_Conf_1.000	250	0							
Locus_19378_Transcript_1/1_Conf_1.000	535	20	8.04E-62	NP_492067.1	85	239.965	148	127	hypothetical protein F13G3.11
Locus_19379_Transcript_1/1_Conf_1.000	595	20	2.21E-38	EFO23010.1	65	162.54	167	109	hypothetical protein LOAG_05474
Locus_1938_Transcript_1/10_Conf_0.208	750	20	2.47E-114	XP_002594632.1	93	415.616	242	227	hypothetical protein BRAFLDRAFT_217516

Locus_1938_Transcript_10/10_Conf_0.333	1691	20	0	XP_002594632.1	84	669.848	458	386	hypothetical protein BRAFLDRAFT_217516
Locus_1938_Transcript_2/10_Conf_0.208	792	20	6.09E-114	XP_002594632.1	93	414.461	244	228	hypothetical protein BRAFLDRAFT_217516

Locus_1938_Transcript_3/10_Conf_0.250	1175	20	0	XP_002594632.1	91	647.121	384	352	hypothetical protein BRAFLDRAFT_217516
Locus_1938_Transcript_4/10_Conf_0.250	1175	20	0	XP_002594632.1	91	649.818	384	352	hypothetical protein BRAFLDRAFT_217516

Locus_1938_Transcript_5/10_Conf_0.333	1703	20	0	XP_002594632.1	83	664.07	462	386	hypothetical protein BRAFLDRAFT_217516
Locus_1938_Transcript_6/10_Conf_0.333	1703	20	0	XP_002594632.1	83	661.374	462	386	hypothetical protein BRAFLDRAFT_217516

Locus_1938_Transcript_7/10_Conf_0.333	1691	20	0	XP_002594632.1	84	667.152	458	386	hypothetical protein BRAFLDRAFT_217516
Locus_1938_Transcript_8/10_Conf_0.333	1691	20	0	XP_002594632.1	84	669.848	458	386	hypothetical protein BRAFLDRAFT_217516

Locus_1938_Transcript_9/10_Conf_0.333	1691	20	0	XP_002594632.1	84	667.152	458	386	hypothetical protein BRAFLDRAFT_217516
Locus_19380_Transcript_1/1_Conf_1.000	139	0							
Locus_19381_Transcript_1/1_Conf_1.000	530	20	4.96E-64	XP_002633755.1	81	247.284	172	140	Hypothetical protein CBG03442
Locus_19382_Transcript_1/3_Conf_0.600	928	20	6.94E-49	XP_002633289.1	61	198.749	302	185	Hypothetical protein CBG06018
Locus_19382_Transcript_2/3_Conf_0.600	911	20	2.73E-42	XP_002633289.1	60	176.792	280	170	Hypothetical protein CBG06018
Locus_19382_Transcript_3/3_Conf_0.600	910	20	1.22E-42	XP_002633289.1	60	177.948	283	171	Hypothetical protein CBG06018
Locus_19383_Transcript_1/1_Conf_1.000	721	20	1.04E-18	EFO20401.1	59	97.8265	155	92	sex-determining protein fem-1
Locus_19384_Transcript_1/1_Conf_1.000	173	20	1.98E-10	XP_001900530.1	75	68.9366	57	43	manba-prov protein
Locus_19385_Transcript_1/1_Conf_1.000	377	0							
Locus_19386_Transcript_1/1_Conf_1.000	418	20	5.26E-59	AAM82167.1	89	230.335	138	123	gamma-butyrobetaine,2-oxoglutarate dioxygenase
Locus_19387_Transcript_1/1_Conf_1.000	1034	2	5.40E-24	XP_001897079.1	46	116.316	372	172	Protein kinase domain containing protein

Locus_19388_Transcript_1/1_Conf_1.000	956	20	1.49E-78	NP_501489.2	68	297.36	311	212	hypothetical protein F08B4.5
Locus_19389_Transcript_1/1_Conf_1.000	280	5	2.76E-04	NP_741176.2	56	48.521	95	54	hypothetical protein C23G10.7
Locus_1939_Transcript_1/1_Conf_1.000	430	20	1.09E-16	CAR63597.1	70	89.7373	80	56	hypothetical protein
Locus_19390_Transcript_1/1_Conf_1.000	786	6	1.99E-16	NP_492861.1	68	90.5077	93	64	hypothetical protein Y52B11A.10
Locus_19391_Transcript_1/2_Conf_0.500	395	0							
Locus_19391_Transcript_2/2_Conf_0.750	116	0							
Locus_19392_Transcript_1/1_Conf_1.000	230	0							
Locus_19393_Transcript_1/1_Conf_1.000	359	8	8.61E-22		50	106.686	155	78	hypothetical protein H19M22.2 - Caenorhabditis elegans
Locus_19394_Transcript_1/1_Conf_1.000	542	0							
Locus_19395_Transcript_1/1_Conf_1.000	153	0							
Locus_19396_Transcript_1/1_Conf_1.000	133	0							
Locus_19397_Transcript_1/1_Conf_1.000	158	20	3.21E-16	XP_001897126.1	94	88.1965	51	48	DnaJ domain containing protein
Locus_19398_Transcript_1/1_Conf_1.000	181	0							
Locus_19399_Transcript_1/1_Conf_1.000	428	6	5.10E-06	EFO23325.1	50	54.299	97	49	hypothetical protein LOAG_05163
Locus_194_Transcript_1/1_Conf_1.000	754	20	5.76E-55	CAR63677.1	89	218.394	124	111	putative SPErmatogenesis family member
Locus_1940_Transcript_1/1_Conf_1.000	258	0							
Locus_19400_Transcript_1/1_Conf_1.000	153	0							

Locus_19401_Transcript_1/1_Conf_1.000	571	20	3.05E-55	XP_002640062.1	81	218.394	161	131	C. briggsae CBR-UNC-120 protein
Locus_19402_Transcript_1/1_Conf_1.000	345	0							
Locus_19403_Transcript_1/1_Conf_1.000	357	3	1.38E-11	XP_002647203.1	72	72.7886	66	48	Hypothetical protein CBG22379
Locus_19404_Transcript_1/1_Conf_1.000	498	2	1.08E-16	NP_497632.1	64	89.7373	159	102	Kruppel-Like Factor (zinc finger protein) family member (klf-1)
Locus_19405_Transcript_1/1_Conf_1.000	447	10	1.29E-33	XP_002639456.1	69	145.976	152	106	Hypothetical protein CBG04051
Locus_19406_Transcript_1/1_Conf_1.000	263	0							
Locus_19407_Transcript_1/1_Conf_1.000	140	0							
Locus_19408_Transcript_1/1_Conf_1.000	144	0							
Locus_19409_Transcript_1/1_Conf_1.000	843	20	1.53E-97	CAA94853.5	79	360.147	266	211	C. elegans protein ZK856.5, confirmed by transcript evidence
Locus_1941_Transcript_1/2_Conf_1.000	3143	1	7.96E-05	XP_001902928.1	49	54.6842	137	68	hypothetical protein Bm1_57350
Locus_1941_Transcript_2/2_Conf_1.000	3120	1	7.89E-05	XP_001902928.1	49	54.6842	137	68	hypothetical protein Bm1_57350
Locus_19410_Transcript_1/1_Conf_1.000	249	0							
Locus_19411_Transcript_1/1_Conf_1.000	190	1	4.83E-04	XP_002646300.1	67	47.7506	49	33	Hypothetical protein CBG12007
Locus_19412_Transcript_1/1_Conf_1.000	362	20	1.50E-42	XP_001901345.1	84	175.637	120	101	Beta-tubulin cofactor D family protein

Locus_19413_Transcript_1/1_Conf_1.000	453	20	3.86E-22	NP_495283.2	57	107.842	139	80	C-type LECtin family member (clec-88)
Locus_19414_Transcript_1/1_Conf_1.000	385	0							
Locus_19415_Transcript_1/1_Conf_1.000	206	0							
Locus_19416_Transcript_1/1_Conf_1.000	671	20	3.96E-51	NP_505312.1	70	205.297	205	144	hypothetical protein T19A5.1
Locus_19417_Transcript_1/1_Conf_1.000	282	20	4.37E-21	XP_002642049.1	71	104.375	82	59	Hypothetical protein CBG17986
Locus_19418_Transcript_1/1_Conf_1.000	458	20	5.28E-72	XP_002638687.1	90	273.478	152	138	Hypothetical protein CBG11882
Locus_19419_Transcript_1/1_Conf_1.000	499	20	1.09E-85	XP_002644182.1	95	318.931	166	158	C. briggsae CBR-UNC-115 protein
Locus_1942_Transcript_1/1_Conf_1.000	667	20	1.15E-26	ACM08416.1	65	124.02	103	67	Lipopolysaccharide-induced tumor necrosis factor-alpha factor homolog
Locus_19420_Transcript_1/1_Conf_1.000	299	17	3.64E-20	EFO24930.1	66	101.293	106	70	hypothetical protein LOAG_03557
Locus_19421_Transcript_1/1_Conf_1.000	252	2	4.23E-16	XP_002630540.1	86	87.8113	66	57	Hypothetical protein CBG12981
Locus_19422_Transcript_1/1_Conf_1.000	174	20	3.48E-23	NP_498516.2	92	111.309	57	53	LEThal family member (let-711)
Locus_19423_Transcript_1/1_Conf_1.000	455	20	2.09E-68	NP_741692.1	88	261.536	151	133	TetraSPanin family member (tsp-13)
Locus_19424_Transcript_1/1_Conf_1.000	280	8	3.97E-11	XP_001894571.1	70	71.2478	62	44	UBX domain containing protein
Locus_19425_Transcript_1/1_Conf_1.000	263	0							
Locus_19426_Transcript_1/1_Conf_1.000	151	1	2.57E-05	XP_002647048.1	70	51.9878	51	36	Hypothetical protein CBG03566
Locus_19427_Transcript_1/1_Conf_1.000	168	0							
Locus_19428_Transcript_1/1_Conf_1.000	500	0							
Locus_19429_Transcript_1/1_Conf_1.000	332	4	4.26E-29	NP_496755.1	74	130.954	110	82	DAF-16/FOXO Controlled, germline Tumor affecting family member (dct-18)
Locus_1943_Transcript_1/1_Conf_1.000	142	0							
Locus_19430_Transcript_1/1_Conf_1.000	762	20	3.15E-40	XP_795502.1	57	169.474	217	124	PREDICTED: similar to ENSANGP00000010363
Locus_19431_Transcript_1/1_Conf_1.000	171	0							
Locus_19432_Transcript_1/1_Conf_1.000	383	20	7.01E-48	XP_002647751.1	84	193.356	126	106	C. briggsae CBR-CYP-42A1 protein
Locus_19433_Transcript_1/1_Conf_1.000	170	0							
Locus_19434_Transcript_1/1_Conf_1.000	294	20	1.74E-38	NP_505616.2	91	162.155	97	89	CULlin family member (cul-5)

Locus_19435_Transcript_1/1_Conf_1.000	165	0							
Locus_19436_Transcript_1/1_Conf_1.000	514	20	3.66E-42	NP_496592.1	82	174.481	120	99	hypothetical protein Y57A10A.15
Locus_19437_Transcript_1/1_Conf_1.000	137	1	3.61E-04	NP_504648.1	71	48.1358	45	32	Carnitine Palmitoyl Transferase family member (cpt-6)
Locus_19438_Transcript_1/1_Conf_1.000	146	0							
Locus_19439_Transcript_1/1_Conf_1.000	213	20	1.67E-17	P30646.4	75	92.4337	70	53	Uncharacterized sugar kinase R08D7.7
Locus_1944_Transcript_1/1_Conf_1.000	1698	20	0	XP_002632610.1	93	766.918	444	414	C. briggsae CBR-GDI-1 protein
Locus_19440_Transcript_1/1_Conf_1.000	253	0							
Locus_19441_Transcript_1/1_Conf_1.000	201	20	2.97E-22	NP_498931.2	84	108.227	65	55	SMAll family member (sma-2)
Locus_19442_Transcript_1/1_Conf_1.000	327	6	3.64E-12	XP_002629686.1	65	74.7146	82	54	Hypothetical protein CBG00906
Locus_19443_Transcript_1/1_Conf_1.000	338	20	1.19E-39	XP_002636314.1	89	166.007	111	99	Hypothetical protein CBG08607
Locus_19444_Transcript_1/1_Conf_1.000	235	0							
Locus_19445_Transcript_1/1_Conf_1.000	795	20	5.27E-65	NP_501024.1	67	251.906	264	179	hypothetical protein C01B10.8
Locus_19446_Transcript_1/1_Conf_1.000	233	20	3.19E-24	XP_002643253.1	96	114.775	59	57	C. briggsae CBR-AEX-3 protein

Locus_19447_Transcript_1/1_Conf_1.000	385	20	9.76E-42	NP_508178.2	79	172.94	128	102	TBC (Tre-2/Bub2/Cdc16) domain family member (tbc-11)
Locus_19448_Transcript_1/1_Conf_1.000	256	0							
Locus_19449_Transcript_1/1_Conf_1.000	1002	20	4.00E-85	NP_505523.1	71	319.316	308	219	hypothetical protein F46B6.4
Locus_1945_Transcript_1/2_Conf_1.000	1387	20	1.11E-36	NP_508806.1	73	159.073	187	137	DNaJ domain (prokaryotic heat shock protein) family member (dnj-14)
Locus_1945_Transcript_2/2_Conf_1.000	1388	20	1.11E-36	NP_508806.1	73	159.073	187	137	DNaJ domain (prokaryotic heat shock protein) family member (dnj-14)
Locus_19450_Transcript_1/1_Conf_1.000	423	20	2.27E-54	EFO24223.1	90	214.927	130	117	hypothetical protein LOAG_04263
Locus_19451_Transcript_1/1_Conf_1.000	147	6	3.04E-06	NP_741010.1	78	55.0694	38	30	hypothetical protein C56C10.7
Locus_19452_Transcript_1/2_Conf_1.000	257	0							
Locus_19452_Transcript_2/2_Conf_1.000	257	0							
Locus_19453_Transcript_1/1_Conf_1.000	142	20	2.10E-12	XP_002433850.1	85	75.485	47	40	conserved hypothetical protein
Locus_19454_Transcript_1/1_Conf_1.000	188	7	9.08E-27	XP_002640720.1	100	123.25	62	62	C. briggsae CBR-TAG-301 protein
Locus_19455_Transcript_1/1_Conf_1.000	804	20	5.82E-35	NP_508178.2	68	152.14	166	114	TBC (Tre-2/Bub2/Cdc16) domain family member (tbc-11)
Locus_19457_Transcript_1/1_Conf_1.000	437	0							
Locus_19458_Transcript_1/1_Conf_1.000	271	0							
Locus_19459_Transcript_1/1_Conf_1.000	362	0							
Locus_1946_Transcript_1/1_Conf_1.000	1208	20	1.24E-134	XP_002641737.1	78	484.182	362	284	C. briggsae CBR-DRS-1 protein
Locus_19460_Transcript_1/1_Conf_1.000	172	0							
Locus_19461_Transcript_1/1_Conf_1.000	725	0							
Locus_19462_Transcript_1/1_Conf_1.000	148	20	2.65E-18	NP_498711.1	85	95.1301	49	42	TYRosinase family member (tyr-1)
Locus_19463_Transcript_1/1_Conf_1.000	213	2	4.11E-08	NP_492278.2	71	61.2326	70	50	hypothetical protein T19A6.4
Locus_19464_Transcript_1/1_Conf_1.000	235	0							
Locus_19465_Transcript_1/1_Conf_1.000	172	0							
Locus_19466_Transcript_1/1_Conf_1.000	217	3	2.24E-14	XP_002634811.1	50	82.0333	112	57	Hypothetical protein CBG13916
Locus_19467_Transcript_1/1_Conf_1.000	248	0							
Locus_19468_Transcript_1/1_Conf_1.000	211	20	8.88E-11	EFO22061.1	61	70.0922	65	40	hypothetical protein LOAG_06422
Locus_19469_Transcript_1/1_Conf_1.000	194	2	4.35E-05	XP_001902022.1	56	51.2174	67	38	hypothetical protein Bm1_52770

Locus_1947_Transcript_1/1_Conf_1.000	1371	2	2.76E-80	XP_002634154.1	64	303.908	395	256	Hypothetical protein CBG01718
Locus_19470_Transcript_1/1_Conf_1.000	185	0							
Locus_19471_Transcript_1/1_Conf_1.000	540	20	3.41E-55	NP_498671.2	82	218.009	179	147	Uridine PhosPhorylase family member (upp-1)
Locus_19472_Transcript_1/1_Conf_1.000	144	20	3.48E-10	XP_002639439.1	78	68.1662	47	37	Hypothetical protein CBG04032
Locus_19473_Transcript_1/1_Conf_1.000	207	0							
Locus_19474_Transcript_1/1_Conf_1.000	138	20	1.67E-17	XP_002812491.1	100	92.4337	45	45	PREDICTED: c-X-C chemokine receptor type 4-like
Locus_19475_Transcript_1/1_Conf_1.000	299	0							
Locus_19476_Transcript_1/1_Conf_1.000	319	0							
Locus_19477_Transcript_1/1_Conf_1.000	1371	0							
Locus_19478_Transcript_1/1_Conf_1.000	424	20	5.26E-27	EFO24868.1	62	124.02	141	88	hypothetical protein LOAG_03617
Locus_19479_Transcript_1/1_Conf_1.000	235	4	5.44E-16	XP_002630800.1	90	87.4261	53	48	Hypothetical protein CBG02500
Locus_1948_Transcript_1/1_Conf_1.000	1671	20	3.76E-138	NP_001122655.1	64	496.508	566	367	Motor AXon guidance family member (max-2)

Locus_19480_Transcript_1/1_Conf_1.000	220	20	3.94E-38	XP_002831505.1	100	160.999	72	72	PREDICTED: diamine acetyltransferase 1-like
Locus_19481_Transcript_1/1_Conf_1.000	360	0							
Locus_19482_Transcript_1/1_Conf_1.000	139	0							
Locus_19483_Transcript_1/1_Conf_1.000	291	20	6.04E-23	XP_002645698.1	75	110.538	96	72	Hypothetical protein CBG07358
Locus_19484_Transcript_1/1_Conf_1.000	853	20	2.43E-66	NP_503353.2	68	256.529	264	180	hypothetical protein H24K24.4
Locus_19485_Transcript_1/1_Conf_1.000	133	4	4.14E-08	ABN08628.1	72	61.2326	43	31	RNA-directed DNA polymerase (Reverse transcriptase)
Locus_19486_Transcript_1/1_Conf_1.000	639	0							
Locus_19487_Transcript_1/1_Conf_1.000	256	0							
Locus_19488_Transcript_1/1_Conf_1.000	278	20	5.18E-27	EFO19307.1	87	124.02	93	81	hypothetical protein LOAG_09187
Locus_19489_Transcript_1/1_Conf_1.000	632	20	1.75E-79	XP_002640158.1	95	299.286	165	157	C. briggsae CBR-TRE-1 protein
Locus_1949_Transcript_1/1_Conf_1.000	398	4	2.23E-17	XP_001892578.1	57	92.0485	134	77	hypothetical protein Bm1_05520
Locus_19490_Transcript_1/1_Conf_1.000	156	3	2.38E-11	AAF66614.1	76	72.0182	52	40	AF142441_1H+/oligopeptide symporter OPT-3

Locus_19491_Transcript_1/1_Conf_1.000	139	20	2.75E-20	BAH13895.1	100	101.679	46	46	unnamed protein product
Locus_19492_Transcript_1/1_Conf_1.000	248	0							
Locus_19493_Transcript_1/1_Conf_1.000	308	5	7.99E-28	XP_001894154.1	75	126.716	101	76	hypothetical protein Bm1_13445
Locus_19494_Transcript_1/1_Conf_1.000	393	2	2.10E-07	XP_001895343.1	52	58.9214	106	56	hypothetical protein Bm1_19440
Locus_19495_Transcript_1/1_Conf_1.000	288	2	2.83E-04	NP_505787.1	61	48.521	77	47	hypothetical protein F58B4.4
Locus_19496_Transcript_1/1_Conf_1.000	165	0							
Locus_19497_Transcript_1/1_Conf_1.000	620	0							
Locus_19498_Transcript_1/1_Conf_1.000	305	0							
Locus_19499_Transcript_1/1_Conf_1.000	495	20	1.72E-38	XP_002642587.1	74	162.155	150	111	Hypothetical protein CBG09137
Locus_195_Transcript_1/1_Conf_1.000	942								

Locus_1950_Transcript_1/1_Conf_1.000	415	20	3.35E-18	NP_492436.1	56	94.7449	119	67	hypothetical protein W06D4.4
Locus_19500_Transcript_1/1_Conf_1.000	138	0							
Locus_19501_Transcript_1/1_Conf_1.000	433	20	1.32E-30	NP_498582.1	79	135.961	130	103	PreFolDin (molecular chaperone) family member (pfd-5)
Locus_19502_Transcript_1/1_Conf_1.000	386	8	1.20E-07	NP_492045.1	53	59.6918	128	68	hypothetical protein R06C7.1
Locus_19503_Transcript_1/1_Conf_1.000	132	0							
Locus_19504_Transcript_1/1_Conf_1.000	154	0							
Locus_19505_Transcript_1/1_Conf_1.000	1039	20	4.39E-50	XP_002638395.1	59	202.986	284	170	Hypothetical protein CBG18604

Locus_19506_Transcript_1/1_Conf_1.000	341	20	1.45E-37	NP_506256.3	82	159.073	113	93	CaDHerin family member (cdh-6)
Locus_19507_Transcript_1/1_Conf_1.000	953	20	1.82E-68	XP_002642783.1	70	263.848	273	193	C. briggsae CBR-GRO-1 protein
Locus_19508_Transcript_1/1_Conf_1.000	154	0							
Locus_19509_Transcript_1/1_Conf_1.000	205	0							
Locus_1951_Transcript_1/1_Conf_1.000	1290	20	1.52E-101	XP_002630594.1	68	374.4	400	275	C. briggsae CBR-AKA-1 protein
Locus_19510_Transcript_1/1_Conf_1.000	273	20	5.53E-45	NP_001021681.1	94	183.726	90	85	hypothetical protein Y105E8A.10
Locus_19511_Transcript_1/1_Conf_1.000	473	0							
Locus_19512_Transcript_1/1_Conf_1.000	352	0							
Locus_19513_Transcript_1/1_Conf_1.000	260	20	2.81E-28	XP_002412610.1	82	128.257	84	69	sorbitol dehydrogenase, putative
Locus_19514_Transcript_1/1_Conf_1.000	236	20	4.75E-20	NP_001023038.1	87	100.908	56	49	EXCretory canal abnormal family member (exc-5)
Locus_19515_Transcript_1/1_Conf_1.000	737	20	1.61E-70	NP_498895.1	77	270.011	245	191	RNA HelicAse family member (rha-2)
Locus_19516_Transcript_1/1_Conf_1.000	277	5	5.37E-16	EFO21774.1	87	87.4261	55	48	hypothetical protein LOAG_06715

Locus_19517_Transcript_1/1_Conf_1.000	241	0							
Locus_19518_Transcript_1/1_Conf_1.000	142	0							
Locus_19519_Transcript_1/1_Conf_1.000	238	0							
Locus_1952_Transcript_1/1_Conf_1.000	1130	20	2.88E-122	NP_502383.1	83	442.965	284	238	hypothetical protein C25G4.11
Locus_19520_Transcript_1/1_Conf_1.000	217	11	8.80E-19	XP_002640798.1	81	96.6709	71	58	C. briggsae CBR-NHR-121 protein
Locus_19521_Transcript_1/1_Conf_1.000	259	14	1.77E-14	XP_002635781.1	68	82.4185	88	60	Hypothetical protein CBG10437
Locus_19522_Transcript_1/1_Conf_1.000	180	0							
Locus_19523_Transcript_1/1_Conf_1.000	369	0							
Locus_19524_Transcript_1/1_Conf_1.000	421	20	3.78E-33	XP_002637497.1	69	144.436	137	95	Hypothetical protein CBG19218
Locus_19525_Transcript_1/1_Conf_1.000	335	4	2.51E-05	NP_740989.1	56	51.9878	76	43	hypothetical protein F07F6.8
Locus_19526_Transcript_1/1_Conf_1.000	319	20	9.91E-50	XP_002631126.1	97	199.519	106	103	C. briggsae CBR-SHN-1 protein
Locus_19527_Transcript_1/1_Conf_1.000	233	2	6.89E-19	NP_497911.1	72	97.0561	79	57	INSulin related family member (ins-17)
Locus_19528_Transcript_1/1_Conf_1.000	377	4	1.17E-26	NP_509961.1	80	122.865	100	80	hypothetical protein C44C10.9
Locus_19529_Transcript_1/1_Conf_1.000	295	20	6.44E-17	XP_002631513.1	64	90.5077	99	64	C. briggsae CBR-HDA-6 protein
Locus_1953_Transcript_1/1_Conf_1.000	554	0							
Locus_19530_Transcript_1/1_Conf_1.000	355	0							
Locus_19531_Transcript_1/1_Conf_1.000	606	20	5.80E-21	XP_002637610.1	61	104.76	142	87	C. briggsae CBR-TAG-120 protein
Locus_19532_Transcript_1/1_Conf_1.000	294	0							
Locus_19533_Transcript_1/1_Conf_1.000	234	1	2.52E-21	CAA26321.1	100	105.145	48	48	unnamed protein product
Locus_19534_Transcript_1/1_Conf_1.000	205	5	7.83E-07	XP_002644215.1	77	56.9954	44	34	C. briggsae CBR-ACL-5 protein

Locus_19535_Transcript_1/1_Conf_1.000	134	0							
Locus_19536_Transcript_1/1_Conf_1.000	320	2	8.78E-06	NP_510289.1	50	53.5286	67	34	hypothetical protein C04A11.2
Locus_19537_Transcript_1/1_Conf_1.000	406	2	8.67E-06	XP_001152656.1	49	53.5286	77	38	PREDICTED: similar to P antigen family, member 2B
Locus_19538_Transcript_1/1_Conf_1.000	262	0							
Locus_19539_Transcript_1/1_Conf_1.000	362	20	1.15E-34	NP_497034.1	74	149.443	119	89	hypothetical protein C01G12.8
Locus_1954_Transcript_1/2_Conf_1.000	425	0							
Locus_1954_Transcript_2/2_Conf_1.000	1076	20	1.83E-38	XP_002631192.1	87	164.466	98	86	C. briggsae CBR-CEY-1 protein
Locus_19540_Transcript_1/1_Conf_1.000	294	6	3.32E-05	CBM41222.1	50	51.6026	69	35	C. elegans protein T10G3.3b, partially confirmed by transcript evidence
Locus_19541_Transcript_1/1_Conf_1.000	327	0							
Locus_19542_Transcript_1/1_Conf_1.000	132	0							
Locus_19543_Transcript_1/1_Conf_1.000	508	20	6.96E-62	XP_002631239.1	81	239.965	164	133	C. briggsae CBR-LACT-3 protein
Locus_19544_Transcript_1/1_Conf_1.000	291	20	2.28E-38	XP_002634996.1	91	161.77	95	87	C. briggsae CBR-KGB-1 protein
Locus_19545_Transcript_1/2_Conf_1.000	454	0							
Locus_19545_Transcript_2/2_Conf_1.000	406	0							
Locus_19546_Transcript_1/1_Conf_1.000	242	0							
Locus_19547_Transcript_1/1_Conf_1.000	129	0							
Locus_19548_Transcript_1/1_Conf_1.000	162	0							
Locus_19549_Transcript_1/1_Conf_1.000	223	0							
Locus_1955_Transcript_1/1_Conf_1.000	380	0							
Locus_19550_Transcript_1/1_Conf_1.000	187	0							
Locus_19551_Transcript_1/1_Conf_1.000	359	0							
Locus_19552_Transcript_1/1_Conf_1.000	158	0							
Locus_19553_Transcript_1/1_Conf_1.000	566	4	3.30E-14	EFO21208.1	75	82.0333	69	52	hypothetical protein LOAG_07284
Locus_19554_Transcript_1/1_Conf_1.000	1027	7	7.43E-42	XP_002636786.1	63	175.637	176	112	Hypothetical protein CBG23525
Locus_19555_Transcript_1/1_Conf_1.000	494	20	8.25E-57	NP_506862.2	78	223.016	155	121	hypothetical protein F21A3.3

Locus_19556_Transcript_1/1_Conf_1.000	130	6	1.58E-07	XP_002633573.1	74	59.3066	43	32	Hypothetical protein CBG05447
Locus_19557_Transcript_1/1_Conf_1.000	226	0							
Locus_19558_Transcript_1/1_Conf_1.000	347	20	6.07E-15	EFA13656.1	60	83.9593	91	55	hypothetical protein TcasGA2_TC016129
Locus_19559_Transcript_1/1_Conf_1.000	222	0							
Locus_1956_Transcript_1/1_Conf_1.000	1180	20	2.71E-78	NP_503386.1	100	296.975	149	149	CalModulin family member (cmd-1)
Locus_19560_Transcript_1/1_Conf_1.000	490	20	9.23E-32	XP_002635570.1	67	139.813	122	82	Hypothetical protein CBG20553
Locus_19561_Transcript_1/1_Conf_1.000	133	0							
Locus_19562_Transcript_1/1_Conf_1.000	258	0							
Locus_19563_Transcript_1/2_Conf_1.000	369	0							
Locus_19563_Transcript_2/2_Conf_1.000	811	0							
Locus_19564_Transcript_1/1_Conf_1.000	200	4	2.80E-04	EFO16977.1	60	48.521	58	35	protein-tyrosine phosphatase

Locus_19565_Transcript_1/1_Conf_1.000	245	0							
Locus_19566_Transcript_1/1_Conf_1.000	227	20	3.80E-25	NP_491658.2	87	117.857	73	64	PaTched Related family member (ptr-10)
Locus_19567_Transcript_1/1_Conf_1.000	130	0							
Locus_19568_Transcript_1/1_Conf_1.000	354	20	1.57E-23	XP_002646774.1	74	112.464	116	86	Hypothetical protein CBG18418
Locus_19569_Transcript_1/1_Conf_1.000	319	20	1.26E-36	NP_509884.1	84	155.992	105	89	hypothetical protein F38B2.4
Locus_1957_Transcript_1/1_Conf_1.000	464	20	1.80E-59	NP_741743.1	84	231.876	152	129	Propionyl Coenzyme A Carboxylase Beta subunit family member (pccb-1)
Locus_19570_Transcript_1/1_Conf_1.000	139	0							
Locus_19571_Transcript_1/1_Conf_1.000	142	0							
Locus_19572_Transcript_1/1_Conf_1.000	158	0							
Locus_19573_Transcript_1/1_Conf_1.000	144	0							
Locus_19574_Transcript_1/1_Conf_1.000	702	20	1.17E-59	EFO26681.1	72	233.802	199	145	glycosyl transferase
Locus_19575_Transcript_1/1_Conf_1.000	417	20	3.42E-42	NP_495445.2	86	174.481	111	96	hypothetical protein ZK1127.5
Locus_19576_Transcript_1/1_Conf_1.000	148	0							
Locus_19577_Transcript_1/1_Conf_1.000	195	0							
Locus_19578_Transcript_1/1_Conf_1.000	313	1	1.01E-09	EDL06708.1	71	66.6254	56	40	mCG51545
Locus_19579_Transcript_1/1_Conf_1.000	219	0							
Locus_1958_Transcript_1/1_Conf_1.000	961	20	1.47E-65	NP_001129880.1	61	254.218	299	185	Nuclear eXport Factor family member (nxf-1)
Locus_19580_Transcript_1/1_Conf_1.000	321	20	1.21E-23	XP_002636926.1	84	112.849	83	70	Hypothetical protein CBG09393

Locus_19581_Transcript_1/1_Conf_1.000	253	20	3.94E-30	XP_001110023.2	100	134.42	82	82	PREDICTED: sentrin-specific protease 3-like isoform 3
Locus_19582_Transcript_1/1_Conf_1.000	492	2	1.38E-11	XP_001900176.1	50	72.7886	199	101	LIM domain containing protein
Locus_19583_Transcript_1/1_Conf_1.000	328	20	3.76E-17	EFN66847.1	60	91.2781	111	67	hypothetical protein EAG_08499
Locus_19584_Transcript_1/1_Conf_1.000	324	20	8.42E-09	XP_001960086.1	55	63.5438	98	54	GF13190
Locus_19585_Transcript_1/1_Conf_1.000	259	0							
Locus_19586_Transcript_1/1_Conf_1.000	429	0							
Locus_19587_Transcript_1/1_Conf_1.000	819	20	2.02E-83	XP_002643051.1	71	313.153	263	189	C. briggsae CBR-DPF-6 protein
Locus_19588_Transcript_1/1_Conf_1.000	247	7	3.46E-31	XP_002633317.1	85	137.887	82	70	Hypothetical protein CBG06054
Locus_19589_Transcript_1/1_Conf_1.000	480	20	6.47E-46	NP_510258.2	68	186.808	158	108	hypothetical protein F18H3.1
Locus_1959_Transcript_1/2_Conf_1.000	1056	20	1.69E-97	XP_002630503.1	81	360.533	291	238	Hypothetical protein CBG24740
Locus_1959_Transcript_2/2_Conf_1.000	1056	20	1.69E-97	XP_002630503.1	81	360.533	291	238	Hypothetical protein CBG24740
Locus_19590_Transcript_1/1_Conf_1.000	153	0							

Locus_19591_Transcript_1/1_Conf_1.000	151	5	4.68E-07	NP_500822.2	70	57.7658	48	34	UNCoordinated family member (unc-5)
Locus_19592_Transcript_1/1_Conf_1.000	132	0							
Locus_19593_Transcript_1/1_Conf_1.000	246	12	3.58E-28	XP_002633158.1	95	127.872	82	78	C. briggsae CBR-UNC-82 protein
Locus_19594_Transcript_1/1_Conf_1.000	214	20	9.44E-21	XP_002644316.1	88	103.219	71	63	C. briggsae CBR-TAG-312 protein
Locus_19595_Transcript_1/1_Conf_1.000	139	2	3.97E-11	NP_506168.2	91	71.2478	45	41	hypothetical protein K10C8.2
Locus_19596_Transcript_1/1_Conf_1.000	263	20	1.26E-28	BAE38513.1	98	129.413	66	65	unnamed protein product
Locus_19597_Transcript_1/1_Conf_1.000	238	0							
Locus_19598_Transcript_1/1_Conf_1.000	333	18	3.38E-10	XP_002637287.1	49	68.1662	117	58	Hypothetical protein CBG18974
Locus_19599_Transcript_1/1_Conf_1.000	291	2	1.59E-23	NP_508764.2	73	112.464	111	82	hypothetical protein F15A8.7
Locus_196_Transcript_1/1_Conf_1.000	597	4	5.39E-08	XP_002641461.1	44	61.6178	179	79	C. briggsae CBR-WAH-1 protein
Locus_1960_Transcript_1/4_Conf_0.222	253	0							
Locus_1960_Transcript_2/4_Conf_0.667	1220	8	8.46E-14	XP_002630572.1	44	82.8037	216	97	Hypothetical protein CBG13025
Locus_1960_Transcript_3/4_Conf_0.444	1126	9	7.54E-14	XP_002630572.1	44	82.8037	216	97	Hypothetical protein CBG13025
Locus_1960_Transcript_4/4_Conf_0.667	1130	9	7.57E-14	XP_002630572.1	44	82.8037	216	97	Hypothetical protein CBG13025
Locus_19600_Transcript_1/1_Conf_1.000	128	0							
Locus_19601_Transcript_1/1_Conf_1.000	651	20	4.12E-74	NP_510485.2	81	281.567	196	160	TBC (Tre-2/Bub2/Cdc16) domain family member (tbc-1)
Locus_19602_Transcript_1/1_Conf_1.000	161	0							
Locus_19603_Transcript_1/1_Conf_1.000	741	0							
Locus_19604_Transcript_1/1_Conf_1.000	134	0							
Locus_19605_Transcript_1/1_Conf_1.000	181	0							
Locus_19606_Transcript_1/1_Conf_1.000	294	20	1.34E-30	XP_002648619.1	78	135.961	98	77	Hypothetical protein CBG24962

Locus_19607_Transcript_1/1_Conf_1.000	484	14	4.95E-25	NP_492859.1	59	117.472	128	76	hypothetical protein Y52B11A.8
Locus_19608_Transcript_1/1_Conf_1.000	602	20	1.02E-62	NP_500647.2	83	243.432	156	131	Dipeptidyl Peptidase Four (IV) family member (dpf-5)
Locus_19609_Transcript_1/1_Conf_1.000	194	7	5.86E-18	NP_001021449.1	77	93.9745	62	48	hypothetical protein F35C12.3
Locus_1961_Transcript_1/1_Conf_1.000	2263	20	0	NP_506192.1	82	798.89	621	512	ABC transporter, class F family member (abcf-1)
Locus_19610_Transcript_1/1_Conf_1.000	134	0							
Locus_19611_Transcript_1/1_Conf_1.000	417	20	2.72E-23	AAK29933.3	81	111.694	83	68	Rab connectin related protein 2, partially confirmed by transcript evidence
Locus_19612_Transcript_1/1_Conf_1.000	370	0							
Locus_19613_Transcript_1/1_Conf_1.000	230	20	1.21E-39	ADN38247.1	100	166.007	76	76	MHC class I antigen
Locus_19614_Transcript_1/1_Conf_1.000	142	0							
Locus_19615_Transcript_1/1_Conf_1.000	418	4	2.31E-22	NP_508552.1	57	108.612	142	81	hypothetical protein F40F4.6
Locus_19616_Transcript_1/1_Conf_1.000	261	0							
Locus_19617_Transcript_1/1_Conf_1.000	777	9	3.41E-29	EFO22071.1	56	132.88	212	120	hypothetical protein LOAG_06415
Locus_19618_Transcript_1/1_Conf_1.000	139	0							
Locus_19619_Transcript_1/1_Conf_1.000	128	0							
Locus_1962_Transcript_1/1_Conf_1.000	378	20	7.28E-45	XP_002634052.1	87	183.341	124	108	C. briggsae CBR-VHA-5 protein
Locus_19620_Transcript_1/1_Conf_1.000	184	0							
Locus_19621_Transcript_1/1_Conf_1.000	136	2	1.47E-05	NP_505920.1	74	52.7582	43	32	hypothetical protein C55A6.6
Locus_19622_Transcript_1/1_Conf_1.000	563	20	1.04E-20	XP_001898035.1	53	103.605	156	84	hypothetical protein Bm1_32955

Locus_19623_Transcript_1/1_Conf_1.000	135	20	3.49E-07	EFO27090.1	82	58.151	35	29	WD repeats and SOF1 domain-containing protein
Locus_19624_Transcript_1/1_Conf_1.000	791	20	7.07E-38	XP_002631305.1	59	161.77	219	131	C. briggsae CBR-DNA-2 protein
Locus_19625_Transcript_1/1_Conf_1.000	320	20	1.34E-46	ACJ65168.1	93	189.119	106	99	Uncoordinated protein 68, isoform b, partially confirmed by transcript evidence
Locus_19626_Transcript_1/1_Conf_1.000	301	0							
Locus_19627_Transcript_1/1_Conf_1.000	167	11	6.63E-14	NP_497035.3	83	80.4925	55	46	Trehalose 6-Phosphate Synthase family member (tps-2)
Locus_19628_Transcript_1/1_Conf_1.000	281	0							
Locus_19629_Transcript_1/1_Conf_1.000	245	0							
Locus_1963_Transcript_1/1_Conf_1.000	474	3	2.58E-26	CAA85490.2	62	121.709	146	91	C. elegans protein C14B1.9, confirmed by transcript evidence
Locus_19630_Transcript_1/1_Conf_1.000	153	0							
Locus_19631_Transcript_1/1_Conf_1.000	141	0							
Locus_19632_Transcript_1/1_Conf_1.000	160	0							
Locus_19633_Transcript_1/1_Conf_1.000	142	3	3.96E-11	NP_505399.1	86	71.2478	44	38	hypothetical protein ZK682.2
Locus_19634_Transcript_1/1_Conf_1.000	372	0							
Locus_19635_Transcript_1/1_Conf_1.000	410	20	2.43E-08	XP_001198782.1	65	62.003	58	38	PREDICTED: similar to ENSANGP00000010363
Locus_19636_Transcript_1/1_Conf_1.000	154	2	2.73E-07	XP_002646320.1	64	58.5362	51	33	C. briggsae CBR-SMP-2 protein
Locus_19637_Transcript_1/1_Conf_1.000	312	2	1.16E-05	XP_002646277.1	67	53.1434	43	29	Hypothetical protein CBG11982
Locus_19638_Transcript_1/1_Conf_1.000	131	0							
Locus_19639_Transcript_1/1_Conf_1.000	188	20	1.04E-22	XP_002194320.1	100	109.768	51	51	PREDICTED: putative eukaryotic translation initiation factor 1 variant 1

Locus_1964_Transcript_1/1_Conf_1.000	410	5	9.83E-18	XP_002640436.1	61	93.2041	127	78	Hypothetical protein CBG08488
Locus_19640_Transcript_1/1_Conf_1.000	225	20	2.02E-18	EFO25092.1	78	95.5153	73	57	hypothetical protein LOAG_03389
Locus_19641_Transcript_1/1_Conf_1.000	363	20	1.27E-33	XP_002647703.1	89	145.976	86	77	Hypothetical protein CBG17892
Locus_19642_Transcript_1/1_Conf_1.000	140	0							
Locus_19643_Transcript_1/1_Conf_1.000	188	20	1.32E-09	EFO20907.1	74	66.2402	50	37	MH2 domain-containing protein
Locus_19644_Transcript_1/1_Conf_1.000	200	20	2.37E-11	XP_001901231.1	78	72.0182	60	47	cation channel family protein
Locus_19645_Transcript_1/1_Conf_1.000	279	20	5.31E-48	NP_502119.2	94	193.741	92	87	hypothetical protein F54D1.6
Locus_19646_Transcript_1/1_Conf_1.000	136	0							
Locus_19647_Transcript_1/1_Conf_1.000	321	0							
Locus_19648_Transcript_1/1_Conf_1.000	545	20	2.10E-60	NP_495125.1	80	235.343	181	146	hypothetical protein C18A3.3
Locus_19649_Transcript_1/1_Conf_1.000	157	0							
Locus_1965_Transcript_1/2_Conf_1.000	769	7	2.89E-49	NP_497909.1	64	199.519	208	134	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-45)

Locus_1965_Transcript_2/2_Conf_1.000	781	8	6.02E-50	NP_497909.1	64	201.83	211	136	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-45)
Locus_19650_Transcript_1/1_Conf_1.000	409	20	5.40E-16	NP_509229.1	58	87.4261	106	62	SUppressor of activated let-60 Ras family member (sur-5)
Locus_19651_Transcript_1/1_Conf_1.000	272	20	3.38E-26	CBW48351.1	80	121.324	86	69	Hypothetical protein C56A3.7c
Locus_19652_Transcript_1/1_Conf_1.000	235	0							
Locus_19653_Transcript_1/1_Conf_1.000	209	0							
Locus_19654_Transcript_1/1_Conf_1.000	158	0							
Locus_19655_Transcript_1/1_Conf_1.000	190	20	1.18E-18	EFO24000.1	87	96.2857	63	55	hypothetical protein LOAG_04486
Locus_19656_Transcript_1/1_Conf_1.000	380	0							
Locus_19657_Transcript_1/1_Conf_1.000	314	4	8.83E-14	NP_505776.1	89	80.1073	47	42	hypothetical protein F32D8.5
Locus_19658_Transcript_1/1_Conf_1.000	304	2	7.31E-05	NP_499025.1	81	50.447	44	36	hypothetical protein ZK512.2
Locus_19659_Transcript_1/1_Conf_1.000	434	20	7.25E-29	XP_001898123.1	70	130.183	145	102	hypothetical protein Bm1_33390

Locus_1966_Transcript_1/1_Conf_1.000	988	20	7.53E-113	XP_002633752.1	83	411.379	261	219	C. briggsae CBR-PYP-1 protein
Locus_19660_Transcript_1/1_Conf_1.000	394	0							
Locus_19661_Transcript_1/1_Conf_1.000	604	20	6.94E-43	NP_495318.2	72	177.563	186	135	hypothetical protein C56E6.2
Locus_19662_Transcript_1/1_Conf_1.000	198	0							
Locus_19663_Transcript_1/1_Conf_1.000	422	5	1.22E-23		63	112.849	141	90	myoblast city protein homolog
Locus_19664_Transcript_1/1_Conf_1.000	194	0							
Locus_19665_Transcript_1/1_Conf_1.000	284	20	6.73E-30	ABC69943.1	76	133.65	94	72	STIP
Locus_19666_Transcript_1/1_Conf_1.000	166	20	4.59E-15	XP_002632772.1	93	84.3445	47	44	C. briggsae CBR-TAT-2 protein
Locus_19667_Transcript_1/1_Conf_1.000	156	1	4.35E-05	EFO17124.1	59	51.2174	49	29	hypothetical protein LOAG_11376
Locus_19668_Transcript_1/1_Conf_1.000	200	0							
Locus_19669_Transcript_1/1_Conf_1.000	674	20	8.89E-59	XP_002642250.1	67	230.72	228	155	Hypothetical protein CBG18235

Locus_1967_Transcript_1/1_Conf_1.000	821	20	1.25E-133	XP_002646763.1	90	479.945	273	246	C. briggsae CBR-GSY-1 protein
Locus_19670_Transcript_1/1_Conf_1.000	573	4	2.31E-34	XP_002644385.1	56	149.058	187	106	Hypothetical protein CBG14225
Locus_19671_Transcript_1/1_Conf_1.000	420	0							
Locus_19672_Transcript_1/1_Conf_1.000	449	0							
Locus_19673_Transcript_1/1_Conf_1.000	309	20	2.85E-09	XP_002130995.1	87	65.0846	40	35	PREDICTED: transcription factor protein
Locus_19674_Transcript_1/2_Conf_1.000	307	20	2.85E-17	XP_002634069.1	65	91.6633	98	64	Hypothetical protein CBG01611
Locus_19674_Transcript_2/2_Conf_1.000	307	20	7.50E-18	XP_002634069.1	65	93.5893	98	64	Hypothetical protein CBG01611
Locus_19675_Transcript_1/1_Conf_1.000	629	20	3.05E-84	ACJ65168.1	87	315.079	208	182	Uncoordinated protein 68, isoform b, partially confirmed by transcript evidence
Locus_19676_Transcript_1/1_Conf_1.000	173	0							
Locus_19677_Transcript_1/1_Conf_1.000	517	20	2.43E-33	XP_001892323.1	80	145.206	109	88	Histone deacetylase family protein
Locus_19678_Transcript_1/1_Conf_1.000	259	0							
Locus_19679_Transcript_1/1_Conf_1.000	138	0							
Locus_1968_Transcript_1/1_Conf_1.000	1263	20	7.66E-58	XP_002631476.1	62	229.18	295	183	Hypothetical protein CBG20630
Locus_19680_Transcript_1/1_Conf_1.000	322	20	1.69E-41	NP_506927.2	91	172.17	106	97	HAlF transporter (PGP related) family member (haf-3)
Locus_19681_Transcript_1/1_Conf_1.000	670	1	2.27E-06	CAR63599.1	41	56.6102	169	70	hypothetical protein
Locus_19682_Transcript_1/1_Conf_1.000	258	4	6.71E-14	XP_002630479.1	78	80.4925	60	47	Hypothetical protein CBG11215
Locus_19683_Transcript_1/1_Conf_1.000	466	20	2.43E-48	NP_500129.1	77	194.897	152	118	hypothetical protein Y41D4A.6
Locus_19684_Transcript_1/1_Conf_1.000	521	12	4.56E-19	EFO16455.1	57	97.8265	156	89	hypothetical protein LOAG_12053

Locus_19685_Transcript_1/1_Conf_1.000	379	20	6.41E-25	XP_002642701.1	65	117.087	127	83	C. briggsae CBR-GLY-3 protein
Locus_19686_Transcript_1/1_Conf_1.000	294	8	5.11E-14	XP_002633220.1	84	80.8777	64	54	C. briggsae CBR-FLP-13 protein
Locus_19687_Transcript_1/1_Conf_1.000	283	0							
Locus_19688_Transcript_1/1_Conf_1.000	173	0							
Locus_19689_Transcript_1/1_Conf_1.000	253	5	1.72E-09	EFO26102.1	63	65.855	82	52	hypothetical protein LOAG_02385
Locus_1969_Transcript_1/1_Conf_1.000	591	0							
Locus_19690_Transcript_1/1_Conf_1.000	595	20	2.78E-49	XP_002634817.1	71	198.749	184	131	C. briggsae CBR-CLP-7 protein
Locus_19691_Transcript_1/1_Conf_1.000	316	0							
Locus_19692_Transcript_1/1_Conf_1.000	408	0							
Locus_19693_Transcript_1/1_Conf_1.000	608	0							
Locus_19694_Transcript_1/1_Conf_1.000	255	0							
Locus_19695_Transcript_1/1_Conf_1.000	227	4	1.83E-11	NP_501363.1	70	72.4034	61	43	P38 Map Kinase family member (pmk-3)
Locus_19696_Transcript_1/1_Conf_1.000	139	0							
Locus_19697_Transcript_1/1_Conf_1.000	146	20	2.18E-12	XP_002641621.1	75	75.485	48	36	Hypothetical protein CBG09941
Locus_19698_Transcript_1/1_Conf_1.000	529	2	7.02E-18	NP_001022051.1	56	93.9745	126	71	SREBP Cleavage activating Protein (SCAP) homolog family member (scp-1)
Locus_19699_Transcript_1/1_Conf_1.000	315	0							
Locus_197_Transcript_1/1_Conf_1.000	1044	20	5.64E-138	NP_001023493.1	84	494.967	327	277	hypothetical protein Y54G2A.2
Locus_1970_Transcript_1/1_Conf_1.000	673	0							
Locus_19700_Transcript_1/1_Conf_1.000	161	3	5.47E-08	NP_501376.2	71	60.8474	53	38	hypothetical protein C07G1.2
Locus_19701_Transcript_1/1_Conf_1.000	930	0							
Locus_19702_Transcript_1/2_Conf_1.000	338	4	5.93E-15	NP_493617.2	92	83.9593	50	46	hypothetical protein F33H2.6
Locus_19702_Transcript_2/2_Conf_1.000	338	4	5.93E-15	NP_493617.2	92	83.9593	50	46	hypothetical protein F33H2.6
Locus_19703_Transcript_1/1_Conf_1.000	817	20	2.09E-56	XP_001897058.1	81	223.402	182	149	SH3 domain-binding protein 5
Locus_19704_Transcript_1/1_Conf_1.000	282	0							
Locus_19705_Transcript_1/1_Conf_1.000	338	0							

Locus_19706_Transcript_1/1_Conf_1.000	565	20	7.32E-30	EAW75449.1	98	134.035	59	58	cathepsin Z, isoform CRA_b
Locus_19707_Transcript_1/1_Conf_1.000	351	20	5.46E-08	XP_001892050.1	56	60.8474	91	51	hypothetical protein Bm1_02740
Locus_19708_Transcript_1/1_Conf_1.000	266	0							
Locus_19709_Transcript_1/1_Conf_1.000	285	0							
Locus_1971_Transcript_1/1_Conf_1.000	734	20	1.79E-05	XP_002646359.1	47	53.9138	118	56	Hypothetical protein CBG12076
Locus_19710_Transcript_1/1_Conf_1.000	411	20	3.21E-69	AAC38987.1	97	264.233	136	133	P-glycoprotein
Locus_19711_Transcript_1/1_Conf_1.000	485	20	3.52E-55	NP_505451.1	80	217.624	161	129	hypothetical protein F11A3.1
Locus_19712_Transcript_1/1_Conf_1.000	252	12	1.66E-20	XP_002639310.1	82	102.449	68	56	Hypothetical protein CBG03881
Locus_19713_Transcript_1/1_Conf_1.000	425	1	3.00E-06	EFO20252.1	50	55.0694	132	67	hypothetical protein LOAG_08240
Locus_19714_Transcript_1/1_Conf_1.000	173	0							
Locus_19715_Transcript_1/1_Conf_1.000	264	0							
Locus_19716_Transcript_1/1_Conf_1.000	298	13	1.93E-13	XP_001901002.1	59	78.9518	99	59	WD40 associated region in TFIID subunit family protein
Locus_19717_Transcript_1/1_Conf_1.000	899	20	1.99E-122	NP_001041015.1	92	442.965	257	238	hypothetical protein Y116A8C.28

Locus_19718_Transcript_1/1_Conf_1.000	603	20	1.11E-48	NP_741839.2	50	196.823	242	123	hypothetical protein F48E3.8
Locus_19719_Transcript_1/1_Conf_1.000	145	0							
Locus_1972_Transcript_1/1_Conf_1.000	1429	20	6.15E-139	NP_694762.1	73	498.819	476	350	5-oxoprolinase
Locus_19720_Transcript_1/1_Conf_1.000	232	20	4.59E-39	ACX42645.1	100	164.081	76	76	MHC class I antigen
Locus_19721_Transcript_1/1_Conf_1.000	151	20	4.37E-13	XP_002635372.1	83	77.7962	42	35	C. briggsae CBR-RPM-1 protein
Locus_19722_Transcript_1/1_Conf_1.000	212	0							
Locus_19723_Transcript_1/1_Conf_1.000	198	20	3.53E-15	CBX25138.1	78	84.7297	64	50	Hypothetical protein C25A1.7a
Locus_19724_Transcript_1/1_Conf_1.000	137	0							
Locus_19725_Transcript_1/1_Conf_1.000	1016	20	7.30E-34	AAK84527.3	87	149.058	87	76	U40420_8Prion-like-(q/n-rich)-domain-bearing protein protein 37, partially confirmed by transcript evidence
Locus_19726_Transcript_1/1_Conf_1.000	130	0							
Locus_19727_Transcript_1/1_Conf_1.000	140	0							
Locus_19728_Transcript_1/1_Conf_1.000	1082	0							
Locus_19729_Transcript_1/1_Conf_1.000	207	0							
Locus_1973_Transcript_1/1_Conf_1.000	339	7	2.49E-05	EFO20860.1	42	51.9878	92	39	hypothetical protein LOAG_07630
Locus_19730_Transcript_1/1_Conf_1.000	227	20	1.82E-19	NP_495578.2	82	98.9821	63	52	hypothetical protein ZK1290.5
Locus_19731_Transcript_1/1_Conf_1.000	206	0							
Locus_19732_Transcript_1/1_Conf_1.000	270	20	7.28E-29	NP_504415.2	92	130.183	68	63	Na/Ca eXchangers family member (ncx-2)
Locus_19733_Transcript_1/1_Conf_1.000	359	5	4.28E-13	XP_002644294.1	74	77.7962	63	47	C. briggsae CBR-DPY-3 protein
Locus_19734_Transcript_1/1_Conf_1.000	195	20	1.75E-30	XP_002832361.1	100	135.576	64	64	PREDICTED: plexin-A3-like

Locus_19735_Transcript_1/1_Conf_1.000	249	3	4.38E-10	NP_493741.1	94	67.781	38	36	hypothetical protein W10D9.5
Locus_19736_Transcript_1/1_Conf_1.000	272	1	2.79E-04	NP_496062.3	68	48.521	50	34	Temporarily Assigned Gene name family member (tag-124)
Locus_19737_Transcript_1/1_Conf_1.000	236	2	7.09E-24	NP_500395.2	73	113.62	78	57	hypothetical protein Y37E11AL.6
Locus_19738_Transcript_1/1_Conf_1.000	343	3	8.18E-36	NP_501400.1	86	153.295	115	100	hypothetical protein F35H10.10
Locus_19739_Transcript_1/1_Conf_1.000	137	0							
Locus_1974_Transcript_1/1_Conf_1.000	1706	20	0	AAK17768.1	96	803.127	516	500	cytochrome c oxidase subunit I
Locus_19740_Transcript_1/1_Conf_1.000	372	0							
Locus_19741_Transcript_1/1_Conf_1.000	346	0							
Locus_19742_Transcript_1/1_Conf_1.000	199	0							
Locus_19743_Transcript_1/1_Conf_1.000	516	20	5.01E-71	CBL43419.1	92	270.396	153	141	C. elegans protein C47E8.4b, confirmed by transcript evidence
Locus_19744_Transcript_1/1_Conf_1.000	136	0							
Locus_19745_Transcript_1/1_Conf_1.000	178	20	4.10E-16	NP_509760.2	87	87.8113	56	49	Temporarily Assigned Gene name family member (tag-289)
Locus_19746_Transcript_1/1_Conf_1.000	548	20	7.68E-34	XP_002629803.1	62	147.132	185	115	Hypothetical protein CBG01047
Locus_19747_Transcript_1/1_Conf_1.000	414	9	1.01E-22	NP_509029.1	65	109.768	103	67	hypothetical protein C15H9.9

Locus_19748_Transcript_1/1_Conf_1.000	419	0							
Locus_19749_Transcript_1/1_Conf_1.000	297	20	7.08E-24	XP_002630866.1	82	113.62	79	65	C. briggsae CBR-HST-3.1 protein
Locus_1975_Transcript_1/1_Conf_1.000	1557	20	0	NP_499778.1	88	767.303	521	460	CU (copper) ATPase family member (cua-1)
Locus_19750_Transcript_1/1_Conf_1.000	527	6	1.02E-21	NP_001023604.1	88	106.686	75	66	hypothetical protein ZC477.3
Locus_19751_Transcript_1/1_Conf_1.000	226	3	1.00E-09	CAR64255.1	93	66.6254	48	45	protein RIO1 kinase
Locus_19752_Transcript_1/1_Conf_1.000	261	0							
Locus_19753_Transcript_1/1_Conf_1.000	142	20	7.96E-20	DAA21858.1	100	100.138	47	47	eukaryotic translation initiation factor 3 subunit M
Locus_19754_Transcript_1/1_Conf_1.000	411	0							
Locus_19755_Transcript_1/1_Conf_1.000	139	0							
Locus_19756_Transcript_1/1_Conf_1.000	212	0							
Locus_19757_Transcript_1/1_Conf_1.000	270	0							

Locus_19758_Transcript_1/1_Conf_1.000	182	20	1.51E-29	BAG65408.1	100	132.494	60	60	unnamed protein product
Locus_19759_Transcript_1/1_Conf_1.000	303	20	1.42E-16	XP_002642179.1	62	89.3521	99	62	C. briggsae CBR-CUTC-1 protein
Locus_1976_Transcript_1/3_Conf_0.500	2042	20	7.90E-40	NP_495036.3	69	170.244	172	120	human DAZ (Deleted in Azoospermia) homolog family member (daz-1)
Locus_1976_Transcript_2/3_Conf_0.667	1754	20	6.53E-40	NP_495036.3	69	170.244	172	120	human DAZ (Deleted in Azoospermia) homolog family member (daz-1)
Locus_1976_Transcript_3/3_Conf_0.667	1766	20	6.59E-40	NP_495036.3	69	170.244	172	120	human DAZ (Deleted in Azoospermia) homolog family member (daz-1)
Locus_19760_Transcript_1/1_Conf_1.000	167	0							
Locus_19761_Transcript_1/1_Conf_1.000	189	2	3.69E-12	XP_002634423.1	84	74.7146	59	50	C. briggsae CBR-PTR-14 protein
Locus_19762_Transcript_1/1_Conf_1.000	175	0							
Locus_19763_Transcript_1/1_Conf_1.000	129	0							
Locus_19764_Transcript_1/1_Conf_1.000	238	0							
Locus_19765_Transcript_1/1_Conf_1.000	356	0							
Locus_19766_Transcript_1/1_Conf_1.000	542	20	6.07E-20	XP_002637670.1	55	100.908	161	89	C. briggsae CBR-RDE-1 protein
Locus_19767_Transcript_1/1_Conf_1.000	258	20	8.13E-44	XP_002810702.1	100	179.874	79	79	PREDICTED: protein CYR61-like isoform 3
Locus_19768_Transcript_1/1_Conf_1.000	471	0							
Locus_19769_Transcript_1/1_Conf_1.000	141	0							
Locus_1977_Transcript_1/1_Conf_1.000	449	0							

Locus_19770_Transcript_1/1_Conf_1.000	382	20	1.37E-27	NP_001021054.1	70	125.946	120	85	Suppressor with Morphological effect on Genitalia family member (smg-1)
Locus_19771_Transcript_1/1_Conf_1.000	146	0							
Locus_19772_Transcript_1/1_Conf_1.000	164	20	1.14E-13	XP_002647593.1	93	79.7221	45	42	C. briggsae CBR-TTR-44 protein
Locus_19773_Transcript_1/1_Conf_1.000	260	0							
Locus_19774_Transcript_1/1_Conf_1.000	174	0							
Locus_19775_Transcript_1/1_Conf_1.000	465	20	6.79E-75	A8XJL7.2	90	283.108	154	140	Serine/threonine-protein kinase sax-1
Locus_19776_Transcript_1/1_Conf_1.000	332	20	1.72E-54	NP_498645.1	93	215.312	110	103	MUscle Positioning family member (mup-4)
Locus_19777_Transcript_1/1_Conf_1.000	173	0							
Locus_19778_Transcript_1/1_Conf_1.000	186	0							
Locus_19779_Transcript_1/1_Conf_1.000	646	20	1.30E-64	AAK62032.1	69	249.98	209	145	metalloprotease 1 precursor
Locus_1978_Transcript_1/2_Conf_1.000	1440	20	7.17E-111	NP_498930.1	75	405.601	345	260	UDP-Galactose Transporter Protein family member (ugtp-1)
Locus_1978_Transcript_2/2_Conf_1.000	1440	20	7.17E-111	NP_498930.1	75	405.601	345	260	UDP-Galactose Transporter Protein family member (ugtp-1)
Locus_19780_Transcript_1/1_Conf_1.000	181	5	1.47E-08	XP_002641239.1	73	62.7734	56	41	Hypothetical protein CBG09106
Locus_19781_Transcript_1/1_Conf_1.000	233	20	5.83E-18	Q17678.6	80	93.9745	71	57	UPF0632 protein C05G5.5
Locus_19782_Transcript_1/1_Conf_1.000	210	20	1.57E-07	NP_500129.1	75	59.3066	45	34	hypothetical protein Y41D4A.6
Locus_19783_Transcript_1/1_Conf_1.000	357	3	9.87E-10	XP_002642316.1	59	66.6254	88	52	Hypothetical protein CBG18309
Locus_19784_Transcript_1/1_Conf_1.000	236	0							
Locus_19785_Transcript_1/1_Conf_1.000	465	0							
Locus_19786_Transcript_1/1_Conf_1.000	159	0							
Locus_19787_Transcript_1/1_Conf_1.000	233	0							
Locus_19788_Transcript_1/1_Conf_1.000	380	6	2.36E-11	NP_001021785.2	53	72.0182	108	58	hypothetical protein Y52B11A.3
Locus_19789_Transcript_1/1_Conf_1.000	817	20	7.22E-41	XP_002629747.1	58	171.785	259	151	Hypothetical protein CBG00981
Locus_1979_Transcript_1/1_Conf_1.000	568	0							
Locus_19790_Transcript_1/1_Conf_1.000	420	1	1.76E-14	ABV03827.1	84	82.4185	51	43	hypothetical protein

Locus_19791_Transcript_1/1_Conf_1.000	414	0							
Locus_19792_Transcript_1/1_Conf_1.000	401	20	4.60E-31	NP_496981.2	86	137.502	115	99	hypothetical protein Y54G11A.9
Locus_19793_Transcript_1/1_Conf_1.000	308	2	3.59E-28	NP_495419.1	78	127.872	100	78	hypothetical protein B0252.1
Locus_19794_Transcript_1/1_Conf_1.000	283	4	3.98E-06	NP_501765.1	60	54.6842	73	44	hypothetical protein K07F5.7
Locus_19795_Transcript_1/1_Conf_1.000	176	0							
Locus_19796_Transcript_1/1_Conf_1.000	159	0							
Locus_19797_Transcript_1/1_Conf_1.000	236	5	5.81E-18	XP_002644134.1	74	93.9745	78	58	C. briggsae CBR-SYD-2 protein
Locus_19798_Transcript_1/1_Conf_1.000	163	0							
Locus_19799_Transcript_1/1_Conf_1.000	367	20	1.47E-25	NP_493353.3	92	86.6557	41	38	Specificity Protein) Transcription Factor family member (sptf-3)
Locus_198_Transcript_1/1_Conf_1.000	1850	20	0	XP_002640154.1	85	803.127	514	441	Hypothetical protein CBG12654
Locus_1980_Transcript_1/1_Conf_1.000	513	0							
Locus_19800_Transcript_1/1_Conf_1.000	777	20	6.42E-28	XP_001896097.1	58	128.642	229	133	Nsp1-like C-terminal region family protein
Locus_19801_Transcript_1/1_Conf_1.000	276	10	4.11E-24	XP_002637177.1	76	114.39	94	72	Hypothetical protein CBG09695
Locus_19802_Transcript_1/1_Conf_1.000	280	0							
Locus_19803_Transcript_1/1_Conf_1.000	223	20	3.82E-17	EFO14895.1	75	91.2781	73	55	CMGC/CDK/CDK9 protein kinase
Locus_19804_Transcript_1/1_Conf_1.000	1239	20	1.25E-145	NP_495680.1	76	520.776	419	319	Nose Resistant to Fluoxetine family member (nrf-6)
Locus_19805_Transcript_1/1_Conf_1.000	280	20	5.18E-19	XP_002645153.1	79	97.4413	69	55	C. briggsae CBR-SFXN-2 protein
Locus_19806_Transcript_1/1_Conf_1.000	446	13	8.34E-57	NP_503543.1	85	223.016	149	128	hypothetical protein T08B1.1

Locus_19807_Transcript_1/1_Conf_1.000	276	20	1.61E-20	XP_001893670.1	75	102.449	92	69	Conserved oligomeric Golgi complex component 6
Locus_19808_Transcript_1/1_Conf_1.000	184	0							
Locus_19809_Transcript_1/1_Conf_1.000	182	0							
Locus_1981_Transcript_1/1_Conf_1.000	1694	20	3.60E-120	XP_002639089.1	89	436.802	269	241	C. briggsae CBR-TAG-163 protein
Locus_19810_Transcript_1/1_Conf_1.000	276	0							
Locus_19811_Transcript_1/1_Conf_1.000	263	0							
Locus_19812_Transcript_1/1_Conf_1.000	325	20	1.69E-25	XP_970656.1	71	119.013	108	77	PREDICTED: similar to Histone deacetylase 11 (HD11)
Locus_19813_Transcript_1/1_Conf_1.000	773	20	1.22E-47	EFO28238.1	82	194.126	141	117	rho GDP-dissociation inhibitor 2
Locus_19814_Transcript_1/1_Conf_1.000	800	13	1.24E-13	NP_504836.1	47	81.2629	254	120	GEX Interacting protein family member (gei-6)
Locus_19815_Transcript_1/1_Conf_1.000	190	20	4.98E-17	AAI43755.1	100	90.8929	63	63	FN1 protein
Locus_19816_Transcript_1/1_Conf_1.000	501	20	3.42E-42	XP_002630693.1	75	174.481	157	118	C. briggsae CBR-SRG-69 protein
Locus_19817_Transcript_1/1_Conf_1.000	325	20	7.79E-47	ADN00780.1	89	189.889	107	96	class 3 lipase protein
Locus_19818_Transcript_1/1_Conf_1.000	462	8	4.64E-23	CAR81373.1	66	110.923	153	102	C. elegans protein F58H1.8, confirmed by transcript evidence
Locus_19819_Transcript_1/1_Conf_1.000	564	11	2.70E-16	XP_002635081.1	50	88.9669	178	90	Hypothetical protein CBG11298
Locus_1982_Transcript_1/1_Conf_1.000	956	6	5.94E-35	NP_001040920.1	54	152.525	217	119	hypothetical protein C35B1.2
Locus_19820_Transcript_1/1_Conf_1.000	202	0							
Locus_19821_Transcript_1/1_Conf_1.000	336	0							

Locus_19822_Transcript_1/1_Conf_1.000	501	4	1.59E-39	NP_871808.3	62	165.622	192	120	hypothetical protein ZC123.4
Locus_19823_Transcript_1/1_Conf_1.000	211	0							
Locus_19824_Transcript_1/1_Conf_1.000	176	0							
Locus_19825_Transcript_1/1_Conf_1.000	147	0							
Locus_19826_Transcript_1/1_Conf_1.000	237	6	2.60E-18	NP_001022476.1	69	95.1301	86	60	Daf-16-Dependent Longevity (WT but not daf-16 lifespan increased) family member (ddl-3)
Locus_19827_Transcript_1/1_Conf_1.000	220	1	4.86E-04	EFO20896.1	67	47.7506	53	36	hypothetical protein LOAG_07593
Locus_19828_Transcript_1/1_Conf_1.000	208	0							
Locus_19829_Transcript_1/1_Conf_1.000	287	0							
Locus_1983_Transcript_1/1_Conf_1.000	1354	20	4.22E-158	XP_002630362.1	86	562.377	406	352	C. briggsae CBR-RPN-5 protein
Locus_19830_Transcript_1/1_Conf_1.000	134	20	1.98E-10	CAG09075.1	81	68.9366	44	36	unnamed protein product
Locus_19831_Transcript_1/1_Conf_1.000	291	0							
Locus_19832_Transcript_1/1_Conf_1.000	284	20	1.36E-30	Q22141.2	81	135.961	91	74	Post-GPI attachment to proteins factor 2
Locus_19833_Transcript_1/1_Conf_1.000	346	0							
Locus_19834_Transcript_1/1_Conf_1.000	201	0							
Locus_19835_Transcript_1/1_Conf_1.000	139	2	4.26E-05	NP_499273.3	77	51.2174	36	28	hypothetical protein R01H10.7
Locus_19836_Transcript_1/1_Conf_1.000	150	0							
Locus_19837_Transcript_1/1_Conf_1.000	274	1	2.78E-04	XP_002640131.1	60	48.521	84	51	Hypothetical protein CBG12630
Locus_19838_Transcript_1/1_Conf_1.000	321	1	4.80E-04	NP_495712.1	57	47.7506	66	38	abnormal EMBroygenesis family member (emb-27)
Locus_19839_Transcript_1/1_Conf_1.000	139	7	8.57E-06	XP_002646356.1	69	53.5286	46	32	Hypothetical protein CBG12070
Locus_1984_Transcript_1/1_Conf_1.000	772	20	2.58E-13	NP_501245.1	57	80.1073	155	89	HMG family member (hmg-5)
Locus_19840_Transcript_1/1_Conf_1.000	276	0							

Locus_19841_Transcript_1/1_Conf_1.000	498	20	1.89E-37	CAA10033.1	66	158.688	163	108	DYS-1 protein
Locus_19842_Transcript_1/1_Conf_1.000	170	1	3.64E-04	XP_002642935.1	68	48.1358	54	37	C. briggsae CBR-NSH-1 protein
Locus_19843_Transcript_1/1_Conf_1.000	294	0							
Locus_19844_Transcript_1/1_Conf_1.000	431	20	9.88E-10	ABG23688.1	50	66.6254	150	76	RNA-dependent RNA polymerase
Locus_19845_Transcript_1/1_Conf_1.000	260	0							
Locus_19846_Transcript_1/1_Conf_1.000	222	4	1.11E-24	XP_001902169.1	89	116.316	73	65	myotactin form B
Locus_19847_Transcript_1/1_Conf_1.000	289	20	2.99E-46	AAY56742.1	96	187.963	96	93	casein kinase I delta isoform
Locus_19848_Transcript_1/1_Conf_1.000	135	1	6.15E-12	EDL23991.1	89	73.9442	38	34	transmembrane protein 147, isoform CRA_a
Locus_19849_Transcript_1/1_Conf_1.000	161	0							
Locus_1985_Transcript_1/1_Conf_1.000	1235	20	3.49E-23	XP_001897562.1	55	114.005	181	101	TSC-22/dip/bun family protein
Locus_19850_Transcript_1/1_Conf_1.000	135	6	2.67E-15	AAA18259.1	90	85.1149	44	40	protein kinase C
Locus_19851_Transcript_1/1_Conf_1.000	168	20	1.85E-24	XP_002816715.1	100	115.546	53	53	PREDICTED: complement C4-B isoform 2

Locus_19852_Transcript_1/1_Conf_1.000	386	20	2.51E-13	XP_002636676.1	54	78.5666	114	62	Hypothetical protein CBG23390
Locus_19853_Transcript_1/1_Conf_1.000	129	0							
Locus_19854_Transcript_1/1_Conf_1.000	298	20	1.16E-50	2BDW	98	202.601	98	97	CrystalStructure OfThe Auto-Inhibited Kinase Domain Of CalciumCALMODULIN ACTIVATED KINASE II
Locus_19855_Transcript_1/1_Conf_1.000	185	0							
Locus_19856_Transcript_1/1_Conf_1.000	145	4	8.58E-09	EFO19864.1	72	63.5438	47	34	hypothetical protein LOAG_08632
Locus_19857_Transcript_1/1_Conf_1.000	415	0							
Locus_19858_Transcript_1/1_Conf_1.000	391	0							
Locus_19859_Transcript_1/1_Conf_1.000	164	0							
Locus_1986_Transcript_1/1_Conf_1.000	1046	20	2.53E-21	NP_496326.1	48	107.457	221	108	hypothetical protein R06F6.6
Locus_19860_Transcript_1/1_Conf_1.000	309	0							

Locus_19861_Transcript_1/1_Conf_1.000	645	20	9.10E-26	XP_001627842.1	69	120.939	117	81	predicted protein
Locus_19862_Transcript_1/1_Conf_1.000	154	0							
Locus_19863_Transcript_1/1_Conf_1.000	226	0							
Locus_19864_Transcript_1/1_Conf_1.000	366	0							
Locus_19865_Transcript_1/1_Conf_1.000	238	20	3.62E-28	CAA30855.1	90	127.872	76	69	myosin heavy chain 2
Locus_19866_Transcript_1/1_Conf_1.000	371	3	1.77E-22	XP_002639247.1	73	108.997	101	74	Hypothetical protein CBG03806
Locus_19867_Transcript_1/1_Conf_1.000	258	0							
Locus_19868_Transcript_1/1_Conf_1.000	230	0							
Locus_19869_Transcript_1/1_Conf_1.000	177	6	3.97E-11	XP_002640845.1	74	71.2478	58	43	C. briggsae CBR-CDH-1 protein
Locus_1987_Transcript_1/1_Conf_1.000	672	20	5.80E-34	CAA21654.2	67	148.288	177	120	C. elegans protein Y48A6C.4, confirmed by transcript evidence
Locus_19870_Transcript_1/1_Conf_1.000	275	0							
Locus_19871_Transcript_1/1_Conf_1.000	211	20	1.12E-21	NP_001090349.1	81	106.301	70	57	sideroflexin 1
Locus_19872_Transcript_1/1_Conf_1.000	306	0							

Locus_19873_Transcript_1/1_Conf_1.000	138	0							
Locus_19874_Transcript_1/1_Conf_1.000	153	5	2.09E-07	CAH04706.3	74	58.9214	47	35	C. elegans protein K04H4.2c, partially confirmed by transcript evidence
Locus_19875_Transcript_1/1_Conf_1.000	378	0							
Locus_19876_Transcript_1/1_Conf_1.000	243	0							
Locus_19877_Transcript_1/1_Conf_1.000	527	20	6.37E-48	XP_002633219.1	71	193.741	178	127	C. briggsae CBR-ITR-1 protein
Locus_19878_Transcript_1/1_Conf_1.000	149	0							
Locus_19879_Transcript_1/1_Conf_1.000	430	20	1.78E-59	ADL62853.1	86	231.876	140	121	thioredoxin reductase 2
Locus_1988_Transcript_1/1_Conf_1.000	893	20	4.50E-26	EFO21777.1	100	122.865	53	53	zinc finger protein
Locus_19880_Transcript_1/1_Conf_1.000	268	20	1.69E-17	NP_501552.1	81	92.4337	91	74	hypothetical protein D1046.3
Locus_19881_Transcript_1/1_Conf_1.000	239	0							
Locus_19882_Transcript_1/1_Conf_1.000	303	20	1.68E-17	NP_491872.1	56	92.4337	103	58	hypothetical protein C55B7.3
Locus_19883_Transcript_1/1_Conf_1.000	224	0							
Locus_19884_Transcript_1/1_Conf_1.000	129	0							
Locus_19885_Transcript_1/1_Conf_1.000	167	4	1.80E-19	XP_002639744.1	85	98.9821	54	46	C. briggsae CBR-LAM-3 protein
Locus_19886_Transcript_1/1_Conf_1.000	276	0							
Locus_19887_Transcript_1/1_Conf_1.000	390	20	7.41E-42	NP_496968.1	86	173.326	109	94	hypothetical protein Y48B6A.12
Locus_19888_Transcript_1/1_Conf_1.000	245	0							
Locus_19889_Transcript_1/1_Conf_1.000	330	0							
Locus_1989_Transcript_1/1_Conf_1.000	821	20	1.99E-22	XP_001894821.1	67	110.538	100	67	MGC80968 protein
Locus_19890_Transcript_1/1_Conf_1.000	302	0							
Locus_19891_Transcript_1/1_Conf_1.000	250	20	6.30E-25	NP_776251.1	100	117.087	83	83	keratinocyte-associated protein 2

Locus_19892_Transcript_1/1_Conf_1.000	353	20	6.01E-23	XP_002648880.1	69	110.538	101	70	C. briggsae CBR-CYP-33A1 protein
Locus_19893_Transcript_1/1_Conf_1.000	355	4	4.42E-34	NP_001033358.2	73	147.517	118	87	DAF-16/FOXO Controlled, germline Tumor affecting family member (dct-6)
Locus_19894_Transcript_1/1_Conf_1.000	812	20	3.69E-122	XP_002646641.1	87	441.81	270	235	Hypothetical protein CBG11073
Locus_19895_Transcript_1/1_Conf_1.000	140	0							
Locus_19896_Transcript_1/1_Conf_1.000	244	0							
Locus_19897_Transcript_1/1_Conf_1.000	357	0							
Locus_19898_Transcript_1/1_Conf_1.000	166	0							
Locus_19899_Transcript_1/1_Conf_1.000	400	20	2.58E-66	NP_501549.1	99	254.603	130	129	RAP homolog (vertebrate Rap GTPase family) family member (rap-1)
Locus_199_Transcript_1/2_Conf_1.000	814	0							
Locus_199_Transcript_2/2_Conf_1.000	813	0							
Locus_1990_Transcript_1/1_Conf_1.000	2284	20	1.31E-139	XP_001901168.1	72	501.901	470	342	Groucho/TLE N-terminal Q-rich domain containing protein
Locus_19900_Transcript_1/1_Conf_1.000	141	0							
Locus_19901_Transcript_1/1_Conf_1.000	254	0							
Locus_19902_Transcript_1/1_Conf_1.000	219	0							
Locus_19903_Transcript_1/1_Conf_1.000	560	0							
Locus_19904_Transcript_1/1_Conf_1.000	350	20	1.87E-32	NP_490888.1	76	142.124	116	89	Mitochondrial Processing Peptidase Alpha family member (mppa-1)
Locus_19905_Transcript_1/1_Conf_1.000	293	20	2.00E-34	NP_502428.1	83	148.673	97	81	hypothetical protein C27D8.1
Locus_19906_Transcript_1/1_Conf_1.000	427	0							

Locus_19907_Transcript_1/1_Conf_1.000	471	20	3.03E-59	NP_001040658.2	95	231.106	129	123	High Incidence of Males (increased X chromosome loss) family member (him-1)
Locus_19908_Transcript_1/1_Conf_1.000	219	20	5.88E-34	XP_001110023.2	100	147.132	73	73	PREDICTED: sentrin-specific protease 3-like isoform 3
Locus_19909_Transcript_1/1_Conf_1.000	139	0							
Locus_1991_Transcript_1/1_Conf_1.000	1973	20	0	NP_001022469.1	84	809.29	541	456	Eukaryotic Initiation Factor family member (eif-3.B)
Locus_19910_Transcript_1/1_Conf_1.000	205	20	6.60E-22	NP_501860.1	88	107.071	68	60	Mitochondrial Sorting of Proteins (yeast MSP) in Nematode family member (mspn-1)
Locus_19911_Transcript_1/1_Conf_1.000	281	20	3.59E-12	XP_002631607.1	94	74.7146	39	37	Hypothetical protein CBG20788

Locus_19912_Transcript_1/1_Conf_1.000	189	7	4.66E-15	XP_002630336.1	77	84.3445	62	48	Hypothetical protein CBG04265
Locus_19913_Transcript_1/1_Conf_1.000	262	0							
Locus_19914_Transcript_1/1_Conf_1.000	377	0							
Locus_19915_Transcript_1/1_Conf_1.000	136	10	1.33E-06	NP_001183823.1	70	56.225	41	29	hypothetical protein LOC100502416
Locus_19916_Transcript_1/1_Conf_1.000	222	20	5.66E-37	NP_001122684.1	100	157.147	74	74	UNCoordinated family member (unc-103)
Locus_19917_Transcript_1/1_Conf_1.000	400	4	3.42E-18	XP_001892604.1	62	94.7449	135	85	Phosphatidylinositol 3- and 4-kinase family protein
Locus_19918_Transcript_1/1_Conf_1.000	306	0							
Locus_19919_Transcript_1/1_Conf_1.000	240	0							
Locus_1992_Transcript_1/1_Conf_1.000	2187	20	9.98E-89	NP_740833.1	58	332.798	472	276	hypothetical protein F53F10.2
Locus_19920_Transcript_1/1_Conf_1.000	342	20	9.33E-40	NP_501928.1	83	166.392	114	95	hypothetical protein F13B12.4
Locus_19921_Transcript_1/1_Conf_1.000	288	0							
Locus_19922_Transcript_1/1_Conf_1.000	259	0							
Locus_19923_Transcript_1/1_Conf_1.000	423	20	2.26E-70	XP_001142154.1	98	268.085	136	134	PREDICTED: similar to Thioredoxin (ATL-derived factor) (ADF) (Surface-associated sulphydryl protein) (SASP)
Locus_19924_Transcript_1/2_Conf_1.000	477	0							
Locus_19924_Transcript_2/2_Conf_1.000	439	0							
Locus_19925_Transcript_1/1_Conf_1.000	298	0							
Locus_19926_Transcript_1/1_Conf_1.000	221	0							
Locus_19927_Transcript_1/1_Conf_1.000	575	5	4.24E-20	NP_001021744.1	68	101.679	103	71	abnormal cell MIGration family member (mig-1)

Locus_19928_Transcript_1/1_Conf_1.000	210	19	1.01E-30	NP_506637.1	98	136.346	68	67	One IG domain family member (oig-3)
Locus_19929_Transcript_1/1_Conf_1.000	291	20	6.22E-36	EAW47423.1	100	153.68	78	78	proteasome (prosome, macropain) subunit, beta type, 1, isoform CRA_d
Locus_1993_Transcript_1/1_Conf_1.000	434	0							
Locus_19930_Transcript_1/1_Conf_1.000	245	0							
Locus_19931_Transcript_1/1_Conf_1.000	559	0							
Locus_19932_Transcript_1/1_Conf_1.000	477	8	2.04E-15	EFO24135.1	72	85.5001	80	58	hypothetical protein LOAG_04354
Locus_19933_Transcript_1/1_Conf_1.000	318	2	4.66E-07	NP_494276.2	63	57.7658	98	62	Variable ABnormal morphology family member (vab-19)
Locus_19934_Transcript_1/1_Conf_1.000	690	20	1.83E-94	XP_001895028.1	88	349.362	226	199	cytoplasmic polyadenylation element binding protein 4
Locus_19935_Transcript_1/1_Conf_1.000	234	0							
Locus_19936_Transcript_1/2_Conf_1.000	901	20	4.28E-32	XP_002640503.1	61	142.895	282	174	Hypothetical protein CBG13642
Locus_19936_Transcript_2/2_Conf_1.000	910	20	4.36E-32	XP_002640503.1	61	142.895	282	174	Hypothetical protein CBG13642
Locus_19937_Transcript_1/1_Conf_1.000	324	0							
Locus_19938_Transcript_1/1_Conf_1.000	217	0							
Locus_19939_Transcript_1/1_Conf_1.000	317	20	1.35E-30	XP_001899898.1	89	135.961	104	93	LMBR1-like conserved region family protein
Locus_1994_Transcript_1/1_Conf_1.000	645	20	4.58E-86	NP_741348.2	88	321.242	214	190	hypothetical protein Y94H6A.5

Locus_19940_Transcript_1/1_Conf_1.000	285	20	4.34E-37	NP_496968.1	92	157.532	92	85	hypothetical protein Y48B6A.12
Locus_19941_Transcript_1/1_Conf_1.000	150	0							
Locus_19942_Transcript_1/1_Conf_1.000	129	2	5.42E-08	XP_001899872.1	78	60.8474	41	32	Protein-tyrosine phosphatase containing protein
Locus_19943_Transcript_1/1_Conf_1.000	538	20	4.88E-14	NP_001021851.2	79	81.2629	54	43	hypothetical protein ZC434.9
Locus_19944_Transcript_1/1_Conf_1.000	133	0							
Locus_19945_Transcript_1/1_Conf_1.000	129	0							
Locus_19946_Transcript_1/1_Conf_1.000	180	0							
Locus_19947_Transcript_1/1_Conf_1.000	305	12	9.52E-13	NP_004490.2	100	76.6406	78	78	heterogeneous nuclear ribonucleoprotein A/B isoform b
Locus_19948_Transcript_1/1_Conf_1.000	371	11	1.60E-07	ABB53347.1	44	59.3066	121	54	secreted protein 5 precursor
Locus_19949_Transcript_1/1_Conf_1.000	291	0							
Locus_1995_Transcript_1/2_Conf_1.000	518	20	1.74E-39	NP_492576.1	89	165.622	120	107	Ribosomal Protein, Large subunit family member (rpl-14)
Locus_1995_Transcript_2/2_Conf_1.000	218	20	1.83E-16	XP_002639221.1	87	88.9669	55	48	C. briggsae CBR-RPL-14 protein
Locus_19950_Transcript_1/1_Conf_1.000	219	0							
Locus_19951_Transcript_1/1_Conf_1.000	201	0							

Locus_19952_Transcript_1/1_Conf_1.000	325	20	2.87E-33	AAD09564.1	86	144.821	104	90	cyclophilin
Locus_19953_Transcript_1/1_Conf_1.000	188	0							
Locus_19954_Transcript_1/1_Conf_1.000	136	0							
Locus_19955_Transcript_1/1_Conf_1.000	369	11	5.82E-50	CBI63216.1	91	200.29	121	111	C. elegans protein F40F8.8b, partially confirmed by transcript evidence
Locus_19956_Transcript_1/1_Conf_1.000	1163	20	7.02E-55	NP_001021782.1	66	219.164	245	163	hypothetical protein Y52B11A.2
Locus_19957_Transcript_1/1_Conf_1.000	245	0							
Locus_19958_Transcript_1/1_Conf_1.000	849	0							
Locus_19959_Transcript_1/2_Conf_1.000	660	20	7.40E-79	XP_002646242.1	95	297.36	162	154	C. briggsae CBR-UNC-13 protein
Locus_19959_Transcript_2/2_Conf_1.000	383	20	2.40E-64	XP_002646242.1	96	248.054	128	123	C. briggsae CBR-UNC-13 protein
Locus_1996_Transcript_1/1_Conf_1.000	371	20	2.82E-20	XP_002643656.1	78	101.679	76	60	Hypothetical protein CBG16408
Locus_19960_Transcript_1/1_Conf_1.000	230	0							
Locus_19961_Transcript_1/1_Conf_1.000	171	20	5.05E-14	XP_002634908.1	76	80.8777	56	43	Hypothetical protein CBG22506
Locus_19962_Transcript_1/1_Conf_1.000	585	20	7.91E-41	NP_495933.1	69	170.629	163	114	hypothetical protein T24B8.2

Locus_19963_Transcript_1/1_Conf_1.000	261	20	7.38E-21	XP_002639570.1	87	103.605	63	55	C. briggsae CBR-ARX-7 protein
Locus_19964_Transcript_1/1_Conf_1.000	402	0							
Locus_19965_Transcript_1/1_Conf_1.000	463	20	1.03E-22	NP_496607.1	75	109.768	88	66	hypothetical protein Y57A10A.29
Locus_19966_Transcript_1/1_Conf_1.000	485	14	1.26E-12	XP_002633316.1	55	76.2554	167	92	C. briggsae CBR-GTL-2 protein
Locus_19967_Transcript_1/1_Conf_1.000	460	11	1.23E-12	NP_510606.1	74	76.2554	59	44	ACyLtransferase-like family member (acl-1)
Locus_19968_Transcript_1/1_Conf_1.000	319	1	2.64E-10	XP_001141980.1	61	68.5514	67	41	PREDICTED: ephrin A1
Locus_19969_Transcript_1/1_Conf_1.000	745	20	3.08E-101	NP_741172.2	91	372.089	220	201	protein KINase family member (kin-18)
Locus_1997_Transcript_1/1_Conf_1.000	198	13	3.19E-24	ACY39994.1	90	114.775	66	60	C. elegans FLN-2 protein, isoform d
Locus_19970_Transcript_1/1_Conf_1.000	182	0							
Locus_19971_Transcript_1/1_Conf_1.000	297	8	2.53E-05	XP_002646337.1	44	51.9878	95	42	Hypothetical protein CBG12050
Locus_19972_Transcript_1/1_Conf_1.000	140	20	3.97E-11	NP_500586.2	82	71.2478	46	38	hypothetical protein ZK185.2
Locus_19973_Transcript_1/1_Conf_1.000	190	0							
Locus_19974_Transcript_1/2_Conf_1.000	509	20	2.56E-56	XP_002632133.1	79	221.476	168	134	Hypothetical protein CBG06989
Locus_19974_Transcript_2/2_Conf_1.000	444	20	4.43E-50	XP_002632133.1	78	200.675	147	116	Hypothetical protein CBG06989

Locus_19975_Transcript_1/1_Conf_1.000	174	1	8.05E-04	XP_001944330.1	73	46.9802	34	25	PREDICTED: similar to CG8213 CG8213-PA
Locus_19976_Transcript_1/1_Conf_1.000	134	0							
Locus_19977_Transcript_1/1_Conf_1.000	425	20	1.59E-07	NP_733845.1	51	59.3066	110	57	nonstructural polyprotein
Locus_19978_Transcript_1/1_Conf_1.000	469	20	6.37E-49	NP_496736.1	85	196.823	121	103	Glycogen SYnthase family member (gsy-1)
Locus_19979_Transcript_1/1_Conf_1.000	322	6	2.55E-05	BAD94515.1	49	51.9878	67	33	peroxisome proliferator-activated receptor gamma
Locus_1998_Transcript_1/4_Conf_0.375	390	20	3.11E-48	NP_495823.1	91	194.512	108	99	Ribosomal Protein, Large subunit family member (rpl-26)
Locus_1998_Transcript_2/4_Conf_0.375	348	20	2.06E-47	NP_871965.1	93	191.815	103	96	Ribosomal Protein, Large subunit family member (rpl-26)
Locus_1998_Transcript_3/4_Conf_0.375	1184	20	2.24E-64	XP_002630145.1	92	250.751	139	129	C. briggsae CBR-RPL-26 protein
Locus_1998_Transcript_4/4_Conf_0.375	1184	20	2.24E-64	XP_002630145.1	92	250.751	139	129	C. briggsae CBR-RPL-26 protein
Locus_19980_Transcript_1/1_Conf_1.000	140	0							
Locus_19981_Transcript_1/1_Conf_1.000	257	0							

Locus_19982_Transcript_1/1_Conf_1.000	147	0							
Locus_19983_Transcript_1/1_Conf_1.000	265	0							
Locus_19984_Transcript_1/1_Conf_1.000	144	0							
Locus_19985_Transcript_1/1_Conf_1.000	143	0							
Locus_19986_Transcript_1/1_Conf_1.000	132	2	8.34E-09	NP_502336.1	89	63.5438	39	35	hypothetical protein C42C1.12
Locus_19987_Transcript_1/1_Conf_1.000	213	20	1.08E-16	EFO20785.1	77	89.7373	67	52	TKL/MLK/HH498 protein kinase
Locus_19988_Transcript_1/1_Conf_1.000	272	0							
Locus_19989_Transcript_1/1_Conf_1.000	347	0							
Locus_1999_Transcript_1/1_Conf_1.000	1887	20	1.43E-96	XP_001897626.1	67	358.607	353	238	Myosin head containing protein
Locus_19990_Transcript_1/1_Conf_1.000	479	2	1.73E-14	NP_509587.1	66	82.4185	110	73	hypothetical protein ZK899.1
Locus_19991_Transcript_1/1_Conf_1.000	162	20	4.46E-10	EDM11526.1	75	67.781	53	40	lactamase, beta 2
Locus_19992_Transcript_1/1_Conf_1.000	178	6	1.23E-20	XP_001896988.1	87	102.834	58	51	UTP--ammonia ligase
Locus_19993_Transcript_1/1_Conf_1.000	564	20	3.38E-51	NP_498172.3	70	204.912	192	136	hypothetical protein R02F2.2
Locus_19994_Transcript_1/1_Conf_1.000	301	20	8.05E-28	XP_002639522.1	76	126.716	99	76	Hypothetical protein CBG04128
Locus_19995_Transcript_1/1_Conf_1.000	554	2	5.38E-06	NP_741780.1	57	54.6842	90	52	hypothetical protein H28G03.2
Locus_19996_Transcript_1/1_Conf_1.000	673	0							

Locus_19997_Transcript_1/1_Conf_1.000	210	20	5.01E-30	AAC19161.1	98	134.035	69	68	unknown
Locus_19998_Transcript_1/1_Conf_1.000	206	20	7.55E-18	NP_496500.1	75	93.5893	66	50	hypothetical protein VF13D12L.3
Locus_19999_Transcript_1/1_Conf_1.000	229	0							
Locus_2_Transcript_1/1_Conf_1.000	285	0							
Locus_20_Transcript_1/1_Conf_1.000	535	7	3.92E-08	XP_002641747.1	63	61.6178	63	40	Hypothetical protein CBG10086
Locus_200_Transcript_1/1_Conf_1.000	730	20	5.66E-36	XP_002631322.1	58	155.221	197	115	C. briggsae CBR-TRS-1 protein
Locus_2000_Transcript_1/1_Conf_1.000	1265	20	6.72E-163	XP_002646193.1	80	578.17	421	341	Hypothetical protein CBG24498
Locus_20000_Transcript_1/1_Conf_1.000	271	2	1.38E-11	XP_002642828.1	68	72.7886	80	55	Hypothetical protein CBG21226
Locus_20001_Transcript_1/1_Conf_1.000	177	20	2.40E-24	BAG59482.1	100	115.161	58	58	unnamed protein product
Locus_20002_Transcript_1/1_Conf_1.000	184	0							

Locus_20003_Transcript_1/1_Conf_1.000	230	0							
Locus_20004_Transcript_1/1_Conf_1.000	621	20	1.22E-45	XP_002637227.1	72	186.808	147	106	Hypothetical protein CBG18895
Locus_20005_Transcript_1/1_Conf_1.000	452	8	7.54E-26	XP_002631168.1	76	120.168	92	70	C. briggsae CBR-PQM-1 protein
Locus_20006_Transcript_1/1_Conf_1.000	240	0							
Locus_20007_Transcript_1/1_Conf_1.000	318	4	1.95E-13	EFO19864.1	64	78.9518	100	64	hypothetical protein LOAG_08632
Locus_20008_Transcript_1/1_Conf_1.000	293	20	2.01E-26	NP_497035.3	78	122.094	97	76	Trehalose 6-Phosphate Synthase family member (tps-2)
Locus_20009_Transcript_1/1_Conf_1.000	348	0							
Locus_2001_Transcript_1/1_Conf_1.000	1103	20	8.64E-116	ACI48996.1	79	421.394	333	264	hypothetical protein Cbre_JD01.003
Locus_20010_Transcript_1/1_Conf_1.000	380	0							
Locus_20011_Transcript_1/1_Conf_1.000	817	0							
Locus_20012_Transcript_1/1_Conf_1.000	385	20	3.58E-44	XP_002633893.1	79	181.03	125	99	C. briggsae CBR-ELO-5 protein
Locus_20013_Transcript_1/1_Conf_1.000	248	20	2.74E-28	XP_001898240.1	84	128.257	82	69	XPA-binding protein 2
Locus_20014_Transcript_1/1_Conf_1.000	120	0							

Locus_20015_Transcript_1/1_Conf_1.000	258	20	6.25E-28	BAG60492.1	100	127.102	59	59	unnamed protein product
Locus_20016_Transcript_1/1_Conf_1.000	338	20	4.53E-23	NP_504239.2	66	110.923	106	71	hypothetical protein Y61A9LA.8
Locus_20017_Transcript_1/1_Conf_1.000	167	0							
Locus_20018_Transcript_1/1_Conf_1.000	188	0							
Locus_20019_Transcript_1/1_Conf_1.000	197	0							
Locus_2002_Transcript_1/1_Conf_1.000	2412	20	0	XP_002637276.1	91	1036.17	591	543	Hypothetical protein CBG18959
Locus_20020_Transcript_1/1_Conf_1.000	221	4	2.84E-12	NP_001076754.1	79	75.0998	73	58	hypothetical protein C14H10.2
Locus_20021_Transcript_1/1_Conf_1.000	392	20	4.64E-44	NP_504292.2	87	180.644	115	101	hypothetical protein C37H5.5
Locus_20022_Transcript_1/1_Conf_1.000	467	20	2.99E-22	EFO27494.1	61	108.227	125	77	hypothetical protein LOAG_00986
Locus_20023_Transcript_1/1_Conf_1.000	735	20	1.90E-63	XP_002646726.1	69	246.514	219	153	Hypothetical protein CBG13109
Locus_20024_Transcript_1/1_Conf_1.000	412	2	1.55E-47	NP_001122963.1	83	192.2	134	112	hypothetical protein F58E6.1
Locus_20025_Transcript_1/1_Conf_1.000	173	0							
Locus_20026_Transcript_1/1_Conf_1.000	129	20	1.47E-13	NP_741632.2	97	79.337	41	40	SMAll family member (sma-1)
Locus_20027_Transcript_1/1_Conf_1.000	312	20	2.84E-12	NP_956980.1	83	75.0998	54	45	mitochondrial fission protein MTP18
Locus_20028_Transcript_1/1_Conf_1.000	209	0							

Locus_20029_Transcript_1/1_Conf_1.000	163	0							
Locus_2003_Transcript_1/1_Conf_1.000	450	20	4.25E-45	XP_002641573.1	81	184.111	138	112	C. briggsae CBR-TTLL-4 protein
Locus_20030_Transcript_1/1_Conf_1.000	260	0							
Locus_20031_Transcript_1/1_Conf_1.000	290	1	6.30E-04	XP_002633908.1	45	47.3654	87	40	Hypothetical protein CBG19972
Locus_20032_Transcript_1/1_Conf_1.000	720	20	9.26E-84	NP_509174.1	83	313.923	206	173	hypothetical protein C16E9.2
Locus_20033_Transcript_1/1_Conf_1.000	333	20	1.12E-21	NP_500647.2	65	106.301	115	75	Dipeptidyl Peptidase Four (IV) family member (dpf-5)
Locus_20034_Transcript_1/1_Conf_1.000	258	8	1.39E-35	NP_502016.2	94	152.525	85	80	hypothetical protein F13E9.1
Locus_20035_Transcript_1/1_Conf_1.000	390	0							
Locus_20036_Transcript_1/1_Conf_1.000	236	0							
Locus_20037_Transcript_1/1_Conf_1.000	306	0							
Locus_20038_Transcript_1/1_Conf_1.000	214	0							
Locus_20039_Transcript_1/1_Conf_1.000	228	20	5.65E-21	EFO26545.1	77	103.99	76	59	kelch domain-containing protein family protein
Locus_2004_Transcript_1/1_Conf_1.000	1174	20	1.76E-53	NP_493375.2	69	214.542	220	153	AuTophaGy (yeast Atg homolog) family member (atg-4.1)
Locus_20040_Transcript_1/1_Conf_1.000	217	1	2.75E-04	YP_001044988.1	53	48.521	56	30	hypothetical protein Rsph17029_3116
Locus_20041_Transcript_1/1_Conf_1.000	464	0							
Locus_20042_Transcript_1/1_Conf_1.000	338	20	1.82E-56	XP_002747692.1	100	221.861	112	112	PREDICTED: 40S ribosomal protein S7-like
Locus_20043_Transcript_1/1_Conf_1.000	222	0							
Locus_20044_Transcript_1/1_Conf_1.000	1103	20	6.31E-50	NP_498604.2	71	202.601	180	129	hypothetical protein B0361.7
Locus_20045_Transcript_1/1_Conf_1.000	247	4	2.49E-13	XP_002645089.1	66	78.5666	93	62	Hypothetical protein CBG16766
Locus_20046_Transcript_1/1_Conf_1.000	513	0							
Locus_20047_Transcript_1/1_Conf_1.000	221	20	3.81E-33	NP_506269.1	100	144.436	73	73	EATing: abnormal pharyngeal pumping family member (eat-6)
Locus_20048_Transcript_1/1_Conf_1.000	134	0							
Locus_20049_Transcript_1/1_Conf_1.000	437	0							

Locus_2005_Transcript_1/1_Conf_1.000	2109	20	0	XP_002638594.1	89	784.252	479	427	C. briggsae CBR-GCK-3 protein
Locus_20050_Transcript_1/1_Conf_1.000	451	2	5.41E-24	XP_002643963.1	60	114.005	130	79	Hypothetical protein CBG17334
Locus_20051_Transcript_1/1_Conf_1.000	240	0							
Locus_20052_Transcript_1/1_Conf_1.000	436	3	8.56E-14	XP_002642011.1	57	80.1073	103	59	Hypothetical protein CBG17944
Locus_20053_Transcript_1/1_Conf_1.000	173	0							
Locus_20054_Transcript_1/1_Conf_1.000	165	0							
Locus_20055_Transcript_1/1_Conf_1.000	299	3	2.21E-09	AAO63577.1	54	65.4698	102	56	secreted protein 5 precursor
Locus_20056_Transcript_1/1_Conf_1.000	241	0							
Locus_20057_Transcript_1/1_Conf_1.000	145	3	1.85E-11	NP_498063.1	86	72.4034	46	40	hypothetical protein R144.11
Locus_20058_Transcript_1/1_Conf_1.000	139	0							
Locus_20059_Transcript_1/1_Conf_1.000	921	20	5.16E-113	ACJ65180.1	78	411.764	304	239	Gaba b receptor subunit protein 2, confirmed by transcript evidence
Locus_2006_Transcript_1/1_Conf_1.000	1118	4	3.93E-31	XP_002638907.1	69	140.198	158	110	Hypothetical protein CBG22133
Locus_20060_Transcript_1/1_Conf_1.000	372	20	2.70E-39	NP_509899.3	89	164.851	118	106	Organic Cation Transporter family member (oct-2)
Locus_20061_Transcript_1/1_Conf_1.000	276	0							
Locus_20062_Transcript_1/1_Conf_1.000	151	0							
Locus_20063_Transcript_1/1_Conf_1.000	161	0							
Locus_20064_Transcript_1/1_Conf_1.000	215	0							
Locus_20065_Transcript_1/1_Conf_1.000	302	0							
Locus_20066_Transcript_1/1_Conf_1.000	302	4	4.15E-16	XP_002641354.1	66	87.8113	96	64	Hypothetical protein CBG13208
Locus_20067_Transcript_1/1_Conf_1.000	311	0							
Locus_20068_Transcript_1/1_Conf_1.000	133	1	2.13E-04	XP_002634830.1	77	48.9062	44	34	Hypothetical protein CBG13938
Locus_20069_Transcript_1/1_Conf_1.000	338	20	3.98E-11	XP_001898083.1	63	71.2478	79	50	hypothetical protein
Locus_2007_Transcript_1/1_Conf_1.000	170	0							
Locus_20070_Transcript_1/1_Conf_1.000	230	0							

Locus_20071_Transcript_1/1_Conf_1.000	466	2	2.81E-04	NP_493556.1	49	48.521	97	48	hypothetical protein Y54E5A.8
Locus_20072_Transcript_1/1_Conf_1.000	147	0							
Locus_20073_Transcript_1/1_Conf_1.000	418	13	2.48E-08	CAR97807.1	48	62.003	115	56	C. elegans protein C23H4.4b, partially confirmed by transcript evidence
Locus_20074_Transcript_1/1_Conf_1.000	304	0							
Locus_20075_Transcript_1/1_Conf_1.000	173	0							
Locus_20076_Transcript_1/1_Conf_1.000	621	20	3.20E-54	NP_508866.1	73	215.312	186	137	Unidentified Vitellogenin-linked Transcript family member (uvt-3)
Locus_20077_Transcript_1/1_Conf_1.000	380	20	4.01E-27	EFO27289.1	69	124.405	123	85	actin family protein
Locus_20078_Transcript_1/1_Conf_1.000	203	0							
Locus_20079_Transcript_1/1_Conf_1.000	294	6	3.20E-16	NP_495366.2	76	88.1965	72	55	DumPY : shorter than wild-type family member (dpy-10)
Locus_2008_Transcript_1/1_Conf_1.000	2313	20	9.50E-154	XP_002631266.1	74	548.895	455	340	C. briggsae CBR-MNK-1 protein
Locus_20080_Transcript_1/1_Conf_1.000	305	0							
Locus_20081_Transcript_1/1_Conf_1.000	260	0							
Locus_20082_Transcript_1/1_Conf_1.000	559	0							
Locus_20083_Transcript_1/1_Conf_1.000	345	1	2.15E-28	BAB93497.1	100	128.642	73	73	OK/SW-CL.24
Locus_20084_Transcript_1/1_Conf_1.000	131	3	3.40E-10	XP_002632407.1	86	68.1662	43	37	Hypothetical protein CBG00431
Locus_20085_Transcript_1/1_Conf_1.000	210	20	2.33E-19	AAN11401.1	74	98.5969	66	49	metalloprotease 1 precursor
Locus_20086_Transcript_1/1_Conf_1.000	524	0							
Locus_20087_Transcript_1/1_Conf_1.000	172	0							

Locus_20088_Transcript_1/1_Conf_1.000	143	10	1.27E-17	BAD93019.1	100	92.8189	46	46	ubiquitin C variant
Locus_20089_Transcript_1/1_Conf_1.000	144	0							
Locus_2009_Transcript_1/1_Conf_1.000	884	0							
Locus_20090_Transcript_1/1_Conf_1.000	336	0							
Locus_20091_Transcript_1/1_Conf_1.000	133	2	1.25E-04	NP_508432.1	74	49.6766	47	35	hypothetical protein F47G3.1
Locus_20092_Transcript_1/1_Conf_1.000	263	4	6.23E-28	XP_002637429.1	84	127.102	83	70	Hypothetical protein CBG19140
Locus_20093_Transcript_1/1_Conf_1.000	391	0							
Locus_20094_Transcript_1/1_Conf_1.000	317	20	7.90E-39	XP_002631100.1	85	163.31	104	89	Hypothetical protein CBG02874
Locus_20095_Transcript_1/1_Conf_1.000	195	0							
Locus_20096_Transcript_1/1_Conf_1.000	159	0							
Locus_20097_Transcript_1/1_Conf_1.000	321	0							
Locus_20098_Transcript_1/1_Conf_1.000	380	0							
Locus_20099_Transcript_1/1_Conf_1.000	445	20	4.17E-32	XP_001897051.1	66	140.969	148	99	RNA polymerase Rpb1, domain 1 family protein
Locus_201_Transcript_1/1_Conf_1.000	906	0							
Locus_2010_Transcript_1/1_Conf_1.000	1579	20	1.77E-166	NP_501365.1	89	590.497	348	313	P38 Map Kinase family member (pmk-1)
Locus_20100_Transcript_1/1_Conf_1.000	545	2	7.07E-24	NP_495419.1	60	114.005	160	96	hypothetical protein B0252.1
Locus_20101_Transcript_1/1_Conf_1.000	157	0							
Locus_20102_Transcript_1/1_Conf_1.000	225	0							
Locus_20103_Transcript_1/1_Conf_1.000	151	0							

Locus_20104_Transcript_1/1_Conf_1.000	769	20	7.77E-95	NP_505613.1	79	350.903	257	204	hypothetical protein C51E3.6
Locus_20105_Transcript_1/1_Conf_1.000	354	20	1.42E-32	NP_505071.1	70	142.51	118	83	hypothetical protein ZC513.5
Locus_20106_Transcript_1/1_Conf_1.000	397	0							
Locus_20107_Transcript_1/1_Conf_1.000	297	20	5.42E-24	NP_492498.1	91	114.005	70	64	hypothetical protein F16A11.2
Locus_20108_Transcript_1/1_Conf_1.000	255	3	2.10E-07	AAA83446.5	70	58.9214	74	52	Hypothetical protein F44A2.3
Locus_20109_Transcript_1/1_Conf_1.000	444	20	1.62E-68	NP_498777.2	92	261.922	147	136	hypothetical protein C14B9.8
Locus_2011_Transcript_1/1_Conf_1.000	706	20	8.35E-42	XP_002642125.1	64	174.481	251	161	Hypothetical protein CBG18072
Locus_20110_Transcript_1/1_Conf_1.000	483	20	3.91E-30	NP_493165.3	60	134.42	156	95	hypothetical protein T27F6.1
Locus_20111_Transcript_1/1_Conf_1.000	350	0							
Locus_20112_Transcript_1/1_Conf_1.000	134	5	3.28E-05	EFA00585.1	70	51.6026	44	31	hypothetical protein TcasGA2_TC003455
Locus_20113_Transcript_1/1_Conf_1.000	261	20	8.96E-43	XP_002811879.1	100	176.407	87	87	PREDICTED: macrophage-capping protein-like isoform 4
Locus_20114_Transcript_1/1_Conf_1.000	437	0							
Locus_20115_Transcript_1/1_Conf_1.000	311	4	1.01E-14	NP_741925.2	81	83.1889	86	70	DYstrophin-like phenotype and CAPON related family member (dyc-1)

Locus_20116_Transcript_1/1_Conf_1.000	180	20	4.86E-20	AAK68292.3	92	100.908	54	50	U28943_4Clc-type chloride channel protein 3, isoform b, confirmed by transcript evidence
Locus_20117_Transcript_1/1_Conf_1.000	357	9	1.20E-15	XP_002633446.1	55	86.2705	120	67	Hypothetical protein CBG06214
Locus_20118_Transcript_1/1_Conf_1.000	290	0							
Locus_20119_Transcript_1/1_Conf_1.000	248	20	1.04E-35	NP_509689.1	96	152.91	82	79	hypothetical protein ZC373.4
Locus_2012_Transcript_1/1_Conf_1.000	1101	20	9.89E-112	NP_497785.1	78	407.912	301	237	TIR (Toll and Interleukin 1 Receptor) domain protein family member (tir-1)
Locus_20120_Transcript_1/1_Conf_1.000	187	0							
Locus_20121_Transcript_1/1_Conf_1.000	147	0							
Locus_20122_Transcript_1/1_Conf_1.000	225	0							
Locus_20123_Transcript_1/1_Conf_1.000	348	0							
Locus_20124_Transcript_1/1_Conf_1.000	369	13	1.27E-20	XP_002641615.1	82	102.834	76	63	Hypothetical protein CBG09935
Locus_20125_Transcript_1/1_Conf_1.000	396	20	1.18E-26	XP_002631717.1	64	122.865	137	88	Hypothetical protein CBG20918
Locus_20126_Transcript_1/1_Conf_1.000	418	7	4.37E-05	XP_002125751.1	40	51.2174	136	55	PREDICTED: similar to Thrombospondin type 1 domain containing protein
Locus_20127_Transcript_1/1_Conf_1.000	326	20	2.20E-33	NP_001022572.1	77	145.206	108	84	Elongation Factor Kinase family member (efk-1)
Locus_20128_Transcript_1/1_Conf_1.000	175	0							
Locus_20129_Transcript_1/1_Conf_1.000	135	0							
Locus_2013_Transcript_1/1_Conf_1.000	1587	20	3.17E-139	NP_001021806.1	72	499.975	494	360	Conserved Oligomeric Golgi (COG) Component family member (cogc-3)
Locus_20130_Transcript_1/1_Conf_1.000	151	0							
Locus_20131_Transcript_1/1_Conf_1.000	356	0							
Locus_20132_Transcript_1/1_Conf_1.000	163	0							
Locus_20133_Transcript_1/2_Conf_1.000	500	0							
Locus_20133_Transcript_2/2_Conf_1.000	511	0							
Locus_20134_Transcript_1/1_Conf_1.000	1114	20	0	NP_492498.1	93	664.84	369	345	hypothetical protein F16A11.2

Locus_20135_Transcript_1/1_Conf_1.000	432	20	1.61E-36	NP_001022174.1	74	155.606	147	110	hypothetical protein F45E10.2
Locus_20136_Transcript_1/1_Conf_1.000	236	0							
Locus_20137_Transcript_1/1_Conf_1.000	482	3	5.91E-15	XP_002641730.1	75	83.9593	62	47	Hypothetical protein CBG10069
Locus_20138_Transcript_1/1_Conf_1.000	654	20	6.48E-51	NP_001022694.1	69	204.527	195	135	hypothetical protein M142.8
Locus_20139_Transcript_1/1_Conf_1.000	158	0							
Locus_2014_Transcript_1/1_Conf_1.000	183	0							
Locus_20140_Transcript_1/1_Conf_1.000	177	0							
Locus_20141_Transcript_1/1_Conf_1.000	175	3	3.49E-07	NP_001022619.1	71	58.151	52	37	NorDiHydroGuaiaretic acid resistant family member (ndg-4)
Locus_20142_Transcript_1/1_Conf_1.000	166	0							
Locus_20143_Transcript_1/1_Conf_1.000	287	0							
Locus_20144_Transcript_1/1_Conf_1.000	294	20	6.02E-23	NP_001024958.1	82	110.538	97	80	hypothetical protein Y34B4A.4
Locus_20145_Transcript_1/2_Conf_1.000	466	0							
Locus_20145_Transcript_2/2_Conf_1.000	367	0							
Locus_20146_Transcript_1/1_Conf_1.000	205	0							
Locus_20147_Transcript_1/1_Conf_1.000	370	0							
Locus_20148_Transcript_1/1_Conf_1.000	268	0							
Locus_20149_Transcript_1/1_Conf_1.000	223	3	8.82E-06	NP_501039.1	63	53.5286	60	38	hypothetical protein C17H12.2
Locus_2015_Transcript_1/3_Conf_0.750	726	0							
Locus_2015_Transcript_2/3_Conf_0.750	818	0							
Locus_2015_Transcript_3/3_Conf_0.750	797	0							
Locus_20150_Transcript_1/1_Conf_1.000	145	2	3.04E-14	XP_002634423.1	89	81.6481	48	43	C. briggsae CBR-PTR-14 protein
Locus_20151_Transcript_1/1_Conf_1.000	138	20	6.12E-20	XP_002816317.1	100	100.523	46	46	PREDICTED: vesicular integral-membrane protein VIP36-like isoform 2

Locus_20152_Transcript_1/1_Conf_1.000	249	3	5.90E-23	NP_497970.1	88	110.538	68	60	Adenylyl CYclase family member (acy-1)
Locus_20153_Transcript_1/1_Conf_1.000	200	20	4.76E-20	NP_496968.1	87	100.908	66	58	hypothetical protein Y48B6A.12
Locus_20154_Transcript_1/1_Conf_1.000	213	20	3.96E-19	NP_500412.1	82	97.8265	69	57	Variable ABnormal morphology family member (vab-2)
Locus_20155_Transcript_1/1_Conf_1.000	371	2	4.97E-25	NP_492185.2	65	117.472	126	82	SMG-associated and Lethal family member (smgl-1)
Locus_20156_Transcript_1/2_Conf_1.000	360	0							
Locus_20156_Transcript_2/2_Conf_1.000	270	0							
Locus_20157_Transcript_1/1_Conf_1.000	231	1	1.44E-08	XP_002634119.1	65	62.7734	72	47	Hypothetical protein CBG01673
Locus_20158_Transcript_1/1_Conf_1.000	148	0							
Locus_20159_Transcript_1/1_Conf_1.000	134	0							
Locus_2016_Transcript_1/1_Conf_1.000	1281	20	1.24E-79	NP_492371.1	74	301.597	258	193	nuclear LaMiN family member (lmn-1)
Locus_20160_Transcript_1/1_Conf_1.000	198	20	1.58E-23	NP_001122833.1	89	112.464	65	58	hypothetical protein ZC518.1
Locus_20161_Transcript_1/1_Conf_1.000	229	20	3.21E-16	NP_741383.1	73	88.1965	72	53	tYrosinyl tRNA Synthetase family member (yrs-1)
Locus_20162_Transcript_1/1_Conf_1.000	211	0							
Locus_20163_Transcript_1/1_Conf_1.000	340	0							
Locus_20165_Transcript_1/1_Conf_1.000	492	20	9.51E-29	XP_002130984.1	63	129.798	145	92	PREDICTED: similar to MGC80593 protein
Locus_20166_Transcript_1/1_Conf_1.000	327	0							
Locus_20167_Transcript_1/1_Conf_1.000	153	0							
Locus_20168_Transcript_1/1_Conf_1.000	275	0							
Locus_20169_Transcript_1/1_Conf_1.000	169	0							

Locus_2017_Transcript_1/1_Conf_1.000	456	20	3.70E-33	XP_002642667.1	95	144.436	73	70	C. briggsae CBR-SNR-5 protein
Locus_20170_Transcript_1/1_Conf_1.000	198	0							
Locus_20171_Transcript_1/1_Conf_1.000	185	20	2.25E-17	NP_497008.1	83	92.0485	61	51	hypothetical protein K10H10.2
Locus_20172_Transcript_1/1_Conf_1.000	304	0							
Locus_20173_Transcript_1/1_Conf_1.000	210	0							
Locus_20174_Transcript_1/1_Conf_1.000	272	0							
Locus_20175_Transcript_1/1_Conf_1.000	146	0							
Locus_20176_Transcript_1/1_Conf_1.000	205	20	1.20E-23	NP_740900.1	88	112.849	68	60	hypothetical protein T08G11.1
Locus_20177_Transcript_1/1_Conf_1.000	318	0							
Locus_20178_Transcript_1/1_Conf_1.000	140	0							
Locus_20179_Transcript_1/1_Conf_1.000	360	20	3.83E-38	XP_002642021.1	93	160.999	90	84	C. briggsae CBR-COQ-8 protein
Locus_2018_Transcript_1/1_Conf_1.000	2111	20	6.94E-172	XP_001899259.1	75	608.986	504	381	Conserved hypothetical protein
Locus_20180_Transcript_1/1_Conf_1.000	427	20	1.48E-21	NP_499961.2	60	105.916	145	87	Nuclear Hormone Receptor family member (nhr-76)
Locus_20181_Transcript_1/1_Conf_1.000	236	0							
Locus_20182_Transcript_1/1_Conf_1.000	309	0							
Locus_20183_Transcript_1/1_Conf_1.000	1127	20	1.07E-84	ADI24662.1	71	318.161	322	230	Hypothetical protein Y110A2AL.12a
Locus_20184_Transcript_1/1_Conf_1.000	131	0							
Locus_20185_Transcript_1/1_Conf_1.000	137	0							
Locus_20186_Transcript_1/1_Conf_1.000	173	0							
Locus_20187_Transcript_1/2_Conf_1.000	318	20	4.15E-56	A8Y236.2	98	220.705	104	102	Putative polypeptide N-acetylgalactosaminyltransferase 10

Locus_20187_Transcript_2/2_Conf_1.000	318	20	4.15E-56	A8Y236.2	98	220.705	104	102	Putative polypeptide N-acetylgalactosaminyltransferase 10
Locus_20188_Transcript_1/1_Conf_1.000	361	6	1.51E-34	XP_002632694.1	79	149.058	111	88	Hypothetical protein CBG21625
Locus_20189_Transcript_1/1_Conf_1.000	144	0							
Locus_2019_Transcript_1/3_Conf_0.357	144	0							
Locus_2019_Transcript_2/3_Conf_0.429	210	0							
Locus_2019_Transcript_3/3_Conf_0.571	407	2	2.79E-04	CAC17797.1	52	48.521	74	39	SXC1 protein
Locus_20190_Transcript_1/1_Conf_1.000	189	4	1.96E-05	NP_001122780.1	73	52.373	56	41	hypothetical protein F41H10.6
Locus_20191_Transcript_1/1_Conf_1.000	209	0							
Locus_20192_Transcript_1/1_Conf_1.000	267	0							
Locus_20193_Transcript_1/1_Conf_1.000	164	9	8.97E-19	XP_002630203.1	92	96.6709	54	50	Hypothetical protein CBG00613
Locus_20194_Transcript_1/1_Conf_1.000	1183	20	1.70E-96	XP_001897426.1	76	357.451	301	231	Rab5 GDP/GTP exchange factor
Locus_20195_Transcript_1/1_Conf_1.000	129	0							
Locus_20196_Transcript_1/2_Conf_1.000	187	0							
Locus_20196_Transcript_2/2_Conf_1.000	264	0							
Locus_20197_Transcript_1/1_Conf_1.000	175	0							
Locus_20198_Transcript_1/1_Conf_1.000	215	12	3.13E-24	NP_493493.2	88	114.775	70	62	hypothetical protein F09C3.2
Locus_20199_Transcript_1/1_Conf_1.000	142	0							
Locus_202_Transcript_1/1_Conf_1.000	227	0							
Locus_2020_Transcript_1/1_Conf_1.000	316	20	5.13E-30	XP_002642349.1	75	134.035	103	78	Hypothetical protein CBG18346
Locus_20200_Transcript_1/1_Conf_1.000	364	0							
Locus_20201_Transcript_1/1_Conf_1.000	135	0							
Locus_20202_Transcript_1/1_Conf_1.000	146	0							
Locus_20203_Transcript_1/1_Conf_1.000	424	0							
Locus_20204_Transcript_1/1_Conf_1.000	142	0							
Locus_20205_Transcript_1/1_Conf_1.000	537	0							
Locus_20206_Transcript_1/1_Conf_1.000	225	20	1.31E-17	NP_510666.1	96	92.8189	50	48	hypothetical protein F01G12.6
Locus_20207_Transcript_1/1_Conf_1.000	627	20	2.13E-61	NP_741746.1	83	239.195	171	142	Kinesin-Like Protein family member (klp-4)

Locus_20208_Transcript_1/1_Conf_1.000	210	20	1.46E-21	XP_002637044.1	84	105.916	69	58	C. briggsae CBR-CUL-5 protein
Locus_20209_Transcript_1/1_Conf_1.000	479	20	3.01E-51	XP_002630906.1	76	204.527	159	121	Hypothetical protein CBG02630
Locus_2021_Transcript_1/1_Conf_1.000	141	0							
Locus_20210_Transcript_1/1_Conf_1.000	379	20	2.43E-32	XP_002643095.1	77	141.739	127	98	C. briggsae CBR-GLY-11 protein
Locus_20211_Transcript_1/1_Conf_1.000	250	20	5.92E-07	XP_001641433.1	57	57.3806	75	43	predicted protein
Locus_20212_Transcript_1/1_Conf_1.000	274	0							
Locus_20213_Transcript_1/1_Conf_1.000	221	0							
Locus_20214_Transcript_1/1_Conf_1.000	964	20	1.05E-71	XP_002643853.1	67	274.633	331	223	Hypothetical protein CBG02083
Locus_20215_Transcript_1/1_Conf_1.000	391	0							
Locus_20216_Transcript_1/1_Conf_1.000	141	0							
Locus_20217_Transcript_1/1_Conf_1.000	177	4	2.26E-06	EFO14006.1	73	55.4546	49	36	hypothetical protein LOAG_14520
Locus_20218_Transcript_1/1_Conf_1.000	189	0							
Locus_20219_Transcript_1/1_Conf_1.000	190	20	2.46E-24	Q60V90.3	95	115.161	60	57	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1
Locus_2022_Transcript_1/1_Conf_1.000	1196	20	1.74E-72	NP_499801.1	70	277.715	278	197	hypothetical protein Y76A2B.5
Locus_20220_Transcript_1/2_Conf_1.000	311	0							
Locus_20220_Transcript_2/2_Conf_1.000	311	0							
Locus_20221_Transcript_1/1_Conf_1.000	197	0							
Locus_20222_Transcript_1/1_Conf_1.000	165	1	8.13E-04	NP_505666.2	68	46.9802	51	35	UDP-GlucuronosylTransferase family member (ugt-49)
Locus_20223_Transcript_1/1_Conf_1.000	210	3	7.89E-19	NP_492219.1	86	91.2781	51	44	hypothetical protein K04G2.9
Locus_20224_Transcript_1/1_Conf_1.000	146	0							
Locus_20225_Transcript_1/1_Conf_1.000	179	20	1.85E-08	XP_002577284.1	66	62.3882	60	40	nuclear factor Y transcription factor subunit B homolog

Locus_20226_Transcript_1/1_Conf_1.000	137	7	1.01E-14	XP_002632396.1	97	83.1889	40	39	C. briggsae CBR-UAF-2 protein
Locus_20227_Transcript_1/1_Conf_1.000	234	6	4.17E-08	NP_001041050.1	58	61.2326	78	46	hypothetical protein Y57G11C.3
Locus_20228_Transcript_1/1_Conf_1.000	264	19	1.18E-10	XP_002639499.1	61	69.707	85	52	C. briggsae CBR-ITX-1 protein
Locus_20229_Transcript_1/1_Conf_1.000	645	1	8.85E-05	EFO26655.1	42	51.2174	133	57	hypothetical protein LOAG_01835
Locus_2023_Transcript_1/1_Conf_1.000	583	0							
Locus_20230_Transcript_1/1_Conf_1.000	194	0							
Locus_20231_Transcript_1/1_Conf_1.000	161	0							
Locus_20232_Transcript_1/1_Conf_1.000	179	0							
Locus_20233_Transcript_1/1_Conf_1.000	206	20	6.41E-09	XP_001745498.1	76	63.929	56	43	hypothetical protein
Locus_20234_Transcript_1/1_Conf_1.000	323	0							
Locus_20235_Transcript_1/1_Conf_1.000	165	0							
Locus_20236_Transcript_1/1_Conf_1.000	166	20	1.93E-21	XP_002644000.1	100	105.531	55	55	C. briggsae CBR-IFA-1 protein
Locus_20237_Transcript_1/1_Conf_1.000	176	0							
Locus_20238_Transcript_1/1_Conf_1.000	268	0							
Locus_20239_Transcript_1/1_Conf_1.000	645	20	2.01E-49	NP_505419.3	70	199.519	210	147	hypothetical protein K07B1.7

Locus_2024_Transcript_1/1_Conf_1.000	1841	20	5.40E-109	XP_002639032.1	57	399.823	606	349	Hypothetical protein CBG22281
Locus_20240_Transcript_1/1_Conf_1.000	297	20	5.24E-27	NP_504827.2	84	124.02	85	72	hypothetical protein F09G2.1
Locus_20241_Transcript_1/1_Conf_1.000	132	0							
Locus_20242_Transcript_1/1_Conf_1.000	276	20	2.85E-17	AAN61521.1	65	91.6633	92	60	301KDa_2 protein
Locus_20243_Transcript_1/1_Conf_1.000	367	0							
Locus_20244_Transcript_1/1_Conf_1.000	312	0							
Locus_20245_Transcript_1/1_Conf_1.000	370	20	1.26E-44	XP_002826560.1	100	182.57	93	93	PREDICTED: protein FAM96B-like
Locus_20246_Transcript_1/1_Conf_1.000	230	20	5.11E-22	NP_569731.2	100	107.457	52	52	putative NPIP-like protein KIAA0220-like
Locus_20247_Transcript_1/1_Conf_1.000	312	0							
Locus_20248_Transcript_1/1_Conf_1.000	257	0							
Locus_20249_Transcript_1/1_Conf_1.000	198	0							
Locus_2025_Transcript_1/1_Conf_1.000	1513	20	3.20E-141	NP_740900.1	75	506.523	507	385	hypothetical protein T08G11.1
Locus_20250_Transcript_1/1_Conf_1.000	251	0							
Locus_20251_Transcript_1/1_Conf_1.000	280	20	1.45E-29	XP_002634888.1	80	132.494	88	71	Hypothetical protein CBG10559
Locus_20252_Transcript_1/1_Conf_1.000	200	20	9.62E-13	XP_001900297.1	75	76.6406	65	49	Importin-beta N-terminal domain containing protein
Locus_20253_Transcript_1/1_Conf_1.000	228	0							
Locus_20254_Transcript_1/1_Conf_1.000	234	0							
Locus_20255_Transcript_1/1_Conf_1.000	520	4	9.14E-36	XP_002631027.1	70	153.295	172	121	Hypothetical protein CBG02784
Locus_20256_Transcript_1/1_Conf_1.000	156	20	5.48E-16	AAV41897.1	92	87.4261	52	48	SAX-2
Locus_20257_Transcript_1/1_Conf_1.000	187	0							
Locus_20258_Transcript_1/1_Conf_1.000	280	20	8.53E-22	NP_001041277.1	81	106.686	69	56	hypothetical protein PDB1.1
Locus_20259_Transcript_1/1_Conf_1.000	262	0							
Locus_2026_Transcript_1/1_Conf_1.000	567	0							
Locus_20260_Transcript_1/1_Conf_1.000	467	5	3.79E-17	XP_001892434.1	58	91.2781	111	65	hypothetical protein Bm1_04780
Locus_20261_Transcript_1/1_Conf_1.000	269	0							

Locus_20262_Transcript_1/1_Conf_1.000	602	10	1.39E-19	EFO17301.1	56	100.138	192	108	hypothetical protein LOAG_11198
Locus_20263_Transcript_1/1_Conf_1.000	223	0							
Locus_20264_Transcript_1/1_Conf_1.000	154	5	1.95E-13	EFO27571.1	76	78.9518	51	39	hypothetical protein LOAG_00907
Locus_20265_Transcript_1/1_Conf_1.000	790	5	2.70E-13	XP_002640068.1	53	80.1073	163	88	Hypothetical protein CBG12552
Locus_20266_Transcript_1/1_Conf_1.000	143	20	3.35E-18	NP_505810.2	95	94.7449	47	45	P21-Activated Kinase family member (pak-2)
Locus_20267_Transcript_1/1_Conf_1.000	410	3	3.39E-10	NP_741003.1	95	68.1662	41	39	hypothetical protein C18A3.4
Locus_20268_Transcript_1/1_Conf_1.000	220	0							
Locus_20269_Transcript_1/1_Conf_1.000	202	0							
Locus_2027_Transcript_1/1_Conf_1.000	1071	3	3.24E-11	NP_497269.1	43	73.9442	230	100	bZIP transcription factor family member (zip-2)
Locus_20270_Transcript_1/1_Conf_1.000	275	0							
Locus_20271_Transcript_1/1_Conf_1.000	226	20	2.30E-22	XP_002640668.1	95	108.612	60	57	C. briggsae CBR-UNC-54 protein
Locus_20272_Transcript_1/1_Conf_1.000	283	20	1.40E-27	NP_497791.1	83	125.946	93	78	NITrilase family member (nit-1)
Locus_20273_Transcript_1/1_Conf_1.000	183	16	5.70E-29	XP_002342629.1	100	130.568	61	61	PREDICTED: hypothetical protein XP_002342629
Locus_20274_Transcript_1/1_Conf_1.000	206	0							
Locus_20275_Transcript_1/1_Conf_1.000	129	0							
Locus_20276_Transcript_1/1_Conf_1.000	213	0							
Locus_20277_Transcript_1/1_Conf_1.000	336	4	7.25E-13	ACM46022.1	62	77.0258	102	64	Troponin t protein 3, isoform d
Locus_20278_Transcript_1/1_Conf_1.000	517	0							

Locus_20279_Transcript_1/1_Conf_1.000	159	0							
Locus_2028_Transcript_1/1_Conf_1.000	881	20	3.98E-136	A8X7H5.2	89	488.419	279	250	Adenylosuccinate synthetase
Locus_20280_Transcript_1/1_Conf_1.000	266	1	3.92E-06	XP_002641855.1	56	54.6842	89	50	Hypothetical protein CBG16529
Locus_20281_Transcript_1/1_Conf_1.000	311	20	9.11E-24	XP_002640257.1	74	113.235	101	75	Hypothetical protein CBG12782
Locus_20282_Transcript_1/1_Conf_1.000	471	20	5.96E-31	NP_001022174.1	68	137.117	129	88	hypothetical protein F45E10.2
Locus_20283_Transcript_1/1_Conf_1.000	610	20	3.65E-55	EFO26301.1	62	218.394	235	148	transcriptional enhancer factor TEF-3
Locus_20284_Transcript_1/1_Conf_1.000	429	20	7.76E-39	XP_002636280.1	78	163.31	128	100	Hypothetical protein CBG08570
Locus_20285_Transcript_1/1_Conf_1.000	294	20	2.69E-39	XP_002632893.1	88	164.851	98	87	Hypothetical protein CBG15101
Locus_20286_Transcript_1/1_Conf_1.000	472	4	2.49E-45	NP_495471.1	78	184.882	144	113	hypothetical protein F10E7.6
Locus_20287_Transcript_1/1_Conf_1.000	584	0							
Locus_20288_Transcript_1/1_Conf_1.000	311	20	7.20E-29	EFO24438.1	78	130.183	102	80	hypothetical protein LOAG_04046
Locus_20289_Transcript_1/1_Conf_1.000	156	0							
Locus_2029_Transcript_1/4_Conf_0.250	534	0							
Locus_2029_Transcript_2/4_Conf_0.250	576	0							
Locus_2029_Transcript_3/4_Conf_0.375	1644	20	0	NP_505657.1	95	692.575	394	377	ARp2/3 compleX component family member (arx-2)

Locus_2029_Transcript_4/4_Conf_0.375	1644	20	0	NP_505657.1	95	694.886	394	377	ARp2/3 compleX component family member (arx-2)
Locus_20290_Transcript_1/1_Conf_1.000	277	0							
Locus_20291_Transcript_1/1_Conf_1.000	401	2	6.91E-11	NP_495928.2	52	70.4774	136	71	hypothetical protein F37B12.3
Locus_20292_Transcript_1/1_Conf_1.000	222	20	7.94E-23	XP_002639618.1	80	110.153	71	57	Hypothetical protein CBG12331
Locus_20293_Transcript_1/1_Conf_1.000	144	0							
Locus_20294_Transcript_1/1_Conf_1.000	229	20	7.38E-21	XP_002811972.1	100	103.605	51	51	PREDICTED: small nuclear ribonucleoprotein G-like isoform 1
Locus_20295_Transcript_1/1_Conf_1.000	373	0							
Locus_20296_Transcript_1/1_Conf_1.000	132	0							
Locus_20297_Transcript_1/1_Conf_1.000	349	20	2.07E-23	EFO20853.1	64	112.079	119	77	aldehyde dehydrogenase 4
Locus_20298_Transcript_1/1_Conf_1.000	210	20	6.32E-33	XP_002800695.1	100	143.665	70	70	PREDICTED: protein disulfide-isomerase-like
Locus_20299_Transcript_1/1_Conf_1.000	243	9	5.21E-11	XP_002636805.1	72	70.8626	81	59	C. briggsae CBR-TTN-1 protein
Locus_203_Transcript_1/1_Conf_1.000	557	5	2.72E-05	XP_002646659.1	49	52.373	85	42	C. briggsae CBR-NURF-1 protein
Locus_2030_Transcript_1/3_Conf_0.500	736	20	5.28E-106	NP_509854.1	90	387.882	230	208	hypothetical protein W04G3.5

Locus_2030_Transcript_2/3_Conf_0.667	2018	20	5.24E-137	NP_509854.1	95	493.041	286	273	hypothetical protein W04G3.5
Locus_2030_Transcript_3/3_Conf_0.667	1622	20	4.83E-167	NP_509854.1	94	592.423	350	330	hypothetical protein W04G3.5
Locus_20300_Transcript_1/1_Conf_1.000	171	0							
Locus_20301_Transcript_1/1_Conf_1.000	140	0							
Locus_20302_Transcript_1/1_Conf_1.000	288	0							
Locus_20303_Transcript_1/1_Conf_1.000	570	4	1.92E-41	NP_741200.1	65	172.555	190	124	DIsplaced Gonad family member (dig-1)
Locus_20304_Transcript_1/1_Conf_1.000	250	20	1.71E-30	XP_002424532.1	89	135.576	83	74	GTP-binding protein Di-Ras2, putative
Locus_20305_Transcript_1/1_Conf_1.000	588	5	1.49E-39	NP_001024333.1	62	166.392	206	128	Olfactory LeaRNing defective family member (olrn-1)
Locus_20306_Transcript_1/1_Conf_1.000	169	0							
Locus_20307_Transcript_1/1_Conf_1.000	408	4	6.78E-35	NP_490772.2	77	150.214	136	105	hypothetical protein Y18H1A.3
Locus_20308_Transcript_1/1_Conf_1.000	143	0							
Locus_20309_Transcript_1/1_Conf_1.000	400	4	3.43E-10	XP_002647225.1	52	68.1662	131	69	Hypothetical protein CBG23815
Locus_2031_Transcript_1/2_Conf_1.000	1332	20	1.45E-86	XP_414473.2	69	324.709	312	217	PREDICTED: similar to multiple ankyrin repeats single KH domain protein
Locus_2031_Transcript_2/2_Conf_1.000	1332	20	1.45E-86	XP_414473.2	69	324.709	312	217	PREDICTED: similar to multiple ankyrin repeats single KH domain protein
Locus_20310_Transcript_1/1_Conf_1.000	138	0							
Locus_20311_Transcript_1/1_Conf_1.000	377	19	2.34E-43	XP_002338056.1	100	144.821	67	67	predicted protein
Locus_20312_Transcript_1/1_Conf_1.000	331	20	3.47E-47	XP_002637345.1	90	191.045	109	99	C. briggsae CBR-UNC-68 protein
Locus_20313_Transcript_1/1_Conf_1.000	397	0							
Locus_20314_Transcript_1/1_Conf_1.000	405	20	9.47E-45	NP_503758.4	79	182.956	134	106	KETtiN (Drosophila actin-binding) homolog family member (ketn-1)

Locus_20315_Transcript_1/1_Conf_1.000	137	1	3.26E-13	EAW60097.1	100	78.1814	36	36	myosin, heavy polypeptide 9, non-muscle, isoform CRA_b
Locus_20316_Transcript_1/1_Conf_1.000	377	9	6.89E-19	XP_002638736.1	68	97.0561	97	66	C. briggsae CBR-EGO-1 protein
Locus_20317_Transcript_1/1_Conf_1.000	231	3	9.31E-16	NP_496235.2	78	86.6557	78	61	Zinc finger Transcription Factor family member (ztf-27)
Locus_20318_Transcript_1/1_Conf_1.000	487	0							
Locus_20319_Transcript_1/1_Conf_1.000	164	20	4.16E-24	XP_002917683.1	100	114.39	54	54	PREDICTED: LOW QUALITY PROTEIN: dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1-like
Locus_2032_Transcript_1/2_Conf_1.000	994	20	1.80E-21	XP_002642942.1	46	107.842	283	132	Hypothetical protein CBG15220
Locus_2032_Transcript_2/2_Conf_1.000	985	20	1.04E-21	XP_002642942.1	46	108.612	283	131	Hypothetical protein CBG15220
Locus_20320_Transcript_1/1_Conf_1.000	404	0							
Locus_20321_Transcript_1/1_Conf_1.000	312	0							
Locus_20322_Transcript_1/1_Conf_1.000	342	0							
Locus_20323_Transcript_1/1_Conf_1.000	406	4	6.20E-12	NP_001021074.1	54	73.9442	133	73	Aboc, EXpulsion defective family member (aex-1)
Locus_20324_Transcript_1/1_Conf_1.000	312	20	7.44E-29	NP_493968.1	78	130.183	103	81	hypothetical protein Y51H7C.9
Locus_20325_Transcript_1/1_Conf_1.000	164	1	8.71E-06	XP_002639187.1	73	53.5286	38	28	Hypothetical protein CBG03729

Locus_20326_Transcript_1/1_Conf_1.000	404	20	3.26E-53	ADL62853.1	88	211.075	134	119	thioredoxin reductase 2
Locus_20327_Transcript_1/1_Conf_1.000	189	0							
Locus_20328_Transcript_1/1_Conf_1.000	313	5	7.20E-24	ABS50363.1	86	113.62	94	81	LIM domain protein variant
Locus_20329_Transcript_1/1_Conf_1.000	245	0							
Locus_2033_Transcript_1/1_Conf_1.000	581	20	6.90E-58	P51535.1	84	227.254	154	130	Myoglobin
Locus_20330_Transcript_1/1_Conf_1.000	146	0							
Locus_20331_Transcript_1/1_Conf_1.000	269	0							
Locus_20332_Transcript_1/1_Conf_1.000	156	8	4.35E-05	XP_002634715.1	65	51.2174	47	31	Hypothetical protein CBG24051
Locus_20333_Transcript_1/1_Conf_1.000	344	0							
Locus_20334_Transcript_1/1_Conf_1.000	344	20	1.55E-26	XP_002630719.1	82	122.479	80	66	C. briggsae CBR-DHS-5 protein
Locus_20335_Transcript_1/1_Conf_1.000	289	0							
Locus_20336_Transcript_1/1_Conf_1.000	258	4	9.69E-13	Q60V67.2	81	76.6406	49	40	Histone-H3-lysine-36 demethylase 1
Locus_20337_Transcript_1/1_Conf_1.000	299	16	2.52E-13	XP_002632937.1	71	78.5666	64	46	Hypothetical protein CBG21692
Locus_20338_Transcript_1/1_Conf_1.000	177	0							
Locus_20339_Transcript_1/1_Conf_1.000	294	20	2.52E-29	ACI49172.1	82	131.724	97	80	hypothetical protein Csp3_JD01.004

Locus_2034_Transcript_1/2_Conf_1.000	1859	20	0	XP_002631329.1	76	653.67	522	401	Hypothetical protein CBG03152
Locus_2034_Transcript_2/2_Conf_1.000	1734	20	2.64E-126	NP_495860.1	78	457.218	338	265	hypothetical protein K08F8.1
Locus_20340_Transcript_1/1_Conf_1.000	133	0							
Locus_20341_Transcript_1/1_Conf_1.000	152	0							
Locus_20342_Transcript_1/1_Conf_1.000	438	3	1.39E-64	NP_495881.2	86	248.825	145	126	hypothetical protein F46C5.2
Locus_20343_Transcript_1/1_Conf_1.000	230	14	5.68E-05	XP_002577435.1	64	50.8322	64	41	nonsense-mediated mRNA decay protein 1 (rent1)
Locus_20344_Transcript_1/1_Conf_1.000	230	20	2.80E-28	XP_002645190.1	89	128.257	75	67	C. briggsae CBR-PPK-3 protein
Locus_20345_Transcript_1/1_Conf_1.000	232	6	7.63E-10	NP_001021653.1	59	67.0106	74	44	FANCI (Fanconi anemia complex component I) homolog family member (fnci-1)
Locus_20346_Transcript_1/1_Conf_1.000	164	0							
Locus_20347_Transcript_1/1_Conf_1.000	182	20	2.04E-18	NP_491138.2	90	95.5153	60	54	SULfate Permease family member (sulp-6)

Locus_20348_Transcript_1/1_Conf_1.000	180	20	2.66E-26	XP_002801767.1	100	121.709	60	60	PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1
Locus_20349_Transcript_1/1_Conf_1.000	272	5	1.80E-11	NP_493664.2	62	72.4034	89	56	hypothetical protein K10B4.3
Locus_2035_Transcript_1/1_Conf_1.000	1141	20	3.02E-103	NP_500218.2	76	379.793	362	277	Sex Peptide Receptor (Drosophila) Related family member (sprr-3)
Locus_20350_Transcript_1/1_Conf_1.000	151	0							
Locus_20351_Transcript_1/1_Conf_1.000	450	0							
Locus_20352_Transcript_1/1_Conf_1.000	160	0							
Locus_20353_Transcript_1/1_Conf_1.000	242	3	9.55E-05	EFO27722.1	56	50.0618	75	42	zinc finger protein
Locus_20354_Transcript_1/1_Conf_1.000	156	0							
Locus_20355_Transcript_1/1_Conf_1.000	468	20	1.98E-50	XP_002632055.1	90	201.83	132	120	C. briggsae CBR-VAB-19 protein
Locus_20356_Transcript_1/1_Conf_1.000	855	20	3.94E-24	P41234.4	48	116.316	321	155	ATP-binding cassette sub-family A member 2

Locus_20357_Transcript_1/1_Conf_1.000	543	4	2.07E-07	NP_494349.1	48	59.3066	152	74	hypothetical protein F29A7.6
Locus_20358_Transcript_1/1_Conf_1.000	604	20	2.49E-08	XP_415310.2	41	62.7734	197	81	PREDICTED: similar to heavy neurofilament protein
Locus_20359_Transcript_1/1_Conf_1.000	178	2	2.04E-07	XP_001894688.1	75	58.9214	41	31	Protein-tyrosine phosphatase containing protein
Locus_2036_Transcript_1/1_Conf_1.000	1530	20	1.33E-126	NP_001041105.1	74	457.988	377	282	EGg Laying defective family member (egl-9)
Locus_20360_Transcript_1/1_Conf_1.000	517	20	9.86E-43	NP_492839.4	74	176.407	171	127	Leucine-rich repeats, Ras-like domain, Kinase family member (lrk-1)
Locus_20361_Transcript_1/1_Conf_1.000	420	4	2.15E-12	NP_504235.2	67	75.485	83	56	Drosophila SOS homolog family member (sos-1)
Locus_20362_Transcript_1/1_Conf_1.000	265	0							
Locus_20363_Transcript_1/1_Conf_1.000	114	0							
Locus_20364_Transcript_1/1_Conf_1.000	250	5	6.31E-17	NP_504166.2	73	90.5077	76	56	hypothetical protein H43I07.2

Locus_20365_Transcript_1/1_Conf_1.000	233	4	1.58E-23	NP_504708.1	80	112.464	80	64	hypothetical protein T25F10.3
Locus_20366_Transcript_1/1_Conf_1.000	183	0							
Locus_20367_Transcript_1/1_Conf_1.000	238	0							
Locus_20368_Transcript_1/1_Conf_1.000	418	0							
Locus_20369_Transcript_1/1_Conf_1.000	276	20	5.37E-16	XP_002637140.1	100	87.4261	43	43	C. briggsae CBR-CAT-4 protein
Locus_2037_Transcript_1/1_Conf_1.000	205	20	1.57E-15	NP_495222.2	85	85.8853	67	57	hypothetical protein F21H12.1
Locus_20370_Transcript_1/1_Conf_1.000	219	0							
Locus_20371_Transcript_1/1_Conf_1.000	155	0							
Locus_20372_Transcript_1/1_Conf_1.000	665	0							
Locus_20373_Transcript_1/1_Conf_1.000	130	20	2.59E-18	BAH14542.1	100	95.1301	43	43	unnamed protein product
Locus_20374_Transcript_1/1_Conf_1.000	399	3	1.76E-06	XP_002423450.1	44	55.8398	127	56	conserved hypothetical protein
Locus_20375_Transcript_1/1_Conf_1.000	303	3	3.06E-11	XP_002642310.1	80	71.633	41	33	Hypothetical protein CBG18302
Locus_20376_Transcript_1/1_Conf_1.000	558	20	2.21E-15	XP_001894167.1	53	85.8853	175	93	Rad9 family protein
Locus_20377_Transcript_1/1_Conf_1.000	382	20	2.94E-54	XP_002640633.1	89	214.542	125	112	C. briggsae CBR-CATP-1 protein
Locus_20378_Transcript_1/1_Conf_1.000	224	0							
Locus_20379_Transcript_1/1_Conf_1.000	169	1	1.63E-04	XP_002632056.1	61	49.2914	54	33	Hypothetical protein CBG20437
Locus_2038_Transcript_1/2_Conf_1.000	2132	9	2.76E-59	XP_002639052.1	50	234.958	542	276	C. briggsae CBR-PQN-59.2 protein
Locus_2038_Transcript_2/2_Conf_1.000	2123	9	2.74E-59	XP_002639052.1	50	234.958	542	276	C. briggsae CBR-PQN-59.2 protein
Locus_20380_Transcript_1/1_Conf_1.000	299	0							
Locus_20381_Transcript_1/1_Conf_1.000	203	0							
Locus_20382_Transcript_1/1_Conf_1.000	251	0							

Locus_20383_Transcript_1/1_Conf_1.000	1124	20	4.21E-166	AAC38987.1	89	588.571	369	329	P-glycoprotein
Locus_20384_Transcript_1/1_Conf_1.000	137	0							
Locus_20385_Transcript_1/1_Conf_1.000	396	20	5.10E-38	ACJ65168.1	98	160.614	75	74	Uncoordinated protein 68, isoform b, partially confirmed by transcript evidence
Locus_20386_Transcript_1/1_Conf_1.000	242	20	1.79E-19	XP_002637220.1	76	98.9821	77	59	Hypothetical protein CBG18886
Locus_20387_Transcript_1/1_Conf_1.000	501	0							
Locus_20388_Transcript_1/1_Conf_1.000	271	0							
Locus_20389_Transcript_1/1_Conf_1.000	299	0							
Locus_2039_Transcript_1/1_Conf_1.000	1598	20	1.38E-166	NP_500596.2	71	590.882	503	362	hypothetical protein F19C7.4
Locus_20390_Transcript_1/1_Conf_1.000	298	0							
Locus_20391_Transcript_1/1_Conf_1.000	160	0							
Locus_20392_Transcript_1/1_Conf_1.000	206	0							
Locus_20393_Transcript_1/1_Conf_1.000	203	20	7.36E-05	EFO21349.1	70	50.447	67	47	hypothetical protein LOAG_07141
Locus_20394_Transcript_1/1_Conf_1.000	330	20	1.28E-41	NP_495662.2	90	172.555	105	95	PaTChed family member (ptc-1)

Locus_20395_Transcript_1/1_Conf_1.000	427	20	1.43E-24	XP_002641664.1	62	115.931	143	90	Hypothetical protein CBG09992
Locus_20396_Transcript_1/1_Conf_1.000	425	20	1.21E-23	CAA90256.2	79	112.849	112	89	C. elegans protein F54C9.11, confirmed by transcript evidence
Locus_20397_Transcript_1/1_Conf_1.000	154	0							
Locus_20398_Transcript_1/1_Conf_1.000	889	4	5.31E-11	NP_499003.1	50	72.7886	184	92	hypothetical protein R107.5
Locus_20399_Transcript_1/1_Conf_1.000	226	0							
Locus_204_Transcript_1/1_Conf_1.000	3308	20	4.04E-15	NP_491244.1	37	88.9669	678	252	HoloCentric chromosome binding Protein family member (hcp-4)
Locus_2040_Transcript_1/1_Conf_1.000	1213	20	2.23E-99	XP_002635668.1	72	367.081	345	249	Hypothetical protein CBG21865
Locus_20400_Transcript_1/1_Conf_1.000	566	0							
Locus_20401_Transcript_1/1_Conf_1.000	508	0							
Locus_20402_Transcript_1/1_Conf_1.000	913	20	1.62E-10	NP_491784.1	45	71.2478	268	123	hypothetical protein T05E7.3
Locus_20403_Transcript_1/1_Conf_1.000	285	20	3.82E-17	XP_001896129.1	68	91.2781	98	67	Hypothetical 216.3 kDa protein R06F6.8 in chromosome II, putative
Locus_20404_Transcript_1/1_Conf_1.000	199	0							
Locus_20405_Transcript_1/1_Conf_1.000	189	0							
Locus_20406_Transcript_1/1_Conf_1.000	329	0							
Locus_20407_Transcript_1/1_Conf_1.000	497	5	3.36E-34	NP_001023038.1	79	147.902	166	132	EXCretory canal abnormal family member (exc-5)
Locus_20408_Transcript_1/1_Conf_1.000	146	3	4.71E-07	NP_498918.3	80	57.7658	40	32	hypothetical protein B0303.7
Locus_20409_Transcript_1/1_Conf_1.000	227	0							
Locus_2041_Transcript_1/1_Conf_1.000	1385	4	1.12E-20	EFO20584.1	62	105.916	127	79	hypothetical protein LOAG_07907
Locus_20410_Transcript_1/1_Conf_1.000	275	0							
Locus_20411_Transcript_1/1_Conf_1.000	242	1	9.86E-10	NP_502377.2	72	66.6254	54	39	hypothetical protein C25G4.3
Locus_20412_Transcript_1/1_Conf_1.000	306	0							

Locus_20413_Transcript_1/1_Conf_1.000	153	20	9.68E-21	XP_002761135.1	100	103.219	50	50	PREDICTED: proteasome subunit beta type-10-like
Locus_20414_Transcript_1/1_Conf_1.000	288	20	3.11E-27	NP_001129887.1	82	124.79	91	75	SEC(selenocysteine)-tRNA Synthase family member (secs-1)
Locus_20415_Transcript_1/1_Conf_1.000	361	20	1.56E-31	XP_002633437.1	78	139.043	119	93	C. briggsae CBR-UNC-22 protein
Locus_20416_Transcript_1/1_Conf_1.000	811	20	8.96E-52	XP_001892617.1	57	207.994	272	156	Protein kinase domain containing protein
Locus_20417_Transcript_1/1_Conf_1.000	420	9	6.92E-19	XP_002634184.1	57	97.0561	138	80	C. briggsae CBR-QUI-1 protein
Locus_20418_Transcript_1/1_Conf_1.000	340	20	1.01E-14	AAD31839.1	56	83.1889	97	55	AF132291_1ancylostoma-secreted protein 1 precursor
Locus_20419_Transcript_1/1_Conf_1.000	294	20	1.05E-51	BAG60276.1	100	206.068	98	98	unnamed protein product
Locus_2042_Transcript_1/1_Conf_1.000	988	20	1.12E-116	NP_497726.2	77	424.091	332	256	hypothetical protein M01F1.7
Locus_20420_Transcript_1/1_Conf_1.000	533	0							

Locus_20421_Transcript_1/1_Conf_1.000	419	20	4.94E-41	NP_499920.1	81	170.629	119	97	hypothetical protein T07A9.8
Locus_20422_Transcript_1/1_Conf_1.000	135	5	2.95E-14	NP_492521.1	95	81.6481	45	43	SynTrophiN family member (stn-1)
Locus_20423_Transcript_1/1_Conf_1.000	206	7	1.93E-05	EFO24901.1	61	52.373	47	29	hypothetical protein LOAG_03581
Locus_20424_Transcript_1/1_Conf_1.000	162	0							
Locus_20425_Transcript_1/1_Conf_1.000	139	20	1.19E-15	XP_002917678.1	100	86.2705	43	43	PREDICTED: protein transport protein Sec61 subunit alpha isoform 1-like
Locus_20426_Transcript_1/1_Conf_1.000	219	8	1.19E-10	XP_002630904.1	67	69.707	65	44	Hypothetical protein CBG02628
Locus_20427_Transcript_1/1_Conf_1.000	467	3	9.33E-16	XP_002641334.1	59	86.6557	126	75	C. briggsae CBR-HMT-1 protein
Locus_20428_Transcript_1/1_Conf_1.000	305	20	4.13E-16	XP_002643868.1	71	87.8113	81	58	Hypothetical protein CBG02104
Locus_20429_Transcript_1/1_Conf_1.000	307	0							
Locus_2043_Transcript_1/1_Conf_1.000	686	0							
Locus_20430_Transcript_1/1_Conf_1.000	286	5	1.65E-36	NP_740906.1	90	155.606	90	81	hypothetical protein F26E4.7
Locus_20431_Transcript_1/1_Conf_1.000	297	0							
Locus_20432_Transcript_1/1_Conf_1.000	135	20	3.49E-07	NP_491634.1	82	58.151	45	37	hypothetical protein M01E11.2

Locus_20433_Transcript_1/1_Conf_1.000	199	20	2.00E-26	CAB00098.2	92	122.094	66	61	C. elegans protein F57F5.1, confirmed by transcript evidence
Locus_20434_Transcript_1/1_Conf_1.000	290	20	5.87E-18	NP_001024053.1	56	93.9745	116	65	UNCoordinated family member (unc-70)
Locus_20435_Transcript_1/1_Conf_1.000	197	20	3.10E-19	XP_002629656.1	89	98.2117	57	51	Hypothetical protein CBG00863
Locus_20436_Transcript_1/2_Conf_1.000	448	20	1.57E-47	XP_002631186.1	75	192.2	150	113	C. briggsae CBR-UNC-53 protein
Locus_20436_Transcript_2/2_Conf_1.000	459	20	6.92E-48	XP_002631186.1	75	193.356	153	115	C. briggsae CBR-UNC-53 protein
Locus_20437_Transcript_1/1_Conf_1.000	162	2	4.18E-08	NP_505894.2	86	61.2326	37	32	hypothetical protein K03B8.6
Locus_20438_Transcript_1/1_Conf_1.000	447	20	9.87E-34	XP_001898089.1	69	146.362	148	103	uridine monophosphate kinase
Locus_20439_Transcript_1/1_Conf_1.000	169	1	6.20E-04	XP_001896579.1	75	47.3654	53	40	hypothetical protein Bm1_25600
Locus_2044_Transcript_1/1_Conf_1.000	1097	20	8.97E-73	XP_002639582.1	80	278.485	225	180	C. briggsae CBR-TRAP-1 protein
Locus_20440_Transcript_1/1_Conf_1.000	232	0							
Locus_20441_Transcript_1/1_Conf_1.000	870	4	1.00E-38	NP_508466.2	68	164.851	155	106	hypothetical protein H01M10.1
Locus_20442_Transcript_1/1_Conf_1.000	178	0							
Locus_20443_Transcript_1/1_Conf_1.000	152	0							
Locus_20444_Transcript_1/1_Conf_1.000	225	0							
Locus_20445_Transcript_1/1_Conf_1.000	399	0							
Locus_20446_Transcript_1/1_Conf_1.000	262	0							
Locus_20447_Transcript_1/1_Conf_1.000	363	20	1.56E-23	XP_001899525.1	65	112.464	126	83	C-terminal binding protein

Locus_20448_Transcript_1/1_Conf_1.000	790	20	4.24E-75	NP_498392.1	70	285.419	265	186	THO Complex (transcription factor/nuclear export) subunit family member (thoc-2)
Locus_20449_Transcript_1/1_Conf_1.000	252	2	9.11E-19	XP_002640627.1	74	96.6709	75	56	C. briggsae CBR-UNC-95 protein
Locus_2045_Transcript_1/2_Conf_1.000	2189	20	4.56E-142	NP_001024503.1	68	509.99	515	355	hypothetical protein C55B6.1
Locus_2045_Transcript_2/2_Conf_1.000	1601	20	2.23E-132	NP_001024503.1	69	477.248	470	326	hypothetical protein C55B6.1
Locus_20450_Transcript_1/1_Conf_1.000	186	0							
Locus_20451_Transcript_1/1_Conf_1.000	184	0							
Locus_20452_Transcript_1/1_Conf_1.000	146	0							
Locus_20453_Transcript_1/1_Conf_1.000	906	20	1.24E-79	NP_001122707.1	75	300.827	247	187	hypothetical protein K02D10.1
Locus_20454_Transcript_1/1_Conf_1.000	258	0							
Locus_20455_Transcript_1/1_Conf_1.000	227	0							
Locus_20456_Transcript_1/1_Conf_1.000	578	4	1.39E-10	NP_001129872.1	53	70.0922	143	76	hypothetical protein T23B5.3
Locus_20457_Transcript_1/1_Conf_1.000	487	0							
Locus_20458_Transcript_1/1_Conf_1.000	400	0							
Locus_20459_Transcript_1/1_Conf_1.000	155	0							
Locus_2046_Transcript_1/2_Conf_1.000	648	2	4.15E-10	ABB53347.1	42	68.9366	186	79	secreted protein 5 precursor
Locus_2046_Transcript_2/2_Conf_1.000	222	0							
Locus_20460_Transcript_1/1_Conf_1.000	517	0							
Locus_20461_Transcript_1/1_Conf_1.000	266	20	1.09E-40	NP_510020.2	88	169.474	88	78	hypothetical protein W03G11.3
Locus_20462_Transcript_1/1_Conf_1.000	173	0							
Locus_20463_Transcript_1/1_Conf_1.000	177	20	8.53E-22	AAV32848.1	91	106.686	59	54	egl-20
Locus_20464_Transcript_1/1_Conf_1.000	251	4	1.01E-06	NP_501580.3	60	56.6102	71	43	LiPoate Ligase family member (lpl-1)
Locus_20465_Transcript_1/1_Conf_1.000	439	4	1.35E-43	NP_510514.2	76	179.104	153	117	hypothetical protein R07D5.2

Locus_20466_Transcript_1/1_Conf_1.000	200	20	1.14E-13	XP_002639317.1	85	79.7221	49	42	C. briggsae CBR-ABT-2 protein
Locus_20467_Transcript_1/1_Conf_1.000	327	20	3.36E-58	NP_509585.1	100	227.639	108	108	Tubulin, Beta family member (tbb-4)
Locus_20468_Transcript_1/1_Conf_1.000	301	0							
Locus_20469_Transcript_1/1_Conf_1.000	159	20	1.18E-18	NP_491028.2	88	96.2857	52	46	abnormal cell LINeage family member (lin-17)
Locus_2047_Transcript_1/1_Conf_1.000	1489	20	0	XP_002638927.1	83	650.588	498	416	Hypothetical protein CBG22153
Locus_20470_Transcript_1/1_Conf_1.000	335	1	6.17E-04	XP_002638631.1	54	47.3654	97	53	Hypothetical protein CBG05684
Locus_20471_Transcript_1/1_Conf_1.000	428	7	7.34E-13	XP_002641828.1	50	77.0258	155	79	C. briggsae CBR-PRK-1 protein
Locus_20472_Transcript_1/1_Conf_1.000	163	4	7.61E-10	NP_001033357.2	82	67.0106	45	37	DAF-16/FOXO Controlled, germline Tumor affecting family member (dct-6)
Locus_20473_Transcript_1/1_Conf_1.000	157	0							
Locus_20474_Transcript_1/1_Conf_1.000	153	0							
Locus_20475_Transcript_1/1_Conf_1.000	271	20	1.74E-22	XP_002646294.1	78	108.997	89	70	C. briggsae CBR-RIC-19 protein
Locus_20476_Transcript_1/1_Conf_1.000	225	0							
Locus_20477_Transcript_1/1_Conf_1.000	210	0							

Locus_20478_Transcript_1/1_Conf_1.000	418	20	5.49E-24	NP_491115.1	64	114.005	137	89	hypothetical protein Y54E10A.6
Locus_20479_Transcript_1/1_Conf_1.000	302	0							
Locus_2048_Transcript_1/1_Conf_1.000	903	20	1.11E-96	NP_001122845.1	87	357.451	234	204	Protein Phosphatase 2A (Two A) Regulatory subunit family member (pptr-2)
Locus_20480_Transcript_1/1_Conf_1.000	148	0							
Locus_20481_Transcript_1/1_Conf_1.000	167	0							
Locus_20482_Transcript_1/1_Conf_1.000	162	0							
Locus_20483_Transcript_1/1_Conf_1.000	129	0							
Locus_20484_Transcript_1/1_Conf_1.000	357	2	1.90E-53	XP_002647011.1	94	211.846	104	98	Hypothetical protein CBG23797
Locus_20485_Transcript_1/1_Conf_1.000	345	0							
Locus_20486_Transcript_1/1_Conf_1.000	502	20	1.13E-77	XP_002637163.1	92	292.352	167	154	C. briggsae CBR-SQV-4 protein

Locus_20487_Transcript_1/1_Conf_1.000	141	20	2.25E-06	XP_002429811.1	76	55.4546	42	32	class A rhodopsin-like G-protein coupled receptor GPRfsh, putative
Locus_20488_Transcript_1/1_Conf_1.000	280	0							
Locus_20489_Transcript_1/1_Conf_1.000	167	0							
Locus_2049_Transcript_1/1_Conf_1.000	668	20	1.51E-111	XP_002640980.1	90	405.986	221	201	Hypothetical protein CBG11728
Locus_20490_Transcript_1/1_Conf_1.000	205	0							
Locus_20491_Transcript_1/1_Conf_1.000	207	20	2.67E-23	NP_496968.1	95	111.694	67	64	hypothetical protein Y48B6A.12
Locus_20492_Transcript_1/1_Conf_1.000	163	1	6.67E-06	XP_002643614.1	72	53.9138	43	31	C. briggsae CBR-SER-1 protein
Locus_20493_Transcript_1/1_Conf_1.000	639	20	1.58E-99	NP_510361.1	89	365.925	212	189	SYnthetic lethal with Mec family member (sym-4)
Locus_20494_Transcript_1/1_Conf_1.000	172	0							
Locus_20495_Transcript_1/1_Conf_1.000	137	0							
Locus_20496_Transcript_1/1_Conf_1.000	294	4	1.53E-18	NP_506256.3	67	95.9005	96	65	CaDHerin family member (cdh-6)
Locus_20497_Transcript_1/1_Conf_1.000	140	0							

Locus_20498_Transcript_1/1_Conf_1.000	396	0							
Locus_20499_Transcript_1/1_Conf_1.000	224	10	4.36E-21	NP_001129803.1	82	104.375	74	61	Leucyl tRNA Synthetase family member (lrs-2)
Locus_205_Transcript_1/1_Conf_1.000	762	20	4.09E-56	NP_496817.1	74	222.246	191	142	hypothetical protein Y48C3A.10
Locus_2050_Transcript_1/1_Conf_1.000	320	0							
Locus_20500_Transcript_1/1_Conf_1.000	230	2	3.56E-07	XP_001893874.1	75	58.151	52	39	Smr domain containing protein
Locus_20501_Transcript_1/1_Conf_1.000	614	20	4.26E-27	XP_002643092.1	62	125.176	211	132	Hypothetical protein CBG23016
Locus_20502_Transcript_1/1_Conf_1.000	484	20	2.04E-87	P13498.2	100	324.709	157	157	Cytochrome b-245 light chain
Locus_20503_Transcript_1/1_Conf_1.000	237	20	7.31E-21	ACI49169.1	78	103.605	76	60	hypothetical protein Csp3_JD01.001
Locus_20504_Transcript_1/1_Conf_1.000	270	0							
Locus_20505_Transcript_1/1_Conf_1.000	157	0							
Locus_20506_Transcript_1/1_Conf_1.000	211	20	1.79E-19	XP_001894872.1	79	98.9821	69	55	hypothetical protein Bm1_17075
Locus_20507_Transcript_1/1_Conf_1.000	194	5	1.49E-13	XP_002637665.1	77	79.337	57	44	C. briggsae CBR-APT-10 protein
Locus_20508_Transcript_1/1_Conf_1.000	133	5	1.98E-10	XP_001893497.1	92	68.9366	41	38	Viral A-type inclusion protein repeat containing protein
Locus_20509_Transcript_1/1_Conf_1.000	346	6	5.13E-22	CAD11605.1	79	107.457	115	91	metalloprotease

Locus_2051_Transcript_1/1_Conf_1.000	202	20	6.00E-15	XP_002637392.1	76	83.9593	67	51	Hypothetical protein CBG19099
Locus_20510_Transcript_1/1_Conf_1.000	551	20	6.85E-30	XP_001900782.1	62	134.035	144	90	mKIAA2025 protein
Locus_20511_Transcript_1/1_Conf_1.000	421	20	4.05E-27	NP_505989.1	72	124.405	140	102	SULfate Permease family member (sulp-4)
Locus_20512_Transcript_1/1_Conf_1.000	549	5	3.65E-15	XP_002633339.1	57	85.1149	110	63	Hypothetical protein CBG06078
Locus_20513_Transcript_1/1_Conf_1.000	367	20	2.17E-17	XP_002643252.1	78	92.0485	74	58	C. briggsae CBR-TRAP-2 protein
Locus_20514_Transcript_1/1_Conf_1.000	148	0							
Locus_20515_Transcript_1/1_Conf_1.000	792	20	1.53E-48	XP_002641022.1	86	197.208	119	103	C. briggsae CBR-GLRX-5 protein
Locus_20516_Transcript_1/1_Conf_1.000	432	20	3.55E-76	CAM84506.1	96	287.345	143	138	serine/threonine phosphatase
Locus_20517_Transcript_1/1_Conf_1.000	203	0							
Locus_20518_Transcript_1/1_Conf_1.000	269	20	3.50E-31	NP_502314.1	91	137.887	73	67	hypothetical protein F35G2.1
Locus_20519_Transcript_1/1_Conf_1.000	265	20	3.64E-28		83	127.872	89	74	myoblast city protein homolog

Locus_2052_Transcript_1/2_Conf_1.000	716	20	3.18E-20	XP_001896583.1	87	102.834	65	57	high mobility group protein
Locus_2052_Transcript_2/2_Conf_1.000	470	0							
Locus_20520_Transcript_1/1_Conf_1.000	204	20	2.28E-06	XP_002181319.1	65	55.4546	63	41	predicted protein
Locus_20521_Transcript_1/1_Conf_1.000	353	2	9.64E-05	EFO18076.1	64	50.0618	59	38	DNA-dependent RNA polymerase
Locus_20522_Transcript_1/1_Conf_1.000	327	20	4.87E-41	NP_492476.1	91	170.629	106	97	hypothetical protein F14B4.3
Locus_20523_Transcript_1/1_Conf_1.000	219	0							
Locus_20524_Transcript_1/1_Conf_1.000	145	0							
Locus_20525_Transcript_1/1_Conf_1.000	140	0							
Locus_20526_Transcript_1/1_Conf_1.000	135	0							
Locus_20527_Transcript_1/1_Conf_1.000	129	0							

Locus_20528_Transcript_1/1_Conf_1.000	414	20	3.00E-59	EFO21414.1	89	231.106	137	122	hypothetical protein LOAG_07072
Locus_20529_Transcript_1/1_Conf_1.000	220	0							
Locus_2053_Transcript_1/1_Conf_1.000	511	20	2.11E-18	XP_001893088.1	61	95.5153	112	69	Glutaredoxin family protein
Locus_20530_Transcript_1/1_Conf_1.000	137	20	6.57E-14	NP_492593.2	93	80.4925	45	42	hypothetical protein F26E4.3
Locus_20531_Transcript_1/1_Conf_1.000	282	0							
Locus_20532_Transcript_1/1_Conf_1.000	415	5	3.24E-21	XP_002630781.1	62	104.76	121	76	Hypothetical protein CBG02477
Locus_20533_Transcript_1/1_Conf_1.000	335	0							
Locus_20534_Transcript_1/1_Conf_1.000	130	0							
Locus_20535_Transcript_1/1_Conf_1.000	165	0							
Locus_20536_Transcript_1/1_Conf_1.000	197	20	9.30E-24	XP_001088441.2	100	113.235	55	55	PREDICTED: transcription elongation factor B polypeptide 2-like
Locus_20537_Transcript_1/1_Conf_1.000	219	0							
Locus_20538_Transcript_1/1_Conf_1.000	504	20	3.62E-47	XP_002633316.1	75	191.045	166	126	C. briggsae CBR-GTL-2 protein
Locus_20539_Transcript_1/1_Conf_1.000	193	0							
Locus_2054_Transcript_1/1_Conf_1.000	1193	7	1.03E-32	XP_002638536.1	45	145.591	430	197	C. briggsae CBR-NUM-1 protein
Locus_20540_Transcript_1/1_Conf_1.000	276	0							
Locus_20541_Transcript_1/1_Conf_1.000	174	0							
Locus_20542_Transcript_1/1_Conf_1.000	350	0							
Locus_20543_Transcript_1/1_Conf_1.000	685	9	3.45E-21	XP_002581843.1	55	105.916	161	90	hypothetical protein

Locus_20544_Transcript_1/1_Conf_1.000	291	20	1.81E-43	NP_496205.2	93	178.718	96	90	PhosphoLipase C family member (plc-3)
Locus_20545_Transcript_1/1_Conf_1.000	273	20	2.18E-25	XP_002638629.1	77	118.627	88	68	C. briggsae CBR-TWK-33 protein
Locus_20546_Transcript_1/1_Conf_1.000	130	0							
Locus_20547_Transcript_1/1_Conf_1.000	204	0							
Locus_20548_Transcript_1/1_Conf_1.000	167	4	1.29E-09	XP_002641345.1	76	66.2402	55	42	Hypothetical protein CBG13198
Locus_20549_Transcript_1/1_Conf_1.000	228	1	7.15E-16	BAG59555.1	100	87.0409	38	38	unnamed protein product
Locus_2055_Transcript_1/1_Conf_1.000	2231	20	7.19E-151	EFO27499.1	75	539.265	473	357	hypothetical protein LOAG_00977
Locus_20550_Transcript_1/1_Conf_1.000	158	0							
Locus_20551_Transcript_1/1_Conf_1.000	225	0							
Locus_20552_Transcript_1/1_Conf_1.000	271	12	2.98E-06	XP_002660579.1	54	55.0694	86	47	PREDICTED: hypothetical protein
Locus_20553_Transcript_1/1_Conf_1.000	247	1	5.03E-06	NP_495345.1	61	54.299	78	48	hypothetical protein F54H5.3
Locus_20554_Transcript_1/1_Conf_1.000	148	0							

Locus_20555_Transcript_1/1_Conf_1.000	346	20	7.89E-31	XP_002635068.1	78	136.732	89	70	C. briggsae CBR-MOM-2 protein
Locus_20556_Transcript_1/1_Conf_1.000	239	3	2.44E-08	NP_001129867.1	69	62.003	72	50	hypothetical protein T05E11.2
Locus_20557_Transcript_1/1_Conf_1.000	373	5	1.27E-04	ZP_02210846.1	40	49.6766	100	40	hypothetical protein CLOBAR_00414
Locus_20558_Transcript_1/1_Conf_1.000	294	20	3.51E-39	NP_496448.1	87	164.466	98	86	hypothetical protein W02B12.10
Locus_20559_Transcript_1/1_Conf_1.000	207	2	1.13E-05	XP_001900715.1	57	53.1434	69	40	hypothetical protein
Locus_2056_Transcript_1/1_Conf_1.000	435	17	1.97E-10	XP_001900570.1	64	68.9366	85	55	ThiS family protein
Locus_20560_Transcript_1/1_Conf_1.000	380	2	4.44E-26	NP_496074.2	74	120.939	109	81	hypothetical protein ZK1307.7
Locus_20561_Transcript_1/1_Conf_1.000	454	20	1.67E-41	XP_002642775.1	78	172.17	132	104	C. briggsae CBR-NEX-1 protein
Locus_20562_Transcript_1/1_Conf_1.000	168	0							
Locus_20563_Transcript_1/1_Conf_1.000	212	0							
Locus_20564_Transcript_1/1_Conf_1.000	222	20	7.81E-31	EAW91906.1	100	87.4261	39	39	hCG2008737
Locus_20565_Transcript_1/1_Conf_1.000	148	0							
Locus_20566_Transcript_1/1_Conf_1.000	137	0							
Locus_20567_Transcript_1/1_Conf_1.000	582	20	1.71E-88	CAR63545.1	91	328.946	196	179	putative Hsp90 protein
Locus_20568_Transcript_1/1_Conf_1.000	275	20	6.78E-35	XP_002644234.1	90	150.214	91	82	C. briggsae CBR-MIG-15 protein
Locus_20569_Transcript_1/1_Conf_1.000	280	0							
Locus_2057_Transcript_1/1_Conf_1.000	2326	20	9.20E-56	NP_001122456.1	49	223.402	500	245	Protein Phosphatase Four Regulatory subunit family member (ppfr-1)
Locus_20570_Transcript_1/1_Conf_1.000	266	20	3.08E-27	XP_002641517.1	82	124.79	88	73	Hypothetical protein CBG09813
Locus_20571_Transcript_1/1_Conf_1.000	324	20	4.74E-36	NP_491855.1	84	154.066	109	92	Nuclear Pore complex Protein family member (npp-12)

Locus_20572_Transcript_1/1_Conf_1.000	172	20	6.17E-12	XP_863776.1	83	73.9442	55	46	PREDICTED: similar to Poly [ADP-ribose] polymerase-1 (PARP-1) (ADPRT) (NAD(+) ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1) isoform 2
Locus_20573_Transcript_1/1_Conf_1.000	175	0							
Locus_20574_Transcript_1/1_Conf_1.000	343	0							
Locus_20575_Transcript_1/1_Conf_1.000	149	0							
Locus_20576_Transcript_1/1_Conf_1.000	182	16	2.04E-10	XP_002631174.1	71	68.9366	60	43	Hypothetical protein CBG02960
Locus_20577_Transcript_1/1_Conf_1.000	362	20	2.18E-25	XP_002642982.1	66	118.627	117	78	Hypothetical protein CBG15266
Locus_20578_Transcript_1/1_Conf_1.000	130	1	6.63E-06	NP_509023.1	88	53.9138	34	30	hypothetical protein C15H9.7
Locus_20579_Transcript_1/1_Conf_1.000	177	5	5.74E-10	NP_492476.1	75	67.3958	58	44	hypothetical protein F14B4.3
Locus_2058_Transcript_1/1_Conf_1.000	879	20	1.14E-74	XP_002647128.1	95	284.263	163	155	Hypothetical protein CBG23912
Locus_20580_Transcript_1/1_Conf_1.000	245	5	3.50E-07	XP_002636960.1	70	58.151	61	43	Hypothetical protein CBG09439
Locus_20581_Transcript_1/1_Conf_1.000	255	0							
Locus_20582_Transcript_1/1_Conf_1.000	211	0							
Locus_20583_Transcript_1/1_Conf_1.000	357	0							
Locus_20584_Transcript_1/1_Conf_1.000	261	20	1.88E-08	EFO16652.1	58	62.3882	68	40	hypothetical protein LOAG_11852
Locus_20585_Transcript_1/1_Conf_1.000	575	11	1.22E-51	NP_498645.1	86	206.453	192	167	MUscle Positioning family member (mup-4)
Locus_20586_Transcript_1/1_Conf_1.000	160	0							
Locus_20587_Transcript_1/1_Conf_1.000	196	0							
Locus_20588_Transcript_1/1_Conf_1.000	174	0							

Locus_20589_Transcript_1/1_Conf_1.000	270	18	1.99E-18	XP_002642615.1	59	95.5153	89	53	C. briggsae CBR-MUP-4 protein
Locus_2059_Transcript_1/1_Conf_1.000	559	5	5.82E-08	NP_001022759.1	53	61.2326	100	53	hypothetical protein T12D8.9
Locus_20590_Transcript_1/1_Conf_1.000	709								
Locus_20591_Transcript_1/1_Conf_1.000	260	0							
Locus_20592_Transcript_1/1_Conf_1.000	302	0							
Locus_20593_Transcript_1/1_Conf_1.000	178	0							
Locus_20594_Transcript_1/1_Conf_1.000	144	0							
Locus_20595_Transcript_1/1_Conf_1.000	149	0							
Locus_20596_Transcript_1/1_Conf_1.000	698	20	3.96E-28	XP_001899546.1	54	129.028	241	131	hypothetical protein
Locus_20597_Transcript_1/1_Conf_1.000	215	3	2.58E-10	XP_002632188.1	70	68.5514	70	49	C. briggsae CBR-SGCB-1 protein
Locus_20598_Transcript_1/1_Conf_1.000	274	19	2.35E-11	XP_002648597.1	63	72.0182	90	57	Hypothetical protein CBG24931
Locus_20599_Transcript_1/1_Conf_1.000	246	20	5.55E-13	NP_001041088.1	71	77.411	63	45	hypothetical protein C27A7.3
Locus_206_Transcript_1/5_Conf_0.450	391	14	1.61E-12	XP_002484510.1	64	75.8702	74	48	hypothetical protein TSTA_040370
Locus_206_Transcript_2/5_Conf_0.400	395	14	1.66E-12	XP_002484510.1	64	75.8702	74	48	hypothetical protein TSTA_040370
Locus_206_Transcript_3/5_Conf_0.650	446	12	1.67E-14	XP_002484510.1	64	75.8702	74	48	hypothetical protein TSTA_040370
Locus_206_Transcript_5/5_Conf_0.750	497	15	1.65E-14	XP_002484510.1	64	75.8702	74	48	hypothetical protein TSTA_040370
Locus_2060_Transcript_1/2_Conf_1.000	1414	0							
Locus_2060_Transcript_2/2_Conf_1.000	1393	0							
Locus_20600_Transcript_1/1_Conf_1.000	278	2	1.46E-13	NP_491385.2	59	79.337	89	53	hypothetical protein Y119C1B.9
Locus_20601_Transcript_1/1_Conf_1.000	132	0							
Locus_20602_Transcript_1/1_Conf_1.000	308	0							
Locus_20603_Transcript_1/1_Conf_1.000	223	11	7.67E-26	XP_002634505.1	90	120.168	74	67	Hypothetical protein CBG08295
Locus_20604_Transcript_1/1_Conf_1.000	180	19	1.08E-19	NP_001065270.1	100	99.7525	46	46	NADH dehydrogenase ubiquinone 1 beta subcomplex subunit 7
Locus_20605_Transcript_1/1_Conf_1.000	385	20	2.18E-33	XP_001893379.1	76	145.206	102	78	Malate/L-lactate dehydrogenase family protein
Locus_20606_Transcript_1/1_Conf_1.000	183	20	5.35E-19	AAD48989.1	86	97.4413	59	51	P-glycoprotein
Locus_20607_Transcript_1/1_Conf_1.000	527	0							
Locus_20608_Transcript_1/1_Conf_1.000	1108	20	1.08E-73	NP_509318.1	62	281.567	315	198	ADAM (disintegrin plus metalloprotease) family member (adm-4)
Locus_20609_Transcript_1/1_Conf_1.000	251	0							
Locus_2061_Transcript_1/1_Conf_1.000	527	1	2.53E-04	NP_001028814.1	41	48.9062	108	45	C4b-binding protein alpha chain precursor

Locus_20610_Transcript_1/1_Conf_1.000	192	0							
Locus_20611_Transcript_1/1_Conf_1.000	372	3	5.67E-13	NP_506162.1	62	77.411	97	61	abnormal cell LINeage family member (lin-25)
Locus_20612_Transcript_1/1_Conf_1.000	312	20	1.36E-30	CAR63696.1	92	135.961	77	71	putative Uncoordinated protein 23
Locus_20613_Transcript_1/1_Conf_1.000	532	20	6.61E-64	XP_002633391.1	83	246.899	161	135	Hypothetical protein CBG06150
Locus_20614_Transcript_1/1_Conf_1.000	146	0							
Locus_20615_Transcript_1/1_Conf_1.000	381	0							
Locus_20616_Transcript_1/1_Conf_1.000	287	0							
Locus_20617_Transcript_1/1_Conf_1.000	647	20	4.81E-35	XP_002633591.1	83	151.754	129	108	Hypothetical protein CBG05468
Locus_20618_Transcript_1/1_Conf_1.000	348	0							
Locus_20619_Transcript_1/1_Conf_1.000	228	0							
Locus_2062_Transcript_1/1_Conf_1.000	1630	20	1.52E-144	NP_498913.2	83	517.694	403	338	FLI-I (Drosophila flightless) homolog family member (fli-1)
Locus_20620_Transcript_1/1_Conf_1.000	159	0							
Locus_20621_Transcript_1/1_Conf_1.000	323	3	1.95E-05	XP_001892569.1	78	52.373	38	30	exonuclease family protein
Locus_20622_Transcript_1/1_Conf_1.000	443	3	4.66E-07	NP_501744.1	51	57.7658	100	51	SM Y trans-splicing-associated snRNA family member (sna-2)
Locus_20623_Transcript_1/1_Conf_1.000	186	20	2.09E-23	XP_002639867.1	95	112.079	62	59	Hypothetical protein CBG12222
Locus_20624_Transcript_1/1_Conf_1.000	204	0							
Locus_20625_Transcript_1/1_Conf_1.000	605	5	3.19E-80	NP_001123175.1	82	301.597	199	165	ImmunoGlobulin-like Cell adhesion Molecule family member (igcm-3)
Locus_20626_Transcript_1/1_Conf_1.000	144	0							
Locus_20627_Transcript_1/1_Conf_1.000	209	0							
Locus_20628_Transcript_1/1_Conf_1.000	149	20	1.90E-24	BAG64777.1	100	115.546	49	49	unnamed protein product
Locus_20629_Transcript_1/1_Conf_1.000	228	0							
Locus_2063_Transcript_1/1_Conf_1.000	859	20	1.39E-77	NP_491892.1	84	293.893	186	157	hypothetical protein F57B10.5

Locus_20630_Transcript_1/1_Conf_1.000	359	20	4.89E-17	XP_002633888.1	74	90.8929	66	49	Hypothetical protein CBG19950
Locus_20631_Transcript_1/1_Conf_1.000	293	20	7.64E-18	EFO13202.1	72	93.5893	93	67	hypothetical protein LOAG_15329
Locus_20632_Transcript_1/1_Conf_1.000	202	20	1.33E-30	XP_002922306.1	100	135.961	66	66	PREDICTED: triosephosphate isomerase-like, partial
Locus_20633_Transcript_1/1_Conf_1.000	179	0							
Locus_20634_Transcript_1/1_Conf_1.000	232	0							
Locus_20635_Transcript_1/1_Conf_1.000	184	20	7.23E-16	EFO27126.1	85	87.0409	61	52	hypothetical protein LOAG_01361
Locus_20636_Transcript_1/1_Conf_1.000	207	0							
Locus_20637_Transcript_1/1_Conf_1.000	396	20	1.49E-13	EFO22336.1	60	79.337	86	52	WW domain-containing protein
Locus_20638_Transcript_1/1_Conf_1.000	562	20	1.45E-38	XP_002641968.1	69	162.925	168	117	Hypothetical protein CBG16675
Locus_20639_Transcript_1/1_Conf_1.000	133	0							
Locus_2064_Transcript_1/1_Conf_1.000	597	20	1.12E-29	EFO20527.1	55	133.65	188	105	hypothetical protein LOAG_07962
Locus_20640_Transcript_1/1_Conf_1.000	256	0							
Locus_20641_Transcript_1/1_Conf_1.000	196	20	5.64E-21	XP_002639870.1	78	103.99	65	51	C. briggsae CBR-IRS-2 protein
Locus_20642_Transcript_1/1_Conf_1.000	155	20	1.14E-21	XP_002914618.1	100	106.301	51	51	PREDICTED: LOW QUALITY PROTEIN: eukaryotic translation initiation factor 3 subunit L-like
Locus_20643_Transcript_1/1_Conf_1.000	195	0							
Locus_20644_Transcript_1/1_Conf_1.000	143	0							

Locus_20645_Transcript_1/1_Conf_1.000	168	2	3.89E-06	XP_002639999.1	68	54.6842	45	31	Hypothetical protein CBG10829
Locus_20646_Transcript_1/1_Conf_1.000	152	0							
Locus_20647_Transcript_1/1_Conf_1.000	309	0							
Locus_20648_Transcript_1/1_Conf_1.000	151	0							
Locus_20649_Transcript_1/1_Conf_1.000	383	0							
Locus_2065_Transcript_1/1_Conf_1.000	1585	8	7.75E-45	XP_002635375.1	75	186.422	141	106	Hypothetical protein CBG00762
Locus_20650_Transcript_1/1_Conf_1.000	261	0							
Locus_20651_Transcript_1/1_Conf_1.000	753	0							
Locus_20652_Transcript_1/1_Conf_1.000	330	0							
Locus_20653_Transcript_1/1_Conf_1.000	283	0							
Locus_20654_Transcript_1/1_Conf_1.000	246	0							
Locus_20655_Transcript_1/1_Conf_1.000	302	20	1.05E-35	NP_001040798.1	87	152.91	100	87	PhosphoDiEsterase family member (pde-4)
Locus_20656_Transcript_1/1_Conf_1.000	408	0							
Locus_20657_Transcript_1/1_Conf_1.000	268	20	1.24E-36	NP_491915.2	89	155.992	89	80	hypothetical protein ZC581.9
Locus_20658_Transcript_1/1_Conf_1.000	121	0							
Locus_20659_Transcript_1/1_Conf_1.000	588	20	4.19E-34	AAK62032.1	61	148.288	206	127	metalloprotease 1 precursor
Locus_2066_Transcript_1/1_Conf_1.000	2578	0							
Locus_20660_Transcript_1/1_Conf_1.000	151	0							
Locus_20661_Transcript_1/1_Conf_1.000	471	20	3.26E-45	NP_508877.1	80	184.496	124	100	hypothetical protein T03G11.4
Locus_20662_Transcript_1/1_Conf_1.000	167	0							

Locus_20663_Transcript_1/1_Conf_1.000	221	6	9.78E-05	XP_001700925.1	65	50.0618	52	34	flagellar associated protein
Locus_20664_Transcript_1/1_Conf_1.000	204	5	3.40E-10	CAA10033.1	71	68.1662	66	47	DYS-1 protein
Locus_20665_Transcript_1/1_Conf_1.000	264	0							
Locus_20666_Transcript_1/1_Conf_1.000	150	0							
Locus_20667_Transcript_1/1_Conf_1.000	150	0							
Locus_20668_Transcript_1/1_Conf_1.000	208	20	7.53E-18	XP_002629821.1	77	93.5893	67	52	C. briggsae CBR-SQV-8 protein
Locus_20669_Transcript_1/1_Conf_1.000	154	0							
Locus_2067_Transcript_1/1_Conf_1.000	533	0							
Locus_20670_Transcript_1/2_Conf_1.000	631	2	1.37E-07	NP_496506.1	60	60.4622	151	91	hypothetical protein F13D12.8
Locus_20670_Transcript_2/2_Conf_1.000	367	0							
Locus_20671_Transcript_1/1_Conf_1.000	549	20	7.98E-79	CAH04706.3	79	296.59	183	146	C. elegans protein K04H4.2c, partially confirmed by transcript evidence
Locus_20672_Transcript_1/1_Conf_1.000	629	4	3.33E-06	NP_001022632.1	48	55.8398	174	85	Gamma-tubulin Interacting Protein family member (gip-1)

Locus_20673_Transcript_1/1_Conf_1.000	430	20	9.19E-32	NP_001021301.1	87	139.813	88	77	hypothetical protein C06A6.4
Locus_20674_Transcript_1/1_Conf_1.000	150	0							
Locus_20675_Transcript_1/1_Conf_1.000	195	0							
Locus_20676_Transcript_1/1_Conf_1.000	217	20	2.02E-23	XP_002632923.1	84	112.079	71	60	C. briggsae CBR-HIM-6 protein
Locus_20677_Transcript_1/1_Conf_1.000	168	0							
Locus_20678_Transcript_1/1_Conf_1.000	195	1	6.27E-04	XP_001512638.1	63	47.3654	60	38	PREDICTED: similar to phospholipase A2 receptor 1
Locus_20679_Transcript_1/1_Conf_1.000	218	20	2.17E-17	CAX65056.1	74	92.0485	67	50	C. elegans protein F25C8.3d, partially confirmed by transcript evidence
Locus_2068_Transcript_1/1_Conf_1.000	1176	20	1.50E-145	CAR63540.1	85	520.39	355	305	putative Uncharacterized GTP-binding protein
Locus_20680_Transcript_1/1_Conf_1.000	233	20	1.21E-23	NP_497616.1	88	112.849	76	67	hypothetical protein Y71H2AM.6
Locus_20681_Transcript_1/1_Conf_1.000	284	20	1.19E-18	XP_002083879.1	67	96.2857	90	61	GD13963
Locus_20682_Transcript_1/1_Conf_1.000	145	20	1.51E-13	NP_493616.1	89	79.337	47	42	hypothetical protein F33H2.5
Locus_20683_Transcript_1/1_Conf_1.000	131	0							
Locus_20684_Transcript_1/1_Conf_1.000	246	0							
Locus_20685_Transcript_1/1_Conf_1.000	208	0							
Locus_20686_Transcript_1/1_Conf_1.000	669	0							
Locus_20687_Transcript_1/1_Conf_1.000	165	0							
Locus_20688_Transcript_1/1_Conf_1.000	157	1	3.33E-05	XP_001895392.1	66	51.6026	51	34	hypothetical protein Bm1_19685

Locus_20689_Transcript_1/1_Conf_1.000	152	0							
Locus_2069_Transcript_1/1_Conf_1.000	462	20	2.81E-20	EFO21743.1	68	101.679	88	60	hypothetical protein LOAG_06744
Locus_20690_Transcript_1/1_Conf_1.000	268	20	6.63E-22	EFO20564.1	76	107.071	81	62	hypothetical protein LOAG_07924
Locus_20691_Transcript_1/1_Conf_1.000	327	7	2.88E-09	NP_498217.2	82	65.0846	46	38	abnormal embryonic PARtitioning of cytoplasm family member (par-3)
Locus_20692_Transcript_1/1_Conf_1.000	187	0							
Locus_20693_Transcript_1/1_Conf_1.000	253	20	2.32E-22	XP_002630114.1	77	108.612	84	65	C. briggsae CBR-PYR-1 protein
Locus_20694_Transcript_1/1_Conf_1.000	1111	0							
Locus_20695_Transcript_1/1_Conf_1.000	334	4	4.40E-18	NP_495032.1	68	94.3597	89	61	hypothetical protein F07F6.1
Locus_20696_Transcript_1/1_Conf_1.000	239	0							
Locus_20697_Transcript_1/1_Conf_1.000	135	9	1.08E-16	XP_002811006.1	100	89.7373	45	45	PREDICTED: LOW QUALITY PROTEIN: nuclease-sensitive element-binding protein 1-like
Locus_20698_Transcript_1/1_Conf_1.000	230	0							
Locus_20699_Transcript_1/1_Conf_1.000	272	0							
Locus_207_Transcript_10/20_Conf_1.000	183	0							
Locus_207_Transcript_11/20_Conf_0.125	786	19	4.57E-13	NP_508612.1	57	79.337	157	90	VITellogenin structural genes (yolk protein genes) family member (vit-4)
Locus_207_Transcript_12/20_Conf_0.125	786	19	2.05E-13	XP_002644391.1	56	80.4925	157	88	C. briggsae CBR-VIT-5 protein
Locus_207_Transcript_13/20_Conf_0.179	429	14	1.20E-15	NP_508612.1	67	86.2705	91	61	VITellogenin structural genes (yolk protein genes) family member (vit-4)
Locus_207_Transcript_14/20_Conf_0.054	151	0							
Locus_207_Transcript_15/20_Conf_0.161	821	14	3.17E-28	NP_508612.1	65	129.798	146	96	VITellogenin structural genes (yolk protein genes) family member (vit-4)

Locus_207_Transcript_16/20_Conf_0.161	863	19	1.62E-33	NP_508612.1	67	147.517	160	108	VITellogenin structural genes (yolk protein genes) family member (vit-4)
Locus_207_Transcript_17/20_Conf_0.196	678	19	3.14E-35	NP_508612.1	63	152.525	224	142	VITellogenin structural genes (yolk protein genes) family member (vit-4)
Locus_207_Transcript_18/20_Conf_0.107	228	5	7.41E-05	NP_509305.1	53	50.447	71	38	VITellogenin structural genes (yolk protein genes) family member (vit-1)
Locus_207_Transcript_19/20_Conf_0.107	228	14	1.22E-07	NP_001123117.1	60	59.6918	73	44	VITellogenin structural genes (yolk protein genes) family member (vit-2)
Locus_207_Transcript_20/20_Conf_0.196	636	14	2.63E-30	NP_508612.1	62	135.961	210	131	VITellogenin structural genes (yolk protein genes) family member (vit-4)
Locus_207_Transcript_7/20_Conf_1.000	183	0							
Locus_207_Transcript_8/20_Conf_1.000	229	0							
Locus_207_Transcript_9/20_Conf_1.000	229	0							
Locus_2070_Transcript_1/1_Conf_1.000	538	20	2.09E-65	XP_001894445.1	80	251.906	177	143	amine oxidase, flavin-containing family protein
Locus_20700_Transcript_1/1_Conf_1.000	258	0							
Locus_20701_Transcript_1/1_Conf_1.000	347	20	1.75E-46	NP_490776.2	93	188.734	103	96	hypothetical protein Y18H1A.9
Locus_20702_Transcript_1/1_Conf_1.000	546	0							
Locus_20703_Transcript_1/1_Conf_1.000	364	2	1.46E-05	NP_499886.1	47	52.7582	107	51	hypothetical protein R02D3.7
Locus_20704_Transcript_1/1_Conf_1.000	152	0							
Locus_20705_Transcript_1/2_Conf_1.000	472	0							
Locus_20705_Transcript_2/2_Conf_1.000	479	0							
Locus_20706_Transcript_1/1_Conf_1.000	409	20	3.14E-40	NP_495209.1	73	167.933	142	104	hypothetical protein R12C12.1
Locus_20707_Transcript_1/1_Conf_1.000	275	0							
Locus_20708_Transcript_1/1_Conf_1.000	129	0							
Locus_20709_Transcript_1/1_Conf_1.000	678	20	4.46E-98	XP_002640633.1	89	361.303	225	201	C. briggsae CBR-CATP-1 protein
Locus_2071_Transcript_1/2_Conf_1.000	1110	20	3.35E-91	XP_002634069.1	67	339.732	337	229	Hypothetical protein CBG01611
Locus_2071_Transcript_2/2_Conf_1.000	1103	20	1.10E-86	XP_002634069.1	70	324.709	298	209	Hypothetical protein CBG01611
Locus_20710_Transcript_1/1_Conf_1.000	204	20	3.87E-22	XP_002647042.1	88	107.842	61	54	Hypothetical protein CBG03560
Locus_20711_Transcript_1/1_Conf_1.000	416	1	8.56E-06	EFO19153.1	57	53.5286	107	61	hypothetical protein LOAG_09341
Locus_20712_Transcript_1/1_Conf_1.000	482	0							

Locus_20713_Transcript_1/1_Conf_1.000	772	0							
Locus_20714_Transcript_1/1_Conf_1.000	187	0							
Locus_20715_Transcript_1/1_Conf_1.000	227	0							
Locus_20716_Transcript_1/1_Conf_1.000	222	0							
Locus_20717_Transcript_1/1_Conf_1.000	333	0							
Locus_20718_Transcript_1/1_Conf_1.000	598	0							
Locus_20719_Transcript_1/1_Conf_1.000	144	0							
Locus_2072_Transcript_1/1_Conf_1.000	1126	20	1.02E-119	XP_002643477.1	84	434.491	300	252	Hypothetical protein CBG16139
Locus_20720_Transcript_1/1_Conf_1.000	788	17	3.62E-127	XP_002633468.1	93	458.373	261	244	C. briggsae CBR-LIN-24 protein
Locus_20721_Transcript_1/1_Conf_1.000	166	0							
Locus_20722_Transcript_1/1_Conf_1.000	439	20	1.82E-48	XP_002637101.1	75	195.282	144	109	Hypothetical protein CBG09600
Locus_20723_Transcript_1/1_Conf_1.000	133	0							
Locus_20724_Transcript_1/1_Conf_1.000	187	0							
Locus_20725_Transcript_1/1_Conf_1.000	231	2	1.82E-11	NP_498172.3	67	72.4034	85	57	hypothetical protein R02F2.2
Locus_20726_Transcript_1/1_Conf_1.000	196	2	5.67E-05	NP_495410.4	61	50.8322	62	38	hypothetical protein C44B7.11
Locus_20727_Transcript_1/1_Conf_1.000	246	20	2.24E-38	NP_497027.1	100	161.77	81	81	Masculinisation Of Germline family member (mog-4)
Locus_20728_Transcript_1/1_Conf_1.000	223	0							
Locus_20729_Transcript_1/2_Conf_1.000	444	0							
Locus_20729_Transcript_2/2_Conf_1.000	327	0							
Locus_2073_Transcript_1/1_Conf_1.000	3304	20	0	NP_498468.2	89	1436.4	930	836	yeast ISW (imitation SWI) homolog family member (isw-1)
Locus_20730_Transcript_1/1_Conf_1.000	186	0							
Locus_20731_Transcript_1/1_Conf_1.000	191	0							
Locus_20732_Transcript_1/1_Conf_1.000	340	4	4.68E-12	ACI49172.1	61	74.3294	112	69	hypothetical protein Csp3_JD01.004
Locus_20733_Transcript_1/2_Conf_1.000	386	0							
Locus_20733_Transcript_2/2_Conf_1.000	386	0							
Locus_20734_Transcript_1/1_Conf_1.000	327	0							
Locus_20735_Transcript_1/1_Conf_1.000	565	20	4.91E-26	NP_495451.1	64	121.324	129	83	High Incidence of Males (increased X chromosome loss) family member (him-14)
Locus_20736_Transcript_1/1_Conf_1.000	134	0							
Locus_20737_Transcript_1/1_Conf_1.000	405	0							

Locus_20738_Transcript_1/1_Conf_1.000	134	5	3.87E-06	NP_001024204.1	74	54.6842	43	32	TiTiN family member (ttn-1)
Locus_20739_Transcript_1/1_Conf_1.000	463	20	3.19E-48	EFO22683.1	77	194.512	153	119	STE/STE11/MEKK2 protein kinase
Locus_2074_Transcript_1/1_Conf_1.000	608	20	3.71E-68	NP_498858.2	91	261.536	157	143	hypothetical protein ZK353.1
Locus_20740_Transcript_1/1_Conf_1.000	205	0							
Locus_20741_Transcript_1/1_Conf_1.000	215	0							
Locus_20742_Transcript_1/1_Conf_1.000	189	0							
Locus_20743_Transcript_1/1_Conf_1.000	570	0							
Locus_20744_Transcript_1/1_Conf_1.000	409	20	1.19E-47	EFO19846.1	83	192.586	136	114	cleavage and polyadenylation specificity factor subunit 2
Locus_20745_Transcript_1/1_Conf_1.000	419	16	7.14E-40	XP_002640063.1	90	166.777	121	109	Hypothetical protein CBG12545
Locus_20746_Transcript_1/1_Conf_1.000	379	0							
Locus_20747_Transcript_1/1_Conf_1.000	209	0							
Locus_20748_Transcript_1/1_Conf_1.000	298	20	5.24E-27	XP_002629701.1	84	124.02	99	84	C. briggsae CBR-SEC-5 protein
Locus_20749_Transcript_1/1_Conf_1.000	248	0							
Locus_2075_Transcript_1/1_Conf_1.000	647	0							
Locus_20750_Transcript_1/1_Conf_1.000	236	0							
Locus_20751_Transcript_1/1_Conf_1.000	521	20	5.45E-89	XP_002630203.1	94	330.102	173	164	Hypothetical protein CBG00613
Locus_20752_Transcript_1/1_Conf_1.000	685	20	2.46E-35	NP_001023694.1	56	152.91	223	125	UDP-GlucuronosylTransferase family member (ugt-35)

Locus_20753_Transcript_1/1_Conf_1.000	355	20	5.80E-18	XP_002643945.1	90	93.9745	60	54	C. briggsae CBR-MIG-2 protein
Locus_20754_Transcript_1/1_Conf_1.000	161	0							
Locus_20755_Transcript_1/1_Conf_1.000	150	5	4.22E-16	CAN82657.1	100	87.8113	38	38	hypothetical protein
Locus_20756_Transcript_1/1_Conf_1.000	379	20	3.86E-46	XP_002632193.1	83	187.578	126	105	Hypothetical protein CBG07059
Locus_20757_Transcript_1/1_Conf_1.000	381	20	9.85E-26	NP_509122.1	78	119.783	95	75	hypothetical protein F38B6.4
Locus_20758_Transcript_1/1_Conf_1.000	209	0							
Locus_20759_Transcript_1/1_Conf_1.000	345	20	5.60E-61	XP_002807879.1	100	236.884	115	115	PREDICTED: LOW QUALITY PROTEIN: heterogeneous nuclear ribonucleoprotein L-like
Locus_2076_Transcript_1/1_Conf_1.000	530	5	2.50E-07	EFO26720.1	47	58.9214	184	87	hypothetical protein LOAG_01771
Locus_20760_Transcript_1/1_Conf_1.000	274	5	5.57E-21	NP_509311.1	70	103.99	95	67	DEGeneration of certain neurons family member (deg-1)
Locus_20761_Transcript_1/1_Conf_1.000	454	5	7.53E-18	EFO21092.1	71	93.5893	80	57	hypothetical protein LOAG_07396
Locus_20762_Transcript_1/1_Conf_1.000	970	20	3.65E-88	XP_002639255.1	69	329.331	325	226	C. briggsae CBR-OCRL-1 protein
Locus_20763_Transcript_1/1_Conf_1.000	181	20	1.79E-14	XP_002640378.1	85	82.4185	60	51	Hypothetical protein CBG20286

Locus_20764_Transcript_1/1_Conf_1.000	316	20	8.73E-38	XP_002644918.1	86	159.844	91	79	C. briggsae CBR-NHR-173 protein
Locus_20765_Transcript_1/1_Conf_1.000	423	4	5.65E-13	NP_493601.2	52	77.411	147	77	FERM domain (protein4.1-ezrin-radixin-moesin) family member (frm-1)
Locus_20766_Transcript_1/1_Conf_1.000	573	20	5.48E-52	AAS78778.1	81	207.608	144	117	thioredoxin
Locus_20767_Transcript_1/1_Conf_1.000	179	0							
Locus_20768_Transcript_1/1_Conf_1.000	435	4	6.14E-12	XP_001892264.1	58	73.9442	89	52	hypothetical protein Bm1_03880
Locus_20769_Transcript_1/1_Conf_1.000	244	0							
Locus_2077_Transcript_1/1_Conf_1.000	1141	20	4.66E-104	NP_001041026.1	81	382.489	296	240	hypothetical protein Y41E3.7
Locus_20770_Transcript_1/1_Conf_1.000	149	0							
Locus_20771_Transcript_1/1_Conf_1.000	186	0							
Locus_20772_Transcript_1/1_Conf_1.000	618	20	2.84E-26	EFO23582.1	54	122.479	192	104	hypothetical protein LOAG_04900
Locus_20773_Transcript_1/1_Conf_1.000	187	0							
Locus_20774_Transcript_1/1_Conf_1.000	135	0							
Locus_20775_Transcript_1/1_Conf_1.000	201	20	2.51E-29	XP_002726116.1	100	131.724	64	64	PREDICTED: ribosomal protein L8-like
Locus_20776_Transcript_1/1_Conf_1.000	304	4	4.56E-23	AAR30497.1	78	110.923	88	69	RhoGEF
Locus_20777_Transcript_1/1_Conf_1.000	604	20	1.83E-27	EFA05576.1	77	126.331	93	72	hypothetical protein TcasGA2_TC015765
Locus_20778_Transcript_1/1_Conf_1.000	246	3	4.68E-28	NP_492219.1	86	127.487	80	69	hypothetical protein K04G2.9
Locus_20779_Transcript_1/1_Conf_1.000	263	3	6.06E-07	XP_002647600.1	55	57.3806	83	46	Hypothetical protein CBG06690

Locus_2078_Transcript_1/1_Conf_1.000	3247	20	0	XP_002641511.1	93	1892.09	1065	998	C. briggsae CBR-CHC-1 protein
Locus_20780_Transcript_1/1_Conf_1.000	484	0							
Locus_20781_Transcript_1/1_Conf_1.000	473	20	2.59E-34	CAN99691.2	70	148.288	154	108	C. elegans protein F54B3.1b, partially confirmed by transcript evidence
Locus_20782_Transcript_1/1_Conf_1.000	264	20	1.14E-13	EFO26936.1	81	79.7221	58	47	DIX domain-containing protein
Locus_20783_Transcript_1/1_Conf_1.000	258	0							
Locus_20784_Transcript_1/1_Conf_1.000	238	0							
Locus_20785_Transcript_1/1_Conf_1.000	269	0							
Locus_20786_Transcript_1/1_Conf_1.000	312	20	9.43E-16	CAQ48388.2	86	86.6557	58	50	C. elegans protein C26H9A.1b, confirmed by transcript evidence
Locus_20787_Transcript_1/1_Conf_1.000	673	20	2.05E-63	NP_496845.1	70	246.128	226	159	hypothetical protein Y48E1B.2
Locus_20788_Transcript_1/1_Conf_1.000	259	0							
Locus_20789_Transcript_1/1_Conf_1.000	193	0							
Locus_2079_Transcript_1/5_Conf_0.417	658	20	2.34E-40	NP_491825.2	72	169.474	153	111	hypothetical protein F26B1.2
Locus_2079_Transcript_2/5_Conf_0.667	843	20	4.97E-52	XP_002640100.1	71	153.68	147	105	Hypothetical protein CBG12588
Locus_2079_Transcript_3/5_Conf_0.167	308	11	3.26E-13	NP_871833.1	72	78.1814	72	52	hypothetical protein F26B1.2
Locus_2079_Transcript_4/5_Conf_0.250	397	20	4.06E-19	XP_002640100.1	80	97.8265	78	63	Hypothetical protein CBG12588

Locus_2079_Transcript_5/5_Conf_0.500	713	20	2.74E-40	NP_491825.2	72	169.474	153	111	hypothetical protein F26B1.2
Locus_20790_Transcript_1/1_Conf_1.000	252	0							
Locus_20791_Transcript_1/1_Conf_1.000	351	0							
Locus_20792_Transcript_1/1_Conf_1.000	271	12	1.52E-26	ACI49247.1	78	122.479	89	70	hypothetical protein Csp3_JD06.013
Locus_20793_Transcript_1/1_Conf_1.000	675	3	9.61E-61	CAR63560.1	79	237.269	188	149	hypothetical protein
Locus_20794_Transcript_1/1_Conf_1.000	306	20	7.25E-21	XP_001629579.1	73	103.605	86	63	predicted protein
Locus_20795_Transcript_1/1_Conf_1.000	200	5	1.21E-15	NP_495375.3	74	86.2705	63	47	hypothetical protein T14B4.1
Locus_20796_Transcript_1/1_Conf_1.000	186	0							
Locus_20797_Transcript_1/1_Conf_1.000	252	20	1.00E-33	XP_002640129.1	93	146.362	83	78	C. briggsae CBR-SNT-4 protein
Locus_20798_Transcript_1/1_Conf_1.000	291	3	5.14E-06	NP_001122477.1	70	54.299	50	35	FERtilization defective (abnormal sperm) family member (fer-1)
Locus_20799_Transcript_1/1_Conf_1.000	139	0							
Locus_208_Transcript_1/1_Conf_1.000	455	20	1.07E-72	NP_508537.1	100	275.789	151	151	SPeCtrin family member (spc-1)
Locus_2080_Transcript_1/1_Conf_1.000	697	20	3.24E-30	XP_002646089.1	73	135.961	116	85	C. briggsae CBR-RSR-1 protein
Locus_20800_Transcript_1/1_Conf_1.000	136	4	5.21E-11	NP_498923.1	84	70.8626	44	37	hypothetical protein B0303.15
Locus_20801_Transcript_1/1_Conf_1.000	426	3	1.09E-32	XP_002631054.1	68	142.895	150	102	C. briggsae CBR-BTF-1 protein
Locus_20802_Transcript_1/1_Conf_1.000	416	20	5.89E-31	EFO16181.1	83	137.117	101	84	hypothetical protein LOAG_12327
Locus_20803_Transcript_1/1_Conf_1.000	478	20	2.11E-12	YP_003357881.1	52	75.485	154	81	DNA repair and recombination protein RadB
Locus_20804_Transcript_1/1_Conf_1.000	744	6	4.85E-30	XP_001897043.1	54	135.576	263	143	Dedicator of cytokinesis family protein
Locus_20805_Transcript_1/1_Conf_1.000	279	20	1.32E-22	NP_504644.1	71	109.383	89	64	ACyLtransferase-like family member (acl-9)

Locus_20806_Transcript_1/1_Conf_1.000	180	20	1.12E-24	EFO22809.1	96	116.316	60	58	hypothetical protein LOAG_05677
Locus_20807_Transcript_1/1_Conf_1.000	133	0							
Locus_20808_Transcript_1/1_Conf_1.000	394	20	4.22E-16	XP_002647917.1	61	87.8113	104	64	Hypothetical protein CBG23791
Locus_20809_Transcript_1/1_Conf_1.000	432	20	1.08E-24	NP_497756.2	65	116.316	126	82	hypothetical protein F34D10.2
Locus_2081_Transcript_1/1_Conf_1.000	804	0							
Locus_20810_Transcript_1/1_Conf_1.000	166	20	1.29E-25	BAG63585.1	100	119.398	55	55	unnamed protein product
Locus_20811_Transcript_1/1_Conf_1.000	348	0							
Locus_20812_Transcript_1/1_Conf_1.000	355	0							
Locus_20813_Transcript_1/1_Conf_1.000	218	0							
Locus_20814_Transcript_1/1_Conf_1.000	889	20	8.57E-86	XP_002638772.1	69	321.242	292	203	C. briggsae CBR-PTR-21 protein
Locus_20815_Transcript_1/1_Conf_1.000	194	20	1.89E-08	XP_001902614.1	78	62.3882	46	36	Elongation factor Tu GTP binding domain containing protein
Locus_20816_Transcript_1/1_Conf_1.000	130	9	5.79E-10	EFO27462.1	89	67.3958	37	33	hypothetical protein LOAG_01021
Locus_20817_Transcript_1/1_Conf_1.000	166	20	3.08E-11	ACI49172.1	70	71.633	54	38	hypothetical protein Csp3_JD01.004
Locus_20818_Transcript_1/1_Conf_1.000	447	0							
Locus_20819_Transcript_1/1_Conf_1.000	276	20	2.49E-21	XP_002631303.1	92	105.145	65	60	C. briggsae CBR-CLH-1 protein
Locus_2082_Transcript_1/2_Conf_1.000	831	0							

Locus_2082_Transcript_2/2_Conf_1.000	780	0							
Locus_20820_Transcript_1/1_Conf_1.000	155	0							
Locus_20821_Transcript_1/1_Conf_1.000	234	20	2.98E-14	XP_002633412.1	73	81.6481	73	54	Hypothetical protein CBG06177
Locus_20822_Transcript_1/1_Conf_1.000	178	0							
Locus_20823_Transcript_1/1_Conf_1.000	283	20	4.83E-28	EFO28229.1	77	127.487	94	73	hypothetical protein LOAG_00257
Locus_20824_Transcript_1/1_Conf_1.000	188	2	3.94E-30	BAC11651.1	98	134.42	60	59	unnamed protein product
Locus_20825_Transcript_1/1_Conf_1.000	132	0							
Locus_20826_Transcript_1/1_Conf_1.000	643	20	4.51E-102	A8X3A7.2	91	374.4	214	196	Integrin alpha pat-2
Locus_20827_Transcript_1/1_Conf_1.000	241	20	1.57E-23	XP_002643333.1	82	112.464	68	56	C. briggsae CBR-VAP-1 protein
Locus_20828_Transcript_1/1_Conf_1.000	131	0							
Locus_20829_Transcript_1/1_Conf_1.000	285	20	2.31E-30	NP_502582.2	81	135.191	95	77	hypothetical protein Y62E10A.13
Locus_2083_Transcript_1/3_Conf_0.714	1199	20	4.84E-123	XP_002635314.1	77	445.662	361	278	Hypothetical protein CBG01477

Locus_2083_Transcript_2/3_Conf_0.571	691	20	5.18E-73	XP_002635314.1	76	278.1	224	172	Hypothetical protein CBG01477
Locus_2083_Transcript_3/3_Conf_0.714	1199	20	4.84E-123	XP_002635314.1	77	445.662	361	278	Hypothetical protein CBG01477
Locus_20830_Transcript_1/1_Conf_1.000	230	2	1.18E-10	NP_740794.1	67	69.707	76	51	hypothetical protein Y51F10.10
Locus_20831_Transcript_1/1_Conf_1.000	187	0							
Locus_20832_Transcript_1/1_Conf_1.000	407	2	4.30E-05	XP_001898007.1	67	51.2174	53	36	Origin recognition complex subunit 5
Locus_20833_Transcript_1/1_Conf_1.000	185	0							
Locus_20834_Transcript_1/1_Conf_1.000	366	0							
Locus_20835_Transcript_1/1_Conf_1.000	152	0							
Locus_20836_Transcript_1/1_Conf_1.000	1263	20	0	EFO25412.1	95	653.67	378	360	hypothetical protein LOAG_03069
Locus_20837_Transcript_1/1_Conf_1.000	140	20	3.59E-12	NP_502549.2	85	74.7146	47	40	TransThyretin-Related family domain family member (ttr-51)
Locus_20838_Transcript_1/1_Conf_1.000	323	0							
Locus_20839_Transcript_1/1_Conf_1.000	427	20	5.95E-47	XP_002644986.1	87	190.274	113	99	C. briggsae CBR-TAG-320 protein
Locus_2084_Transcript_1/1_Conf_1.000	3760	20	0	NP_495221.1	60	741.88	1073	650	hypothetical protein F21H12.6
Locus_20840_Transcript_1/1_Conf_1.000	131	0							
Locus_20841_Transcript_1/1_Conf_1.000	165	0							
Locus_20842_Transcript_1/1_Conf_1.000	294	0							

Locus_20843_Transcript_1/1_Conf_1.000	202	5	1.58E-07	XP_002637497.1	68	59.3066	54	37	Hypothetical protein CBG19218
Locus_20844_Transcript_1/1_Conf_1.000	131	0							
Locus_20845_Transcript_1/1_Conf_1.000	204	4	6.39E-17	XP_002647777.1	85	90.5077	60	51	C. briggsae CBR-TSP-13 protein
Locus_20846_Transcript_1/1_Conf_1.000	455	0							
Locus_20847_Transcript_1/1_Conf_1.000	133	20	1.98E-10	NP_001129928.1	90	68.9366	43	39	CHoline Transporter-Like family member (chtl-1)
Locus_20848_Transcript_1/1_Conf_1.000	166	0							
Locus_20849_Transcript_1/1_Conf_1.000	142	0							
Locus_2085_Transcript_1/1_Conf_1.000	364	20	6.08E-44	NP_496492.1	86	180.259	121	105	hypothetical protein C47D12.2
Locus_20850_Transcript_1/1_Conf_1.000	268	0							
Locus_20851_Transcript_1/1_Conf_1.000	505	4	5.64E-16	NP_496906.2	55	87.4261	127	70	hypothetical protein Y51H1A.2
Locus_20852_Transcript_1/1_Conf_1.000	172	20	1.12E-21	NP_498528.1	94	106.301	53	50	Pim (mammalian oncogene) Related Kinase family member (prk-1)
Locus_20853_Transcript_1/1_Conf_1.000	239	2	1.69E-09	EFO24512.1	63	65.855	76	48	hypothetical protein LOAG_03972
Locus_20854_Transcript_1/1_Conf_1.000	346	2	4.35E-13	NP_506285.1	61	77.7962	111	68	hypothetical protein F57B1.5
Locus_20855_Transcript_1/1_Conf_1.000	287	0							
Locus_20856_Transcript_1/1_Conf_1.000	144	0							
Locus_20857_Transcript_1/1_Conf_1.000	206	20	3.07E-19	NP_500987.3	85	98.2117	68	58	hypothetical protein Y73B6BL.1
Locus_20858_Transcript_1/1_Conf_1.000	136	0							
Locus_20859_Transcript_1/1_Conf_1.000	173	0							
Locus_2086_Transcript_1/1_Conf_1.000	986	20	2.91E-40	NP_001171768.1	70	170.244	180	126	hypothetical protein LOC100376325
Locus_20860_Transcript_1/1_Conf_1.000	297	5	4.28E-37	XP_002643254.1	88	157.532	98	87	Hypothetical protein CBG08123
Locus_20861_Transcript_1/1_Conf_1.000	183	0							
Locus_20862_Transcript_1/1_Conf_1.000	236	2	3.41E-10	XP_002631009.1	63	68.1662	80	51	Hypothetical protein CBG02761

Locus_20863_Transcript_1/1_Conf_1.000	412	20	5.55E-21	XP_002636677.1	60	103.99	133	81	Hypothetical protein CBG23391
Locus_20864_Transcript_1/1_Conf_1.000	240	20	1.05E-27	XP_002639713.1	88	126.331	79	70	C. briggsae CBR-RAD-54 protein
Locus_20865_Transcript_1/1_Conf_1.000	144	0							
Locus_20866_Transcript_1/1_Conf_1.000	264	0							
Locus_20867_Transcript_1/1_Conf_1.000	188	0							
Locus_20868_Transcript_1/1_Conf_1.000	188	0							
Locus_20869_Transcript_1/1_Conf_1.000	277	2	1.85E-16	XP_002638587.1	67	88.9669	91	61	Hypothetical protein CBG05635
Locus_2087_Transcript_1/1_Conf_1.000	1131	20	2.61E-131	NP_001021405.1	90	473.011	292	263	asparagiNyl tRNA Synthetase family member (nrs-1)
Locus_20870_Transcript_1/2_Conf_1.000	519	20	2.26E-18	NP_001022032.1	55	95.5153	173	96	TRRAP-like (transcription/transformation domain-associated protein) family member (trr-1)
Locus_20870_Transcript_2/2_Conf_1.000	519	20	1.01E-18	EFO19589.1	50	96.6709	170	86	hypothetical protein LOAG_08898
Locus_20871_Transcript_1/1_Conf_1.000	151	0							
Locus_20872_Transcript_1/1_Conf_1.000	249	0							
Locus_20873_Transcript_1/1_Conf_1.000	214	0							
Locus_20874_Transcript_1/1_Conf_1.000	572	20	9.31E-12	EFO20177.1	55	73.9442	107	59	hypothetical protein LOAG_08313
Locus_20875_Transcript_1/1_Conf_1.000	414	20	1.07E-32	XP_002645073.1	90	142.895	71	64	C. briggsae CBR-ADT-2 protein
Locus_20876_Transcript_1/1_Conf_1.000	154	0							

Locus_20877_Transcript_1/1_Conf_1.000	313	0							
Locus_20878_Transcript_1/1_Conf_1.000	154	0							
Locus_20879_Transcript_1/1_Conf_1.000	290	6	2.15E-28	XP_002642067.1	94	128.642	67	63	Hypothetical protein CBG18006
Locus_2088_Transcript_1/2_Conf_1.000	2677	20	4.73E-35	XP_684510.2	43	154.836	718	313	PREDICTED: im:7150991
Locus_2088_Transcript_2/2_Conf_1.000	2317	20	4.00E-35	XP_684510.2	43	154.836	718	313	PREDICTED: im:7150991
Locus_20880_Transcript_1/1_Conf_1.000	284	0							
Locus_20881_Transcript_1/1_Conf_1.000	155	20	4.81E-12	XP_001893740.1	88	74.3294	45	40	ATP-dependent helicase DDX1
Locus_20882_Transcript_1/1_Conf_1.000	280	0							
Locus_20883_Transcript_1/1_Conf_1.000	425	5	1.59E-07	EFO27260.1	80	59.3066	41	33	RNA recognition domain-containing protein domain-containing protein
Locus_20884_Transcript_1/1_Conf_1.000	194	20	1.35E-22	P27442.1	90	109.383	64	58	GMP reductase
Locus_20885_Transcript_1/1_Conf_1.000	1807	20	6.28E-86	NP_495931.2	52	323.168	642	336	hypothetical protein T24B8.7
Locus_20886_Transcript_1/1_Conf_1.000	333	20	3.35E-42	ACY39994.1	92	174.481	95	88	C. elegans FLN-2 protein, isoform d
Locus_20887_Transcript_1/1_Conf_1.000	241	0							
Locus_20888_Transcript_1/1_Conf_1.000	175	5	1.51E-10	EFO21331.1	72	69.3218	58	42	expressed sequence
Locus_20889_Transcript_1/1_Conf_1.000	139	0							
Locus_2089_Transcript_1/4_Conf_0.667	842	9	8.79E-21	NP_510235.2	46	105.145	281	132	hypothetical protein C29F7.2
Locus_2089_Transcript_2/4_Conf_0.222	394	4	1.15E-13	NP_510234.1	54	79.7221	135	73	hypothetical protein C29F7.1
Locus_2089_Transcript_3/4_Conf_0.667	860	10	1.41E-21	XP_002645614.1	49	107.842	278	138	Hypothetical protein CBG05337

Locus_2089_Transcript_4/4_Conf_0.667	827	12	1.71E-21	XP_002645614.1	49	107.457	278	138	Hypothetical protein CBG05337
Locus_20890_Transcript_1/1_Conf_1.000	293	0							
Locus_20891_Transcript_1/1_Conf_1.000	139	1	1.12E-05	EDL24903.1	78	53.1434	37	29	mCG14133
Locus_20892_Transcript_1/1_Conf_1.000	198	0							
Locus_20893_Transcript_1/1_Conf_1.000	368	0							
Locus_20894_Transcript_1/1_Conf_1.000	381	20	5.21E-35	NP_499648.3	71	150.599	127	91	ELongator complex Protein Component family member (elpc-2)
Locus_20895_Transcript_1/1_Conf_1.000	719	0							
Locus_20896_Transcript_1/1_Conf_1.000	251	20	2.32E-11	EFO20608.1	62	72.0182	83	52	ran-binding protein 7
Locus_20897_Transcript_1/1_Conf_1.000	221	0							
Locus_20898_Transcript_1/1_Conf_1.000	147	0							
Locus_20899_Transcript_1/1_Conf_1.000	213	10	1.50E-34	NP_872018.1	100	149.058	70	70	Anion/Bicarbonate TranSporter family member (abts-3)
Locus_209_Transcript_1/1_Conf_1.000	1555	20	0	NP_490816.4	88	669.848	432	382	related to yeast Vacuolar Protein Sorting factor family member (vps-4)

Locus_2090_Transcript_1/1_Conf_1.000	583	5	7.81E-33	NP_509903.1	72	144.05	179	129	TweeTY transmembrane/cell surface protein Homolog family member (ttyh-1)
Locus_20900_Transcript_1/1_Conf_1.000	141	0							
Locus_20901_Transcript_1/1_Conf_1.000	789	0							
Locus_20902_Transcript_1/1_Conf_1.000	247	0							
Locus_20903_Transcript_1/1_Conf_1.000	181	20	2.66E-18	BAG61688.1	100	95.1301	46	46	unnamed protein product
Locus_20904_Transcript_1/1_Conf_1.000	422	0							
Locus_20905_Transcript_1/1_Conf_1.000	161	0							
Locus_20906_Transcript_1/1_Conf_1.000	131	0							
Locus_20907_Transcript_1/1_Conf_1.000	173	3	5.77E-10	XP_002639131.1	72	67.3958	58	42	Hypothetical protein CBG14951
Locus_20908_Transcript_1/1_Conf_1.000	458	20	6.93E-56	NP_508379.1	82	219.935	151	125	ACyLtransferase-like family member (acl-4)
Locus_20909_Transcript_1/1_Conf_1.000	305	0							
Locus_2091_Transcript_1/1_Conf_1.000	647	2	1.12E-07	XP_002634773.1	70	60.8474	57	40	Hypothetical protein CBG13872
Locus_20910_Transcript_1/1_Conf_1.000	155	20	6.29E-12	XP_002637345.1	82	73.9442	47	39	C. briggsae CBR-UNC-68 protein
Locus_20911_Transcript_1/1_Conf_1.000	505	20	2.69E-34	NP_504148.1	61	148.288	138	85	PHAryngeal gland Toxin-related family member (phat-5)
Locus_20912_Transcript_1/1_Conf_1.000	132	0							
Locus_20913_Transcript_1/1_Conf_1.000	205	0							
Locus_20914_Transcript_1/1_Conf_1.000	263	8	3.32E-13	XP_002638527.1	72	78.1814	87	63	C. briggsae CBR-UNC-80 protein
Locus_20915_Transcript_1/1_Conf_1.000	217	0							
Locus_20916_Transcript_1/1_Conf_1.000	136	0							
Locus_20917_Transcript_1/1_Conf_1.000	143	0							
Locus_20918_Transcript_1/1_Conf_1.000	313	0							
Locus_20919_Transcript_1/1_Conf_1.000	136	0							
Locus_2092_Transcript_1/1_Conf_1.000	767	20	2.28E-30	XP_002641311.1	94	136.732	94	89	C. briggsae CBR-UNC-69 protein
Locus_20920_Transcript_1/1_Conf_1.000	168	0							
Locus_20921_Transcript_1/1_Conf_1.000	328	0							
Locus_20922_Transcript_1/1_Conf_1.000	197	0							
Locus_20923_Transcript_1/1_Conf_1.000	374	0							
Locus_20924_Transcript_1/1_Conf_1.000	310	0							

Locus_20925_Transcript_1/1_Conf_1.000	372	20	2.99E-38	NP_502432.1	77	161.384	124	96	RBD (RNA binding domain) protein family member (rbd-1)
Locus_20926_Transcript_1/1_Conf_1.000	290	0							
Locus_20927_Transcript_1/1_Conf_1.000	269	0							
Locus_20928_Transcript_1/1_Conf_1.000	178	0							
Locus_20929_Transcript_1/1_Conf_1.000	267	0							
Locus_2093_Transcript_1/2_Conf_1.000	1210	2	2.43E-13	NP_505850.1	88	81.2629	51	45	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-70)
Locus_2093_Transcript_2/2_Conf_1.000	1176	2	2.33E-13	NP_505850.1	88	81.2629	51	45	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-70)
Locus_20930_Transcript_1/1_Conf_1.000	566	20	2.68E-40	XP_001894156.1	69	168.703	191	132	MutS domain V family protein
Locus_20931_Transcript_1/2_Conf_1.000	232	0							
Locus_20931_Transcript_2/2_Conf_1.000	231	0							
Locus_20932_Transcript_1/1_Conf_1.000	183	0							
Locus_20933_Transcript_1/1_Conf_1.000	322	0							
Locus_20934_Transcript_1/1_Conf_1.000	147	0							
Locus_20935_Transcript_1/1_Conf_1.000	130	2	7.33E-05	XP_001893489.1	70	50.447	41	29	Hepatocellular carcinoma-associated antigen 66
Locus_20936_Transcript_1/1_Conf_1.000	199	20	3.76E-25	NP_509205.2	93	117.857	66	62	P-GlycoProtein related family member (pgp-10)
Locus_20937_Transcript_1/2_Conf_1.000	817	4	2.32E-39	NP_508552.1	62	166.777	202	126	hypothetical protein F40F4.6
Locus_20937_Transcript_2/2_Conf_1.000	817	4	2.32E-39	NP_508552.1	62	166.777	202	126	hypothetical protein F40F4.6
Locus_20938_Transcript_1/1_Conf_1.000	229	0							
Locus_20939_Transcript_1/1_Conf_1.000	310	0							
Locus_2094_Transcript_1/1_Conf_1.000	475	7	3.39E-10	NP_499022.1	46	68.1662	151	70	hypothetical protein ZK512.5
Locus_20940_Transcript_1/1_Conf_1.000	164	0							
Locus_20941_Transcript_1/1_Conf_1.000	291	0							
Locus_20942_Transcript_1/1_Conf_1.000	141	0							
Locus_20943_Transcript_1/1_Conf_1.000	395	0							
Locus_20944_Transcript_1/1_Conf_1.000	228	20	1.44E-16	CBW44372.1	76	89.3521	72	55	C. elegans protein F21A10.2e, partially confirmed by transcript evidence

Locus_20945_Transcript_1/1_Conf_1.000	203	20	5.99E-23	XP_002643622.1	84	110.538	66	56	C. briggsae CBR-NAS-39 protein
Locus_20946_Transcript_1/1_Conf_1.000	202	0							
Locus_20947_Transcript_1/1_Conf_1.000	249	0							
Locus_20948_Transcript_1/1_Conf_1.000	614	3	3.50E-13	NP_497273.2	53	78.9518	166	89	Fatty Acid/Retinol binding protein family member (far-8)
Locus_20949_Transcript_1/1_Conf_1.000	343	2	5.85E-42	AAQ18782.1	80	173.711	115	92	GATA transcription factor
Locus_2095_Transcript_1/1_Conf_1.000	846	20	7.51E-36	NP_506009.1	55	155.221	274	152	hypothetical protein C52E4.7
Locus_20950_Transcript_1/1_Conf_1.000	387	20	1.95E-50	XP_002645256.1	84	201.83	129	109	Hypothetical protein CBG00135
Locus_20951_Transcript_1/1_Conf_1.000	232	0							
Locus_20952_Transcript_1/1_Conf_1.000	157	0							
Locus_20953_Transcript_1/1_Conf_1.000	150	20	8.24E-12	NP_741684.2	87	73.559	48	42	PROximal proliferation in germline family member (pro-3)
Locus_20954_Transcript_1/1_Conf_1.000	141	10	3.58E-12	CAA92456.3	91	74.7146	47	43	C. elegans protein C53B4.4b, partially confirmed by transcript evidence
Locus_20955_Transcript_1/1_Conf_1.000	227	1	2.89E-41	EAW61183.1	100	171.4	75	75	basigin (Ok blood group), isoform CRA_d
Locus_20956_Transcript_1/1_Conf_1.000	207	0							

Locus_20957_Transcript_1/1_Conf_1.000	214	20	2.75E-20	EFO18082.1	94	101.679	70	66	hypothetical protein LOAG_10417
Locus_20958_Transcript_1/1_Conf_1.000	284	0							
Locus_20959_Transcript_1/1_Conf_1.000	646	9	2.22E-56	NP_509677.1	70	222.631	216	153	hypothetical protein F19C6.2
Locus_2096_Transcript_1/1_Conf_1.000	278	0							
Locus_20960_Transcript_1/1_Conf_1.000	646	6	1.70E-48	XP_002636775.1	68	196.438	190	131	Hypothetical protein CBG23509
Locus_20961_Transcript_1/1_Conf_1.000	188	0							
Locus_20962_Transcript_1/1_Conf_1.000	140	0							
Locus_20963_Transcript_1/1_Conf_1.000	246	20	1.61E-12	NP_505977.1	73	75.8702	67	49	PYruvate Carboxylase family member (pyc-1)
Locus_20964_Transcript_1/1_Conf_1.000	137	20	4.87E-09	XP_797921.2	90	64.3142	43	39	PREDICTED: similar to MGC82686 protein
Locus_20965_Transcript_1/1_Conf_1.000	302	20	3.87E-22	NP_491200.1	72	107.842	102	74	hypothetical protein D1037.1
Locus_20966_Transcript_1/1_Conf_1.000	686	0							
Locus_20967_Transcript_1/1_Conf_1.000	191	20	5.49E-24	XP_002632893.1	95	114.005	63	60	Hypothetical protein CBG15101
Locus_20968_Transcript_1/1_Conf_1.000	164	4	3.65E-12	ACJ65180.1	86	74.7146	45	39	Gaba b receptor subunit protein 2, confirmed by transcript evidence

Locus_20969_Transcript_1/1_Conf_1.000	357	20	3.48E-39	EFO23704.1	80	164.466	117	94	hypothetical protein LOAG_04778
Locus_2097_Transcript_1/1_Conf_1.000	2466	20	0	NP_492319.2	84	820.846	590	497	RSK-pNinety (RSK-p90 kinase) homolog family member (rskn-1)
Locus_20970_Transcript_1/1_Conf_1.000	479	0							
Locus_20971_Transcript_1/1_Conf_1.000	191	0							
Locus_20972_Transcript_1/1_Conf_1.000	161	20	8.16E-12	NP_503578.1	84	73.559	45	38	hypothetical protein F22F7.7
Locus_20973_Transcript_1/1_Conf_1.000	743	20	1.13E-63	ACI49160.1	70	247.284	231	162	hypothetical protein Cbre_JD21.007
Locus_20974_Transcript_1/1_Conf_1.000	172	0							
Locus_20975_Transcript_1/1_Conf_1.000	351	0							
Locus_20976_Transcript_1/1_Conf_1.000	133	20	8.32E-17	ACJ65168.1	100	90.1225	44	44	Uncoordinated protein 68, isoform b, partially confirmed by transcript evidence
Locus_20977_Transcript_1/1_Conf_1.000	242	15	2.19E-17	ADI88500.1	71	92.0485	77	55	DRAG-1
Locus_20978_Transcript_1/1_Conf_1.000	153	0							
Locus_20979_Transcript_1/1_Conf_1.000	130	0							

Locus_2098_Transcript_1/1_Conf_1.000	564	20	9.80E-59	NP_492601.1	89	229.95	133	119	Cytochrome C Oxidase family member (cco-1)
Locus_20980_Transcript_1/1_Conf_1.000	157	1	1.65E-04	EFO17639.1	68	49.2914	35	24	hypothetical protein LOAG_10859
Locus_20981_Transcript_1/1_Conf_1.000	276	0							
Locus_20982_Transcript_1/1_Conf_1.000	179	20	6.55E-14	NP_496814.1	80	80.4925	60	48	Member of AAA family binding CED-4 family member (mac-1)
Locus_20983_Transcript_1/1_Conf_1.000	562	0							
Locus_20984_Transcript_1/1_Conf_1.000	134	20	1.47E-13	NP_510705.1	93	79.337	44	41	hypothetical protein C10E2.6
Locus_20985_Transcript_1/1_Conf_1.000	685	20	1.86E-83	XP_002645520.1	85	312.768	206	176	C. briggsae CBR-NHR-14 protein
Locus_20986_Transcript_1/1_Conf_1.000	304	20	1.56E-39	CAX65056.1	92	165.622	101	93	C. elegans protein F25C8.3d, partially confirmed by transcript evidence
Locus_20987_Transcript_1/1_Conf_1.000	225	0							

Locus_20988_Transcript_1/1_Conf_1.000	281	20	6.74E-27	NP_501743.1	77	123.635	92	71	CAVeolin family member (cav-1)
Locus_20989_Transcript_1/1_Conf_1.000	129	1	4.75E-04	XP_002937788.1	69	47.7506	39	27	PREDICTED: collagen alpha-6(VI) chain-like, partial
Locus_2099_Transcript_1/2_Conf_1.000	861	7	1.98E-23	NP_492047.1	55	114.005	139	77	Chondroitin ProteoGlycan family member (cpg-3)
Locus_2099_Transcript_2/2_Conf_1.000	716	7	1.38E-23	NP_492047.1	55	114.005	139	77	Chondroitin ProteoGlycan family member (cpg-3)
Locus_20990_Transcript_1/1_Conf_1.000	319	0							
Locus_20991_Transcript_1/1_Conf_1.000	129	0							
Locus_20992_Transcript_1/1_Conf_1.000	242	0							
Locus_20993_Transcript_1/1_Conf_1.000	128	0							
Locus_20994_Transcript_1/1_Conf_1.000	160	0							
Locus_20995_Transcript_1/2_Conf_1.000	476	0							
Locus_20995_Transcript_2/2_Conf_1.000	464	0							
Locus_20996_Transcript_1/1_Conf_1.000	245	3	2.67E-15	XP_002643880.1	69	85.1149	83	58	Hypothetical protein CBG02118
Locus_20997_Transcript_1/1_Conf_1.000	511	20	7.87E-82	XP_002645216.1	94	306.22	169	159	Hypothetical protein CBG00074
Locus_20998_Transcript_1/1_Conf_1.000	583	20	1.16E-52	NP_741293.1	69	209.92	204	142	Enhanced RNAI (RNA interference) family member (eri-1)

Locus_20999_Transcript_1/1_Conf_1.000	153	20	1.40E-11	EFO25550.1	78	72.7886	50	39	nucleolar protein 10
Locus_21_Transcript_1/1_Conf_1.000	1484	20	5.83E-156	NP_502269.1	96	555.444	350	336	hypothetical protein ZK829.7
Locus_210_Transcript_1/3_Conf_0.375	562	8	7.13E-62	ADN00782.1	80	240.35	175	141	parasitic stage specific protein 1
Locus_210_Transcript_2/3_Conf_0.500	851	20	1.47E-39	XP_002637073.1	56	167.548	207	117	C. briggsae CBR-LYS-1 protein
Locus_210_Transcript_3/3_Conf_0.375	696	8	4.04E-73	ADN00782.1	79	278.485	204	162	parasitic stage specific protein 1
Locus_2100_Transcript_1/9_Conf_0.692	3844	20	0	NP_491069.1	86	1819.67	1231	1059	hypothetical protein Y71F9AL.17
Locus_2100_Transcript_2/9_Conf_0.692	3844	20	0	NP_491069.1	86	1819.67	1231	1059	hypothetical protein Y71F9AL.17

Locus_2100_Transcript_3/9_Conf_0.692	3844	20	0	NP_491069.1	86	1819.67	1231	1059	hypothetical protein Y71F9AL.17
Locus_2100_Transcript_4/9_Conf_0.692	3844	20	0	NP_491069.1	86	1819.67	1231	1059	hypothetical protein Y71F9AL.17
Locus_2100_Transcript_5/9_Conf_0.692	3844	20	0	NP_491069.1	86	1819.67	1231	1059	hypothetical protein Y71F9AL.17

Locus_2100_Transcript_6/9_Conf_0.692	3844	20	0	NP_491069.1	86	1819.67	1231	1059	hypothetical protein Y71F9AL.17
Locus_2100_Transcript_7/9_Conf_0.692	3844	20	0	NP_491069.1	86	1819.67	1231	1059	hypothetical protein Y71F9AL.17
Locus_2100_Transcript_8/9_Conf_0.692	3844	20	0	NP_491069.1	86	1819.67	1231	1059	hypothetical protein Y71F9AL.17

Locus_2100_Transcript_9/9_Conf_0.692	3844	20	0	NP_491069.1	86	1819.67	1231	1059	hypothetical protein Y71F9AL.17
Locus_21000_Transcript_1/1_Conf_1.000	577	20	3.61E-51	NP_499668.1	71	204.912	184	131	hypothetical protein Y37D8A.2
Locus_21001_Transcript_1/1_Conf_1.000	233	0							
Locus_21002_Transcript_1/1_Conf_1.000	175	0							
Locus_21003_Transcript_1/1_Conf_1.000	226	0							
Locus_21004_Transcript_1/1_Conf_1.000	282	4	4.24E-16	NP_500204.2	70	87.8113	94	66	CaDHerin family member (cdh-10)
Locus_21005_Transcript_1/1_Conf_1.000	150	0							
Locus_21006_Transcript_1/1_Conf_1.000	329	20	7.59E-10	XP_002640649.1	60	67.0106	70	42	Hypothetical protein CBG19707
Locus_21007_Transcript_1/1_Conf_1.000	218	0							
Locus_21008_Transcript_1/1_Conf_1.000	489	0							
Locus_21009_Transcript_1/1_Conf_1.000	252	0							
Locus_2101_Transcript_1/2_Conf_1.000	1582	20	8.84E-158	EFO22806.1	77	561.607	441	341	N-myristoyltransferase 2
Locus_2101_Transcript_2/2_Conf_1.000	1582	20	8.84E-158	EFO22806.1	77	561.607	441	341	N-myristoyltransferase 2
Locus_21010_Transcript_1/1_Conf_1.000	191	0							
Locus_21011_Transcript_1/1_Conf_1.000	515	1	5.32E-17	EFO16507.1	56	90.8929	162	91	hypothetical protein LOAG_12000
Locus_21012_Transcript_1/1_Conf_1.000	270	20	7.27E-37	NP_497786.2	95	156.762	89	85	MethylMalonylCoA Mutase homolog family member (mmcm-1)

Locus_21013_Transcript_1/1_Conf_1.000	254	0							
Locus_21014_Transcript_1/1_Conf_1.000	162	10	1.34E-06	ZP_06280939.1	58	56.225	53	31	LPXTG-motif cell wall anchor domain protein
Locus_21015_Transcript_1/1_Conf_1.000	241	20	2.43E-08	XP_002155142.1	75	62.003	48	36	PREDICTED: similar to ezrin-binding partner PACE-1
Locus_21016_Transcript_1/1_Conf_1.000	349	2	1.26E-20	NP_506224.1	59	102.834	118	70	hypothetical protein R90.1
Locus_21017_Transcript_1/1_Conf_1.000	288	1	1.96E-05	XP_002642656.1	74	52.373	35	26	Hypothetical protein CBG00040
Locus_21018_Transcript_1/1_Conf_1.000	236	2	3.66E-04	NP_740912.2	46	48.1358	86	40	SCP(Small C-terminal domain Phosphatase)-Like phosphatase family member (scpl-1)
Locus_21019_Transcript_1/1_Conf_1.000	197	0							
Locus_2102_Transcript_1/1_Conf_1.000	1094	4	6.52E-07	XP_002631720.1	54	59.6918	120	65	C. briggsae CBR-PQN-87 protein
Locus_21020_Transcript_1/1_Conf_1.000	292	0							
Locus_21021_Transcript_1/1_Conf_1.000	467	4	2.78E-52	NP_492775.2	80	207.994	154	124	LAMinin related. See also lmb- family member (lam-3)
Locus_21022_Transcript_1/1_Conf_1.000	331	0							
Locus_21023_Transcript_1/1_Conf_1.000	220	0							
Locus_21024_Transcript_1/1_Conf_1.000	141	0							
Locus_21025_Transcript_1/1_Conf_1.000	134	0							
Locus_21026_Transcript_1/1_Conf_1.000	183	0							
Locus_21027_Transcript_1/1_Conf_1.000	187	4	4.37E-13	NP_491022.2	83	77.7962	61	51	hypothetical protein F32B5.7
Locus_21028_Transcript_1/1_Conf_1.000	159	0							
Locus_21029_Transcript_1/1_Conf_1.000	157	20	2.08E-23	ACV89490.1	100	112.079	52	52	MHC class II antigen
Locus_2103_Transcript_1/1_Conf_1.000	596	20	4.47E-23	EFO22749.1	61	111.694	157	97	hypothetical protein LOAG_05738
Locus_21030_Transcript_1/1_Conf_1.000	246	20	1.12E-21	NP_501999.2	78	106.301	80	63	hypothetical protein T25B9.10
Locus_21031_Transcript_1/1_Conf_1.000	227	10	3.32E-21	XP_002644127.1	77	104.76	75	58	C. briggsae CBR-TAG-289 protein
Locus_21032_Transcript_1/1_Conf_1.000	350	0							
Locus_21033_Transcript_1/1_Conf_1.000	143	11	5.35E-08	NP_496800.1	71	60.8474	45	32	hypothetical protein W09H1.5

Locus_21034_Transcript_1/1_Conf_1.000	154	20	1.00E-17	NP_491165.2	94	93.2041	50	47	human SPG (spastic paraplegia) family member (spg-7)
Locus_21035_Transcript_1/1_Conf_1.000	500	2	2.33E-11	NP_740794.1	47	72.0182	168	79	hypothetical protein Y51F10.10
Locus_21036_Transcript_1/1_Conf_1.000	481	20	5.12E-51	XP_002646593.1	89	203.756	131	117	C. briggsae CBR-PRPF-4 protein
Locus_21037_Transcript_1/1_Conf_1.000	363	0							
Locus_21038_Transcript_1/1_Conf_1.000	156	0							
Locus_21039_Transcript_1/1_Conf_1.000	154	0							
Locus_2104_Transcript_1/1_Conf_1.000	2329	20	0	CAX32485.1	68	697.582	790	539	C. elegans protein T20D3.11b, partially confirmed by transcript evidence
Locus_21040_Transcript_1/1_Conf_1.000	416	20	2.75E-12	XP_001894417.1	59	75.0998	100	59	Nuclear hormone receptor family member nhr-25
Locus_21041_Transcript_1/1_Conf_1.000	197	0							
Locus_21042_Transcript_1/1_Conf_1.000	204	20	2.78E-12	XP_002645018.1	69	75.0998	68	47	C. briggsae CBR-SUR-5 protein
Locus_21043_Transcript_1/1_Conf_1.000	196	0							
Locus_21044_Transcript_1/1_Conf_1.000	263	20	1.87E-32	NP_491529.2	87	142.124	87	76	hypothetical protein Y110A7A.6
Locus_21045_Transcript_1/1_Conf_1.000	129	0							
Locus_21046_Transcript_1/1_Conf_1.000	220	2	6.90E-06	XP_001892872.1	61	50.0618	52	32	hypothetical protein Bm1_07015
Locus_21047_Transcript_1/1_Conf_1.000	447	0							
Locus_21048_Transcript_1/1_Conf_1.000	177	20	5.72E-18	NP_493618.1	87	93.9745	56	49	Deletions Of G-rich DNA family member (dog-1)
Locus_21049_Transcript_1/1_Conf_1.000	213	4	1.61E-28	NP_495365.1	97	129.028	70	68	RaPsYn family member (rpy-1)

Locus_2105_Transcript_1/1_Conf_1.000	1036	20	7.53E-42	XP_002639656.1	58	175.637	239	141	Hypothetical protein CBG12372
Locus_21050_Transcript_1/1_Conf_1.000	192	0							
Locus_21051_Transcript_1/1_Conf_1.000	272	20	2.41E-40	NP_001122445.1	96	168.318	89	86	hypothetical protein F08A10.1
Locus_21052_Transcript_1/1_Conf_1.000	222	0							
Locus_21053_Transcript_1/1_Conf_1.000	210	20	3.59E-28	NP_502747.1	94	127.872	69	65	hypothetical protein F55B11.1
Locus_21054_Transcript_1/1_Conf_1.000	161	0							
Locus_21055_Transcript_1/1_Conf_1.000	318	0							
Locus_21056_Transcript_1/1_Conf_1.000	136	0							
Locus_21057_Transcript_1/1_Conf_1.000	161	2	1.03E-14	EFO27604.1	83	83.1889	53	44	hypothetical protein LOAG_00873
Locus_21058_Transcript_1/1_Conf_1.000	375	20	6.84E-43	XP_001900176.1	77	176.792	135	104	LIM domain containing protein
Locus_21059_Transcript_1/1_Conf_1.000	406	20	2.26E-46	ACZ13335.1	90	188.348	133	120	60S ribosomal protein L5
Locus_2106_Transcript_1/4_Conf_0.667	1634	20	1.57E-173	XP_002637767.1	87	613.994	400	349	C. briggsae CBR-UNC-61 protein
Locus_2106_Transcript_2/4_Conf_0.667	1639	20	6.61E-172	XP_002637767.1	86	608.601	407	351	C. briggsae CBR-UNC-61 protein

Locus_2106_Transcript_3/4_Conf_0.667	1627	20	6.55E-172	XP_002637767.1	86	608.601	403	349	C. briggsae CBR-UNC-61 protein
Locus_2106_Transcript_4/4_Conf_0.667	1618	20	1.55E-173	XP_002637767.1	87	613.994	400	349	C. briggsae CBR-UNC-61 protein
Locus_21060_Transcript_1/1_Conf_1.000	145	0							
Locus_21061_Transcript_1/1_Conf_1.000	402	17	4.15E-32	NP_502894.1	68	140.969	122	84	hypothetical protein Y105C5B.5
Locus_21062_Transcript_1/1_Conf_1.000	155	0							
Locus_21063_Transcript_1/1_Conf_1.000	450	0							
Locus_21064_Transcript_1/1_Conf_1.000	386	15	8.32E-17	NP_509219.1	55	90.1225	138	76	hypothetical protein F46H5.4
Locus_21065_Transcript_1/1_Conf_1.000	268	2	1.06E-11	XP_002637628.1	72	73.1738	65	47	Hypothetical protein CBG19373
Locus_21066_Transcript_1/1_Conf_1.000	138	20	1.90E-21	XP_002800676.1	100	105.531	45	45	PREDICTED: galectin-3-binding protein isoform 3
Locus_21067_Transcript_1/1_Conf_1.000	502	5	1.15E-13	XP_002636935.1	55	79.7221	145	81	C. briggsae CBR-UIG-1 protein
Locus_21068_Transcript_1/1_Conf_1.000	351	20	5.62E-21	XP_002629947.1	85	103.99	71	61	C. briggsae CBR-PFD-2 protein

Locus_21069_Transcript_1/1_Conf_1.000	308	20	1.90E-29	EFO24692.1	75	132.109	100	75	protein-tyrosine phosphatase
Locus_2107_Transcript_1/1_Conf_1.000	751	20	1.05E-88	XP_001899666.1	82	330.487	235	194	Putative activator 1 36 kDa subunit
Locus_21070_Transcript_1/1_Conf_1.000	131	4	5.60E-13	NP_501176.1	95	77.411	41	39	hypothetical protein T12B3.3
Locus_21071_Transcript_1/2_Conf_1.000	297	0							
Locus_21071_Transcript_2/2_Conf_1.000	195	0							
Locus_21072_Transcript_1/1_Conf_1.000	397	20	4.48E-26	XP_002643199.1	69	120.939	113	79	C. briggsae CBR-TTR-37 protein
Locus_21073_Transcript_1/1_Conf_1.000	436	0							
Locus_21074_Transcript_1/1_Conf_1.000	348	0							
Locus_21075_Transcript_1/1_Conf_1.000	440	20	5.50E-29	XP_002648469.1	73	130.568	110	81	Hypothetical protein CBG24757
Locus_21076_Transcript_1/1_Conf_1.000	165	20	1.69E-17	CAX65056.1	78	92.4337	66	52	C. elegans protein F25C8.3d, partially confirmed by transcript evidence
Locus_21077_Transcript_1/1_Conf_1.000	233	20	1.43E-24	NP_492944.2	87	115.931	70	61	hypothetical protein F32B4.5
Locus_21078_Transcript_1/1_Conf_1.000	141	5	1.84E-08	XP_002641945.1	85	62.3882	35	30	C. briggsae CBR-TAG-198 protein
Locus_21079_Transcript_1/1_Conf_1.000	163	0							
Locus_2108_Transcript_1/1_Conf_1.000	328	9	7.26E-45	XP_002632886.1	89	183.341	109	98	Hypothetical protein CBG15094
Locus_21080_Transcript_1/1_Conf_1.000	308	20	1.02E-06	NP_001082522.1	65	56.6102	60	39	UTP14, U3 small nucleolar ribonucleoprotein, homolog A

Locus_21081_Transcript_1/1_Conf_1.000	634	20	9.42E-81	XP_002638487.1	80	303.523	211	170	Hypothetical protein CBG12917
Locus_21082_Transcript_1/1_Conf_1.000	275	6	1.51E-26	NP_001122724.1	86	122.479	67	58	hypothetical protein Y22D7AL.6
Locus_21083_Transcript_1/1_Conf_1.000	170	20	9.88E-10	XP_002642493.1	77	66.6254	58	45	Hypothetical protein CBG06913
Locus_21084_Transcript_1/1_Conf_1.000	418	20	1.31E-25	XP_002430986.1	56	119.398	146	82	zinc finger protein DHHC domain containing protein, putative
Locus_21085_Transcript_1/1_Conf_1.000	522	20	2.99E-50	XP_002643964.1	71	201.445	173	124	C. briggsae CBR-HUM-4 protein
Locus_21086_Transcript_1/1_Conf_1.000	224	0							
Locus_21087_Transcript_1/1_Conf_1.000	168	0							
Locus_21088_Transcript_1/1_Conf_1.000	342	0							
Locus_21089_Transcript_1/1_Conf_1.000	209	0							
Locus_2109_Transcript_1/1_Conf_1.000	4169	20	0	XP_002638675.1	61	1021.15	1304	799	C. briggsae CBR-PBRM-1 protein
Locus_21090_Transcript_1/1_Conf_1.000	441	0							
Locus_21091_Transcript_1/1_Conf_1.000	408	20	2.85E-25	NP_001022060.1	56	118.242	165	94	CLC-type chloride cHannel family member (clh-3)
Locus_21092_Transcript_1/1_Conf_1.000	280	0							
Locus_21093_Transcript_1/1_Conf_1.000	604	20	2.90E-65	XP_002629799.1	80	251.906	204	165	Hypothetical protein CBG01042
Locus_21094_Transcript_1/1_Conf_1.000	363	4	4.85E-17	XP_001900557.1	57	90.8929	130	75	Bromodomain containing protein
Locus_21095_Transcript_1/1_Conf_1.000	185	0							
Locus_21096_Transcript_1/1_Conf_1.000	319	0							

Locus_21097_Transcript_1/1_Conf_1.000	463	2	1.26E-28	NP_492185.2	69	129.413	153	107	SMG-associated and Lethal family member (smgl-1)
Locus_21098_Transcript_1/1_Conf_1.000	506	0							
Locus_21099_Transcript_1/1_Conf_1.000	242	2	3.28E-05	NP_503409.1	71	51.6026	73	52	SyNapTotagmin family member (snt-5)
Locus_211_Transcript_1/5_Conf_0.588	459	20	8.77E-35	Q94637.1	70	149.828	156	110	Vitellogenin-6
Locus_211_Transcript_2/5_Conf_0.529	314	20	6.74E-22	Q94637.1	72	107.071	108	78	Vitellogenin-6
Locus_211_Transcript_3/5_Conf_0.353	231	20	3.66E-12	NP_001023274.1	65	74.7146	78	51	VITellogenin structural genes (yolk protein genes) family member (vit-6)
Locus_211_Transcript_4/5_Conf_0.471	311	20	4.23E-21	Q94637.1	71	104.375	107	77	Vitellogenin-6
Locus_211_Transcript_5/5_Conf_0.765	551	20	8.07E-39	Q94637.1	68	163.696	188	128	Vitellogenin-6
Locus_2110_Transcript_1/1_Conf_1.000	558	20	3.27E-43	NP_491843.3	88	178.333	100	88	hypothetical protein ZC328.2
Locus_21100_Transcript_1/1_Conf_1.000	163	1	2.60E-26	AAG23764.1	100	121.709	54	54	AF258561_1PP3686
Locus_21101_Transcript_1/1_Conf_1.000	167	20	5.43E-16	XP_002640833.1	87	87.4261	55	48	C. briggsae CBR-KLP-20 protein
Locus_21102_Transcript_1/1_Conf_1.000	297	0							
Locus_21103_Transcript_1/1_Conf_1.000	239	20	8.34E-25	CAR63597.1	87	116.701	70	61	hypothetical protein
Locus_21104_Transcript_1/1_Conf_1.000	175	0							
Locus_21105_Transcript_1/1_Conf_1.000	365	0							

Locus_21106_Transcript_1/1_Conf_1.000	237	0							
Locus_21107_Transcript_1/1_Conf_1.000	275	20	5.54E-37	XP_002646729.1	89	157.147	87	78	C. briggsae CBR-PRX-13 protein
Locus_21108_Transcript_1/1_Conf_1.000	198	0							
Locus_21109_Transcript_1/1_Conf_1.000	309	0							
Locus_2111_Transcript_1/2_Conf_1.000	301	20	3.06E-27	AAT40500.1	72	124.79	94	68	Putative reverse transcriptase, identical
Locus_2111_Transcript_2/2_Conf_1.000	170	15	6.19E-12	ABN08556.1	81	73.9442	53	43	Polyprotein, putative
Locus_21110_Transcript_1/1_Conf_1.000	144	1	1.67E-04	NP_510249.2	61	49.2914	47	29	TREhalase family member (tre-4)
Locus_21111_Transcript_1/1_Conf_1.000	326	0							
Locus_21112_Transcript_1/1_Conf_1.000	276	0							
Locus_21113_Transcript_1/1_Conf_1.000	232	0							
Locus_21114_Transcript_1/1_Conf_1.000	385	20	1.46E-29	XP_002646129.1	84	132.494	86	73	Hypothetical protein CBG08008
Locus_21115_Transcript_1/1_Conf_1.000	353	0							
Locus_21116_Transcript_1/1_Conf_1.000	351	3	1.44E-08	XP_002641791.1	66	62.7734	71	47	Hypothetical protein CBG10142
Locus_21117_Transcript_1/1_Conf_1.000	332	20	1.45E-61	XP_002801767.1	100	238.81	110	110	PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1
Locus_21118_Transcript_1/1_Conf_1.000	191	0							
Locus_21119_Transcript_1/1_Conf_1.000	229	0							

Locus_2112_Transcript_1/2_Conf_1.000	829	20	5.35E-23	EFO19187.1	100	112.464	54	54	ets-domain-containing protein
Locus_2112_Transcript_2/2_Conf_1.000	829	20	5.35E-23	EFO19187.1	100	112.464	54	54	ets-domain-containing protein
Locus_21120_Transcript_1/1_Conf_1.000	447	20	7.80E-39	XP_002661248.1	74	163.31	147	109	PREDICTED: ATP-binding cassette, sub-family C, member 1
Locus_21121_Transcript_1/1_Conf_1.000	254	0							
Locus_21122_Transcript_1/1_Conf_1.000	178	0							

Locus_21123_Transcript_1/1_Conf_1.000	284	20	4.53E-18	XP_001895789.1	73	94.3597	91	67	Timeless protein
Locus_21124_Transcript_1/1_Conf_1.000	358	0							
Locus_21125_Transcript_1/1_Conf_1.000	270	20	7.52E-34	XP_002630757.1	84	146.747	90	76	Hypothetical protein CBG02451
Locus_21126_Transcript_1/1_Conf_1.000	148	0							
Locus_21127_Transcript_1/1_Conf_1.000	305	0							
Locus_21128_Transcript_1/1_Conf_1.000	491	20	1.02E-46	NP_506182.2	79	189.504	149	118	DeHydrogenases, Short chain family member (dhs-21)
Locus_21129_Transcript_1/1_Conf_1.000	259	9	1.60E-15	NP_499482.1	69	85.8853	85	59	defective SPErmatogenesis family member (spe-6)
Locus_2113_Transcript_1/2_Conf_1.000	1452	3	4.50E-28	XP_002630981.1	55	130.568	206	114	Hypothetical protein CBG02720
Locus_2113_Transcript_2/2_Conf_1.000	1454	3	4.50E-28	XP_002630981.1	55	130.568	206	114	Hypothetical protein CBG02720
Locus_21130_Transcript_1/1_Conf_1.000	157	0							
Locus_21131_Transcript_1/1_Conf_1.000	167	0							

Locus_21132_Transcript_1/1_Conf_1.000	188	20	5.68E-29	XP_001109998.2	100	130.568	62	62	PREDICTED: glucose-6-phosphate isomerase
Locus_21133_Transcript_1/1_Conf_1.000	264	0							
Locus_21134_Transcript_1/1_Conf_1.000	133	12	3.17E-08	NP_001041301.1	89	61.6178	37	33	hypothetical protein ZK54.1
Locus_21135_Transcript_1/1_Conf_1.000	139	0							
Locus_21136_Transcript_1/1_Conf_1.000	236	2	2.07E-07	EFO26611.1	65	58.9214	72	47	hypothetical protein LOAG_01867
Locus_21137_Transcript_1/1_Conf_1.000	219	4	1.51E-13	ACI49219.1	90	79.337	42	38	hypothetical protein Csp3_JD05.004
Locus_21138_Transcript_1/1_Conf_1.000	148	0							
Locus_21139_Transcript_1/1_Conf_1.000	174	0							
Locus_2114_Transcript_1/1_Conf_1.000	351	4	1.94E-13	XP_002640867.1	73	78.9518	60	44	Hypothetical protein CBG15758
Locus_21140_Transcript_1/1_Conf_1.000	139	0							
Locus_21141_Transcript_1/1_Conf_1.000	195	0							
Locus_21142_Transcript_1/1_Conf_1.000	262	0							
Locus_21143_Transcript_1/1_Conf_1.000	189	0							
Locus_21144_Transcript_1/1_Conf_1.000	192	0							
Locus_21145_Transcript_1/1_Conf_1.000	190	0							
Locus_21146_Transcript_1/1_Conf_1.000	187	20	1.15E-29	EAW90757.1	100	132.88	61	61	microsomal glutathione S-transferase 3, isoform CRA_d
Locus_21147_Transcript_1/1_Conf_1.000	136	20	1.67E-09	XP_002104105.1	84	65.855	44	37	GD18625
Locus_21148_Transcript_1/1_Conf_1.000	197	0							

Locus_21149_Transcript_1/1_Conf_1.000	197	0							
Locus_2115_Transcript_1/1_Conf_1.000	2245	20	2.00E-100	NP_501805.1	59	371.703	694	413	hypothetical protein F44D12.1
Locus_21150_Transcript_1/1_Conf_1.000	271	0							
Locus_21151_Transcript_1/1_Conf_1.000	469	1	1.25E-12	NP_500548.1	52	76.2554	162	85	hypothetical protein W03B1.9
Locus_21152_Transcript_1/1_Conf_1.000	343	20	5.66E-37	ACI49016.1	83	157.147	112	94	hypothetical protein Cbre_JD04.001
Locus_21153_Transcript_1/1_Conf_1.000	205	0							
Locus_21154_Transcript_1/1_Conf_1.000	204	20	2.77E-20	NP_503846.1	82	101.679	67	55	CYtochrome P450 family member (cyp-33C9)
Locus_21155_Transcript_1/1_Conf_1.000	182	0							
Locus_21156_Transcript_1/1_Conf_1.000	274	2	8.89E-19	NP_001024902.1	68	96.6709	90	62	hypothetical protein T10B10.4
Locus_21157_Transcript_1/1_Conf_1.000	302	0							
Locus_21158_Transcript_1/1_Conf_1.000	505	20	2.51E-40	EFO24958.1	71	168.318	151	108	hypothetical protein LOAG_03524
Locus_21159_Transcript_1/1_Conf_1.000	169	0							
Locus_2116_Transcript_1/1_Conf_1.000	284	0							
Locus_21160_Transcript_1/1_Conf_1.000	193	0							
Locus_21161_Transcript_1/1_Conf_1.000	136	3	1.98E-10	NP_491382.1	90	68.9366	44	40	hypothetical protein Y119C1B.5
Locus_21162_Transcript_1/1_Conf_1.000	323	5	5.12E-14	3N9L	60	80.8777	110	66	Cekdm7a
Locus_21163_Transcript_1/1_Conf_1.000	418	0							
Locus_21164_Transcript_1/1_Conf_1.000	128	0							
Locus_21165_Transcript_1/1_Conf_1.000	149	0							
Locus_21166_Transcript_1/1_Conf_1.000	322	20	1.53E-42	NP_505019.2	81	175.637	107	87	hypothetical protein C37C3.7
Locus_21167_Transcript_1/1_Conf_1.000	187	0							
Locus_21168_Transcript_1/1_Conf_1.000	229	13	1.93E-37	EAW74622.1	100	158.688	75	75	protein tyrosine phosphatase, receptor type, C-associated protein
Locus_21169_Transcript_1/1_Conf_1.000	210	0							
Locus_2117_Transcript_1/1_Conf_1.000	503	20	1.43E-48	NP_497411.2	76	195.667	170	130	hypothetical protein Y82E9BR.18
Locus_21170_Transcript_1/1_Conf_1.000	339	0							
Locus_21171_Transcript_1/1_Conf_1.000	288	0							
Locus_21172_Transcript_1/1_Conf_1.000	197	5	2.38E-11	NP_001122672.1	76	72.0182	63	48	Regulator of G protein Signaling family member (rgs-5)
Locus_21173_Transcript_1/1_Conf_1.000	274	5	3.87E-06	XP_002595725.1	55	54.6842	90	50	hypothetical protein BRAFLDRAFT_200329
Locus_21174_Transcript_1/1_Conf_1.000	202	0							
Locus_21175_Transcript_1/1_Conf_1.000	155	0							
Locus_21176_Transcript_1/1_Conf_1.000	140	15	1.97E-10	BAH14685.1	100	68.9366	46	46	unnamed protein product
Locus_21177_Transcript_1/2_Conf_1.000	560	11	5.15E-89	XP_001900400.1	87	330.487	187	163	Zinc finger, C2H2 type family protein

Locus_21177_Transcript_2/2_Conf_1.000	560	11	5.15E-89	XP_001900400.1	87	330.487	187	163	Zinc finger, C2H2 type family protein
Locus_21178_Transcript_1/1_Conf_1.000	419	20	6.47E-33	XP_002640010.1	72	143.665	128	93	Hypothetical protein CBG12480
Locus_21179_Transcript_1/1_Conf_1.000	346	0							
Locus_2118_Transcript_1/1_Conf_1.000	835	4	2.44E-23	NP_492051.1	49	113.62	250	124	yeast BUB homolog family member (bub-1)
Locus_21180_Transcript_1/1_Conf_1.000	397	20	6.72E-06	XP_002871971.1	49	53.9138	91	45	PAZ domain-containing protein
Locus_21181_Transcript_1/1_Conf_1.000	210	5	2.75E-20	XP_002641791.1	85	101.679	70	60	Hypothetical protein CBG10142
Locus_21182_Transcript_1/1_Conf_1.000	136	0							
Locus_21183_Transcript_1/1_Conf_1.000	260	20	1.82E-19	XP_002646198.1	69	98.9821	86	60	Hypothetical protein CBG04359
Locus_21184_Transcript_1/1_Conf_1.000	252	20	4.53E-10	XP_001897797.1	82	67.781	46	38	Ets-domain containing protein
Locus_21185_Transcript_1/1_Conf_1.000	364	18	9.15E-16	XP_002647704.1	59	86.6557	108	64	Hypothetical protein CBG17893
Locus_21186_Transcript_1/1_Conf_1.000	139	0							
Locus_21187_Transcript_1/1_Conf_1.000	153	2	6.51E-09	XP_002634130.1	80	63.929	45	36	Hypothetical protein CBG01688
Locus_21188_Transcript_1/1_Conf_1.000	149	0							
Locus_21189_Transcript_1/1_Conf_1.000	377	20	2.62E-10	XP_002415173.1	61	68.5514	71	44	sentrin/sumo-specific protease, putative
Locus_2119_Transcript_1/1_Conf_1.000	256	20	1.27E-20	EFO17214.1	78	102.834	71	56	DOMON domain-containing protein
Locus_21190_Transcript_1/1_Conf_1.000	245	0							
Locus_21191_Transcript_1/1_Conf_1.000	150	0							
Locus_21192_Transcript_1/1_Conf_1.000	328	20	7.05E-32	NP_505775.3	77	140.198	104	81	hypothetical protein F32D8.4
Locus_21193_Transcript_1/1_Conf_1.000	212	0							
Locus_21194_Transcript_1/1_Conf_1.000	145	0							
Locus_21195_Transcript_1/1_Conf_1.000	205	20	5.59E-21	EFO25626.1	96	103.99	56	54	hypothetical protein LOAG_02863
Locus_21196_Transcript_1/1_Conf_1.000	477								
Locus_21197_Transcript_1/1_Conf_1.000	374	20	6.47E-17	XP_001356645.1	58	90.5077	124	73	GA20218

Locus_21198_Transcript_1/1_Conf_1.000	137	0							
Locus_21199_Transcript_1/1_Conf_1.000	537	0							
Locus_212_Transcript_1/1_Conf_1.000	449	20	3.75E-33	XP_001900551.1	63	144.436	148	94	Protein kinase domain containing protein
Locus_2120_Transcript_1/1_Conf_1.000	619	20	1.54E-64	NP_001122891.1	75	249.595	213	160	hypothetical protein C53A5.2
Locus_21200_Transcript_1/1_Conf_1.000	226	20	2.47E-16	XP_001894892.1	76	88.5817	75	57	RhoGAP domain containing protein
Locus_21201_Transcript_1/1_Conf_1.000	415								
Locus_21202_Transcript_1/1_Conf_1.000	232	20	2.00E-18	NP_499164.1	76	95.5153	75	57	SQuashed Vulva family member (sqv-3)
Locus_21203_Transcript_1/1_Conf_1.000	135	0							
Locus_21204_Transcript_1/1_Conf_1.000	138	0							
Locus_21205_Transcript_1/1_Conf_1.000	165	20	2.28E-14	EFO21603.1	85	82.0333	55	47	hypothetical protein LOAG_06885
Locus_21206_Transcript_1/1_Conf_1.000	130	0							
Locus_21207_Transcript_1/1_Conf_1.000	165	0							
Locus_21208_Transcript_1/1_Conf_1.000	618	0							
Locus_21209_Transcript_1/1_Conf_1.000	492	0							
Locus_2121_Transcript_1/1_Conf_1.000	1563	20	4.01E-62	NP_496095.1	63	243.817	276	174	WEE homolog family member (wee-1.3)
Locus_21210_Transcript_1/1_Conf_1.000	356	0							
Locus_21211_Transcript_1/1_Conf_1.000	338	0							
Locus_21212_Transcript_1/1_Conf_1.000	131	0							
Locus_21213_Transcript_1/1_Conf_1.000	171	0							
Locus_21214_Transcript_1/1_Conf_1.000	162	5	1.49E-05	NP_492318.1	80	52.7582	40	32	hypothetical protein T01H8.2

Locus_21215_Transcript_1/1_Conf_1.000	429	20	7.53E-26	XP_001901553.1	60	120.168	146	89	Protein-tyrosine phosphatase containing protein
Locus_21216_Transcript_1/1_Conf_1.000	199	20	7.08E-32	BAG60652.1	100	140.198	66	66	unnamed protein product
Locus_21217_Transcript_1/1_Conf_1.000	350	0							
Locus_21218_Transcript_1/1_Conf_1.000	337	4	1.85E-08	XP_002641335.1	60	62.3882	88	53	Hypothetical protein CBG13183
Locus_21219_Transcript_1/1_Conf_1.000	204	0							
Locus_2122_Transcript_1/1_Conf_1.000	1418	20	1.26E-144	NP_494771.1	77	517.694	420	325	hypothetical protein B0286.3
Locus_21220_Transcript_1/1_Conf_1.000	299	2	2.44E-16	NP_492118.1	68	88.5817	98	67	hypothetical protein D2030.3
Locus_21221_Transcript_1/1_Conf_1.000	479	20	3.13E-40	NP_500629.1	86	167.933	104	90	CYtochrome C family member (cyc-2.1)
Locus_21222_Transcript_1/1_Conf_1.000	180	0							
Locus_21223_Transcript_1/1_Conf_1.000	359	20	2.74E-52	XP_002638749.1	92	207.994	119	110	Hypothetical protein CBG18552
Locus_21224_Transcript_1/1_Conf_1.000	169	0							

Locus_21225_Transcript_1/1_Conf_1.000	237	20	4.73E-28	NP_500379.1	79	127.487	78	62	hypothetical protein Y37E11B.5
Locus_21226_Transcript_1/1_Conf_1.000	319	20	1.03E-22	NP_494841.3	69	109.768	91	63	hypothetical protein F10G7.10
Locus_21227_Transcript_1/1_Conf_1.000	221	0							
Locus_21228_Transcript_1/1_Conf_1.000	201	4	5.07E-22	CAR63710.1	88	107.457	67	59	putative C2 domain containing protein
Locus_21229_Transcript_1/1_Conf_1.000	172	20	7.52E-18	XP_002639780.1	85	93.5893	56	48	Hypothetical protein CBG02227
Locus_2123_Transcript_1/1_Conf_1.000	623	20	1.16E-88	XP_002639761.1	89	329.717	200	179	C. briggsae CBR-PAB-1 protein
Locus_21230_Transcript_1/1_Conf_1.000	391	0							
Locus_21231_Transcript_1/1_Conf_1.000	405	20	8.04E-36	2OS5	82	153.295	114	94	Macrophage Migration Inhibitory Factor
Locus_21232_Transcript_1/1_Conf_1.000	200	0							

Locus_21233_Transcript_1/1_Conf_1.000	717	20	6.35E-85	NP_497203.1	81	317.775	228	185	Metaphase-to-Anaphase Transition defect family member (mat-3)
Locus_21234_Transcript_1/1_Conf_1.000	311	0							
Locus_21235_Transcript_1/1_Conf_1.000	228	20	2.62E-26	NP_001022450.1	92	121.709	75	69	hypothetical protein Y48E1A.1
Locus_21236_Transcript_1/1_Conf_1.000	278	0							
Locus_21237_Transcript_1/1_Conf_1.000	266	0							
Locus_21238_Transcript_1/1_Conf_1.000	197	20	5.29E-11	XP_001894671.1	79	70.8626	59	47	Protein kinase domain containing protein
Locus_21239_Transcript_1/1_Conf_1.000	159	0							
Locus_2124_Transcript_1/1_Conf_1.000	187	0							
Locus_21240_Transcript_1/1_Conf_1.000	148	0							
Locus_21241_Transcript_1/1_Conf_1.000	260	0							
Locus_21242_Transcript_1/1_Conf_1.000	239	1	2.52E-05	XP_002630993.1	63	51.9878	57	36	Hypothetical protein CBG02738
Locus_21243_Transcript_1/1_Conf_1.000	163	20	8.97E-19	NP_505312.1	90	96.6709	54	49	hypothetical protein T19A5.1
Locus_21244_Transcript_1/1_Conf_1.000	169	20	3.63E-12	NP_741501.1	70	74.7146	55	39	hypothetical protein F11E6.1
Locus_21245_Transcript_1/1_Conf_1.000	152	0							
Locus_21246_Transcript_1/1_Conf_1.000	133	0							

Locus_21247_Transcript_1/1_Conf_1.000	180	0							
Locus_21248_Transcript_1/1_Conf_1.000	166	0							
Locus_21249_Transcript_1/1_Conf_1.000	165	0							
Locus_2125_Transcript_1/3_Conf_0.714	1468	2	2.97E-19	XP_002634618.1	41	101.293	523	217	Hypothetical protein CBG18472
Locus_2125_Transcript_2/3_Conf_0.714	1468	2	1.13E-18	NP_501436.1	41	99.3673	526	216	hypothetical protein T26A8.1
Locus_2125_Transcript_3/3_Conf_0.714	1468	2	1.13E-18	NP_501436.1	41	99.3673	526	216	hypothetical protein T26A8.1
Locus_21250_Transcript_1/1_Conf_1.000	248	17	2.67E-07	XP_517936.2	80	58.5362	40	32	PREDICTED: PHD finger protein 15
Locus_21251_Transcript_1/1_Conf_1.000	207	0							
Locus_21252_Transcript_1/1_Conf_1.000	261	0							
Locus_21253_Transcript_1/1_Conf_1.000	848	20	2.50E-31	AAO63576.1	55	140.198	183	101	secreted protein 4 precursor
Locus_21254_Transcript_1/1_Conf_1.000	393	20	1.22E-39	EFO19650.1	75	166.007	129	98	NAK/GAK protein kinase
Locus_21255_Transcript_1/1_Conf_1.000	203	0							
Locus_21256_Transcript_1/1_Conf_1.000	142	0							
Locus_21257_Transcript_1/1_Conf_1.000	509	0							
Locus_21258_Transcript_1/1_Conf_1.000	393	20	3.30E-53	XP_002645892.1	92	211.075	118	109	Hypothetical protein CBG07642
Locus_21259_Transcript_1/1_Conf_1.000	237	20	7.31E-21	NP_001123159.1	74	103.605	78	58	SYnaptoGenesis abnormal family member (syg-1)

Locus_2126_Transcript_1/1_Conf_1.000	2907	20	3.03E-168	EFO26291.1	57	597.43	911	520	hypothetical protein LOAG_02191
Locus_21260_Transcript_1/1_Conf_1.000	268	20	1.38E-35	ACZ64269.1	98	152.525	88	87	astacin metalloprotease b
Locus_21261_Transcript_1/1_Conf_1.000	147	0							
Locus_21262_Transcript_1/1_Conf_1.000	253	20	1.04E-14	XP_002629772.1	63	83.1889	86	55	Hypothetical protein CBG01012
Locus_21263_Transcript_1/1_Conf_1.000	137	0							
Locus_21264_Transcript_1/1_Conf_1.000	144	20	1.67E-12	AAF82410.1	87	75.8702	47	41	AF221132_1diacylglycerol acyltransferase
Locus_21265_Transcript_1/1_Conf_1.000	147	20	3.70E-20	XP_002809166.1	100	101.293	48	48	PREDICTED: antigen peptide transporter 1-like
Locus_21266_Transcript_1/1_Conf_1.000	305	3	1.86E-08	NP_497061.1	62	62.3882	66	41	hypothetical protein Y54E2A.5
Locus_21267_Transcript_1/1_Conf_1.000	142	20	3.70E-17	NP_497809.1	97	91.2781	47	46	Heavy chain, Unconventional Myosin family member (hum-5)

Locus_21268_Transcript_1/1_Conf_1.000	244	20	1.41E-24	NP_491242.2	86	115.931	80	69	hypothetical protein T03F1.7
Locus_21269_Transcript_1/1_Conf_1.000	176	4	1.02E-06	EFO23768.1	66	56.6102	60	40	hypothetical protein LOAG_04713
Locus_2127_Transcript_1/1_Conf_1.000	145	0							
Locus_21270_Transcript_1/1_Conf_1.000	301	0							
Locus_21271_Transcript_1/1_Conf_1.000	190	0							
Locus_21272_Transcript_1/1_Conf_1.000	218	20	3.57E-20	NP_001181828.1	100	101.293	44	44	cathepsin B
Locus_21273_Transcript_1/1_Conf_1.000	132	0							
Locus_21274_Transcript_1/1_Conf_1.000	251	0							
Locus_21275_Transcript_1/1_Conf_1.000	470	20	8.28E-65	NP_500551.2	89	249.595	155	138	hypothetical protein F55F10.1
Locus_21276_Transcript_1/1_Conf_1.000	203	20	1.17E-18	NP_509676.1	98	96.2857	67	66	G-protein-coupled Receptor Kinase family member (grk-1)
Locus_21277_Transcript_1/1_Conf_1.000	814	0							

Locus_21278_Transcript_1/1_Conf_1.000	161	16	9.64E-13	NP_001122528.1	78	76.6406	52	41	Cation transporting ATPase family member (catp-1)
Locus_21279_Transcript_1/1_Conf_1.000	250	20	4.67E-20	NP_500531.1	82	100.908	81	67	hypothetical protein F15E6.6
Locus_2128_Transcript_1/4_Conf_0.429	1076	15	1.96E-24	XP_002630067.1	89	117.857	74	66	C. briggsae CBR-IPLA-1 protein
Locus_2128_Transcript_2/4_Conf_0.571	1204	20	5.36E-29	XP_002630067.1	77	133.265	111	86	C. briggsae CBR-IPLA-1 protein
Locus_2128_Transcript_3/4_Conf_0.571	2720	20	0	XP_002630067.1	73	731.865	664	490	C. briggsae CBR-IPLA-1 protein
Locus_2128_Transcript_4/4_Conf_0.571	2754	20	0	XP_002630067.1	73	731.865	664	490	C. briggsae CBR-IPLA-1 protein
Locus_21280_Transcript_1/1_Conf_1.000	289	0							
Locus_21281_Transcript_1/1_Conf_1.000	330	1	2.43E-08	NP_741467.1	67	62.003	59	40	hypothetical protein C09G4.2
Locus_21282_Transcript_1/1_Conf_1.000	323	20	2.29E-22	EFO17955.1	73	108.612	102	75	hypothetical protein LOAG_10542
Locus_21283_Transcript_1/1_Conf_1.000	216	5	1.84E-08	NP_741348.2	68	62.3882	66	45	hypothetical protein Y94H6A.5
Locus_21284_Transcript_1/1_Conf_1.000	274	0							
Locus_21285_Transcript_1/1_Conf_1.000	166	5	8.94E-19	NP_001122868.1	92	96.6709	54	50	GLIoTactin (Drosophila neuroligin-like) homolog family member (nrx-1)
Locus_21286_Transcript_1/1_Conf_1.000	218	8	1.01E-06	XP_001900229.1	62	56.6102	67	42	FAT domain containing protein
Locus_21287_Transcript_1/1_Conf_1.000	208	2	7.31E-05	XP_001901751.1	61	50.447	68	42	mKIAA0368 protein
Locus_21288_Transcript_1/1_Conf_1.000	232	6	4.05E-11	NP_492132.1	67	71.2478	71	48	Enhancer of Glp-One (glp-1) family member (ego-1)
Locus_21289_Transcript_1/1_Conf_1.000	276	0							

Locus_2129_Transcript_1/1_Conf_1.000	361	20	7.93E-60	XP_001156335.1	100	233.032	113	113	PREDICTED: similar to proliferation associated gene (pag) isoform 1
Locus_21290_Transcript_1/1_Conf_1.000	166	0							
Locus_21291_Transcript_1/1_Conf_1.000	291	12	1.49E-13	XP_002637289.1	69	79.337	96	67	Hypothetical protein CBG18976
Locus_21292_Transcript_1/1_Conf_1.000	167	0							
Locus_21293_Transcript_1/1_Conf_1.000	236	0							
Locus_21294_Transcript_1/1_Conf_1.000	283	0							
Locus_21295_Transcript_1/1_Conf_1.000	314	20	1.00E-33	XP_002643878.1	73	146.362	102	75	Hypothetical protein CBG02116
Locus_21296_Transcript_1/1_Conf_1.000	224	0							
Locus_21297_Transcript_1/1_Conf_1.000	457	20	1.84E-24	EFO15194.1	54	115.546	175	95	hypothetical protein LOAG_13318
Locus_21298_Transcript_1/1_Conf_1.000	129	2	5.98E-15	NP_491129.1	95	83.9593	42	40	hypothetical protein Y54E10A.16
Locus_21299_Transcript_1/1_Conf_1.000	230	0							
Locus_213_Transcript_1/6_Conf_0.727	1047	20	7.12E-40	XP_002639074.1	83	169.088	114	95	C. briggsae CBR-CEY-2 protein
Locus_213_Transcript_2/6_Conf_0.727	1047	20	1.59E-39	XP_002639074.1	85	167.933	109	93	C. briggsae CBR-CEY-2 protein
Locus_213_Transcript_3/6_Conf_0.409	1026	20	1.15E-42	XP_002639788.1	73	178.333	145	107	Hypothetical protein CBG02238

Locus_213_Transcript_4/6_Conf_0.409	1068	20	5.44E-43	XP_002639788.1	72	179.489	150	109	Hypothetical protein CBG02238
Locus_213_Transcript_5/6_Conf_0.409	1155	20	6.11E-43	XP_002639788.1	72	179.489	150	109	Hypothetical protein CBG02238
Locus_213_Transcript_6/6_Conf_0.409	1155	20	1.36E-42	XP_002639788.1	73	178.333	145	107	Hypothetical protein CBG02238
Locus_2130_Transcript_1/1_Conf_1.000	1047	20	2.01E-26	XP_002636810.1	49	124.405	247	123	C. briggsae CBR-MUT-14 protein
Locus_21300_Transcript_1/1_Conf_1.000	220	0							
Locus_21301_Transcript_1/1_Conf_1.000	303	20	1.52E-18	NP_741664.1	82	95.9005	76	63	hypothetical protein Y39B6A.33
Locus_21302_Transcript_1/1_Conf_1.000	381	0							
Locus_21303_Transcript_1/1_Conf_1.000	443	20	6.21E-52	AAN11401.1	75	206.838	147	111	metalloprotease 1 precursor
Locus_21304_Transcript_1/1_Conf_1.000	275	20	1.56E-39	XP_002811594.1	100	165.622	82	82	PREDICTED: protein DJ-1-like isoform 1
Locus_21305_Transcript_1/1_Conf_1.000	230	0							
Locus_21306_Transcript_1/1_Conf_1.000	336	0							
Locus_21307_Transcript_1/1_Conf_1.000	558	0							

Locus_21308_Transcript_1/1_Conf_1.000	224	20	7.66E-34	NP_001040798.1	98	146.747	74	73	PhosphoDiEsterase family member (pde-4)
Locus_21309_Transcript_1/1_Conf_1.000	247	6	8.29E-09	XP_001896275.1	71	63.5438	64	46	Ubiquitin carboxyl-terminal hydrolase family protein
Locus_2131_Transcript_1/1_Conf_1.000	723	20	1.10E-108	ABS45067.1	87	396.741	239	208	latrophilin-like protein 2
Locus_21310_Transcript_1/1_Conf_1.000	194	20	1.65E-12	XP_002630862.1	82	75.8702	58	48	C. briggsae CBR-RRT-2 protein
Locus_21311_Transcript_1/1_Conf_1.000	558	20	3.61E-50	XP_002631065.1	75	201.445	185	140	C. briggsae CBR-SFXN-1.4 protein
Locus_21312_Transcript_1/1_Conf_1.000	189	3	4.08E-11	NP_490976.1	70	71.2478	62	44	hypothetical protein F23C8.8
Locus_21313_Transcript_1/1_Conf_1.000	237	0							
Locus_21314_Transcript_1/1_Conf_1.000	280	0							
Locus_21315_Transcript_1/1_Conf_1.000	193	20	1.65E-20	XP_001896049.1	95	102.449	63	60	Patched family protein
Locus_21316_Transcript_1/1_Conf_1.000	132	0							
Locus_21317_Transcript_1/1_Conf_1.000	175	0							
Locus_21318_Transcript_1/1_Conf_1.000	223	0							
Locus_21319_Transcript_1/1_Conf_1.000	230	0							
Locus_2132_Transcript_1/1_Conf_1.000	260	20	1.70E-33	EFO18852.1	94	145.591	84	79	RNA polymerase III 128kD subunit-PA
Locus_21320_Transcript_1/1_Conf_1.000	172	0							
Locus_21321_Transcript_1/1_Conf_1.000	156	0							
Locus_21322_Transcript_1/1_Conf_1.000	207	9	3.38E-18	AAX36081.1	84	94.7449	69	58	transforming growth factor beta
Locus_21323_Transcript_1/1_Conf_1.000	461	10	1.08E-16	NP_498049.2	77	89.7373	66	51	FLYWCH zinc finger transcription factor homolog family member (flh-2)

Locus_21324_Transcript_1/1_Conf_1.000	446	20	7.86E-31	ABJ99064.1	67	136.732	145	98	Hypothetical protein W03A3.2
Locus_21325_Transcript_1/1_Conf_1.000	245	0							
Locus_21326_Transcript_1/1_Conf_1.000	197	0							
Locus_21327_Transcript_1/1_Conf_1.000	203	0							
Locus_21328_Transcript_1/1_Conf_1.000	183	20	3.83E-17	XP_002912747.1	100	91.2781	60	60	PREDICTED: tropomyosin alpha-1 chain-like isoform 2
Locus_21329_Transcript_1/1_Conf_1.000	158	1	3.54E-23	AAQ15254.1	100	111.309	52	52	AF370418_1PP14214
Locus_2133_Transcript_1/2_Conf_1.000	1256	20	8.58E-86	XP_002633413.1	81	322.013	250	203	C. briggsae CBR-ECH-2 protein
Locus_2133_Transcript_2/2_Conf_1.000	1132	20	2.92E-90	XP_002633413.1	80	336.65	266	214	C. briggsae CBR-ECH-2 protein
Locus_21330_Transcript_1/1_Conf_1.000	281	0							
Locus_21331_Transcript_1/1_Conf_1.000	423	0							
Locus_21332_Transcript_1/1_Conf_1.000	228	19	6.23E-28	NP_505844.2	90	127.102	75	68	hypothetical protein K10D6.2
Locus_21333_Transcript_1/1_Conf_1.000	244	0							
Locus_21334_Transcript_1/1_Conf_1.000	259	0							
Locus_21335_Transcript_1/1_Conf_1.000	391	20	6.12E-12	NP_492367.1	49	73.9442	139	69	Glycogen Synthase Kinase Alpha subunit family member (gska-3)
Locus_21336_Transcript_1/1_Conf_1.000	137	0							
Locus_21337_Transcript_1/1_Conf_1.000	249	3	6.10E-20	NP_493486.2	84	100.523	72	61	hypothetical protein C49A1.10

Locus_21338_Transcript_1/1_Conf_1.000	303	0							
Locus_21339_Transcript_1/1_Conf_1.000	168	0							
Locus_2134_Transcript_1/1_Conf_1.000	524	1	3.24E-04	XP_001639273.1	42	48.521	109	46	predicted protein
Locus_21340_Transcript_1/1_Conf_1.000	154	20	1.14E-21	XP_002745917.1	100	106.301	50	50	PREDICTED: heterogeneous nuclear ribonucleoproteins A2/B1-like
Locus_21341_Transcript_1/2_Conf_1.000	299	4	2.80E-04	EDL38626.1	73	48.521	49	36	multiple coagulation factor deficiency 2, isoform CRA_b
Locus_21341_Transcript_2/2_Conf_1.000	282	4	2.85E-04	EDL38626.1	73	48.521	49	36	multiple coagulation factor deficiency 2, isoform CRA_b
Locus_21342_Transcript_1/1_Conf_1.000	261	0							
Locus_21343_Transcript_1/1_Conf_1.000	378	20	1.29E-17	XP_002634314.1	72	92.8189	74	54	Hypothetical protein CBG17655
Locus_21344_Transcript_1/1_Conf_1.000	168	9	1.09E-24	ACR27076.1	100	116.316	56	56	transforming growth protein 2-like protein
Locus_21345_Transcript_1/1_Conf_1.000	241	2	4.41E-26	XP_002634586.1	88	120.939	79	70	Hypothetical protein CBG08397
Locus_21346_Transcript_1/1_Conf_1.000	154	20	1.07E-19	XP_002929569.1	100	99.7525	49	49	PREDICTED: transcription factor BTF3-like
Locus_21347_Transcript_1/1_Conf_1.000	261	7	1.26E-04	XP_002413556.1	61	49.6766	60	37	RB13-6 antigen, putative
Locus_21348_Transcript_1/1_Conf_1.000	194	0							
Locus_21349_Transcript_1/1_Conf_1.000	141	17	5.16E-19	XP_002820885.1	100	97.4413	46	46	PREDICTED: DNA damage-inducible transcript 4 protein-like isoform 1

Locus_2135_Transcript_1/1_Conf_1.000	436	20	5.87E-47	NP_508413.1	98	190.274	117	115	Ribosomal Protein, Large subunit family member (rpl-11.2)
Locus_21350_Transcript_1/1_Conf_1.000	458	20	5.94E-15	XP_001896061.1	52	83.9593	146	77	hypothetical protein Bm1_23020
Locus_21351_Transcript_1/1_Conf_1.000	371	0							
Locus_21352_Transcript_1/1_Conf_1.000	138	0							
Locus_21353_Transcript_1/1_Conf_1.000	194	0							
Locus_21354_Transcript_1/1_Conf_1.000	333	20	5.38E-16	NP_506227.1	54	87.4261	111	61	TransThyretin-Related family domain family member (ttr-29)
Locus_21355_Transcript_1/1_Conf_1.000	235	20	7.07E-32	XP_002632463.1	96	140.198	78	75	Hypothetical protein CBG13687
Locus_21356_Transcript_1/1_Conf_1.000	130	0							
Locus_21357_Transcript_1/1_Conf_1.000	281	1	3.60E-04	XP_002630436.1	70	48.1358	41	29	Hypothetical protein CBG11167
Locus_21358_Transcript_1/1_Conf_1.000	225	0							
Locus_21359_Transcript_1/1_Conf_1.000	465	20	3.76E-41	NP_001024271.1	69	171.014	152	105	CHeckpoint Kinase family member (chk-2)
Locus_2136_Transcript_1/1_Conf_1.000	2284	20	0	NP_741567.1	84	1033.86	710	601	eXPOrtin (nuclear export receptor) family member (xpo-1)
Locus_21360_Transcript_1/1_Conf_1.000	202	0							

Locus_21361_Transcript_1/1_Conf_1.000	219	10	1.37E-06	XP_001901212.1	52	56.225	61	32	Furin-like cysteine rich region family protein
Locus_21362_Transcript_1/1_Conf_1.000	907	20	4.00E-78	CAB16487.2	79	295.819	260	206	C. elegans protein Y53C12A.3, confirmed by transcript evidence
Locus_21363_Transcript_1/1_Conf_1.000	160	0							
Locus_21364_Transcript_1/1_Conf_1.000	294	3	1.54E-10	NP_491682.1	59	69.3218	101	60	MTK1/MEKK4 homolog family member (mtk-1)
Locus_21365_Transcript_1/1_Conf_1.000	281	20	4.83E-25	XP_002647206.1	73	117.472	91	67	Hypothetical protein CBG22384
Locus_21366_Transcript_1/1_Conf_1.000	165	0							
Locus_21367_Transcript_1/1_Conf_1.000	271	0							
Locus_21368_Transcript_1/1_Conf_1.000	186	0							
Locus_21369_Transcript_1/1_Conf_1.000	252	0							
Locus_2137_Transcript_1/1_Conf_1.000	667	20	1.55E-31	XP_001898376.1	61	140.198	215	132	corneal wound healing-related protein
Locus_21370_Transcript_1/1_Conf_1.000	376	20	4.17E-24	XP_002640523.1	82	114.39	78	64	Hypothetical protein CBG18685
Locus_21371_Transcript_1/1_Conf_1.000	165	20	8.96E-11	EFO27900.1	71	70.0922	57	41	ATP-dependent DNA helicase
Locus_21372_Transcript_1/1_Conf_1.000	110	0							
Locus_21373_Transcript_1/1_Conf_1.000	351	0							
Locus_21374_Transcript_1/1_Conf_1.000	269	0							
Locus_21375_Transcript_1/1_Conf_1.000	154	0							

Locus_21376_Transcript_1/1_Conf_1.000	186	1	4.85E-04	XP_002632226.1	66	47.7506	50	33	Hypothetical protein CBG07097
Locus_21377_Transcript_1/1_Conf_1.000	299	0							
Locus_21378_Transcript_1/1_Conf_1.000	252	20	2.46E-40	NP_001024999.1	97	168.318	80	78	Nuclear Hormone Receptor family member (nhr-48)
Locus_21379_Transcript_1/1_Conf_1.000	333	20	2.75E-28	EFO24634.1	71	128.257	110	79	hypothetical protein LOAG_03853
Locus_2138_Transcript_1/1_Conf_1.000	901	20	3.01E-102	ACN93881.1	88	375.941	254	224	putative glutamate-cysteine ligase modifier subunit
Locus_21380_Transcript_1/2_Conf_1.000	383	20	1.99E-10	XP_002637015.1	59	68.9366	87	52	Hypothetical protein CBG09507
Locus_21380_Transcript_2/2_Conf_1.000	407	20	1.29E-17	NP_507628.1	59	92.8189	124	74	TransThyretin-Related family domain family member (ttr-24)
Locus_21381_Transcript_1/1_Conf_1.000	539	0							
Locus_21382_Transcript_1/1_Conf_1.000	130	0							
Locus_21383_Transcript_1/1_Conf_1.000	283	18	8.86E-06	NP_504810.2	75	53.5286	36	27	UDP-GlucuronosylTransferase family member (ugt-40)
Locus_21384_Transcript_1/1_Conf_1.000	276	0							
Locus_21385_Transcript_1/1_Conf_1.000	313	20	1.32E-17	NP_500737.1	64	92.8189	97	63	hypothetical protein W03F8.3
Locus_21386_Transcript_1/2_Conf_1.000	779	20	2.05E-50	EFO28439.1	62	203.371	250	157	transcription factor E2F-4

Locus_21386_Transcript_2/2_Conf_1.000	764	20	9.77E-50	EFO28439.1	62	201.06	249	155	transcription factor E2F-4
Locus_21387_Transcript_1/1_Conf_1.000	238	20	2.51E-21	XP_002646431.1	81	105.145	79	64	Hypothetical protein CBG18813
Locus_21388_Transcript_1/1_Conf_1.000	314	9	1.15E-13	XP_001895480.1	60	79.7221	100	60	Immunoglobulin I-set domain containing protein
Locus_21389_Transcript_1/1_Conf_1.000	349	8	3.67E-12	NP_001021225.1	62	74.7146	98	61	CEll Death abnormality family member (ced-7)
Locus_2139_Transcript_1/1_Conf_1.000	1861	0							
Locus_21390_Transcript_1/1_Conf_1.000	242	20	3.37E-26	XP_002644773.1	86	121.324	67	58	Hypothetical protein CBG14786
Locus_21391_Transcript_1/1_Conf_1.000	381	20	7.47E-58	XP_002643489.1	94	226.483	127	120	C. briggsae CBR-APA-2 protein
Locus_21392_Transcript_1/1_Conf_1.000	281	20	1.05E-11	XP_002629730.1	87	73.1738	48	42	Hypothetical protein CBG00961
Locus_21393_Transcript_1/1_Conf_1.000	171	0							
Locus_21394_Transcript_1/1_Conf_1.000	559	2	7.59E-16	XP_002643026.1	54	87.4261	192	104	Hypothetical protein CBG22933
Locus_21395_Transcript_1/1_Conf_1.000	283	20	5.02E-09	XP_002595424.1	55	64.3142	94	52	hypothetical protein BRAFLDRAFT_69255
Locus_21396_Transcript_1/1_Conf_1.000	237	0							
Locus_21397_Transcript_1/1_Conf_1.000	366	0							

Locus_21398_Transcript_1/1_Conf_1.000	156	0							
Locus_21399_Transcript_1/1_Conf_1.000	172	0							
Locus_214_Transcript_1/1_Conf_1.000	793	0							
Locus_2140_Transcript_1/1_Conf_1.000	1934	20	1.91E-96	XP_001900109.1	78	358.221	266	210	SPRY domain-containing SOCS box protein SSB-4
Locus_21400_Transcript_1/1_Conf_1.000	366	20	1.30E-46	NP_001122650.1	90	189.119	121	109	PaTChed family member (ptc-3)
Locus_21401_Transcript_1/1_Conf_1.000	306	20	7.74E-23	XP_002631676.1	74	110.153	100	74	Hypothetical protein CBG20869
Locus_21402_Transcript_1/1_Conf_1.000	363	3	8.52E-30	NP_499313.2	67	133.265	119	80	hypothetical protein F43D9.1
Locus_21403_Transcript_1/1_Conf_1.000	380	1	8.14E-04	NP_504527.2	61	46.9802	54	33	hypothetical protein F26F12.3
Locus_21404_Transcript_1/1_Conf_1.000	419	0							
Locus_21405_Transcript_1/1_Conf_1.000	505	20	2.19E-52	XP_002635088.1	79	208.379	156	124	C. briggsae CBR-ASP-6 protein
Locus_21406_Transcript_1/1_Conf_1.000	242	0							
Locus_21407_Transcript_1/1_Conf_1.000	293	1	1.49E-21	NP_498957.1	72	105.916	97	70	hypothetical protein F44E2.9
Locus_21408_Transcript_1/1_Conf_1.000	296	20	5.08E-30	NP_491653.2	85	134.035	92	79	hypothetical protein F55F8.3
Locus_21409_Transcript_1/1_Conf_1.000	129	3	1.29E-09	NP_508449.1	79	66.2402	43	34	hypothetical protein R04B3.3
Locus_2141_Transcript_1/1_Conf_1.000	309	0							
Locus_21410_Transcript_1/1_Conf_1.000	132	0							

Locus_21411_Transcript_1/1_Conf_1.000	171	20	6.14E-28	EAX10909.1	98	127.102	57	56	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant), isoform CRA_a
Locus_21412_Transcript_1/1_Conf_1.000	254	0							
Locus_21413_Transcript_1/1_Conf_1.000	155	0							
Locus_21414_Transcript_1/1_Conf_1.000	422	2	4.20E-16	XP_002631299.1	67	87.8113	98	66	Hypothetical protein CBG03113
Locus_21415_Transcript_1/1_Conf_1.000	240	0							
Locus_21416_Transcript_1/1_Conf_1.000	339	0							
Locus_21417_Transcript_1/1_Conf_1.000	173	0							
Locus_21418_Transcript_1/1_Conf_1.000	231	0							
Locus_21419_Transcript_1/1_Conf_1.000	143	0							
Locus_2142_Transcript_1/2_Conf_1.000	1427	20	1.15E-52	AAD13340.1	48	212.231	450	218	ancylostoma secreted protein 1 precursor
Locus_2142_Transcript_2/2_Conf_1.000	322	1	4.80E-04	AAD13339.1	57	47.7506	83	48	ancylostoma-secreted protein 1 precursor
Locus_21420_Transcript_1/1_Conf_1.000	458	15	1.61E-20	NP_491122.2	59	102.449	119	71	hypothetical protein Y54E10A.17
Locus_21421_Transcript_1/1_Conf_1.000	243	0							
Locus_21422_Transcript_1/1_Conf_1.000	149	0							
Locus_21423_Transcript_1/1_Conf_1.000	171	7	9.85E-10	NP_501376.2	67	66.6254	55	37	hypothetical protein C07G1.2
Locus_21424_Transcript_1/1_Conf_1.000	191	20	4.81E-20	XP_002635377.1	82	100.908	63	52	Hypothetical protein CBG00768
Locus_21425_Transcript_1/1_Conf_1.000	2573	20	0	NP_497274.2	92	1009.59	591	545	hypothetical protein K02F3.2

Locus_21426_Transcript_1/1_Conf_1.000	135	0							
Locus_21427_Transcript_1/1_Conf_1.000	335	2	5.57E-13	XP_002630454.1	65	77.411	86	56	Hypothetical protein CBG11187
Locus_21428_Transcript_1/1_Conf_1.000	289	20	7.90E-31	NP_492594.2	83	136.732	95	79	hypothetical protein F26E4.5
Locus_21429_Transcript_1/1_Conf_1.000	307	7	1.32E-14	NP_001021268.1	71	82.8037	84	60	UNCoordinated family member (unc-44)
Locus_2143_Transcript_1/1_Conf_1.000	1279	20	0	EFO27018.1	94	720.694	408	387	hypothetical protein LOAG_01458
Locus_21430_Transcript_1/1_Conf_1.000	334	20	2.34E-11	AAN05752.1	65	72.0182	107	70	heat shock protein 20
Locus_21431_Transcript_1/1_Conf_1.000	407	0							
Locus_21432_Transcript_1/1_Conf_1.000	450	0							
Locus_21433_Transcript_1/1_Conf_1.000	341	0							
Locus_21434_Transcript_1/1_Conf_1.000	344	20	6.95E-19	CAO03461.1	61	97.0561	112	69	SET binding factor 1
Locus_21435_Transcript_1/1_Conf_1.000	166	20	3.51E-23	BAD92403.1	100	111.309	55	55	major histocompatibility complex, class II, DR alpha precursor variant
Locus_21436_Transcript_1/1_Conf_1.000	148	0							
Locus_21437_Transcript_1/1_Conf_1.000	171	7	2.05E-07	NP_001122684.1	90	58.9214	40	36	UNCoordinated family member (unc-103)
Locus_21438_Transcript_1/1_Conf_1.000	207	20	2.41E-32	XP_001899245.1	100	141.739	68	68	Dumpy : shorter than wild-type protein 23, isoform b

Locus_21439_Transcript_1/1_Conf_1.000	199	20	4.45E-26	AAV38526.1	100	120.939	58	58	proteasome (prosome, macropain) subunit, beta type, 3
Locus_2144_Transcript_1/3_Conf_0.714	1075	20	2.36E-86	EFO18208.1	88	323.553	199	177	hypothetical protein LOAG_10291
Locus_2144_Transcript_2/3_Conf_0.714	1079	20	2.37E-86	EFO18208.1	88	323.553	199	177	hypothetical protein LOAG_10291
Locus_2144_Transcript_3/3_Conf_0.714	1081	20	2.38E-86	EFO18208.1	88	323.553	199	177	hypothetical protein LOAG_10291
Locus_21440_Transcript_1/1_Conf_1.000	163	17	8.38E-25	BAF84240.1	100	116.701	54	54	unnamed protein product

Locus_21441_Transcript_1/1_Conf_1.000	237	15	6.00E-07	XP_002116347.1	60	57.3806	66	40	hypothetical protein TRIADDRAFT_64268
Locus_21442_Transcript_1/1_Conf_1.000	135	0							
Locus_21443_Transcript_1/1_Conf_1.000	138	0							
Locus_21444_Transcript_1/1_Conf_1.000	185	0							
Locus_21445_Transcript_1/1_Conf_1.000	314	0							
Locus_21446_Transcript_1/1_Conf_1.000	189	0							
Locus_21447_Transcript_1/1_Conf_1.000	355	20	6.85E-19	NP_001090394.1	64	97.0561	115	74	putative deoxyribonuclease tatdn3-A
Locus_21448_Transcript_1/1_Conf_1.000	140	19	2.95E-06	XP_001113618.2	100	55.0694	44	44	PREDICTED: CD82 antigen isoform 2
Locus_21449_Transcript_1/1_Conf_1.000	129	0							
Locus_2145_Transcript_1/1_Conf_1.000	456	0							
Locus_21450_Transcript_1/1_Conf_1.000	526	0							
Locus_21451_Transcript_1/1_Conf_1.000	140	0							
Locus_21452_Transcript_1/1_Conf_1.000	143	3	3.47E-07	NP_498645.1	66	58.151	48	32	MUscle Positioning family member (mup-4)

Locus_21453_Transcript_1/1_Conf_1.000	537	20	2.38E-69	XP_001894059.1	87	265.003	177	154	SMC family, C-terminal domain containing protein
Locus_21454_Transcript_1/1_Conf_1.000	202	20	1.87E-08	XP_001011065.1	54	62.3882	66	36	LIM domain containing protein
Locus_21455_Transcript_1/1_Conf_1.000	176	5	1.37E-11	NP_001022925.1	68	72.7886	58	40	hypothetical protein Y56A3A.36
Locus_21456_Transcript_1/1_Conf_1.000	176	0							
Locus_21457_Transcript_1/1_Conf_1.000	339	8	3.55E-44	ABS45067.1	87	181.03	113	99	latrophilin-like protein 2
Locus_21458_Transcript_1/1_Conf_1.000	175	0							
Locus_21459_Transcript_1/1_Conf_1.000	326	7	4.00E-43	XP_002646632.1	92	177.563	108	100	C. briggsae CBR-UNC-52 protein
Locus_2146_Transcript_1/1_Conf_1.000	1454	20	1.88E-42	XP_001895237.1	62	178.333	222	139	hypothetical protein
Locus_21460_Transcript_1/1_Conf_1.000	243	0							
Locus_21461_Transcript_1/1_Conf_1.000	230	0							
Locus_21462_Transcript_1/1_Conf_1.000	760	5	8.15E-73	XP_002645124.1	75	277.715	237	179	Hypothetical protein CBG16818
Locus_21463_Transcript_1/1_Conf_1.000	159	0							
Locus_21464_Transcript_1/1_Conf_1.000	257	5	7.71E-10	EFO23218.1	66	67.0106	59	39	hypothetical protein LOAG_05263
Locus_21465_Transcript_1/1_Conf_1.000	498	0							
Locus_21466_Transcript_1/1_Conf_1.000	323	0							
Locus_21467_Transcript_1/1_Conf_1.000	515	20	2.30E-28	XP_001899869.1	57	128.642	171	99	hypothetical protein Bm1_42035

Locus_21468_Transcript_1/1_Conf_1.000	165	2	1.25E-04	NP_509647.1	70	49.6766	51	36	hypothetical protein F47A4.5
Locus_21469_Transcript_1/1_Conf_1.000	133	0							
Locus_2147_Transcript_1/2_Conf_1.000	417	0							
Locus_2147_Transcript_2/2_Conf_1.000	413	0							
Locus_21470_Transcript_1/1_Conf_1.000	188	3	3.95E-22	XP_002633497.1	95	107.842	61	58	Hypothetical protein CBG06269
Locus_21471_Transcript_1/1_Conf_1.000	157	0							
Locus_21472_Transcript_1/1_Conf_1.000	242	0							
Locus_21473_Transcript_1/1_Conf_1.000	199	0							
Locus_21474_Transcript_1/1_Conf_1.000	321	3	1.10E-24	XP_002635291.1	67	116.316	105	71	Hypothetical protein CBG11538
Locus_21475_Transcript_1/1_Conf_1.000	271	0							
Locus_21476_Transcript_1/1_Conf_1.000	149	2	2.57E-05	NP_491716.1	78	51.9878	41	32	hypothetical protein B0207.7
Locus_21477_Transcript_1/1_Conf_1.000	182	0							
Locus_21478_Transcript_1/1_Conf_1.000	179	0							
Locus_21479_Transcript_1/1_Conf_1.000	149	0							
Locus_2148_Transcript_1/1_Conf_1.000	1485	20	2.19E-94	NP_496624.2	59	350.903	471	282	hypothetical protein Y57A10B.1
Locus_21480_Transcript_1/1_Conf_1.000	481	20	2.55E-34	XP_001893384.1	65	148.288	160	104	Plasmid Maintenance Protein containing protein
Locus_21481_Transcript_1/1_Conf_1.000	470	0							
Locus_21482_Transcript_1/1_Conf_1.000	151	0							
Locus_21483_Transcript_1/1_Conf_1.000	335	20	1.08E-32	NP_502386.1	74	142.895	111	83	hypothetical protein T04A11.2
Locus_21484_Transcript_1/1_Conf_1.000	518	20	6.17E-45	XP_002630506.1	70	183.726	167	118	C. briggsae CBR-HIM-14 protein
Locus_21485_Transcript_1/1_Conf_1.000	522	0							
Locus_21486_Transcript_1/1_Conf_1.000	475	2	1.47E-21	NP_502182.2	77	105.916	86	67	hypothetical protein F12F6.1
Locus_21487_Transcript_1/1_Conf_1.000	491	0							
Locus_21488_Transcript_1/1_Conf_1.000	314	1	7.70E-26	AAB02411.1	100	120.168	55	55	CoxII/D-loop DNA fusion protein

Locus_21489_Transcript_1/1_Conf_1.000	133	20	2.76E-20	3MQL	100	101.679	43	43	CrystalStructure OfThe Fibronectin 6fni1-2fnii7fni Fragment
Locus_2149_Transcript_1/1_Conf_1.000	644	7	6.66E-21	CBI83239.1	54	104.76	130	71	C. elegans protein W06F12.2e, confirmed by transcript evidence
Locus_21490_Transcript_1/1_Conf_1.000	154	1	1.66E-04	NP_001076620.1	60	49.2914	45	27	hypothetical protein Y34D9A.8
Locus_21491_Transcript_1/1_Conf_1.000	242	20	4.55E-31	NP_001021650.1	90	137.502	80	72	HaMmeRhead embryonic lethal family member (hmr-1)
Locus_21492_Transcript_1/1_Conf_1.000	775	0							
Locus_21493_Transcript_1/1_Conf_1.000	297	0							
Locus_21494_Transcript_1/1_Conf_1.000	377	4	5.81E-34	NP_493078.2	73	147.132	125	92	hypothetical protein R05D7.5
Locus_21495_Transcript_1/1_Conf_1.000	398	0							
Locus_21496_Transcript_1/1_Conf_1.000	194	0							
Locus_21497_Transcript_1/1_Conf_1.000	281	3	2.33E-11	NP_499961.2	65	72.0182	93	61	Nuclear Hormone Receptor family member (nhr-76)
Locus_21498_Transcript_1/1_Conf_1.000	170	0							
Locus_21499_Transcript_1/1_Conf_1.000	137	0							
Locus_215_Transcript_1/2_Conf_1.000	983	16	4.01E-58	CAR63537.1	67	229.565	202	137	putative Lipid Binding Protein
Locus_215_Transcript_2/2_Conf_1.000	854	20	1.74E-64	CAR63537.1	86	250.366	159	137	putative Lipid Binding Protein
Locus_2150_Transcript_1/1_Conf_1.000	342	20	5.13E-30	NP_494366.2	78	134.035	111	87	hypothetical protein F08D12.1
Locus_21500_Transcript_1/1_Conf_1.000	384	0							
Locus_21501_Transcript_1/1_Conf_1.000	137	0							
Locus_21502_Transcript_1/1_Conf_1.000	309	0							

Locus_21503_Transcript_1/1_Conf_1.000	328	20	3.28E-29	NP_496542.1	76	131.339	108	83	hypothetical protein ZK930.1
Locus_21504_Transcript_1/1_Conf_1.000	189	1	1.83E-11	NP_499637.2	77	72.4034	61	47	hypothetical protein Y111B2A.8
Locus_21505_Transcript_1/1_Conf_1.000	621	0							
Locus_21506_Transcript_1/1_Conf_1.000	213	4	3.15E-08	XP_002636889.1	62	61.6178	67	42	C. briggsae CBR-HEX-2 protein
Locus_21507_Transcript_1/1_Conf_1.000	271	0							
Locus_21508_Transcript_1/1_Conf_1.000	128	0							
Locus_21509_Transcript_1/1_Conf_1.000	168	0							
Locus_2151_Transcript_1/1_Conf_1.000	773	20	1.75E-86	XP_002640077.1	81	323.168	253	206	Hypothetical protein CBG12562
Locus_21510_Transcript_1/1_Conf_1.000	444	0							
Locus_21511_Transcript_1/1_Conf_1.000	134	0							
Locus_21512_Transcript_1/1_Conf_1.000	178	0							
Locus_21513_Transcript_1/1_Conf_1.000	129	0							
Locus_21514_Transcript_1/1_Conf_1.000	177	20	5.92E-15	NP_499784.2	84	83.9593	58	49	KELch-repeat containing protein family member (kel-3)
Locus_21515_Transcript_1/1_Conf_1.000	201	0							
Locus_21516_Transcript_1/1_Conf_1.000	227	0							
Locus_21517_Transcript_1/1_Conf_1.000	160	0							
Locus_21518_Transcript_1/1_Conf_1.000	137	11	1.46E-13	NP_871654.2	93	79.337	45	42	GEX Interacting protein family member (gei-4)
Locus_21519_Transcript_1/1_Conf_1.000	315	6	1.45E-16	AAV41897.1	69	89.3521	94	65	SAX-2
Locus_2152_Transcript_1/1_Conf_1.000	2478	20	0	NP_498283.1	77	983.786	817	632	hypothetical protein C28H8.3
Locus_21520_Transcript_1/1_Conf_1.000	209	0							
Locus_21521_Transcript_1/1_Conf_1.000	155	0							
Locus_21522_Transcript_1/1_Conf_1.000	219	0							

Locus_21523_Transcript_1/1_Conf_1.000	138	20	6.13E-12	EFO27870.1	89	73.9442	46	41	CMGC/CDK/CDK7 protein kinase
Locus_21524_Transcript_1/1_Conf_1.000	306	4	1.84E-24	NP_508923.1	77	115.546	98	76	hypothetical protein C41A3.1
Locus_21525_Transcript_1/1_Conf_1.000	273	20	7.79E-15	XP_001900299.1	60	83.5741	87	53	Protein-tyrosine phosphatase containing protein
Locus_21526_Transcript_1/1_Conf_1.000	554	0							
Locus_21527_Transcript_1/1_Conf_1.000	142	11	7.71E-15	ACJ65168.1	93	83.5741	44	41	Uncoordinated protein 68, isoform b, partially confirmed by transcript evidence
Locus_21528_Transcript_1/1_Conf_1.000	131	0							
Locus_21529_Transcript_1/1_Conf_1.000	180	0							
Locus_2153_Transcript_1/1_Conf_1.000	443	0							
Locus_21530_Transcript_1/1_Conf_1.000	356	2	3.30E-05	XP_001901347.1	55	51.6026	76	42	DNA excision repair protein ERCC-6
Locus_21531_Transcript_1/1_Conf_1.000	324	0							
Locus_21532_Transcript_1/1_Conf_1.000	264	0							
Locus_21533_Transcript_1/2_Conf_1.000	731	0							
Locus_21533_Transcript_2/2_Conf_1.000	731	0							
Locus_21534_Transcript_1/1_Conf_1.000	277	2	3.27E-05	EFO19241.1	53	51.6026	88	47	hypothetical protein LOAG_09252
Locus_21535_Transcript_1/1_Conf_1.000	173	0							
Locus_21536_Transcript_1/1_Conf_1.000	223	20	1.27E-20	XP_002645688.1	83	102.834	62	52	C. briggsae CBR-ELT-3 protein

Locus_21537_Transcript_1/1_Conf_1.000	170	17	1.74E-06	NP_001165114.1	70	55.8398	54	38	collagen
Locus_21538_Transcript_1/1_Conf_1.000	542	20	4.95E-30	XP_002636579.1	75	134.42	103	78	Hypothetical protein CBG23273
Locus_21539_Transcript_1/1_Conf_1.000	152	4	1.89E-16	EFO25124.1	89	88.9669	47	42	bromodomain containing protein
Locus_2154_Transcript_1/1_Conf_1.000	1064	20	7.66E-98	NP_494772.1	74	361.688	281	209	NOT-Like (yeast CCR4/NOT complex component) family member (ntl-2)
Locus_21540_Transcript_1/1_Conf_1.000	411	20	8.84E-27	XP_002114490.1	65	123.25	127	83	hypothetical protein TRIADDRAFT_27462
Locus_21541_Transcript_1/1_Conf_1.000	171	0							
Locus_21542_Transcript_1/1_Conf_1.000	645	1	1.61E-06	XP_002634576.1	60	56.9954	75	45	C. briggsae CBR-SRB-17 protein
Locus_21543_Transcript_1/1_Conf_1.000	332	1	4.15E-08	XP_002640024.1	66	61.2326	115	77	Hypothetical protein CBG12496
Locus_21544_Transcript_1/1_Conf_1.000	302	20	3.86E-30	NP_500647.2	78	134.42	99	78	Dipeptidyl Peptidase Four (IV) family member (dpf-5)
Locus_21545_Transcript_1/1_Conf_1.000	860	20	9.45E-26	XP_001893874.1	48	121.709	284	139	Smr domain containing protein
Locus_21546_Transcript_1/1_Conf_1.000	151	20	1.27E-20	XP_001107614.2	100	102.834	49	49	PREDICTED: inorganic pyrophosphatase-like
Locus_21547_Transcript_1/1_Conf_1.000	145	0							
Locus_21548_Transcript_1/1_Conf_1.000	323	20	7.11E-32	XP_002630378.1	77	140.198	109	84	Hypothetical protein CBG04317
Locus_21549_Transcript_1/1_Conf_1.000	143	0							
Locus_2155_Transcript_1/2_Conf_1.000	295	0							
Locus_2155_Transcript_2/2_Conf_1.000	293	0							
Locus_21550_Transcript_1/1_Conf_1.000	258	4	4.65E-15	XP_002646447.1	69	84.3445	73	51	Hypothetical protein CBG18852
Locus_21551_Transcript_1/1_Conf_1.000	151	0							
Locus_21552_Transcript_1/1_Conf_1.000	232	0							

Locus_21553_Transcript_1/1_Conf_1.000	139	0							
Locus_21554_Transcript_1/1_Conf_1.000	155	6	2.17E-04	XP_002648446.1	68	48.9062	45	31	Hypothetical protein CBG24721
Locus_21555_Transcript_1/1_Conf_1.000	132	0							
Locus_21556_Transcript_1/1_Conf_1.000	524	20	7.42E-25	XP_001894749.1	59	117.087	162	97	galactokinase family protein
Locus_21557_Transcript_1/1_Conf_1.000	187	0							
Locus_21558_Transcript_1/1_Conf_1.000	590	20	1.24E-78	XP_002633788.1	83	296.204	189	157	C. briggsae CBR-FAT-4 protein
Locus_21559_Transcript_1/1_Conf_1.000	231	0							
Locus_2156_Transcript_1/2_Conf_1.000	1078	12	6.52E-44	XP_002640218.1	51	182.57	276	142	C. briggsae CBR-ZTF-4 protein
Locus_2156_Transcript_2/2_Conf_1.000	336	0							
Locus_21560_Transcript_1/1_Conf_1.000	263	0							
Locus_21561_Transcript_1/1_Conf_1.000	171	0							
Locus_21562_Transcript_1/1_Conf_1.000	298	0							
Locus_21563_Transcript_1/1_Conf_1.000	187	20	8.79E-22	XP_001898118.1	94	106.686	59	56	FYVE finger-containing phosphoinositide kinase
Locus_21564_Transcript_1/1_Conf_1.000	193	0							
Locus_21565_Transcript_1/1_Conf_1.000	279	0							
Locus_21566_Transcript_1/1_Conf_1.000	129	0							
Locus_21567_Transcript_1/2_Conf_1.000	198	0							
Locus_21567_Transcript_2/2_Conf_1.000	272	0							
Locus_21568_Transcript_1/1_Conf_1.000	378	20	8.07E-36	XP_002642916.1	91	153.295	87	80	C. briggsae CBR-TAG-168 protein
Locus_21569_Transcript_1/1_Conf_1.000	489	2	8.70E-06	XP_002634144.1	64	53.5286	48	31	Hypothetical protein CBG01705
Locus_2157_Transcript_1/2_Conf_1.000	1640	20	0	NP_001021071.1	83	675.626	452	378	hypothetical protein D1007.5
Locus_2157_Transcript_2/2_Conf_1.000	1640	20	0	NP_001021071.1	83	675.626	452	378	hypothetical protein D1007.5

Locus_21570_Transcript_1/1_Conf_1.000	229	20	2.22E-17	EFO19956.1	77	92.0485	68	53	hypothetical protein LOAG_08535
Locus_21571_Transcript_1/1_Conf_1.000	497	20	1.77E-51	XP_002636314.1	81	205.297	166	135	Hypothetical protein CBG08607
Locus_21572_Transcript_1/1_Conf_1.000	158	0							
Locus_21573_Transcript_1/1_Conf_1.000	168	0							
Locus_21574_Transcript_1/1_Conf_1.000	149	2	2.66E-10	NP_497053.1	83	68.5514	48	40	hypothetical protein C09F9.2
Locus_21575_Transcript_1/1_Conf_1.000	178	0							
Locus_21576_Transcript_1/1_Conf_1.000	329	0							
Locus_21577_Transcript_1/1_Conf_1.000	318	0							
Locus_21578_Transcript_1/1_Conf_1.000	149	20	8.83E-14	XP_002920932.1	100	80.1073	35	35	PREDICTED: lipolysis-stimulated lipoprotein receptor-like
Locus_21579_Transcript_1/1_Conf_1.000	259	20	3.67E-20	NP_493023.1	80	101.293	67	54	hypothetical protein R09B3.3
Locus_2158_Transcript_1/2_Conf_1.000	581	12	9.31E-63	XP_002637005.1	87	243.432	166	146	Hypothetical protein CBG09497
Locus_2158_Transcript_2/2_Conf_1.000	581	12	9.31E-63	XP_002637005.1	87	243.432	166	146	Hypothetical protein CBG09497
Locus_21580_Transcript_1/1_Conf_1.000	132	0							
Locus_21581_Transcript_1/1_Conf_1.000	330	0							
Locus_21582_Transcript_1/1_Conf_1.000	485	20	6.91E-27	NP_491361.1	59	123.635	161	96	hypothetical protein ZK973.11
Locus_21583_Transcript_1/1_Conf_1.000	291	20	9.04E-11	XP_970144.1	63	70.0922	96	61	PREDICTED: similar to conserved hypothetical protein
Locus_21584_Transcript_1/1_Conf_1.000	426	12	3.35E-74	XP_002633317.1	95	280.796	141	134	Hypothetical protein CBG06054

Locus_21585_Transcript_1/1_Conf_1.000	184	0							
Locus_21586_Transcript_1/1_Conf_1.000	366	20	5.68E-34	XP_002639355.1	73	147.132	122	90	Hypothetical protein CBG03934
Locus_21587_Transcript_1/1_Conf_1.000	483	0							
Locus_21588_Transcript_1/1_Conf_1.000	130	1	2.13E-04	XP_002646581.1	77	48.9062	44	34	Hypothetical protein CBG20463
Locus_21589_Transcript_1/1_Conf_1.000	234	20	5.97E-39	BAG58796.1	100	163.696	78	78	unnamed protein product
Locus_2159_Transcript_1/1_Conf_1.000	1025	8	3.34E-18	XP_002637670.1	40	97.0561	360	145	C. briggsae CBR-RDE-1 protein
Locus_21590_Transcript_1/1_Conf_1.000	136	2	7.52E-10	NP_495168.1	84	67.0106	45	38	hypothetical protein H41C03.1
Locus_21591_Transcript_1/1_Conf_1.000	197	0							
Locus_21592_Transcript_1/1_Conf_1.000	220	20	7.99E-15	NP_494994.1	75	83.5741	73	55	hypothetical protein ZK622.1
Locus_21593_Transcript_1/1_Conf_1.000	150	0							
Locus_21594_Transcript_1/1_Conf_1.000	190	0							
Locus_21595_Transcript_1/1_Conf_1.000	132	0							
Locus_21596_Transcript_1/1_Conf_1.000	198	1	6.25E-04	XP_001915506.1	74	47.3654	35	26	PREDICTED: similar to alpha-2-glycoprotein 1, zinc-binding
Locus_21597_Transcript_1/1_Conf_1.000	605	20	8.23E-72	NP_503138.1	82	210.305	151	125	hypothetical protein W03F9.1
Locus_21598_Transcript_1/1_Conf_1.000	141	20	7.96E-20	BAD96655.1	100	100.138	46	46	transcription factor-like 1 variant
Locus_21599_Transcript_1/1_Conf_1.000	503	0							

Locus_216_Transcript_1/1_Conf_1.000	891	20	8.35E-81	XP_002636473.1	80	304.679	220	177	Hypothetical protein CBG23144
Locus_2160_Transcript_1/1_Conf_1.000	569	20	9.35E-49	NP_001040840.1	75	196.823	179	136	hypothetical protein C02D5.2
Locus_21600_Transcript_1/1_Conf_1.000	192	0							
Locus_21601_Transcript_1/1_Conf_1.000	504	20	7.77E-58	NP_501991.2	80	226.483	153	123	hypothetical protein T25B9.1
Locus_21602_Transcript_1/1_Conf_1.000	129	0							
Locus_21603_Transcript_1/1_Conf_1.000	1342	4	9.34E-25	XP_002645538.1	71	119.398	91	65	Hypothetical protein CBG22805
Locus_21604_Transcript_1/1_Conf_1.000	130	0							
Locus_21605_Transcript_1/1_Conf_1.000	803	20	2.03E-72	NP_509284.2	76	276.559	190	146	UNCoordinated family member (unc-98)
Locus_21606_Transcript_1/1_Conf_1.000	273	7	2.25E-38	XP_002633317.1	91	161.77	90	82	Hypothetical protein CBG06054
Locus_21607_Transcript_1/1_Conf_1.000	648	20	4.29E-15	NP_491348.1	88	85.5001	68	60	SCP(Small C-terminal domain Phosphatase)-Like phosphatase family member (scpl-3)
Locus_21608_Transcript_1/1_Conf_1.000	241	20	3.05E-27	NP_500943.1	82	124.79	76	63	hypothetical protein F58F9.7
Locus_21609_Transcript_1/1_Conf_1.000	520	20	1.31E-58	XP_002629752.1	86	229.18	145	126	Hypothetical protein CBG00986

Locus_2161_Transcript_1/2_Conf_1.000	568	20	6.35E-05	ZP_01908754.1	60	51.2174	70	42	putative transcriptional regulator
Locus_2161_Transcript_2/2_Conf_1.000	692	20	4.31E-11	XP_002191349.1	59	72.4034	110	65	PREDICTED: hypothetical protein, partial
Locus_21610_Transcript_1/1_Conf_1.000	322	0							
Locus_21611_Transcript_1/1_Conf_1.000	363	0							
Locus_21612_Transcript_1/1_Conf_1.000	188	0							
Locus_21613_Transcript_1/1_Conf_1.000	130	20	8.36E-09	XP_001899525.1	80	63.5438	42	34	C-terminal binding protein
Locus_21614_Transcript_1/1_Conf_1.000	180	1	5.94E-18	NP_510548.2	100	93.9745	43	43	hypothetical protein F39D8.3
Locus_21615_Transcript_1/1_Conf_1.000	284	20	6.32E-20	NP_501792.2	74	100.523	93	69	abnormal GONad development family member (gon-1)
Locus_21616_Transcript_1/1_Conf_1.000	156	20	4.79E-20	NP_001021901.1	98	100.908	51	50	CLC-type chloride cHannel family member (clh-2)
Locus_21617_Transcript_1/1_Conf_1.000	145	3	1.85E-11	NP_001021685.1	83	72.4034	48	40	ZO-1 (Zonula Occludens tight junctional protein) Ortholog family member (zoo-1)
Locus_21618_Transcript_1/1_Conf_1.000	354	20	1.87E-08	EFO14379.1	80	62.3882	42	34	hypothetical protein LOAG_14143
Locus_21619_Transcript_1/1_Conf_1.000	281	2	9.78E-10	NP_001032983.1	74	66.6254	78	58	hypothetical protein W05F2.4

Locus_2162_Transcript_1/1_Conf_1.000	1136	20	7.53E-62	NP_505962.2	60	242.276	336	202	Nuclear Pore complex Protein family member (npp-22)
Locus_21620_Transcript_1/1_Conf_1.000	168	0							
Locus_21621_Transcript_1/1_Conf_1.000	447	0							
Locus_21622_Transcript_1/1_Conf_1.000	242	20	4.00E-19	EFO22882.1	86	97.8265	61	53	TK/FER protein kinase
Locus_21623_Transcript_1/1_Conf_1.000	144	3	1.62E-07	XP_002639976.1	83	59.3066	48	40	C. briggsae CBR-KIN-32 protein
Locus_21624_Transcript_1/1_Conf_1.000	159	0							
Locus_21625_Transcript_1/1_Conf_1.000	132	0							
Locus_21626_Transcript_1/1_Conf_1.000	241	20	1.38E-11	XP_002630247.1	72	72.7886	79	57	Hypothetical protein CBG00666
Locus_21627_Transcript_1/1_Conf_1.000	195	0							
Locus_21628_Transcript_1/1_Conf_1.000	291	1	2.72E-15	NP_001076618.1	73	85.1149	76	56	hypothetical protein Y110A7A.21
Locus_21629_Transcript_1/1_Conf_1.000	603	20	5.72E-21	XP_002632199.1	52	104.76	180	95	C. briggsae CBR-NOL-1 protein
Locus_2163_Transcript_1/1_Conf_1.000	162	0							
Locus_21630_Transcript_1/1_Conf_1.000	267	20	2.36E-19	XP_002633705.1	80	98.5969	77	62	C. briggsae CBR-ECH-9 protein
Locus_21631_Transcript_1/1_Conf_1.000	157	0							
Locus_21632_Transcript_1/1_Conf_1.000	232	1	4.33E-05	NP_490917.3	45	51.2174	87	40	hypothetical protein Y20F4.2
Locus_21633_Transcript_1/1_Conf_1.000	141	20	2.25E-06	BAG60188.1	100	55.4546	46	46	unnamed protein product
Locus_21634_Transcript_1/1_Conf_1.000	289	0							
Locus_21635_Transcript_1/1_Conf_1.000	216	0							

Locus_21636_Transcript_1/1_Conf_1.000	392	9	1.07E-32	XP_002640798.1	75	142.895	131	99	C. briggsae CBR-NHR-121 protein
Locus_21637_Transcript_1/1_Conf_1.000	309	0							
Locus_21638_Transcript_1/1_Conf_1.000	195	20	6.44E-25	XP_002829151.1	100	117.087	53	53	PREDICTED: tubulin-folding cofactor B-like
Locus_21639_Transcript_1/1_Conf_1.000	206	20	3.07E-19	XP_002633255.1	82	98.2117	68	56	Hypothetical protein CBG05980
Locus_2164_Transcript_1/2_Conf_1.000	330	0							
Locus_2164_Transcript_2/2_Conf_1.000	273	0							
Locus_21640_Transcript_1/1_Conf_1.000	332	0							
Locus_21641_Transcript_1/1_Conf_1.000	295	20	3.78E-17	EFO25770.1	100	91.2781	61	61	hypothetical protein LOAG_02719
Locus_21642_Transcript_1/1_Conf_1.000	324	3	2.80E-04	XP_002128277.1	50	48.521	77	39	PREDICTED: hypothetical protein
Locus_21643_Transcript_1/1_Conf_1.000	322	0							
Locus_21644_Transcript_1/1_Conf_1.000	153	0							
Locus_21645_Transcript_1/1_Conf_1.000	162	0							
Locus_21646_Transcript_1/1_Conf_1.000	305	2	2.96E-14	NP_498845.2	78	81.6481	55	43	hypothetical protein R05D3.9
Locus_21647_Transcript_1/1_Conf_1.000	408	20	5.87E-71	XP_002705104.1	100	270.011	135	135	PREDICTED: ribosomal protein L9-like

Locus_21648_Transcript_1/1_Conf_1.000	353	20	4.62E-07	XP_001636445.1	45	57.7658	137	63	predicted protein
Locus_21649_Transcript_1/1_Conf_1.000	186	20	5.15E-22	XP_002639246.1	83	107.457	62	52	Hypothetical protein CBG03805
Locus_2165_Transcript_1/2_Conf_0.500	351	20	7.31E-37	NP_501862.1	67	156.762	141	95	GABA TransAminase family member (gta-1)
Locus_2165_Transcript_2/2_Conf_0.750	891	20	1.96E-130	NP_501862.1	87	469.544	286	251	GABA TransAminase family member (gta-1)
Locus_21650_Transcript_1/1_Conf_1.000	341	0							
Locus_21651_Transcript_1/1_Conf_1.000	267	0							
Locus_21652_Transcript_1/1_Conf_1.000	255	0							
Locus_21653_Transcript_1/1_Conf_1.000	153	0							
Locus_21654_Transcript_1/2_Conf_1.000	714	8	1.93E-09	AAT40504.2	50	67.0106	121	61	Polyprotein, putative
Locus_21654_Transcript_2/2_Conf_1.000	714	8	1.93E-09	AAT40504.2	50	67.0106	121	61	Polyprotein, putative
Locus_21655_Transcript_1/1_Conf_1.000	181	0							

Locus_21656_Transcript_1/1_Conf_1.000	240	20	7.80E-15	CAD44516.1	73	83.5741	78	57	VAB-10B protein
Locus_21657_Transcript_1/1_Conf_1.000	149	0							
Locus_21658_Transcript_1/1_Conf_1.000	579								
Locus_21659_Transcript_1/1_Conf_1.000	196	0							
Locus_2166_Transcript_1/1_Conf_1.000	696	5	7.03E-09	XP_002639759.1	47	65.0846	93	44	Hypothetical protein CBG02205
Locus_21660_Transcript_1/1_Conf_1.000	291	0							
Locus_21661_Transcript_1/1_Conf_1.000	175	0							
Locus_21662_Transcript_1/1_Conf_1.000	181	0							
Locus_21663_Transcript_1/1_Conf_1.000	219	20	5.36E-11	XP_002639380.1	65	70.8626	70	46	Hypothetical protein CBG03966
Locus_21664_Transcript_1/1_Conf_1.000	1792	20	1.42E-98	EFO26157.1	59	365.155	561	333	type III restriction enzyme
Locus_21665_Transcript_1/1_Conf_1.000	145	0							
Locus_21666_Transcript_1/1_Conf_1.000	983	20	4.08E-119	XP_002639292.1	76	432.18	338	258	C. briggsae CBR-NHR-62 protein
Locus_21667_Transcript_1/1_Conf_1.000	219	0							
Locus_21668_Transcript_1/1_Conf_1.000	298	0							
Locus_21669_Transcript_1/1_Conf_1.000	249	7	1.55E-23	NP_491915.2	83	112.464	77	64	hypothetical protein ZC581.9
Locus_2167_Transcript_1/1_Conf_1.000	1206	20	8.23E-54	EFO26832.1	70	215.698	179	126	hypothetical protein LOAG_01653

Locus_21670_Transcript_1/1_Conf_1.000	142	20	2.32E-19	XP_002923631.1	100	98.5969	47	47	PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like isoform 2
Locus_21671_Transcript_1/1_Conf_1.000	338	0							
Locus_21672_Transcript_1/1_Conf_1.000	297	0							
Locus_21673_Transcript_1/1_Conf_1.000	140	0							
Locus_21674_Transcript_1/1_Conf_1.000	344	20	7.64E-42	ACT52846.1	84	173.326	112	95	GMP reductase
Locus_21675_Transcript_1/1_Conf_1.000	180	0							
Locus_21676_Transcript_1/1_Conf_1.000	156	2	2.63E-10	NP_492746.2	82	68.5514	50	41	Temporarily Assigned Gene name family member (tag-68)
Locus_21677_Transcript_1/1_Conf_1.000	446	0							
Locus_21678_Transcript_1/1_Conf_1.000	487	20	6.63E-38	NP_498761.1	68	160.229	166	114	DiCer Related family member (dcr-1)
Locus_21679_Transcript_1/1_Conf_1.000	360	0							
Locus_2168_Transcript_1/1_Conf_1.000	155	0							
Locus_21680_Transcript_1/1_Conf_1.000	140	7	8.01E-12	XP_002634930.1	91	73.559	46	42	Hypothetical protein CBG22529
Locus_21681_Transcript_1/1_Conf_1.000	224	0							
Locus_21682_Transcript_1/1_Conf_1.000	406	6	1.13E-13	NP_501855.1	61	79.7221	100	61	TransThyretin-Related family domain family member (ttr-54)

Locus_21683_Transcript_1/1_Conf_1.000	431	20	6.55E-46	EFO19591.1	92	186.808	107	99	hypothetical protein LOAG_08901
Locus_21684_Transcript_1/1_Conf_1.000	138	2	4.11E-08	XP_511489.2	79	61.2326	39	31	PREDICTED: similar to isolog of yeast sui1 and rice gos2; putative
Locus_21685_Transcript_1/1_Conf_1.000	156	20	3.43E-18	EFO22882.1	92	94.7449	52	48	TK/FER protein kinase
Locus_21686_Transcript_1/1_Conf_1.000	195	20	4.18E-24	BAJ21087.1	100	114.39	56	56	transcription elongation factor B (SIII), polypeptide 2
Locus_21687_Transcript_1/1_Conf_1.000	189	0							
Locus_21688_Transcript_1/1_Conf_1.000	182	20	9.78E-21	XP_002639101.1	88	103.219	60	53	Hypothetical protein CBG14920
Locus_21689_Transcript_1/1_Conf_1.000	370	20	2.82E-20	XP_001894671.1	66	101.679	113	75	Protein kinase domain containing protein
Locus_2169_Transcript_1/1_Conf_1.000	2527	20	0	XP_002630210.1	71	853.203	829	596	C. briggsae CBR-ZYG-9 protein
Locus_21690_Transcript_1/1_Conf_1.000	180	0							
Locus_21691_Transcript_1/1_Conf_1.000	693	20	3.25E-107	XP_001902629.1	87	391.734	230	201	Zinc finger, C2H2 type family protein

Locus_21692_Transcript_1/1_Conf_1.000	145	20	2.04E-10	NP_495516.2	85	68.9366	48	41	hypothetical protein F32A5.8
Locus_21693_Transcript_1/1_Conf_1.000	139	20	1.28E-17	XP_002750292.1	100	92.8189	46	46	PREDICTED: alpha-enolase isoform 1
Locus_21694_Transcript_1/1_Conf_1.000	360	0							
Locus_21695_Transcript_1/1_Conf_1.000	289	20	8.17E-28	NP_496501.2	77	126.716	94	73	hypothetical protein F13D12.9
Locus_21696_Transcript_1/1_Conf_1.000	128	0							
Locus_21697_Transcript_1/1_Conf_1.000	173	0							
Locus_21698_Transcript_1/1_Conf_1.000	403	20	3.89E-22	XP_002648413.1	76	107.842	77	59	Hypothetical protein CBG24676
Locus_21699_Transcript_1/1_Conf_1.000	174	20	2.11E-20	XP_002636607.1	90	102.064	53	48	C. briggsae CBR-DHS-20 protein
Locus_217_Transcript_1/2_Conf_1.000	195	2	1.35E-06	XP_002425519.1	64	56.225	64	41	conserved hypothetical protein
Locus_217_Transcript_2/2_Conf_1.000	223	4	4.36E-13	XP_002425519.1	68	77.7962	73	50	conserved hypothetical protein
Locus_2170_Transcript_1/1_Conf_1.000	320	0							
Locus_21700_Transcript_1/1_Conf_1.000	224	0							
Locus_21701_Transcript_1/1_Conf_1.000	334	15	9.46E-29	XP_002638532.1	84	129.798	92	78	Hypothetical protein CBG05566
Locus_21702_Transcript_1/1_Conf_1.000	701	20	6.89E-113	XP_002638687.1	90	410.609	233	212	Hypothetical protein CBG11882
Locus_21703_Transcript_1/1_Conf_1.000	154	0							
Locus_21704_Transcript_1/1_Conf_1.000	196	20	1.22E-15	XP_002630450.1	75	86.2705	64	48	C. briggsae CBR-ASM-1 protein
Locus_21705_Transcript_1/1_Conf_1.000	149	0							

Locus_21706_Transcript_1/1_Conf_1.000	274	0							
Locus_21707_Transcript_1/1_Conf_1.000	314	0							
Locus_21708_Transcript_1/1_Conf_1.000	264	0							
Locus_21709_Transcript_1/1_Conf_1.000	351	20	6.04E-07	ZP_04769408.1	49	57.3806	109	54	gamma-glutamyltransferase
Locus_2171_Transcript_1/1_Conf_1.000	990	20	1.12E-31	XP_002731938.1	51	141.739	281	146	PREDICTED: sestrin 1-like
Locus_21710_Transcript_1/1_Conf_1.000	132	5	1.09E-08	XP_001901288.1	80	63.1586	42	34	hypothetical protein Bm1_49115
Locus_21711_Transcript_1/1_Conf_1.000	217	0							
Locus_21712_Transcript_1/1_Conf_1.000	148	20	8.24E-20	XP_001099130.2	100	100.138	48	48	PREDICTED: collagen alpha-2(VI) chain-like isoform 3
Locus_21713_Transcript_1/1_Conf_1.000	345	5	1.54E-34	NP_492157.2	79	149.058	112	89	hypothetical protein D2005.6
Locus_21714_Transcript_1/1_Conf_1.000	377	20	1.62E-60	NP_506269.1	99	235.343	125	124	EATing: abnormal pharyngeal pumping family member (eat-6)
Locus_21715_Transcript_1/1_Conf_1.000	138	0							
Locus_21716_Transcript_1/1_Conf_1.000	172	0							
Locus_21717_Transcript_1/1_Conf_1.000	470	4	2.78E-36	A8Y3Q1.2	81	154.836	101	82	Putative 28S ribosomal protein S5
Locus_21718_Transcript_1/1_Conf_1.000	207	20	1.80E-11	XP_002632023.1	65	72.4034	63	41	Hypothetical protein CBG10312
Locus_21719_Transcript_1/1_Conf_1.000	183	0							

Locus_2172_Transcript_1/1_Conf_1.000	1676	20	0	AAX36933.1	100	877.856	432	432	eukaryotic translation elongation factor 1 alpha 1
Locus_21720_Transcript_1/1_Conf_1.000	175	0							
Locus_21721_Transcript_1/1_Conf_1.000	373	20	4.46E-34	XP_001898170.1	75	147.517	121	91	Ubiquitin-conjugating enzyme family protein
Locus_21722_Transcript_1/1_Conf_1.000	178	0							
Locus_21723_Transcript_1/1_Conf_1.000	320	4	5.86E-18	NP_495792.1	68	93.9745	95	65	hypothetical protein M05D6.6
Locus_21724_Transcript_1/1_Conf_1.000	288	0							
Locus_21725_Transcript_1/1_Conf_1.000	377	0							
Locus_21726_Transcript_1/1_Conf_1.000	201	0							
Locus_21727_Transcript_1/1_Conf_1.000	157	20	2.15E-20	XP_002822113.1	100	102.064	51	51	PREDICTED: eukaryotic translation initiation factor 3 subunit F-like isoform 3
Locus_21728_Transcript_1/1_Conf_1.000	433	20	4.24E-37	NP_502676.3	70	157.532	143	101	hypothetical protein Y37A1A.2
Locus_21729_Transcript_1/1_Conf_1.000	523	20	4.05E-39	XP_002631431.1	75	164.466	161	121	C. briggsae CBR-TAG-341 protein
Locus_2173_Transcript_1/2_Conf_1.000	456	20	2.40E-24	NP_741102.1	84	115.161	119	100	UBiquitin-Like family member (ubl-1)
Locus_2173_Transcript_2/2_Conf_1.000	144	0							
Locus_21730_Transcript_1/1_Conf_1.000	239	0							

Locus_21731_Transcript_1/1_Conf_1.000	145	1	1.28E-04	XP_002638613.1	86	49.6766	43	37	C. briggsae CBR-PGP-9 protein
Locus_21732_Transcript_1/1_Conf_1.000	231	0							
Locus_21733_Transcript_1/2_Conf_1.000	219	0							
Locus_21733_Transcript_2/2_Conf_1.000	219	0							
Locus_21734_Transcript_1/1_Conf_1.000	508	20	2.58E-32	XP_002640010.1	77	141.739	132	102	Hypothetical protein CBG12480
Locus_21735_Transcript_1/1_Conf_1.000	213	0							
Locus_21736_Transcript_1/1_Conf_1.000	421	13	5.11E-30	AAK31453.4	64	134.035	151	97	Hypothetical protein C25H3.8
Locus_21737_Transcript_1/1_Conf_1.000	411	0							
Locus_21738_Transcript_1/1_Conf_1.000	218	20	3.35E-10	XP_002647313.1	68	68.1662	66	45	Hypothetical protein CBG06354
Locus_21739_Transcript_1/1_Conf_1.000	147	20	4.68E-15	NP_500551.2	87	84.3445	49	43	hypothetical protein F55F10.1
Locus_2174_Transcript_1/1_Conf_1.000	877	20	4.01E-88	XP_002631317.1	78	328.946	233	183	Hypothetical protein CBG03139
Locus_21740_Transcript_1/1_Conf_1.000	299	20	1.16E-34	XP_002645875.1	82	149.443	99	82	Hypothetical protein CBG07619
Locus_21741_Transcript_1/1_Conf_1.000	230	3	2.38E-11	NP_494819.3	89	72.0182	47	42	abnormal DYe Filling family member (dyf-14)
Locus_21742_Transcript_1/1_Conf_1.000	223	0							
Locus_21743_Transcript_1/1_Conf_1.000	147	0							
Locus_21744_Transcript_1/1_Conf_1.000	257	2	6.75E-06	XP_001898661.1	61	53.9138	71	44	MGC88946 protein
Locus_21745_Transcript_1/1_Conf_1.000	410	0							

Locus_21746_Transcript_1/1_Conf_1.000	128	3	2.79E-04	NP_001129839.1	66	48.521	42	28	hypothetical protein R05D3.12
Locus_21747_Transcript_1/1_Conf_1.000	231	0							
Locus_21748_Transcript_1/1_Conf_1.000	420	0							
Locus_21749_Transcript_1/1_Conf_1.000	216	0							
Locus_2175_Transcript_1/1_Conf_1.000	798	20	4.59E-109	ADL62852.1	84	398.282	266	225	thioredoxin reductase 1
Locus_21750_Transcript_1/1_Conf_1.000	285	0							
Locus_21751_Transcript_1/1_Conf_1.000	170	0							
Locus_21752_Transcript_1/1_Conf_1.000	249	0							
Locus_21753_Transcript_1/1_Conf_1.000	175	19	7.50E-18	XP_002811165.1	100	93.5893	57	57	PREDICTED: MARCKS-related protein-like
Locus_21754_Transcript_1/1_Conf_1.000	161	0							
Locus_21755_Transcript_1/1_Conf_1.000	149	0							
Locus_21756_Transcript_1/1_Conf_1.000	130	0							
Locus_21757_Transcript_1/1_Conf_1.000	151	0							
Locus_21758_Transcript_1/1_Conf_1.000	233	4	2.70E-31	NP_492127.1	89	138.272	77	69	Low-density lipoprotein Receptor Related family member (lrp-1)
Locus_21759_Transcript_1/1_Conf_1.000	435	20	1.00E-46	XP_002632693.1	81	189.504	144	117	Hypothetical protein CBG21624
Locus_2176_Transcript_1/1_Conf_1.000	650	20	2.91E-88	NP_497035.3	86	328.561	216	186	Trehalose 6-Phosphate Synthase family member (tps-2)
Locus_21760_Transcript_1/1_Conf_1.000	203	0							
Locus_21761_Transcript_1/1_Conf_1.000	195	16	1.70E-09	NP_001021671.2	75	65.855	44	33	hypothetical protein W09G3.7
Locus_21762_Transcript_1/1_Conf_1.000	443	0							

Locus_21763_Transcript_1/1_Conf_1.000	268	20	8.34E-33	NP_496251.1	96	143.28	76	73	TropoNin C family member (tnc-2)
Locus_21764_Transcript_1/1_Conf_1.000	401	20	2.61E-34	NP_496813.1	77	148.288	131	101	hypothetical protein Y48C3A.3
Locus_21765_Transcript_1/1_Conf_1.000	228	0							
Locus_21766_Transcript_1/1_Conf_1.000	408	17	5.53E-45	NP_502746.1	84	183.726	133	113	hypothetical protein Y67A10A.9
Locus_21767_Transcript_1/1_Conf_1.000	271	20	8.09E-12	XP_002631859.1	60	73.559	87	53	Hypothetical protein CBG07809
Locus_21768_Transcript_1/1_Conf_1.000	347	20	2.64E-10	XP_969308.1	77	68.5514	49	38	PREDICTED: similar to required for meiotic nuclear division 5 homolog A
Locus_21769_Transcript_1/1_Conf_1.000	365	20	8.56E-14	EFO27901.1	64	80.1073	106	68	hypothetical protein LOAG_00581
Locus_2177_Transcript_1/1_Conf_1.000	415	4	4.08E-24	XP_002629793.1	77	114.39	95	74	Hypothetical protein CBG01035
Locus_21770_Transcript_1/1_Conf_1.000	129	4	5.07E-06	XP_002647771.1	85	54.299	42	36	C. briggsae CBR-PPH-5 protein
Locus_21771_Transcript_1/1_Conf_1.000	244	20	4.25E-21	AAK31453.4	83	104.375	71	59	Hypothetical protein C25H3.8
Locus_21772_Transcript_1/1_Conf_1.000	135	0							
Locus_21773_Transcript_1/1_Conf_1.000	148	20	2.40E-19	XP_001249905.2	100	98.5969	49	49	PREDICTED: endothelial differentiation-related factor 1
Locus_21774_Transcript_1/1_Conf_1.000	353	1	8.16E-04	NP_508782.2	61	46.9802	39	24	hypothetical protein C05E11.6
Locus_21775_Transcript_1/1_Conf_1.000	237	0							
Locus_21776_Transcript_1/1_Conf_1.000	409	0							
Locus_21777_Transcript_1/1_Conf_1.000	146	0							
Locus_21778_Transcript_1/1_Conf_1.000	281	0							
Locus_21779_Transcript_1/1_Conf_1.000	154	0							
Locus_2178_Transcript_1/1_Conf_1.000	899	20	1.26E-84	XP_002642931.1	69	317.39	293	204	C. briggsae CBR-ALH-11 protein

Locus_21780_Transcript_1/1_Conf_1.000	188	2	3.96E-06	NP_508797.3	71	54.6842	52	37	Nuclear Hormone Receptor family member (nhr-45)
Locus_21781_Transcript_1/3_Conf_0.667	456	0							
Locus_21781_Transcript_2/3_Conf_0.667	475	0							
Locus_21781_Transcript_3/3_Conf_0.667	469	0							
Locus_21782_Transcript_1/1_Conf_1.000	145	0							
Locus_21783_Transcript_1/1_Conf_1.000	246	1	6.15E-04	NP_001002222.1	75	47.3654	36	27	serine/threonine-protein kinase PAK 4
Locus_21784_Transcript_1/1_Conf_1.000	151	0							
Locus_21785_Transcript_1/1_Conf_1.000	268	0							
Locus_21786_Transcript_1/1_Conf_1.000	133	0							
Locus_21787_Transcript_1/1_Conf_1.000	201	2	2.61E-10	NP_001022224.1	76	68.5514	63	48	hypothetical protein H20J04.9
Locus_21788_Transcript_1/1_Conf_1.000	295	20	2.51E-45	XP_002646290.1	90	184.882	97	88	C. briggsae CBR-INX-13 protein
Locus_21789_Transcript_1/1_Conf_1.000	140	0							
Locus_2179_Transcript_1/2_Conf_1.000	808	20	6.61E-79	NP_502295.1	75	298.13	265	200	yeast MON (monensin-resistant) homolog family member (mon-2)
Locus_2179_Transcript_2/2_Conf_1.000	3007	20	0	NP_502295.1	72	1091.64	1027	743	yeast MON (monensin-resistant) homolog family member (mon-2)
Locus_21790_Transcript_1/1_Conf_1.000	438	4	9.73E-18	CAN99691.2	53	93.2041	162	87	C. elegans protein F54B3.1b, partially confirmed by transcript evidence
Locus_21791_Transcript_1/2_Conf_1.000	426	0							
Locus_21791_Transcript_2/2_Conf_1.000	426	0							
Locus_21792_Transcript_1/1_Conf_1.000	535	0							

Locus_21793_Transcript_1/1_Conf_1.000	179	20	2.83E-25	XP_002918048.1	100	118.242	59	59	PREDICTED: signal transducer and activator of transcription 1-like
Locus_21794_Transcript_1/1_Conf_1.000	277	0							
Locus_21795_Transcript_1/1_Conf_1.000	294	0							
Locus_21796_Transcript_1/1_Conf_1.000	259	20	2.82E-12	NP_495376.1	64	75.0998	77	50	EXOSome (multiexonuclease complex) component family member (exos-8)
Locus_21797_Transcript_1/1_Conf_1.000	135	0							
Locus_21798_Transcript_1/1_Conf_1.000	265	0							
Locus_21799_Transcript_1/1_Conf_1.000	350	0							
Locus_218_Transcript_1/2_Conf_1.000	3101	20	1.52E-157	EFO23451.1	66	561.992	580	388	hypothetical protein LOAG_05033
Locus_218_Transcript_2/2_Conf_1.000	3101	20	1.52E-157	EFO23451.1	66	561.992	580	388	hypothetical protein LOAG_05033
Locus_2180_Transcript_1/1_Conf_1.000	919	0							
Locus_21800_Transcript_1/1_Conf_1.000	335	0							
Locus_21801_Transcript_1/1_Conf_1.000	258	0							
Locus_21802_Transcript_1/1_Conf_1.000	157	1	2.55E-05	NP_497340.2	62	51.9878	50	31	CaDHerin family member (cdh-12)

Locus_21803_Transcript_1/1_Conf_1.000	207	20	3.26E-29	XP_002646095.1	95	131.339	68	65	C. briggsae CBR-HMR-1 protein
Locus_21804_Transcript_1/1_Conf_1.000	143	0							
Locus_21805_Transcript_1/1_Conf_1.000	366	12	3.95E-19	EFO24904.1	59	97.8265	122	73	hypothetical protein LOAG_03584
Locus_21806_Transcript_1/1_Conf_1.000	395	3	2.56E-13	EFO20675.1	78	78.5666	66	52	hypothetical protein LOAG_07811
Locus_21807_Transcript_1/1_Conf_1.000	194	5	2.55E-05	XP_002648112.1	63	51.9878	52	33	C. briggsae CBR-PQN-83 protein
Locus_21808_Transcript_1/1_Conf_1.000	228	0							
Locus_21809_Transcript_1/1_Conf_1.000	202	0							
Locus_2181_Transcript_1/1_Conf_1.000	531	0							
Locus_21810_Transcript_1/1_Conf_1.000	234	0							
Locus_21811_Transcript_1/1_Conf_1.000	157	0							
Locus_21812_Transcript_1/1_Conf_1.000	271	4	8.94E-11	XP_002642332.1	67	70.0922	61	41	Hypothetical protein CBG18327
Locus_21813_Transcript_1/1_Conf_1.000	220	20	5.53E-16	XP_001850222.1	78	87.4261	66	52	phosphatidylethanolamine-binding protein
Locus_21814_Transcript_1/1_Conf_1.000	151	0							
Locus_21815_Transcript_1/1_Conf_1.000	128	20	5.61E-13	YP_002725704.1	97	77.411	42	41	NADH dehydrogenase subunit 1
Locus_21816_Transcript_1/1_Conf_1.000	407	0							
Locus_21817_Transcript_1/1_Conf_1.000	169	2	7.83E-07	XP_001899881.1	67	56.9954	55	37	cytochrome P450
Locus_21818_Transcript_1/1_Conf_1.000	231	5	1.10E-16	XP_001900525.1	76	89.7373	75	57	Lung seven transmembrane receptor family protein
Locus_21819_Transcript_1/1_Conf_1.000	233	6	6.24E-12	NP_500144.2	73	73.9442	71	52	Erythroid-Like Transcription factor family member (elt-6)
Locus_2182_Transcript_1/1_Conf_1.000	333	0							
Locus_21820_Transcript_1/1_Conf_1.000	151	20	1.60E-15	XP_002647214.1	94	85.8853	50	47	Hypothetical protein CBG22398
Locus_21821_Transcript_1/1_Conf_1.000	149	19	1.90E-16	XP_002633114.1	85	88.9669	49	42	C. briggsae CBR-UNC-8 protein
Locus_21822_Transcript_1/1_Conf_1.000	218	7	2.40E-08	XP_002630441.1	59	62.003	72	43	Hypothetical protein CBG11172
Locus_21823_Transcript_1/1_Conf_1.000	239	0							

Locus_21824_Transcript_1/1_Conf_1.000	330	20	8.26E-49	CAA21622.4	94	196.438	110	104	C. elegans protein Y43F8C.12, partially confirmed by transcript evidence
Locus_21825_Transcript_1/1_Conf_1.000	257	0							
Locus_21826_Transcript_1/1_Conf_1.000	290	6	4.31E-45	NP_001022641.1	95	184.111	96	92	LEThal family member (let-805)
Locus_21827_Transcript_1/1_Conf_1.000	154	15	3.02E-14	NP_076949.1	100	81.6481	34	34	structure-specific endonuclease subunit SLX1 isoform 1
Locus_21828_Transcript_1/1_Conf_1.000	201	0							
Locus_21829_Transcript_1/1_Conf_1.000	137	1	1.02E-06	NP_501709.2	77	56.6102	44	34	Membrane Calcium ATPase family member (mca-1)
Locus_2183_Transcript_1/1_Conf_1.000	339	20	6.98E-16	AAD51334.1	66	87.0409	80	53	Kunitz type serine protease inhibitor
Locus_21830_Transcript_1/1_Conf_1.000	251	20	3.58E-12	EFO23283.1	71	74.7146	67	48	hypothetical protein LOAG_05201
Locus_21831_Transcript_1/1_Conf_1.000	438	20	1.95E-34	NP_499155.1	65	148.673	144	95	hypothetical protein T05G5.5
Locus_21832_Transcript_1/1_Conf_1.000	510	20	3.94E-49	CAA97764.2	76	197.593	160	122	C. elegans protein B0564.2, confirmed by transcript evidence
Locus_21833_Transcript_1/1_Conf_1.000	249	0							

Locus_21834_Transcript_1/1_Conf_1.000	208	20	8.34E-09	EFO17055.1	64	63.5438	70	45	thiamin pyrophosphokinase
Locus_21835_Transcript_1/1_Conf_1.000	299	4	5.82E-10	NP_496134.1	58	67.3958	96	56	hypothetical protein C08H9.1
Locus_21836_Transcript_1/1_Conf_1.000	146	0							
Locus_21837_Transcript_1/1_Conf_1.000	169	11	4.15E-08	NP_001024812.1	75	61.2326	37	28	hypothetical protein M163.8
Locus_21838_Transcript_1/1_Conf_1.000	184	20	2.40E-19	NP_503175.1	83	98.5969	61	51	ABC Transporter family member (abt-4)
Locus_21839_Transcript_1/1_Conf_1.000	339	0							
Locus_2184_Transcript_1/1_Conf_1.000	184	0							
Locus_21840_Transcript_1/1_Conf_1.000	275	0							
Locus_21841_Transcript_1/1_Conf_1.000	180	20	8.87E-14	NP_495410.4	81	80.1073	60	49	hypothetical protein C44B7.11
Locus_21842_Transcript_1/1_Conf_1.000	325	20	1.17E-18	Q21012.3	75	96.2857	93	70	Enolase-phosphatase E1
Locus_21843_Transcript_1/1_Conf_1.000	259	4	2.16E-12	NP_001040741.1	54	75.485	84	46	hypothetical protein C15F1.5
Locus_21844_Transcript_1/1_Conf_1.000	185	3	7.48E-13	NP_495697.2	94	77.0258	34	32	Lim and Transglutaminase Domain family member (ltd-1)
Locus_21845_Transcript_1/1_Conf_1.000	139	0							
Locus_21846_Transcript_1/1_Conf_1.000	273	0							
Locus_21847_Transcript_1/1_Conf_1.000	170	0							
Locus_21848_Transcript_1/1_Conf_1.000	240	0							
Locus_21849_Transcript_1/1_Conf_1.000	161	0							
Locus_2185_Transcript_1/4_Conf_0.667	2646	20	0	NP_499080.3	78	730.324	588	462	SR Protein Kinase family member (spk-1)
Locus_2185_Transcript_2/4_Conf_0.667	2736	20	0	NP_499080.3	76	729.169	617	471	SR Protein Kinase family member (spk-1)

Locus_2185_Transcript_3/4_Conf_0.667	2847	20	0	NP_001021134.1	73	744.577	671	495	SR Protein Kinase family member (spk-1)
Locus_2185_Transcript_4/4_Conf_0.667	2697	20	0	NP_499080.3	77	731.865	604	467	SR Protein Kinase family member (spk-1)
Locus_21850_Transcript_1/1_Conf_1.000	139	0							
Locus_21851_Transcript_1/1_Conf_1.000	138	20	7.49E-10	XP_001510147.1	80	67.0106	46	37	PREDICTED: hypothetical protein, partial
Locus_21852_Transcript_1/1_Conf_1.000	609	0							
Locus_21853_Transcript_1/1_Conf_1.000	348	20	1.88E-16	NP_502195.3	72	88.9669	77	56	hypothetical protein F58B3.4
Locus_21854_Transcript_1/1_Conf_1.000	277	0							
Locus_21855_Transcript_1/1_Conf_1.000	147	0							
Locus_21856_Transcript_1/1_Conf_1.000	554	20	6.06E-58	NP_498895.1	75	227.254	184	138	RNA HelicAse family member (rha-2)
Locus_21857_Transcript_1/1_Conf_1.000	172	0							
Locus_21858_Transcript_1/1_Conf_1.000	132	0							
Locus_21859_Transcript_1/1_Conf_1.000	142	0							
Locus_2186_Transcript_1/1_Conf_1.000	147	0							
Locus_21860_Transcript_1/1_Conf_1.000	199	0							
Locus_21861_Transcript_1/1_Conf_1.000	128	0							
Locus_21862_Transcript_1/1_Conf_1.000	446	0							
Locus_21863_Transcript_1/1_Conf_1.000	226	1	1.27E-04	EFO19311.1	55	49.6766	67	37	hypothetical protein LOAG_09182
Locus_21864_Transcript_1/1_Conf_1.000	361	0							
Locus_21865_Transcript_1/1_Conf_1.000	243	0							
Locus_21866_Transcript_1/1_Conf_1.000	180	0							

Locus_21867_Transcript_1/1_Conf_1.000	406	20	4.01E-19	NP_498361.1	64	97.8265	104	67	hypothetical protein T12A2.8
Locus_21868_Transcript_1/1_Conf_1.000	1355	20	5.05E-119	CBK19468.1	66	432.565	463	308	C. elegans protein R11A8.4b, partially confirmed by transcript evidence
Locus_21869_Transcript_1/1_Conf_1.000	278	0							
Locus_2187_Transcript_1/1_Conf_1.000	1325	20	1.81E-81	NP_493544.2	68	307.76	362	249	hypothetical protein Y105E8B.3
Locus_21870_Transcript_1/1_Conf_1.000	208	20	8.34E-09	XP_002644943.1	61	63.5438	67	41	Hypothetical protein CBG10898
Locus_21871_Transcript_1/1_Conf_1.000	130	0							
Locus_21872_Transcript_1/1_Conf_1.000	188	20	3.47E-10	EFO27462.1	61	68.1662	70	43	hypothetical protein LOAG_01021
Locus_21873_Transcript_1/1_Conf_1.000	218	4	1.72E-14	XP_002638865.1	80	82.4185	72	58	Hypothetical protein CBG22082
Locus_21874_Transcript_1/1_Conf_1.000	655	0							
Locus_21875_Transcript_1/1_Conf_1.000	201	16	6.21E-12	NP_501217.2	85	73.9442	67	57	hypothetical protein R05G6.10
Locus_21876_Transcript_1/1_Conf_1.000	199	0							
Locus_21877_Transcript_1/1_Conf_1.000	255	20	5.87E-26	NP_499922.1	85	120.553	76	65	Kinase, GLH-Binding family member (kgb-1)
Locus_21878_Transcript_1/1_Conf_1.000	184	0							
Locus_21879_Transcript_1/1_Conf_1.000	199	0							

Locus_2188_Transcript_1/3_Conf_0.600	566	20	7.31E-38	XP_002637185.1	68	160.614	163	112	Hypothetical protein CBG09704
Locus_2188_Transcript_2/3_Conf_0.600	603	20	4.65E-39	XP_002637185.1	69	164.851	163	113	Hypothetical protein CBG09704
Locus_2188_Transcript_3/3_Conf_0.600	603	20	8.78E-38	XP_002637185.1	68	160.614	163	112	Hypothetical protein CBG09704
Locus_21880_Transcript_1/1_Conf_1.000	166	0							
Locus_21881_Transcript_1/1_Conf_1.000	216	0							
Locus_21882_Transcript_1/1_Conf_1.000	132	0							
Locus_21883_Transcript_1/1_Conf_1.000	171	0							
Locus_21884_Transcript_1/1_Conf_1.000	143	0							
Locus_21885_Transcript_1/1_Conf_1.000	429	20	1.24E-36	XP_001901596.1	74	155.992	143	106	oxidoreductase, short chain dehydrogenase/reductase family protein
Locus_21886_Transcript_1/1_Conf_1.000	214	0							
Locus_21887_Transcript_1/1_Conf_1.000	137	0							
Locus_21888_Transcript_1/1_Conf_1.000	147	0							
Locus_21889_Transcript_1/1_Conf_1.000	228	0							
Locus_2189_Transcript_1/2_Conf_1.000	967	20	1.17E-70	Q95PP1.1	86	271.166	227	197	Aspartyl protease inhibitor
Locus_2189_Transcript_2/2_Conf_1.000	961	20	1.16E-70	Q95PP1.1	86	271.166	227	197	Aspartyl protease inhibitor
Locus_21890_Transcript_1/1_Conf_1.000	167	0							
Locus_21891_Transcript_1/1_Conf_1.000	136	0							
Locus_21892_Transcript_1/1_Conf_1.000	207	2	1.80E-11	XP_002633609.1	68	72.4034	67	46	Hypothetical protein CBG05491
Locus_21893_Transcript_1/2_Conf_1.000	292	0							
Locus_21893_Transcript_2/2_Conf_1.000	291	0							
Locus_21894_Transcript_1/1_Conf_1.000	462	20	1.18E-26	XP_002630318.1	62	122.865	115	72	Hypothetical protein CBG04241
Locus_21895_Transcript_1/1_Conf_1.000	443	0							
Locus_21896_Transcript_1/1_Conf_1.000	150	0							
Locus_21897_Transcript_1/1_Conf_1.000	134	0							
Locus_21898_Transcript_1/1_Conf_1.000	189	20	8.18E-28	XP_002750079.1	100	126.716	63	63	PREDICTED: ATP synthase subunit gamma, mitochondrial-like
Locus_21899_Transcript_1/1_Conf_1.000	134	0							
Locus_219_Transcript_1/1_Conf_1.000	593	20	8.20E-70	XP_002645843.1	78	266.929	201	158	C. briggsae CBR-TAG-53 protein
Locus_2190_Transcript_1/2_Conf_1.000	1427	20	3.74E-112	XP_002639282.1	82	409.838	338	279	C. briggsae CBR-NHR-69 protein

Locus_2190_Transcript_2/2_Conf_1.000	1427	20	3.74E-112	XP_002639282.1	82	409.838	338	279	C. briggsae CBR-NHR-69 protein
Locus_21900_Transcript_1/1_Conf_1.000	151	2	3.35E-05	XP_002641207.1	66	51.6026	50	33	Hypothetical protein CBG09068
Locus_21901_Transcript_1/1_Conf_1.000	970	20	3.70E-40	EFO23919.1	57	169.859	319	185	hypothetical protein LOAG_04568
Locus_21902_Transcript_1/1_Conf_1.000	277	20	2.50E-13	AAY99638.1	90	78.5666	51	46	mca-1
Locus_21903_Transcript_1/1_Conf_1.000	274	3	2.05E-07	ABD39381.1	72	58.9214	36	26	putative galectin protein 10
Locus_21904_Transcript_1/1_Conf_1.000	415	0							
Locus_21905_Transcript_1/1_Conf_1.000	554	0							
Locus_21906_Transcript_1/1_Conf_1.000	277	1	8.60E-06	EFN73640.1	85	53.5286	34	29	Probable phospholipid-transporting ATPase ID
Locus_21907_Transcript_1/1_Conf_1.000	421	5	1.75E-30	ACI49226.1	77	135.576	121	94	hypothetical protein Csp3_JD05.011
Locus_21908_Transcript_1/1_Conf_1.000	145	20	1.67E-12	EFN69115.1	87	75.8702	47	41	Peroxisome biogenesis factor 1
Locus_21909_Transcript_1/1_Conf_1.000	333	0							
Locus_2191_Transcript_1/1_Conf_1.000	1559	20	6.02E-143	XP_002634371.1	70	512.301	521	367	C. briggsae CBR-RIG-4 protein
Locus_21910_Transcript_1/1_Conf_1.000	141	0							
Locus_21911_Transcript_1/1_Conf_1.000	309	0							
Locus_21912_Transcript_1/1_Conf_1.000	185	0							
Locus_21913_Transcript_1/1_Conf_1.000	152	0							
Locus_21914_Transcript_1/1_Conf_1.000	209	0							
Locus_21915_Transcript_1/1_Conf_1.000	244	20	1.50E-42	ADN00778.1	97	175.637	81	79	LON-1 protein
Locus_21916_Transcript_1/1_Conf_1.000	226	0							

Locus_21917_Transcript_1/1_Conf_1.000	289	1	1.50E-05	NP_501999.2	48	52.7582	95	46	hypothetical protein T25B9.10
Locus_21918_Transcript_1/1_Conf_1.000	294	20	8.40E-25	XP_002644815.1	82	116.701	73	60	Hypothetical protein CBG14833
Locus_21919_Transcript_1/1_Conf_1.000	204	5	3.52E-07	NP_507251.2	56	58.151	67	38	Proline HYdroxylase family member (phy-3)
Locus_2192_Transcript_1/1_Conf_1.000	516	20	1.29E-42	NP_493258.1	80	176.022	131	105	ProFiliN family member (pfn-1)
Locus_21920_Transcript_1/1_Conf_1.000	166	20	4.45E-10	NP_498037.2	87	67.781	40	35	yeast ULA (ubiquitin activating) homolog family member (ula-1)
Locus_21921_Transcript_1/1_Conf_1.000	161	0							
Locus_21922_Transcript_1/1_Conf_1.000	416	0							
Locus_21923_Transcript_1/1_Conf_1.000	147	0							
Locus_21924_Transcript_1/1_Conf_1.000	372	3	2.71E-23	CAC35853.2	62	111.694	124	78	C. elegans protein Y111B2A.24, partially confirmed by transcript evidence
Locus_21925_Transcript_1/2_Conf_1.000	407	3	3.40E-10	NP_491390.2	52	68.1662	103	54	hypothetical protein D1007.15
Locus_21925_Transcript_2/2_Conf_1.000	407	3	4.02E-11	NP_491390.2	52	71.2478	106	56	hypothetical protein D1007.15
Locus_21926_Transcript_1/1_Conf_1.000	382	0							
Locus_21927_Transcript_1/1_Conf_1.000	188	0							
Locus_21928_Transcript_1/1_Conf_1.000	274	20	8.04E-20	XP_001896429.1	84	100.138	89	75	Hypothetical WD-repeat protein F21H12.1 in chromosome II, putative
Locus_21929_Transcript_1/1_Conf_1.000	248	0							
Locus_2193_Transcript_1/1_Conf_1.000	511	0							
Locus_21930_Transcript_1/1_Conf_1.000	318	20	4.48E-26	NP_491734.1	84	120.939	86	73	UNCoordinated family member (unc-94)
Locus_21931_Transcript_1/1_Conf_1.000	261	0							
Locus_21932_Transcript_1/1_Conf_1.000	165	0							
Locus_21933_Transcript_1/1_Conf_1.000	238	20	7.56E-18	XP_002632693.1	73	93.5893	78	57	Hypothetical protein CBG21624

Locus_21934_Transcript_1/1_Conf_1.000	272	20	8.09E-12	XP_002638675.1	63	73.559	83	53	C. briggsae CBR-PBRM-1 protein
Locus_21935_Transcript_1/1_Conf_1.000	259	20	4.95E-25	NP_499717.1	91	117.472	67	61	ABC transporter, class E family member (abce-1)
Locus_21936_Transcript_1/1_Conf_1.000	571	4	1.94E-09	XP_002642383.1	52	66.2402	130	68	Hypothetical protein CBG18387
Locus_21937_Transcript_1/1_Conf_1.000	231	0							
Locus_21938_Transcript_1/1_Conf_1.000	170	0							
Locus_21939_Transcript_1/1_Conf_1.000	240	0							
Locus_2194_Transcript_1/1_Conf_1.000	2311	0							
Locus_21940_Transcript_1/1_Conf_1.000	363	1	1.67E-17	NP_001041053.1	68	92.4337	92	63	hypothetical protein Y62E10A.20
Locus_21941_Transcript_1/1_Conf_1.000	412	0							
Locus_21942_Transcript_1/1_Conf_1.000	154	0							
Locus_21943_Transcript_1/1_Conf_1.000	194	0							
Locus_21944_Transcript_1/1_Conf_1.000	360	12	3.36E-26	XP_002639929.1	82	121.324	106	87	Hypothetical protein CBG08265
Locus_21945_Transcript_1/1_Conf_1.000	312	20	8.78E-30	ACV73031.1	94	133.265	71	67	AHA-1

Locus_21946_Transcript_1/1_Conf_1.000	254	15	4.09E-19	XP_001898877.1	79	97.8265	84	67	oxidoreductase, short chain dehydrogenase/reductase family protein
Locus_21947_Transcript_1/1_Conf_1.000	206	0							
Locus_21948_Transcript_1/1_Conf_1.000	429	20	3.18E-08	EFO25642.1	56	61.6178	85	48	hypothetical protein LOAG_02841
Locus_21949_Transcript_1/1_Conf_1.000	304	0							
Locus_2195_Transcript_1/1_Conf_1.000	823	20	1.03E-119	XP_002636728.1	86	433.721	268	231	C. briggsae CBR-FRM-7 protein
Locus_21950_Transcript_1/1_Conf_1.000	303	0							
Locus_21951_Transcript_1/1_Conf_1.000	263	0							
Locus_21952_Transcript_1/1_Conf_1.000	311	20	1.82E-48	NP_001033411.1	96	195.282	102	98	hypothetical protein F53H1.1
Locus_21953_Transcript_1/1_Conf_1.000	207	0							
Locus_21954_Transcript_1/2_Conf_1.000	409	0							
Locus_21954_Transcript_2/2_Conf_1.000	409	0							
Locus_21955_Transcript_1/1_Conf_1.000	315	20	6.97E-11	NP_491270.2	51	70.4774	101	52	Low-density lipoprotein Receptor Related family member (lrp-2)
Locus_21956_Transcript_1/1_Conf_1.000	254	0							
Locus_21957_Transcript_1/1_Conf_1.000	602	1	2.08E-07	NP_491543.1	51	59.6918	133	68	FANCM (Fanconi anemia complex component M) homolog family member (fncm-1)
Locus_21958_Transcript_1/1_Conf_1.000	158	1	2.16E-04	XP_001842842.1	62	48.9062	54	34	plasma glutamate carboxypeptidase
Locus_21959_Transcript_1/1_Conf_1.000	281	0							
Locus_2196_Transcript_1/2_Conf_1.000	1525	20	1.89E-141	EFO24230.1	67	507.294	527	358	hypothetical protein LOAG_04252
Locus_2196_Transcript_2/2_Conf_1.000	1525	20	1.89E-141	EFO24230.1	67	507.294	527	358	hypothetical protein LOAG_04252
Locus_21960_Transcript_1/1_Conf_1.000	137	0							
Locus_21961_Transcript_1/1_Conf_1.000	190	1	6.48E-25	XP_002751331.1	90	117.087	62	56	PREDICTED: stathmin-like
Locus_21962_Transcript_1/1_Conf_1.000	195	2	1.03E-06	XP_002641391.1	67	56.6102	62	42	C. briggsae CBR-GLY-8 protein
Locus_21963_Transcript_1/1_Conf_1.000	209	2	3.36E-34	EAW76268.1	100	147.902	69	69	hCG38498, isoform CRA_b
Locus_21964_Transcript_1/1_Conf_1.000	174	0							
Locus_21965_Transcript_1/1_Conf_1.000	137	0							
Locus_21966_Transcript_1/1_Conf_1.000	130	0							
Locus_21967_Transcript_1/1_Conf_1.000	514	0							

Locus_21968_Transcript_1/1_Conf_1.000	170	20	8.92E-19	NP_494991.1	89	96.6709	56	50	Phosphoethanolamine MethyTransferase family member (pmt-1)
Locus_21969_Transcript_1/1_Conf_1.000	176	0							
Locus_2197_Transcript_1/1_Conf_1.000	1071	20	7.66E-146	NP_493279.1	85	521.161	356	303	Suppressor of Mec and Unc defects family member (smu-1)
Locus_21970_Transcript_1/1_Conf_1.000	289	14	5.69E-13	EFO20293.1	65	77.411	89	58	PDZ domain-containing protein
Locus_21971_Transcript_1/1_Conf_1.000	197	0							
Locus_21972_Transcript_1/1_Conf_1.000	392	2	1.27E-33	NP_495168.1	77	145.976	117	91	hypothetical protein H41C03.1
Locus_21973_Transcript_1/1_Conf_1.000	142	3	9.13E-08	NP_497765.2	78	60.077	42	33	Adenylyl CYclase family member (acy-3)
Locus_21974_Transcript_1/1_Conf_1.000	330	20	1.13E-13	NP_496307.1	60	79.7221	103	62	hypothetical protein C09G5.2
Locus_21975_Transcript_1/1_Conf_1.000	214	20	4.25E-13	XP_002634303.1	82	77.7962	62	51	C. briggsae CBR-NCX-3 protein
Locus_21976_Transcript_1/1_Conf_1.000	342	6	6.95E-19	XP_002631746.1	61	97.0561	111	68	C. briggsae CBR-TAG-280 protein
Locus_21977_Transcript_1/1_Conf_1.000	456	0							
Locus_21978_Transcript_1/1_Conf_1.000	125	0							
Locus_21979_Transcript_1/1_Conf_1.000	262	0							
Locus_2198_Transcript_1/2_Conf_1.000	899	20	6.46E-89	EFO20496.1	73	331.643	304	223	hypothetical protein LOAG_07994
Locus_2198_Transcript_2/2_Conf_1.000	899	20	6.46E-89	EFO20496.1	73	331.643	304	223	hypothetical protein LOAG_07994
Locus_21980_Transcript_1/1_Conf_1.000	168	0							
Locus_21981_Transcript_1/1_Conf_1.000	579	20	2.73E-38	NP_001022032.1	67	162.155	187	126	TRRAP-like (transcription/transformation domain-associated protein) family member (trr-1)
Locus_21982_Transcript_1/1_Conf_1.000	129	0							
Locus_21983_Transcript_1/1_Conf_1.000	132	5	9.85E-10	NP_500647.2	82	66.6254	41	34	Dipeptidyl Peptidase Four (IV) family member (dpf-5)
Locus_21984_Transcript_1/1_Conf_1.000	200	4	9.31E-08	XP_001900237.1	64	60.077	64	41	mucosa associated lymphoid tissue lymphoma translocation protein 1, isoform b
Locus_21985_Transcript_1/1_Conf_1.000	540	0							
Locus_21986_Transcript_1/1_Conf_1.000	186	1	1.67E-04	XP_002632203.1	71	49.2914	45	32	Hypothetical protein CBG07070
Locus_21987_Transcript_1/1_Conf_1.000	499	5	1.72E-22	XP_002642061.1	55	108.997	167	93	Hypothetical protein CBG17999
Locus_21988_Transcript_1/1_Conf_1.000	389	0							
Locus_21989_Transcript_1/1_Conf_1.000	143	0							
Locus_2199_Transcript_1/6_Conf_0.357	409	20	2.95E-30	NP_497777.1	72	134.806	124	90	hypothetical protein C36A4.4
Locus_2199_Transcript_2/6_Conf_0.500	1473	20	4.92E-139	NP_497777.1	71	499.204	454	324	hypothetical protein C36A4.4

Locus_2199_Transcript_3/6_Conf_0.429	1181	20	2.43E-119	NP_497777.1	74	433.335	364	270	hypothetical protein C36A4.4
Locus_2199_Transcript_4/6_Conf_0.500	1473	20	4.16E-138	NP_497777.1	71	496.123	454	323	hypothetical protein C36A4.4
Locus_2199_Transcript_5/6_Conf_0.429	1188	20	1.59E-118	NP_497777.1	74	430.639	360	268	hypothetical protein C36A4.4
Locus_2199_Transcript_6/6_Conf_0.429	1181	20	5.41E-119	NP_497777.1	74	432.18	364	270	hypothetical protein C36A4.4
Locus_21990_Transcript_1/1_Conf_1.000	139	0							
Locus_21991_Transcript_1/1_Conf_1.000	279	0							
Locus_21992_Transcript_1/1_Conf_1.000	361	20	6.78E-27	XP_001896664.1	69	123.635	119	83	Protein kinase domain containing protein
Locus_21993_Transcript_1/1_Conf_1.000	400	0							
Locus_21994_Transcript_1/1_Conf_1.000	252	19	4.38E-13	XP_002640231.1	75	77.7962	52	39	Hypothetical protein CBG12746
Locus_21995_Transcript_1/1_Conf_1.000	129	0							
Locus_21996_Transcript_1/1_Conf_1.000	176	20	8.29E-17	ACI49101.1	88	90.1225	54	48	hypothetical protein Cbre_JD13.003
Locus_21997_Transcript_1/1_Conf_1.000	300	20	2.77E-28	NP_496066.2	90	128.257	86	78	Nuclear Hormone Receptor family member (nhr-19)
Locus_21998_Transcript_1/1_Conf_1.000	206	0							

Locus_21999_Transcript_1/1_Conf_1.000	151	5	3.96E-06	ACI49239.1	85	54.6842	35	30	hypothetical protein Csp3_JD06.005
Locus_22_Transcript_1/1_Conf_1.000	2388	16	6.91E-06	AAH84352.1	35	57.7658	562	197	LOC495149 protein
Locus_220_Transcript_1/2_Conf_1.000	1383	20	7.76E-123	CAJ45481.1	67	445.277	424	286	legumain
Locus_220_Transcript_2/2_Conf_1.000	1059	20	6.90E-99	XP_002636781.1	69	365.155	332	231	Hypothetical protein CBG23516
Locus_2200_Transcript_1/2_Conf_1.000	523	20	3.08E-63	NP_500191.3	86	244.588	175	151	ParaPleGiN AAA protease family member (ppgn-1)
Locus_2200_Transcript_2/2_Conf_1.000	523	20	3.08E-63	NP_500191.3	86	244.588	175	151	ParaPleGiN AAA protease family member (ppgn-1)

Locus_22000_Transcript_1/1_Conf_1.000	450	1	5.25E-11	CAR63594.1	55	70.8626	127	71	hypothetical protein
Locus_22001_Transcript_1/1_Conf_1.000	166	0							
Locus_22002_Transcript_1/1_Conf_1.000	302	20	6.79E-43	EFO27430.1	95	176.792	93	89	GTP-binding protein GTR1
Locus_22003_Transcript_1/1_Conf_1.000	256	3	6.97E-11	AAF82410.1	77	70.4774	53	41	AF221132_1diacylglycerol acyltransferase
Locus_22004_Transcript_1/1_Conf_1.000	145	2	9.81E-05	XP_002635479.1	73	50.0618	45	33	C. briggsae CBR-PMT-2 protein
Locus_22005_Transcript_1/1_Conf_1.000	132	0							
Locus_22006_Transcript_1/1_Conf_1.000	228	14	5.14E-06	EFN62076.1	68	54.299	38	26	hypothetical protein EAG_04210
Locus_22007_Transcript_1/1_Conf_1.000	325	0							
Locus_22008_Transcript_1/1_Conf_1.000	212	0							
Locus_22009_Transcript_1/1_Conf_1.000	294	0							
Locus_2201_Transcript_1/1_Conf_1.000	275	0							
Locus_22010_Transcript_1/1_Conf_1.000	160	20	5.10E-22	XP_002913146.1	100	107.457	53	53	PREDICTED: transmembrane emp24 domain-containing protein 2-like isoform 1
Locus_22011_Transcript_1/1_Conf_1.000	340	20	5.33E-24	XP_001899060.1	66	114.005	112	75	acetyltransferase, GNAT family protein
Locus_22012_Transcript_1/1_Conf_1.000	132	0							
Locus_22013_Transcript_1/1_Conf_1.000	151	8	9.40E-16	CAB00107.2	85	86.6557	49	42	C. elegans protein F58H1.4, confirmed by transcript evidence

Locus_22014_Transcript_1/1_Conf_1.000	233	0							
Locus_22015_Transcript_1/1_Conf_1.000	144	0							
Locus_22016_Transcript_1/1_Conf_1.000	343	20	3.09E-59	ABU93237.1	97	231.106	114	111	ligand-gated ion channel subunit
Locus_22017_Transcript_1/1_Conf_1.000	138	0							
Locus_22018_Transcript_1/1_Conf_1.000	373	0							
Locus_22019_Transcript_1/1_Conf_1.000	197	20	1.64E-20	BAG65407.1	100	102.449	50	50	unnamed protein product
Locus_2202_Transcript_1/1_Conf_1.000	341	0							
Locus_22020_Transcript_1/1_Conf_1.000	146	0							
Locus_22021_Transcript_1/1_Conf_1.000	380	20	9.93E-10	NP_495244.1	77	66.6254	48	37	Transbilayer Amphipath Transporters (subfamily IV P-type ATPase) family member (tat-4)
Locus_22022_Transcript_1/1_Conf_1.000	349	20	8.67E-38	AAK62032.1	74	159.844	116	86	metalloprotease 1 precursor
Locus_22023_Transcript_1/1_Conf_1.000	217	0							
Locus_22024_Transcript_1/1_Conf_1.000	206	4	4.00E-19	NP_504292.2	89	97.8265	68	61	hypothetical protein C37H5.5
Locus_22025_Transcript_1/1_Conf_1.000	160	20	3.54E-15	XP_001896329.1	90	84.7297	53	48	calcium ATPase
Locus_22026_Transcript_1/1_Conf_1.000	312	7	1.96E-21	NP_001021268.1	87	105.531	78	68	UNCoordinated family member (unc-44)

Locus_22027_Transcript_1/1_Conf_1.000	234	3	9.93E-10	A8X3A7.2	85	66.6254	75	64	Integrin alpha pat-2
Locus_22028_Transcript_1/1_Conf_1.000	147	0							
Locus_22029_Transcript_1/1_Conf_1.000	235	20	4.44E-26	NP_498128.1	96	120.939	65	63	CLocK (biological timing) abnormality family member (clk-1)
Locus_2203_Transcript_1/1_Conf_1.000	854	20	2.54E-132	XP_002634111.1	94	475.707	280	264	Hypothetical protein CBG01664
Locus_22030_Transcript_1/1_Conf_1.000	353	0							
Locus_22031_Transcript_1/1_Conf_1.000	267	20	4.72E-44	XP_002808235.1	100	180.644	88	88	PREDICTED: LOW QUALITY PROTEIN: calpain small subunit 1-like
Locus_22032_Transcript_1/1_Conf_1.000	144	0							
Locus_22033_Transcript_1/1_Conf_1.000	165	20	1.69E-17	EFO18251.1	87	92.4337	55	48	hypothetical protein LOAG_10243
Locus_22034_Transcript_1/1_Conf_1.000	164	20	2.06E-23	XP_002799431.1	100	112.079	54	54	PREDICTED: pyruvate kinase isozymes M1/M2 isoform 2

Locus_22035_Transcript_1/1_Conf_1.000	154	20	3.81E-17	EFO24654.1	92	91.2781	51	47	RNA polymerase Rpb1
Locus_22036_Transcript_1/1_Conf_1.000	176	0							
Locus_22037_Transcript_1/1_Conf_1.000	156	3	4.20E-08	NP_001022683.1	67	61.2326	55	37	hypothetical protein M01A8.2
Locus_22038_Transcript_1/1_Conf_1.000	418	20	5.64E-45	NP_001023958.1	85	183.726	124	106	Heat Shock Protein family member (hsp-17)
Locus_22039_Transcript_1/1_Conf_1.000	439	0							
Locus_2204_Transcript_1/1_Conf_1.000	681	20	1.42E-59	EFO25906.1	68	233.417	206	142	steroid hormone receptor
Locus_22040_Transcript_1/1_Conf_1.000	396	4	5.87E-10	EFO16079.1	55	67.3958	129	72	hypothetical protein LOAG_12429
Locus_22041_Transcript_1/1_Conf_1.000	199	0							
Locus_22042_Transcript_1/1_Conf_1.000	164	20	1.58E-23	NP_498711.1	96	112.464	54	52	TYRosinase family member (tyr-1)
Locus_22043_Transcript_1/1_Conf_1.000	478	0							
Locus_22044_Transcript_1/1_Conf_1.000	215	0							
Locus_22045_Transcript_1/1_Conf_1.000	145	0							
Locus_22046_Transcript_1/1_Conf_1.000	323	0							
Locus_22047_Transcript_1/1_Conf_1.000	132	2	8.63E-06	NP_491776.1	75	53.5286	44	33	hypothetical protein T09B4.7
Locus_22048_Transcript_1/1_Conf_1.000	345	4	2.23E-09	EFO23701.1	55	65.4698	103	57	TPR Domain containing protein
Locus_22049_Transcript_1/1_Conf_1.000	325	1	7.41E-16	CAR63646.1	80	84.7297	46	37	putative Homeobox family member
Locus_2205_Transcript_1/1_Conf_1.000	491	5	1.58E-23	CAB04203.2	62	112.464	156	98	C. elegans protein F26H9.2, confirmed by transcript evidence
Locus_22050_Transcript_1/1_Conf_1.000	172	0							
Locus_22051_Transcript_1/1_Conf_1.000	976	1	9.61E-04	CBI61474.1	45	48.9062	150	68	unnamed protein product
Locus_22052_Transcript_1/1_Conf_1.000	142	1	8.55E-06	EFO27222.1	72	53.5286	47	34	hypothetical protein LOAG_01266
Locus_22053_Transcript_1/1_Conf_1.000	455	20	1.56E-39	XP_001896270.1	66	165.622	149	99	Zinc finger, C2H2 type family protein
Locus_22054_Transcript_1/1_Conf_1.000	298	20	4.31E-13	EFO28436.1	54	77.7962	92	50	zinc finger protein
Locus_22055_Transcript_1/1_Conf_1.000	313	0							

Locus_22056_Transcript_1/1_Conf_1.000	352	20	1.94E-13	XP_002637085.1	77	78.9518	58	45	Hypothetical protein CBG09584
Locus_22057_Transcript_1/1_Conf_1.000	505	0							
Locus_22058_Transcript_1/1_Conf_1.000	139	0							
Locus_22059_Transcript_1/1_Conf_1.000	164	0							
Locus_2206_Transcript_1/1_Conf_1.000	345	20	5.12E-22	XP_002630467.1	86	107.457	74	64	C. briggsae CBR-UNC-104 protein
Locus_22060_Transcript_1/1_Conf_1.000	129	0							
Locus_22061_Transcript_1/1_Conf_1.000	405	0							
Locus_22062_Transcript_1/1_Conf_1.000	432	20	4.84E-41	NP_504578.1	76	170.629	131	100	hypothetical protein F17A9.4
Locus_22063_Transcript_1/1_Conf_1.000	565	0							
Locus_22064_Transcript_1/1_Conf_1.000	240	0							
Locus_22065_Transcript_1/1_Conf_1.000	129	0							
Locus_22066_Transcript_1/1_Conf_1.000	236	3	4.58E-31	NP_500132.3	87	137.502	78	68	hypothetical protein Y41D4A.7
Locus_22067_Transcript_1/1_Conf_1.000	321	20	3.31E-21	NP_593736.1	70	104.76	105	74	histone acetyltransferase Mst2
Locus_22068_Transcript_1/1_Conf_1.000	232	0							
Locus_22069_Transcript_1/1_Conf_1.000	234	20	8.41E-09	NP_504512.1	71	63.5438	74	53	hypothetical protein F44E7.2
Locus_2207_Transcript_1/2_Conf_1.000	1526	3	5.54E-08	NP_492411.1	46	63.929	167	77	GEX Interacting protein family member (gei-11)
Locus_2207_Transcript_2/2_Conf_1.000	2627	3	1.07E-07	NP_492411.1	46	63.929	167	77	GEX Interacting protein family member (gei-11)
Locus_22070_Transcript_1/1_Conf_1.000	214	20	4.09E-24	XP_002646410.1	91	114.39	67	61	Hypothetical protein CBG18783
Locus_22071_Transcript_1/1_Conf_1.000	481	0							
Locus_22072_Transcript_1/1_Conf_1.000	146	0							
Locus_22073_Transcript_1/1_Conf_1.000	623	0							

Locus_22074_Transcript_1/1_Conf_1.000	492	0							
Locus_22075_Transcript_1/1_Conf_1.000	210	20	3.98E-19	NP_509186.3	78	97.8265	71	56	Carbonic AnHydrase family member (cah-5)
Locus_22076_Transcript_1/1_Conf_1.000	208	2	1.20E-07	XP_002642021.1	65	59.6918	69	45	C. briggsae CBR-COQ-8 protein
Locus_22077_Transcript_1/1_Conf_1.000	264	20	5.10E-14	XP_002642804.1	72	80.8777	75	54	Hypothetical protein CBG21200
Locus_22078_Transcript_1/1_Conf_1.000	341	20	1.90E-21	CAB07368.3	67	105.531	113	76	C. elegans protein F22G12.4, confirmed by transcript evidence
Locus_22079_Transcript_1/1_Conf_1.000	143	20	6.53E-14	XP_002640379.1	87	80.4925	47	41	C. briggsae CBR-OPT-3 protein
Locus_2208_Transcript_1/2_Conf_1.000	4847	20	0	NP_001024981.1	79	1048.88	844	674	Lin-5 (Five) Interacting protein family member (lfi-1)
Locus_2208_Transcript_2/2_Conf_1.000	4847	20	0	NP_001024981.1	79	1044.65	843	673	Lin-5 (Five) Interacting protein family member (lfi-1)
Locus_22080_Transcript_1/1_Conf_1.000	302	3	5.43E-08	XP_002645016.1	62	60.8474	81	51	Hypothetical protein CBG11012
Locus_22081_Transcript_1/1_Conf_1.000	307	20	9.77E-26	NP_498284.1	75	119.783	93	70	hypothetical protein C28H8.11
Locus_22082_Transcript_1/1_Conf_1.000	154	0							

Locus_22083_Transcript_1/1_Conf_1.000	250	2	1.15E-10	NP_505353.1	94	69.707	39	37	hypothetical protein T27E4.7
Locus_22084_Transcript_1/1_Conf_1.000	346	0							
Locus_22085_Transcript_1/1_Conf_1.000	432	0							
Locus_22086_Transcript_1/1_Conf_1.000	319	20	1.43E-48	XP_002633294.1	95	195.667	94	90	C. briggsae CBR-NHR-67 protein
Locus_22087_Transcript_1/1_Conf_1.000	167	20	5.07E-22	NP_500379.1	98	107.457	53	52	hypothetical protein Y37E11B.5
Locus_22088_Transcript_1/1_Conf_1.000	142	0							
Locus_22089_Transcript_1/1_Conf_1.000	362	20	2.96E-06	XP_001361765.2	43	55.0694	116	51	GA21047
Locus_2209_Transcript_1/1_Conf_1.000	782	20	1.64E-55	XP_002642013.1	85	220.32	185	159	Hypothetical protein CBG17947
Locus_22090_Transcript_1/1_Conf_1.000	182	20	2.84E-28	XP_002641773.1	98	128.257	60	59	Hypothetical protein CBG10119
Locus_22091_Transcript_1/1_Conf_1.000	404	2	1.70E-09	NP_496236.1	57	65.855	124	71	hypothetical protein T09F3.2
Locus_22092_Transcript_1/1_Conf_1.000	219	0							
Locus_22093_Transcript_1/1_Conf_1.000	212	0							
Locus_22094_Transcript_1/1_Conf_1.000	190	0							
Locus_22095_Transcript_1/1_Conf_1.000	524	0							
Locus_22096_Transcript_1/1_Conf_1.000	147	0							
Locus_22097_Transcript_1/1_Conf_1.000	173	0							
Locus_22098_Transcript_1/1_Conf_1.000	154	0							
Locus_22099_Transcript_1/1_Conf_1.000	273	0							
Locus_221_Transcript_1/3_Conf_0.571	588	1	3.01E-16	EFO15932.1	65	88.9669	112	73	hypothetical protein LOAG_12576
Locus_221_Transcript_2/3_Conf_0.429	588	1	3.01E-16	EFO15932.1	65	88.9669	112	73	hypothetical protein LOAG_12576
Locus_221_Transcript_3/3_Conf_0.571	2214	20	1.02E-72	EFO15932.1	67	279.641	286	192	hypothetical protein LOAG_12576
Locus_2210_Transcript_1/3_Conf_0.400	1914	20	0	XP_002636622.1	83	884.019	643	537	C. briggsae CBR-SMA-1 protein
Locus_2210_Transcript_2/3_Conf_0.400	1905	20	0	XP_002636622.1	85	883.248	625	532	C. briggsae CBR-SMA-1 protein

Locus_2210_Transcript_3/3_Conf_0.600	1954	20	0	XP_002636622.1	85	882.478	623	531	C. briggsae CBR-SMA-1 protein
Locus_22100_Transcript_1/1_Conf_1.000	319	0							
Locus_22101_Transcript_1/1_Conf_1.000	167	0							
Locus_22102_Transcript_1/1_Conf_1.000	169	20	1.24E-28	XP_002913159.1	100	129.413	56	56	PREDICTED: serine/threonine-protein phosphatase PP1-gamma catalytic subunit-like
Locus_22103_Transcript_1/1_Conf_1.000	181	0							
Locus_22104_Transcript_1/1_Conf_1.000	162	0							
Locus_22105_Transcript_1/1_Conf_1.000	668	20	7.73E-07	XP_001894189.1	53	58.151	149	79	hypothetical protein
Locus_22106_Transcript_1/1_Conf_1.000	179	0							
Locus_22107_Transcript_1/1_Conf_1.000	407	5	1.74E-14	NP_492265.1	66	82.4185	77	51	MYST family histone acetyltransferase-like family member (mys-4)
Locus_22108_Transcript_1/1_Conf_1.000	393	6	1.90E-08	XP_002645850.1	58	62.3882	73	43	Hypothetical protein CBG07586
Locus_22109_Transcript_1/1_Conf_1.000	191	0							
Locus_2211_Transcript_1/1_Conf_1.000	903	5	3.79E-12	NP_496595.1	73	76.6406	67	49	SR protein related family member (rsr-2)
Locus_22110_Transcript_1/1_Conf_1.000	250	0							

Locus_22111_Transcript_1/1_Conf_1.000	441	20	7.85E-47	EFO21836.1	77	189.889	146	113	hypothetical protein LOAG_06649
Locus_22112_Transcript_1/1_Conf_1.000	301	3	2.13E-04	XP_002646170.1	59	48.9062	72	43	C. briggsae CBR-TAF-5 protein
Locus_22113_Transcript_1/1_Conf_1.000	762	20	6.82E-27	XP_002131847.1	73	125.176	127	93	PREDICTED: similar to riboflavin kinase
Locus_22114_Transcript_1/1_Conf_1.000	157	2	2.23E-09	XP_002634423.1	75	65.4698	52	39	C. briggsae CBR-PTR-14 protein
Locus_22115_Transcript_1/1_Conf_1.000	513	20	5.99E-69	NP_741582.2	86	263.462	170	147	hypothetical protein H14N18.4
Locus_22116_Transcript_1/1_Conf_1.000	131	0							
Locus_22117_Transcript_1/1_Conf_1.000	305	0							
Locus_22118_Transcript_1/1_Conf_1.000	292	20	3.41E-34	XP_002629844.1	89	147.902	97	87	C. briggsae CBR-SCP-1 protein
Locus_22119_Transcript_1/1_Conf_1.000	302	0							
Locus_2212_Transcript_1/1_Conf_1.000	889	20	9.52E-69	NP_493412.2	68	264.618	316	218	hypothetical protein Y37H9A.3
Locus_22120_Transcript_1/1_Conf_1.000	130	0							
Locus_22121_Transcript_1/1_Conf_1.000	633	20	7.79E-43	NP_504651.1	75	177.563	152	114	MOlybdenum Cofactor biosynthesis family member (moc-2)
Locus_22122_Transcript_1/1_Conf_1.000	361	0							
Locus_22123_Transcript_1/1_Conf_1.000	148	0							
Locus_22124_Transcript_1/1_Conf_1.000	197	6	2.22E-09	EFO16773.1	69	65.4698	66	46	hypothetical protein LOAG_11731
Locus_22125_Transcript_1/1_Conf_1.000	286	0							
Locus_22126_Transcript_1/1_Conf_1.000	614	20	1.49E-88	1LLQ	89	329.331	201	180	CrystalStructure Of Malic Enzyme From Ascaris Suum Complexed With Nicotinamide Adenine Dinucleotide
Locus_22127_Transcript_1/1_Conf_1.000	262	0							
Locus_22128_Transcript_1/1_Conf_1.000	129	0							
Locus_22129_Transcript_1/1_Conf_1.000	379	9	3.19E-16	XP_002638736.1	71	88.1965	84	60	C. briggsae CBR-EGO-1 protein

Locus_2213_Transcript_1/1_Conf_1.000	2658	20	0	XP_002645233.1	76	946.421	777	597	C. briggsae CBR-TAG-147 protein
Locus_22130_Transcript_1/1_Conf_1.000	173	20	2.59E-10	YP_001413705.1	71	68.5514	57	41	D-lactate dehydrogenase (cytochrome)
Locus_22131_Transcript_1/1_Conf_1.000	222	20	2.64E-18	NP_497641.2	83	95.1301	68	57	CaDHerin family member (cdh-1)
Locus_22132_Transcript_1/1_Conf_1.000	288	0							
Locus_22133_Transcript_1/1_Conf_1.000	359	1	1.68E-17	EFO25272.1	58	92.4337	116	68	hypothetical protein LOAG_03210
Locus_22134_Transcript_1/1_Conf_1.000	284	0							
Locus_22135_Transcript_1/1_Conf_1.000	502	20	1.93E-53	NP_741714.1	80	211.846	167	134	related to yeast Vacuolar Protein Sorting factor family member (vps-45)
Locus_22136_Transcript_1/1_Conf_1.000	373	0							
Locus_22137_Transcript_1/1_Conf_1.000	133	0							
Locus_22138_Transcript_1/1_Conf_1.000	165	0							
Locus_22139_Transcript_1/1_Conf_1.000	174	17	5.04E-06	XP_002740793.1	62	54.299	54	34	PREDICTED: hypothetical protein
Locus_2214_Transcript_1/2_Conf_1.000	1072	20	2.79E-63	EFO18993.1	56	246.899	362	203	hypothetical protein LOAG_09502
Locus_2214_Transcript_2/2_Conf_1.000	1033	20	4.37E-66	EFO18993.1	58	256.144	349	203	hypothetical protein LOAG_09502
Locus_22140_Transcript_1/1_Conf_1.000	169	2	7.31E-13	NP_491499.1	80	77.0258	56	45	hypothetical protein F54C1.1
Locus_22141_Transcript_1/1_Conf_1.000	172	0							
Locus_22142_Transcript_1/1_Conf_1.000	157	0							
Locus_22143_Transcript_1/1_Conf_1.000	155	0							
Locus_22144_Transcript_1/1_Conf_1.000	251	2	8.00E-04	NP_503880.1	58	46.9802	50	29	hypothetical protein Y73C8B.1
Locus_22145_Transcript_1/1_Conf_1.000	260	0							
Locus_22146_Transcript_1/1_Conf_1.000	168	0							
Locus_22147_Transcript_1/1_Conf_1.000	276	0							
Locus_22148_Transcript_1/2_Conf_1.000	276	4	3.05E-11	NP_495478.1	82	71.633	50	41	hypothetical protein T07F8.4
Locus_22148_Transcript_2/2_Conf_1.000	270	2	1.43E-08	NP_495478.1	78	62.7734	50	39	hypothetical protein T07F8.4

Locus_22149_Transcript_1/1_Conf_1.000	291	20	2.29E-22	NP_061932.1	100	108.612	51	51	mitochondrial import receptor subunit TOM7 homolog
Locus_2215_Transcript_1/2_Conf_1.000	1365	2	1.44E-04	XP_001751006.1	30	52.373	325	98	hypothetical protein
Locus_2215_Transcript_2/2_Conf_1.000	1365	4	7.63E-06	XP_001751006.1	29	56.6102	325	95	hypothetical protein
Locus_22150_Transcript_1/1_Conf_1.000	206	4	1.74E-14	NP_496984.1	72	82.4185	68	49	hypothetical protein R06A4.8
Locus_22151_Transcript_1/1_Conf_1.000	229	0							
Locus_22152_Transcript_1/1_Conf_1.000	319	20	1.34E-46	XP_002831374.1	99	189.119	106	105	PREDICTED: ADP/ATP translocase 3-like, partial
Locus_22153_Transcript_1/1_Conf_1.000	410	1	4.28E-05	NP_504468.2	61	51.2174	72	44	hypothetical protein C18C4.7
Locus_22154_Transcript_1/1_Conf_1.000	213	2	4.54E-15	XP_002638798.1	76	84.3445	71	54	C. briggsae CBR-PIF-1 protein
Locus_22155_Transcript_1/1_Conf_1.000	251	20	1.83E-24	XP_002643979.1	95	115.546	68	65	C. briggsae CBR-PGP-3 protein
Locus_22156_Transcript_1/1_Conf_1.000	148	15	7.24E-08	XP_002630579.1	75	60.4622	48	36	C. briggsae CBR-NHX-2 protein
Locus_22157_Transcript_1/1_Conf_1.000	263	0							
Locus_22158_Transcript_1/1_Conf_1.000	248	0							
Locus_22159_Transcript_1/1_Conf_1.000	327	20	4.43E-26	NP_502164.1	86	120.939	105	91	WHiTe (Drosophila) related ABC transporte family member (wht-2)
Locus_2216_Transcript_1/2_Conf_1.000	2128	20	2.68E-147	NP_505969.1	91	527.324	309	284	HRD (yeast Hmg-coa Reductase Degradation) homolog family member (hrd-1)

Locus_2216_Transcript_2/2_Conf_1.000	2053	20	2.57E-147	NP_505969.1	91	527.324	309	284	HRD (yeast Hmg-coa Reductase Degradation) homolog family member (hrd-1)
Locus_22160_Transcript_1/1_Conf_1.000	372	2	4.35E-05	NP_506364.2	50	51.2174	122	62	hypothetical protein C50B8.5
Locus_22161_Transcript_1/1_Conf_1.000	184	0							
Locus_22162_Transcript_1/1_Conf_1.000	151	0							
Locus_22163_Transcript_1/1_Conf_1.000	473	20	2.26E-46	XP_001895190.1	74	188.348	157	117	Receptor family ligand binding region containing protein
Locus_22164_Transcript_1/1_Conf_1.000	156	0							
Locus_22165_Transcript_1/1_Conf_1.000	225	20	3.21E-24	XP_001100810.2	100	114.775	72	72	PREDICTED: 60S ribosomal protein L5-like isoform 3
Locus_22166_Transcript_1/1_Conf_1.000	167	0							
Locus_22167_Transcript_1/1_Conf_1.000	169	0							
Locus_22168_Transcript_1/1_Conf_1.000	300	0							
Locus_22169_Transcript_1/1_Conf_1.000	923	20	9.69E-11	XP_001464299.1	42	72.0182	293	124	kinesin K39
Locus_2217_Transcript_1/1_Conf_1.000	1332	20	6.06E-101	NP_498411.1	81	372.474	281	228	related to yeast Vacuolar Protein Sorting factor family member (vps-16)
Locus_22170_Transcript_1/1_Conf_1.000	120	0							

Locus_22171_Transcript_1/1_Conf_1.000	174	20	2.33E-19	XP_002643811.1	94	98.5969	57	54	C. briggsae CBR-NMY-1 protein
Locus_22172_Transcript_1/1_Conf_1.000	246	4	8.84E-19	NP_496968.1	77	96.6709	74	57	hypothetical protein Y48B6A.12
Locus_22173_Transcript_1/1_Conf_1.000	134	0							
Locus_22174_Transcript_1/1_Conf_1.000	284	20	1.23E-15	ABJ99064.1	64	86.2705	96	62	Hypothetical protein W03A3.2
Locus_22175_Transcript_1/1_Conf_1.000	210	20	2.75E-20	EFO25043.1	86	101.679	69	60	hypothetical protein LOAG_03439
Locus_22176_Transcript_1/1_Conf_1.000	197	20	5.83E-26	XP_002640668.1	96	120.553	65	63	C. briggsae CBR-UNC-54 protein
Locus_22177_Transcript_1/1_Conf_1.000	215	2	1.91E-05	XP_002636455.1	65	52.373	47	31	Hypothetical protein CBG23119
Locus_22178_Transcript_1/1_Conf_1.000	574	20	1.76E-58	CAR63670.1	84	229.18	152	129	hypothetical protein
Locus_22179_Transcript_1/1_Conf_1.000	211	0							
Locus_2218_Transcript_1/1_Conf_1.000	324	0							
Locus_22180_Transcript_1/1_Conf_1.000	177	0							
Locus_22181_Transcript_1/1_Conf_1.000	359	0							
Locus_22182_Transcript_1/1_Conf_1.000	255	0							
Locus_22183_Transcript_1/1_Conf_1.000	374	20	5.42E-56	XP_002642222.1	90	220.32	122	111	C. briggsae CBR-FSN-1 protein
Locus_22184_Transcript_1/1_Conf_1.000	345	10	3.20E-40	XP_002631802.1	84	167.933	115	97	Hypothetical protein CBG21021
Locus_22185_Transcript_1/1_Conf_1.000	273	20	2.12E-20	NP_492278.2	69	102.064	91	63	hypothetical protein T19A6.4
Locus_22186_Transcript_1/1_Conf_1.000	331	4	2.52E-05	XP_001204017.1	53	51.9878	111	59	PREDICTED: similar to Pdcd6ip protein
Locus_22187_Transcript_1/1_Conf_1.000	552	5	2.03E-37	ACM46022.1	70	159.073	150	105	Troponin t protein 3, isoform d
Locus_22188_Transcript_1/1_Conf_1.000	141	0							
Locus_22189_Transcript_1/1_Conf_1.000	136	0							
Locus_2219_Transcript_1/1_Conf_1.000	242	0							
Locus_22190_Transcript_1/1_Conf_1.000	346	20	2.79E-44	NP_498014.2	86	181.415	115	100	COenzyme Q (ubiquinone) biosynthesis family member (coq-8)

Locus_22191_Transcript_1/1_Conf_1.000	379	20	1.92E-29	XP_002634543.1	71	132.109	118	84	C. briggsae CBR-CED-5 protein
Locus_22192_Transcript_1/1_Conf_1.000	128	0							
Locus_22193_Transcript_1/1_Conf_1.000	497	0							
Locus_22194_Transcript_1/1_Conf_1.000	143	20	4.22E-21	3JYH	100	104.375	47	47	Human Dipeptidyl Peptidase Dpp7
Locus_22195_Transcript_1/1_Conf_1.000	230	7	1.14E-05	B4XT00.1	60	53.1434	71	43	C-type lectin B1
Locus_22196_Transcript_1/1_Conf_1.000	255	0							
Locus_22197_Transcript_1/1_Conf_1.000	496	20	3.47E-39	XP_001899820.1	85	164.466	132	113	Hexokinase family protein
Locus_22198_Transcript_1/1_Conf_1.000	132	9	2.27E-06	CBA11992.1	80	55.4546	41	33	endonuclease-reverse transcriptase HmRTE-e01
Locus_22199_Transcript_1/1_Conf_1.000	311	0							
Locus_222_Transcript_1/3_Conf_0.625	1227	20	1.16E-127	P54813.2	83	461.07	323	270	Protein YME1 homolog
Locus_222_Transcript_2/3_Conf_0.750	2500	20	0	P54813.2	86	921.383	636	551	Protein YME1 homolog
Locus_222_Transcript_3/3_Conf_0.750	2518	20	0	P54813.2	87	935.636	636	556	Protein YME1 homolog

Locus_2220_Transcript_1/1_Conf_1.000	2000	20	0	NP_498887.2	91	1072.77	628	574	GLutamate Receptor family (AMPA) family member (glr-1)
Locus_22200_Transcript_1/1_Conf_1.000	349	0							
Locus_22201_Transcript_1/1_Conf_1.000	146	1	6.36E-04	EFO24319.1	64	47.3654	48	31	hypothetical protein LOAG_04165
Locus_22202_Transcript_1/1_Conf_1.000	162	0							
Locus_22203_Transcript_1/1_Conf_1.000	291	4	1.59E-31	XP_002642450.1	83	139.043	92	77	Hypothetical protein CBG06858
Locus_22204_Transcript_1/1_Conf_1.000	261	20	2.01E-18	NP_740780.1	94	95.5153	71	67	AdaPtin, Small chain (clathrin associated complex) family member (aps-3)
Locus_22205_Transcript_1/1_Conf_1.000	376	0							
Locus_22206_Transcript_1/1_Conf_1.000	462	0							
Locus_22207_Transcript_1/1_Conf_1.000	163	0							
Locus_22208_Transcript_1/1_Conf_1.000	452	20	1.85E-32	XP_002636579.1	76	142.124	103	79	Hypothetical protein CBG23273
Locus_22209_Transcript_1/1_Conf_1.000	206	0							
Locus_2221_Transcript_1/1_Conf_1.000	864	0							
Locus_22210_Transcript_1/1_Conf_1.000	174	20	5.93E-23	BAG11032.1	100	110.538	52	52	FERM, RhoGEF and pleckstrin domain-containing protein 1
Locus_22211_Transcript_1/1_Conf_1.000	152	0							
Locus_22212_Transcript_1/1_Conf_1.000	229	0							

Locus_22213_Transcript_1/1_Conf_1.000	206	0							
Locus_22214_Transcript_1/1_Conf_1.000	149	0							
Locus_22215_Transcript_1/1_Conf_1.000	413	20	9.70E-50	NP_501127.2	85	199.519	126	108	RNA Polymerase, Class III (C) family member (rpc-1)
Locus_22216_Transcript_1/1_Conf_1.000	317	20	1.76E-38	NP_495009.1	90	162.155	96	87	hypothetical protein F09E5.3
Locus_22217_Transcript_1/1_Conf_1.000	270	20	4.01E-19	NP_490706.2	64	97.8265	90	58	hypothetical protein Y48G1BM.1
Locus_22218_Transcript_1/1_Conf_1.000	219	20	1.46E-16	XP_001894229.1	84	89.3521	58	49	Variant SH3 domain containing protein
Locus_22219_Transcript_1/1_Conf_1.000	159	0							
Locus_2222_Transcript_1/2_Conf_1.000	344	4	5.15E-14	XP_002640676.1	89	80.8777	47	42	Hypothetical protein CBG19738
Locus_2222_Transcript_2/2_Conf_1.000	340	2	6.53E-14	XP_002640676.1	85	80.4925	70	60	Hypothetical protein CBG19738
Locus_22220_Transcript_1/1_Conf_1.000	281	1	2.04E-07	NP_502613.2	62	58.9214	91	57	QUInine non-avoider family member (qui-1)
Locus_22221_Transcript_1/1_Conf_1.000	364	0							
Locus_22222_Transcript_1/1_Conf_1.000	158	0							
Locus_22223_Transcript_1/1_Conf_1.000	229	1	8.18E-12	XP_001896987.1	63	73.559	79	50	Zinc finger, C2H2 type family protein
Locus_22224_Transcript_1/1_Conf_1.000	327	1	2.98E-14	NP_508445.1	60	81.6481	82	50	hypothetical protein T07D1.3
Locus_22225_Transcript_1/1_Conf_1.000	227	0							
Locus_22226_Transcript_1/1_Conf_1.000	175	0							
Locus_22227_Transcript_1/1_Conf_1.000	243	0							
Locus_22228_Transcript_1/1_Conf_1.000	544	7	2.52E-05	CAB55122.3	56	52.373	51	29	C. elegans protein Y116A8C.16a, partially confirmed by transcript evidence
Locus_22229_Transcript_1/1_Conf_1.000	407	20	1.32E-62	XP_002642870.1	89	242.276	135	121	Hypothetical protein CBG15140
Locus_2223_Transcript_1/1_Conf_1.000	2261	20	0	NP_496721.2	87	1045.42	664	578	Carnitine Palmitoyl Transferase family member (cpt-1)

Locus_22230_Transcript_1/1_Conf_1.000	319	20	4.94E-33	NP_504750.2	80	144.05	91	73	hypothetical protein K11C4.2
Locus_22231_Transcript_1/1_Conf_1.000	145	20	1.97E-21	BAG60853.1	100	105.531	47	47	unnamed protein product
Locus_22232_Transcript_1/1_Conf_1.000	329	0							
Locus_22233_Transcript_1/1_Conf_1.000	224	0							
Locus_22234_Transcript_1/1_Conf_1.000	289	20	4.19E-32	NP_491653.2	84	140.969	95	80	hypothetical protein F55F8.3
Locus_22235_Transcript_1/1_Conf_1.000	312	0							
Locus_22236_Transcript_1/1_Conf_1.000	422	0							
Locus_22237_Transcript_1/1_Conf_1.000	160	0							
Locus_22238_Transcript_1/1_Conf_1.000	837	20	5.54E-92	XP_002630799.1	72	341.658	285	208	Hypothetical protein CBG02498
Locus_22239_Transcript_1/1_Conf_1.000	435	5	1.97E-26	NP_503502.2	75	122.094	86	65	hypothetical protein F36H9.7
Locus_2224_Transcript_1/2_Conf_1.000	2466	20	2.43E-38	XP_002640658.1	39	165.622	746	298	Hypothetical protein CBG19716
Locus_2224_Transcript_2/2_Conf_1.000	2403	20	5.28E-38	XP_002640658.1	39	164.466	731	286	Hypothetical protein CBG19716
Locus_22240_Transcript_1/1_Conf_1.000	247	0							
Locus_22241_Transcript_1/1_Conf_1.000	289	20	1.23E-07	NP_001037879.1	69	59.6918	63	44	CTF8, chromosome transmission fidelity factor 8 homolog
Locus_22242_Transcript_1/1_Conf_1.000	163	0							
Locus_22243_Transcript_1/1_Conf_1.000	267	20	3.89E-14	NP_505919.3	63	81.2629	86	55	hypothetical protein C55A6.3
Locus_22244_Transcript_1/1_Conf_1.000	140	2	5.94E-07	XP_002641999.1	78	57.3806	46	36	C. briggsae CBR-ACY-3 protein
Locus_22245_Transcript_1/1_Conf_1.000	204	18	4.13E-24	XP_002641899.1	89	114.39	68	61	C. briggsae CBR-NHR-10 protein
Locus_22246_Transcript_1/1_Conf_1.000	152	0							
Locus_22247_Transcript_1/1_Conf_1.000	438	0							
Locus_22248_Transcript_1/1_Conf_1.000	164	0							
Locus_22249_Transcript_1/1_Conf_1.000	133	0							

Locus_2225_Transcript_1/1_Conf_1.000	2231	20	0	XP_002633925.1	88	749.584	551	487	C. briggsae CBR-SOC-2 protein
Locus_22250_Transcript_1/1_Conf_1.000	351	2	6.64E-22	XP_002638987.1	75	107.071	113	85	Hypothetical protein CBG22233
Locus_22251_Transcript_1/1_Conf_1.000	959	20	2.68E-43	XP_002630256.1	53	180.259	308	166	Hypothetical protein CBG00675
Locus_22252_Transcript_1/1_Conf_1.000	236	0							
Locus_22253_Transcript_1/1_Conf_1.000	177	20	7.97E-28	XP_002811367.1	100	126.716	58	58	PREDICTED: complement C1q subcomponent subunit C-like isoform 1
Locus_22254_Transcript_1/1_Conf_1.000	322	16	7.30E-53	NP_001129826.1	98	209.92	106	104	hypothetical protein T13H5.1
Locus_22255_Transcript_1/1_Conf_1.000	131	0							
Locus_22256_Transcript_1/1_Conf_1.000	132	20	8.89E-19	XP_002802333.1	100	96.6709	43	43	PREDICTED: eukaryotic translation initiation factor 3 subunit I-like
Locus_22257_Transcript_1/1_Conf_1.000	143	20	1.23E-20	XP_002915235.1	100	102.834	47	47	PREDICTED: spectrin alpha chain, brain-like isoform 2
Locus_22258_Transcript_1/1_Conf_1.000	262	0							

Locus_22259_Transcript_1/1_Conf_1.000	237	20	1.57E-39	ADI78884.1	100	165.622	79	79	plasma membrane citrate carrier
Locus_2226_Transcript_1/1_Conf_1.000	576	4	5.82E-17	XP_001899796.1	70	91.2781	82	58	Uncoordinated protein 40
Locus_22260_Transcript_1/1_Conf_1.000	147	0							
Locus_22261_Transcript_1/1_Conf_1.000	130	0							
Locus_22262_Transcript_1/1_Conf_1.000	273	20	2.11E-28	XP_002644906.1	92	128.642	88	81	Hypothetical protein CBG10845
Locus_22263_Transcript_1/1_Conf_1.000	208	0							
Locus_22264_Transcript_1/1_Conf_1.000	264	0							
Locus_22265_Transcript_1/1_Conf_1.000	210	2	1.09E-08	NP_001023357.2	67	63.1586	68	46	hypothetical protein T04C4.1
Locus_22266_Transcript_1/1_Conf_1.000	145	0							
Locus_22267_Transcript_1/1_Conf_1.000	295	20	2.52E-29	XP_002631704.1	80	131.724	96	77	Hypothetical protein CBG20903
Locus_22268_Transcript_1/1_Conf_1.000	206	0							
Locus_22269_Transcript_1/1_Conf_1.000	210	0							
Locus_2227_Transcript_1/1_Conf_1.000	188	1	6.11E-07	XP_001898414.1	85	57.3806	35	30	collagen col-34
Locus_22270_Transcript_1/1_Conf_1.000	173	20	7.79E-15	XP_002636770.1	85	83.5741	56	48	Hypothetical protein CBG23501
Locus_22271_Transcript_1/1_Conf_1.000	767	20	1.78E-75	XP_002630049.1	73	286.574	238	176	C. briggsae CBR-APN-1 protein
Locus_22272_Transcript_1/1_Conf_1.000	382	20	2.83E-65	XP_002646694.1	95	251.136	126	120	C. briggsae CBR-SPON-1 protein
Locus_22273_Transcript_1/1_Conf_1.000	204	0							
Locus_22274_Transcript_1/1_Conf_1.000	182	0							
Locus_22275_Transcript_1/1_Conf_1.000	328	0							
Locus_22276_Transcript_1/1_Conf_1.000	278	0							
Locus_22277_Transcript_1/1_Conf_1.000	307	9	5.93E-23	NP_499482.1	78	110.538	83	65	defective SPErmatogenesis family member (spe-6)
Locus_22278_Transcript_1/1_Conf_1.000	167	0							
Locus_22279_Transcript_1/1_Conf_1.000	464	20	9.54E-69	XP_002629875.1	90	262.692	154	139	C. briggsae CBR-LET-75 protein
Locus_2228_Transcript_1/1_Conf_1.000	549	0							
Locus_22280_Transcript_1/1_Conf_1.000	247	20	5.51E-37	XP_002641343.1	96	157.147	81	78	C. briggsae CBR-DPY-18 protein

Locus_22281_Transcript_1/1_Conf_1.000	286	20	3.93E-30	NP_501419.2	84	134.42	95	80	hypothetical protein D2096.3
Locus_22282_Transcript_1/1_Conf_1.000	188	0							
Locus_22283_Transcript_1/1_Conf_1.000	423	0							
Locus_22284_Transcript_1/1_Conf_1.000	160	3	4.63E-07	NP_509676.1	68	57.7658	54	37	G-protein-coupled Receptor Kinase family member (grk-1)
Locus_22285_Transcript_1/1_Conf_1.000	158	0							
Locus_22286_Transcript_1/1_Conf_1.000	133	3	1.09E-08	EFO24958.1	79	63.1586	43	34	hypothetical protein LOAG_03524
Locus_22287_Transcript_1/1_Conf_1.000	357	20	1.24E-28	NP_001021200.1	70	129.413	116	82	tryptophanyl (W) tRNA Synthetase family member (wrs-2)
Locus_22288_Transcript_1/1_Conf_1.000	138	0							
Locus_22289_Transcript_1/1_Conf_1.000	287	0							
Locus_2229_Transcript_1/2_Conf_1.000	2011	20	0	NP_498777.2	84	619.772	437	370	hypothetical protein C14B9.8
Locus_2229_Transcript_2/2_Conf_1.000	1987	20	0	NP_498777.2	84	619.772	437	370	hypothetical protein C14B9.8
Locus_22290_Transcript_1/1_Conf_1.000	327	0							
Locus_22291_Transcript_1/1_Conf_1.000	172	0							
Locus_22292_Transcript_1/1_Conf_1.000	337	20	4.35E-50	XP_002632347.1	92	200.675	113	105	Hypothetical protein CBG00360
Locus_22293_Transcript_1/1_Conf_1.000	186	20	3.81E-25	NP_509174.1	96	117.857	61	59	hypothetical protein C16E9.2
Locus_22294_Transcript_1/1_Conf_1.000	321	20	6.90E-19	XP_001893826.1	66	97.0561	104	69	Protein-tyrosine phosphatase containing protein
Locus_22295_Transcript_1/1_Conf_1.000	325	0							
Locus_22296_Transcript_1/1_Conf_1.000	235	20	4.58E-31	XP_002927413.1	100	137.502	67	67	PREDICTED: eukaryotic translation initiation factor 3 subunit C-like
Locus_22297_Transcript_1/1_Conf_1.000	188	0							
Locus_22298_Transcript_1/1_Conf_1.000	147	0							
Locus_22299_Transcript_1/1_Conf_1.000	172	0							

Locus_223_Transcript_1/1_Conf_1.000	2106	20	0	XP_001894294.1	87	899.427	592	517	protein phosphatase PP2A regulatory subunit
Locus_2230_Transcript_1/1_Conf_1.000	916	0							
Locus_22300_Transcript_1/1_Conf_1.000	368	0							
Locus_22301_Transcript_1/1_Conf_1.000	140	0							
Locus_22302_Transcript_1/1_Conf_1.000	433	20	6.05E-76	BAG60350.1	100	286.574	144	144	unnamed protein product
Locus_22303_Transcript_1/1_Conf_1.000	293	20	1.18E-18	XP_002632873.1	64	96.2857	97	63	Hypothetical protein CBG15077
Locus_22304_Transcript_1/1_Conf_1.000	145	0							
Locus_22305_Transcript_1/1_Conf_1.000	367	0							
Locus_22306_Transcript_1/1_Conf_1.000	218	8	5.70E-18	NP_501928.1	80	93.9745	71	57	hypothetical protein F13B12.4
Locus_22307_Transcript_1/1_Conf_1.000	139	0							

Locus_22308_Transcript_1/1_Conf_1.000	381	20	1.57E-23	NP_494994.1	67	112.464	129	87	hypothetical protein ZK622.1
Locus_22309_Transcript_1/1_Conf_1.000	350	1	4.06E-11	EFO24286.1	76	71.2478	50	38	hypothetical protein LOAG_04203
Locus_2231_Transcript_1/1_Conf_1.000	563	20	1.95E-43	CAR63593.1	83	179.104	110	92	putative PQ loop repeat family protein
Locus_22310_Transcript_1/2_Conf_1.000	423	0							
Locus_22310_Transcript_2/2_Conf_1.000	475	0							
Locus_22311_Transcript_1/1_Conf_1.000	493	3	1.48E-05	XP_002633421.1	53	52.7582	94	50	C. briggsae CBR-NHR-43 protein
Locus_22312_Transcript_1/1_Conf_1.000	131	20	4.29E-13	NP_505370.2	97	77.7962	43	42	hypothetical protein B0222.2
Locus_22313_Transcript_1/1_Conf_1.000	637	20	4.57E-83	XP_002641813.1	95	311.227	180	171	C. briggsae CBR-INF-1 protein
Locus_22314_Transcript_1/1_Conf_1.000	283	0							
Locus_22315_Transcript_1/1_Conf_1.000	787	7	2.55E-72		74	276.174	255	189	hypothetical protein Y105C5A.r
Locus_22316_Transcript_1/1_Conf_1.000	458	2	6.16E-04	NP_001024104.1	61	47.3654	59	36	hypothetical protein T05B11.7
Locus_22317_Transcript_1/1_Conf_1.000	312	0							
Locus_22318_Transcript_1/1_Conf_1.000	407	0							
Locus_22319_Transcript_1/1_Conf_1.000	164	5	1.70E-09	NP_495484.1	80	65.855	50	40	hypothetical protein C27H5.2

Locus_2232_Transcript_1/1_Conf_1.000	500	20	4.85E-17	NP_500336.1	89	90.8929	57	51	Mitochondrial ATPase Inhibitor family member (mai-2)
Locus_22320_Transcript_1/1_Conf_1.000	379	0							
Locus_22321_Transcript_1/1_Conf_1.000	351	0							
Locus_22322_Transcript_1/1_Conf_1.000	305	2	4.29E-28	EAW71418.1	100	92.0485	57	57	RNA binding motif protein 8A, isoform CRA_a
Locus_22323_Transcript_1/1_Conf_1.000	143	0							
Locus_22324_Transcript_1/1_Conf_1.000	290	0							
Locus_22325_Transcript_1/1_Conf_1.000	175	0							
Locus_22326_Transcript_1/1_Conf_1.000	154	0							
Locus_22327_Transcript_1/1_Conf_1.000	347	20	1.26E-36	EFO24516.1	73	155.992	115	85	TBL1X protein
Locus_22328_Transcript_1/1_Conf_1.000	194	4	1.27E-04	XP_002639323.1	59	49.6766	67	40	C. briggsae CBR-HUM-7 protein
Locus_22329_Transcript_1/1_Conf_1.000	147	0							
Locus_2233_Transcript_1/1_Conf_1.000	256	20	7.65E-34	NP_001129862.1	90	146.747	85	77	UNCoordinated family member (unc-26)
Locus_22330_Transcript_1/1_Conf_1.000	269	0							

Locus_22331_Transcript_1/1_Conf_1.000	162	0							
Locus_22332_Transcript_1/1_Conf_1.000	417	20	2.71E-39	NP_505978.1	69	164.851	138	96	hypothetical protein D2023.4
Locus_22333_Transcript_1/1_Conf_1.000	206	11	1.33E-14	ADD13547.1	91	82.8037	68	62	Inositol triphosphate receptor protein 1, isoform h
Locus_22334_Transcript_1/1_Conf_1.000	393	20	2.99E-54	NP_001022450.1	89	214.542	130	116	hypothetical protein Y48E1A.1
Locus_22335_Transcript_1/1_Conf_1.000	260	4	7.39E-29	NP_510438.1	95	130.183	67	64	CalSeQuestrin family member (csq-1)
Locus_22336_Transcript_1/1_Conf_1.000	255	20	4.83E-12	NP_509417.2	71	74.3294	67	48	hypothetical protein F40B5.2
Locus_22337_Transcript_1/1_Conf_1.000	163	0							
Locus_22338_Transcript_1/1_Conf_1.000	261	0							
Locus_22339_Transcript_1/1_Conf_1.000	343	1	1.55E-10	NP_001041292.1	71	69.3218	59	42	hypothetical protein T23E7.6
Locus_2234_Transcript_1/1_Conf_1.000	2782	20	0	XP_002633929.1	86	1461.82	878	756	C. briggsae CBR-LAM-1 protein
Locus_22340_Transcript_1/1_Conf_1.000	243	0							
Locus_22341_Transcript_1/1_Conf_1.000	370	0							
Locus_22342_Transcript_1/1_Conf_1.000	283	20	6.78E-06	ZP_04074401.1	64	53.9138	53	34	hypothetical protein bthur0013_47340
Locus_22343_Transcript_1/1_Conf_1.000	131	0							
Locus_22344_Transcript_1/1_Conf_1.000	186	0							
Locus_22345_Transcript_1/1_Conf_1.000	540	2	2.74E-04	NP_001033432.1	65	48.9062	47	31	hypothetical protein T19E7.6
Locus_22346_Transcript_1/1_Conf_1.000	312	20	2.17E-20	NP_502560.1	67	102.064	81	55	FATty acid desaturase family member (fat-2)
Locus_22347_Transcript_1/1_Conf_1.000	143	0							
Locus_22348_Transcript_1/1_Conf_1.000	587	0							
Locus_22349_Transcript_1/1_Conf_1.000	203	0							
Locus_2235_Transcript_1/1_Conf_1.000	1801	20	1.11E-58	ACI32657.1	53	232.646	274	147	Delta protein
Locus_22350_Transcript_1/1_Conf_1.000	354	20	1.73E-46	XP_002638742.1	92	188.734	117	108	C. briggsae CBR-PDE-6 protein
Locus_22351_Transcript_1/1_Conf_1.000	139	0							

Locus_22352_Transcript_1/1_Conf_1.000	609	20	2.28E-65	NP_001021681.1	77	252.292	209	162	hypothetical protein Y105E8A.10
Locus_22353_Transcript_1/1_Conf_1.000	346	0							
Locus_22354_Transcript_1/1_Conf_1.000	206	20	5.07E-14	XP_002633760.1	68	80.8777	58	40	C. briggsae CBR-GON-1 protein
Locus_22355_Transcript_1/1_Conf_1.000	389	0							
Locus_22356_Transcript_1/1_Conf_1.000	263	20	7.15E-16	CAR63522.1	72	87.0409	86	62	putative heat shock protein
Locus_22357_Transcript_1/1_Conf_1.000	181	20	8.57E-17	XP_002637669.1	88	90.1225	51	45	Hypothetical protein CBG19425
Locus_22358_Transcript_1/1_Conf_1.000	133	1	6.18E-04	XP_002637804.1	70	47.3654	37	26	Hypothetical protein CBG04590
Locus_22359_Transcript_1/1_Conf_1.000	180	1	1.68E-04	NP_499757.2	60	49.2914	51	31	hypothetical protein T03F6.4
Locus_2236_Transcript_1/5_Conf_0.444	342	0							
Locus_2236_Transcript_2/5_Conf_0.222	475	0							
Locus_2236_Transcript_3/5_Conf_0.333	333	0							
Locus_2236_Transcript_4/5_Conf_0.333	1724	20	7.87E-123	XP_002637706.1	77	445.662	339	264	Hypothetical protein CBG11571
Locus_2236_Transcript_5/5_Conf_0.222	342	0							
Locus_22360_Transcript_1/1_Conf_1.000	199	2	1.94E-05	XP_001891532.1	62	52.373	66	41	hypothetical protein Bm1_00020
Locus_22361_Transcript_1/1_Conf_1.000	374	20	2.31E-06	EFN78575.1	57	55.4546	83	48	Histone-lysine N-methyltransferase SETMAR
Locus_22362_Transcript_1/1_Conf_1.000	147	0							
Locus_22363_Transcript_1/1_Conf_1.000	274	0							
Locus_22364_Transcript_1/1_Conf_1.000	139	0							
Locus_22365_Transcript_1/1_Conf_1.000	215	0							
Locus_22366_Transcript_1/1_Conf_1.000	248	0							

Locus_22367_Transcript_1/1_Conf_1.000	275	6	2.59E-10	NP_001033378.1	67	68.5514	73	49	Acyl CoA DeHydrogenase family member (acdh-11)
Locus_22368_Transcript_1/1_Conf_1.000	167	0							
Locus_22369_Transcript_1/1_Conf_1.000	460	20	3.22E-37	CAB55118.2	73	157.918	143	105	C. elegans protein Y48C3A.18a, confirmed by transcript evidence
Locus_2237_Transcript_1/1_Conf_1.000	399	20	8.68E-30	XP_001895262.1	90	133.265	66	60	Hypothetical UPF0222 protein Y54G11A.11 in chromosome II, putative
Locus_22370_Transcript_1/1_Conf_1.000	145	1	6.36E-04	NP_491653.2	65	47.3654	47	31	hypothetical protein F55F8.3
Locus_22371_Transcript_1/1_Conf_1.000	312	0							
Locus_22372_Transcript_1/1_Conf_1.000	172	6	5.05E-14	NP_490755.1	87	80.8777	54	47	Heavy chain, Unconventional Myosin family member (hum-7)
Locus_22373_Transcript_1/1_Conf_1.000	467	14	1.59E-15	NP_001024064.1	53	85.8853	123	66	hypothetical protein R02C2.7
Locus_22374_Transcript_1/1_Conf_1.000	165	9	4.44E-18	XP_002647278.1	87	94.3597	55	48	C. briggsae CBR-KETN-1 protein
Locus_22375_Transcript_1/1_Conf_1.000	322	0							
Locus_22376_Transcript_1/1_Conf_1.000	169	0							
Locus_22377_Transcript_1/1_Conf_1.000	198	20	3.65E-20	XP_002634787.1	80	101.293	65	52	C. briggsae CBR-NPP-20 protein
Locus_22378_Transcript_1/1_Conf_1.000	268	0							
Locus_22379_Transcript_1/1_Conf_1.000	172	0							
Locus_2238_Transcript_1/1_Conf_1.000	438	6	3.45E-23	XP_002646549.1	63	111.309	144	91	Hypothetical protein CBG20406
Locus_22380_Transcript_1/1_Conf_1.000	497	20	6.42E-102	NP_492020.1	99	372.859	165	164	hypothetical protein K10D3.4
Locus_22381_Transcript_1/1_Conf_1.000	134	0							
Locus_22382_Transcript_1/1_Conf_1.000	301	0							
Locus_22383_Transcript_1/1_Conf_1.000	256	20	4.83E-12	XP_002646299.1	63	74.3294	77	49	Hypothetical protein CBG12006

Locus_22384_Transcript_1/1_Conf_1.000	485	20	1.58E-55	ACD61693.1	81	218.779	164	133	UDP-galactose transporter-related protein
Locus_22385_Transcript_1/1_Conf_1.000	205	6	1.63E-12	XP_002639055.1	71	75.8702	70	50	C. briggsae CBR-GCY-28 protein
Locus_22386_Transcript_1/1_Conf_1.000	129	0							
Locus_22387_Transcript_1/1_Conf_1.000	236	0							
Locus_22388_Transcript_1/1_Conf_1.000	177	0							
Locus_22389_Transcript_1/1_Conf_1.000	450	3	1.93E-13	ACH87166.1	54	78.9518	142	78	GLO-3
Locus_2239_Transcript_1/1_Conf_1.000	898	20	3.82E-57	XP_001898424.1	68	226.098	241	165	DEAD/H
Locus_22390_Transcript_1/1_Conf_1.000	191	0							
Locus_22391_Transcript_1/1_Conf_1.000	173	0							
Locus_22392_Transcript_1/1_Conf_1.000	340	20	6.07E-36	NP_502129.1	84	153.68	113	95	hypothetical protein B0035.5
Locus_22393_Transcript_1/1_Conf_1.000	513	1	3.58E-05	XP_002640597.1	42	51.6026	168	71	C. briggsae CBR-DLK-1 protein
Locus_22394_Transcript_1/2_Conf_1.000	345	0							
Locus_22394_Transcript_2/2_Conf_1.000	345	0							
Locus_22395_Transcript_1/1_Conf_1.000	145	0							
Locus_22396_Transcript_1/1_Conf_1.000	377	0							
Locus_22397_Transcript_1/1_Conf_1.000	179	0							
Locus_22398_Transcript_1/1_Conf_1.000	137	0							
Locus_22399_Transcript_1/1_Conf_1.000	134	0							
Locus_224_Transcript_1/2_Conf_1.000	2197	20	0	NP_502350.1	80	701.049	543	439	hypothetical protein F19B6.1
Locus_224_Transcript_2/2_Conf_1.000	2197	20	0	NP_502350.1	80	701.049	543	439	hypothetical protein F19B6.1
Locus_2240_Transcript_1/1_Conf_1.000	708	0							
Locus_22400_Transcript_1/1_Conf_1.000	187	0							

Locus_22401_Transcript_1/1_Conf_1.000	133	20	2.68E-15	XP_002744859.1	100	85.1149	43	43	PREDICTED: L-lactate dehydrogenase B chain-like isoform 1
Locus_22402_Transcript_1/1_Conf_1.000	142	0							
Locus_22403_Transcript_1/1_Conf_1.000	188	20	1.27E-12	CAO72177.1	79	76.2554	62	49	hexosaminidase
Locus_22404_Transcript_1/1_Conf_1.000	144	0							
Locus_22405_Transcript_1/1_Conf_1.000	164	0							
Locus_22406_Transcript_1/1_Conf_1.000	310	0							
Locus_22407_Transcript_1/1_Conf_1.000	146	3	6.15E-07	XP_002633895.1	70	57.3806	48	34	C. briggsae CBR-SAND-1 protein
Locus_22408_Transcript_1/1_Conf_1.000	265	20	6.44E-17	EFO24933.1	75	90.5077	86	65	AGC/PKN protein kinase
Locus_22409_Transcript_1/1_Conf_1.000	284	0							
Locus_2241_Transcript_1/1_Conf_1.000	149	0							
Locus_22410_Transcript_1/1_Conf_1.000	296	0							
Locus_22411_Transcript_1/1_Conf_1.000	260	20	6.07E-15	XP_786956.2	64	83.9593	81	52	PREDICTED: similar to MGC140497 protein
Locus_22412_Transcript_1/1_Conf_1.000	206	0							
Locus_22413_Transcript_1/1_Conf_1.000	320	2	2.82E-12	XP_001893183.1	53	75.0998	115	61	Zinc finger, C2H2 type family protein
Locus_22414_Transcript_1/1_Conf_1.000	288	20	5.14E-14	XP_002635477.1	85	80.8777	48	41	Hypothetical protein CBG08772
Locus_22415_Transcript_1/1_Conf_1.000	130	0							
Locus_22416_Transcript_1/1_Conf_1.000	194	20	6.26E-20	NP_501657.1	84	100.523	64	54	hypothetical protein F56D5.3
Locus_22417_Transcript_1/1_Conf_1.000	743	20	6.27E-38	XP_002637600.1	67	161.77	179	120	C. briggsae CBR-SULP-8 protein
Locus_22418_Transcript_1/1_Conf_1.000	173	0							
Locus_22419_Transcript_1/1_Conf_1.000	282	0							
Locus_2242_Transcript_1/1_Conf_1.000	881	0							
Locus_22420_Transcript_1/1_Conf_1.000	160	20	3.66E-12	XP_002641552.1	80	74.7146	51	41	C. briggsae CBR-RBC-2 protein
Locus_22421_Transcript_1/1_Conf_1.000	317	3	1.77E-14	NP_492775.2	62	82.4185	108	67	LAMinin related. See also lmb- family member (lam-3)
Locus_22422_Transcript_1/1_Conf_1.000	251	0							
Locus_22423_Transcript_1/1_Conf_1.000	212	0							
Locus_22424_Transcript_1/1_Conf_1.000	236	20	3.77E-17	EFO15057.1	66	91.2781	77	51	DNA polymerase epsilon catalytic subunit
Locus_22425_Transcript_1/1_Conf_1.000	264	0							

Locus_22426_Transcript_1/1_Conf_1.000	252	0							
Locus_22427_Transcript_1/1_Conf_1.000	153	0							
Locus_22428_Transcript_1/1_Conf_1.000	179	0							
Locus_22429_Transcript_1/1_Conf_1.000	312	0							
Locus_2243_Transcript_1/4_Conf_0.154	715	8	6.01E-11	NP_741488.1	40	72.0182	227	93	abnormal cell LINeage family member (lin-3)
Locus_2243_Transcript_2/4_Conf_0.692	1505	9	3.75E-17	NP_741489.1	45	94.3597	246	111	abnormal cell LINeage family member (lin-3)
Locus_2243_Transcript_3/4_Conf_0.769	1505	9	3.75E-17	NP_741489.1	45	94.3597	246	111	abnormal cell LINeage family member (lin-3)
Locus_2243_Transcript_4/4_Conf_0.692	1505	9	3.75E-17	NP_741489.1	45	94.3597	246	111	abnormal cell LINeage family member (lin-3)
Locus_22430_Transcript_1/1_Conf_1.000	218	20	8.76E-35	XP_002917081.1	100	149.828	72	72	PREDICTED: alpha-actinin-1-like
Locus_22431_Transcript_1/1_Conf_1.000	182	0							
Locus_22432_Transcript_1/1_Conf_1.000	312	20	2.47E-32	NP_001040998.1	83	141.739	103	86	hypothetical protein W07G9.2
Locus_22433_Transcript_1/1_Conf_1.000	192	0							
Locus_22434_Transcript_1/1_Conf_1.000	512	20	1.85E-14	EFO23916.1	55	82.4185	177	98	transcription accessory protein
Locus_22435_Transcript_1/1_Conf_1.000	267	0							
Locus_22436_Transcript_1/1_Conf_1.000	328	0							
Locus_22437_Transcript_1/1_Conf_1.000	463	0							
Locus_22438_Transcript_1/1_Conf_1.000	129	0							
Locus_22439_Transcript_1/1_Conf_1.000	135	0							
Locus_2244_Transcript_1/1_Conf_1.000	443	20	1.88E-32	NP_871953.1	86	142.124	90	78	hypothetical protein T05H10.6
Locus_22440_Transcript_1/1_Conf_1.000	163	7	8.12E-20	XP_002644337.1	98	100.138	52	51	C. briggsae CBR-KLP-4 protein
Locus_22441_Transcript_1/1_Conf_1.000	185	20	2.03E-26	AAH05159.2	100	122.094	61	61	COL6A1 protein

Locus_22442_Transcript_1/1_Conf_1.000	319	0							
Locus_22443_Transcript_1/1_Conf_1.000	145	0							
Locus_22444_Transcript_1/1_Conf_1.000	141	0							
Locus_22445_Transcript_1/1_Conf_1.000	249	0							
Locus_22446_Transcript_1/1_Conf_1.000	241	20	3.61E-28	XP_002632693.1	83	127.872	80	67	Hypothetical protein CBG21624
Locus_22447_Transcript_1/1_Conf_1.000	308	0							
Locus_22448_Transcript_1/1_Conf_1.000	893	20	1.29E-89	NP_001040689.1	71	333.954	301	216	Prolyl tRNA Synthetase family member (prs-2)
Locus_22449_Transcript_1/1_Conf_1.000	218	0							
Locus_2245_Transcript_1/1_Conf_1.000	480	20	4.76E-73	XP_002756083.1	99	276.944	159	158	PREDICTED: fructose-bisphosphate aldolase A isoform 1
Locus_22450_Transcript_1/1_Conf_1.000	203	0							
Locus_22451_Transcript_1/1_Conf_1.000	130	0							
Locus_22452_Transcript_1/1_Conf_1.000	221	0							
Locus_22453_Transcript_1/1_Conf_1.000	139	0							
Locus_22454_Transcript_1/1_Conf_1.000	197	20	2.71E-15	XP_002635154.1	77	85.1149	62	48	C. briggsae CBR-VRS-1 protein
Locus_22455_Transcript_1/1_Conf_1.000	229	0							
Locus_22456_Transcript_1/1_Conf_1.000	202	0							
Locus_22457_Transcript_1/1_Conf_1.000	414	2	4.10E-16	NP_510476.2	75	87.8113	68	51	hypothetical protein Y70D2A.1
Locus_22458_Transcript_1/1_Conf_1.000	173	0							
Locus_22459_Transcript_1/1_Conf_1.000	425	0							
Locus_2246_Transcript_1/1_Conf_1.000	221	0							

Locus_22460_Transcript_1/1_Conf_1.000	319	1	5.15E-06	NP_492051.1	54	54.299	105	57	yeast BUB homolog family member (bub-1)
Locus_22461_Transcript_1/1_Conf_1.000	141	0							
Locus_22462_Transcript_1/1_Conf_1.000	145	20	2.26E-09	EFO26209.1	83	65.4698	43	36	hypothetical protein LOAG_02281
Locus_22463_Transcript_1/1_Conf_1.000	486	20	2.00E-34	XP_002641244.1	66	148.673	156	103	Hypothetical protein CBG09112
Locus_22464_Transcript_1/1_Conf_1.000	268	0							
Locus_22465_Transcript_1/1_Conf_1.000	204	3	5.08E-06	AAZ82850.2	67	54.299	62	42	Hypothetical protein C01B10.11
Locus_22466_Transcript_1/1_Conf_1.000	271	0							
Locus_22467_Transcript_1/2_Conf_1.000	256	0							
Locus_22467_Transcript_2/2_Conf_1.000	256	0							
Locus_22468_Transcript_1/1_Conf_1.000	270	0							
Locus_22469_Transcript_1/1_Conf_1.000	187	1	1.46E-08	EFO26588.1	70	62.7734	62	44	hypothetical protein LOAG_01892
Locus_2247_Transcript_1/1_Conf_1.000	500	20	1.94E-74	XP_001135183.1	99	281.567	138	137	PREDICTED: similar to ubiquitin A-52 residue ribosomal protein fusion product 1
Locus_22470_Transcript_1/1_Conf_1.000	271	0							
Locus_22471_Transcript_1/1_Conf_1.000	228	0							
Locus_22472_Transcript_1/1_Conf_1.000	321	0							
Locus_22473_Transcript_1/1_Conf_1.000	233	0							
Locus_22474_Transcript_1/1_Conf_1.000	483	0							
Locus_22475_Transcript_1/1_Conf_1.000	138	1	2.76E-04	NP_493647.1	70	48.521	44	31	hypothetical protein C23H3.5
Locus_22476_Transcript_1/1_Conf_1.000	295	0							

Locus_22477_Transcript_1/1_Conf_1.000	703	2	6.07E-08	XP_001898083.1	50	62.003	173	87	hypothetical protein
Locus_22478_Transcript_1/1_Conf_1.000	182	2	4.41E-05	XP_001897754.1	58	51.2174	62	36	Poly
Locus_22479_Transcript_1/1_Conf_1.000	260	0							
Locus_2248_Transcript_1/1_Conf_1.000	1524	20	1.32E-110	NP_495161.1	86	404.831	280	241	FZO (Fzo mitochondrial fusion protein) related family member (fzo-1)
Locus_22480_Transcript_1/1_Conf_1.000	189	0							
Locus_22481_Transcript_1/1_Conf_1.000	222	9	1.36E-06	XP_002648400.1	62	56.225	62	39	C. briggsae CBR-DPF-1 protein
Locus_22482_Transcript_1/1_Conf_1.000	137	0							
Locus_22483_Transcript_1/1_Conf_1.000	416	0							
Locus_22484_Transcript_1/1_Conf_1.000	203	2	5.63E-05	XP_002646533.1	64	50.8322	48	31	C. briggsae CBR-SPTF-3 protein
Locus_22485_Transcript_1/1_Conf_1.000	284	20	5.87E-48	NP_001034936.1	100	127.487	57	57	phospholipid hydroperoxide glutathione peroxidase, mitochondrial isoform B precursor
Locus_22486_Transcript_1/1_Conf_1.000	199	0							
Locus_22487_Transcript_1/1_Conf_1.000	487	5	7.64E-10	XP_002647866.1	55	67.0106	93	52	C. briggsae CBR-PRS-2 protein
Locus_22488_Transcript_1/1_Conf_1.000	255	2	4.67E-07	XP_001900629.1	63	57.7658	73	46	hypothetical protein Bm1_45825
Locus_22489_Transcript_1/1_Conf_1.000	185	0							
Locus_2249_Transcript_1/1_Conf_1.000	746	20	4.30E-103	NP_500125.1	94	378.252	219	207	Proteasome Beta Subunit family member (pbs-1)

Locus_22490_Transcript_1/1_Conf_1.000	282	20	2.04E-10	NP_502532.1	55	68.9366	79	44	SCP-Like extracellular protein family member (scl-14)
Locus_22491_Transcript_1/1_Conf_1.000	545	0							
Locus_22492_Transcript_1/1_Conf_1.000	433	20	1.31E-62	NP_505810.2	91	242.276	143	131	P21-Activated Kinase family member (pak-2)
Locus_22493_Transcript_1/1_Conf_1.000	138	0							
Locus_22494_Transcript_1/1_Conf_1.000	216	20	1.35E-35	XP_001164037.1	100	152.525	71	71	PREDICTED: similar to macrophage inflammatory protein 3 beta isoform 1
Locus_22495_Transcript_1/1_Conf_1.000	323	2	3.55E-07	NP_502859.2	62	58.151	69	43	hypothetical protein Y73F8A.24
Locus_22496_Transcript_1/1_Conf_1.000	206	5	9.25E-08	NP_505281.1	59	60.077	62	37	hypothetical protein F07B7.12
Locus_22497_Transcript_1/1_Conf_1.000	147	0							
Locus_22498_Transcript_1/1_Conf_1.000	234	0							
Locus_22499_Transcript_1/1_Conf_1.000	193	0							
Locus_225_Transcript_1/1_Conf_1.000	651	8	2.47E-111	NP_510149.1	93	405.216	216	203	hypothetical protein C34E7.4
Locus_2250_Transcript_1/1_Conf_1.000	480	0							
Locus_22500_Transcript_1/1_Conf_1.000	197	0							
Locus_22501_Transcript_1/1_Conf_1.000	198	5	8.40E-17	NP_499157.2	84	90.1225	65	55	hypothetical protein T05G5.8
Locus_22502_Transcript_1/1_Conf_1.000	129	0							
Locus_22503_Transcript_1/1_Conf_1.000	363	5	1.91E-05	XP_001945045.1	50	52.373	89	45	PREDICTED: similar to conserved hypothetical protein
Locus_22504_Transcript_1/1_Conf_1.000	236	0							
Locus_22505_Transcript_1/1_Conf_1.000	184	0							

Locus_22506_Transcript_1/1_Conf_1.000	135	20	1.73E-14	NP_496037.1	93	82.4185	44	41	Guanylyl CYclase family member (gcy-3)
Locus_22507_Transcript_1/1_Conf_1.000	164	0							
Locus_22508_Transcript_1/1_Conf_1.000	148	20	1.01E-09	NP_001122772.1	77	66.6254	45	35	Poly(ADP-ribose) Metabolism Enzyme family member (pme-3)
Locus_22509_Transcript_1/1_Conf_1.000	434	5	1.13E-05	NP_001021813.1	55	53.1434	89	49	abnormal cell LINeage family member (lin-17)
Locus_2251_Transcript_1/1_Conf_1.000	259	0							
Locus_22510_Transcript_1/1_Conf_1.000	410	20	2.95E-22	P34569.4	69	108.227	94	65	Kelch repeat-containing protein kel-10
Locus_22511_Transcript_1/1_Conf_1.000	185	20	3.70E-28	XP_002931439.1	100	127.872	61	61	PREDICTED: heat shock 70 kDa protein 1A/1B-like, partial
Locus_22512_Transcript_1/1_Conf_1.000	240	0							
Locus_22513_Transcript_1/1_Conf_1.000	141	0							
Locus_22514_Transcript_1/1_Conf_1.000	140	0							
Locus_22515_Transcript_1/1_Conf_1.000	249	0							
Locus_22516_Transcript_1/1_Conf_1.000	128	0							
Locus_22517_Transcript_1/1_Conf_1.000	185	0							
Locus_22518_Transcript_1/1_Conf_1.000	408	10	1.41E-32	XP_002645844.1	75	142.51	131	99	C. briggsae CBR-TSP-8 protein
Locus_22519_Transcript_1/1_Conf_1.000	363	1	2.11E-04	XP_002643891.1	49	48.9062	102	50	Hypothetical protein CBG02143

Locus_2252_Transcript_1/1_Conf_1.000	444	20	9.19E-64	EFO27339.1	90	246.128	148	134	dynein heavy chain protein 1
Locus_22520_Transcript_1/1_Conf_1.000	184	3	3.71E-12	NP_491803.1	87	74.7146	48	42	SaPosin-like Protein family member (spp-15)
Locus_22521_Transcript_1/1_Conf_1.000	284	2	8.27E-12	NP_001023948.1	62	73.559	70	44	hypothetical protein F48F5.6
Locus_22522_Transcript_1/1_Conf_1.000	413	3	1.05E-11	XP_002638813.1	61	73.1738	98	60	C. briggsae CBR-ATM-1 protein
Locus_22523_Transcript_1/1_Conf_1.000	150	20	2.02E-18	CAC43204.1	96	95.5153	50	48	immunoglobulin heavy chain variable region
Locus_22524_Transcript_1/1_Conf_1.000	176	20	1.42E-08	XP_002633529.1	70	62.7734	54	38	Hypothetical protein CBG05395
Locus_22525_Transcript_1/1_Conf_1.000	159	0							
Locus_22526_Transcript_1/1_Conf_1.000	186	0							
Locus_22527_Transcript_1/1_Conf_1.000	128	6	1.21E-07	EFO13288.1	80	59.6918	41	33	hypothetical protein LOAG_15242
Locus_22528_Transcript_1/1_Conf_1.000	208	20	1.24E-20	NP_496814.1	82	102.834	70	58	Member of AAA family binding CED-4 family member (mac-1)
Locus_22529_Transcript_1/1_Conf_1.000	293	0							
Locus_2253_Transcript_1/2_Conf_1.000	924	20	4.14E-86	NP_498620.1	84	322.398	227	191	hypothetical protein F08F8.7
Locus_2253_Transcript_2/2_Conf_1.000	904	20	3.97E-86	NP_498620.1	84	322.398	227	191	hypothetical protein F08F8.7
Locus_22530_Transcript_1/1_Conf_1.000	518	4	3.75E-42	XP_001898170.1	73	174.481	172	126	Ubiquitin-conjugating enzyme family protein
Locus_22531_Transcript_1/1_Conf_1.000	313	0							
Locus_22532_Transcript_1/1_Conf_1.000	567	20	7.96E-32	XP_002634048.1	59	140.584	197	118	Hypothetical protein CBG01587

Locus_22533_Transcript_1/1_Conf_1.000	174	20	1.36E-27	XP_614269.5	100	125.946	58	58	PREDICTED: filamin A, alpha
Locus_22534_Transcript_1/1_Conf_1.000	158	0							
Locus_22535_Transcript_1/1_Conf_1.000	222	3	1.23E-07	NP_502249.3	64	59.6918	73	47	TRPA cation channel homolog family member (trpa-1)
Locus_22536_Transcript_1/1_Conf_1.000	337	0							
Locus_22537_Transcript_1/1_Conf_1.000	466	20	2.07E-23	NP_001086849.1	66	112.079	154	102	dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase
Locus_22538_Transcript_1/1_Conf_1.000	136	0							
Locus_22539_Transcript_1/1_Conf_1.000	303	0							
Locus_2254_Transcript_1/1_Conf_1.000	714	9	7.10E-12	EFO26833.1	56	75.0998	117	66	hypothetical protein LOAG_01654
Locus_22540_Transcript_1/1_Conf_1.000	197	0							
Locus_22541_Transcript_1/1_Conf_1.000	255	0							
Locus_22542_Transcript_1/1_Conf_1.000	567	0							
Locus_22543_Transcript_1/1_Conf_1.000	359	5	4.71E-28	XP_002645442.1	72	127.487	115	83	C. briggsae CBR-TAG-241 protein
Locus_22544_Transcript_1/1_Conf_1.000	145	0							
Locus_22545_Transcript_1/1_Conf_1.000	437	20	9.36E-53	XP_002639554.1	83	209.534	148	123	Hypothetical protein CBG04185
Locus_22546_Transcript_1/1_Conf_1.000	442	0							
Locus_22547_Transcript_1/1_Conf_1.000	147	0							
Locus_22548_Transcript_1/1_Conf_1.000	162	20	5.26E-19	XP_002637506.1	86	97.4413	53	46	C. briggsae CBR-INX-10 protein
Locus_22549_Transcript_1/1_Conf_1.000	275	1	2.97E-06	NP_502390.2	52	55.0694	85	45	High Incidence of Males (increased X chromosome loss) family member (him-6)

Locus_2255_Transcript_1/1_Conf_1.000	1317	20	4.49E-157	NP_499188.2	89	558.91	346	309	Glycerol-3-Phosphate DeHydrogenase family member (gpdh-2)
Locus_22550_Transcript_1/1_Conf_1.000	208	3	1.25E-04	NP_491050.3	58	49.6766	73	43	InTestinal Neurexin-like family member (itx-1)
Locus_22551_Transcript_1/1_Conf_1.000	168	20	3.75E-17	NP_497990.1	83	91.2781	56	47	hypothetical protein C38D4.9
Locus_22552_Transcript_1/1_Conf_1.000	149	0							
Locus_22553_Transcript_1/1_Conf_1.000	129	0							
Locus_22554_Transcript_1/1_Conf_1.000	163	0							
Locus_22555_Transcript_1/1_Conf_1.000	280	6	9.14E-16	XP_002640853.1	62	86.6557	88	55	Hypothetical protein CBG15741
Locus_22556_Transcript_1/1_Conf_1.000	188	3	6.53E-09	NP_741241.1	66	63.929	60	40	Dipeptidyl Peptidase Four (IV) family member (dpf-6)
Locus_22557_Transcript_1/1_Conf_1.000	355	17	6.63E-14	EFO22315.1	60	80.4925	105	64	hypothetical protein LOAG_06169
Locus_22558_Transcript_1/1_Conf_1.000	145	0							
Locus_22559_Transcript_1/1_Conf_1.000	269	1	1.48E-05	ACI49192.1	59	52.7582	81	48	hypothetical protein Csp3_JD03.001
Locus_2256_Transcript_1/2_Conf_1.000	893	11	3.83E-09	XP_002733735.1	47	66.6254	138	65	PREDICTED: receptor for egg jelly 6-like
Locus_2256_Transcript_2/2_Conf_1.000	902	12	7.86E-10	NP_001021459.2	40	68.9366	188	76	hypothetical protein F36H2.3
Locus_22560_Transcript_1/1_Conf_1.000	283	20	1.88E-48	NP_492127.1	92	195.282	94	87	Low-density lipoprotein Receptor Related family member (lrp-1)
Locus_22561_Transcript_1/1_Conf_1.000	167	0							
Locus_22562_Transcript_1/1_Conf_1.000	258	0							
Locus_22563_Transcript_1/1_Conf_1.000	149	4	6.78E-06	XP_001894015.1	68	53.9138	47	32	hypothetical protein Bm1_12730
Locus_22564_Transcript_1/1_Conf_1.000	288	0							
Locus_22565_Transcript_1/1_Conf_1.000	150	0							
Locus_22566_Transcript_1/1_Conf_1.000	191	1	1.36E-06	XP_002643591.1	76	56.225	63	48	Hypothetical protein CBG16316
Locus_22567_Transcript_1/1_Conf_1.000	183	20	3.84E-09	NP_001023008.1	66	64.6994	57	38	CULlin family member (cul-2)

Locus_22568_Transcript_1/1_Conf_1.000	401	20	2.19E-57	NP_001022438.1	96	224.942	127	122	Ligand-Gated ion Channel family member (lgc-35)
Locus_22569_Transcript_1/1_Conf_1.000	164	0							
Locus_2257_Transcript_1/1_Conf_1.000	1700	20	5.45E-84	CAD44516.1	59	316.62	564	334	VAB-10B protein
Locus_22570_Transcript_1/1_Conf_1.000	276	0							
Locus_22571_Transcript_1/1_Conf_1.000	276	0							
Locus_22572_Transcript_1/1_Conf_1.000	332	0							
Locus_22573_Transcript_1/1_Conf_1.000	430	4	4.71E-36	NP_505948.2	72	154.066	143	104	hypothetical protein T27F2.2
Locus_22574_Transcript_1/1_Conf_1.000	271	0							
Locus_22575_Transcript_1/1_Conf_1.000	349	0							
Locus_22576_Transcript_1/1_Conf_1.000	185	20	8.52E-25	XP_002641621.1	90	116.701	61	55	Hypothetical protein CBG09941
Locus_22577_Transcript_1/1_Conf_1.000	219	0							
Locus_22578_Transcript_1/1_Conf_1.000	369	20	2.46E-24	NP_495529.1	73	115.161	91	67	SCP(Small C-terminal domain Phosphatase)-Like phosphatase family member (scpl-2)
Locus_22579_Transcript_1/1_Conf_1.000	611	20	2.05E-82	NP_497814.3	89	308.916	203	181	UNCoordinated family member (unc-79)
Locus_2258_Transcript_1/2_Conf_1.000	685	20	4.77E-55	ACX55058.1	92	218.394	127	117	glutathione peroxidase
Locus_2258_Transcript_2/2_Conf_1.000	679	20	1.45E-56	ACX55058.1	93	223.402	125	117	glutathione peroxidase
Locus_22580_Transcript_1/1_Conf_1.000	161	20	1.87E-24	EFO18724.1	98	115.546	53	52	voltage and ligand gated potassium channel
Locus_22581_Transcript_1/1_Conf_1.000	271	0							
Locus_22582_Transcript_1/1_Conf_1.000	146	0							
Locus_22583_Transcript_1/1_Conf_1.000	230	20	1.53E-34	XP_002710954.1	100	149.058	72	72	PREDICTED: small nuclear ribonucleoprotein polypeptide B/B-like
Locus_22584_Transcript_1/1_Conf_1.000	221	0							
Locus_22585_Transcript_1/1_Conf_1.000	283	0							
Locus_22586_Transcript_1/1_Conf_1.000	149	4	1.41E-11	XP_002644189.1	85	72.7886	49	42	Hypothetical protein CBG17172

Locus_22587_Transcript_1/1_Conf_1.000	287	11	1.66E-12	EFO24938.1	78	75.8702	87	68	hypothetical protein LOAG_03545
Locus_22588_Transcript_1/1_Conf_1.000	313	20	1.07E-35	NP_495634.1	84	152.91	104	88	hypothetical protein C06A8.6
Locus_22589_Transcript_1/1_Conf_1.000	293	20	3.65E-36	CAN70790.1	97	154.451	80	78	hypothetical protein
Locus_2259_Transcript_1/1_Conf_1.000	1021	0							
Locus_22590_Transcript_1/1_Conf_1.000	175	6	2.50E-13	EAW66059.1	100	78.5666	47	47	neural precursor cell expressed, developmentally down-regulated 8
Locus_22591_Transcript_1/1_Conf_1.000	166	0							
Locus_22592_Transcript_1/1_Conf_1.000	342	0							
Locus_22593_Transcript_1/1_Conf_1.000	246	20	1.78E-27	NP_502312.2	86	125.561	81	70	Neurexin Like receptor family member (nlr-1)
Locus_22594_Transcript_1/1_Conf_1.000	179	0							
Locus_22595_Transcript_1/1_Conf_1.000	138	0							
Locus_22596_Transcript_1/1_Conf_1.000	215	0							
Locus_22597_Transcript_1/1_Conf_1.000	284	4	1.16E-05	EFO13647.1	59	53.1434	67	40	hypothetical protein LOAG_14881
Locus_22598_Transcript_1/1_Conf_1.000	448	8	2.27E-38	XP_002636678.1	75	161.77	145	109	C. briggsae CBR-CHE-11 protein
Locus_22599_Transcript_1/1_Conf_1.000	131	20	5.24E-11	AAF82410.1	88	70.8626	43	38	AF221132_1diacylglycerol acyltransferase
Locus_226_Transcript_1/1_Conf_1.000	379	0							
Locus_2260_Transcript_1/2_Conf_1.000	609	20	7.94E-18	EFO17801.1	100	94.3597	47	47	hypothetical protein LOAG_10696
Locus_2260_Transcript_2/2_Conf_1.000	609	20	1.77E-17	EFO17801.1	97	93.2041	47	46	hypothetical protein LOAG_10696

Locus_22600_Transcript_1/1_Conf_1.000	137	19	6.35E-17	XP_002647760.1	97	90.5077	45	44	Hypothetical protein CBG20513
Locus_22601_Transcript_1/1_Conf_1.000	228	0							
Locus_22602_Transcript_1/1_Conf_1.000	238	0							
Locus_22603_Transcript_1/1_Conf_1.000	152	1	2.17E-04	XP_001896667.1	63	48.9062	46	29	Zinc finger, C2H2 type family protein
Locus_22604_Transcript_1/1_Conf_1.000	145	20	2.04E-10	EFO20586.1	80	68.9366	47	38	anion exchange protein
Locus_22605_Transcript_1/1_Conf_1.000	145	9	5.56E-08	NP_001020988.1	71	60.8474	45	32	UNCoordinated family member (unc-89)
Locus_22606_Transcript_1/1_Conf_1.000	184	0							
Locus_22607_Transcript_1/1_Conf_1.000	248	0							
Locus_22608_Transcript_1/1_Conf_1.000	202	0							
Locus_22609_Transcript_1/1_Conf_1.000	138	0							
Locus_2261_Transcript_1/1_Conf_1.000	444	20	3.52E-39	P27613.1	81	164.466	125	102	Globin-like host-protective antigen
Locus_22610_Transcript_1/1_Conf_1.000	301	2	7.09E-08	NP_499962.2	63	60.4622	88	56	hypothetical protein K11H12.9
Locus_22611_Transcript_1/1_Conf_1.000	164	20	1.87E-16	NP_506256.3	88	88.9669	54	48	CaDHerin family member (cdh-6)
Locus_22612_Transcript_1/1_Conf_1.000	249	2	2.94E-06	EFO23679.1	61	55.0694	94	58	hypothetical protein LOAG_04806
Locus_22613_Transcript_1/1_Conf_1.000	235	20	2.96E-38	BAG51482.1	100	161.384	78	78	unnamed protein product
Locus_22614_Transcript_1/1_Conf_1.000	142	0							
Locus_22615_Transcript_1/1_Conf_1.000	468	20	5.05E-46	NP_508419.1	76	187.193	139	107	hypothetical protein T10H10.2
Locus_22616_Transcript_1/1_Conf_1.000	158	0							
Locus_22617_Transcript_1/1_Conf_1.000	189	20	1.44E-24	NP_001024984.1	89	115.931	59	53	DVE (Defective proVEntriculus in Drosophila) homolog family member (dve-1)
Locus_22618_Transcript_1/1_Conf_1.000	349	20	2.53E-29	NP_510434.2	82	131.724	76	63	hypothetical protein F54E4.4
Locus_22619_Transcript_1/1_Conf_1.000	156	0							

Locus_2262_Transcript_1/1_Conf_1.000	3456	20	0	XP_001895813.1	61	806.594	1073	659	F/Y-rich N-terminus family protein
Locus_22620_Transcript_1/1_Conf_1.000	163	0							
Locus_22621_Transcript_1/1_Conf_1.000	328	0							
Locus_22622_Transcript_1/1_Conf_1.000	320	20	1.31E-17	NP_505966.1	82	92.8189	69	57	hypothetical protein T04F3.4
Locus_22623_Transcript_1/1_Conf_1.000	440	0							
Locus_22624_Transcript_1/1_Conf_1.000	167	0							
Locus_22625_Transcript_1/1_Conf_1.000	211	20	2.75E-28	XP_002831615.1	100	128.257	64	64	PREDICTED: LOW QUALITY PROTEIN: cell division protein kinase 16-like
Locus_22626_Transcript_1/1_Conf_1.000	401	0							
Locus_22627_Transcript_1/1_Conf_1.000	252	0							
Locus_22628_Transcript_1/1_Conf_1.000	195	0							
Locus_22629_Transcript_1/1_Conf_1.000	141	20	2.17E-17	XP_001110023.2	100	92.0485	46	46	PREDICTED: sentrin-specific protease 3-like isoform 3
Locus_2263_Transcript_1/1_Conf_1.000	219	0							
Locus_22630_Transcript_1/1_Conf_1.000	172	3	8.63E-06	NP_001122749.1	66	53.5286	57	38	hypothetical protein ZK643.3
Locus_22631_Transcript_1/1_Conf_1.000	196	20	2.45E-16	XP_426592.2	95	88.5817	42	40	PREDICTED: hypothetical protein
Locus_22632_Transcript_1/1_Conf_1.000	334	4	2.05E-07	XP_002642528.1	69	58.9214	66	46	Hypothetical protein CBG20151
Locus_22633_Transcript_1/1_Conf_1.000	316	20	2.23E-25	NP_510713.1	72	118.627	113	82	Cyclase ASsociated protein Homolog family member (cas-1)
Locus_22634_Transcript_1/1_Conf_1.000	406	5	1.01E-46	ACY39996.1	83	189.504	133	111	Hypothetical protein C30F12.5a
Locus_22635_Transcript_1/1_Conf_1.000	178	0							
Locus_22636_Transcript_1/1_Conf_1.000	229	0							
Locus_22637_Transcript_1/1_Conf_1.000	184	0							
Locus_22638_Transcript_1/1_Conf_1.000	155	0							
Locus_22639_Transcript_1/1_Conf_1.000	137	0							
Locus_2264_Transcript_1/1_Conf_1.000	462	0							
Locus_22640_Transcript_1/1_Conf_1.000	135	0							
Locus_22641_Transcript_1/1_Conf_1.000	168	0							

Locus_22642_Transcript_1/1_Conf_1.000	207	0							
Locus_22643_Transcript_1/1_Conf_1.000	387	0							
Locus_22644_Transcript_1/1_Conf_1.000	275	20	9.22E-08	XP_002585751.1	57	60.077	80	46	hypothetical protein BRAFLDRAFT_111201
Locus_22645_Transcript_1/1_Conf_1.000	145	0							
Locus_22646_Transcript_1/1_Conf_1.000	408	0							
Locus_22647_Transcript_1/1_Conf_1.000	196	2	3.93E-06	XP_001895789.1	66	54.6842	65	43	Timeless protein
Locus_22648_Transcript_1/1_Conf_1.000	365	5	1.61E-28	XP_002638930.1	87	129.028	121	106	C. briggsae CBR-CPX-1 protein
Locus_22649_Transcript_1/1_Conf_1.000	132	0							
Locus_2265_Transcript_1/1_Conf_1.000	1188	20	3.15E-66	XP_002429272.1	55	256.914	353	197	G-protein signaling modulator, putative
Locus_22650_Transcript_1/1_Conf_1.000	202	0							
Locus_22651_Transcript_1/1_Conf_1.000	187	0							
Locus_22652_Transcript_1/1_Conf_1.000	136	2	1.98E-10	NP_502231.1	81	68.9366	44	36	LiPocalin-Related protein family member (lpr-2)
Locus_22653_Transcript_1/1_Conf_1.000	176	0							
Locus_22654_Transcript_1/1_Conf_1.000	544	20	2.17E-65	NP_500551.2	86	251.906	172	148	hypothetical protein F55F10.1
Locus_22655_Transcript_1/1_Conf_1.000	134	0							
Locus_22656_Transcript_1/1_Conf_1.000	312	20	3.23E-32	EFO15665.1	85	141.354	89	76	hypothetical protein LOAG_12844
Locus_22657_Transcript_1/1_Conf_1.000	251	0							
Locus_22658_Transcript_1/1_Conf_1.000	166	20	3.88E-22	XP_002630655.1	96	107.842	55	53	C. briggsae CBR-MPK-2 protein
Locus_22659_Transcript_1/1_Conf_1.000	173	0							
Locus_2266_Transcript_1/1_Conf_1.000	2199	20	0	EFO25169.1	84	907.131	625	526	trehalose 6-phosphate synthase 1
Locus_22660_Transcript_1/1_Conf_1.000	160	20	6.04E-15	XP_002630143.1	88	83.9593	50	44	Hypothetical protein CBG00545
Locus_22661_Transcript_1/1_Conf_1.000	206	2	3.52E-07	XP_001895139.1	63	58.151	65	41	MGC84124 protein
Locus_22662_Transcript_1/1_Conf_1.000	285	0							

Locus_22663_Transcript_1/1_Conf_1.000	252	20	1.50E-29	CBW48349.1	85	132.494	84	72	Hypothetical protein C52E4.5b
Locus_22664_Transcript_1/1_Conf_1.000	175	0							
Locus_22665_Transcript_1/1_Conf_1.000	144	20	3.98E-14	NP_490693.2	86	81.2629	46	40	ATM (ataxia telangectasia mutated) family member (atm-1)
Locus_22666_Transcript_1/1_Conf_1.000	243	17	1.42E-08	XP_002634032.1	55	62.7734	85	47	Hypothetical protein CBG01569
Locus_22667_Transcript_1/1_Conf_1.000	184	0							
Locus_22668_Transcript_1/1_Conf_1.000	542	20	1.10E-53	Q60QP4.2	80	213.001	150	120	UPF0359 membrane protein CBG21730
Locus_22669_Transcript_1/1_Conf_1.000	226	0							
Locus_2267_Transcript_1/1_Conf_1.000	546	0							
Locus_22670_Transcript_1/1_Conf_1.000	313	0							
Locus_22671_Transcript_1/1_Conf_1.000	372	2	2.30E-14	NP_498398.1	71	82.0333	125	89	LEThal family member (let-716)
Locus_22672_Transcript_1/1_Conf_1.000	155	20	1.31E-09	XP_002633495.1	74	66.2402	51	38	Hypothetical protein CBG06267
Locus_22673_Transcript_1/1_Conf_1.000	328	0							
Locus_22674_Transcript_1/1_Conf_1.000	315	0							
Locus_22675_Transcript_1/1_Conf_1.000	158	0							
Locus_22676_Transcript_1/1_Conf_1.000	390	0							

Locus_22677_Transcript_1/1_Conf_1.000	218	20	8.80E-19	NP_508493.1	81	96.6709	64	52	protein KINase family member (kin-29)
Locus_22678_Transcript_1/1_Conf_1.000	313	0							
Locus_22679_Transcript_1/1_Conf_1.000	242	0							
Locus_2268_Transcript_1/1_Conf_1.000	809	2	1.11E-17	NP_509937.1	64	94.7449	156	100	hypothetical protein F52D10.2
Locus_22680_Transcript_1/1_Conf_1.000	313	0							
Locus_22681_Transcript_1/1_Conf_1.000	134	0							
Locus_22682_Transcript_1/1_Conf_1.000	379	20	2.88E-25	XP_001901557.1	66	118.242	113	75	Protein kinase domain containing protein
Locus_22683_Transcript_1/1_Conf_1.000	192	3	2.01E-18	XP_002633133.1	77	95.5153	68	53	C. briggsae CBR-GRL-4 protein
Locus_22684_Transcript_1/2_Conf_1.000	542	2	2.48E-05	NP_001122966.1	50	52.373	124	63	hypothetical protein F59A1.11
Locus_22684_Transcript_2/2_Conf_1.000	651	4	6.07E-09	NP_001122966.1	52	65.0846	153	80	hypothetical protein F59A1.11
Locus_22685_Transcript_1/1_Conf_1.000	280	0							
Locus_22686_Transcript_1/1_Conf_1.000	331	20	2.27E-14	EFO16615.1	68	82.0333	83	57	hypothetical protein LOAG_11891
Locus_22687_Transcript_1/1_Conf_1.000	353	0							
Locus_22688_Transcript_1/1_Conf_1.000	136	0							
Locus_22689_Transcript_1/1_Conf_1.000	157	0							
Locus_2269_Transcript_1/1_Conf_1.000	1064	20	1.38E-38	CAA86058.2	52	164.851	210	111	C. elegans protein B0393.5, partially confirmed by transcript evidence
Locus_22690_Transcript_1/1_Conf_1.000	128	5	5.09E-06	NP_001021995.1	76	54.299	42	32	hypothetical protein C27D6.11
Locus_22691_Transcript_1/1_Conf_1.000	129	20	9.55E-13	A8WRV1.2	83	76.6406	42	35	Serine/threonine-protein kinase kin-29
Locus_22692_Transcript_1/1_Conf_1.000	323	20	5.99E-47	CAR97828.1	88	190.274	106	94	C. elegans protein F44G4.8b, confirmed by transcript evidence

Locus_22693_Transcript_1/1_Conf_1.000	207	0							
Locus_22694_Transcript_1/1_Conf_1.000	182	0							
Locus_22695_Transcript_1/1_Conf_1.000	241	0							
Locus_22696_Transcript_1/1_Conf_1.000	162	0							
Locus_22697_Transcript_1/1_Conf_1.000	269	0							
Locus_22698_Transcript_1/1_Conf_1.000	299	0							
Locus_22699_Transcript_1/1_Conf_1.000	437	20	2.17E-33	NP_490828.3	73	145.206	123	91	HAlF transporter (PGP related) family member (haf-6)
Locus_227_Transcript_1/4_Conf_0.500	2580	20	0	NP_500329.1	74	724.931	707	528	mammalian ELKS/CAST/ERC/Rab6 interacting protein homolog family member (elks-1)
Locus_227_Transcript_2/4_Conf_0.400	842	3	3.13E-10	XP_002634742.1	63	70.0922	79	50	C. briggsae CBR-ELKS-1 protein
Locus_227_Transcript_3/4_Conf_0.700	3093	20	0	NP_500329.1	69	750.355	819	573	mammalian ELKS/CAST/ERC/Rab6 interacting protein homolog family member (elks-1)
Locus_227_Transcript_4/4_Conf_0.700	3093	20	0	NP_500329.1	69	750.355	819	573	mammalian ELKS/CAST/ERC/Rab6 interacting protein homolog family member (elks-1)
Locus_2270_Transcript_1/1_Conf_1.000	1071	0							
Locus_22700_Transcript_1/1_Conf_1.000	320	1	5.65E-29	CAR63539.1	77	130.568	102	79	hypothetical protein
Locus_22701_Transcript_1/1_Conf_1.000	344	0							
Locus_22702_Transcript_1/1_Conf_1.000	342	20	9.73E-13	XP_002647591.1	51	76.6406	95	49	Hypothetical protein CBG06679
Locus_22703_Transcript_1/1_Conf_1.000	154	0							
Locus_22704_Transcript_1/1_Conf_1.000	312	3	2.25E-09	NP_741925.2	62	65.4698	100	62	DYstrophin-like phenotype and CAPON related family member (dyc-1)
Locus_22705_Transcript_1/1_Conf_1.000	132	0							
Locus_22706_Transcript_1/1_Conf_1.000	261	20	8.75E-06	NP_001087602.1	58	53.5286	67	39	zinc finger, MIZ-type containing 2
Locus_22707_Transcript_1/1_Conf_1.000	237	20	1.74E-14	NP_741251.1	68	82.4185	76	52	hypothetical protein C02F5.6
Locus_22708_Transcript_1/1_Conf_1.000	270	3	1.63E-04	XP_001194422.1	52	49.2914	72	38	PREDICTED: similar to contactin associated protein
Locus_22709_Transcript_1/1_Conf_1.000	182	0							
Locus_2271_Transcript_1/1_Conf_1.000	819	20	6.76E-63	NP_001129866.1	71	244.973	212	152	Kinesin-Like Protein family member (klp-12)

Locus_22710_Transcript_1/1_Conf_1.000	431	20	2.98E-06	EFN51338.1	82	55.0694	39	32	hypothetical protein CHLNCDRAFT_141133
Locus_22711_Transcript_1/1_Conf_1.000	156	0							
Locus_22712_Transcript_1/1_Conf_1.000	423	14	4.17E-24	CAR63608.1	72	114.39	74	54	hypothetical protein
Locus_22713_Transcript_1/1_Conf_1.000	387	0							
Locus_22714_Transcript_1/1_Conf_1.000	373	20	2.22E-25	XP_518438.2	66	118.627	123	82	PREDICTED: copine V isoform 3
Locus_22715_Transcript_1/1_Conf_1.000	309	20	4.25E-05	XP_002108615.1	48	51.2174	72	35	hypothetical protein TRIADDRAFT_19102
Locus_22716_Transcript_1/1_Conf_1.000	161	0							
Locus_22717_Transcript_1/1_Conf_1.000	225	20	2.15E-28	EFO21576.1	86	128.642	74	64	hypothetical protein LOAG_06912
Locus_22718_Transcript_1/1_Conf_1.000	314	3	1.77E-22	NP_508833.1	86	108.997	67	58	hypothetical protein T07F12.4
Locus_22719_Transcript_1/1_Conf_1.000	180	0							
Locus_2272_Transcript_1/2_Conf_1.000	734	20	5.56E-15	ABH88210.1	65	85.5001	103	67	saposin-like protein 1
Locus_2272_Transcript_2/2_Conf_1.000	739	20	5.66E-15	ABH88210.1	65	85.5001	103	67	saposin-like protein 1
Locus_22720_Transcript_1/1_Conf_1.000	554	20	1.01E-28	XP_002630751.1	63	130.183	133	85	Hypothetical protein CBG02443

Locus_22721_Transcript_1/1_Conf_1.000	270	20	1.84E-48	XP_002803216.1	100	195.282	89	89	PREDICTED: amyloid beta A4 protein-like, partial
Locus_22722_Transcript_1/1_Conf_1.000	361	20	8.87E-19	XP_001900618.1	63	96.6709	117	74	Leucine Rich Repeat family protein
Locus_22723_Transcript_1/1_Conf_1.000	177	20	2.25E-14	CAR63659.1	82	82.0333	57	47	putative Collagen protein 20
Locus_22724_Transcript_1/1_Conf_1.000	242	0							
Locus_22725_Transcript_1/1_Conf_1.000	521	0							
Locus_22726_Transcript_1/1_Conf_1.000	165	0							
Locus_22727_Transcript_1/1_Conf_1.000	177	0							
Locus_22728_Transcript_1/1_Conf_1.000	242	6	3.88E-06	XP_002630353.1	61	54.6842	57	35	Hypothetical protein CBG04283
Locus_22729_Transcript_1/1_Conf_1.000	718	3	1.75E-34	NP_498060.2	57	150.214	244	140	hypothetical protein R144.5
Locus_2273_Transcript_1/1_Conf_1.000	1338	20	9.65E-14	XP_002664350.1	69	82.8037	59	41	PREDICTED: hypothetical protein LOC322903
Locus_22730_Transcript_1/1_Conf_1.000	128	20	2.88E-09	NP_001024131.1	76	65.0846	42	32	Peroxisomal Membrane Protein related family member (pmp-5)
Locus_22731_Transcript_1/1_Conf_1.000	128	0							

Locus_22732_Transcript_1/1_Conf_1.000	148	20	7.72E-18	XP_002823344.1	100	93.5893	49	49	PREDICTED: keratin, type I cytoskeletal 18-like
Locus_22733_Transcript_1/1_Conf_1.000	228	20	9.32E-24	AAQ06435.1	96	113.235	76	73	ABC6 protein
Locus_22734_Transcript_1/1_Conf_1.000	157	0							
Locus_22735_Transcript_1/1_Conf_1.000	203	2	3.90E-06	EFO23663.1	61	54.6842	68	42	myosin xviiia
Locus_22736_Transcript_1/1_Conf_1.000	194	0							
Locus_22737_Transcript_1/2_Conf_1.000	303	20	6.58E-22	XP_002632609.1	72	107.071	100	72	C. briggsae CBR-COQ-3 protein
Locus_22737_Transcript_2/2_Conf_1.000	309	20	2.10E-20	XP_002632609.1	70	102.064	102	72	C. briggsae CBR-COQ-3 protein
Locus_22738_Transcript_1/1_Conf_1.000	640	20	2.11E-27	NP_509145.2	68	126.331	104	71	AuTophaGy (yeast Atg homolog) family member (atg-2)
Locus_22739_Transcript_1/1_Conf_1.000	504	20	3.49E-58	XP_001894372.1	75	227.639	180	136	Immunoglobulin I-set domain containing protein
Locus_2274_Transcript_1/1_Conf_1.000	1028	20	4.97E-46	XP_001893845.1	57	189.504	303	173	Mov34/MPN/PAD-1 family protein
Locus_22740_Transcript_1/1_Conf_1.000	220	0							
Locus_22741_Transcript_1/1_Conf_1.000	368	0							
Locus_22742_Transcript_1/1_Conf_1.000	135	0							
Locus_22743_Transcript_1/1_Conf_1.000	525	20	2.48E-76	XP_002644087.1	90	288.115	173	157	Hypothetical protein CBG17560
Locus_22744_Transcript_1/1_Conf_1.000	172	0							

Locus_22745_Transcript_1/1_Conf_1.000	330	20	6.61E-14	XP_002643183.1	60	80.4925	98	59	Hypothetical protein CBG24152
Locus_22746_Transcript_1/1_Conf_1.000	168	0							
Locus_22747_Transcript_1/1_Conf_1.000	381	20	3.74E-25	XP_002639036.1	75	117.857	122	92	C. briggsae CBR-DYB-1 protein
Locus_22748_Transcript_1/1_Conf_1.000	178	0							
Locus_22749_Transcript_1/1_Conf_1.000	138	0							
Locus_2275_Transcript_1/2_Conf_1.000	566	6	4.17E-17	XP_002633345.1	52	91.6633	163	86	Hypothetical protein CBG06087
Locus_2275_Transcript_2/2_Conf_1.000	560	6	2.36E-17	XP_002633345.1	53	92.4337	161	86	Hypothetical protein CBG06087
Locus_22750_Transcript_1/1_Conf_1.000	137	0							
Locus_22751_Transcript_1/1_Conf_1.000	355	20	4.44E-18	EFO24692.1	65	94.3597	120	79	protein-tyrosine phosphatase
Locus_22752_Transcript_1/1_Conf_1.000	139	1	2.75E-12	NP_001122963.1	86	75.0998	46	40	hypothetical protein F58E6.1
Locus_22753_Transcript_1/1_Conf_1.000	216	0							
Locus_22754_Transcript_1/1_Conf_1.000	448	0							
Locus_22755_Transcript_1/1_Conf_1.000	148	0							
Locus_22756_Transcript_1/1_Conf_1.000	196	0							
Locus_22757_Transcript_1/1_Conf_1.000	198	0							
Locus_22758_Transcript_1/1_Conf_1.000	245	0							
Locus_22759_Transcript_1/1_Conf_1.000	207	20	8.57E-30	XP_002818459.1	100	133.265	67	67	PREDICTED: hypothetical protein LOC100441808
Locus_2276_Transcript_1/4_Conf_0.500	854	20	1.64E-38	AAG36874.1	76	164.081	178	136	AF242767_1SF2
Locus_2276_Transcript_3/4_Conf_0.375	566	9	7.36E-14	AAG36874.1	69	80.8777	134	93	AF242767_1SF2

Locus_2276_Transcript_4/4_Conf_0.500	970	20	2.03E-38	AAG36874.1	76	164.081	178	136	AF242767_1SF2
Locus_22760_Transcript_1/1_Conf_1.000	180	0							
Locus_22761_Transcript_1/1_Conf_1.000	188	2	2.18E-04	NP_500597.1	62	48.9062	35	22	hypothetical protein F19C7.1
Locus_22762_Transcript_1/1_Conf_1.000	165	0							
Locus_22763_Transcript_1/1_Conf_1.000	319	20	2.72E-15	XP_002641345.1	63	85.1149	103	65	Hypothetical protein CBG13198
Locus_22764_Transcript_1/1_Conf_1.000	179	1	1.46E-05	AAG43143.1	100	52.7582	53	53	AF061732_1My029 protein
Locus_22765_Transcript_1/1_Conf_1.000	179	1	2.76E-04	XP_001895772.1	59	48.521	57	34	hypothetical protein Bm1_21590
Locus_22766_Transcript_1/1_Conf_1.000	166	0							
Locus_22767_Transcript_1/1_Conf_1.000	686	20	4.64E-34	NP_495011.1	87	148.673	90	79	Protein Kinase C family member (pkc-3)
Locus_22768_Transcript_1/1_Conf_1.000	423	1	1.54E-10	EFO21344.1	56	69.3218	91	51	hypothetical protein LOAG_07145
Locus_22769_Transcript_1/1_Conf_1.000	210	0							
Locus_2277_Transcript_1/1_Conf_1.000	1707	20	9.80E-158	XP_002640778.1	74	561.607	491	365	C. briggsae CBR-FRL-1 protein

Locus_22770_Transcript_1/1_Conf_1.000	361	20	1.45E-45	EFO25590.1	84	185.652	120	101	hypothetical protein LOAG_02898
Locus_22771_Transcript_1/1_Conf_1.000	147	0							
Locus_22772_Transcript_1/1_Conf_1.000	232	0							
Locus_22773_Transcript_1/1_Conf_1.000	353	0							
Locus_22774_Transcript_1/1_Conf_1.000	298	20	2.06E-23	XP_002427603.1	84	112.079	88	74	mitochondrial 2-oxoglutarate/malate carrier protein, putative
Locus_22775_Transcript_1/1_Conf_1.000	311	20	2.66E-07	XP_001897863.1	76	58.5362	56	43	rab6
Locus_22776_Transcript_1/1_Conf_1.000	403	3	2.60E-26	NP_500870.2	80	121.709	112	90	hypothetical protein C06E7.2
Locus_22777_Transcript_1/1_Conf_1.000	280	0							
Locus_22778_Transcript_1/1_Conf_1.000	325	0							
Locus_22779_Transcript_1/1_Conf_1.000	153	20	9.37E-16	EFO27858.1	90	86.6557	50	45	hypothetical protein LOAG_00620
Locus_2278_Transcript_1/1_Conf_1.000	587	0							
Locus_22780_Transcript_1/1_Conf_1.000	179	0							
Locus_22781_Transcript_1/1_Conf_1.000	583	20	1.20E-33	NP_500530.1	61	146.747	191	118	Nuclear Hormone Receptor family member (nhr-78)
Locus_22782_Transcript_1/1_Conf_1.000	170	3	3.29E-05	AAA82423.2	62	51.6026	58	36	Hypothetical protein F10E7.9
Locus_22783_Transcript_1/1_Conf_1.000	180	0							

Locus_22784_Transcript_1/1_Conf_1.000	131	0							
Locus_22785_Transcript_1/1_Conf_1.000	228	20	6.68E-22	NP_497205.1	89	107.071	75	67	UNCoordinated family member (unc-45)
Locus_22786_Transcript_1/1_Conf_1.000	404	20	3.76E-25	XP_002639857.1	68	117.857	134	92	Hypothetical protein CBG12210
Locus_22787_Transcript_1/1_Conf_1.000	203	0							
Locus_22788_Transcript_1/2_Conf_1.000	320	0							
Locus_22788_Transcript_2/2_Conf_1.000	294	0							
Locus_22789_Transcript_1/1_Conf_1.000	302	0							
Locus_2279_Transcript_1/1_Conf_1.000	1312	20	1.47E-176	XP_002639838.1	87	623.624	401	351	Hypothetical protein CBG12186
Locus_22790_Transcript_1/1_Conf_1.000	141	0							
Locus_22791_Transcript_1/1_Conf_1.000	134	0							
Locus_22792_Transcript_1/1_Conf_1.000	240	20	6.15E-28	NP_001122569.1	86	127.102	81	70	hypothetical protein ZK849.2
Locus_22793_Transcript_1/1_Conf_1.000	304	20	3.58E-52	EAW85022.1	100	207.608	100	100	px19-like protein, isoform CRA_b
Locus_22794_Transcript_1/1_Conf_1.000	326	0							
Locus_22795_Transcript_1/1_Conf_1.000	188	5	5.18E-06	CBK19511.1	68	54.299	47	32	C. elegans protein Y67H2A.10b, partially confirmed by transcript evidence
Locus_22796_Transcript_1/1_Conf_1.000	289	0							
Locus_22797_Transcript_1/1_Conf_1.000	182	5	5.04E-09	CAE47474.2	72	64.3142	54	39	C. elegans protein Y79H2A.3b, partially confirmed by transcript evidence
Locus_22798_Transcript_1/1_Conf_1.000	423	20	7.86E-23	XP_002630155.1	58	110.153	154	90	Hypothetical protein CBG00558
Locus_22799_Transcript_1/1_Conf_1.000	256	3	5.68E-29	NP_493358.1	90	130.568	83	75	hypothetical protein C01A2.2
Locus_228_Transcript_1/1_Conf_1.000	1269	20	3.77E-105	ACO15793.1	85	386.341	253	217	Hypothetical protein Y71G12B.23a
Locus_2280_Transcript_1/1_Conf_1.000	1611	20	2.29E-177	XP_002633188.1	78	626.706	449	354	C. briggsae CBR-PAM-1 protein
Locus_22800_Transcript_1/1_Conf_1.000	194	0							
Locus_22801_Transcript_1/1_Conf_1.000	172	20	1.20E-23	AAW29117.1	96	112.849	57	55	AF1 non-allergic IgE heavy chain VH3-30-3

Locus_22802_Transcript_1/1_Conf_1.000	364	20	1.08E-16	NP_506711.1	58	89.7373	127	74	DNaJ domain (prokaryotic heat shock protein) family member (dnj-3)
Locus_22803_Transcript_1/1_Conf_1.000	297	20	1.17E-18	EFO22690.1	80	96.2857	62	50	4-hydroxybenzoate polyprenyl transferase
Locus_22804_Transcript_1/1_Conf_1.000	140	0							
Locus_22805_Transcript_1/1_Conf_1.000	409	0							
Locus_22806_Transcript_1/1_Conf_1.000	355	4	1.25E-04	ACP31595.1	62	49.6766	72	45	Hypothetical protein Y32H12A.2b
Locus_22807_Transcript_1/1_Conf_1.000	175	0							
Locus_22808_Transcript_1/1_Conf_1.000	317	0							
Locus_22809_Transcript_1/1_Conf_1.000	187	0							
Locus_2281_Transcript_1/1_Conf_1.000	2804	20	0	XP_002644134.1	81	1070.84	835	684	C. briggsae CBR-SYD-2 protein
Locus_22810_Transcript_1/1_Conf_1.000	190	0							
Locus_22811_Transcript_1/1_Conf_1.000	261	2	5.48E-08	NP_505736.2	75	60.8474	48	36	yeast MRE recombination/repair homolog family member (mre-11)
Locus_22812_Transcript_1/1_Conf_1.000	168	0							
Locus_22813_Transcript_1/1_Conf_1.000	354	11	1.48E-13	EFO21218.1	97	79.337	40	39	CAMK/CAMKL/NUAK protein kinase
Locus_22814_Transcript_1/1_Conf_1.000	195	0							
Locus_22815_Transcript_1/1_Conf_1.000	146	0							
Locus_22816_Transcript_1/1_Conf_1.000	183	0							
Locus_22817_Transcript_1/1_Conf_1.000	377	20	3.55E-07	XP_700974.4	60	58.151	65	39	PREDICTED: transmembrane protein 67
Locus_22818_Transcript_1/1_Conf_1.000	134	0							
Locus_22819_Transcript_1/1_Conf_1.000	350	0							

Locus_2282_Transcript_1/1_Conf_1.000	278	20	1.90E-37	ABC40752.1	94	158.688	88	83	myosin heavy chain
Locus_22820_Transcript_1/1_Conf_1.000	434	20	1.27E-49	AAH13586.2	100	199.134	108	108	PRKCSH protein
Locus_22821_Transcript_1/1_Conf_1.000	130	4	1.43E-08	NP_490840.2	87	62.7734	41	36	DAP (Death-Associated Protein) Kinase homolog family member (dapk-1)
Locus_22822_Transcript_1/1_Conf_1.000	180	0							
Locus_22823_Transcript_1/1_Conf_1.000	364	0							
Locus_22824_Transcript_1/1_Conf_1.000	246	8	6.32E-25	XP_002634052.1	87	117.087	82	72	C. briggsae CBR-VHA-5 protein
Locus_22825_Transcript_1/1_Conf_1.000	176	0							
Locus_22826_Transcript_1/1_Conf_1.000	129	0							
Locus_22827_Transcript_1/1_Conf_1.000	346	20	4.78E-36	NP_001022673.1	85	154.066	111	95	NADC (Na+-coupled dicarboxylate transporter) family member (nac-3)
Locus_22828_Transcript_1/1_Conf_1.000	259	20	3.66E-36	XP_002632226.1	90	154.451	85	77	Hypothetical protein CBG07097
Locus_22829_Transcript_1/1_Conf_1.000	295	20	1.53E-34	ADL62853.1	84	149.058	98	83	thioredoxin reductase 2

Locus_2283_Transcript_1/1_Conf_1.000	241	20	1.56E-31	XP_002636221.1	88	139.043	80	71	Hypothetical protein CBG12142
Locus_22830_Transcript_1/1_Conf_1.000	309	20	1.19E-23	NP_500418.1	70	112.849	96	68	hypothetical protein M02B7.2
Locus_22831_Transcript_1/1_Conf_1.000	219	0							
Locus_22832_Transcript_1/1_Conf_1.000	224	20	8.48E-25	NP_001022123.1	86	116.701	76	66	hypothetical protein F28C6.4
Locus_22833_Transcript_1/1_Conf_1.000	205	0							
Locus_22834_Transcript_1/1_Conf_1.000	1423	20	1.44E-164	XP_002636960.1	82	583.948	439	362	Hypothetical protein CBG09439
Locus_22835_Transcript_1/1_Conf_1.000	141	0							
Locus_22836_Transcript_1/1_Conf_1.000	199	0							
Locus_22837_Transcript_1/1_Conf_1.000	232	0							
Locus_22838_Transcript_1/1_Conf_1.000	154	0							
Locus_22839_Transcript_1/1_Conf_1.000	417	0							
Locus_2284_Transcript_1/2_Conf_0.500	3023	20	0	XP_002635006.1	86	1407.89	935	811	Hypothetical protein CBG13546
Locus_2284_Transcript_2/2_Conf_0.500	925	20	2.42E-102	XP_001900408.1	98	376.326	194	192	GTP-binding nuclear protein RAN/TC4

Locus_22840_Transcript_1/1_Conf_1.000	263	20	2.70E-39	XP_002633776.1	89	164.851	87	78	C. briggsae CBR-NHR-4 protein
Locus_22841_Transcript_1/1_Conf_1.000	280	0							
Locus_22842_Transcript_1/1_Conf_1.000	257	0							
Locus_22843_Transcript_1/1_Conf_1.000	201	0							
Locus_22844_Transcript_1/1_Conf_1.000	246	20	3.46E-31	XP_001093980.2	100	137.887	60	60	PREDICTED: hypothetical protein LOC705622
Locus_22845_Transcript_1/1_Conf_1.000	282	1	9.79E-05	EFO22051.1	58	50.0618	78	46	hypothetical protein LOAG_06433
Locus_22846_Transcript_1/1_Conf_1.000	140	4	2.41E-08	XP_001901959.1	79	62.003	39	31	hypothetical protein
Locus_22847_Transcript_1/1_Conf_1.000	324	0							
Locus_22848_Transcript_1/1_Conf_1.000	160	20	2.70E-23	XP_002810196.1	100	111.694	53	53	PREDICTED: protein S100-A4-like isoform 2
Locus_22849_Transcript_1/1_Conf_1.000	281	0							
Locus_2285_Transcript_1/1_Conf_1.000	212	0							
Locus_22850_Transcript_1/1_Conf_1.000	653	7	2.62E-28	NP_498592.1	55	129.413	216	119	hypothetical protein R151.8
Locus_22851_Transcript_1/1_Conf_1.000	187	0							
Locus_22852_Transcript_1/1_Conf_1.000	275	0							
Locus_22853_Transcript_1/1_Conf_1.000	338	0							
Locus_22854_Transcript_1/1_Conf_1.000	133	0							
Locus_22855_Transcript_1/1_Conf_1.000	204	0							
Locus_22856_Transcript_1/1_Conf_1.000	138	0							
Locus_22857_Transcript_1/1_Conf_1.000	235	0							
Locus_22858_Transcript_1/1_Conf_1.000	523	20	8.72E-42	AAO18224.1	95	173.326	92	88	FMRFamide-like prepropeptide

Locus_22859_Transcript_1/1_Conf_1.000	388	20	1.14E-58	XP_002637345.1	92	229.18	128	118	C. briggsae CBR-UNC-68 protein
Locus_2286_Transcript_1/1_Conf_1.000	660	4	7.26E-26	NP_501779.1	52	121.324	198	103	hypothetical protein F32B6.4
Locus_22860_Transcript_1/1_Conf_1.000	199	0							
Locus_22861_Transcript_1/1_Conf_1.000	610	0							
Locus_22862_Transcript_1/1_Conf_1.000	297	0							
Locus_22863_Transcript_1/1_Conf_1.000	209	20	6.58E-22	XP_001899774.1	88	107.071	68	60	Guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif family protein
Locus_22864_Transcript_1/1_Conf_1.000	360	20	4.23E-45	NP_490690.1	86	184.111	104	90	hypothetical protein F56C11.3
Locus_22865_Transcript_1/1_Conf_1.000	161	0							
Locus_22866_Transcript_1/1_Conf_1.000	182	9	3.05E-14	NP_001020988.1	79	81.6481	62	49	UNCoordinated family member (unc-89)
Locus_22867_Transcript_1/1_Conf_1.000	241	0							
Locus_22868_Transcript_1/1_Conf_1.000	339	2	1.15E-10	NP_500240.1	91	69.707	36	33	hypothetical protein Y69A2AR.31
Locus_22869_Transcript_1/1_Conf_1.000	278	8	9.15E-24	XP_002639434.1	79	113.235	91	72	Hypothetical protein CBG04027
Locus_2287_Transcript_1/4_Conf_0.625	1135	20	2.06E-43	NP_506352.1	82	181.03	137	113	TransThyretin-Related family domain family member (ttr-44)
Locus_2287_Transcript_2/4_Conf_0.625	1094	20	1.94E-43	NP_506352.1	82	181.03	137	113	TransThyretin-Related family domain family member (ttr-44)
Locus_2287_Transcript_3/4_Conf_0.375	532	20	2.21E-51	EFO24957.1	84	205.297	122	103	hypothetical protein LOAG_03532
Locus_2287_Transcript_4/4_Conf_0.625	1135	20	2.06E-43	NP_506352.1	82	181.03	137	113	TransThyretin-Related family domain family member (ttr-44)
Locus_22870_Transcript_1/1_Conf_1.000	173	20	5.20E-27	XP_002825204.1	100	124.02	57	57	PREDICTED: apoptosis regulatory protein Siva-like
Locus_22871_Transcript_1/1_Conf_1.000	191	0							

Locus_22872_Transcript_1/1_Conf_1.000	161	20	7.87E-23	NP_001024865.1	100	110.153	53	53	DumPY : shorter than wild-type family member (dpy-23)
Locus_22873_Transcript_1/1_Conf_1.000	217	7	9.13E-08	NP_502367.2	69	60.077	59	41	hypothetical protein F28D1.9
Locus_22874_Transcript_1/1_Conf_1.000	191	0							
Locus_22875_Transcript_1/1_Conf_1.000	136	0							
Locus_22876_Transcript_1/1_Conf_1.000	188	5	7.99E-07	NP_504937.3	57	56.9954	56	32	hypothetical protein C54F6.6
Locus_22877_Transcript_1/1_Conf_1.000	305	20	1.57E-23	ABD75715.1	95	112.464	80	76	vacuolar protein sorting factor
Locus_22878_Transcript_1/1_Conf_1.000	142	0							
Locus_22879_Transcript_1/1_Conf_1.000	242	20	6.60E-14	CAA96571.1	74	80.4925	79	59	parasite pepsinogen
Locus_2288_Transcript_1/1_Conf_1.000	1890	20	0	NP_499949.2	82	783.097	558	459	Gut on EXterior family member (gex-2)
Locus_22880_Transcript_1/1_Conf_1.000	324	0							
Locus_22881_Transcript_1/1_Conf_1.000	159	0							
Locus_22882_Transcript_1/1_Conf_1.000	265	20	4.32E-13	NP_001024930.1	68	77.7962	79	54	Choline Kinase C family member (ckc-1)
Locus_22883_Transcript_1/1_Conf_1.000	152	0							
Locus_22884_Transcript_1/1_Conf_1.000	230	20	2.45E-24	NP_872193.1	80	115.161	76	61	hypothetical protein K07C11.7
Locus_22885_Transcript_1/1_Conf_1.000	161	0							
Locus_22886_Transcript_1/1_Conf_1.000	364	20	9.15E-16	NP_508641.2	82	86.6557	73	60	Temporarily Assigned Gene name family member (tag-81)
Locus_22887_Transcript_1/1_Conf_1.000	243	0							
Locus_22888_Transcript_1/1_Conf_1.000	172	0							
Locus_22889_Transcript_1/1_Conf_1.000	217	0							

Locus_2289_Transcript_1/4_Conf_0.700	2494	20	0	EFO23774.1	80	902.123	740	594	replication licensing factor MCM7
Locus_2289_Transcript_2/4_Conf_0.700	2494	20	0	EFO23774.1	80	902.123	740	594	replication licensing factor MCM7

Locus_2289_Transcript_3/4_Conf_0.700	2494	20	0	EFO23774.1	80	901.353	740	593	replication licensing factor MCM7
Locus_2289_Transcript_4/4_Conf_0.700	2494	20	0	EFO23774.1	80	902.123	740	594	replication licensing factor MCM7
Locus_22890_Transcript_1/1_Conf_1.000	431	0							
Locus_22891_Transcript_1/1_Conf_1.000	145	1	6.78E-14	NP_001021158.1	83	80.4925	48	40	UDP-GlucuronosylTransferase family member (ugt-60)
Locus_22892_Transcript_1/1_Conf_1.000	499	0							
Locus_22893_Transcript_1/1_Conf_1.000	206	0							
Locus_22894_Transcript_1/1_Conf_1.000	151	0							
Locus_22895_Transcript_1/1_Conf_1.000	203	0							
Locus_22896_Transcript_1/1_Conf_1.000	248	0							
Locus_22897_Transcript_1/1_Conf_1.000	137	11	4.40E-18	CAH73152.1	100	94.3597	45	45	golgi membrane protein 1
Locus_22898_Transcript_1/1_Conf_1.000	339	0							
Locus_22899_Transcript_1/1_Conf_1.000	354	10	1.25E-12	XP_001895198.1	57	76.2554	111	64	PAZ domain containing protein

Locus_229_Transcript_1/1_Conf_1.000	1740	20	0	XP_002642779.1	94	870.922	511	482	C. briggsae CBR-ATP-2 protein
Locus_2290_Transcript_1/1_Conf_1.000	613	20	2.94E-44	ACD88894.1	73	182.185	138	102	transthyretin-like protein
Locus_22900_Transcript_1/1_Conf_1.000	148	20	7.73E-10	NP_001122772.1	77	67.0106	45	35	Poly(ADP-ribose) Metabolism Enzyme family member (pme-3)
Locus_22901_Transcript_1/1_Conf_1.000	182	0							
Locus_22902_Transcript_1/1_Conf_1.000	257	20	6.97E-11	NP_494994.1	70	70.4774	60	42	hypothetical protein ZK622.1
Locus_22903_Transcript_1/1_Conf_1.000	190	2	7.20E-08	NP_498149.1	69	60.4622	63	44	hypothetical protein Y32H12A.6
Locus_22904_Transcript_1/1_Conf_1.000	420	0							
Locus_22905_Transcript_1/1_Conf_1.000	150	0							
Locus_22906_Transcript_1/1_Conf_1.000	306	20	4.23E-37	1UH6	98	157.532	75	74	SolutionStructure OfThe Murine Ubiquitin-Like 5 Protein From Riken Cdna 0610031k06
Locus_22907_Transcript_1/1_Conf_1.000	243	0							
Locus_22908_Transcript_1/1_Conf_1.000	147	16	1.08E-19	XP_002831355.1	100	99.7525	48	48	PREDICTED: kelch domain-containing protein 7B-like
Locus_22909_Transcript_1/1_Conf_1.000	360	20	2.12E-12	XP_002402660.1	59	75.485	77	46	engulfment and cell motility, putative
Locus_2291_Transcript_1/1_Conf_1.000	620	19	1.93E-83	XP_002646662.1	84	312.383	206	174	C. briggsae CBR-DDL-3 protein

Locus_22910_Transcript_1/1_Conf_1.000	182	20	3.05E-14	XP_001901250.1	83	81.6481	56	47	MGC80217 protein
Locus_22911_Transcript_1/1_Conf_1.000	170	0							
Locus_22912_Transcript_1/1_Conf_1.000	233	20	4.78E-12	AAC39118.1	72	74.3294	74	54	high-affinity peptide transporter
Locus_22913_Transcript_1/1_Conf_1.000	132	0							
Locus_22914_Transcript_1/1_Conf_1.000	292	20	4.47E-26	NP_498248.2	82	120.939	89	73	hypothetical protein Y37B11A.2
Locus_22915_Transcript_1/1_Conf_1.000	231	14	8.40E-25	AAZ42352.1	76	116.701	76	58	degeneration of certain neurons protein 1
Locus_22916_Transcript_1/1_Conf_1.000	214	0							
Locus_22917_Transcript_1/1_Conf_1.000	264	20	3.64E-28	NP_502011.1	81	127.872	83	68	hypothetical protein T11G6.3
Locus_22918_Transcript_1/1_Conf_1.000	133	0							
Locus_22919_Transcript_1/1_Conf_1.000	230	3	2.55E-05	NP_001022134.1	60	51.9878	64	39	hypothetical protein F32A5.1
Locus_2292_Transcript_1/1_Conf_1.000	319	0							
Locus_22920_Transcript_1/1_Conf_1.000	151	0							
Locus_22921_Transcript_1/1_Conf_1.000	199	20	5.26E-19	XP_002636781.1	83	97.4413	66	55	Hypothetical protein CBG23516
Locus_22922_Transcript_1/1_Conf_1.000	140	0							
Locus_22923_Transcript_1/1_Conf_1.000	132	0							
Locus_22924_Transcript_1/1_Conf_1.000	148	0							

Locus_22925_Transcript_1/1_Conf_1.000	130	20	3.39E-18	XP_002914592.1	100	94.7449	43	43	PREDICTED: casein kinase I isoform epsilon-like
Locus_22926_Transcript_1/1_Conf_1.000	157	0							
Locus_22927_Transcript_1/1_Conf_1.000	224	0							
Locus_22928_Transcript_1/1_Conf_1.000	147	0							
Locus_22929_Transcript_1/1_Conf_1.000	138	0							
Locus_2293_Transcript_1/1_Conf_1.000	1402	20	1.20E-163	XP_002633437.1	77	580.867	470	364	C. briggsae CBR-UNC-22 protein
Locus_22930_Transcript_1/1_Conf_1.000	138	0							
Locus_22931_Transcript_1/1_Conf_1.000	173	0							
Locus_22932_Transcript_1/1_Conf_1.000	225	3	3.94E-14	NP_496398.2	76	81.2629	55	42	hypothetical protein T06D8.1
Locus_22933_Transcript_1/1_Conf_1.000	330	0							
Locus_22934_Transcript_1/1_Conf_1.000	266	2	9.96E-10	NP_741424.1	86	66.6254	38	33	hypothetical protein Y73B6BL.35
Locus_22935_Transcript_1/1_Conf_1.000	218	2	1.15E-10	NP_505963.3	70	69.707	61	43	hypothetical protein T04F3.1
Locus_22936_Transcript_1/1_Conf_1.000	262	0							
Locus_22937_Transcript_1/1_Conf_1.000	292	2	2.31E-06	XP_002645672.1	53	55.4546	102	55	Hypothetical protein CBG07319
Locus_22938_Transcript_1/1_Conf_1.000	185	0							
Locus_22939_Transcript_1/1_Conf_1.000	131	0							
Locus_2294_Transcript_1/1_Conf_1.000	195	20	5.11E-14	XP_002633575.1	79	80.8777	62	49	C. briggsae CBR-EXOS-2 protein
Locus_22940_Transcript_1/1_Conf_1.000	284	20	3.14E-11	XP_002630279.1	58	71.633	72	42	Hypothetical protein CBG00710
Locus_22941_Transcript_1/1_Conf_1.000	358	20	6.80E-27	XP_002638874.1	87	123.635	100	87	Hypothetical protein CBG22093
Locus_22942_Transcript_1/1_Conf_1.000	207	0							
Locus_22943_Transcript_1/1_Conf_1.000	241	0							
Locus_22944_Transcript_1/1_Conf_1.000	432	5	2.42E-08	XP_001897081.1	62	62.003	94	59	hypothetical protein
Locus_22945_Transcript_1/1_Conf_1.000	416	20	1.22E-60	XP_002638579.1	88	235.728	137	121	Hypothetical protein CBG05625
Locus_22946_Transcript_1/1_Conf_1.000	159	0							
Locus_22947_Transcript_1/1_Conf_1.000	324	20	4.43E-34	XP_002639978.1	85	147.517	107	91	C. briggsae CBR-FHOD-1 protein

Locus_22948_Transcript_1/1_Conf_1.000	192	20	4.95E-25	NP_502317.1	95	117.472	60	57	Proline HYdroxylase family member (phy-2)
Locus_22949_Transcript_1/1_Conf_1.000	309	20	9.13E-16	NP_493574.2	71	86.6557	67	48	hypothetical protein F39B2.5
Locus_2295_Transcript_1/1_Conf_1.000	1397	20	1.24E-19	NP_001012918.1	45	102.449	328	148	G2/M phase-specific E3 ubiquitin-protein ligase
Locus_22950_Transcript_1/1_Conf_1.000	183	20	1.27E-20	XP_002637401.1	88	102.834	59	52	C. briggsae CBR-FKB-3 protein
Locus_22951_Transcript_1/1_Conf_1.000	289	20	3.80E-25	XP_002648446.1	72	117.857	92	67	Hypothetical protein CBG24721
Locus_22952_Transcript_1/1_Conf_1.000	277	5	1.12E-21	XP_002629678.1	81	106.301	83	68	Hypothetical protein CBG00897
Locus_22953_Transcript_1/1_Conf_1.000	204	0							
Locus_22954_Transcript_1/1_Conf_1.000	231	0							
Locus_22955_Transcript_1/1_Conf_1.000	283	0							
Locus_22956_Transcript_1/1_Conf_1.000	199	20	1.03E-14	NP_505237.1	71	83.1889	66	47	human CLN (neuronal ceroid lipofuscinosis) related family member (cln-3.3)
Locus_22957_Transcript_1/1_Conf_1.000	508	20	2.13E-10	AAD13339.1	45	68.9366	167	76	ancylostoma-secreted protein 1 precursor

Locus_22958_Transcript_1/1_Conf_1.000	199	20	3.19E-24	XP_002634309.1	89	114.775	65	58	Hypothetical protein CBG17650
Locus_22959_Transcript_1/1_Conf_1.000	142	0							
Locus_2296_Transcript_1/1_Conf_1.000	788	20	1.26E-79	NP_506570.1	73	300.442	250	183	DeHydrogenases, Short chain family member (dhs-22)
Locus_22960_Transcript_1/1_Conf_1.000	298	20	1.14E-05	XP_001523646.1	60	53.1434	78	47	conserved hypothetical protein
Locus_22961_Transcript_1/1_Conf_1.000	137	0							
Locus_22962_Transcript_1/1_Conf_1.000	150	0							
Locus_22963_Transcript_1/1_Conf_1.000	135	0							
Locus_22964_Transcript_1/1_Conf_1.000	157	0							
Locus_22965_Transcript_1/1_Conf_1.000	129	0							
Locus_22966_Transcript_1/1_Conf_1.000	245	0							
Locus_22967_Transcript_1/1_Conf_1.000	142	20	1.45E-13	XP_002631429.1	85	79.337	47	40	Hypothetical protein CBG03286
Locus_22968_Transcript_1/1_Conf_1.000	383	6	9.89E-10	NP_510686.4	63	66.6254	116	74	hypothetical protein F59C12.3
Locus_22969_Transcript_1/1_Conf_1.000	244	0							
Locus_2297_Transcript_1/6_Conf_0.556	1657	20	3.85E-18	EEE52502.1	34	97.8265	374	129	hypothetical protein OsJ_34704
Locus_2297_Transcript_2/6_Conf_0.389	1133	20	1.34E-18	EEE52502.1	35	98.5969	370	130	hypothetical protein OsJ_34704
Locus_2297_Transcript_3/6_Conf_0.167	445	0							
Locus_2297_Transcript_4/6_Conf_0.333	922	20	8.18E-18	YP_068003.1	36	95.5153	355	130	LF3
Locus_2297_Transcript_5/6_Conf_0.500	2112	20	2.11E-19	XP_001427121.1	39	102.449	415	164	hypothetical protein
Locus_2297_Transcript_6/6_Conf_0.556	1675	20	3.91E-18	EEE52502.1	34	97.8265	374	129	hypothetical protein OsJ_34704
Locus_22970_Transcript_1/1_Conf_1.000	343	0							

Locus_22971_Transcript_1/1_Conf_1.000	279	0							
Locus_22972_Transcript_1/1_Conf_1.000	134	20	4.27E-13	CBL87054.2	97	77.7962	44	43	C. elegans protein F54E4.1, partially confirmed by transcript evidence
Locus_22973_Transcript_1/1_Conf_1.000	305	20	7.24E-37	XP_002640083.1	89	156.762	101	90	C. briggsae CBR-FRK-1 protein
Locus_22974_Transcript_1/1_Conf_1.000	254	20	2.09E-31	XP_396338.2	98	138.658	84	83	PREDICTED: similar to Tubulin alpha-1 chain
Locus_22975_Transcript_1/1_Conf_1.000	228	2	2.16E-04	NP_001041050.1	65	48.9062	55	36	hypothetical protein Y57G11C.3
Locus_22976_Transcript_1/1_Conf_1.000	187	0							
Locus_22977_Transcript_1/1_Conf_1.000	130	0							
Locus_22978_Transcript_1/1_Conf_1.000	473	0							
Locus_22979_Transcript_1/1_Conf_1.000	199	0							
Locus_2298_Transcript_1/1_Conf_1.000	708	20	6.93E-28	NP_492608.2	74	128.257	119	89	2 (Zwei) IG-domain protein family member (zig-1)
Locus_22980_Transcript_1/1_Conf_1.000	137	0							
Locus_22981_Transcript_1/1_Conf_1.000	229	0							
Locus_22982_Transcript_1/1_Conf_1.000	130	1	5.79E-10	NP_506678.2	80	67.3958	41	33	hypothetical protein W09D12.1
Locus_22983_Transcript_1/1_Conf_1.000	161	11	1.18E-18	NP_491003.2	94	96.2857	53	50	Amino Acid Transporter family member (aat-5)

Locus_22984_Transcript_1/1_Conf_1.000	179	2	4.39E-10	NP_492730.2	79	67.781	49	39	hypothetical protein Y106G6H.5
Locus_22985_Transcript_1/1_Conf_1.000	269	20	3.64E-20	NP_001024342.1	84	101.293	76	64	Aboc, EXpulsion defective family member (aex-3)
Locus_22986_Transcript_1/1_Conf_1.000	181	0							
Locus_22987_Transcript_1/1_Conf_1.000	148	17	1.72E-09	A8X3A7.2	78	65.855	50	39	Integrin alpha pat-2
Locus_22988_Transcript_1/1_Conf_1.000	128	0							
Locus_22989_Transcript_1/1_Conf_1.000	321	0							
Locus_2299_Transcript_1/1_Conf_1.000	1902	20	4.54E-58	XP_001899184.1	75	230.72	208	158	SWIM zinc finger family protein
Locus_22990_Transcript_1/1_Conf_1.000	217	6	1.23E-12	NP_001021463.1	65	76.2554	69	45	SUppressor of activated let-60 Ras family member (sur-2)
Locus_22991_Transcript_1/1_Conf_1.000	269	0							
Locus_22992_Transcript_1/1_Conf_1.000	297	4	3.28E-29	XP_002644323.1	81	131.339	93	76	C. briggsae CBR-SEC-3 protein
Locus_22993_Transcript_1/1_Conf_1.000	357	20	8.04E-28	XP_002631304.1	81	126.716	85	69	Hypothetical protein CBG03118
Locus_22994_Transcript_1/1_Conf_1.000	184	0							
Locus_22995_Transcript_1/1_Conf_1.000	196	0							
Locus_22996_Transcript_1/1_Conf_1.000	440	20	7.35E-66	XP_002637345.1	89	253.062	146	130	C. briggsae CBR-UNC-68 protein
Locus_22997_Transcript_1/1_Conf_1.000	137	0							
Locus_22998_Transcript_1/1_Conf_1.000	252	0							
Locus_22999_Transcript_1/1_Conf_1.000	468	20	1.17E-18	EFO22869.1	81	96.2857	92	75	hypothetical protein LOAG_05613

Locus_23_Transcript_1/1_Conf_1.000	1555	20	0	XP_002645954.1	92	862.833	482	446	C. briggsae CBR-GAS-1 protein
Locus_230_Transcript_1/1_Conf_1.000	1380	16	2.66E-14	XP_001901969.1	49	84.7297	216	106	hypothetical protein
Locus_2300_Transcript_1/1_Conf_1.000	1112	20	7.98E-93	EFO19759.1	67	345.125	354	240	hypothetical protein LOAG_08726
Locus_23000_Transcript_1/1_Conf_1.000	388	0							
Locus_23001_Transcript_1/1_Conf_1.000	177	0							
Locus_23002_Transcript_1/1_Conf_1.000	262	20	5.66E-13	XP_002631622.1	62	77.411	87	54	Hypothetical protein CBG20808
Locus_23003_Transcript_1/1_Conf_1.000	136	0							
Locus_23004_Transcript_1/1_Conf_1.000	308	20	1.04E-35	XP_002629821.1	84	152.91	101	85	C. briggsae CBR-SQV-8 protein
Locus_23005_Transcript_1/1_Conf_1.000	266	0							
Locus_23006_Transcript_1/1_Conf_1.000	432	20	7.73E-39	EFO17002.1	80	163.31	122	98	rab5-interacting protein
Locus_23007_Transcript_1/1_Conf_1.000	374	5	4.61E-39	NP_001123075.1	86	164.081	123	106	hypothetical protein ZC455.1
Locus_23008_Transcript_1/1_Conf_1.000	351	0							
Locus_23009_Transcript_1/1_Conf_1.000	167	20	4.30E-13	XP_002635372.1	86	77.7962	51	44	C. briggsae CBR-RPM-1 protein
Locus_2301_Transcript_1/1_Conf_1.000	3724	20	0	NP_497506.3	85	1672.14	1246	1066	hypothetical protein Y48G9A.3
Locus_23010_Transcript_1/1_Conf_1.000	182	11	9.48E-16	XP_002648958.1	77	86.6557	61	47	Hypothetical protein CBG21275
Locus_23011_Transcript_1/1_Conf_1.000	175	0							

Locus_23012_Transcript_1/1_Conf_1.000	185	0							
Locus_23013_Transcript_1/1_Conf_1.000	152	0							
Locus_23014_Transcript_1/1_Conf_1.000	208	1	1.25E-04	NP_497103.1	62	49.6766	61	38	hypothetical protein Y53F4B.18
Locus_23015_Transcript_1/1_Conf_1.000	146	6	8.86E-14	NP_495550.1	82	80.1073	51	42	BTB and MATH domain containing family member (bath-44)
Locus_23016_Transcript_1/1_Conf_1.000	156	0							
Locus_23017_Transcript_1/1_Conf_1.000	222	4	9.73E-13	EFO20262.1	88	76.6406	53	47	zinc finger protein
Locus_23018_Transcript_1/1_Conf_1.000	145	20	2.66E-18	XP_001369724.1	93	95.1301	46	43	PREDICTED: similar to LOC539180 protein
Locus_23019_Transcript_1/1_Conf_1.000	299	0							
Locus_2302_Transcript_1/1_Conf_1.000	2013	20	6.32E-175	NP_505638.1	69	619.002	593	413	RO (Ro) ribonucleoProtein family member (rop-1)
Locus_23020_Transcript_1/1_Conf_1.000	283	0							
Locus_23021_Transcript_1/1_Conf_1.000	204	0							
Locus_23022_Transcript_1/1_Conf_1.000	169	0							
Locus_23023_Transcript_1/1_Conf_1.000	243	12	4.57E-07	EFO17581.1	76	57.7658	63	48	bestrophin family protein
Locus_23024_Transcript_1/1_Conf_1.000	537	5	2.84E-38	XP_002647112.1	73	161.77	146	107	C. briggsae CBR-FRM-8 protein
Locus_23025_Transcript_1/1_Conf_1.000	780	1	2.64E-21	EFO16834.1	64	106.686	136	88	hypothetical protein LOAG_11670
Locus_23026_Transcript_1/1_Conf_1.000	267	8	1.09E-24	NP_001022643.1	76	116.316	88	67	LEThal family member (let-805)

Locus_23027_Transcript_1/1_Conf_1.000	284	20	9.42E-24	XP_002634423.1	79	113.235	88	70	C. briggsae CBR-PTR-14 protein
Locus_23028_Transcript_1/2_Conf_1.000	384	20	3.74E-09	ZP_05656155.1	47	64.6994	87	41	predicted protein
Locus_23028_Transcript_2/2_Conf_1.000	293	20	3.80E-09	ZP_05656155.1	47	64.6994	87	41	predicted protein
Locus_23029_Transcript_1/1_Conf_1.000	280	0							
Locus_2303_Transcript_1/1_Conf_1.000	552	0							
Locus_23030_Transcript_1/1_Conf_1.000	385	20	1.31E-54	CAR63666.1	90	215.698	128	116	putative Zinc finger C-x8-C-x5-C-x3-H type
Locus_23031_Transcript_1/1_Conf_1.000	166	3	1.06E-11	CAR63674.1	85	73.1738	54	46	putative PeRoXisome assembly factor
Locus_23032_Transcript_1/1_Conf_1.000	198	20	6.23E-12	XP_002645757.1	88	73.9442	44	39	Hypothetical protein CBG07432
Locus_23033_Transcript_1/1_Conf_1.000	253	0							
Locus_23034_Transcript_1/1_Conf_1.000	188	1	8.25E-12	CAJ45481.1	76	73.559	60	46	legumain
Locus_23035_Transcript_1/1_Conf_1.000	218	0							
Locus_23036_Transcript_1/1_Conf_1.000	235	0							
Locus_23037_Transcript_1/1_Conf_1.000	312	1	5.73E-05	XP_002642902.1	45	50.8322	105	48	Hypothetical protein CBG15176
Locus_23038_Transcript_1/1_Conf_1.000	144	20	1.01E-17	EFO25442.1	95	93.2041	48	46	TWK-7 protein

Locus_23039_Transcript_1/1_Conf_1.000	145	4	1.46E-08	XP_002640845.1	76	62.7734	46	35	C. briggsae CBR-CDH-1 protein
Locus_2304_Transcript_1/1_Conf_1.000	284	0							
Locus_23040_Transcript_1/1_Conf_1.000	141	0							
Locus_23041_Transcript_1/1_Conf_1.000	224	20	2.31E-22	NP_498057.1	89	108.612	67	60	hypothetical protein C27F2.10
Locus_23042_Transcript_1/1_Conf_1.000	221	0							
Locus_23043_Transcript_1/1_Conf_1.000	254	0							
Locus_23044_Transcript_1/2_Conf_1.000	271	0							
Locus_23044_Transcript_2/2_Conf_1.000	424	0							
Locus_23045_Transcript_1/1_Conf_1.000	146	0							
Locus_23046_Transcript_1/1_Conf_1.000	256	9	7.20E-16	NP_499308.1	70	87.0409	77	54	hypothetical protein D2045.5
Locus_23047_Transcript_1/1_Conf_1.000	181	2	7.53E-05	XP_002631385.1	61	50.447	57	35	Hypothetical protein CBG03227
Locus_23048_Transcript_1/1_Conf_1.000	203	0							
Locus_23049_Transcript_1/1_Conf_1.000	162	0							
Locus_2305_Transcript_1/1_Conf_1.000	1074	4	3.48E-122	XP_002631137.1	75	442.58	328	248	Hypothetical protein CBG02921
Locus_23050_Transcript_1/1_Conf_1.000	312	20	7.64E-50	NP_505708.2	94	199.904	102	96	hypothetical protein F32G8.4
Locus_23051_Transcript_1/1_Conf_1.000	141	0							
Locus_23052_Transcript_1/1_Conf_1.000	163	0							
Locus_23053_Transcript_1/1_Conf_1.000	395	0							
Locus_23054_Transcript_1/1_Conf_1.000	133	0							
Locus_23055_Transcript_1/1_Conf_1.000	181	0							
Locus_23056_Transcript_1/1_Conf_1.000	135	4	2.85E-17	ABU93237.1	100	91.6633	44	44	ligand-gated ion channel subunit
Locus_23057_Transcript_1/1_Conf_1.000	253	2	4.83E-20	XP_002719154.1	73	100.908	83	61	PREDICTED: alpha 1 type I collagen
Locus_23058_Transcript_1/1_Conf_1.000	132	0							
Locus_23059_Transcript_1/1_Conf_1.000	185	20	5.52E-24	XP_001640743.1	95	114.005	60	57	predicted protein

Locus_2306_Transcript_1/2_Conf_1.000	1217	20	4.42E-55	XP_002633667.1	67	219.935	230	156	Hypothetical protein CBG03342
Locus_2306_Transcript_2/2_Conf_1.000	2247	20	0	O18023.4	72	824.313	761	548	Ig-like and fibronectin type-III domain-containing protein C25G4.10
Locus_23060_Transcript_1/1_Conf_1.000	180	1	1.05E-06	XP_001083984.1	75	56.6102	45	34	PREDICTED: hypothetical protein LOC695354
Locus_23061_Transcript_1/1_Conf_1.000	298	20	9.18E-48	XP_001901913.1	95	192.971	97	93	F-box only protein 11
Locus_23062_Transcript_1/1_Conf_1.000	165	0							
Locus_23063_Transcript_1/1_Conf_1.000	215	20	1.85E-08	XP_002742403.1	72	62.3882	68	49	PREDICTED: TIP30-like
Locus_23064_Transcript_1/1_Conf_1.000	256	0							
Locus_23065_Transcript_1/1_Conf_1.000	179	4	1.08E-08	XP_001892742.1	83	63.1586	56	47	hypothetical protein
Locus_23066_Transcript_1/1_Conf_1.000	468	20	1.51E-58	XP_002633219.1	84	228.794	152	128	C. briggsae CBR-ITR-1 protein
Locus_23067_Transcript_1/1_Conf_1.000	184	17	7.25E-08	NP_998128.1	94	60.4622	34	32	disco-interacting protein 2 homolog B
Locus_23068_Transcript_1/1_Conf_1.000	137	0							
Locus_23069_Transcript_1/1_Conf_1.000	325	20	7.56E-34	XP_002645153.1	84	146.747	99	84	C. briggsae CBR-SFXN-2 protein
Locus_2307_Transcript_1/2_Conf_1.000	2933	20	2.70E-23	EFO22438.1	54	115.931	206	112	R3H domain-containing protein

Locus_2307_Transcript_2/2_Conf_1.000	2933	20	6.01E-23	XP_001900693.1	44	114.775	327	147	R3H domain containing protein
Locus_23070_Transcript_1/1_Conf_1.000	297	0							
Locus_23071_Transcript_1/1_Conf_1.000	240	0							
Locus_23072_Transcript_1/1_Conf_1.000	165	0							
Locus_23073_Transcript_1/1_Conf_1.000	247	0							
Locus_23074_Transcript_1/1_Conf_1.000	156	11	2.81E-12	XP_002633999.1	90	75.0998	43	39	C. briggsae CBR-TNI-4 protein
Locus_23075_Transcript_1/1_Conf_1.000	358	20	1.01E-30	XP_001899166.1	74	136.346	116	86	GTP-ase activating protein for Arf containing protein
Locus_23076_Transcript_1/1_Conf_1.000	143	0							
Locus_23077_Transcript_1/1_Conf_1.000	138	0							
Locus_23078_Transcript_1/1_Conf_1.000	298	4	6.64E-14	XP_002638288.1	61	80.4925	89	55	Hypothetical protein CBG22835
Locus_23079_Transcript_1/1_Conf_1.000	184	0							
Locus_2308_Transcript_1/1_Conf_1.000	1637	20	0	P50719.1	100	843.188	440	440	Tubulin alpha chain
Locus_23080_Transcript_1/1_Conf_1.000	339	20	3.47E-07	BAC36271.1	51	58.151	104	54	unnamed protein product
Locus_23081_Transcript_1/1_Conf_1.000	224	0							
Locus_23082_Transcript_1/1_Conf_1.000	137	0							
Locus_23083_Transcript_1/1_Conf_1.000	286	0							
Locus_23084_Transcript_1/1_Conf_1.000	213	0							
Locus_23085_Transcript_1/1_Conf_1.000	145	19	8.29E-12	XP_002640829.1	91	73.559	48	44	C. briggsae CBR-ADS-1 protein
Locus_23086_Transcript_1/1_Conf_1.000	415	0							

Locus_23087_Transcript_1/1_Conf_1.000	181	2	4.41E-05	NP_502795.2	68	51.2174	51	35	Homolog of Hedgehog AcylTransferase family member (hhat-2)
Locus_23088_Transcript_1/1_Conf_1.000	251	1	3.84E-06	XP_001897820.1	61	54.6842	81	50	hypothetical protein Bm1_31875
Locus_23089_Transcript_1/1_Conf_1.000	193	8	1.14E-13	EFO12672.1	79	79.7221	64	51	hypothetical protein LOAG_15862
Locus_2309_Transcript_1/1_Conf_1.000	762	20	3.25E-45	NP_499537.2	61	186.037	267	164	hypothetical protein Y56A3A.2
Locus_23090_Transcript_1/1_Conf_1.000	165	0							
Locus_23091_Transcript_1/1_Conf_1.000	187	0							
Locus_23092_Transcript_1/1_Conf_1.000	232	0							
Locus_23093_Transcript_1/1_Conf_1.000	132	3	7.06E-08	NP_508964.2	75	60.4622	45	34	Regulator of G protein Signaling family member (rgs-6)
Locus_23094_Transcript_1/1_Conf_1.000	172	2	3.28E-05	XP_002630912.1	63	51.6026	57	36	Hypothetical protein CBG02636
Locus_23095_Transcript_1/1_Conf_1.000	544	4	5.25E-11	NP_001021653.1	45	71.2478	191	87	FANCI (Fanconi anemia complex component I) homolog family member (fnci-1)
Locus_23096_Transcript_1/1_Conf_1.000	168	0							
Locus_23097_Transcript_1/1_Conf_1.000	322	20	1.14E-21	XP_001899134.1	73	106.301	102	75	hypothetical protein Bm1_38405
Locus_23098_Transcript_1/1_Conf_1.000	228	2	7.64E-18	XP_002632364.1	93	93.5893	75	70	Hypothetical protein CBG00382
Locus_23099_Transcript_1/1_Conf_1.000	129	0							
Locus_231_Transcript_1/2_Conf_1.000	536	20	1.87E-34	XP_002698333.1	90	149.058	103	93	PREDICTED: hypothetical protein
Locus_231_Transcript_2/2_Conf_1.000	497	20	1.05E-27	XP_002698333.1	89	126.331	92	82	PREDICTED: hypothetical protein

Locus_2310_Transcript_1/4_Conf_0.429	194	4	2.82E-04	XP_002641892.1	62	48.521	50	31	Hypothetical protein CBG16586
Locus_2310_Transcript_2/4_Conf_0.571	297	4	2.61E-10	XP_002641892.1	60	68.5514	76	46	Hypothetical protein CBG16586
Locus_2310_Transcript_3/4_Conf_0.571	238	4	1.34E-06	NP_001021172.1	69	56.225	46	32	PDF Receptor homolog family member (pdfr-1)
Locus_2310_Transcript_4/4_Conf_0.571	289	4	2.64E-10	XP_002641892.1	60	68.5514	76	46	Hypothetical protein CBG16586
Locus_23100_Transcript_1/1_Conf_1.000	137	0							
Locus_23101_Transcript_1/1_Conf_1.000	237	20	4.27E-29	NP_496802.2	89	130.954	79	71	BTAF (TBP-associated factor) homolog family member (btf-1)
Locus_23102_Transcript_1/1_Conf_1.000	135	0							
Locus_23103_Transcript_1/1_Conf_1.000	465	5	8.17E-12	XP_002642202.1	47	73.559	123	59	Hypothetical protein CBG18175
Locus_23104_Transcript_1/1_Conf_1.000	177	0							
Locus_23105_Transcript_1/1_Conf_1.000	204	20	2.05E-23	NP_502390.2	84	112.079	66	56	High Incidence of Males (increased X chromosome loss) family member (him-6)
Locus_23106_Transcript_1/1_Conf_1.000	545	20	5.94E-47	NP_001129830.1	62	190.66	182	113	LEThal family member (let-23)

Locus_23107_Transcript_1/1_Conf_1.000	237	20	2.43E-24	CAR63538.1	79	115.161	78	62	putative MFP2
Locus_23108_Transcript_1/1_Conf_1.000	142	20	6.10E-20	XP_002828013.1	100	100.523	46	46	PREDICTED: tRNA-dihydrouridine synthase 1-like isoform 2
Locus_23109_Transcript_1/1_Conf_1.000	248	0							
Locus_2311_Transcript_1/1_Conf_1.000	1074	20	1.06E-62	NP_496320.3	63	244.973	337	213	Cell Death Lethal family member (cdl-1)
Locus_23110_Transcript_1/1_Conf_1.000	177	1	5.56E-05	XP_002640523.1	79	50.8322	44	35	Hypothetical protein CBG18685
Locus_23111_Transcript_1/1_Conf_1.000	147	3	1.37E-06	EFO17834.1	76	56.225	47	36	hypothetical protein LOAG_10662
Locus_23112_Transcript_1/1_Conf_1.000	551	0							
Locus_23113_Transcript_1/1_Conf_1.000	140	0							
Locus_23114_Transcript_1/1_Conf_1.000	144	0							
Locus_23115_Transcript_1/1_Conf_1.000	478	20	2.03E-39	XP_002735023.1	75	165.236	157	119	PREDICTED: CG8129-like
Locus_23116_Transcript_1/1_Conf_1.000	221	0							
Locus_23117_Transcript_1/1_Conf_1.000	188	0							
Locus_23118_Transcript_1/1_Conf_1.000	200	0							
Locus_23119_Transcript_1/1_Conf_1.000	165	20	9.56E-21	AAH18938.4	100	103.219	45	45	NSMCE1 protein
Locus_2312_Transcript_1/2_Conf_1.000	2781	20	0	XP_002642644.1	85	1073.15	796	678	C. briggsae CBR-EGL-45 protein
Locus_2312_Transcript_2/2_Conf_1.000	2835	20	0	XP_002642644.1	85	1073.15	796	678	C. briggsae CBR-EGL-45 protein
Locus_23120_Transcript_1/1_Conf_1.000	155	0							
Locus_23121_Transcript_1/1_Conf_1.000	212	0							
Locus_23122_Transcript_1/1_Conf_1.000	189	0							

Locus_23123_Transcript_1/1_Conf_1.000	342	20	2.45E-48	XP_002637013.1	82	194.897	113	93	C. briggsae CBR-NID-1 protein
Locus_23124_Transcript_1/1_Conf_1.000	151	0							
Locus_23125_Transcript_1/1_Conf_1.000	369	20	3.32E-37	NP_001024306.1	78	157.918	114	90	Poly(ADP-ribose) Metabolism Enzyme family member (pme-5)
Locus_23126_Transcript_1/1_Conf_1.000	375	7	9.29E-24	XP_002640437.1	68	113.235	113	77	Hypothetical protein CBG08489
Locus_23127_Transcript_1/1_Conf_1.000	625	20	1.72E-63	NP_001040789.1	84	246.128	178	150	hypothetical protein H20J04.4
Locus_23128_Transcript_1/1_Conf_1.000	269	0							
Locus_23129_Transcript_1/1_Conf_1.000	225	7	3.33E-13	XP_001894370.1	69	78.1814	72	50	Immunoglobulin I-set domain containing protein
Locus_2313_Transcript_1/1_Conf_1.000	551	20	1.45E-96	BAE90788.1	100	355.525	183	183	unnamed protein product
Locus_23130_Transcript_1/1_Conf_1.000	327	8	2.34E-43	ACI49226.1	87	178.333	109	95	hypothetical protein Csp3_JD05.011
Locus_23131_Transcript_1/1_Conf_1.000	157	0							
Locus_23132_Transcript_1/1_Conf_1.000	498	0							
Locus_23133_Transcript_1/1_Conf_1.000	146	0							
Locus_23134_Transcript_1/1_Conf_1.000	191	2	3.23E-08	XP_002634150.1	71	61.6178	39	28	Hypothetical protein CBG01711
Locus_23135_Transcript_1/1_Conf_1.000	227	20	4.05E-35	XP_002828602.1	100	150.984	75	75	PREDICTED: trafficking protein particle complex subunit 5-like isoform 1
Locus_23136_Transcript_1/1_Conf_1.000	396	20	9.02E-27	NP_493980.1	64	123.25	132	85	hypothetical protein H17B01.4
Locus_23137_Transcript_1/1_Conf_1.000	291	13	8.18E-12	XP_002646276.1	63	73.559	66	42	C. briggsae CBR-ABF-2 protein
Locus_23138_Transcript_1/1_Conf_1.000	180	0							
Locus_23139_Transcript_1/1_Conf_1.000	169	0							
Locus_2314_Transcript_1/1_Conf_1.000	1573	20	9.32E-59	NP_494334.3	59	232.646	255	152	SET (trithorax/polycomb) domain containing family member (set-11)
Locus_23140_Transcript_1/1_Conf_1.000	203	0							
Locus_23141_Transcript_1/1_Conf_1.000	181	0							
Locus_23142_Transcript_1/1_Conf_1.000	488	1	2.22E-09	XP_001900122.1	58	65.4698	90	53	hypothetical protein Bm1_43305
Locus_23143_Transcript_1/1_Conf_1.000	187	5	1.11E-24	ACD85816.1	95	116.316	61	58	forkhead transcription factor DAF-16

Locus_23144_Transcript_1/1_Conf_1.000	157	17	4.06E-11	XP_002635426.1	92	71.2478	51	47	Hypothetical protein CBG00823
Locus_23145_Transcript_1/1_Conf_1.000	167	0							
Locus_23146_Transcript_1/1_Conf_1.000	175	5	4.56E-07	NP_001041091.2	67	57.7658	55	37	Motor AXon guidance family member (max-1)
Locus_23147_Transcript_1/1_Conf_1.000	251	0							
Locus_23148_Transcript_1/1_Conf_1.000	191	20	2.81E-28	XP_002642963.1	96	128.257	63	61	Hypothetical protein CBG15247
Locus_23149_Transcript_1/1_Conf_1.000	152	0							
Locus_2315_Transcript_1/1_Conf_1.000	551	20	6.96E-91	NP_506055.2	95	336.65	183	175	ELongator complex Protein Component family member (elpc-3)
Locus_23150_Transcript_1/1_Conf_1.000	169	0							
Locus_23151_Transcript_1/1_Conf_1.000	741	10	7.44E-23	XP_002633684.1	53	111.694	209	112	C. briggsae CBR-EEL-1 protein
Locus_23152_Transcript_1/1_Conf_1.000	151	0							
Locus_23153_Transcript_1/1_Conf_1.000	214	0							
Locus_23154_Transcript_1/1_Conf_1.000	344								
Locus_23155_Transcript_1/1_Conf_1.000	169	0							
Locus_23156_Transcript_1/1_Conf_1.000	173	0							
Locus_23157_Transcript_1/1_Conf_1.000	175	8	7.48E-26	XP_001893452.1	98	120.168	58	57	basement membrane proteoglycan
Locus_23158_Transcript_1/1_Conf_1.000	202	0							
Locus_23159_Transcript_1/1_Conf_1.000	200	0							
Locus_2316_Transcript_1/1_Conf_1.000	1085	20	7.44E-80	XP_001510286.1	59	301.982	364	217	PREDICTED: similar to Phosphoenolpyruvate carboxykinase, cytosolic [GTP] (Phosphoenolpyruvate carboxylase) (PEPCK-C) [Ornithorhynchus anatinus]

Locus_23160_Transcript_1/2_Conf_1.000	778	20	4.44E-37	NP_491390.2	65	159.073	217	142	hypothetical protein D1007.15
Locus_23160_Transcript_2/2_Conf_1.000	778	20	4.44E-37	NP_491390.2	65	159.073	217	142	hypothetical protein D1007.15
Locus_23161_Transcript_1/1_Conf_1.000	154	0							
Locus_23162_Transcript_1/1_Conf_1.000	243	6	9.50E-13	CBX25138.1	69	76.6406	69	48	Hypothetical protein C25A1.7a
Locus_23163_Transcript_1/1_Conf_1.000	181	0							
Locus_23164_Transcript_1/1_Conf_1.000	318	0							
Locus_23165_Transcript_1/1_Conf_1.000	277	0							
Locus_23166_Transcript_1/1_Conf_1.000	185	0							
Locus_23167_Transcript_1/1_Conf_1.000	212	0							
Locus_23168_Transcript_1/1_Conf_1.000	448	20	1.62E-60	XP_002635876.1	89	235.343	149	133	C. briggsae CBR-PTR-16 protein
Locus_23169_Transcript_1/1_Conf_1.000	187	3	1.97E-05	EFO13949.1	72	52.373	58	42	hypothetical protein LOAG_14577
Locus_2317_Transcript_1/1_Conf_1.000	1249	3	5.27E-43	XP_002646302.1	49	179.874	429	214	Hypothetical protein CBG12009
Locus_23170_Transcript_1/1_Conf_1.000	176	0							
Locus_23171_Transcript_1/1_Conf_1.000	160	20	2.99E-22	NP_502576.1	100	108.227	53	53	RAB family member (rab-19)
Locus_23172_Transcript_1/1_Conf_1.000	220	0							
Locus_23173_Transcript_1/1_Conf_1.000	298	0							
Locus_23174_Transcript_1/1_Conf_1.000	227	0							
Locus_23175_Transcript_1/1_Conf_1.000	141	0							
Locus_23176_Transcript_1/1_Conf_1.000	173	0							
Locus_23177_Transcript_1/1_Conf_1.000	131	20	9.86E-18	XP_002813192.1	100	93.2041	43	43	PREDICTED: plexin-D1-like

Locus_23178_Transcript_1/1_Conf_1.000	299	20	2.34E-51	NP_001024972.1	100	204.912	99	99	abnormal cell MIGration family member (mig-15)
Locus_23179_Transcript_1/1_Conf_1.000	625	20	4.85E-50	XP_002646339.1	75	201.445	174	131	C. briggsae CBR-INX-16 protein
Locus_2318_Transcript_1/2_Conf_1.000	2402	20	5.84E-29	AAK18978.3	47	134.42	267	128	Hypothetical protein T20F7.1
Locus_2318_Transcript_2/2_Conf_1.000	2381	20	2.87E-28	AAK18978.3	47	132.109	263	126	Hypothetical protein T20F7.1
Locus_23180_Transcript_1/1_Conf_1.000	154	3	2.64E-10	XP_001900332.1	97	68.5514	34	33	hypothetical protein
Locus_23181_Transcript_1/1_Conf_1.000	343	0							
Locus_23182_Transcript_1/1_Conf_1.000	225	0							
Locus_23183_Transcript_1/1_Conf_1.000	791	20	4.85E-71	XP_002635154.1	74	271.937	230	172	C. briggsae CBR-VRS-1 protein
Locus_23184_Transcript_1/1_Conf_1.000	179	2	4.55E-07	NP_505266.1	73	57.7658	65	48	hypothetical protein C01B7.5
Locus_23185_Transcript_1/1_Conf_1.000	249	6	1.27E-17	AAV41897.1	77	92.8189	70	54	SAX-2
Locus_23186_Transcript_1/1_Conf_1.000	250	0							
Locus_23187_Transcript_1/1_Conf_1.000	150	0							
Locus_23188_Transcript_1/1_Conf_1.000	235	0							
Locus_23189_Transcript_1/1_Conf_1.000	299	0							
Locus_2319_Transcript_1/1_Conf_1.000	830	20	5.86E-54	NP_741763.1	62	215.312	276	172	Homeodomain interacting Protein Kinase family member (hpk-1)
Locus_23190_Transcript_1/1_Conf_1.000	213	0							
Locus_23191_Transcript_1/1_Conf_1.000	207	20	6.56E-30	NP_508833.1	94	133.65	68	64	hypothetical protein T07F12.4
Locus_23192_Transcript_1/1_Conf_1.000	214	0							
Locus_23193_Transcript_1/1_Conf_1.000	662	20	1.01E-35	XP_002639186.1	69	154.066	146	102	C. briggsae CBR-LEM-3 protein

Locus_23194_Transcript_1/1_Conf_1.000	239	4	1.80E-27	XP_002638826.1	84	125.561	79	67	Hypothetical protein CBG22031
Locus_23195_Transcript_1/1_Conf_1.000	461	0							
Locus_23196_Transcript_1/1_Conf_1.000	163	20	9.28E-16	NP_501335.1	92	86.6557	53	49	UNCoordinated family member (unc-24)
Locus_23197_Transcript_1/1_Conf_1.000	148	0							
Locus_23198_Transcript_1/1_Conf_1.000	237	5	2.98E-06	XP_002637807.1	64	55.0694	71	46	Hypothetical protein CBG04593
Locus_23199_Transcript_1/1_Conf_1.000	130	2	1.25E-04	NP_001023038.1	77	49.6766	40	31	EXCretory canal abnormal family member (exc-5)
Locus_232_Transcript_1/1_Conf_1.000	1047	20	1.18E-34	NP_505179.1	54	151.754	251	137	hypothetical protein T23B12.4
Locus_2320_Transcript_1/1_Conf_1.000	1692	20	8.96E-79	NP_498203.2	57	299.286	510	292	CEll Death abnormality family member (ced-6)
Locus_23200_Transcript_1/1_Conf_1.000	276	20	3.97E-27	XP_002638736.1	81	124.405	92	75	C. briggsae CBR-EGO-1 protein
Locus_23201_Transcript_1/1_Conf_1.000	248	20	1.27E-41	XP_002823653.1	100	172.555	82	82	PREDICTED: hypothetical protein LOC100451758
Locus_23202_Transcript_1/1_Conf_1.000	234	0							
Locus_23203_Transcript_1/1_Conf_1.000	259	0							
Locus_23204_Transcript_1/1_Conf_1.000	148	5	8.85E-06	NP_493023.1	85	53.5286	34	29	hypothetical protein R09B3.3
Locus_23205_Transcript_1/1_Conf_1.000	195	7	9.34E-08	XP_002636803.1	68	60.077	63	43	Hypothetical protein CBG09244
Locus_23206_Transcript_1/1_Conf_1.000	133	3	2.51E-05	XP_002639821.1	79	51.9878	39	31	C. briggsae CBR-ERS-2 protein

Locus_23207_Transcript_1/1_Conf_1.000	131	20	4.14E-16	EFN87947.1	100	87.8113	43	43	26S protease regulatory subunit 8
Locus_23208_Transcript_1/1_Conf_1.000	138	0							
Locus_23209_Transcript_1/1_Conf_1.000	264	4	1.94E-05	NP_001023935.1	56	52.373	67	38	hypothetical protein F46B6.5
Locus_2321_Transcript_1/1_Conf_1.000	1394	20	0	XP_002643863.1	86	710.294	449	390	C. briggsae CBR-HID-1 protein
Locus_23210_Transcript_1/1_Conf_1.000	310	20	7.42E-42	EAW52759.1	100	173.326	82	82	transgelin 2, isoform CRA_a
Locus_23211_Transcript_1/1_Conf_1.000	227	5	4.98E-09	CBW48343.1	86	64.3142	38	33	Hypothetical protein C29A12.4d
Locus_23212_Transcript_1/1_Conf_1.000	317	1	6.32E-04	EFO26583.1	53	47.3654	98	52	hypothetical protein LOAG_01905
Locus_23213_Transcript_1/1_Conf_1.000	326	0							
Locus_23214_Transcript_1/1_Conf_1.000	184	0							
Locus_23215_Transcript_1/1_Conf_1.000	383	20	2.66E-47	NP_001024720.1	88	191.43	126	111	Na/H eXchanger family member (nhx-5)
Locus_23216_Transcript_1/1_Conf_1.000	188	0							
Locus_23217_Transcript_1/1_Conf_1.000	288	0							
Locus_23218_Transcript_1/1_Conf_1.000	165	8	2.88E-09	CAA46190.1	80	65.0846	51	41	P-glycoprotein A
Locus_23219_Transcript_1/1_Conf_1.000	141	1	1.72E-06	EAW50361.1	88	55.8398	44	39	hCG2041296
Locus_2322_Transcript_1/1_Conf_1.000	758	20	1.09E-85	NP_503105.1	80	320.472	255	204	Peroxisomal Membrane Protein related family member (pmp-4)
Locus_23220_Transcript_1/1_Conf_1.000	167	0							
Locus_23221_Transcript_1/1_Conf_1.000	192	2	4.81E-04	XP_002637532.1	80	47.7506	36	29	Hypothetical protein CBG19257
Locus_23222_Transcript_1/1_Conf_1.000	300	0							
Locus_23223_Transcript_1/1_Conf_1.000	181	0							

Locus_23224_Transcript_1/1_Conf_1.000	346	20	3.54E-31	NP_501928.1	70	137.887	116	82	hypothetical protein F13B12.4
Locus_23225_Transcript_1/1_Conf_1.000	135	0							
Locus_23226_Transcript_1/1_Conf_1.000	212	3	2.41E-16	XP_002636913.1	75	88.5817	70	53	Hypothetical protein CBG09377
Locus_23227_Transcript_1/1_Conf_1.000	199	3	3.78E-09	XP_002638395.1	67	64.6994	61	41	Hypothetical protein CBG18604
Locus_23228_Transcript_1/1_Conf_1.000	221	7	2.48E-16	EFO21619.1	76	88.5817	71	54	DOMON domain-containing protein
Locus_23229_Transcript_1/1_Conf_1.000	169	20	2.19E-25	XP_002828392.1	100	118.627	55	55	PREDICTED: LOW QUALITY PROTEIN: lipid phosphate phosphohydrolase 2-like, partial
Locus_2323_Transcript_1/1_Conf_1.000	523	0							
Locus_23230_Transcript_1/1_Conf_1.000	168								
Locus_23231_Transcript_1/1_Conf_1.000	168	8	3.88E-14	XP_001894372.1	78	81.2629	56	44	Immunoglobulin I-set domain containing protein
Locus_23232_Transcript_1/1_Conf_1.000	151	0							
Locus_23233_Transcript_1/1_Conf_1.000	129	0							
Locus_23234_Transcript_1/1_Conf_1.000	330	5	2.32E-51	CAR63666.1	94	204.912	110	104	putative Zinc finger C-x8-C-x5-C-x3-H type
Locus_23235_Transcript_1/1_Conf_1.000	140	0							
Locus_23236_Transcript_1/1_Conf_1.000	157	2	2.15E-12	XP_002634505.1	82	75.485	52	43	Hypothetical protein CBG08295
Locus_23237_Transcript_1/1_Conf_1.000	202	0							
Locus_23238_Transcript_1/1_Conf_1.000	128	20	1.06E-11	NP_502846.2	90	73.1738	42	38	hypothetical protein Y73F8A.11
Locus_23239_Transcript_1/1_Conf_1.000	132	0							
Locus_2324_Transcript_1/2_Conf_1.000	345	20	1.03E-14	NP_504416.1	68	83.1889	51	35	hypothetical protein C10G8.4
Locus_2324_Transcript_2/2_Conf_1.000	462	20	1.04E-14	NP_504416.1	68	83.1889	51	35	hypothetical protein C10G8.4
Locus_23240_Transcript_1/1_Conf_1.000	144	0							
Locus_23241_Transcript_1/1_Conf_1.000	270	0							
Locus_23242_Transcript_1/1_Conf_1.000	153	0							
Locus_23243_Transcript_1/1_Conf_1.000	200	2	1.26E-04	EFO16396.1	60	49.6766	66	40	hypothetical protein LOAG_12108
Locus_23244_Transcript_1/1_Conf_1.000	385	20	3.94E-59	CAB55030.2	96	230.72	128	123	C. elegans protein Y57A10A.10, partially confirmed by transcript evidence

Locus_23245_Transcript_1/1_Conf_1.000	146	20	2.33E-22	BAH13667.1	100	108.612	48	48	unnamed protein product
Locus_23246_Transcript_1/1_Conf_1.000	548	6	2.31E-30	EFO19771.1	59	135.576	189	113	hypothetical protein LOAG_08718
Locus_23247_Transcript_1/1_Conf_1.000	319	20	2.71E-31	NP_495273.1	79	138.272	106	84	hypothetical protein C32D5.6
Locus_23248_Transcript_1/1_Conf_1.000	186	3	3.83E-09	NP_495267.1	85	64.6994	35	30	hypothetical protein C29F5.1
Locus_23249_Transcript_1/1_Conf_1.000	270	20	3.75E-17	NP_505501.1	68	91.2781	85	58	Temporarily Assigned Gene name family member (tag-120)
Locus_2325_Transcript_1/2_Conf_1.000	766	20	2.04E-63	NP_741181.1	74	246.514	213	158	hypothetical protein T12A2.15
Locus_2325_Transcript_2/2_Conf_1.000	743	20	1.93E-63	NP_741181.1	73	246.514	213	157	hypothetical protein T12A2.15
Locus_23250_Transcript_1/1_Conf_1.000	163	0							
Locus_23251_Transcript_1/1_Conf_1.000	337	0							
Locus_23252_Transcript_1/1_Conf_1.000	170	0							
Locus_23253_Transcript_1/1_Conf_1.000	132	0							
Locus_23254_Transcript_1/1_Conf_1.000	317	0							
Locus_23255_Transcript_1/1_Conf_1.000	262	0							
Locus_23256_Transcript_1/1_Conf_1.000	428	20	2.29E-06	XP_002648766.1	45	55.4546	146	66	Hypothetical protein CBG10699
Locus_23257_Transcript_1/1_Conf_1.000	184	20	5.35E-19	CAR63646.1	98	97.4413	60	59	putative Homeobox family member
Locus_23258_Transcript_1/1_Conf_1.000	205	0							

Locus_23259_Transcript_1/1_Conf_1.000	154	0							
Locus_2326_Transcript_1/1_Conf_1.000	356	20	1.06E-19	ACI49172.1	60	99.7525	121	73	hypothetical protein Csp3_JD01.004
Locus_23260_Transcript_1/1_Conf_1.000	138	0							
Locus_23261_Transcript_1/1_Conf_1.000	137	0							
Locus_23262_Transcript_1/1_Conf_1.000	474	0							
Locus_23263_Transcript_1/1_Conf_1.000	489	20	1.93E-21	XP_001636445.1	49	105.531	180	89	predicted protein
Locus_23264_Transcript_1/1_Conf_1.000	338	20	5.35E-24	EFO26090.1	72	114.005	111	80	hypothetical protein LOAG_02402
Locus_23265_Transcript_1/1_Conf_1.000	153	0							
Locus_23266_Transcript_1/1_Conf_1.000	156	0							
Locus_23267_Transcript_1/1_Conf_1.000	222	20	1.77E-14	NP_506322.1	81	82.4185	55	45	hypothetical protein F53F1.2
Locus_23268_Transcript_1/1_Conf_1.000	407	20	8.61E-30	XP_002638851.1	69	133.265	136	94	C. briggsae CBR-IMB-5 protein
Locus_23269_Transcript_1/1_Conf_1.000	239	0							
Locus_2327_Transcript_1/1_Conf_1.000	128	0							
Locus_23270_Transcript_1/1_Conf_1.000	187	0							
Locus_23271_Transcript_1/1_Conf_1.000	188	20	3.13E-11	BAG10454.1	100	71.633	62	62	ribosome-binding protein 1
Locus_23272_Transcript_1/1_Conf_1.000	199	1	3.91E-06	NP_001022861.1	76	54.6842	43	33	CREB Homolog family member (crh-1)
Locus_23273_Transcript_1/1_Conf_1.000	140	0							
Locus_23274_Transcript_1/1_Conf_1.000	135	0							
Locus_23275_Transcript_1/1_Conf_1.000	265	0							

Locus_23276_Transcript_1/1_Conf_1.000	133	7	2.34E-11	XP_002634396.1	86	72.0182	44	38	Hypothetical protein CBG04396
Locus_23277_Transcript_1/1_Conf_1.000	274	5	2.77E-12	EFO24919.1	64	75.0998	90	58	RGC/RGC protein kinase
Locus_23278_Transcript_1/1_Conf_1.000	142	0							
Locus_23279_Transcript_1/1_Conf_1.000	143	20	5.34E-16	XP_002342425.1	100	87.4261	41	41	PREDICTED: hypothetical protein XP_002342425
Locus_2328_Transcript_1/2_Conf_1.000	570	0							
Locus_2328_Transcript_2/2_Conf_1.000	438	0							
Locus_23280_Transcript_1/1_Conf_1.000	159	8	6.02E-23	XP_002632635.1	98	110.538	51	50	C. briggsae CBR-DMD-6 protein
Locus_23281_Transcript_1/1_Conf_1.000	244	0							
Locus_23282_Transcript_1/1_Conf_1.000	219	0							
Locus_23283_Transcript_1/1_Conf_1.000	221	3	4.24E-08	XP_002636414.1	61	61.2326	72	44	Hypothetical protein CBG23067
Locus_23284_Transcript_1/1_Conf_1.000	202	0							
Locus_23285_Transcript_1/1_Conf_1.000	492	0							
Locus_23286_Transcript_1/2_Conf_1.000	409	9	1.51E-34	NP_496430.1	90	149.058	82	74	hypothetical protein C33B4.2
Locus_23286_Transcript_2/2_Conf_1.000	409	7	5.19E-35	NP_496430.1	91	150.599	82	75	hypothetical protein C33B4.2
Locus_23287_Transcript_1/1_Conf_1.000	240	3	2.96E-14	XP_002634119.1	69	81.6481	79	55	Hypothetical protein CBG01673
Locus_23288_Transcript_1/1_Conf_1.000	164	20	1.29E-25	2DDY	100	119.398	54	54	SolutionStructure Of Matrilysin (Mmp-7) Complexed To Constraint Conformational Sulfonamide Inhibitor
Locus_23289_Transcript_1/1_Conf_1.000	263	20	7.39E-13	XP_001897247.1	65	77.0258	85	56	Strictosidine synthase family protein
Locus_2329_Transcript_1/1_Conf_1.000	226	4	1.76E-22	XP_002631267.1	81	108.997	75	61	C. briggsae CBR-PRO-1 protein
Locus_23290_Transcript_1/1_Conf_1.000	159	0							
Locus_23291_Transcript_1/1_Conf_1.000	193	0							
Locus_23292_Transcript_1/1_Conf_1.000	324	0							
Locus_23293_Transcript_1/1_Conf_1.000	168	7	2.13E-04	XP_002848567.1	73	48.9062	41	30	ADP-ribosylation factor
Locus_23294_Transcript_1/1_Conf_1.000	328	1	1.09E-16	AAB32534.1	100	89.7373	39	39	histone H1 transcription factor large subunit 2A
Locus_23295_Transcript_1/1_Conf_1.000	212	0							
Locus_23296_Transcript_1/1_Conf_1.000	134	0							
Locus_23297_Transcript_1/1_Conf_1.000	198	0							
Locus_23298_Transcript_1/1_Conf_1.000	130	0							
Locus_23299_Transcript_1/1_Conf_1.000	349	0							
Locus_233_Transcript_1/1_Conf_1.000	506	20	8.67E-25	XP_002644823.1	59	116.701	153	91	C. briggsae CBR-TAG-275 protein
Locus_2330_Transcript_1/2_Conf_1.000	600	0							
Locus_2330_Transcript_2/2_Conf_1.000	596	0							

Locus_23300_Transcript_1/1_Conf_1.000	176	0							
Locus_23301_Transcript_1/1_Conf_1.000	329	5	4.75E-12	XP_002630535.1	57	74.3294	89	51	C. briggsae CBR-TAG-308 protein
Locus_23302_Transcript_1/1_Conf_1.000	199	0							
Locus_23303_Transcript_1/1_Conf_1.000	287	20	1.26E-36	ACI49226.1	87	155.992	95	83	hypothetical protein Csp3_JD05.011
Locus_23304_Transcript_1/1_Conf_1.000	405	0							
Locus_23305_Transcript_1/1_Conf_1.000	286	0							
Locus_23306_Transcript_1/1_Conf_1.000	150	0							
Locus_23307_Transcript_1/1_Conf_1.000	240	0							
Locus_23308_Transcript_1/1_Conf_1.000	255	1	9.75E-05	CBH39183.1	57	50.0618	73	42	conserved hypothetical protein, DUF255 family
Locus_23309_Transcript_1/1_Conf_1.000	194	20	7.65E-18	XP_002637256.1	77	93.5893	63	49	Hypothetical protein CBG18935
Locus_2331_Transcript_1/1_Conf_1.000	1737	20	4.28E-76	XP_002735266.1	50	290.426	542	271	PREDICTED: lethal giant larvae homolog 1-like
Locus_23310_Transcript_1/1_Conf_1.000	143	0							
Locus_23311_Transcript_1/1_Conf_1.000	158	0							
Locus_23312_Transcript_1/1_Conf_1.000	283	0							
Locus_23313_Transcript_1/1_Conf_1.000	256	4	6.06E-31	XP_002643867.1	91	137.117	83	76	Hypothetical protein CBG02103
Locus_23314_Transcript_1/1_Conf_1.000	221	0							
Locus_23315_Transcript_1/1_Conf_1.000	181	13	7.03E-11	XP_002648535.1	77	70.4774	59	46	Hypothetical protein CBG24833
Locus_23316_Transcript_1/1_Conf_1.000	306	20	5.01E-30	NP_497814.3	77	134.035	101	78	UNCoordinated family member (unc-79)
Locus_23317_Transcript_1/1_Conf_1.000	380	11	1.29E-17	XP_001896168.1	62	92.8189	108	68	SET domain containing protein
Locus_23318_Transcript_1/1_Conf_1.000	164	1	1.64E-04	EFO14283.1	69	49.2914	52	36	hypothetical protein LOAG_14239
Locus_23319_Transcript_1/1_Conf_1.000	231	0							
Locus_2332_Transcript_1/1_Conf_1.000	1141	20	1.29E-154	XP_002642936.1	90	550.436	341	310	C. briggsae CBR-MDH-1 protein
Locus_23320_Transcript_1/1_Conf_1.000	263	0							
Locus_23321_Transcript_1/1_Conf_1.000	145	0							
Locus_23322_Transcript_1/1_Conf_1.000	134	0							
Locus_23323_Transcript_1/1_Conf_1.000	199	20	2.88E-25	NP_496219.1	90	118.242	66	60	Guanylyl CYclase family member (gcy-5)
Locus_23324_Transcript_1/1_Conf_1.000	406	0							

Locus_23325_Transcript_1/1_Conf_1.000	143	1	2.25E-06	NP_001021657.2	77	55.4546	36	28	hypothetical protein W03F11.5
Locus_23326_Transcript_1/1_Conf_1.000	255	0							
Locus_23327_Transcript_1/1_Conf_1.000	184	0							
Locus_23328_Transcript_1/1_Conf_1.000	189	20	7.18E-16	EFN89112.1	82	87.0409	57	47	F-actin-capping protein subunit alpha
Locus_23329_Transcript_1/1_Conf_1.000	195	0							
Locus_2333_Transcript_1/1_Conf_1.000	1837	20	1.64E-65	XP_002642511.1	54	255.373	430	233	Hypothetical protein CBG06936
Locus_23330_Transcript_1/1_Conf_1.000	444	0							
Locus_23331_Transcript_1/1_Conf_1.000	159	5	4.19E-08	AAB42328.2	70	61.2326	51	36	Hypothetical protein C32E8.11
Locus_23332_Transcript_1/1_Conf_1.000	155	0							
Locus_23333_Transcript_1/1_Conf_1.000	251	0							
Locus_23334_Transcript_1/1_Conf_1.000	129	20	2.77E-20	XP_002924566.1	100	101.679	42	42	PREDICTED: LIM domain-containing protein 2-like
Locus_23335_Transcript_1/1_Conf_1.000	147	0							
Locus_23336_Transcript_1/1_Conf_1.000	151	0							
Locus_23337_Transcript_1/1_Conf_1.000	186	0							
Locus_23338_Transcript_1/1_Conf_1.000	208	0							
Locus_23339_Transcript_1/1_Conf_1.000	134	20	2.86E-17	XP_002919669.1	100	91.6633	44	44	PREDICTED: n-alpha-acetyltransferase 20, NatB catalytic subunit-like isoform 3
Locus_2334_Transcript_1/1_Conf_1.000	323	0							
Locus_23340_Transcript_1/1_Conf_1.000	189	20	1.40E-11	CAX65070.1	81	72.7886	53	43	C. elegans protein R74.4b, confirmed by transcript evidence
Locus_23341_Transcript_1/1_Conf_1.000	141	20	8.24E-17	NP_510700.3	91	90.1225	47	43	Histone DeAcetylase family member (hda-4)
Locus_23342_Transcript_1/1_Conf_1.000	133	0							
Locus_23343_Transcript_1/1_Conf_1.000	297	20	1.58E-23	XP_002634426.1	67	112.464	98	66	Hypothetical protein CBG04437
Locus_23344_Transcript_1/1_Conf_1.000	139	0							

Locus_23345_Transcript_1/1_Conf_1.000	136	16	6.15E-12	NP_510520.4	91	73.9442	45	41	Osm-9 and Capsaicin receptor-Related family member (ocr-3)
Locus_23346_Transcript_1/1_Conf_1.000	179								
Locus_23347_Transcript_1/1_Conf_1.000	160	0							
Locus_23348_Transcript_1/1_Conf_1.000	140	0							
Locus_23349_Transcript_1/1_Conf_1.000	305	0							
Locus_2335_Transcript_1/1_Conf_1.000	1570	1	2.48E-11	XP_001902673.1	44	75.0998	396	175	hypothetical protein Bm1_56075
Locus_23350_Transcript_1/1_Conf_1.000	236	0							
Locus_23351_Transcript_1/1_Conf_1.000	128	0							
Locus_23352_Transcript_1/1_Conf_1.000	933	4	5.99E-24	NP_509471.2	59	115.931	233	138	hypothetical protein F53A9.4
Locus_23353_Transcript_1/1_Conf_1.000	325	20	3.75E-41	NP_508154.2	89	171.014	93	83	Nematode AStacin protease family member (nas-15)
Locus_23354_Transcript_1/1_Conf_1.000	255	0							
Locus_23355_Transcript_1/1_Conf_1.000	148	7	7.24E-08	ACJ65168.1	77	60.4622	49	38	Uncoordinated protein 68, isoform b, partially confirmed by transcript evidence
Locus_23356_Transcript_1/1_Conf_1.000	157	20	3.00E-22	EFO27462.1	100	108.227	52	52	hypothetical protein LOAG_01021
Locus_23357_Transcript_1/1_Conf_1.000	187	0							
Locus_23358_Transcript_1/1_Conf_1.000	129	20	1.09E-16	XP_002829423.1	100	89.7373	42	42	PREDICTED: LOW QUALITY PROTEIN: mitochondrial import receptor subunit TOM40 homolog
Locus_23359_Transcript_1/1_Conf_1.000	363	0							
Locus_2336_Transcript_1/2_Conf_1.000	139	0							
Locus_2336_Transcript_2/2_Conf_1.000	132	0							

Locus_23360_Transcript_1/1_Conf_1.000	251	20	3.23E-21	XP_002640311.1	79	104.76	82	65	C. briggsae CBR-LET-363 protein
Locus_23361_Transcript_1/1_Conf_1.000	131	0							
Locus_23362_Transcript_1/1_Conf_1.000	159	0							
Locus_23363_Transcript_1/1_Conf_1.000	250	0							
Locus_23364_Transcript_1/1_Conf_1.000	259	20	2.72E-23	XP_002636068.1	76	111.694	84	64	Hypothetical protein CBG01308
Locus_23365_Transcript_1/1_Conf_1.000	263	5	5.30E-11	NP_497641.2	72	70.8626	86	62	CaDHerin family member (cdh-1)
Locus_23366_Transcript_1/1_Conf_1.000	232	5	3.31E-13	Q60UZ5.2	71	78.1814	77	55	Mediator of RNA polymerase II transcription subunit 23
Locus_23367_Transcript_1/1_Conf_1.000	235	0							
Locus_23368_Transcript_1/1_Conf_1.000	214	20	9.74E-26	XP_001891908.1	98	119.783	66	65	SNF7 family protein
Locus_23369_Transcript_1/1_Conf_1.000	172	4	8.59E-22	NP_001022641.1	91	106.686	57	52	LEThal family member (let-805)
Locus_2337_Transcript_1/1_Conf_1.000	534	20	1.58E-41	XP_002629939.1	89	172.555	103	92	Hypothetical protein CBG03659
Locus_23370_Transcript_1/1_Conf_1.000	178	0							

Locus_23371_Transcript_1/1_Conf_1.000	130	0							
Locus_23372_Transcript_1/1_Conf_1.000	163	14	4.62E-07	AAK64493.1	67	57.7658	49	33	AF388311_1C-type lectin CTL-2 precursor
Locus_23373_Transcript_1/1_Conf_1.000	314	2	2.56E-21	ACE63491.1	67	105.145	97	65	GABAB2 receptor subunit
Locus_23374_Transcript_1/1_Conf_1.000	306	0							
Locus_23375_Transcript_1/1_Conf_1.000	148	0							
Locus_23376_Transcript_1/1_Conf_1.000	141	0							
Locus_23377_Transcript_1/1_Conf_1.000	156	20	2.54E-13	XP_002918275.1	100	78.5666	35	35	PREDICTED: collagen alpha-2(I) chain-like
Locus_23378_Transcript_1/1_Conf_1.000	176	0							
Locus_23379_Transcript_1/1_Conf_1.000	223	0							
Locus_2338_Transcript_1/2_Conf_1.000	510	0							
Locus_2338_Transcript_2/2_Conf_1.000	510	0							
Locus_23380_Transcript_1/1_Conf_1.000	171	2	2.43E-08	XP_002641539.1	70	62.003	54	38	C. briggsae CBR-SET-27 protein
Locus_23381_Transcript_1/1_Conf_1.000	336	0							
Locus_23382_Transcript_1/1_Conf_1.000	163	0							
Locus_23383_Transcript_1/1_Conf_1.000	156	0							
Locus_23384_Transcript_1/1_Conf_1.000	184	20	9.42E-24	XP_002919957.1	100	113.235	53	53	PREDICTED: activated RNA polymerase II transcriptional coactivator p15-like
Locus_23385_Transcript_1/1_Conf_1.000	149	2	5.92E-10	XP_002643350.1	77	67.3958	45	35	Hypothetical protein CBG15947
Locus_23386_Transcript_1/1_Conf_1.000	243	0							
Locus_23387_Transcript_1/1_Conf_1.000	288	0							
Locus_23388_Transcript_1/1_Conf_1.000	160	0							
Locus_23389_Transcript_1/1_Conf_1.000	318	7	8.20E-12	NP_497229.1	70	73.559	93	66	hypothetical protein W06E11.1
Locus_2339_Transcript_1/1_Conf_1.000	1339	20	1.14E-22	EFO18116.1	46	112.464	463	215	api5-prov protein
Locus_23390_Transcript_1/1_Conf_1.000	158	0							

Locus_23391_Transcript_1/1_Conf_1.000	147	0							
Locus_23392_Transcript_1/1_Conf_1.000	149	0							
Locus_23393_Transcript_1/1_Conf_1.000	163	0							
Locus_23394_Transcript_1/1_Conf_1.000	160	20	1.76E-06	NP_490949.3	69	55.8398	53	37	ABC Transporter family member (abt-2)
Locus_23395_Transcript_1/1_Conf_1.000	262	0							
Locus_23396_Transcript_1/1_Conf_1.000	365	9	3.13E-32	AAA83446.5	80	141.354	109	88	Hypothetical protein F44A2.3
Locus_23397_Transcript_1/1_Conf_1.000	270	0							
Locus_23398_Transcript_1/1_Conf_1.000	152	0							
Locus_23399_Transcript_1/1_Conf_1.000	142	20	3.03E-19	XP_002921914.1	100	98.2117	47	47	PREDICTED: eukaryotic translation initiation factor 3 subunit I-like
Locus_234_Transcript_1/1_Conf_1.000	568	20	2.80E-61	NP_506256.3	67	238.424	187	126	CaDHerin family member (cdh-6)
Locus_2340_Transcript_1/1_Conf_1.000	666	6	1.21E-60	NP_492439.1	83	236.884	160	133	hypothetical protein T06D10.1
Locus_23400_Transcript_1/1_Conf_1.000	140	0							
Locus_23401_Transcript_1/1_Conf_1.000	229	0							

Locus_23402_Transcript_1/1_Conf_1.000	410	20	6.98E-48	XP_002639323.1	78	193.356	134	105	C. briggsae CBR-HUM-7 protein
Locus_23403_Transcript_1/1_Conf_1.000	137	4	3.99E-11	XP_002646095.1	86	71.2478	45	39	C. briggsae CBR-HMR-1 protein
Locus_23404_Transcript_1/1_Conf_1.000	183	1	4.25E-08	XP_002641351.1	73	61.2326	60	44	C. briggsae CBR-TEG-1 protein
Locus_23405_Transcript_1/1_Conf_1.000	214	0							
Locus_23406_Transcript_1/1_Conf_1.000	655	0							
Locus_23407_Transcript_1/1_Conf_1.000	319	0							
Locus_23408_Transcript_1/1_Conf_1.000	658	0							
Locus_23409_Transcript_1/1_Conf_1.000	240	20	4.71E-28	XP_002632772.1	82	127.487	79	65	C. briggsae CBR-TAT-2 protein
Locus_2341_Transcript_1/1_Conf_1.000	348	0							
Locus_23410_Transcript_1/1_Conf_1.000	284	0							
Locus_23411_Transcript_1/1_Conf_1.000	147	0							
Locus_23412_Transcript_1/1_Conf_1.000	278	9	6.31E-41	NP_001022641.1	89	170.244	92	82	LEThal family member (let-805)
Locus_23413_Transcript_1/1_Conf_1.000	174	20	5.74E-18	AAF36480.1	87	93.9745	56	49	glutathione S-transferase 2
Locus_23414_Transcript_1/1_Conf_1.000	172	20	5.38E-24	XP_002834167.1	100	114.005	56	56	PREDICTED: peptidyl-tRNA hydrolase 2, mitochondrial-like isoform 2
Locus_23415_Transcript_1/1_Conf_1.000	240	20	1.23E-44	NP_001182611.1	100	182.57	78	78	metalloproteinase inhibitor 3
Locus_23416_Transcript_1/1_Conf_1.000	338	20	1.11E-45	XP_002642615.1	81	186.037	112	91	C. briggsae CBR-MUP-4 protein

Locus_23417_Transcript_1/1_Conf_1.000	160	0							
Locus_23418_Transcript_1/1_Conf_1.000	386	4	8.91E-11	NP_001021653.1	61	70.0922	126	78	FANCI (Fanconi anemia complex component I) homolog family member (fnci-1)
Locus_23419_Transcript_1/1_Conf_1.000	683	20	9.46E-72	NP_499173.1	82	273.863	206	169	hypothetical protein ZK632.3
Locus_2342_Transcript_1/1_Conf_1.000	374	20	9.61E-37	XP_002643252.1	78	156.377	114	89	C. briggsae CBR-TRAP-2 protein
Locus_23420_Transcript_1/1_Conf_1.000	137	0							
Locus_23421_Transcript_1/1_Conf_1.000	290	3	7.18E-16	XP_002637525.1	74	87.0409	75	56	Hypothetical protein CBG19248
Locus_23422_Transcript_1/1_Conf_1.000	157	0							
Locus_23423_Transcript_1/1_Conf_1.000	212	0							
Locus_23424_Transcript_1/1_Conf_1.000	172	0							
Locus_23425_Transcript_1/1_Conf_1.000	169	20	2.51E-13	NP_001024724.2	80	78.5666	56	45	EGg Laying defective family member (egl-15)
Locus_23426_Transcript_1/1_Conf_1.000	182	0							
Locus_23427_Transcript_1/1_Conf_1.000	151	0							
Locus_23428_Transcript_1/1_Conf_1.000	152	0							
Locus_23429_Transcript_1/1_Conf_1.000	137	0							
Locus_2343_Transcript_1/2_Conf_1.000	1864	20	6.27E-113	XP_002630571.1	70	412.92	403	285	Hypothetical protein CBG13024
Locus_2343_Transcript_2/2_Conf_1.000	1788	20	5.94E-113	XP_002630571.1	70	412.92	403	285	Hypothetical protein CBG13024
Locus_23430_Transcript_1/1_Conf_1.000	187	0							
Locus_23431_Transcript_1/1_Conf_1.000	306	3	2.50E-05	XP_002642803.1	82	51.9878	40	33	C. briggsae CBR-TAG-164 protein
Locus_23432_Transcript_1/1_Conf_1.000	136	0							
Locus_23433_Transcript_1/1_Conf_1.000	255	0							
Locus_23434_Transcript_1/1_Conf_1.000	194	20	9.66E-21	CAA86821.1	87	103.219	64	56	excretory/secretory antigen
Locus_23435_Transcript_1/1_Conf_1.000	261	0							
Locus_23436_Transcript_1/1_Conf_1.000	209	20	2.18E-25	XP_002634716.1	95	118.627	69	66	C. briggsae CBR-EXC-5 protein
Locus_23437_Transcript_1/1_Conf_1.000	261	0							
Locus_23438_Transcript_1/1_Conf_1.000	157	20	4.63E-23	NP_001034792.3	100	110.923	52	52	neuroblastoma breakpoint family member 10
Locus_23439_Transcript_1/1_Conf_1.000	165	4	7.10E-08	XP_001893303.1	67	60.4622	53	36	ribosomal RNA adenine dimethylase family protein
Locus_2344_Transcript_1/2_Conf_1.000	1084	20	3.64E-10	XP_002641794.1	65	70.4774	61	40	Hypothetical protein CBG10147
Locus_2344_Transcript_2/2_Conf_1.000	1095	20	3.71E-10	XP_002641794.1	65	70.4774	61	40	Hypothetical protein CBG10147
Locus_23440_Transcript_1/1_Conf_1.000	159	20	1.35E-14	XP_002640523.1	84	82.8037	51	43	Hypothetical protein CBG18685
Locus_23441_Transcript_1/1_Conf_1.000	301	0							

Locus_23442_Transcript_1/1_Conf_1.000	169	0							
Locus_23443_Transcript_1/1_Conf_1.000	504	20	1.32E-65	NP_490772.2	88	252.292	159	141	hypothetical protein Y18H1A.3
Locus_23444_Transcript_1/1_Conf_1.000	165	20	4.02E-11	XP_002639959.1	86	71.2478	46	40	Hypothetical protein CBG10779
Locus_23445_Transcript_1/1_Conf_1.000	330	0							
Locus_23446_Transcript_1/1_Conf_1.000	274	0							
Locus_23447_Transcript_1/1_Conf_1.000	161	0							
Locus_23448_Transcript_1/1_Conf_1.000	165	20	1.38E-19	NP_004137.2	100	99.3673	42	42	NADH dehydrogenase ubiquinone 1 beta subcomplex subunit 7
Locus_23449_Transcript_1/1_Conf_1.000	352	0							
Locus_2345_Transcript_1/1_Conf_1.000	1819	20	0	NP_001040881.1	71	650.588	582	414	WHiTe (Drosophila) related ABC transporte family member (wht-7)
Locus_23450_Transcript_1/1_Conf_1.000	198	2	2.70E-15	NP_001076730.1	86	85.1149	52	45	hypothetical protein Y41E3.22
Locus_23451_Transcript_1/1_Conf_1.000	139	2	2.26E-06	XP_002630900.1	79	55.4546	43	34	Hypothetical protein CBG02622
Locus_23452_Transcript_1/1_Conf_1.000	202	0							
Locus_23453_Transcript_1/1_Conf_1.000	159	0							
Locus_23454_Transcript_1/1_Conf_1.000	308	0							
Locus_23455_Transcript_1/1_Conf_1.000	221	0							
Locus_23456_Transcript_1/1_Conf_1.000	184	20	8.52E-25	NP_509350.2	90	116.701	61	55	hypothetical protein C34D10.2
Locus_23457_Transcript_1/1_Conf_1.000	162	0							
Locus_23458_Transcript_1/1_Conf_1.000	134	0							
Locus_23459_Transcript_1/1_Conf_1.000	382	1	4.76E-04	EFO21065.1	50	47.7506	89	45	hypothetical protein LOAG_07427
Locus_2346_Transcript_1/2_Conf_1.000	4361	20	7.65E-118	NP_498678.3	42	430.639	1286	548	abnormal cell LINeage family member (lin-13)
Locus_2346_Transcript_2/2_Conf_1.000	2584	20	9.64E-86	NP_498678.3	46	323.168	703	329	abnormal cell LINeage family member (lin-13)
Locus_23460_Transcript_1/1_Conf_1.000	132	0							
Locus_23461_Transcript_1/1_Conf_1.000	389	0							

Locus_23462_Transcript_1/1_Conf_1.000	307	20	1.91E-13	NP_001006002.1	67	78.9518	67	45	galactokinase
Locus_23463_Transcript_1/1_Conf_1.000	332	0							
Locus_23464_Transcript_1/1_Conf_1.000	201	0							
Locus_23465_Transcript_1/1_Conf_1.000	300	6	8.07E-20	AAX48771.1	95	100.138	60	57	FMRF amide-like protein 7
Locus_23466_Transcript_1/1_Conf_1.000	505	0							
Locus_23467_Transcript_1/1_Conf_1.000	334	20	1.98E-10	XP_001901255.1	60	68.9366	106	64	COMM domain containing 4
Locus_23468_Transcript_1/1_Conf_1.000	320	0							
Locus_23469_Transcript_1/1_Conf_1.000	313	20	6.11E-15	XP_002633416.1	56	83.9593	125	70	Hypothetical protein CBG06181
Locus_2347_Transcript_1/1_Conf_1.000	2252	20	0	NP_502420.2	77	916.376	760	591	hypothetical protein C26H9A.2
Locus_23470_Transcript_1/1_Conf_1.000	263	1	8.19E-04	XP_002613981.1	45	46.9802	70	32	hypothetical protein BRAFLDRAFT_118457
Locus_23471_Transcript_1/1_Conf_1.000	278	7	6.53E-43	XP_002644616.1	91	170.244	87	80	Hypothetical protein CBG14575
Locus_23472_Transcript_1/1_Conf_1.000	412	20	5.51E-45	NP_495209.1	81	183.726	138	113	hypothetical protein R12C12.1
Locus_23473_Transcript_1/1_Conf_1.000	235	20	1.75E-14	XP_001524562.1	72	82.4185	77	56	26S proteasome regulatory subunit RPN6
Locus_23474_Transcript_1/1_Conf_1.000	158	0							
Locus_23475_Transcript_1/1_Conf_1.000	354	2	4.45E-10	XP_001899872.1	55	67.781	87	48	Protein-tyrosine phosphatase containing protein

Locus_23476_Transcript_1/1_Conf_1.000	190	20	1.35E-30	XP_002913719.1	100	135.961	63	63	PREDICTED: actin-related protein 2/3 complex subunit 2-like
Locus_23477_Transcript_1/1_Conf_1.000	308	20	8.29E-17	NP_500127.2	60	90.1225	102	62	hypothetical protein K08D12.2
Locus_23478_Transcript_1/1_Conf_1.000	232	3	4.63E-07	XP_002635372.1	68	57.7658	73	50	C. briggsae CBR-RPM-1 protein
Locus_23479_Transcript_1/1_Conf_1.000	136	0							
Locus_2348_Transcript_1/2_Conf_1.000	1264	20	1.03E-62	XP_002643530.1	55	245.358	400	223	C. briggsae CBR-CAB-1 protein
Locus_2348_Transcript_2/2_Conf_1.000	1188	20	2.20E-46	XP_002643530.1	86	115.161	75	65	C. briggsae CBR-CAB-1 protein
Locus_23480_Transcript_1/1_Conf_1.000	312	0							
Locus_23481_Transcript_1/1_Conf_1.000	222	0							
Locus_23482_Transcript_1/1_Conf_1.000	576	20	2.64E-94	NP_503410.3	92	348.206	176	162	hypothetical protein R12A1.3
Locus_23483_Transcript_1/1_Conf_1.000	144	0							
Locus_23484_Transcript_1/1_Conf_1.000	181	4	2.26E-17	XP_002648388.1	84	92.0485	57	48	Hypothetical protein CBG24638
Locus_23485_Transcript_1/1_Conf_1.000	284	0							
Locus_23486_Transcript_1/1_Conf_1.000	347	20	1.10E-48	XP_001897519.1	91	196.052	115	105	symbol
Locus_23487_Transcript_1/1_Conf_1.000	179	0							
Locus_23488_Transcript_1/1_Conf_1.000	135	3	5.58E-05	NP_506407.1	73	50.8322	42	31	hypothetical protein F20G2.2
Locus_23489_Transcript_1/1_Conf_1.000	147	4	1.01E-09	XP_002644860.1	86	66.6254	46	40	Hypothetical protein CBG05033
Locus_2349_Transcript_1/1_Conf_1.000	432	2	3.38E-10	XP_002646300.1	66	68.1662	78	52	Hypothetical protein CBG12007
Locus_23490_Transcript_1/1_Conf_1.000	477	10	1.37E-19	NP_494916.1	68	99.3673	106	73	SHC (Src Homology domain C-terminal) adaptor homolog family member (shc-2)
Locus_23491_Transcript_1/1_Conf_1.000	237	0							
Locus_23492_Transcript_1/1_Conf_1.000	211	0							
Locus_23493_Transcript_1/1_Conf_1.000	156	0							
Locus_23494_Transcript_1/1_Conf_1.000	394	0							

Locus_23495_Transcript_1/1_Conf_1.000	567	20	2.63E-59	NP_491658.2	74	231.876	190	141	PaTched Related family member (ptr-10)
Locus_23496_Transcript_1/1_Conf_1.000	162	20	1.03E-14	XP_002632718.1	75	83.1889	54	41	Hypothetical protein CBG18748
Locus_23497_Transcript_1/1_Conf_1.000	168	0							
Locus_23498_Transcript_1/1_Conf_1.000	286	20	3.35E-13	XP_002642338.1	70	78.1814	81	57	C. briggsae CBR-DHS-11 protein
Locus_23499_Transcript_1/2_Conf_1.000	175	0							
Locus_23499_Transcript_2/2_Conf_1.000	187	0							
Locus_235_Transcript_1/1_Conf_1.000	1048	7	4.65E-15	XP_001892092.1	72	86.6557	94	68	reticulocyte binding-like protein 2b
Locus_2350_Transcript_1/1_Conf_1.000	258	20	1.65E-20	NP_500837.1	72	102.449	85	62	hypothetical protein C39H7.1
Locus_23500_Transcript_1/1_Conf_1.000	216	0							
Locus_23501_Transcript_1/1_Conf_1.000	319	20	1.03E-30	EFO26545.1	79	136.346	105	83	kelch domain-containing protein family protein
Locus_23502_Transcript_1/1_Conf_1.000	143	1	1.56E-07	NP_001123118.1	80	59.3066	35	28	hypothetical protein C44C10.9
Locus_23503_Transcript_1/1_Conf_1.000	158	2	9.69E-05	NP_496542.1	83	50.0618	43	36	hypothetical protein ZK930.1
Locus_23504_Transcript_1/1_Conf_1.000	358	0							
Locus_23505_Transcript_1/1_Conf_1.000	665	2	1.10E-29	NP_499472.1	67	134.035	125	84	Sterol regulatory element Binding Protein family member (sbp-1)
Locus_23506_Transcript_1/1_Conf_1.000	158	20	2.54E-21	XP_002829216.1	96	105.145	52	50	PREDICTED: eukaryotic translation initiation factor 3 subunit K-like
Locus_23507_Transcript_1/1_Conf_1.000	212	0							
Locus_23508_Transcript_1/1_Conf_1.000	228	0							
Locus_23509_Transcript_1/1_Conf_1.000	145	0							
Locus_2351_Transcript_1/1_Conf_1.000	443	20	1.81E-43	EFO27551.1	76	178.718	147	112	hypothetical protein LOAG_00931
Locus_23510_Transcript_1/1_Conf_1.000	339	12	4.95E-46	NP_506408.1	85	187.193	113	97	hypothetical protein F20G2.3
Locus_23511_Transcript_1/1_Conf_1.000	186	0							
Locus_23512_Transcript_1/1_Conf_1.000	182	0							

Locus_23513_Transcript_1/1_Conf_1.000	157	6	2.46E-08	NP_001021110.1	70	62.003	51	36	CAlSYntenin/Alcadein homolog family member (casy-1)
Locus_23514_Transcript_1/1_Conf_1.000	168	20	5.41E-16	NP_493642.1	92	87.4261	56	52	hypothetical protein F23F1.6
Locus_23515_Transcript_1/1_Conf_1.000	381	20	2.86E-25	XP_002645261.1	80	118.242	86	69	Hypothetical protein CBG00142
Locus_23516_Transcript_1/1_Conf_1.000	163	0							
Locus_23517_Transcript_1/1_Conf_1.000	195	0							
Locus_23518_Transcript_1/1_Conf_1.000	197	0							
Locus_23519_Transcript_1/1_Conf_1.000	163	0							
Locus_2352_Transcript_1/1_Conf_1.000	554	0							
Locus_23520_Transcript_1/1_Conf_1.000	144	3	7.26E-08	EFO24290.1	73	60.4622	46	34	hypothetical protein LOAG_04198
Locus_23521_Transcript_1/1_Conf_1.000	178	0							
Locus_23522_Transcript_1/1_Conf_1.000	194	2	9.37E-08	XP_002630446.1	61	60.077	60	37	Hypothetical protein CBG11179
Locus_23523_Transcript_1/1_Conf_1.000	205	20	1.63E-20	XP_002633097.1	79	102.449	68	54	C. briggsae CBR-RPC-1 protein
Locus_23524_Transcript_1/1_Conf_1.000	164	0							
Locus_23525_Transcript_1/1_Conf_1.000	318	3	3.22E-08	EFO16242.1	53	61.6178	83	44	hypothetical protein LOAG_12266
Locus_23526_Transcript_1/1_Conf_1.000	180	2	7.53E-05	XP_002648586.1	52	50.447	91	48	Hypothetical protein CBG24916
Locus_23527_Transcript_1/1_Conf_1.000	179	0							
Locus_23528_Transcript_1/1_Conf_1.000	174	0							
Locus_23529_Transcript_1/1_Conf_1.000	141	0							
Locus_2353_Transcript_1/3_Conf_0.600	721	20	8.76E-42	NP_001041048.1	59	174.481	204	122	EPS (human endocytosis) related family member (eps-8)
Locus_2353_Transcript_2/3_Conf_0.400	751	20	7.62E-31	NP_502803.3	53	138.272	213	113	EPS (human endocytosis) related family member (eps-8)
Locus_2353_Transcript_3/3_Conf_0.600	698	20	8.23E-42	NP_001041048.1	59	174.481	204	122	EPS (human endocytosis) related family member (eps-8)
Locus_23530_Transcript_1/1_Conf_1.000	277	20	2.10E-28	EFO24787.1	89	128.642	83	74	ATP-dependent Clp protease

Locus_23531_Transcript_1/1_Conf_1.000	313	20	4.05E-51	XP_002822113.1	100	204.142	104	104	PREDICTED: eukaryotic translation initiation factor 3 subunit F-like isoform 3
Locus_23532_Transcript_1/1_Conf_1.000	128	0							
Locus_23533_Transcript_1/1_Conf_1.000	255	20	1.27E-20	XP_002633417.1	84	102.834	76	64	C. briggsae CBR-TRPA-1 protein
Locus_23534_Transcript_1/1_Conf_1.000	208	20	7.75E-31	NP_001023038.1	98	136.732	69	68	EXCretory canal abnormal family member (exc-5)
Locus_23535_Transcript_1/1_Conf_1.000	279	20	4.49E-47	XP_002803216.1	100	190.66	93	93	PREDICTED: amyloid beta A4 protein-like, partial
Locus_23536_Transcript_1/1_Conf_1.000	155	0							
Locus_23537_Transcript_1/1_Conf_1.000	1347	20	4.79E-162	XP_002641814.1	80	575.474	437	351	C. briggsae CBR-BYN-1 protein

Locus_23538_Transcript_1/1_Conf_1.000	130	20	4.89E-17	XP_002931287.1	100	90.8929	43	43	PREDICTED: filamin-A-like, partial
Locus_23539_Transcript_1/1_Conf_1.000	187								
Locus_2354_Transcript_1/2_Conf_1.000	1575	20	1.62E-119	XP_001898426.1	56	434.491	575	325	Bromodomain containing protein
Locus_2354_Transcript_2/2_Conf_1.000	499	20	5.14E-43	NP_509770.2	76	177.178	135	103	hypothetical protein F57C7.1
Locus_23540_Transcript_1/1_Conf_1.000	174	1	9.51E-05	NP_499670.1	59	50.0618	57	34	hypothetical protein Y37D8A.4
Locus_23541_Transcript_1/1_Conf_1.000	213	0							
Locus_23542_Transcript_1/1_Conf_1.000	371	0							
Locus_23543_Transcript_1/1_Conf_1.000	169	20	1.92E-21	NP_001122771.1	88	105.531	53	47	hypothetical protein F13H10.4
Locus_23544_Transcript_1/1_Conf_1.000	261	0							
Locus_23545_Transcript_1/1_Conf_1.000	744	4	3.36E-31	EFO25848.1	69	139.428	175	122	zinc finger protein
Locus_23546_Transcript_1/1_Conf_1.000	149	0							
Locus_23547_Transcript_1/1_Conf_1.000	324	0							
Locus_23548_Transcript_1/1_Conf_1.000	228	0							
Locus_23549_Transcript_1/1_Conf_1.000	333	0							

Locus_2355_Transcript_1/1_Conf_1.000	348	20	6.83E-51	AAZ42325.1	98	203.371	103	101	translation elongation factor 1-alpha
Locus_23550_Transcript_1/1_Conf_1.000	810	20	9.95E-35	NP_501226.2	67	151.369	157	106	hypothetical protein F49E8.1
Locus_23551_Transcript_1/1_Conf_1.000	366	20	1.78E-11	XP_001899513.1	67	72.4034	68	46	AIDA-1b
Locus_23552_Transcript_1/1_Conf_1.000	214	1	2.76E-04	XP_002634850.1	65	48.521	60	39	Hypothetical protein CBG13967
Locus_23553_Transcript_1/1_Conf_1.000	321	20	1.13E-37	NP_492438.1	87	159.458	106	93	RADiation sensitivity abnormal/yeast RAD-related family member (rad-54)
Locus_23554_Transcript_1/1_Conf_1.000	131	0							
Locus_23555_Transcript_1/1_Conf_1.000	146	0							
Locus_23556_Transcript_1/1_Conf_1.000	206	0							
Locus_23557_Transcript_1/1_Conf_1.000	358	7	1.05E-11	NP_001021268.1	71	73.1738	115	82	UNCoordinated family member (unc-44)
Locus_23558_Transcript_1/1_Conf_1.000	181	20	9.16E-19	NP_491003.2	91	96.6709	60	55	Amino Acid Transporter family member (aat-5)
Locus_23559_Transcript_1/1_Conf_1.000	249	20	2.65E-23	NP_500943.1	86	111.694	65	56	hypothetical protein F58F9.7
Locus_2356_Transcript_1/3_Conf_0.714	1423	20	4.21E-47	NP_001018536.1	44	193.741	421	188	drebrin-like protein
Locus_2356_Transcript_2/3_Conf_0.714	1423	20	7.17E-47	NP_001018536.1	44	192.971	424	190	drebrin-like protein

Locus_2356_Transcript_3/3_Conf_0.714	1423	20	4.21E-47	NP_001018536.1	44	193.741	421	188	drebrin-like protein
Locus_23560_Transcript_1/1_Conf_1.000	323	4	3.50E-55	XP_002629930.1	96	217.624	105	101	Hypothetical protein CBG21978
Locus_23561_Transcript_1/1_Conf_1.000	260	4	3.94E-06	XP_002641855.1	62	54.6842	66	41	Hypothetical protein CBG16529
Locus_23562_Transcript_1/1_Conf_1.000	147	3	4.69E-07	XP_002639522.1	76	57.7658	43	33	Hypothetical protein CBG04128
Locus_23563_Transcript_1/1_Conf_1.000	150	0							
Locus_23564_Transcript_1/1_Conf_1.000	243	2	8.32E-09	XP_002634329.1	79	63.5438	48	38	C. briggsae CBR-TAG-321 protein
Locus_23565_Transcript_1/1_Conf_1.000	202	0							
Locus_23566_Transcript_1/1_Conf_1.000	174	20	9.77E-26	XP_001115060.2	100	119.783	57	57	PREDICTED: heat shock 70 kDa protein 1A/1B, partial
Locus_23567_Transcript_1/1_Conf_1.000	235	9	7.05E-40	ADN00778.1	97	166.777	77	75	LON-1 protein
Locus_23568_Transcript_1/1_Conf_1.000	412	20	1.31E-38	NP_496802.2	73	162.54	133	98	BTAF (TBP-associated factor) homolog family member (btf-1)
Locus_23569_Transcript_1/1_Conf_1.000	197	0							
Locus_2357_Transcript_1/1_Conf_1.000	774	20	2.10E-63	XP_001895436.1	66	246.514	268	177	Micro-fibrillar-associated protein 1 C-terminus containing protein
Locus_23570_Transcript_1/1_Conf_1.000	157	2	1.65E-12	CBL43426.1	84	75.8702	52	44	C. elegans protein C54E10.2b, confirmed by transcript evidence
Locus_23571_Transcript_1/1_Conf_1.000	136	20	7.52E-10	XP_002171431.1	86	67.0106	45	39	vacuolar ATP synthase subunit B
Locus_23572_Transcript_1/1_Conf_1.000	180	20	8.00E-23	EFO22245.1	96	110.153	59	57	ubiquitin-conjugating enzyme family protein

Locus_23573_Transcript_1/1_Conf_1.000	241	3	1.20E-23	NP_001022992.1	80	112.849	80	64	CYtoKinesis defect family member (cyk-3)
Locus_23574_Transcript_1/1_Conf_1.000	156	0							
Locus_23575_Transcript_1/1_Conf_1.000	190	0							
Locus_23576_Transcript_1/1_Conf_1.000	166	0							
Locus_23577_Transcript_1/1_Conf_1.000	212	0							
Locus_23578_Transcript_1/1_Conf_1.000	229	0							
Locus_23579_Transcript_1/1_Conf_1.000	129	0							
Locus_2358_Transcript_1/1_Conf_1.000	1379	5	1.54E-38	NP_872024.1	63	165.236	211	134	hypothetical protein F18C5.10
Locus_23580_Transcript_1/1_Conf_1.000	439	20	2.21E-62	XP_002752629.1	100	241.506	140	140	PREDICTED: CD63 antigen-like isoform 1
Locus_23581_Transcript_1/1_Conf_1.000	503	0							
Locus_23582_Transcript_1/1_Conf_1.000	158	0							
Locus_23583_Transcript_1/1_Conf_1.000	170	13	1.42E-24	BAG65491.1	100	115.931	56	56	unnamed protein product
Locus_23584_Transcript_1/1_Conf_1.000	334	20	3.47E-39	NP_491529.2	89	164.466	101	90	hypothetical protein Y110A7A.6
Locus_23585_Transcript_1/1_Conf_1.000	164	0							
Locus_23586_Transcript_1/1_Conf_1.000	204	20	4.28E-21	EFO18824.1	83	104.375	66	55	hypothetical protein LOAG_09672
Locus_23587_Transcript_1/1_Conf_1.000	210	20	3.14E-24	EFO21237.1	87	114.775	66	58	hypothetical protein LOAG_07254
Locus_23588_Transcript_1/1_Conf_1.000	196	0							
Locus_23589_Transcript_1/1_Conf_1.000	233	0							
Locus_2359_Transcript_1/2_Conf_1.000	1640	20	1.60E-125	NP_741885.1	77	454.521	366	284	NUCleoBindin homolog family member (nucb-1)

Locus_2359_Transcript_2/2_Conf_1.000	1601	20	5.69E-120	XP_002644192.1	76	436.032	375	285	C. briggsae CBR-NUCB-1 protein
Locus_23590_Transcript_1/1_Conf_1.000	662	6	1.41E-37	XP_002638375.1	67	160.229	190	128	Hypothetical protein CBG18580
Locus_23591_Transcript_1/1_Conf_1.000	318	0							
Locus_23592_Transcript_1/1_Conf_1.000	345	0							
Locus_23593_Transcript_1/1_Conf_1.000	141	0							
Locus_23594_Transcript_1/1_Conf_1.000	329	0							
Locus_23595_Transcript_1/1_Conf_1.000	129	20	4.89E-17	XP_002831617.1	100	90.8929	43	43	PREDICTED: serine/threonine-protein kinase A-Raf-like
Locus_23596_Transcript_1/1_Conf_1.000	216	0							
Locus_23597_Transcript_1/1_Conf_1.000	237	0							
Locus_23598_Transcript_1/1_Conf_1.000	296	0							
Locus_23599_Transcript_1/1_Conf_1.000	159	20	1.44E-16	XP_002639507.1	84	89.3521	52	44	C. briggsae CBR-LIN-17 protein
Locus_236_Transcript_1/4_Conf_0.250	844	20	2.94E-16	EFO27939.1	71	90.1225	85	61	hypothetical protein LOAG_00532
Locus_236_Transcript_2/4_Conf_0.500	976	20	3.76E-16	EFO27939.1	71	90.1225	85	61	hypothetical protein LOAG_00532
Locus_236_Transcript_3/4_Conf_0.500	1137	20	4.80E-16	EFO27939.1	71	90.1225	85	61	hypothetical protein LOAG_00532
Locus_236_Transcript_4/4_Conf_0.375	1156	20	5.39E-15	EFO27939.1	75	86.6557	74	56	hypothetical protein LOAG_00532
Locus_2360_Transcript_1/4_Conf_0.444	1248	20	1.59E-156	NP_503064.2	78	556.984	409	323	Amino acid Transporter GlycoProtein subunit family member (atgp-1)
Locus_2360_Transcript_2/4_Conf_0.667	1905	20	0	NP_503064.2	74	756.518	617	461	Amino acid Transporter GlycoProtein subunit family member (atgp-1)
Locus_2360_Transcript_3/4_Conf_0.667	1905	20	0	NP_503064.2	74	756.133	617	461	Amino acid Transporter GlycoProtein subunit family member (atgp-1)
Locus_2360_Transcript_4/4_Conf_0.667	1905	20	0	NP_503064.2	74	756.133	617	461	Amino acid Transporter GlycoProtein subunit family member (atgp-1)
Locus_23600_Transcript_1/1_Conf_1.000	150	20	1.23E-15	EFO17879.1	87	86.2705	48	42	hypothetical protein LOAG_10616
Locus_23601_Transcript_1/1_Conf_1.000	189	0							

Locus_23602_Transcript_1/1_Conf_1.000	225	20	1.39E-27	XP_002634807.1	85	125.946	74	63	Hypothetical protein CBG13912
Locus_23603_Transcript_1/1_Conf_1.000	155	0							
Locus_23604_Transcript_1/1_Conf_1.000	241	0							
Locus_23605_Transcript_1/1_Conf_1.000	169	0							
Locus_23606_Transcript_1/1_Conf_1.000	159	0							
Locus_23607_Transcript_1/1_Conf_1.000	187	20	2.17E-12	XP_002648059.1	78	75.485	60	47	Hypothetical protein CBG24048
Locus_23608_Transcript_1/1_Conf_1.000	199	20	3.19E-16	EDL39643.1	100	88.1965	55	55	small nuclear ribonucleoprotein E, isoform CRA_a
Locus_23609_Transcript_1/1_Conf_1.000	184	0							
Locus_2361_Transcript_1/1_Conf_1.000	1589	20	1.49E-96	XP_002642323.1	60	358.221	526	317	C. briggsae CBR-RIB-2 protein
Locus_23610_Transcript_1/1_Conf_1.000	321	0							
Locus_23611_Transcript_1/1_Conf_1.000	275	20	7.03E-24	XP_002647685.1	76	113.62	91	70	Hypothetical protein CBG17873
Locus_23612_Transcript_1/1_Conf_1.000	170	20	1.05E-19	CAB57891.2	91	99.7525	56	51	C. elegans protein Y47D3A.11, partially confirmed by transcript evidence
Locus_23613_Transcript_1/1_Conf_1.000	254	0							
Locus_23614_Transcript_1/1_Conf_1.000	230	0							
Locus_23615_Transcript_1/1_Conf_1.000	128	0							
Locus_23616_Transcript_1/1_Conf_1.000	155	0							
Locus_23617_Transcript_1/1_Conf_1.000	131	2	1.09E-16	NP_001023062.1	100	89.7373	43	43	Ligand-Gated ion Channel family member (lgc-43)
Locus_23618_Transcript_1/1_Conf_1.000	248	12	7.02E-08	EFO19578.1	72	60.4622	72	52	hypothetical protein LOAG_08912
Locus_23619_Transcript_1/1_Conf_1.000	159	0							
Locus_2362_Transcript_1/1_Conf_1.000	618	20	4.68E-29	NP_501149.1	57	131.724	198	113	hypothetical protein D2024.2
Locus_23620_Transcript_1/1_Conf_1.000	197	0							

Locus_23621_Transcript_1/1_Conf_1.000	233	20	1.64E-12	NP_503528.2	82	75.8702	64	53	SeRPin family member (srp-3)
Locus_23622_Transcript_1/1_Conf_1.000	174	0							
Locus_23623_Transcript_1/1_Conf_1.000	289	13	3.44E-18	NP_001041303.1	65	94.7449	93	61	Trehalose 6-Phosphate Synthase family member (tps-1)
Locus_23624_Transcript_1/1_Conf_1.000	131	1	4.75E-04	XP_001121351.1	79	47.7506	39	31	PREDICTED: similar to SET domain and mariner transposase fusion
Locus_23625_Transcript_1/1_Conf_1.000	761	20	3.10E-72	NP_500284.2	81	275.789	213	174	Enhancer of EfL-1 mutant phenotype family member (eel-1)
Locus_23626_Transcript_1/2_Conf_1.000	390	3	3.84E-06	XP_002642918.1	57	54.6842	107	61	Hypothetical protein CBG15194
Locus_23626_Transcript_2/2_Conf_1.000	417	6	7.20E-08	NP_498462.3	52	60.4622	112	59	hypothetical protein C13B9.2
Locus_23627_Transcript_1/1_Conf_1.000	179	0							
Locus_23628_Transcript_1/1_Conf_1.000	454	0							
Locus_23629_Transcript_1/1_Conf_1.000	143	0							
Locus_2363_Transcript_1/1_Conf_1.000	1280	20	2.94E-81	EFO22000.1	60	306.99	392	239	hypothetical protein LOAG_06484
Locus_23630_Transcript_1/1_Conf_1.000	160	0							
Locus_23631_Transcript_1/1_Conf_1.000	295	0							
Locus_23632_Transcript_1/1_Conf_1.000	147	7	2.49E-08	AAN61521.1	82	62.003	47	39	301KDa_2 protein
Locus_23633_Transcript_1/1_Conf_1.000	178	0							
Locus_23634_Transcript_1/2_Conf_1.000	668	20	2.72E-44	XP_002643134.1	67	182.57	205	139	Hypothetical protein CBG15311

Locus_23634_Transcript_2/2_Conf_1.000	668	20	2.72E-44	XP_002643134.1	67	182.57	205	139	Hypothetical protein CBG15311
Locus_23635_Transcript_1/1_Conf_1.000	355	20	2.51E-21	CAB40412.1	73	105.145	93	68	hexokinase
Locus_23636_Transcript_1/1_Conf_1.000	144	3	4.41E-05	NP_501448.1	68	51.2174	45	31	hypothetical protein C28C12.4
Locus_23637_Transcript_1/1_Conf_1.000	147	0							
Locus_23638_Transcript_1/1_Conf_1.000	211	12	5.38E-16	XP_002639999.1	82	87.4261	68	56	Hypothetical protein CBG10829
Locus_23639_Transcript_1/1_Conf_1.000	140	20	1.08E-08	XP_002926200.1	100	63.1586	46	46	PREDICTED: l-lactate dehydrogenase A chain-like
Locus_2364_Transcript_1/1_Conf_1.000	270	0							
Locus_23640_Transcript_1/1_Conf_1.000	333	0							
Locus_23641_Transcript_1/1_Conf_1.000	206	0							
Locus_23642_Transcript_1/1_Conf_1.000	549	20	3.61E-55	NP_491390.2	74	218.009	181	135	hypothetical protein D1007.15

Locus_23643_Transcript_1/1_Conf_1.000	445	20	5.60E-45	XP_002634229.1	77	183.726	146	113	C. briggsae CBR-UNC-26 protein
Locus_23644_Transcript_1/1_Conf_1.000	148	0							
Locus_23645_Transcript_1/1_Conf_1.000	432	2	2.77E-12	XP_002634200.1	53	75.0998	135	72	C. briggsae CBR-NOL-9 protein
Locus_23646_Transcript_1/1_Conf_1.000	134	20	4.13E-16	NP_506269.1	100	87.8113	44	44	EATing: abnormal pharyngeal pumping family member (eat-6)
Locus_23647_Transcript_1/1_Conf_1.000	265	0							
Locus_23648_Transcript_1/1_Conf_1.000	208	20	3.87E-14	NP_504523.1	76	81.2629	67	51	LEThal family member (let-418)
Locus_23649_Transcript_1/1_Conf_1.000	207	0							

Locus_2365_Transcript_1/1_Conf_1.000	1466	20	4.23E-167	CAJ43810.1	74	592.423	483	361	astacin-like metalloprotease
Locus_23650_Transcript_1/1_Conf_1.000	165	0							
Locus_23651_Transcript_1/1_Conf_1.000	335	0							
Locus_23652_Transcript_1/1_Conf_1.000	219	20	3.58E-15	CAB01717.3	84	84.7297	51	43	C. elegans protein C07A4.1, partially confirmed by transcript evidence
Locus_23653_Transcript_1/1_Conf_1.000	274	0							
Locus_23654_Transcript_1/1_Conf_1.000	202	0							
Locus_23655_Transcript_1/1_Conf_1.000	138	13	2.18E-17	XP_002630534.1	97	92.0485	45	44	Hypothetical protein CBG12974
Locus_23656_Transcript_1/1_Conf_1.000	340	20	8.83E-11	XP_001902350.1	56	70.0922	103	58	Myosin XVIIIA
Locus_23657_Transcript_1/1_Conf_1.000	314	20	2.81E-52	XP_002346307.1	99	207.994	104	103	PREDICTED: similar to complement component 4B (Childo blood group), partial
Locus_23658_Transcript_1/1_Conf_1.000	371	1	4.83E-04	XP_002641128.1	46	47.7506	130	60	Hypothetical protein CBG08978
Locus_23659_Transcript_1/1_Conf_1.000	186	20	1.83E-19	NP_501991.2	83	98.9821	61	51	hypothetical protein T25B9.1
Locus_2366_Transcript_1/2_Conf_1.000	2579	20	0	XP_001901889.1	68	675.241	712	487	Kelch motif family protein
Locus_2366_Transcript_2/2_Conf_1.000	2573	20	0	XP_001901889.1	68	676.011	712	488	Kelch motif family protein
Locus_23660_Transcript_1/1_Conf_1.000	219	0							
Locus_23661_Transcript_1/1_Conf_1.000	198	1	4.33E-05	NP_497340.2	55	51.2174	65	36	CaDHerin family member (cdh-12)
Locus_23662_Transcript_1/1_Conf_1.000	147	0							
Locus_23663_Transcript_1/1_Conf_1.000	244	0							
Locus_23664_Transcript_1/1_Conf_1.000	359	0							

Locus_23665_Transcript_1/1_Conf_1.000	390	20	2.25E-06	XP_418071.2	48	55.4546	117	57	PREDICTED: similar to mannose receptor, C type 2
Locus_23666_Transcript_1/1_Conf_1.000	157	0							
Locus_23667_Transcript_1/1_Conf_1.000	240	1	8.09E-04	NP_498765.1	54	46.9802	79	43	hypothetical protein K06H7.3
Locus_23668_Transcript_1/1_Conf_1.000	129	0							
Locus_23669_Transcript_1/1_Conf_1.000	287	0							
Locus_2367_Transcript_1/3_Conf_0.375	1482	20	2.08E-145	Q24702.1	77	520.39	417	325	DVA-1 polyprotein
Locus_2367_Transcript_3/3_Conf_0.375	226	0							
Locus_23670_Transcript_1/1_Conf_1.000	140	1	1.01E-06	NP_502390.2	73	56.6102	46	34	High Incidence of Males (increased X chromosome loss) family member (him-6)
Locus_23671_Transcript_1/1_Conf_1.000	206	20	6.18E-20	BAG63346.1	100	100.523	48	48	unnamed protein product
Locus_23672_Transcript_1/1_Conf_1.000	148	4	8.85E-06	XP_001901521.1	70	53.5286	47	33	Protein kinase domain containing protein
Locus_23673_Transcript_1/1_Conf_1.000	166	20	9.23E-24	BAG63075.1	100	113.235	55	55	unnamed protein product
Locus_23674_Transcript_1/1_Conf_1.000	448	20	1.74E-30	NP_502434.1	69	135.576	147	102	hypothetical protein C36H8.1

Locus_23675_Transcript_1/1_Conf_1.000	287	20	7.68E-26	XP_002633316.1	74	120.168	99	74	C. briggsae CBR-GTL-2 protein
Locus_23676_Transcript_1/1_Conf_1.000	630	20	4.59E-96	NP_492775.2	87	354.369	213	187	LAMinin related. See also lmb- family member (lam-3)
Locus_23677_Transcript_1/1_Conf_1.000	138	1	6.57E-06	XP_002635510.1	75	53.9138	44	33	Hypothetical protein CBG08814
Locus_23678_Transcript_1/1_Conf_1.000	137	0							
Locus_23679_Transcript_1/1_Conf_1.000	278	0							
Locus_2368_Transcript_1/1_Conf_1.000	342	20	5.67E-29	EEZ99728.1	77	130.568	89	69	hypothetical protein TcasGA2_TC002495
Locus_23680_Transcript_1/1_Conf_1.000	351	0							
Locus_23681_Transcript_1/1_Conf_1.000	175	0							
Locus_23682_Transcript_1/1_Conf_1.000	332	20	2.18E-33	NP_001022190.1	85	145.206	95	81	hypothetical protein F53A10.2
Locus_23683_Transcript_1/1_Conf_1.000	141	0							
Locus_23684_Transcript_1/1_Conf_1.000	295	0							
Locus_23685_Transcript_1/1_Conf_1.000	244	20	1.56E-31	XP_002719808.1	100	139.043	64	64	PREDICTED: actin related protein 2/3 complex subunit 3-like
Locus_23686_Transcript_1/1_Conf_1.000	493	20	1.16E-42	XP_002642732.1	75	176.022	132	100	C. briggsae CBR-KIN-18 protein
Locus_23687_Transcript_1/1_Conf_1.000	247	20	1.51E-18	XP_001898877.1	79	95.9005	81	64	oxidoreductase, short chain dehydrogenase/reductase family protein
Locus_23688_Transcript_1/1_Conf_1.000	264	0							
Locus_23689_Transcript_1/1_Conf_1.000	220	0							
Locus_2369_Transcript_1/2_Conf_1.000	1648	5	2.60E-68	XP_002638678.1	56	179.874	274	156	Hypothetical protein CBG11870
Locus_2369_Transcript_2/2_Conf_1.000	1598	5	8.30E-71	NP_492101.1	57	272.707	479	274	hypothetical protein T28F4.4
Locus_23690_Transcript_1/1_Conf_1.000	177	0							
Locus_23691_Transcript_1/1_Conf_1.000	242	0							
Locus_23692_Transcript_1/1_Conf_1.000	203	0							
Locus_23693_Transcript_1/1_Conf_1.000	389	0							

Locus_23694_Transcript_1/1_Conf_1.000	215	20	5.33E-32	XP_002807990.1	100	140.584	68	68	PREDICTED: LOW QUALITY PROTEIN: ATP-dependent DNA helicase 2 subunit 1-like
Locus_23695_Transcript_1/1_Conf_1.000	168	0							
Locus_23696_Transcript_1/1_Conf_1.000	194	2	1.15E-05	XP_002644087.1	74	53.1434	39	29	Hypothetical protein CBG17560
Locus_23697_Transcript_1/1_Conf_1.000	162	20	1.75E-22	BAG59422.1	100	108.997	53	53	unnamed protein product
Locus_23698_Transcript_1/1_Conf_1.000	276	0							
Locus_23699_Transcript_1/1_Conf_1.000	197	20	1.21E-23	NP_506269.1	89	112.849	65	58	EATing: abnormal pharyngeal pumping family member (eat-6)

Locus_237_Transcript_1/1_Conf_1.000	1085	10	6.02E-05	ZP_04598122.1	45	53.1434	174	80	immunoglobulin A1 protease
Locus_2370_Transcript_1/1_Conf_1.000	229	7	3.22E-08	EFO22616.1	72	61.6178	59	43	TK/ABL protein kinase
Locus_23700_Transcript_1/1_Conf_1.000	166	20	7.57E-18	NP_001040798.1	87	93.5893	55	48	PhosphoDiEsterase family member (pde-4)
Locus_23701_Transcript_1/1_Conf_1.000	198	5	2.54E-05	A8WRJ2.2	61	51.9878	71	44	GTPase-activating protein rrc-1
Locus_23702_Transcript_1/1_Conf_1.000	304	20	1.78E-51	XP_002928507.1	100	205.297	101	101	PREDICTED: elongation factor 2-like
Locus_23703_Transcript_1/1_Conf_1.000	291	20	1.89E-08	XP_001641575.1	58	62.3882	70	41	predicted protein
Locus_23704_Transcript_1/1_Conf_1.000	203	20	1.25E-28	NP_497796.1	95	129.413	67	64	hypothetical protein F37A8.5
Locus_23705_Transcript_1/1_Conf_1.000	246	0							
Locus_23706_Transcript_1/1_Conf_1.000	215	9	3.04E-11	XP_002630557.1	71	71.633	71	51	Hypothetical protein CBG13002
Locus_23707_Transcript_1/1_Conf_1.000	137	0							
Locus_23708_Transcript_1/1_Conf_1.000	174	5	1.91E-13	ABU49430.1	82	78.9518	57	47	PRO-2

Locus_23709_Transcript_1/1_Conf_1.000	292	6	7.64E-18	ADJ37280.1	70	93.5893	99	70	Hypothetical protein F26G1.2a
Locus_2371_Transcript_1/1_Conf_1.000	3023	20	0	XP_002636622.1	79	1228.77	1002	794	C. briggsae CBR-SMA-1 protein
Locus_23710_Transcript_1/1_Conf_1.000	138	20	5.36E-16	ACT68329.1	86	87.4261	45	39	cysteine proteinase
Locus_23711_Transcript_1/1_Conf_1.000	174	0							
Locus_23712_Transcript_1/1_Conf_1.000	229	0							
Locus_23713_Transcript_1/1_Conf_1.000	880	20	2.13E-105	NP_001022916.1	82	386.341	292	242	STIM (mammalian STromal Interaction Molecule) homolog family member (stim-1)
Locus_23714_Transcript_1/1_Conf_1.000	184	0							
Locus_23715_Transcript_1/1_Conf_1.000	144	5	2.76E-07	EFO26737.1	85	58.5362	48	41	hypothetical protein LOAG_01753
Locus_23716_Transcript_1/1_Conf_1.000	161	3	4.34E-05	XP_002647546.1	71	51.2174	45	32	C. briggsae CBR-PME-5 protein
Locus_23717_Transcript_1/1_Conf_1.000	357	20	8.04E-28	XP_002637952.1	76	126.716	117	90	Hypothetical protein CBG04769
Locus_23718_Transcript_1/1_Conf_1.000	197	1	8.19E-04	XP_001898052.1	62	46.9802	54	34	Importin-beta N-terminal domain containing protein
Locus_23719_Transcript_1/1_Conf_1.000	142	20	2.84E-09	EFO25060.1	82	65.0846	45	37	UDP-glucoronosyl and UDP-glucosyl transferase
Locus_2372_Transcript_1/1_Conf_1.000	253	0							
Locus_23720_Transcript_1/1_Conf_1.000	308	20	1.27E-33	XP_002634145.1	85	145.976	101	86	Hypothetical protein CBG01706
Locus_23721_Transcript_1/1_Conf_1.000	128	2	7.85E-07	XP_002634289.1	87	56.9954	41	36	Hypothetical protein CBG17623
Locus_23722_Transcript_1/1_Conf_1.000	150	20	1.96E-13	AAZ82849.1	87	78.9518	49	43	Cam kinase kinase protein 1, isoform b

Locus_23723_Transcript_1/1_Conf_1.000	266	13	7.33E-29	XP_002631169.1	92	130.183	88	81	Hypothetical protein CBG02955
Locus_23724_Transcript_1/1_Conf_1.000	211	5	1.33E-06	XP_001946729.1	59	56.225	61	36	PREDICTED: similar to DNA ligase IV
Locus_23725_Transcript_1/1_Conf_1.000	244	0							
Locus_23726_Transcript_1/1_Conf_1.000	208	0							
Locus_23727_Transcript_1/1_Conf_1.000	439	0							
Locus_23728_Transcript_1/1_Conf_1.000	213	6	8.85E-11	NP_001021303.1	76	70.0922	67	51	Nuclear Hormone Receptor family member (nhr-105)
Locus_23729_Transcript_1/1_Conf_1.000	270	20	2.33E-51	XP_540489.1	100	204.912	85	85	PREDICTED: similar to anaphase promoting complex subunit 11 homolog
Locus_2373_Transcript_1/1_Conf_1.000	2283	20	2.07E-177	AAD45354.1	91	627.476	348	319	AF159950_1GSK-3

Locus_23730_Transcript_1/1_Conf_1.000	302	20	1.46E-37	XP_002639432.1	81	159.073	100	81	C. briggsae CBR-TYR-4 protein
Locus_23731_Transcript_1/1_Conf_1.000	151	0							
Locus_23732_Transcript_1/1_Conf_1.000	146	0							
Locus_23733_Transcript_1/1_Conf_1.000	189	20	6.27E-28	XP_002914618.1	100	127.102	62	62	PREDICTED: LOW QUALITY PROTEIN: eukaryotic translation initiation factor 3 subunit L-like
Locus_23734_Transcript_1/1_Conf_1.000	148	0							
Locus_23735_Transcript_1/1_Conf_1.000	159	20	3.92E-06	XP_002735062.1	60	54.6842	48	29	PREDICTED: Alk-like, partial
Locus_23736_Transcript_1/1_Conf_1.000	239	20	2.21E-09	XP_002639475.1	64	65.4698	75	48	Hypothetical protein CBG04073
Locus_23737_Transcript_1/1_Conf_1.000	645	20	2.15E-43	XP_002629985.1	79	179.489	137	109	Hypothetical protein CBG13347
Locus_23738_Transcript_1/1_Conf_1.000	267	0							
Locus_23739_Transcript_1/1_Conf_1.000	200	0							
Locus_2374_Transcript_1/3_Conf_0.571	477	0							
Locus_2374_Transcript_2/3_Conf_0.571	1546	20	1.18E-82		63	311.997	329	208	hypothetical protein Y105C5B.t - Caenorhabditis elegans
Locus_2374_Transcript_3/3_Conf_0.714	1461	20	1.10E-82		63	311.997	329	208	hypothetical protein Y105C5B.t - Caenorhabditis elegans
Locus_23740_Transcript_1/1_Conf_1.000	229	0							
Locus_23741_Transcript_1/1_Conf_1.000	128	0							
Locus_23742_Transcript_1/1_Conf_1.000	214	20	1.15E-34	ACJ65168.1	100	149.443	71	71	Uncoordinated protein 68, isoform b, partially confirmed by transcript evidence
Locus_23743_Transcript_1/1_Conf_1.000	130	0							

Locus_23744_Transcript_1/1_Conf_1.000	254	20	9.37E-40	EFO24654.1	96	166.392	84	81	RNA polymerase Rpb1
Locus_23745_Transcript_1/1_Conf_1.000	138	20	1.51E-18	XP_002924501.1	100	95.9005	45	45	PREDICTED: eukaryotic translation initiation factor 5A-1-like
Locus_23746_Transcript_1/1_Conf_1.000	615	20	4.23E-99	NP_001122963.1	94	364.385	204	193	hypothetical protein F58E6.1
Locus_23747_Transcript_1/1_Conf_1.000	287	5	5.33E-19	NP_001122928.1	74	97.4413	79	59	hypothetical protein F23H12.3
Locus_23748_Transcript_1/1_Conf_1.000	228	20	2.70E-31	XP_002745237.1	100	138.272	68	68	PREDICTED: 40S ribosomal protein S13-like

Locus_23749_Transcript_1/1_Conf_1.000	243	0							
Locus_2375_Transcript_1/1_Conf_1.000	2868	20	0	XP_001899340.1	63	783.867	990	624	c-MYC promoter-binding protein IRLB
Locus_23750_Transcript_1/1_Conf_1.000	132	2	1.13E-05	EFO21756.1	70	53.1434	44	31	PAN domain-containing protein
Locus_23751_Transcript_1/1_Conf_1.000	182	18	2.66E-18	XP_002642115.1	82	95.1301	57	47	C. briggsae CBR-NDG-4 protein
Locus_23752_Transcript_1/1_Conf_1.000	305	20	9.16E-32	XP_002644203.1	81	139.813	101	82	Hypothetical protein CBG17194
Locus_23753_Transcript_1/1_Conf_1.000	135	20	1.05E-11	NP_493662.1	90	73.1738	44	40	hypothetical protein C50D2.2
Locus_23754_Transcript_1/1_Conf_1.000	138	0							
Locus_23755_Transcript_1/1_Conf_1.000	199	20	9.00E-11	NP_503517.1	66	70.0922	65	43	hypothetical protein T10B5.7
Locus_23756_Transcript_1/1_Conf_1.000	161	0							
Locus_23757_Transcript_1/1_Conf_1.000	324	20	1.68E-41	NP_001122686.1	100	172.17	103	103	UNCoordinated family member (unc-103)
Locus_23758_Transcript_1/1_Conf_1.000	309	0							
Locus_23759_Transcript_1/1_Conf_1.000	179	2	5.94E-07	NP_508708.2	71	57.3806	45	32	hypothetical protein ZK470.1
Locus_2376_Transcript_1/3_Conf_0.600	922	20	1.26E-10	NP_495957.1	77	71.633	57	44	vertebrate transcription factor DP-Like family member (dpl-1)
Locus_2376_Transcript_2/3_Conf_0.400	2018	20	9.73E-75	XP_001897870.1	78	286.189	235	184	transcription factor DP1

Locus_2376_Transcript_3/3_Conf_0.400	1648	20	1.83E-137	XP_001897504.1	76	494.197	413	316	SNF2 family N-terminal domain containing protein
Locus_23760_Transcript_1/1_Conf_1.000	129	0							
Locus_23761_Transcript_1/1_Conf_1.000	235	0							
Locus_23762_Transcript_1/1_Conf_1.000	227	0							
Locus_23763_Transcript_1/1_Conf_1.000	205	20	3.07E-11	XP_001381283.1	73	71.633	56	41	PREDICTED: similar to haloacid dehalogenase-like hydrolase domain containing 1A
Locus_23764_Transcript_1/1_Conf_1.000	277	20	8.56E-22	XP_002642776.1	79	106.686	77	61	C. briggsae CBR-WRS-2 protein
Locus_23765_Transcript_1/1_Conf_1.000	152	0							
Locus_23766_Transcript_1/1_Conf_1.000	140	4	3.26E-05	XP_002641225.1	82	51.6026	35	29	C. briggsae CBR-SMA-4 protein
Locus_23767_Transcript_1/1_Conf_1.000	282	0							

Locus_23768_Transcript_1/1_Conf_1.000	249	20	4.82E-25	XP_002633897.1	82	117.472	80	66	Hypothetical protein CBG19959
Locus_23769_Transcript_1/1_Conf_1.000	284	0							
Locus_2377_Transcript_1/1_Conf_1.000	593	20	1.91E-34	XP_002637821.1	70	149.443	179	126	Hypothetical protein CBG04610
Locus_23770_Transcript_1/1_Conf_1.000	455	0							
Locus_23771_Transcript_1/1_Conf_1.000	140	0							
Locus_23772_Transcript_1/1_Conf_1.000	213	20	4.82E-33	A8Y3Q1.2	100	144.05	70	70	Putative 28S ribosomal protein S5
Locus_23773_Transcript_1/1_Conf_1.000	171	0							
Locus_23774_Transcript_1/1_Conf_1.000	321	18	1.75E-22	EFO19513.1	75	108.997	88	66	hypothetical protein LOAG_08980

Locus_23775_Transcript_1/1_Conf_1.000	323	20	5.64E-21	NP_741839.2	58	103.99	104	61	hypothetical protein F48E3.8
Locus_23776_Transcript_1/1_Conf_1.000	292	20	9.04E-11	EFO25944.1	56	70.0922	95	54	hypothetical protein LOAG_02539
Locus_23777_Transcript_1/1_Conf_1.000	140	0							
Locus_23778_Transcript_1/1_Conf_1.000	143	2	2.11E-04	NP_490886.2	70	48.9062	48	34	hypothetical protein Y71G12B.11
Locus_23779_Transcript_1/1_Conf_1.000	149	0							
Locus_2378_Transcript_1/1_Conf_1.000	957	16	5.07E-26	XP_002639372.1	54	122.865	296	160	C. briggsae CBR-RPA-2 protein
Locus_23780_Transcript_1/1_Conf_1.000	207	20	7.27E-21	XP_002640853.1	77	103.605	67	52	Hypothetical protein CBG15741
Locus_23781_Transcript_1/1_Conf_1.000	258	0							
Locus_23782_Transcript_1/1_Conf_1.000	161	20	2.01E-18	XP_002636919.1	88	95.5153	51	45	Hypothetical protein CBG09383
Locus_23783_Transcript_1/1_Conf_1.000	187	10	1.90E-08	XP_001901648.1	72	62.3882	61	44	Conserved hypothetical protein
Locus_23784_Transcript_1/1_Conf_1.000	274	0							
Locus_23785_Transcript_1/1_Conf_1.000	171	0							
Locus_23786_Transcript_1/1_Conf_1.000	198	2	1.21E-15	NP_496015.1	80	86.2705	65	52	hypothetical protein M176.5
Locus_23787_Transcript_1/1_Conf_1.000	277	20	2.25E-30	NP_493616.1	85	135.191	91	78	hypothetical protein F33H2.5

Locus_23788_Transcript_1/1_Conf_1.000	266	20	3.51E-39	CAX51641.1	92	164.466	88	81	C. elegans protein F11E6.8b, partially confirmed by transcript evidence
Locus_23789_Transcript_1/1_Conf_1.000	232	0							
Locus_2379_Transcript_1/1_Conf_1.000	1394	20	1.05E-119	NP_491213.1	69	434.876	400	277	INneXin family member (inx-12)
Locus_23790_Transcript_1/1_Conf_1.000	129	0							
Locus_23791_Transcript_1/1_Conf_1.000	317	18	4.14E-49	NP_001002032.1	100	177.178	78	78	hematological and neurological expressed 1 protein isoform 2
Locus_23792_Transcript_1/1_Conf_1.000	196	0							
Locus_23793_Transcript_1/1_Conf_1.000	534	2	7.85E-33	NP_498567.1	70	143.665	164	116	hypothetical protein K04G7.1
Locus_23794_Transcript_1/1_Conf_1.000	137	0							
Locus_23795_Transcript_1/1_Conf_1.000	265	0							
Locus_23796_Transcript_1/1_Conf_1.000	186	20	3.23E-24	XP_002631133.1	96	114.775	61	59	C. briggsae CBR-CLH-2 protein
Locus_23797_Transcript_1/1_Conf_1.000	620	20	4.35E-51	XP_002637127.1	75	204.912	205	154	Hypothetical protein CBG09629
Locus_23798_Transcript_1/1_Conf_1.000	131	20	6.19E-12	NP_510155.3	93	73.9442	43	40	PIP Kinase family member (ppk-3)
Locus_23799_Transcript_1/1_Conf_1.000	198	0							
Locus_238_Transcript_1/1_Conf_1.000	608	0							
Locus_2380_Transcript_1/1_Conf_1.000	802	0							
Locus_23800_Transcript_1/1_Conf_1.000	278	0							
Locus_23801_Transcript_1/1_Conf_1.000	446	0							

Locus_23802_Transcript_1/1_Conf_1.000	154	20	1.44E-24	XP_002737593.1	100	115.931	51	51	PREDICTED: protein phosphatase 4, catalytic subunit-like
Locus_23803_Transcript_1/1_Conf_1.000	201	0							
Locus_23804_Transcript_1/1_Conf_1.000	234	0							
Locus_23805_Transcript_1/1_Conf_1.000	174	0							
Locus_23806_Transcript_1/1_Conf_1.000	347	0							
Locus_23807_Transcript_1/1_Conf_1.000	338	0							
Locus_23808_Transcript_1/1_Conf_1.000	143	0							
Locus_23809_Transcript_1/1_Conf_1.000	237	0							
Locus_2381_Transcript_1/1_Conf_1.000	2060	20	2.81E-77	Q09275.2	67	294.664	328	223	Putative thiol protease ulp-4
Locus_23810_Transcript_1/1_Conf_1.000	143	0							
Locus_23811_Transcript_1/1_Conf_1.000	279	4	1.11E-21	NP_501142.1	70	106.301	94	66	GLoBin family member (glb-23)
Locus_23812_Transcript_1/1_Conf_1.000	144	0							
Locus_23813_Transcript_1/1_Conf_1.000	288	0							
Locus_23814_Transcript_1/1_Conf_1.000	357	1	5.61E-05	XP_002641620.1	60	50.8322	53	32	C. briggsae CBR-BUB-1 protein
Locus_23815_Transcript_1/1_Conf_1.000	163	0							
Locus_23816_Transcript_1/1_Conf_1.000	134	0							
Locus_23817_Transcript_1/1_Conf_1.000	162	0							
Locus_23818_Transcript_1/1_Conf_1.000	137	0							
Locus_23819_Transcript_1/1_Conf_1.000	218	20	8.80E-19	XP_001891673.1	86	96.6709	65	56	hypothetical protein Bm1_00760
Locus_2382_Transcript_1/3_Conf_0.714	4636	20	0	XP_002630260.1	81	1592.4	1126	913	Hypothetical protein CBG00683
Locus_2382_Transcript_2/3_Conf_0.714	4612	20	0	XP_002630260.1	80	1583.93	1126	911	Hypothetical protein CBG00683
Locus_2382_Transcript_3/3_Conf_0.714	4618	20	0	XP_002630260.1	81	1592.4	1126	913	Hypothetical protein CBG00683
Locus_23820_Transcript_1/1_Conf_1.000	292	20	2.07E-39	XP_002630350.1	87	165.236	97	85	Hypothetical protein CBG04280
Locus_23821_Transcript_1/1_Conf_1.000	136	8	1.57E-07	XP_002639522.1	74	59.3066	43	32	Hypothetical protein CBG04128

Locus_23822_Transcript_1/1_Conf_1.000	206	20	8.07E-20	XP_002917175.1	100	100.138	68	68	PREDICTED: proteasome subunit beta type-2-like
Locus_23823_Transcript_1/1_Conf_1.000	208	2	3.39E-10	XP_002638587.1	78	68.1662	55	43	Hypothetical protein CBG05635
Locus_23824_Transcript_1/1_Conf_1.000	208	0							
Locus_23825_Transcript_1/1_Conf_1.000	205	0							
Locus_23826_Transcript_1/1_Conf_1.000	153	20	3.33E-21	CAR63641.1	100	104.76	50	50	putative 26S proteasome regulatory chain 4
Locus_23827_Transcript_1/1_Conf_1.000	323	0							
Locus_23828_Transcript_1/1_Conf_1.000	384	20	1.55E-47	NP_491030.1	91	192.2	128	117	DNaJ domain (prokaryotic heat shock protein) family member (dnj-30)
Locus_23829_Transcript_1/1_Conf_1.000	151	0							
Locus_2383_Transcript_1/3_Conf_0.667	1039	20	1.44E-101	XP_001902124.1	73	374.015	317	233	sterol carrier protein
Locus_2383_Transcript_2/3_Conf_0.667	918	20	7.71E-85	XP_001902124.1	71	318.161	277	197	sterol carrier protein

Locus_2383_Transcript_3/3_Conf_0.667	1039	20	1.10E-101	XP_001902124.1	73	374.4	317	233	sterol carrier protein
Locus_23830_Transcript_1/1_Conf_1.000	155	0							
Locus_23831_Transcript_1/1_Conf_1.000	234	0							
Locus_23832_Transcript_1/1_Conf_1.000	322	0							
Locus_23833_Transcript_1/1_Conf_1.000	166	0							
Locus_23834_Transcript_1/1_Conf_1.000	178	0							
Locus_23835_Transcript_1/1_Conf_1.000	128	5	4.45E-10	NP_509586.1	92	67.781	42	39	GOlgi Snap Receptor complex member family member (gosr-2.1)
Locus_23836_Transcript_1/1_Conf_1.000	179	4	5.01E-14	XP_002637214.1	75	80.8777	60	45	Hypothetical protein CBG09740
Locus_23837_Transcript_1/1_Conf_1.000	232	20	7.58E-34	NP_741181.1	97	146.747	77	75	hypothetical protein T12A2.15
Locus_23838_Transcript_1/1_Conf_1.000	353	20	7.29E-45	NP_490755.1	89	183.341	120	107	Heavy chain, Unconventional Myosin family member (hum-7)
Locus_23839_Transcript_1/1_Conf_1.000	145	0							
Locus_2384_Transcript_1/2_Conf_1.000	1699	20	8.68E-90	XP_001897752.1	95	335.88	182	173	Ubiquitin-conjugating enzyme E2 1

Locus_2384_Transcript_2/2_Conf_1.000	511	20	1.81E-78	1Z3D	98	295.049	146	144	ProteinCrystal Growth Improvement Leading ToThe 2.5aCrystallographicStructure Of Ubiquitin-Conjugating Enzyme (Ubc-1) From Caenorhabditis Elegans
Locus_23840_Transcript_1/1_Conf_1.000	304	5	2.05E-07	NP_499641.2	53	58.9214	73	39	hypothetical protein Y111B2A.10
Locus_23841_Transcript_1/1_Conf_1.000	179	0							
Locus_23842_Transcript_1/1_Conf_1.000	390	13	7.25E-05	XP_652875.1	54	50.447	116	63	hypothetical protein
Locus_23843_Transcript_1/1_Conf_1.000	251	0							

Locus_23844_Transcript_1/1_Conf_1.000	162	20	2.70E-15	XP_002832350.1	100	85.1149	53	53	PREDICTED: LOW QUALITY PROTEIN: filamin-A-like
Locus_23845_Transcript_1/1_Conf_1.000	363	20	1.22E-52	XP_002633950.1	85	209.149	120	102	C. briggsae CBR-FBL-1 protein
Locus_23846_Transcript_1/1_Conf_1.000	152	20	2.56E-13	XP_002703534.1	100	78.5666	50	50	PREDICTED: signal recognition particle receptor subunit alpha-like
Locus_23847_Transcript_1/1_Conf_1.000	212	0							
Locus_23848_Transcript_1/1_Conf_1.000	386	20	1.60E-68	ADF56012.1	97	261.922	128	125	nicotinic acetylcholine receptor non-alpha subunit LEV-1
Locus_23849_Transcript_1/1_Conf_1.000	191	20	8.78E-14	XP_002642807.1	79	80.1073	63	50	C. briggsae CBR-KEL-3 protein
Locus_2385_Transcript_1/1_Conf_1.000	913	20	9.29E-91	NP_498012.1	83	337.806	263	219	hypothetical protein C35D10.10
Locus_23850_Transcript_1/1_Conf_1.000	130	5	3.18E-08	NP_501599.1	80	61.6178	41	33	Prolyl Carboxy Peptidase like family member (pcp-2)
Locus_23851_Transcript_1/1_Conf_1.000	192	0							
Locus_23852_Transcript_1/1_Conf_1.000	212	0							

Locus_23853_Transcript_1/1_Conf_1.000	141	0							
Locus_23854_Transcript_1/1_Conf_1.000	277	20	1.50E-34	NP_501127.2	89	149.058	92	82	RNA Polymerase, Class III (C) family member (rpc-1)
Locus_23855_Transcript_1/1_Conf_1.000	158	0							
Locus_23856_Transcript_1/1_Conf_1.000	143	0							
Locus_23857_Transcript_1/1_Conf_1.000	171	0							
Locus_23858_Transcript_1/1_Conf_1.000	128	18	4.02E-11	NP_494777.1	90	71.2478	42	38	MoLTing defective family member (mlt-7)
Locus_23859_Transcript_1/1_Conf_1.000	136	4	2.19E-09	NP_500615.1	81	65.4698	44	36	hypothetical protein T22B11.2
Locus_2386_Transcript_1/1_Conf_1.000	1394	20	3.97E-137	NP_492839.4	81	347.436	271	220	Leucine-rich repeats, Ras-like domain, Kinase family member (lrk-1)
Locus_23860_Transcript_1/1_Conf_1.000	133	0							
Locus_23861_Transcript_1/1_Conf_1.000	299	2	1.34E-06	XP_001899503.1	56	56.225	107	60	hypothetical protein Bm1_40230
Locus_23862_Transcript_1/1_Conf_1.000	182	0							
Locus_23863_Transcript_1/1_Conf_1.000	191	0							
Locus_23864_Transcript_1/1_Conf_1.000	356	0							
Locus_23865_Transcript_1/1_Conf_1.000	272	0							
Locus_23866_Transcript_1/1_Conf_1.000	204	0							
Locus_23867_Transcript_1/1_Conf_1.000	274	0							
Locus_23868_Transcript_1/1_Conf_1.000	507	0							
Locus_23869_Transcript_1/1_Conf_1.000	173	0							
Locus_2387_Transcript_1/3_Conf_0.571	792	0							
Locus_2387_Transcript_2/3_Conf_0.714	1343	0							
Locus_2387_Transcript_3/3_Conf_0.714	1382	0							
Locus_23870_Transcript_1/1_Conf_1.000	171	0							
Locus_23871_Transcript_1/1_Conf_1.000	165	20	4.14E-24	AAH46345.1	100	114.39	55	55	AURKAIP1 protein

Locus_23872_Transcript_1/1_Conf_1.000	164	20	1.87E-16	XP_002929659.1	100	88.9669	43	43	PREDICTED: GTP-binding nuclear protein Ran-like, partial
Locus_23873_Transcript_1/1_Conf_1.000	170	0							
Locus_23874_Transcript_1/1_Conf_1.000	389	0							
Locus_23875_Transcript_1/1_Conf_1.000	439	0							
Locus_23876_Transcript_1/1_Conf_1.000	171	0							
Locus_23877_Transcript_1/1_Conf_1.000	277	0							
Locus_23878_Transcript_1/1_Conf_1.000	163	20	2.99E-14	NP_509229.1	90	81.6481	51	46	SUppressor of activated let-60 Ras family member (sur-5)
Locus_23879_Transcript_1/1_Conf_1.000	174	0							
Locus_2388_Transcript_1/1_Conf_1.000	1053	20	9.22E-104	NP_500892.1	85	381.333	287	244	hypothetical protein K02B2.3
Locus_23880_Transcript_1/1_Conf_1.000	320	20	3.41E-42	XP_001891823.1	90	174.481	106	96	2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial precursor
Locus_23881_Transcript_1/1_Conf_1.000	159	0							
Locus_23882_Transcript_1/1_Conf_1.000	233	0							
Locus_23883_Transcript_1/1_Conf_1.000	189	0							
Locus_23884_Transcript_1/1_Conf_1.000	196	0							
Locus_23885_Transcript_1/1_Conf_1.000	176	0							
Locus_23886_Transcript_1/1_Conf_1.000	263	0							
Locus_23887_Transcript_1/1_Conf_1.000	138	0							
Locus_23888_Transcript_1/1_Conf_1.000	128	6	1.48E-05	EFO20090.1	86	52.7582	37	32	hypothetical protein LOAG_08398
Locus_23889_Transcript_1/1_Conf_1.000	160	0							

Locus_2389_Transcript_1/2_Conf_1.000	991	20	7.28E-15	EFO27344.1	43	85.8853	314	138	double-stranded RNA binding domain-containing protein family protein
Locus_2389_Transcript_2/2_Conf_1.000	995	20	7.32E-15	EFO27344.1	43	85.8853	314	138	double-stranded RNA binding domain-containing protein family protein
Locus_23890_Transcript_1/1_Conf_1.000	155	0							
Locus_23891_Transcript_1/1_Conf_1.000	192	0							
Locus_23892_Transcript_1/1_Conf_1.000	135	0							
Locus_23893_Transcript_1/1_Conf_1.000	206	0							
Locus_23894_Transcript_1/1_Conf_1.000	192	20	1.64E-28	XP_002828455.1	100	129.028	63	63	PREDICTED: LOW QUALITY PROTEIN: ornithine decarboxylase antizyme 1-like
Locus_23895_Transcript_1/1_Conf_1.000	551	20	3.09E-14	NP_507654.1	46	82.0333	169	79	SCP-Like extracellular protein family member (scl-19)
Locus_23896_Transcript_1/1_Conf_1.000	187	0							
Locus_23897_Transcript_1/1_Conf_1.000	392	0							
Locus_23898_Transcript_1/1_Conf_1.000	129	0							

Locus_23899_Transcript_1/1_Conf_1.000	284	20	3.02E-30	CAF97585.1	80	134.806	88	71	unnamed protein product
Locus_239_Transcript_1/1_Conf_1.000	180	0							
Locus_2390_Transcript_1/1_Conf_1.000	498	20	6.90E-64	CAG25499.1	88	246.514	144	128	heat shock protein 20
Locus_23900_Transcript_1/1_Conf_1.000	133	1	3.63E-04	XP_002642828.1	64	48.1358	42	27	Hypothetical protein CBG21226
Locus_23901_Transcript_1/1_Conf_1.000	205	20	5.96E-31	BAG64784.1	100	137.117	68	68	unnamed protein product
Locus_23902_Transcript_1/1_Conf_1.000	208	20	4.11E-32	XP_002920795.1	100	140.969	59	59	PREDICTED: LOW QUALITY PROTEIN: SPARC-like
Locus_23903_Transcript_1/1_Conf_1.000	227	0							
Locus_23904_Transcript_1/1_Conf_1.000	171	20	1.67E-25	XP_002810873.1	100	119.013	57	57	PREDICTED: nardilysin-like isoform 2
Locus_23905_Transcript_1/1_Conf_1.000	742	0							
Locus_23906_Transcript_1/1_Conf_1.000	370	20	3.33E-21	NP_503012.2	67	104.76	102	69	hypothetical protein Y116A8C.13
Locus_23907_Transcript_1/1_Conf_1.000	356	0							
Locus_23908_Transcript_1/1_Conf_1.000	164	0							
Locus_23909_Transcript_1/1_Conf_1.000	423	7	2.12E-60	CAA92681.2	89	234.958	125	112	C. elegans protein K08E4.3, confirmed by transcript evidence

Locus_2391_Transcript_1/1_Conf_1.000	730	20	2.62E-41	NP_492270.1	58	172.94	235	137	hypothetical protein F16D3.4
Locus_23910_Transcript_1/1_Conf_1.000	212	0							
Locus_23911_Transcript_1/1_Conf_1.000	395	20	1.17E-50	NP_497814.3	84	202.601	131	111	UNCoordinated family member (unc-79)
Locus_23912_Transcript_1/1_Conf_1.000	470	10	5.59E-37	NP_499042.2	71	157.147	156	112	hypothetical protein T23G5.6
Locus_23913_Transcript_1/1_Conf_1.000	345	2	6.28E-12	NP_494997.1	67	73.9442	76	51	VH1 dual-specificity phosphatase family member (vhp-1)
Locus_23914_Transcript_1/1_Conf_1.000	317	2	7.95E-15	NP_001024845.1	69	83.5741	89	62	hypothetical protein R08B4.5
Locus_23915_Transcript_1/1_Conf_1.000	174	6	5.56E-13	XP_523970.2	90	77.411	42	38	PREDICTED: similar to Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived) isoform 2
Locus_23916_Transcript_1/1_Conf_1.000	183	0							
Locus_23917_Transcript_1/1_Conf_1.000	226	3	6.47E-25	NP_740934.2	93	117.087	75	70	UNCoordinated family member (unc-95)
Locus_23918_Transcript_1/1_Conf_1.000	459	20	3.84E-06	XP_002130348.1	48	54.6842	128	62	PREDICTED: similar to protease, serine, 7 (enterokinase)
Locus_23919_Transcript_1/1_Conf_1.000	304	11	7.55E-10		54	67.0106	100	54	hypothetical protein T28B8.4
Locus_2392_Transcript_1/1_Conf_1.000	2200	20	2.86E-160	XP_002641169.1	66	570.466	528	353	C. briggsae CBR-FRM-2 protein
Locus_23920_Transcript_1/1_Conf_1.000	147	0							
Locus_23921_Transcript_1/1_Conf_1.000	522	20	9.64E-41	NP_502553.2	79	169.859	162	128	Cleavage and Polyadenylation Specificity Factor family member (cpsf-3)
Locus_23922_Transcript_1/1_Conf_1.000	268	0							
Locus_23923_Transcript_1/1_Conf_1.000	389	0							
Locus_23924_Transcript_1/1_Conf_1.000	235	0							
Locus_23925_Transcript_1/1_Conf_1.000	169	0							
Locus_23926_Transcript_1/1_Conf_1.000	290	20	1.82E-19	NP_493592.1	68	98.9821	104	71	hypothetical protein F32A7.4
Locus_23927_Transcript_1/1_Conf_1.000	418	0							
Locus_23928_Transcript_1/1_Conf_1.000	254	0							

Locus_23929_Transcript_1/1_Conf_1.000	239	20	2.35E-27	AAM11895.1	86	125.176	79	68	high-affinity dicarboxylate transporter INDY3
Locus_2393_Transcript_1/1_Conf_1.000	451	20	1.66E-57	NP_497721.1	87	225.328	138	121	Ribosomal Protein, Large subunit family member (rpl-16)
Locus_23930_Transcript_1/1_Conf_1.000	376	0							
Locus_23931_Transcript_1/1_Conf_1.000	132	0							
Locus_23932_Transcript_1/1_Conf_1.000	226	0							
Locus_23933_Transcript_1/1_Conf_1.000	226	0							
Locus_23934_Transcript_1/1_Conf_1.000	242	0							
Locus_23935_Transcript_1/1_Conf_1.000	152	0							
Locus_23936_Transcript_1/1_Conf_1.000	278	20	3.25E-29	EFO19658.1	82	131.339	92	76	hypothetical protein LOAG_08833
Locus_23937_Transcript_1/1_Conf_1.000	187	0							
Locus_23938_Transcript_1/1_Conf_1.000	320	20	2.14E-36	XP_002643176.1	87	155.221	99	87	Hypothetical protein CBG24142
Locus_23939_Transcript_1/1_Conf_1.000	367	20	4.08E-24	XP_002646775.1	66	114.39	116	77	Hypothetical protein CBG18419
Locus_2394_Transcript_1/2_Conf_1.000	1214	0							
Locus_2394_Transcript_2/2_Conf_1.000	621	0							
Locus_23940_Transcript_1/1_Conf_1.000	347	20	8.43E-33	XP_002637479.1	78	143.28	112	88	Hypothetical protein CBG19196

Locus_23941_Transcript_1/1_Conf_1.000	340	19	1.04E-19	NP_497235.2	94	99.7525	57	54	G-protein-coupled Receptor Kinase family member (grk-2)
Locus_23942_Transcript_1/1_Conf_1.000	154	0							
Locus_23943_Transcript_1/1_Conf_1.000	143	0							
Locus_23944_Transcript_1/1_Conf_1.000	133	0							
Locus_23945_Transcript_1/1_Conf_1.000	332	0							
Locus_23946_Transcript_1/1_Conf_1.000	207	0							
Locus_23947_Transcript_1/1_Conf_1.000	350	0							
Locus_23948_Transcript_1/1_Conf_1.000	155	0							
Locus_23949_Transcript_1/1_Conf_1.000	240	0							
Locus_2395_Transcript_1/1_Conf_1.000	808	20	3.70E-122	NP_492775.2	80	441.81	265	213	LAMinin related. See also lmb- family member (lam-3)
Locus_23950_Transcript_1/1_Conf_1.000	136	1	4.72E-04	NP_491418.1	76	47.7506	39	30	hypothetical protein B0041.5
Locus_23951_Transcript_1/1_Conf_1.000	154	0							
Locus_23952_Transcript_1/1_Conf_1.000	426	7	5.74E-58	Q20548.2	89	226.868	141	126	Probable RING finger protein 207 homolog
Locus_23953_Transcript_1/1_Conf_1.000	226	0							
Locus_23954_Transcript_1/1_Conf_1.000	135	0							
Locus_23955_Transcript_1/1_Conf_1.000	217	0							
Locus_23956_Transcript_1/1_Conf_1.000	377	20	1.18E-18	EFO24235.1	60	96.2857	118	71	hypothetical protein LOAG_04250
Locus_23957_Transcript_1/1_Conf_1.000	189	0							
Locus_23958_Transcript_1/1_Conf_1.000	178	4	8.85E-11	NP_500790.1	82	70.0922	57	47	hypothetical protein F41H10.4
Locus_23959_Transcript_1/1_Conf_1.000	197	0							
Locus_2396_Transcript_1/1_Conf_1.000	1005	1	7.75E-04	NP_504247.2	38	49.2914	226	87	hypothetical protein F54D11.2

Locus_23960_Transcript_1/1_Conf_1.000	1207	20	1.97E-156	NP_497007.1	81	556.599	403	327	hypothetical protein K10H10.1
Locus_23961_Transcript_1/1_Conf_1.000	239	20	3.40E-10	EFO26171.1	68	68.1662	60	41	tyrosyl-DNA phosphodiesterase
Locus_23962_Transcript_1/1_Conf_1.000	455	20	2.32E-43	NP_502044.1	76	178.333	150	115	AQuaPorin or aquaglyceroporin related family member (aqp-3)
Locus_23963_Transcript_1/1_Conf_1.000	147	3	4.38E-13	XP_001897744.1	91	77.7962	48	44	ABC transporter family protein
Locus_23964_Transcript_1/1_Conf_1.000	153	20	1.15E-13	EAX10112.1	82	79.7221	47	39	hCG2018900
Locus_23965_Transcript_1/1_Conf_1.000	208	20	1.68E-17	XP_002642043.1	73	92.4337	72	53	C. briggsae CBR-PAL-1 protein
Locus_23966_Transcript_1/1_Conf_1.000	201	0							
Locus_23967_Transcript_1/1_Conf_1.000	222	0							
Locus_23968_Transcript_1/1_Conf_1.000	313	0							
Locus_23969_Transcript_1/1_Conf_1.000	168	0							

Locus_2397_Transcript_1/1_Conf_1.000	2178	20	4.59E-102	EFO15014.1	73	377.096	314	230	CAMK/PIM protein kinase
Locus_23970_Transcript_1/1_Conf_1.000	311	4	1.23E-28	NP_500851.2	79	129.413	101	80	hypothetical protein H35B03.1
Locus_23971_Transcript_1/1_Conf_1.000	143	0							
Locus_23972_Transcript_1/1_Conf_1.000	192	1	9.70E-05	XP_002633562.1	63	50.0618	65	41	Hypothetical protein CBG05433
Locus_23973_Transcript_1/1_Conf_1.000	324	0							
Locus_23974_Transcript_1/1_Conf_1.000	368	20	2.61E-63	XP_002926784.1	100	244.588	122	122	PREDICTED: heat shock protein HSP 90-alpha-like
Locus_23975_Transcript_1/1_Conf_1.000	163	20	3.53E-15	XP_002631757.1	86	84.7297	53	46	Hypothetical protein CBG20965
Locus_23976_Transcript_1/1_Conf_1.000	390	7	5.54E-13	XP_001901143.1	70	77.411	93	66	Protein kinase domain containing protein

Locus_23977_Transcript_1/1_Conf_1.000	196	20	2.46E-08	XP_001900312.1	80	62.003	66	53	Krr1 family protein
Locus_23978_Transcript_1/1_Conf_1.000	593	12	1.08E-45	XP_002644583.1	74	186.808	150	112	C. briggsae CBR-GLIT-1 protein
Locus_23979_Transcript_1/1_Conf_1.000	276	20	5.54E-29	NP_509689.1	84	130.568	95	80	hypothetical protein ZC373.4
Locus_2398_Transcript_1/1_Conf_1.000	468	5	3.91E-06	AAR03713.1	49	54.6842	103	51	secreted protein 4 precursor
Locus_23980_Transcript_1/1_Conf_1.000	261	20	2.46E-16	XP_002634885.1	75	88.5817	76	57	Hypothetical protein CBG10553
Locus_23981_Transcript_1/1_Conf_1.000	194	9	7.16E-16	NP_503758.4	77	87.0409	63	49	KETtiN (Drosophila actin-binding) homolog family member (ketn-1)
Locus_23982_Transcript_1/1_Conf_1.000	198	20	3.91E-06	YP_779412.1	60	54.6842	64	39	malonyl-CoA synthase
Locus_23983_Transcript_1/1_Conf_1.000	269	20	9.25E-24	EFO16116.1	79	113.235	88	70	hypothetical protein LOAG_12392
Locus_23984_Transcript_1/1_Conf_1.000	138	0							
Locus_23985_Transcript_1/1_Conf_1.000	755	20	3.51E-36	XP_002636125.1	52	155.992	257	136	Hypothetical protein CBG01375
Locus_23986_Transcript_1/1_Conf_1.000	276	0							
Locus_23987_Transcript_1/1_Conf_1.000	304	19	6.82E-11	NP_502296.1	58	70.4774	92	54	hypothetical protein M18.3
Locus_23988_Transcript_1/1_Conf_1.000	183	0							
Locus_23989_Transcript_1/1_Conf_1.000	229	0							
Locus_2399_Transcript_1/1_Conf_1.000	2816	20	0	XP_002644820.1	87	1172.15	864	757	C. briggsae CBR-NNT-1 protein
Locus_23990_Transcript_1/1_Conf_1.000	186	0							
Locus_23991_Transcript_1/1_Conf_1.000	192	0							
Locus_23992_Transcript_1/1_Conf_1.000	148	20	3.47E-10	YP_466652.1	83	68.1662	43	36	L-threonine ammonia-lyase

Locus_23993_Transcript_1/1_Conf_1.000	132	3	9.54E-05		67	50.0618	43	29	ypothetical protein Y39B6B.h
Locus_23994_Transcript_1/1_Conf_1.000	298	4	1.06E-27	XP_002638375.1	80	126.331	97	78	Hypothetical protein CBG18580
Locus_23995_Transcript_1/1_Conf_1.000	145	1	4.87E-04	NP_494953.3	72	47.7506	40	29	Nematode AStacin protease family member (nas-29)
Locus_23996_Transcript_1/1_Conf_1.000	497	0							
Locus_23997_Transcript_1/1_Conf_1.000	417	0							
Locus_23998_Transcript_1/1_Conf_1.000	219	0							
Locus_23999_Transcript_1/1_Conf_1.000	186	0							
Locus_24_Transcript_1/1_Conf_1.000	315	0							
Locus_240_Transcript_1/1_Conf_1.000	2181	20	0	NP_496273.1	96	1174.07	702	674	Cell Division Cycle related family member (cdc-48.1)
Locus_2400_Transcript_1/1_Conf_1.000	506	20	1.57E-42	XP_002631189.1	90	175.637	103	93	C. briggsae CBR-SDHD-1 protein
Locus_24000_Transcript_1/1_Conf_1.000	172	0							
Locus_24001_Transcript_1/1_Conf_1.000	131	0							
Locus_24002_Transcript_1/1_Conf_1.000	161	0							
Locus_24003_Transcript_1/1_Conf_1.000	138	0							
Locus_24004_Transcript_1/1_Conf_1.000	188	0							
Locus_24005_Transcript_1/1_Conf_1.000	164	0							
Locus_24006_Transcript_1/1_Conf_1.000	187	20	1.19E-18	Q03566.2	88	96.2857	51	45	Probable G-protein coupled receptor tkr-1
Locus_24007_Transcript_1/1_Conf_1.000	317	20	9.68E-29	XP_002630524.1	69	129.798	105	73	Hypothetical protein CBG12962

Locus_24008_Transcript_1/1_Conf_1.000	183	1	6.35E-04	XP_002641413.1	65	47.3654	60	39	Hypothetical protein CBG13279
Locus_24009_Transcript_1/1_Conf_1.000	170	0							
Locus_2401_Transcript_1/1_Conf_1.000	620	5	7.64E-64	NP_001123059.1	76	247.284	204	156	hypothetical protein Y61A9LA.11
Locus_24010_Transcript_1/1_Conf_1.000	330	0							
Locus_24011_Transcript_1/1_Conf_1.000	156	6	3.01E-06	EFO20752.1	73	55.0694	41	30	AMOP domain-containing protein
Locus_24012_Transcript_1/1_Conf_1.000	684	20	7.13E-51	XP_001897894.1	66	204.527	247	165	ancient conserved domain protein 4
Locus_24013_Transcript_1/1_Conf_1.000	152	0							
Locus_24014_Transcript_1/1_Conf_1.000	211	20	1.16E-18	XP_002640591.1	77	96.2857	68	53	Hypothetical protein CBG15874
Locus_24015_Transcript_1/1_Conf_1.000	242	20	5.19E-35	EFO28104.1	97	150.599	76	74	hypothetical protein LOAG_00390
Locus_24016_Transcript_1/1_Conf_1.000	161	0							
Locus_24017_Transcript_1/1_Conf_1.000	411	2	1.79E-11	NP_497340.2	59	72.4034	139	83	CaDHerin family member (cdh-12)
Locus_24018_Transcript_1/1_Conf_1.000	265	0							
Locus_24019_Transcript_1/1_Conf_1.000	301	0							
Locus_2402_Transcript_1/1_Conf_1.000	281	8	3.26E-05	NP_498849.3	57	51.6026	84	48	hypothetical protein R05D3.1
Locus_24020_Transcript_1/1_Conf_1.000	204	0							
Locus_24021_Transcript_1/1_Conf_1.000	284	0							

Locus_24022_Transcript_1/1_Conf_1.000	214	20	1.36E-27	NP_503175.1	92	125.946	71	66	ABC Transporter family member (abt-4)
Locus_24023_Transcript_1/1_Conf_1.000	193	20	1.65E-12	NP_500785.1	70	75.8702	64	45	hypothetical protein Y4C6B.6
Locus_24024_Transcript_1/1_Conf_1.000	210	20	2.25E-30	NP_004532.1	100	135.191	62	62	NADH dehydrogenase ubiquinone 1 alpha subcomplex subunit 1
Locus_24025_Transcript_1/1_Conf_1.000	250	0							
Locus_24026_Transcript_1/1_Conf_1.000	235	0							
Locus_24027_Transcript_1/1_Conf_1.000	225	20	5.12E-30	BAI49947.1	85	134.035	74	63	GLI family zinc finger protein
Locus_24028_Transcript_1/1_Conf_1.000	344	0							
Locus_24029_Transcript_1/1_Conf_1.000	320	5	5.29E-27	NP_001024085.2	95	124.02	71	68	hypothetical protein R186.8
Locus_2403_Transcript_1/1_Conf_1.000	1475	20	1.24E-166	NP_502560.1	82	590.882	376	311	FATty acid desaturase family member (fat-2)
Locus_24030_Transcript_1/1_Conf_1.000	133	0							
Locus_24031_Transcript_1/1_Conf_1.000	226	2	6.49E-17	XP_002634566.1	85	90.5077	64	55	Hypothetical protein CBG08372
Locus_24032_Transcript_1/1_Conf_1.000	228	0							

Locus_24033_Transcript_1/1_Conf_1.000	135	2	1.73E-06	NP_504508.1	76	55.8398	47	36	hypothetical protein K09H11.1
Locus_24034_Transcript_1/1_Conf_1.000	136	0							
Locus_24035_Transcript_1/1_Conf_1.000	165	0							
Locus_24036_Transcript_1/1_Conf_1.000	183	2	8.82E-22	NP_001122963.1	88	106.686	60	53	hypothetical protein F58E6.1
Locus_24037_Transcript_1/1_Conf_1.000	232	20	1.48E-37	BAG62774.1	100	159.073	77	77	unnamed protein product
Locus_24038_Transcript_1/1_Conf_1.000	162	9	1.34E-06	AAO63576.1	66	56.225	53	35	secreted protein 4 precursor
Locus_24039_Transcript_1/1_Conf_1.000	275	2	1.29E-09	NP_491915.2	81	66.2402	43	35	hypothetical protein ZC581.9
Locus_2404_Transcript_1/1_Conf_1.000	2087	20	1.81E-39	XP_002640179.1	52	169.088	411	217	Hypothetical protein CBG12682
Locus_24040_Transcript_1/1_Conf_1.000	141	0							
Locus_24041_Transcript_1/1_Conf_1.000	139	0							
Locus_24042_Transcript_1/1_Conf_1.000	376	20	9.93E-26	NP_871661.1	75	119.783	106	80	hypothetical protein F54C8.7
Locus_24043_Transcript_1/1_Conf_1.000	237	0							
Locus_24044_Transcript_1/1_Conf_1.000	252	0							
Locus_24045_Transcript_1/1_Conf_1.000	546	20	1.90E-08	ADI61829.1	76	62.7734	56	43	endonuclease-reverse transcriptase
Locus_24046_Transcript_1/1_Conf_1.000	183	0							
Locus_24047_Transcript_1/1_Conf_1.000	301	0							
Locus_24048_Transcript_1/1_Conf_1.000	169	20	2.87E-09	XP_002648446.1	67	65.0846	53	36	Hypothetical protein CBG24721
Locus_24049_Transcript_1/1_Conf_1.000	241	2	2.35E-11	NP_494213.2	84	72.0182	51	43	hypothetical protein Y59C2A.1
Locus_2405_Transcript_1/4_Conf_0.600	721	20	2.48E-20	AAO63578.1	46	103.219	204	94	secreted protein 6 precursor

Locus_2405_Transcript_2/4_Conf_0.500	416	20	2.48E-13	NP_502498.1	52	78.5666	99	52	SCP-Like extracellular protein family member (scl-10)
Locus_2405_Transcript_3/4_Conf_0.600	766	20	4.77E-20	AAO63578.1	45	102.449	204	92	secreted protein 6 precursor
Locus_2405_Transcript_4/4_Conf_0.700	766	20	8.14E-20	AAO63578.1	45	101.679	204	93	secreted protein 6 precursor
Locus_24050_Transcript_1/1_Conf_1.000	275	1	8.08E-04	ZP_05532439.1	50	46.9802	85	43	hypothetical protein SvirD4_18528
Locus_24051_Transcript_1/1_Conf_1.000	145	5	1.91E-08	CAA10033.1	75	62.3882	48	36	DYS-1 protein
Locus_24052_Transcript_1/1_Conf_1.000	176	2	5.57E-05	NP_508178.2	63	50.8322	58	37	TBC (Tre-2/Bub2/Cdc16) domain family member (tbc-11)
Locus_24053_Transcript_1/1_Conf_1.000	145	0							
Locus_24054_Transcript_1/1_Conf_1.000	320	20	3.79E-25	NP_001022327.2	67	117.857	105	71	CalEXcitin family member (cex-2)
Locus_24055_Transcript_1/1_Conf_1.000	254	20	3.83E-17	XP_002647073.1	66	91.2781	84	56	Hypothetical protein CBG03599
Locus_24056_Transcript_1/1_Conf_1.000	142	0							
Locus_24057_Transcript_1/1_Conf_1.000	155	0							
Locus_24058_Transcript_1/1_Conf_1.000	184	4	1.19E-10	AAK31527.3	74	69.707	58	43	Neuronal symmetry protein 1, partially confirmed by transcript evidence
Locus_24059_Transcript_1/1_Conf_1.000	226	0							
Locus_2406_Transcript_1/3_Conf_0.714	1282	4	3.45E-05	AAH48067.1	44	54.299	201	89	Nolc1l protein
Locus_2406_Transcript_2/3_Conf_0.714	1306	4	1.59E-05	YP_708893.1	43	55.4546	216	93	hypothetical protein RHA1_ro11088
Locus_2406_Transcript_3/3_Conf_0.714	1306	4	4.63E-05	YP_708893.1	42	53.9138	216	92	hypothetical protein RHA1_ro11088
Locus_24060_Transcript_1/1_Conf_1.000	160	0							
Locus_24061_Transcript_1/1_Conf_1.000	151	0							
Locus_24062_Transcript_1/1_Conf_1.000	285	0							
Locus_24063_Transcript_1/1_Conf_1.000	263	0							
Locus_24064_Transcript_1/1_Conf_1.000	236	20	4.31E-13	XP_002640318.1	64	77.7962	76	49	C. briggsae CBR-CLN-3.2 protein
Locus_24065_Transcript_1/1_Conf_1.000	190	0							
Locus_24066_Transcript_1/1_Conf_1.000	131	0							
Locus_24067_Transcript_1/1_Conf_1.000	187	0							
Locus_24068_Transcript_1/1_Conf_1.000	176	0							
Locus_24069_Transcript_1/1_Conf_1.000	259	0							
Locus_2407_Transcript_1/1_Conf_1.000	160	0							
Locus_24070_Transcript_1/1_Conf_1.000	285	20	3.45E-18	NP_491128.4	72	94.7449	84	61	Conserved Oligomeric Golgi (COG) Component family member (cogc-1)
Locus_24071_Transcript_1/1_Conf_1.000	155	5	8.79E-06	CAD44090.2	80	53.5286	46	37	C. elegans protein C27H6.4b, confirmed by transcript evidence
Locus_24072_Transcript_1/1_Conf_1.000	402	0							

Locus_24073_Transcript_1/1_Conf_1.000	139	0							
Locus_24074_Transcript_1/1_Conf_1.000	129	0							
Locus_24075_Transcript_1/1_Conf_1.000	308	20	9.47E-21	NP_491496.1	68	103.219	103	71	Downstream Of Mes (in same operon) family member (dom-3)
Locus_24076_Transcript_1/1_Conf_1.000	132	0							
Locus_24077_Transcript_1/1_Conf_1.000	144	20	2.41E-11	XP_002639452.1	92	72.0182	42	39	Hypothetical protein CBG04047
Locus_24078_Transcript_1/1_Conf_1.000	172	0							
Locus_24079_Transcript_1/1_Conf_1.000	201	0							
Locus_2408_Transcript_1/1_Conf_1.000	160	0							
Locus_24080_Transcript_1/1_Conf_1.000	335	3	1.62E-12	EFO17724.1	55	75.8702	109	61	hypothetical protein LOAG_10773
Locus_24081_Transcript_1/1_Conf_1.000	234	0							
Locus_24082_Transcript_1/1_Conf_1.000	147	3	1.12E-08	XP_002642237.1	82	63.1586	40	33	Hypothetical protein CBG18219
Locus_24083_Transcript_1/1_Conf_1.000	221	20	7.47E-13	ACI49160.1	67	77.0258	74	50	hypothetical protein Cbre_JD21.007
Locus_24084_Transcript_1/1_Conf_1.000	375	20	1.34E-30	NP_509266.1	73	135.961	125	92	hypothetical protein F48E3.2
Locus_24085_Transcript_1/1_Conf_1.000	473	13	3.71E-57	NP_001040915.1	84	224.172	144	121	hypothetical protein C27D8.3
Locus_24086_Transcript_1/1_Conf_1.000	194	20	2.63E-18	EFO22374.1	83	95.1301	62	52	hypothetical protein LOAG_06111
Locus_24087_Transcript_1/1_Conf_1.000	280	0							
Locus_24088_Transcript_1/1_Conf_1.000	179	9	1.01E-22	NP_492127.1	89	109.768	59	53	Low-density lipoprotein Receptor Related family member (lrp-1)
Locus_24089_Transcript_1/1_Conf_1.000	184	0							
Locus_2409_Transcript_1/1_Conf_1.000	1275	20	7.04E-168	NP_492451.2	93	594.734	333	313	hypothetical protein ZK858.6
Locus_24090_Transcript_1/1_Conf_1.000	411	0							
Locus_24091_Transcript_1/1_Conf_1.000	369	5	1.71E-17	AAA97973.2	79	92.4337	78	62	Hypothetical protein F21C10.7
Locus_24092_Transcript_1/1_Conf_1.000	248	0							
Locus_24093_Transcript_1/1_Conf_1.000	372	0							
Locus_24094_Transcript_1/1_Conf_1.000	152	0							
Locus_24095_Transcript_1/1_Conf_1.000	141	0							
Locus_24096_Transcript_1/1_Conf_1.000	139	20	1.51E-10	XP_002596899.1	78	69.3218	46	36	hypothetical protein BRAFLDRAFT_76408
Locus_24097_Transcript_1/1_Conf_1.000	190	0							

Locus_24098_Transcript_1/1_Conf_1.000	233	2	4.32E-13	NP_493385.2	85	77.7962	56	48	hypothetical protein Y87G2A.13
Locus_24099_Transcript_1/1_Conf_1.000	309	20	5.72E-18	XP_002636521.1	67	93.9745	96	65	Hypothetical protein CBG23202
Locus_241_Transcript_1/2_Conf_1.000	1101	20	4.03E-97	NP_498934.1	74	359.377	303	226	abnormal cell MIGration family member (mig-22)
Locus_241_Transcript_2/2_Conf_1.000	1053	20	2.77E-100	NP_498934.1	78	369.777	287	226	abnormal cell MIGration family member (mig-22)
Locus_2410_Transcript_1/1_Conf_1.000	311	0							
Locus_24100_Transcript_1/1_Conf_1.000	136	0							
Locus_24101_Transcript_1/1_Conf_1.000	136	20	1.97E-18	BAD92458.1	100	95.5153	44	44	hypothetical protein FLJ41407 variant
Locus_24102_Transcript_1/1_Conf_1.000	150	0							
Locus_24103_Transcript_1/1_Conf_1.000	384	0							
Locus_24104_Transcript_1/1_Conf_1.000	201	20	4.03E-11	NP_001122921.1	66	71.2478	68	45	hypothetical protein F17C11.12
Locus_24105_Transcript_1/1_Conf_1.000	242	0							
Locus_24106_Transcript_1/1_Conf_1.000	158	0							

Locus_24107_Transcript_1/1_Conf_1.000	191	20	3.00E-30	XP_002916731.1	100	134.806	63	63	PREDICTED: u4/U6.U5 tri-snRNP-associated protein 1-like
Locus_24108_Transcript_1/1_Conf_1.000	134	20	6.61E-06	DAA27257.1	95	53.9138	44	42	SPARC
Locus_24109_Transcript_1/1_Conf_1.000	218	20	2.16E-25	NP_502044.1	86	118.627	72	62	AQuaPorin or aquaglyceroporin related family member (aqp-3)
Locus_2411_Transcript_1/1_Conf_1.000	2614	20	2.92E-106	XP_001902470.1	55	391.349	585	326	SET domain containing protein
Locus_24110_Transcript_1/1_Conf_1.000	254	0							
Locus_24111_Transcript_1/1_Conf_1.000	137	0							
Locus_24112_Transcript_1/1_Conf_1.000	175	20	1.84E-24	NP_497696.2	96	115.546	58	56	Pim (mammalian oncogene) Related Kinase family member (prk-2)
Locus_24113_Transcript_1/1_Conf_1.000	403								
Locus_24114_Transcript_1/1_Conf_1.000	263	0							
Locus_24115_Transcript_1/1_Conf_1.000	269	0							
Locus_24116_Transcript_1/1_Conf_1.000	135	0							
Locus_24117_Transcript_1/1_Conf_1.000	139	0							

Locus_24118_Transcript_1/1_Conf_1.000	251	20	2.55E-34	NP_001001392.1	98	148.288	70	69	CD44 antigen isoform 5 precursor
Locus_24119_Transcript_1/1_Conf_1.000	140	1	6.15E-04	XP_002640263.1	63	47.3654	46	29	Hypothetical protein CBG12788
Locus_2412_Transcript_1/1_Conf_1.000	1672	20	2.59E-163	AAF63404.1	99	580.096	285	283	AF105967_1galectin
Locus_24120_Transcript_1/1_Conf_1.000	206	0							
Locus_24121_Transcript_1/1_Conf_1.000	272	0							
Locus_24122_Transcript_1/1_Conf_1.000	388	2	1.98E-10	XP_002634119.1	56	68.9366	116	65	Hypothetical protein CBG01673
Locus_24123_Transcript_1/1_Conf_1.000	347	20	1.10E-24	EFO26647.1	73	116.316	114	84	FYVE zinc finger family protein
Locus_24124_Transcript_1/1_Conf_1.000	332	20	2.35E-46	EAX00616.1	100	110.538	46	46	chromosome 2 open reading frame 28, isoform CRA_b
Locus_24125_Transcript_1/1_Conf_1.000	364	20	1.08E-32	XP_001901809.1	70	142.895	118	83	Serine/threonine protein phosphatase PP1-1

Locus_24126_Transcript_1/1_Conf_1.000	296	0							
Locus_24127_Transcript_1/1_Conf_1.000	294	20	2.37E-19	NP_741638.1	70	98.5969	92	65	CYtochrome P450 family member (cyp-35C1)
Locus_24128_Transcript_1/1_Conf_1.000	492	20	2.41E-48	XP_002642154.1	76	194.897	161	123	Hypothetical protein CBG18111
Locus_24129_Transcript_1/1_Conf_1.000	144	20	1.16E-13	XP_001628405.1	93	79.7221	45	42	predicted protein
Locus_2413_Transcript_1/1_Conf_1.000	1443	0							
Locus_24130_Transcript_1/1_Conf_1.000	184	2	9.80E-05	AAN10061.1	71	50.0618	38	27	Kunitz-like protease inhibitor precursor
Locus_24131_Transcript_1/1_Conf_1.000	173	0							
Locus_24132_Transcript_1/1_Conf_1.000	459	1	2.75E-04	XP_002647046.1	56	48.521	73	41	Hypothetical protein CBG03564
Locus_24133_Transcript_1/1_Conf_1.000	321	7	4.33E-13	XP_001901084.1	66	77.7962	77	51	hypothetical protein Bm1_48110
Locus_24134_Transcript_1/1_Conf_1.000	174	0							
Locus_24135_Transcript_1/1_Conf_1.000	218	0							
Locus_24136_Transcript_1/1_Conf_1.000	140	0							
Locus_24137_Transcript_1/1_Conf_1.000	128	0							
Locus_24138_Transcript_1/1_Conf_1.000	236	2	2.21E-17	NP_492944.2	73	92.0485	75	55	hypothetical protein F32B4.5
Locus_24139_Transcript_1/1_Conf_1.000	244	20	1.98E-18	NP_510410.1	75	95.5153	77	58	HIStone family member (his-24)
Locus_2414_Transcript_1/2_Conf_1.000	1323	20	3.46E-40	XP_002641351.1	72	170.629	148	108	C. briggsae CBR-TEG-1 protein
Locus_2414_Transcript_2/2_Conf_1.000	820	20	1.09E-20	NP_510410.1	73	104.76	89	65	HIStone family member (his-24)

Locus_24140_Transcript_1/1_Conf_1.000	141	20	8.80E-19	XP_002829265.1	100	96.6709	47	47	PREDICTED: rRNA 2'-O-methyltransferase fibrillarin-like
Locus_24141_Transcript_1/1_Conf_1.000	236	0							
Locus_24142_Transcript_1/1_Conf_1.000	174	20	2.57E-26	AAA18259.1	100	121.709	57	57	protein kinase C
Locus_24143_Transcript_1/1_Conf_1.000	328	20	7.59E-10	XP_001184423.1	51	67.0106	106	55	PREDICTED: similar to alpha-2-macroglobulin receptor
Locus_24144_Transcript_1/1_Conf_1.000	133	0							
Locus_24145_Transcript_1/1_Conf_1.000	246	20	6.78E-11	XP_001990298.1	71	70.4774	67	48	GH18314
Locus_24146_Transcript_1/1_Conf_1.000	130	0							

Locus_24147_Transcript_1/1_Conf_1.000	379	20	6.62E-30	XP_002639618.1	72	133.65	118	85	Hypothetical protein CBG12331
Locus_24148_Transcript_1/1_Conf_1.000	151	0							
Locus_24149_Transcript_1/1_Conf_1.000	339	0							
Locus_2415_Transcript_1/1_Conf_1.000	1170	20	0	XP_002642268.1	98	711.064	375	370	C. briggsae CBR-ACT-5 protein
Locus_24150_Transcript_1/1_Conf_1.000	206	20	1.13E-21	XP_001099076.2	100	106.301	49	49	PREDICTED: hypothetical protein LOC710457
Locus_24151_Transcript_1/1_Conf_1.000	347	0							
Locus_24152_Transcript_1/1_Conf_1.000	343	6	3.32E-37	AAK09440.1	93	157.918	86	80	AF339097_1fasciclin-like precursor protein
Locus_24153_Transcript_1/1_Conf_1.000	160	0							
Locus_24154_Transcript_1/1_Conf_1.000	128	0							
Locus_24155_Transcript_1/1_Conf_1.000	278	0							
Locus_24156_Transcript_1/1_Conf_1.000	328	0							
Locus_24157_Transcript_1/1_Conf_1.000	323	20	1.53E-34	NP_492266.2	84	149.058	106	90	hypothetical protein C34B7.2
Locus_24158_Transcript_1/1_Conf_1.000	237	0							
Locus_24159_Transcript_1/1_Conf_1.000	200	20	9.95E-10	NP_499001.1	70	66.6254	57	40	hypothetical protein R107.2
Locus_2416_Transcript_1/1_Conf_1.000	1155	20	9.92E-102	NP_492781.2	81	374.785	277	226	hypothetical protein B0511.7

Locus_24160_Transcript_1/1_Conf_1.000	450	20	6.19E-20	EFO19584.1	51	100.523	156	80	histone acetyltransferase MYST1
Locus_24161_Transcript_1/1_Conf_1.000	153	20	8.48E-17	XP_002643253.1	94	90.1225	50	47	C. briggsae CBR-AEX-3 protein
Locus_24162_Transcript_1/1_Conf_1.000	407	0							
Locus_24163_Transcript_1/1_Conf_1.000	314	20	1.89E-32	XP_002429721.1	75	142.124	104	79	low-density lipoprotein receptor, putative

Locus_24164_Transcript_1/1_Conf_1.000	285	20	3.79E-41	CAD44516.1	93	171.014	95	89	VAB-10B protein
Locus_24165_Transcript_1/1_Conf_1.000	132	0							
Locus_24166_Transcript_1/1_Conf_1.000	153	0							
Locus_24167_Transcript_1/1_Conf_1.000	228	0							
Locus_24168_Transcript_1/1_Conf_1.000	219	0							
Locus_24169_Transcript_1/1_Conf_1.000	217	18	1.04E-19	XP_002643289.1	82	99.7525	68	56	C. briggsae CBR-DVE-1 protein
Locus_2417_Transcript_1/2_Conf_1.000	896	0							
Locus_2417_Transcript_2/2_Conf_1.000	887	0							
Locus_24170_Transcript_1/1_Conf_1.000	138	0							
Locus_24171_Transcript_1/1_Conf_1.000	179	0							
Locus_24172_Transcript_1/1_Conf_1.000	198	0							
Locus_24173_Transcript_1/1_Conf_1.000	368	2	2.10E-12	XP_002630024.1	76	75.485	51	39	Hypothetical protein CBG13391
Locus_24174_Transcript_1/1_Conf_1.000	351	0							
Locus_24175_Transcript_1/1_Conf_1.000	131	0							
Locus_24176_Transcript_1/1_Conf_1.000	251	20	8.49E-30	XP_002634445.1	81	133.265	83	68	Hypothetical protein CBG04460
Locus_24177_Transcript_1/1_Conf_1.000	281	0							
Locus_24178_Transcript_1/1_Conf_1.000	234	20	7.83E-23	XP_002603816.1	81	110.153	76	62	hypothetical protein BRAFLDRAFT_124685
Locus_24179_Transcript_1/1_Conf_1.000	331	4	6.61E-14	EFO19179.1	61	80.4925	115	71	hypothetical protein LOAG_09315
Locus_2418_Transcript_1/1_Conf_1.000	485	20	2.37E-27	NP_497641.2	60	125.176	150	91	CaDHerin family member (cdh-1)

Locus_24180_Transcript_1/1_Conf_1.000	359	14	6.82E-19	NP_505989.1	57	97.0561	135	78	SULfate Permease family member (sulp-4)
Locus_24181_Transcript_1/1_Conf_1.000	291	0							
Locus_24182_Transcript_1/1_Conf_1.000	155	0							
Locus_24183_Transcript_1/1_Conf_1.000	203	0							
Locus_24184_Transcript_1/1_Conf_1.000	208	0							
Locus_24185_Transcript_1/1_Conf_1.000	208	20	7.49E-34	XP_002809493.1	100	146.747	65	65	PREDICTED: bifunctional aminoacyl-tRNA synthetase
Locus_24186_Transcript_1/1_Conf_1.000	166	0							
Locus_24187_Transcript_1/1_Conf_1.000	306	2	1.98E-10	NP_509809.2	60	68.9366	88	53	hypothetical protein C05A9.2
Locus_24188_Transcript_1/1_Conf_1.000	245	0							
Locus_24189_Transcript_1/1_Conf_1.000	164	0							
Locus_2419_Transcript_1/1_Conf_1.000	1171	20	3.20E-47	XP_002645722.1	63	193.741	234	149	C. briggsae CBR-ADM-2 protein
Locus_24190_Transcript_1/1_Conf_1.000	206	0							
Locus_24191_Transcript_1/1_Conf_1.000	166	20	3.28E-21	AAI00854.1	100	104.76	52	52	Cytochrome c oxidase subunit VIIa polypeptide 2 (liver)
Locus_24192_Transcript_1/1_Conf_1.000	154	20	3.33E-13	XP_002642408.1	84	78.1814	50	42	C. briggsae CBR-NHL-1 protein
Locus_24193_Transcript_1/1_Conf_1.000	178	0							
Locus_24194_Transcript_1/1_Conf_1.000	312	20	3.23E-24	XP_001901686.1	72	114.775	99	72	Cohesin subunit SA-1
Locus_24195_Transcript_1/1_Conf_1.000	279	0							
Locus_24196_Transcript_1/1_Conf_1.000	286	0							
Locus_24197_Transcript_1/1_Conf_1.000	146	0							
Locus_24198_Transcript_1/1_Conf_1.000	432	20	1.40E-64	NP_871810.1	93	248.825	143	133	HAlF transporter (PGP related) family member (haf-9)
Locus_24199_Transcript_1/1_Conf_1.000	264	20	1.81E-27	NP_495790.1	81	125.561	87	71	beta-LACTamase domain containing family member (lact-4)
Locus_242_Transcript_1/1_Conf_1.000	464	20	1.48E-37	NP_001021606.1	72	159.073	131	95	hypothetical protein T03F1.12
Locus_2420_Transcript_1/1_Conf_1.000	296	0							
Locus_24200_Transcript_1/1_Conf_1.000	144	5	2.11E-07	NP_001129925.1	74	58.9214	47	35	High Incidence of Males (increased X chromosome loss) family member (him-4)

Locus_24201_Transcript_1/1_Conf_1.000	240	20	9.53E-13	EFO15112.1	69	76.6406	76	53	hypothetical protein LOAG_13403
Locus_24202_Transcript_1/1_Conf_1.000	131	0							
Locus_24203_Transcript_1/1_Conf_1.000	216	0							
Locus_24204_Transcript_1/1_Conf_1.000	311	0							
Locus_24205_Transcript_1/1_Conf_1.000	150	20	1.19E-10	XP_002634930.1	82	69.707	46	38	Hypothetical protein CBG22529
Locus_24206_Transcript_1/1_Conf_1.000	138	0							
Locus_24207_Transcript_1/1_Conf_1.000	194	4	6.32E-14	XP_002631791.1	77	68.1662	48	37	Hypothetical protein CBG21009
Locus_24208_Transcript_1/1_Conf_1.000	168	14	1.47E-13	XP_002644186.1	85	79.337	54	46	Hypothetical protein CBG17168
Locus_24209_Transcript_1/1_Conf_1.000	522	20	6.05E-35	XP_002632055.1	61	150.599	181	111	C. briggsae CBR-VAB-19 protein
Locus_2421_Transcript_1/1_Conf_1.000	882	20	4.08E-72	XP_001900701.1	65	275.789	286	187	hypothetical protein Bm1_46195
Locus_24210_Transcript_1/1_Conf_1.000	265	20	1.29E-41	XP_002633950.1	87	172.555	88	77	C. briggsae CBR-FBL-1 protein
Locus_24211_Transcript_1/1_Conf_1.000	292	0							
Locus_24212_Transcript_1/1_Conf_1.000	163	0							
Locus_24213_Transcript_1/1_Conf_1.000	137	0							
Locus_24214_Transcript_1/1_Conf_1.000	159	20	5.64E-21	XP_002923631.1	100	103.99	52	52	PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like isoform 2

Locus_24215_Transcript_1/1_Conf_1.000	270	10	1.21E-15	EFO20077.1	75	86.2705	72	54	hypothetical protein LOAG_08413
Locus_24216_Transcript_1/1_Conf_1.000	253	0							
Locus_24217_Transcript_1/1_Conf_1.000	405	1	2.70E-07	YP_002000086.1	45	58.5362	97	44	virulence-associated lipoprotein MIA
Locus_24218_Transcript_1/1_Conf_1.000	184	1	3.72E-04	AAO63576.1	53	48.1358	62	33	secreted protein 4 precursor
Locus_24219_Transcript_1/1_Conf_1.000	379	4	7.85E-15	XP_002631397.1	56	83.5741	121	68	C. briggsae CBR-DEP-1 protein
Locus_2422_Transcript_1/1_Conf_1.000	360	0							
Locus_24220_Transcript_1/1_Conf_1.000	375	20	4.75E-36	XP_002635372.1	80	154.066	118	95	C. briggsae CBR-RPM-1 protein
Locus_24221_Transcript_1/1_Conf_1.000	151	20	3.95E-14	ADM44660.1	82	81.2629	51	42	immunoglobulin epsilon heavy chain variable region
Locus_24222_Transcript_1/1_Conf_1.000	139	0							
Locus_24223_Transcript_1/1_Conf_1.000	195	20	9.94E-26	NP_495986.3	98	119.783	65	64	EATing: abnormal pharyngeal pumping family member (eat-3)
Locus_24224_Transcript_1/1_Conf_1.000	136	0							
Locus_24225_Transcript_1/1_Conf_1.000	298	0							
Locus_24226_Transcript_1/1_Conf_1.000	142	20	9.41E-21	XP_001713909.1	100	103.219	46	46	PREDICTED: similar to MHC class II antigen
Locus_24227_Transcript_1/1_Conf_1.000	253	7	5.91E-18	NP_494897.3	66	93.9745	80	53	hypothetical protein R05F9.12
Locus_24228_Transcript_1/1_Conf_1.000	221	0							
Locus_24229_Transcript_1/1_Conf_1.000	244	0							

Locus_2423_Transcript_1/2_Conf_1.000	1601	20	1.59E-138	XP_002637274.1	81	497.664	356	291	Hypothetical protein CBG18957
Locus_2423_Transcript_2/2_Conf_1.000	1541	20	6.60E-142	XP_002637274.1	86	508.834	336	289	Hypothetical protein CBG18957
Locus_24230_Transcript_1/1_Conf_1.000	266	20	1.53E-18	EFO24692.1	70	95.9005	86	61	protein-tyrosine phosphatase
Locus_24231_Transcript_1/1_Conf_1.000	265	12	5.64E-13	XP_002640224.1	68	77.411	83	57	C. briggsae CBR-SMG-1 protein
Locus_24232_Transcript_1/1_Conf_1.000	129	0							
Locus_24233_Transcript_1/1_Conf_1.000	132	0							
Locus_24234_Transcript_1/1_Conf_1.000	162	20	1.58E-23	DAA31575.1	100	112.464	53	53	cold shock domain containing E1, RNA-binding
Locus_24235_Transcript_1/1_Conf_1.000	520	0							
Locus_24236_Transcript_1/1_Conf_1.000	221	20	3.95E-30	NP_741812.1	89	134.42	73	65	hypothetical protein T07H6.1
Locus_24237_Transcript_1/1_Conf_1.000	200	20	2.00E-18	NP_872022.1	80	95.5153	65	52	CysTiNoSin (lysosomal protein) homolog family member (ctns-1)
Locus_24238_Transcript_1/1_Conf_1.000	149	0							
Locus_24239_Transcript_1/1_Conf_1.000	234	0							
Locus_2424_Transcript_1/2_Conf_1.000	1973	20	3.29E-152	NP_491664.1	61	543.502	685	423	UNCoordinated family member (unc-40)
Locus_2424_Transcript_2/2_Conf_1.000	1793	20	3.67E-171	NP_491664.1	69	606.29	625	432	UNCoordinated family member (unc-40)
Locus_24240_Transcript_1/1_Conf_1.000	313	0							
Locus_24241_Transcript_1/1_Conf_1.000	418	0							
Locus_24242_Transcript_1/1_Conf_1.000	357	3	6.18E-12	NP_001023197.1	64	73.9442	111	72	hypothetical protein F38E11.6
Locus_24243_Transcript_1/1_Conf_1.000	181	2	4.12E-11	XP_001898554.1	72	71.2478	59	43	DOMON domain containing protein

Locus_24244_Transcript_1/1_Conf_1.000	150	20	6.09E-15	XP_002640668.1	97	83.9593	45	44	C. briggsae CBR-UNC-54 protein
Locus_24245_Transcript_1/1_Conf_1.000	249	0							
Locus_24246_Transcript_1/1_Conf_1.000	280	0							
Locus_24247_Transcript_1/1_Conf_1.000	212	20	1.41E-24	NP_508573.1	85	115.931	70	60	Discoidin Domain Receptor family member (ddr-2)
Locus_24248_Transcript_1/1_Conf_1.000	220	0							
Locus_24249_Transcript_1/1_Conf_1.000	415	0							

Locus_2425_Transcript_1/1_Conf_1.000	1947	20	0	NP_490866.4	95	833.558	463	442	SRC oncogene related family member (src-1)
Locus_24250_Transcript_1/1_Conf_1.000	412	20	3.37E-18	XP_002631639.1	62	94.7449	116	73	Hypothetical protein CBG20828
Locus_24251_Transcript_1/1_Conf_1.000	169	0							
Locus_24252_Transcript_1/1_Conf_1.000	165	0							
Locus_24253_Transcript_1/1_Conf_1.000	195	20	2.53E-21	NP_495697.2	90	105.145	64	58	Lim and Transglutaminase Domain family member (ltd-1)
Locus_24254_Transcript_1/1_Conf_1.000	246	0							
Locus_24255_Transcript_1/1_Conf_1.000	174	2	9.19E-08	XP_002646794.1	75	60.077	53	40	C. briggsae CBR-RHGF-2 protein
Locus_24256_Transcript_1/1_Conf_1.000	219	0							
Locus_24257_Transcript_1/1_Conf_1.000	131	0							
Locus_24258_Transcript_1/1_Conf_1.000	208	2	4.89E-09	NP_490719.1	69	64.3142	53	37	hypothetical protein Y48G1A.3
Locus_24259_Transcript_1/1_Conf_1.000	600	6	1.06E-35	CAR63655.1	94	153.68	73	69	hypothetical protein
Locus_2426_Transcript_1/1_Conf_1.000	502	20	1.71E-09	EFO21554.1	56	65.855	81	46	hypothetical protein LOAG_06935
Locus_24260_Transcript_1/1_Conf_1.000	297	20	7.28E-45	NP_498931.2	91	183.341	101	92	SMAll family member (sma-2)
Locus_24261_Transcript_1/1_Conf_1.000	142	0							
Locus_24262_Transcript_1/1_Conf_1.000	204	0							
Locus_24263_Transcript_1/1_Conf_1.000	168	0							
Locus_24264_Transcript_1/1_Conf_1.000	181	0							

Locus_24265_Transcript_1/1_Conf_1.000	186	20	4.35E-29	XP_002831612.1	100	130.954	61	61	PREDICTED: NADH dehydrogenase ubiquinone 1 alpha subcomplex subunit 4
Locus_24266_Transcript_1/1_Conf_1.000	278	9	7.76E-15	NP_498229.3	74	83.5741	81	60	Regulator of G protein Signaling family member (rgs-5)
Locus_24267_Transcript_1/1_Conf_1.000	178	0							
Locus_24268_Transcript_1/1_Conf_1.000	189	0							
Locus_24269_Transcript_1/1_Conf_1.000	160	0							
Locus_2427_Transcript_1/3_Conf_0.714	957	20	3.62E-32	EFO20353.1	60	143.28	175	106	hypothetical protein LOAG_08138
Locus_2427_Transcript_2/3_Conf_0.429	888	20	9.31E-32	EFO20353.1	62	141.739	158	99	hypothetical protein LOAG_08138
Locus_2427_Transcript_3/3_Conf_0.714	888	20	9.31E-32	EFO20353.1	62	141.739	158	99	hypothetical protein LOAG_08138
Locus_24270_Transcript_1/1_Conf_1.000	216	20	7.73E-07	BAC54021.1	58	56.9954	58	34	C-type lectin 2
Locus_24271_Transcript_1/1_Conf_1.000	150	0							
Locus_24272_Transcript_1/1_Conf_1.000	240	20	3.28E-13	XP_002634543.1	80	78.1814	71	57	C. briggsae CBR-CED-5 protein
Locus_24273_Transcript_1/1_Conf_1.000	156	0							
Locus_24274_Transcript_1/1_Conf_1.000	225	4	3.68E-12	EFO20220.1	80	74.7146	56	45	hypothetical protein LOAG_08273
Locus_24275_Transcript_1/1_Conf_1.000	228	9	3.21E-16	NP_001122921.1	74	88.1965	74	55	hypothetical protein F17C11.12

Locus_24276_Transcript_1/1_Conf_1.000	145	20	3.48E-10	NP_496115.1	81	68.1662	48	39	CYtochrome P450 family member (cyp-13A8)
Locus_24277_Transcript_1/1_Conf_1.000	357	20	4.68E-52	XP_002629849.1	94	207.223	117	110	C. briggsae CBR-RAB-39 protein
Locus_24278_Transcript_1/1_Conf_1.000	213	0							
Locus_24279_Transcript_1/1_Conf_1.000	240	0							
Locus_2428_Transcript_1/1_Conf_1.000	604	20	3.13E-27	NP_492063.1	80	125.561	89	72	DYnein Light chain (Tctex type family member (dylt-1)
Locus_24280_Transcript_1/1_Conf_1.000	484	20	2.45E-40	NP_495790.1	73	168.318	145	107	beta-LACTamase domain containing family member (lact-4)
Locus_24281_Transcript_1/1_Conf_1.000	137	0							
Locus_24282_Transcript_1/1_Conf_1.000	206	2	6.19E-12	XP_002633595.1	88	73.9442	43	38	Hypothetical protein CBG05472
Locus_24283_Transcript_1/1_Conf_1.000	184	0							
Locus_24284_Transcript_1/1_Conf_1.000	154	0							
Locus_24285_Transcript_1/1_Conf_1.000	143	0							
Locus_24286_Transcript_1/1_Conf_1.000	141	0							
Locus_24287_Transcript_1/1_Conf_1.000	334	11	9.48E-21	NP_496106.2	72	103.219	88	64	hypothetical protein ZK1321.4
Locus_24288_Transcript_1/1_Conf_1.000	198	0							
Locus_24289_Transcript_1/1_Conf_1.000	161	0							
Locus_2429_Transcript_1/2_Conf_1.000	1332	20	1.81E-121	NP_501711.1	68	440.654	445	307	AMPHiphysin homolog family member (amph-1)
Locus_2429_Transcript_2/2_Conf_1.000	756	20	1.71E-22	XP_002633971.1	80	110.538	73	59	C. briggsae CBR-AMPH-1 protein
Locus_24290_Transcript_1/1_Conf_1.000	179	0							
Locus_24291_Transcript_1/1_Conf_1.000	288	0							
Locus_24292_Transcript_1/1_Conf_1.000	177	20	2.10E-20	NP_741242.1	91	102.064	59	54	Dipeptidyl Peptidase Four (IV) family member (dpf-6)
Locus_24293_Transcript_1/1_Conf_1.000	132	20	1.68E-17	DAA31575.1	100	92.4337	43	43	cold shock domain containing E1, RNA-binding

Locus_24294_Transcript_1/1_Conf_1.000	259	20	6.49E-17	XP_001899548.1	66	90.5077	87	58	Immunoglobulin I-set domain containing protein
Locus_24295_Transcript_1/1_Conf_1.000	144	0							
Locus_24296_Transcript_1/1_Conf_1.000	302	0							
Locus_24297_Transcript_1/1_Conf_1.000	273	6	4.58E-07	EFO18390.1	54	57.7658	83	45	hypothetical protein LOAG_10106
Locus_24298_Transcript_1/1_Conf_1.000	135	20	6.36E-09	NP_001014338.1	79	63.929	44	35	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial precursor
Locus_24299_Transcript_1/1_Conf_1.000	389	20	2.64E-47	NP_508711.1	83	191.43	128	107	Vacuolar H ATPase family member (vha-12)
Locus_243_Transcript_1/2_Conf_1.000	330	20	3.24E-53	EFO21508.1	100	211.075	109	109	ubiquitin C II
Locus_243_Transcript_2/2_Conf_1.000	828	20	3.59E-136	EFO21508.1	100	488.419	255	255	ubiquitin C II
Locus_2430_Transcript_1/1_Conf_1.000	497	20	6.92E-72	XP_001477246.1	100	273.092	135	135	PREDICTED: similar to ribosomal protein
Locus_24300_Transcript_1/1_Conf_1.000	155	0							
Locus_24301_Transcript_1/1_Conf_1.000	163	20	6.87E-19	XP_001895981.1	94	97.0561	53	50	probable spectrin beta chain
Locus_24302_Transcript_1/1_Conf_1.000	145	0							
Locus_24303_Transcript_1/1_Conf_1.000	161	0							

Locus_24304_Transcript_1/1_Conf_1.000	313	20	2.10E-15	XP_002426250.1	67	85.5001	67	45	Ubl carboxyl-terminal hydrolase, putative
Locus_24305_Transcript_1/1_Conf_1.000	157	0							
Locus_24306_Transcript_1/1_Conf_1.000	233	0							
Locus_24307_Transcript_1/1_Conf_1.000	141	7	7.22E-13	XP_001899214.1	80	77.0258	46	37	MSP domain protein 2
Locus_24308_Transcript_1/1_Conf_1.000	154	0							
Locus_24309_Transcript_1/1_Conf_1.000	198	0							
Locus_2431_Transcript_1/1_Conf_1.000	1226	20	0	AAF86584.1	95	649.047	339	323	cathepsin L cysteine protease
Locus_24310_Transcript_1/1_Conf_1.000	221	0							
Locus_24311_Transcript_1/1_Conf_1.000	230	0							
Locus_24312_Transcript_1/1_Conf_1.000	866	17	1.17E-15	NP_001022738.1	47	88.1965	270	127	hypothetical protein R74.8
Locus_24313_Transcript_1/1_Conf_1.000	304	20	3.15E-32	XP_002647589.1	84	141.354	100	84	Hypothetical protein CBG06677
Locus_24314_Transcript_1/1_Conf_1.000	295	0							
Locus_24315_Transcript_1/1_Conf_1.000	278	14	1.67E-09	NP_741839.2	52	65.855	78	41	hypothetical protein F48E3.8
Locus_24316_Transcript_1/1_Conf_1.000	442	20	6.43E-49	XP_002634964.1	77	196.823	146	113	Hypothetical protein CBG13500
Locus_24317_Transcript_1/1_Conf_1.000	146	5	1.67E-12	XP_001893342.1	87	75.8702	48	42	chloride channel protein 7
Locus_24318_Transcript_1/1_Conf_1.000	361	0							
Locus_24319_Transcript_1/1_Conf_1.000	219	1	2.57E-13	NP_508464.2	77	78.5666	68	53	hypothetical protein F52H2.7
Locus_2432_Transcript_1/2_Conf_1.000	590	20	7.59E-52	NP_492097.1	77	207.223	164	127	hypothetical protein ZK524.4
Locus_2432_Transcript_2/2_Conf_1.000	649	20	9.77E-52	NP_492097.1	77	207.223	164	127	hypothetical protein ZK524.4
Locus_24320_Transcript_1/1_Conf_1.000	191	19	2.02E-18	XP_002642115.1	84	95.5153	57	48	C. briggsae CBR-NDG-4 protein

Locus_24321_Transcript_1/1_Conf_1.000	189	20	8.76E-22	NP_001020988.1	87	106.686	62	54	UNCoordinated family member (unc-89)
Locus_24322_Transcript_1/1_Conf_1.000	169	0							
Locus_24323_Transcript_1/1_Conf_1.000	321	0							
Locus_24324_Transcript_1/1_Conf_1.000	373	1	8.21E-04	NP_509241.1	52	46.9802	124	65	AuTophaGy (yeast Atg homolog) family member (atg-11)
Locus_24325_Transcript_1/1_Conf_1.000	260	0							
Locus_24326_Transcript_1/1_Conf_1.000	311	0							
Locus_24327_Transcript_1/1_Conf_1.000	143	0							
Locus_24328_Transcript_1/1_Conf_1.000	204	1	2.69E-15	XP_861221.1	87	85.1149	48	42	PREDICTED: similar to protein phosphatase 1G isoform 3
Locus_24329_Transcript_1/1_Conf_1.000	152	0							
Locus_2433_Transcript_1/1_Conf_1.000	842	20	1.62E-99	XP_002591721.1	78	366.696	279	220	hypothetical protein BRAFLDRAFT_80816
Locus_24330_Transcript_1/1_Conf_1.000	315	11	8.81E-06	NP_001129799.1	78	53.5286	50	39	Nuclear Hormone Receptor family member (nhr-62)
Locus_24331_Transcript_1/1_Conf_1.000	178	10	1.61E-12	NP_001122601.1	69	75.8702	73	51	Multiple PDZ domain protein family member (mpz-1)
Locus_24332_Transcript_1/1_Conf_1.000	192	6	1.26E-12	XP_002639323.1	75	76.2554	66	50	C. briggsae CBR-HUM-7 protein

Locus_24333_Transcript_1/1_Conf_1.000	172	20	5.57E-21	EFO16323.1	92	103.99	57	53	CAMK/PSK protein kinase
Locus_24334_Transcript_1/1_Conf_1.000	145	0							
Locus_24335_Transcript_1/1_Conf_1.000	130	0							
Locus_24336_Transcript_1/1_Conf_1.000	166	20	3.07E-19	NP_001122814.1	92	98.2117	53	49	STAT transcription factor family member (sta-1)
Locus_24337_Transcript_1/1_Conf_1.000	178	0							
Locus_24338_Transcript_1/1_Conf_1.000	178	0							
Locus_24339_Transcript_1/1_Conf_1.000	144	0							
Locus_2434_Transcript_1/1_Conf_1.000	469	20	2.84E-73	XP_002815481.1	98	277.715	156	154	PREDICTED: 60S ribosomal protein L27a-like
Locus_24340_Transcript_1/1_Conf_1.000	185	20	1.78E-22	XP_002641381.1	88	108.997	61	54	Hypothetical protein CBG13238
Locus_24341_Transcript_1/1_Conf_1.000	134	0							
Locus_24342_Transcript_1/1_Conf_1.000	220	0							
Locus_24343_Transcript_1/1_Conf_1.000	260	0							
Locus_24344_Transcript_1/1_Conf_1.000	344	0							
Locus_24345_Transcript_1/1_Conf_1.000	133	0							
Locus_24346_Transcript_1/1_Conf_1.000	132	20	4.88E-17	XP_002927181.1	100	90.8929	43	43	PREDICTED: LOW QUALITY PROTEIN: Golgi apparatus protein 1-like
Locus_24347_Transcript_1/1_Conf_1.000	225	20	1.11E-16	YP_003885693.1	70	89.7373	75	53	alpha/beta hydrolase fold protein
Locus_24348_Transcript_1/1_Conf_1.000	144	0							
Locus_24349_Transcript_1/1_Conf_1.000	216	0							
Locus_2435_Transcript_1/2_Conf_1.000	151	0							
Locus_2435_Transcript_2/2_Conf_1.000	170	1	2.69E-07	P51536.1	71	58.5362	49	35	Globin
Locus_24350_Transcript_1/1_Conf_1.000	199	5	2.44E-24	NP_001022641.1	87	115.161	66	58	LEThal family member (let-805)
Locus_24351_Transcript_1/1_Conf_1.000	154	0							

Locus_24352_Transcript_1/1_Conf_1.000	137	20	1.05E-11	NP_495799.1	91	73.1738	45	41	hypothetical protein T13H5.4
Locus_24353_Transcript_1/1_Conf_1.000	292	10	3.11E-11	NP_001023172.1	62	71.633	102	64	Inositol Triphosphate Receptor family member (itr-1)
Locus_24354_Transcript_1/1_Conf_1.000	224								
Locus_24355_Transcript_1/1_Conf_1.000	505	6	1.34E-25	NP_492101.1	59	119.398	144	86	hypothetical protein T28F4.4
Locus_24356_Transcript_1/1_Conf_1.000	171	8	1.16E-10	NP_001024200.1	83	69.707	54	45	TiTiN family member (ttn-1)
Locus_24357_Transcript_1/1_Conf_1.000	154	1	2.47E-08	NP_509760.2	68	62.003	48	33	Temporarily Assigned Gene name family member (tag-289)
Locus_24358_Transcript_1/1_Conf_1.000	288	0							
Locus_24359_Transcript_1/1_Conf_1.000	239	20	1.17E-10	NP_492984.1	60	69.707	70	42	O-ACyltransferase homolog family member (oac-19)
Locus_2436_Transcript_1/1_Conf_1.000	402	0							
Locus_24360_Transcript_1/1_Conf_1.000	288	20	1.49E-21	XP_002643681.1	77	105.916	94	73	Hypothetical protein CBG01860
Locus_24361_Transcript_1/1_Conf_1.000	236	0							
Locus_24362_Transcript_1/1_Conf_1.000	284	0							
Locus_24363_Transcript_1/1_Conf_1.000	135	0							
Locus_24364_Transcript_1/1_Conf_1.000	129	0							
Locus_24365_Transcript_1/1_Conf_1.000	272	0							
Locus_24366_Transcript_1/1_Conf_1.000	361	2	7.01E-24	NP_508797.3	68	113.62	116	79	Nuclear Hormone Receptor family member (nhr-45)
Locus_24367_Transcript_1/1_Conf_1.000	149	0							
Locus_24368_Transcript_1/1_Conf_1.000	236								
Locus_24369_Transcript_1/1_Conf_1.000	300	0							
Locus_2437_Transcript_1/1_Conf_1.000	4194	20	0	EFO20269.1	56	702.59	1020	581	hypothetical protein LOAG_08219
Locus_24370_Transcript_1/1_Conf_1.000	187	0							
Locus_24371_Transcript_1/1_Conf_1.000	265	0							
Locus_24372_Transcript_1/1_Conf_1.000	252	7	3.23E-24	Q09600.2	78	114.775	82	64	Vacuolar protein sorting-associated protein 11 homolog
Locus_24373_Transcript_1/1_Conf_1.000	423	0							
Locus_24374_Transcript_1/1_Conf_1.000	251	2	1.97E-10	XP_002640291.1	83	68.9366	49	41	Hypothetical protein CBG12817
Locus_24375_Transcript_1/1_Conf_1.000	164	0							

Locus_24376_Transcript_1/1_Conf_1.000	243	20	3.59E-28	ABW80085.1	84	127.872	82	69	immunoglobulin heavy chain variable region
Locus_24377_Transcript_1/1_Conf_1.000	282	7	5.02E-09	Q60LV7.3	61	64.3142	86	53	Kinesin-like protein vab-8
Locus_24378_Transcript_1/1_Conf_1.000	209	0							
Locus_24379_Transcript_1/1_Conf_1.000	221	0							
Locus_2438_Transcript_1/1_Conf_1.000	974	20	3.92E-82	XP_002631685.1	74	309.301	255	191	Hypothetical protein CBG20878
Locus_24380_Transcript_1/1_Conf_1.000	217	20	3.34E-18	XP_002629800.1	80	94.7449	56	45	C. briggsae CBR-MAB-3.1 protein
Locus_24381_Transcript_1/1_Conf_1.000	133	0							
Locus_24382_Transcript_1/1_Conf_1.000	288	20	3.56E-15	ADK91433.1	60	84.7297	86	52	c-type lectin 1
Locus_24383_Transcript_1/1_Conf_1.000	528	20	1.12E-23	EFO20021.1	52	113.235	161	84	hypothetical protein LOAG_08471
Locus_24384_Transcript_1/1_Conf_1.000	171	20	5.38E-24	XP_002825166.1	100	114.005	56	56	PREDICTED: cytoplasmic dynein 1 heavy chain 1-like, partial
Locus_24385_Transcript_1/1_Conf_1.000	130	0							
Locus_24386_Transcript_1/1_Conf_1.000	396	20	2.99E-38	CAA92456.3	85	161.384	124	106	C. elegans protein C53B4.4b, partially confirmed by transcript evidence
Locus_24387_Transcript_1/1_Conf_1.000	139	20	2.94E-14	XP_002641617.1	91	81.6481	46	42	C. briggsae CBR-MOG-1 protein
Locus_24388_Transcript_1/1_Conf_1.000	139	0							
Locus_24389_Transcript_1/1_Conf_1.000	137	0							
Locus_2439_Transcript_1/1_Conf_1.000	705	0							

Locus_24390_Transcript_1/1_Conf_1.000	195	0							
Locus_24391_Transcript_1/1_Conf_1.000	266	0							
Locus_24392_Transcript_1/1_Conf_1.000	343	17	2.01E-34	XP_002634184.1	78	148.673	114	89	C. briggsae CBR-QUI-1 protein
Locus_24393_Transcript_1/1_Conf_1.000	200	0							
Locus_24394_Transcript_1/1_Conf_1.000	258	0							
Locus_24395_Transcript_1/1_Conf_1.000	256	0							
Locus_24396_Transcript_1/1_Conf_1.000	294	0							
Locus_24397_Transcript_1/1_Conf_1.000	330	20	2.05E-15	XP_002130849.1	57	85.5001	105	60	PREDICTED: similar to predicted protein
Locus_24398_Transcript_1/1_Conf_1.000	190	0							
Locus_24399_Transcript_1/1_Conf_1.000	211	0							
Locus_244_Transcript_1/3_Conf_0.714	1927	20	1.47E-165	XP_002631704.1	78	587.8	514	402	Hypothetical protein CBG20903
Locus_244_Transcript_2/3_Conf_0.714	1927	20	1.47E-165	XP_002631704.1	78	587.8	514	402	Hypothetical protein CBG20903
Locus_244_Transcript_3/3_Conf_0.714	1927	20	1.47E-165	XP_002631704.1	78	587.8	514	402	Hypothetical protein CBG20903
Locus_2440_Transcript_1/1_Conf_1.000	483	0							
Locus_24400_Transcript_1/1_Conf_1.000	144	0							
Locus_24401_Transcript_1/1_Conf_1.000	432	0							
Locus_24402_Transcript_1/1_Conf_1.000	178	0							
Locus_24403_Transcript_1/1_Conf_1.000	306	0							
Locus_24404_Transcript_1/1_Conf_1.000	169	0							
Locus_24405_Transcript_1/1_Conf_1.000	233	0							
Locus_24406_Transcript_1/1_Conf_1.000	206	20	4.74E-12	NP_504354.1	79	74.3294	48	38	hypothetical protein K11D12.9
Locus_24407_Transcript_1/1_Conf_1.000	177	2	1.05E-11	XP_002634565.1	64	73.1738	64	41	C. briggsae CBR-INS-1 protein

Locus_24408_Transcript_1/1_Conf_1.000	247	20	1.32E-22	EFO19136.1	77	109.383	81	63	TKL/STKR/TYPE1 protein kinase
Locus_24409_Transcript_1/1_Conf_1.000	131	0							
Locus_2441_Transcript_1/1_Conf_1.000	498	0							
Locus_24410_Transcript_1/1_Conf_1.000	370	0							
Locus_24411_Transcript_1/1_Conf_1.000	130	0							
Locus_24412_Transcript_1/1_Conf_1.000	130	20	1.09E-08	NP_494912.1	80	63.1586	42	34	NuDiX family member (ndx-3)
Locus_24413_Transcript_1/1_Conf_1.000	132	0							
Locus_24414_Transcript_1/1_Conf_1.000	414	20	3.79E-54	NP_502964.2	89	214.157	136	122	hypothetical protein Y51H4A.7
Locus_24415_Transcript_1/1_Conf_1.000	136	0							
Locus_24416_Transcript_1/1_Conf_1.000	164	0							
Locus_24417_Transcript_1/1_Conf_1.000	182	5	1.42E-11	NP_509645.1	77	72.7886	49	38	DumPY : shorter than wild-type family member (dpy-22)
Locus_24418_Transcript_1/1_Conf_1.000	442	3	1.04E-14	XP_002642231.1	59	83.1889	122	73	Hypothetical protein CBG18209
Locus_24419_Transcript_1/1_Conf_1.000	211	0							
Locus_2442_Transcript_1/1_Conf_1.000	379	20	1.09E-24	NP_502571.1	80	116.316	110	89	Ribosomal protein, Large subunit, Acidic (P1) family member (rla-2)
Locus_24420_Transcript_1/1_Conf_1.000	143	0							

Locus_24421_Transcript_1/1_Conf_1.000	201	4	5.62E-13	CAR63703.1	73	77.411	56	41	hypothetical protein
Locus_24422_Transcript_1/1_Conf_1.000	373	0							
Locus_24423_Transcript_1/1_Conf_1.000	173	20	1.37E-19	ADN38247.1	100	99.3673	57	57	MHC class I antigen
Locus_24424_Transcript_1/1_Conf_1.000	276	20	1.28E-09	NP_509658.1	72	66.2402	51	37	Multidrug Resistance Protein family member (mrp-4)
Locus_24425_Transcript_1/1_Conf_1.000	194	0							
Locus_24426_Transcript_1/1_Conf_1.000	306	0							
Locus_24427_Transcript_1/1_Conf_1.000	133	0							
Locus_24428_Transcript_1/1_Conf_1.000	217	20	4.36E-26	AAA62207.1	89	120.939	69	62	prolyl 4-hydroxylase alpha subunit
Locus_24429_Transcript_1/1_Conf_1.000	287	3	2.74E-15	NP_494848.3	70	85.1149	81	57	fatty Acid CoA Synthetase family member (acs-11)
Locus_2443_Transcript_1/1_Conf_1.000	437	3	3.85E-06	NP_506662.1	51	54.6842	97	50	hypothetical protein ZC412.3
Locus_24430_Transcript_1/1_Conf_1.000	308	4	3.05E-19	XP_002640160.1	69	98.2117	102	71	Hypothetical protein CBG12661
Locus_24431_Transcript_1/1_Conf_1.000	163	0							
Locus_24432_Transcript_1/1_Conf_1.000	275	12	3.60E-28	XP_002636027.1	79	127.872	88	70	C. briggsae CBR-ABT-4 protein
Locus_24433_Transcript_1/1_Conf_1.000	140	0							
Locus_24434_Transcript_1/1_Conf_1.000	180	0							
Locus_24435_Transcript_1/1_Conf_1.000	181	20	1.51E-13	XP_002633107.1	78	79.337	60	47	Hypothetical protein CBG05798
Locus_24436_Transcript_1/1_Conf_1.000	258	20	3.67E-20	NP_001040940.1	67	101.293	84	57	PhosphatidylSerine Receptor family member (psr-1)
Locus_24437_Transcript_1/1_Conf_1.000	228	0							
Locus_24438_Transcript_1/1_Conf_1.000	293	0							
Locus_24439_Transcript_1/1_Conf_1.000	306	0							
Locus_2444_Transcript_1/1_Conf_1.000	891	5	1.19E-26	XP_002634353.1	53	124.79	247	131	Hypothetical protein CBG17703
Locus_24440_Transcript_1/1_Conf_1.000	128	0							
Locus_24441_Transcript_1/1_Conf_1.000	176	0							
Locus_24442_Transcript_1/1_Conf_1.000	277	0							
Locus_24443_Transcript_1/1_Conf_1.000	185	20	1.04E-22	XP_002639077.1	83	109.768	61	51	Hypothetical protein CBG14895

Locus_24444_Transcript_1/1_Conf_1.000	463	2	1.65E-28	NP_493079.1	76	129.028	143	110	hypothetical protein C15C6.1
Locus_24445_Transcript_1/1_Conf_1.000	164	0							
Locus_24446_Transcript_1/1_Conf_1.000	131	4	1.48E-05	NP_496976.2	72	52.7582	43	31	hypothetical protein Y54G11A.7
Locus_24447_Transcript_1/1_Conf_1.000	397	0							
Locus_24448_Transcript_1/1_Conf_1.000	250	0							
Locus_24449_Transcript_1/1_Conf_1.000	135	0							
Locus_2445_Transcript_1/1_Conf_1.000	1244	20	5.89E-95	XP_002642343.1	68	352.443	434	297	C. briggsae CBR-CNT-2 protein
Locus_24450_Transcript_1/1_Conf_1.000	201	0							
Locus_24451_Transcript_1/1_Conf_1.000	184	0							
Locus_24452_Transcript_1/1_Conf_1.000	242	20	3.48E-39	NP_506014.1	97	164.466	80	78	Protein Kinase C family member (pkc-1)
Locus_24453_Transcript_1/1_Conf_1.000	163	20	1.10E-16	XP_002646949.1	90	89.7373	52	47	C. briggsae CBR-APD-3 protein
Locus_24454_Transcript_1/1_Conf_1.000	161	4	6.05E-07	XP_001897054.1	75	57.3806	41	31	Fes/CIP4 homology domain containing protein
Locus_24455_Transcript_1/1_Conf_1.000	212	0							
Locus_24456_Transcript_1/1_Conf_1.000	178	20	2.57E-18	ADI24637.1	84	95.1301	59	50	Lin-12 and glp-1 x-hybridizing protein 1, isoform a, partially confirmed by transcript evidence
Locus_24457_Transcript_1/1_Conf_1.000	143	0							
Locus_24458_Transcript_1/1_Conf_1.000	146	0							
Locus_24459_Transcript_1/1_Conf_1.000	292	0							
Locus_2446_Transcript_1/3_Conf_0.750	1744	20	4.61E-70	XP_002639919.1	61	270.396	332	203	Hypothetical protein CBG08251
Locus_2446_Transcript_2/3_Conf_0.750	1744	20	4.61E-70	XP_002639919.1	61	270.396	332	203	Hypothetical protein CBG08251
Locus_2446_Transcript_3/3_Conf_0.750	1744	20	4.61E-70	XP_002639919.1	61	270.396	332	203	Hypothetical protein CBG08251
Locus_24460_Transcript_1/1_Conf_1.000	385	0							

Locus_24461_Transcript_1/1_Conf_1.000	142	20	4.38E-10	EFO14895.1	82	67.781	46	38	CMGC/CDK/CDK9 protein kinase
Locus_24462_Transcript_1/1_Conf_1.000	160	0							
Locus_24463_Transcript_1/1_Conf_1.000	187	0							
Locus_24464_Transcript_1/1_Conf_1.000	183	0							
Locus_24465_Transcript_1/1_Conf_1.000	408	0							
Locus_24466_Transcript_1/1_Conf_1.000	206	0							
Locus_24467_Transcript_1/1_Conf_1.000	391	3	6.99E-16	XP_002649017.1	54	87.0409	132	72	Hypothetical protein CBG21465
Locus_24468_Transcript_1/1_Conf_1.000	255	0							
Locus_24469_Transcript_1/1_Conf_1.000	276	0							
Locus_2447_Transcript_1/1_Conf_1.000	346	20	5.86E-11	Q6T269.1	63	64.3142	52	33	Bitisilin-3
Locus_24470_Transcript_1/1_Conf_1.000	228	20	7.60E-34	BAG59376.1	100	146.747	75	75	unnamed protein product
Locus_24471_Transcript_1/1_Conf_1.000	185	3	3.03E-22	CBI83238.1	93	108.227	59	55	C. elegans protein W06F12.2d, confirmed by transcript evidence
Locus_24472_Transcript_1/1_Conf_1.000	183	7	2.04E-10	NP_490781.1	69	68.9366	66	46	hypothetical protein ZC123.3
Locus_24473_Transcript_1/1_Conf_1.000	158	0							
Locus_24474_Transcript_1/1_Conf_1.000	156	20	4.79E-20	AAY99638.1	98	100.908	51	50	mca-1
Locus_24475_Transcript_1/1_Conf_1.000	201	20	4.29E-21	XP_002643587.1	86	104.375	66	57	Hypothetical protein CBG16309
Locus_24476_Transcript_1/1_Conf_1.000	231	3	1.18E-10	NP_001122838.1	65	69.707	75	49	hypothetical protein B0399.1
Locus_24477_Transcript_1/1_Conf_1.000	400	0							
Locus_24478_Transcript_1/1_Conf_1.000	162	0							
Locus_24479_Transcript_1/1_Conf_1.000	172	0							
Locus_2448_Transcript_1/1_Conf_1.000	967	20	8.95E-79	CAA52188.1	77	298.13	281	219	lamin
Locus_24480_Transcript_1/1_Conf_1.000	225	0							

Locus_24481_Transcript_1/1_Conf_1.000	178	0							
Locus_24482_Transcript_1/1_Conf_1.000	224	17	1.96E-21	NP_001129905.1	78	105.531	74	58	hypothetical protein T03D8.6
Locus_24483_Transcript_1/1_Conf_1.000	138	20	1.91E-13	XP_002829097.1	100	78.9518	37	37	PREDICTED: GRAM domain-containing protein 1A-like, partial
Locus_24484_Transcript_1/1_Conf_1.000	149	20	6.55E-09	XP_001961184.1	73	63.929	49	36	GF13738
Locus_24485_Transcript_1/1_Conf_1.000	346	0							
Locus_24486_Transcript_1/1_Conf_1.000	301	0							
Locus_24487_Transcript_1/1_Conf_1.000	183	20	6.12E-15	ACY40018.1	93	83.9593	46	43	C. elegans FLN-1 protein, isoform g
Locus_24488_Transcript_1/1_Conf_1.000	162	20	1.93E-21	NP_510672.2	94	105.531	52	49	Nematode AStacin protease family member (nas-39)
Locus_24489_Transcript_1/1_Conf_1.000	143	0							
Locus_2449_Transcript_1/1_Conf_1.000	210	3	3.49E-07	NP_492018.1	74	58.151	47	35	UNCoordinated family member (unc-14)
Locus_24490_Transcript_1/1_Conf_1.000	188	0							
Locus_24491_Transcript_1/1_Conf_1.000	202	20	1.13E-21	XP_002644000.1	92	106.301	66	61	C. briggsae CBR-IFA-1 protein
Locus_24492_Transcript_1/1_Conf_1.000	133	0							
Locus_24493_Transcript_1/1_Conf_1.000	217	0							
Locus_24494_Transcript_1/1_Conf_1.000	218	20	5.01E-06	XP_002807830.1	55	54.299	67	37	PREDICTED: LOW QUALITY PROTEIN: SH2 domain-containing adapter protein D-like, partial
Locus_24495_Transcript_1/1_Conf_1.000	219	0							
Locus_24496_Transcript_1/1_Conf_1.000	152	5	1.27E-04	NP_001024175.1	68	49.6766	48	33	UNCoordinated family member (unc-62)
Locus_24497_Transcript_1/1_Conf_1.000	305	0							
Locus_24498_Transcript_1/1_Conf_1.000	179	0							

Locus_24499_Transcript_1/1_Conf_1.000	186	2	7.97E-15	ABU93237.1	81	83.5741	59	48	ligand-gated ion channel subunit
Locus_245_Transcript_1/1_Conf_1.000	638	20	1.24E-96	CAR63548.1	98	356.295	188	186	putative Ribosomal Protein
Locus_2450_Transcript_1/1_Conf_1.000	1068	4	5.20E-86	EFO19071.1	66	322.398	358	239	hypothetical protein LOAG_09424
Locus_24500_Transcript_1/1_Conf_1.000	321	0							
Locus_24501_Transcript_1/1_Conf_1.000	214	0							
Locus_24502_Transcript_1/1_Conf_1.000	293	4	1.03E-06	XP_002643707.1	52	56.6102	97	51	Hypothetical protein CBG01897
Locus_24503_Transcript_1/1_Conf_1.000	226	20	5.86E-26	NP_502164.1	85	120.553	74	63	WHiTe (Drosophila) related ABC transporte family member (wht-2)
Locus_24504_Transcript_1/1_Conf_1.000	139	0							
Locus_24505_Transcript_1/1_Conf_1.000	208	0							
Locus_24506_Transcript_1/1_Conf_1.000	332	20	7.29E-21	NP_499580.1	72	103.605	114	83	hypothetical protein Y75B8A.7
Locus_24507_Transcript_1/1_Conf_1.000	204	0							
Locus_24508_Transcript_1/1_Conf_1.000	173	0							
Locus_24509_Transcript_1/1_Conf_1.000	343	20	6.28E-28	XP_002646550.1	88	127.102	81	72	C. briggsae CBR-PRP-17 protein
Locus_2451_Transcript_1/8_Conf_0.150	1777	20	2.94E-88	NP_505392.2	61	330.872	444	271	Gut granule LOss family member (glo-4)
Locus_2451_Transcript_2/8_Conf_0.150	1819	20	1.61E-89	NP_505392.2	61	335.109	445	272	Gut granule LOss family member (glo-4)

Locus_2451_Transcript_3/8_Conf_0.300	4245	20	0	NP_505392.2	62	979.163	1295	805	Gut granule LOss family member (glo-4)
Locus_2451_Transcript_4/8_Conf_0.350	4512	20	0	NP_505392.2	62	1038.48	1368	852	Gut granule LOss family member (glo-4)
Locus_2451_Transcript_5/8_Conf_0.350	4512	20	0	NP_505392.2	62	1040.02	1368	852	Gut granule LOss family member (glo-4)
Locus_2451_Transcript_6/8_Conf_0.350	4512	20	0	NP_505392.2	62	1045.42	1368	854	Gut granule LOss family member (glo-4)
Locus_2451_Transcript_7/8_Conf_0.300	4245	20	0	NP_505392.2	62	980.319	1295	805	Gut granule LOss family member (glo-4)
Locus_2451_Transcript_8/8_Conf_0.350	4512	20	0	NP_505392.2	62	1039.64	1368	852	Gut granule LOss family member (glo-4)
Locus_24510_Transcript_1/1_Conf_1.000	253	0							
Locus_24511_Transcript_1/1_Conf_1.000	187	0							
Locus_24512_Transcript_1/1_Conf_1.000	155	0							
Locus_24513_Transcript_1/1_Conf_1.000	304	15	1.05E-27	NP_491312.2	67	126.331	99	67	hypothetical protein R12E2.8
Locus_24514_Transcript_1/1_Conf_1.000	134	0							

Locus_24515_Transcript_1/1_Conf_1.000	205	20	5.59E-21	CBI31608.3	86	103.99	66	57	unnamed protein product
Locus_24516_Transcript_1/1_Conf_1.000	393	20	8.48E-25	XP_001623156.1	76	116.701	97	74	predicted protein
Locus_24517_Transcript_1/1_Conf_1.000	134	2	2.13E-04	NP_504235.2	73	48.9062	46	34	Drosophila SOS homolog family member (sos-1)
Locus_24518_Transcript_1/1_Conf_1.000	165	1	8.96E-11	BAG60969.1	90	70.0922	51	46	unnamed protein product
Locus_24519_Transcript_1/1_Conf_1.000	282	0							
Locus_2452_Transcript_1/1_Conf_1.000	2027	20	4.14E-49	XP_002630773.1	58	201.06	321	189	Hypothetical protein CBG02468
Locus_24520_Transcript_1/1_Conf_1.000	153	20	5.14E-14	EFO17784.1	86	80.8777	51	44	hypothetical protein LOAG_10715
Locus_24521_Transcript_1/1_Conf_1.000	155	8	1.15E-05	AAN61521.1	62	53.1434	51	32	301KDa_2 protein
Locus_24522_Transcript_1/1_Conf_1.000	298	0							
Locus_24523_Transcript_1/1_Conf_1.000	170	1	2.78E-04	XP_001899312.1	62	48.521	50	31	nuclear receptor NHR-67
Locus_24524_Transcript_1/1_Conf_1.000	165	0							

Locus_24525_Transcript_1/1_Conf_1.000	174	20	1.37E-11	NP_001182132.1	100	72.7886	58	58	elongation factor 1-delta isoform 5
Locus_24526_Transcript_1/1_Conf_1.000	228	0							
Locus_24527_Transcript_1/1_Conf_1.000	139	5	2.67E-07	XP_002637772.1	69	58.5362	42	29	Hypothetical protein CBG04555
Locus_24528_Transcript_1/1_Conf_1.000	162	0							
Locus_24529_Transcript_1/1_Conf_1.000	199	0							
Locus_2453_Transcript_1/2_Conf_1.000	681	20	7.21E-88	XP_002644811.1	89	327.405	209	187	C. briggsae CBR-HSP-3 protein
Locus_2453_Transcript_2/2_Conf_1.000	699	20	3.33E-91	XP_002644811.1	89	338.576	215	193	C. briggsae CBR-HSP-3 protein
Locus_24530_Transcript_1/1_Conf_1.000	220	0							
Locus_24531_Transcript_1/1_Conf_1.000	199	20	4.92E-25	EFO22480.1	89	117.472	65	58	BSD domain-containing protein
Locus_24532_Transcript_1/1_Conf_1.000	129	20	2.87E-09	XP_002932324.1	88	65.0846	42	37	PREDICTED: putative ATP-dependent RNA helicase DHX33
Locus_24533_Transcript_1/1_Conf_1.000	272	0							
Locus_24534_Transcript_1/1_Conf_1.000	163	0							
Locus_24535_Transcript_1/1_Conf_1.000	175	20	2.11E-20	NP_501972.1	84	102.064	57	48	Flavin-containing MonoOxygenase family member (fmo-2)
Locus_24536_Transcript_1/1_Conf_1.000	229	0							
Locus_24537_Transcript_1/1_Conf_1.000	192	0							
Locus_24538_Transcript_1/1_Conf_1.000	310	20	1.50E-34	XP_002636957.1	82	149.058	103	85	C. briggsae CBR-EAT-6 protein
Locus_24539_Transcript_1/1_Conf_1.000	486	20	1.47E-53	NP_495222.2	79	212.231	162	128	hypothetical protein F21H12.1
Locus_2454_Transcript_1/1_Conf_1.000	502	20	1.30E-41	EFO26496.1	73	172.555	171	125	hypothetical protein LOAG_01982

Locus_24540_Transcript_1/1_Conf_1.000	160	2	1.49E-05	XP_002643029.1	75	52.7582	36	27	Hypothetical protein CBG22937
Locus_24541_Transcript_1/1_Conf_1.000	244	0							
Locus_24542_Transcript_1/1_Conf_1.000	696	17	3.83E-31	XP_002643226.1	52	139.043	232	122	Hypothetical protein CBG08091
Locus_24543_Transcript_1/1_Conf_1.000	284	20	3.81E-33	NP_001021871.1	87	144.436	90	79	UNCoordinated family member (unc-13)
Locus_24544_Transcript_1/1_Conf_1.000	141	0							
Locus_24545_Transcript_1/1_Conf_1.000	170	8	1.48E-05	NP_001040941.1	78	52.7582	47	37	PhosphatidylSerine Receptor family member (psr-1)
Locus_24546_Transcript_1/1_Conf_1.000	413	20	1.70E-62	EFO20273.1	91	241.891	137	125	RNA-metabolising metallo-beta-lactamase
Locus_24547_Transcript_1/1_Conf_1.000	170	20	8.64E-14	2DIZ	100	80.1073	38	38	The SolutionStructure OfThe Third Thioredoxin Domain Of Human Thioredoxin Domain-Containing Protein 5
Locus_24548_Transcript_1/1_Conf_1.000	178	0							
Locus_24549_Transcript_1/1_Conf_1.000	270	20	1.20E-31	CAJ43276.1	86	139.428	90	78	hypothetical protein
Locus_2455_Transcript_1/1_Conf_1.000	3007	20	0	XP_002637229.1	74	752.666	675	503	C. briggsae CBR-TAG-59 protein
Locus_24550_Transcript_1/1_Conf_1.000	239	2	1.38E-11	NP_508799.1	69	72.7886	78	54	hypothetical protein F16H11.1
Locus_24551_Transcript_1/1_Conf_1.000	174	9	7.25E-21	ADI24623.1	100	103.605	54	54	Copine domain protein, atypical protein 2, isoform c, partially confirmed by transcript evidence

Locus_24552_Transcript_1/1_Conf_1.000	199	20	1.13E-29	BAH13680.1	100	132.88	66	66	unnamed protein product
Locus_24553_Transcript_1/1_Conf_1.000	202	4	5.26E-11	NP_501686.2	63	70.8626	65	41	hypothetical protein C33A12.3
Locus_24554_Transcript_1/1_Conf_1.000	171	0							
Locus_24555_Transcript_1/1_Conf_1.000	195	0							
Locus_24556_Transcript_1/1_Conf_1.000	208	20	5.39E-16	XP_002634584.1	79	87.4261	68	54	Hypothetical protein CBG08395
Locus_24557_Transcript_1/1_Conf_1.000	153	0							
Locus_24558_Transcript_1/1_Conf_1.000	156	0							
Locus_24559_Transcript_1/1_Conf_1.000	322	20	6.02E-31	AAI16568.1	71	137.117	98	70	Sp5 transcription factor-like
Locus_2456_Transcript_1/1_Conf_1.000	195	20	2.46E-08	XP_002052742.1	61	62.003	62	38	GJ17725
Locus_24560_Transcript_1/1_Conf_1.000	865	20	4.14E-45	EFO20328.1	54	186.037	289	158	cytochrome P450 family protein

Locus_24561_Transcript_1/1_Conf_1.000	266	20	3.53E-15	NP_508145.2	72	84.7297	68	49	Suppressor of LIneage defect family member (sli-1)
Locus_24562_Transcript_1/1_Conf_1.000	379	20	5.21E-51	EAX09478.1	100	203.756	102	102	hCG401289, isoform CRA_d
Locus_24563_Transcript_1/1_Conf_1.000	166	0							
Locus_24564_Transcript_1/1_Conf_1.000	313	3	5.01E-09	XP_001893739.1	57	64.3142	82	47	Protein kinase domain containing protein
Locus_24565_Transcript_1/1_Conf_1.000	268	20	1.86E-32	XP_002634119.1	89	142.124	87	78	Hypothetical protein CBG01673
Locus_24566_Transcript_1/1_Conf_1.000	270	1	3.64E-04	NP_499445.2	56	48.1358	67	38	hypothetical protein Y47D3A.14
Locus_24567_Transcript_1/1_Conf_1.000	131	0							
Locus_24568_Transcript_1/1_Conf_1.000	157	0							
Locus_24569_Transcript_1/1_Conf_1.000	182	0							
Locus_2457_Transcript_1/1_Conf_1.000	1156	5	3.96E-42	NP_498283.1	65	176.792	206	134	hypothetical protein C28H8.3
Locus_24570_Transcript_1/1_Conf_1.000	176	20	3.15E-16	NP_001163592.1	87	88.1965	56	49	CG31116, isoform H
Locus_24571_Transcript_1/1_Conf_1.000	305	20	3.95E-51	XP_002924108.1	100	204.142	101	101	PREDICTED: LOW QUALITY PROTEIN: transmembrane emp24 domain-containing protein 9-like
Locus_24572_Transcript_1/1_Conf_1.000	203	2	2.29E-06	EFO23663.1	61	55.4546	68	42	myosin xviiia
Locus_24573_Transcript_1/1_Conf_1.000	146	0							
Locus_24574_Transcript_1/1_Conf_1.000	660	0							

Locus_24575_Transcript_1/1_Conf_1.000	175	0							
Locus_24576_Transcript_1/1_Conf_1.000	138	0							
Locus_24577_Transcript_1/1_Conf_1.000	484	20	1.49E-29	NP_001024342.1	77	132.494	127	98	Aboc, EXpulsion defective family member (aex-3)
Locus_24578_Transcript_1/1_Conf_1.000	385	20	7.04E-16	AAO63576.1	59	87.0409	106	63	secreted protein 4 precursor
Locus_24579_Transcript_1/1_Conf_1.000	168	0							
Locus_2458_Transcript_1/1_Conf_1.000	180	4	8.28E-20	NP_493560.1	84	100.138	58	49	hypothetical protein K05C4.11
Locus_24580_Transcript_1/1_Conf_1.000	258	0							
Locus_24581_Transcript_1/1_Conf_1.000	954	20	6.87E-108	XP_002640180.1	92	394.815	252	232	Hypothetical protein CBG12683
Locus_24582_Transcript_1/1_Conf_1.000	303	0							
Locus_24583_Transcript_1/1_Conf_1.000	135	0							
Locus_24584_Transcript_1/1_Conf_1.000	256	20	2.57E-05	XP_002875012.1	52	51.9878	84	44	RNA recognition motif-containing protein
Locus_24585_Transcript_1/1_Conf_1.000	286	2	5.48E-40	NP_001022371.1	96	167.162	86	83	hypothetical protein T26C5.5
Locus_24587_Transcript_1/1_Conf_1.000	370	4	2.37E-43	XP_002631789.1	81	178.333	122	100	Hypothetical protein CBG21003
Locus_24588_Transcript_1/1_Conf_1.000	128	0							
Locus_24589_Transcript_1/1_Conf_1.000	131	20	7.81E-15	XP_001894369.1	100	83.5741	43	43	Voltage-gated potassium channel, Shab-family (KCNB, Kv2-like) alpha-subunit. C. elegans exp-2 ortholog

Locus_2459_Transcript_1/1_Conf_1.000	570	20	3.29E-33	XP_001900388.1	83	145.206	114	95	GTP-binding protein Rheb homolog
Locus_24590_Transcript_1/1_Conf_1.000	265	0							
Locus_24591_Transcript_1/1_Conf_1.000	257	0							
Locus_24592_Transcript_1/1_Conf_1.000	300	0							
Locus_24593_Transcript_1/1_Conf_1.000	132	0							
Locus_24594_Transcript_1/1_Conf_1.000	138	0							
Locus_24595_Transcript_1/1_Conf_1.000	151	0							
Locus_24596_Transcript_1/1_Conf_1.000	145	17	5.56E-08	NP_504022.2	74	60.8474	47	35	hypothetical protein F59B1.8
Locus_24597_Transcript_1/1_Conf_1.000	132	0							
Locus_24598_Transcript_1/1_Conf_1.000	218	20	4.07E-32	ABO36652.1	97	140.969	72	70	latrophilin-like protein 2
Locus_24599_Transcript_1/1_Conf_1.000	155	0							
Locus_246_Transcript_1/1_Conf_1.000	340	0							
Locus_2460_Transcript_1/1_Conf_1.000	812	20	3.08E-52	NP_510201.2	70	209.534	238	167	Nuclear Hormone Receptor family member (nhr-32)
Locus_24600_Transcript_1/1_Conf_1.000	291	0							

Locus_24601_Transcript_1/1_Conf_1.000	337	20	2.17E-25	XP_001901457.1	73	118.627	109	80	Hypothetical UPF0202 protein F55A12.8 in chromosome I
Locus_24602_Transcript_1/1_Conf_1.000	357	20	8.61E-22	XP_002640146.1	66	106.686	110	73	C. briggsae CBR-GLY-2 protein
Locus_24603_Transcript_1/1_Conf_1.000	257	20	3.43E-42	EFO25047.1	96	174.481	85	82	serine/threonine protein phosphatase 5
Locus_24604_Transcript_1/1_Conf_1.000	157	20	2.01E-18	BAG58382.1	100	95.5153	52	52	unnamed protein product
Locus_24605_Transcript_1/1_Conf_1.000	159	0							
Locus_24606_Transcript_1/1_Conf_1.000	158	20	9.32E-24	AAP36779.1	100	113.235	52	52	Homo sapiens jumping translocation breakpoint
Locus_24607_Transcript_1/1_Conf_1.000	208	6	3.38E-18	XP_002645082.1	82	94.7449	68	56	C. briggsae CBR-DHS-29 protein
Locus_24608_Transcript_1/1_Conf_1.000	211	18	1.25E-10	XP_002638474.1	59	47.3654	47	28	C. briggsae CBR-TTR-26 protein
Locus_24609_Transcript_1/1_Conf_1.000	306	0							
Locus_2461_Transcript_1/1_Conf_1.000	145	0							
Locus_24610_Transcript_1/1_Conf_1.000	374	4	2.63E-18	XP_002643890.1	78	95.1301	120	94	Hypothetical protein CBG02142
Locus_24611_Transcript_1/1_Conf_1.000	222	0							
Locus_24612_Transcript_1/1_Conf_1.000	222	0							
Locus_24613_Transcript_1/1_Conf_1.000	150	0							
Locus_24614_Transcript_1/1_Conf_1.000	565	20	2.03E-80	NP_496205.2	87	301.982	187	163	PhosphoLipase C family member (plc-3)

Locus_24615_Transcript_1/1_Conf_1.000	253	20	4.23E-16	NP_001020988.1	64	87.8113	84	54	UNCoordinated family member (unc-89)
Locus_24616_Transcript_1/1_Conf_1.000	253	20	3.35E-13	XP_002631113.1	68	78.1814	86	59	C. briggsae CBR-ARS-1 protein
Locus_24617_Transcript_1/1_Conf_1.000	182	20	2.49E-16	XP_001893904.1	87	88.5817	55	48	Protein-tyrosine phosphatase containing protein
Locus_24618_Transcript_1/1_Conf_1.000	151	0							
Locus_24619_Transcript_1/1_Conf_1.000	128	9	3.90E-06	XP_002748769.1	100	54.6842	42	42	PREDICTED: hematological and neurological expressed 1 protein-like
Locus_2462_Transcript_1/1_Conf_1.000	171	0							
Locus_24620_Transcript_1/1_Conf_1.000	131	20	5.07E-06	AAZ67097.1	78	54.299	42	33	transposase
Locus_24621_Transcript_1/1_Conf_1.000	250	20	3.46E-15	NP_509351.1	66	84.7297	83	55	hypothetical protein C34D10.1
Locus_24622_Transcript_1/1_Conf_1.000	385	20	3.74E-17	NP_510174.3	56	91.2781	127	72	hypothetical protein R03G8.3
Locus_24623_Transcript_1/1_Conf_1.000	152	0							
Locus_24624_Transcript_1/1_Conf_1.000	147	0							
Locus_24625_Transcript_1/1_Conf_1.000	346	2	8.20E-12	XP_002642236.1	64	73.559	105	68	Hypothetical protein CBG18218
Locus_24626_Transcript_1/1_Conf_1.000	142	0							
Locus_24627_Transcript_1/1_Conf_1.000	326	0							
Locus_24628_Transcript_1/1_Conf_1.000	226	20	1.66E-23	CAI15068.1	100	74.7146	38	38	guanylate kinase 1

Locus_24629_Transcript_1/1_Conf_1.000	525	20	1.75E-13	NP_496914.1	53	79.337	189	101	hypothetical protein W02B8.2
Locus_2463_Transcript_1/1_Conf_1.000	1421	20	0	NP_491134.1	87	676.781	455	399	NucleOLar protein family member (nol-5)
Locus_24630_Transcript_1/1_Conf_1.000	341	20	6.47E-46	XP_002637940.1	89	186.808	113	101	C. briggsae CBR-CTG-2 protein
Locus_24631_Transcript_1/1_Conf_1.000	157	0							
Locus_24632_Transcript_1/1_Conf_1.000	136	0							
Locus_24633_Transcript_1/1_Conf_1.000	359	5	5.37E-40	NP_741363.1	91	167.162	117	107	hypothetical protein F37C4.4
Locus_24634_Transcript_1/1_Conf_1.000	200	0							
Locus_24635_Transcript_1/1_Conf_1.000	417	20	4.06E-27	XP_795502.1	62	124.405	135	85	PREDICTED: similar to ENSANGP00000010363
Locus_24636_Transcript_1/1_Conf_1.000	242	0							
Locus_24637_Transcript_1/1_Conf_1.000	235	4	7.10E-16	NP_493170.1	79	87.0409	64	51	hypothetical protein T27F6.7
Locus_24638_Transcript_1/1_Conf_1.000	162	0							
Locus_24639_Transcript_1/1_Conf_1.000	243	20	1.01E-38	A8XQD5.2	98	162.925	80	79	Serine/threonine-protein kinase dkf-2
Locus_2464_Transcript_1/1_Conf_1.000	174	0							
Locus_24640_Transcript_1/1_Conf_1.000	231	0							
Locus_24641_Transcript_1/1_Conf_1.000	160	0							
Locus_24642_Transcript_1/1_Conf_1.000	194	0							

Locus_24643_Transcript_1/1_Conf_1.000	236	7	3.05E-12	XP_002631921.1	85	56.9954	34	29	Hypothetical protein CBG07909
Locus_24644_Transcript_1/1_Conf_1.000	389	0							
Locus_24645_Transcript_1/1_Conf_1.000	227	0							
Locus_24646_Transcript_1/1_Conf_1.000	148	20	5.01E-09	XP_002641345.1	79	64.3142	48	38	Hypothetical protein CBG13198
Locus_24647_Transcript_1/1_Conf_1.000	130	0							
Locus_24648_Transcript_1/1_Conf_1.000	221	0							
Locus_24649_Transcript_1/1_Conf_1.000	287	0							
Locus_2465_Transcript_1/3_Conf_0.286	550	1	4.94E-04	NP_001022722.1	82	48.1358	40	33	Coelomocyte UPtake defective family member (cup-5)
Locus_2465_Transcript_2/3_Conf_0.714	2391	20	0	NP_001022722.1	79	597.045	452	361	Coelomocyte UPtake defective family member (cup-5)
Locus_2465_Transcript_3/3_Conf_0.714	2429	20	0	NP_001022722.1	82	823.928	587	485	Coelomocyte UPtake defective family member (cup-5)
Locus_24650_Transcript_1/1_Conf_1.000	286	0							
Locus_24651_Transcript_1/1_Conf_1.000	265	0							
Locus_24652_Transcript_1/1_Conf_1.000	201	2	4.92E-09	XP_002639479.1	77	64.3142	63	49	Hypothetical protein CBG04077
Locus_24653_Transcript_1/1_Conf_1.000	196	20	2.15E-12	YP_388711.1	76	75.485	64	49	ATP-dependent protease ATP-binding subunit ClpX
Locus_24654_Transcript_1/1_Conf_1.000	710	20	3.39E-83	XP_001892306.1	77	311.997	235	181	Ser/Thr protein phosphatase family protein
Locus_24655_Transcript_1/1_Conf_1.000	150	0							
Locus_24656_Transcript_1/1_Conf_1.000	259	1	3.68E-12	XP_001161286.1	100	74.7146	34	34	PREDICTED: hypothetical protein
Locus_24657_Transcript_1/1_Conf_1.000	346	20	9.96E-34	NP_498081.2	83	146.362	103	86	ALdehyde deHydrogenase family member (alh-1)
Locus_24658_Transcript_1/1_Conf_1.000	278	0							
Locus_24659_Transcript_1/1_Conf_1.000	1389	20	5.06E-98	XP_001895789.1	62	362.844	473	295	Timeless protein
Locus_2466_Transcript_1/2_Conf_1.000	1416	20	5.41E-79	XP_002634331.1	76	299.671	261	200	C. briggsae CBR-IMP-3 protein
Locus_2466_Transcript_2/2_Conf_1.000	1416	20	5.41E-79	XP_002634331.1	76	299.671	261	200	C. briggsae CBR-IMP-3 protein
Locus_24660_Transcript_1/1_Conf_1.000	387	0							

Locus_24661_Transcript_1/1_Conf_1.000	379	0							
Locus_24662_Transcript_1/1_Conf_1.000	300	20	2.69E-15	NP_491806.2	65	85.1149	101	66	LiPid Depleted family member (lpd-2)
Locus_24663_Transcript_1/2_Conf_1.000	228	0							
Locus_24663_Transcript_2/2_Conf_1.000	236	0							
Locus_24664_Transcript_1/1_Conf_1.000	156	0							
Locus_24665_Transcript_1/1_Conf_1.000	547	20	1.90E-16	XP_002642886.1	54	89.3521	182	99	C. briggsae CBR-INFT-1 protein
Locus_24666_Transcript_1/1_Conf_1.000	275	2	5.39E-16	EDL12487.1	62	87.4261	86	54	eukaryotic translation initiation factor 5A, isoform CRA_i
Locus_24667_Transcript_1/1_Conf_1.000	259	0							
Locus_24668_Transcript_1/1_Conf_1.000	131	0							
Locus_24669_Transcript_1/1_Conf_1.000	287	20	1.03E-46	ABI63362.1	100	189.504	88	88	immunoglobulin J chain
Locus_2467_Transcript_1/2_Conf_1.000	1601	20	6.23E-34	XP_002633700.1	53	150.214	316	168	Hypothetical protein CBG03383
Locus_2467_Transcript_2/2_Conf_1.000	1601	20	6.23E-34	XP_002633700.1	53	150.214	316	168	Hypothetical protein CBG03383
Locus_24670_Transcript_1/1_Conf_1.000	248	2	3.48E-07	XP_001902364.1	64	58.151	57	37	Myotubularin-related family protein
Locus_24671_Transcript_1/1_Conf_1.000	332	0							
Locus_24672_Transcript_1/1_Conf_1.000	239	20	3.08E-11	XP_002599652.1	65	71.633	61	40	hypothetical protein BRAFLDRAFT_119367
Locus_24673_Transcript_1/1_Conf_1.000	133	0							
Locus_24674_Transcript_1/1_Conf_1.000	142	6	2.49E-05	XP_002637217.1	67	51.9878	46	31	Hypothetical protein CBG18883
Locus_24675_Transcript_1/1_Conf_1.000	145	0							
Locus_24676_Transcript_1/1_Conf_1.000	175	20	1.01E-14	NP_001020992.1	82	83.1889	57	47	hypothetical protein C09D4.1
Locus_24677_Transcript_1/1_Conf_1.000	346	0							
Locus_24678_Transcript_1/1_Conf_1.000	146	0							
Locus_24679_Transcript_1/1_Conf_1.000	193	0							
Locus_2468_Transcript_1/1_Conf_1.000	212	8	1.73E-14	EFO23768.1	83	82.4185	48	40	hypothetical protein LOAG_04713

Locus_24680_Transcript_1/1_Conf_1.000	176	0							
Locus_24681_Transcript_1/1_Conf_1.000	176	20	1.33E-06	EFN62814.1	69	56.225	56	39	Myosin-2 essential light chain
Locus_24682_Transcript_1/1_Conf_1.000	132	0							
Locus_24683_Transcript_1/1_Conf_1.000	177	0							
Locus_24684_Transcript_1/1_Conf_1.000	130	0							
Locus_24685_Transcript_1/1_Conf_1.000	427	0							
Locus_24686_Transcript_1/1_Conf_1.000	151	0							
Locus_24687_Transcript_1/1_Conf_1.000	451	0							
Locus_24688_Transcript_1/1_Conf_1.000	136	0							
Locus_24689_Transcript_1/1_Conf_1.000	208	0							
Locus_2469_Transcript_1/1_Conf_1.000	204	0							
Locus_24690_Transcript_1/1_Conf_1.000	154	17	1.15E-05	NP_498151.2	66	53.1434	51	34	hypothetical protein Y32H12A.8
Locus_24691_Transcript_1/1_Conf_1.000	139	0							
Locus_24692_Transcript_1/1_Conf_1.000	198	0							
Locus_24693_Transcript_1/1_Conf_1.000	144	3	1.12E-08	EFO21461.1	69	63.1586	52	36	AGC/NDR protein kinase
Locus_24694_Transcript_1/1_Conf_1.000	533	0							
Locus_24695_Transcript_1/1_Conf_1.000	407	0							
Locus_24696_Transcript_1/1_Conf_1.000	130	20	1.42E-16	NP_500130.1	97	89.3521	43	42	hypothetical protein Y41D4A.4
Locus_24697_Transcript_1/1_Conf_1.000	234	20	8.09E-28	XP_001902612.1	92	126.716	77	71	PWI domain containing protein

Locus_24698_Transcript_1/1_Conf_1.000	329	20	2.18E-49	3FGA	100	198.364	99	99	Structural Basis Of Pp2a And Sgo Interaction
Locus_24699_Transcript_1/1_Conf_1.000	132	20	4.42E-10	XP_002158814.1	81	67.781	43	35	PREDICTED: similar to predicted protein
Locus_247_Transcript_1/3_Conf_0.714	2780	20	3.49E-65	ACI49190.1	58	254.988	346	204	hypothetical protein Csp3_JD02.018
Locus_247_Transcript_2/3_Conf_0.714	2693	20	2.50E-76	ACI49190.1	63	291.967	319	204	hypothetical protein Csp3_JD02.018
Locus_247_Transcript_3/3_Conf_0.714	2702	20	1.74E-69	ACI49190.1	63	269.24	320	204	hypothetical protein Csp3_JD02.018
Locus_2470_Transcript_1/1_Conf_1.000	268	0							
Locus_24700_Transcript_1/1_Conf_1.000	278	20	3.71E-25	EFO27066.1	82	117.857	90	74	hypothetical protein LOAG_01421
Locus_24701_Transcript_1/1_Conf_1.000	371	11	4.50E-18	XP_002629874.1	65	94.3597	102	67	C. briggsae CBR-TWK-1 protein
Locus_24702_Transcript_1/1_Conf_1.000	249	5	1.08E-16	CBW48341.1	63	89.7373	86	55	Hypothetical protein C27H6.1c
Locus_24703_Transcript_1/1_Conf_1.000	131	0							

Locus_24704_Transcript_1/1_Conf_1.000	151	3	1.78E-06	XP_002630904.1	72	55.8398	43	31	Hypothetical protein CBG02628
Locus_24705_Transcript_1/1_Conf_1.000	316	20	2.37E-51	NP_491193.2	97	204.912	105	102	Calcium Channel, Beta subunit family member (ccb-1)
Locus_24706_Transcript_1/1_Conf_1.000	131	2	8.94E-11	XP_002645194.1	88	70.0922	43	38	Hypothetical protein CBG16926
Locus_24707_Transcript_1/1_Conf_1.000	167	20	2.35E-27	BAG64777.1	100	125.176	55	55	unnamed protein product
Locus_24708_Transcript_1/1_Conf_1.000	166	0							
Locus_24709_Transcript_1/1_Conf_1.000	183	0							
Locus_2471_Transcript_1/1_Conf_1.000	772	20	4.76E-84	Q27666.1	96	315.079	159	153	cytoplasmic superoxide dismutase
Locus_24710_Transcript_1/1_Conf_1.000	166	0							
Locus_24711_Transcript_1/1_Conf_1.000	292	20	7.66E-10	NP_001074358.1	66	67.0106	75	50	hypothetical protein LOC771987
Locus_24712_Transcript_1/1_Conf_1.000	204	0							
Locus_24713_Transcript_1/1_Conf_1.000	153	20	3.33E-21	ABI74141.1	100	104.76	51	51	immunoglobulin light chain variable region
Locus_24714_Transcript_1/1_Conf_1.000	135	0							
Locus_24715_Transcript_1/1_Conf_1.000	138	0							
Locus_24716_Transcript_1/1_Conf_1.000	151	0							
Locus_24717_Transcript_1/1_Conf_1.000	260	0							
Locus_24718_Transcript_1/1_Conf_1.000	229	0							

Locus_24719_Transcript_1/1_Conf_1.000	154	0							
Locus_2472_Transcript_1/1_Conf_1.000	504	20	1.06E-38	XP_002631813.1	66	162.925	167	111	Hypothetical protein CBG21034
Locus_24720_Transcript_1/1_Conf_1.000	145	0							
Locus_24721_Transcript_1/1_Conf_1.000	554	3	7.77E-05	XP_001902040.1	45	50.8322	127	58	Conserved hypothetical protein
Locus_24722_Transcript_1/1_Conf_1.000	140	0							
Locus_24723_Transcript_1/1_Conf_1.000	403	20	1.02E-30	NP_491275.2	62	136.346	133	83	hypothetical protein F47B3.6
Locus_24724_Transcript_1/1_Conf_1.000	142	0							
Locus_24725_Transcript_1/1_Conf_1.000	437	20	6.29E-41	NP_491293.1	72	170.244	143	104	hypothetical protein C24G7.4
Locus_24726_Transcript_1/1_Conf_1.000	200	0							
Locus_24727_Transcript_1/1_Conf_1.000	206	19	1.69E-09	ACI22689.1	62	65.855	67	42	Hypothetical protein F52C12.6
Locus_24728_Transcript_1/1_Conf_1.000	210	20	1.97E-18	NP_495675.1	81	95.5153	69	56	hypothetical protein DH11.1

Locus_24729_Transcript_1/1_Conf_1.000	325	20	5.57E-53	XP_002750116.1	100	210.305	108	108	PREDICTED: vimentin-like isoform 2
Locus_2473_Transcript_1/1_Conf_1.000	621	20	5.97E-93	NP_504721.1	95	343.969	180	171	Germinal Center Kinase family member (gck-2)
Locus_24730_Transcript_1/1_Conf_1.000	264	2	1.75E-22	XP_002640985.1	73	108.997	87	64	C. briggsae CBR-CDH-12 protein
Locus_24731_Transcript_1/1_Conf_1.000	323	20	3.20E-16	AAN11402.1	55	88.1965	109	61	secreted-protein 1 precursor
Locus_24732_Transcript_1/1_Conf_1.000	145	0							
Locus_24733_Transcript_1/1_Conf_1.000	205	0							
Locus_24734_Transcript_1/1_Conf_1.000	262	0							
Locus_24735_Transcript_1/1_Conf_1.000	205	20	2.34E-27	NP_498931.2	91	125.176	68	62	SMAll family member (sma-2)
Locus_24736_Transcript_1/1_Conf_1.000	130	0							
Locus_24737_Transcript_1/1_Conf_1.000	146	20	4.54E-18	AAC18189.1	97	94.3597	48	47	immunoglobulin heavy chain variable region
Locus_24738_Transcript_1/1_Conf_1.000	218	0							
Locus_24739_Transcript_1/1_Conf_1.000	228	11	3.33E-05	XP_002401086.1	62	51.6026	64	40	rolling pebbles, putative

Locus_2474_Transcript_1/1_Conf_1.000	1096	20	6.98E-134	CAB77052.1	95	481.485	260	247	putative integrin-linked kinase
Locus_24740_Transcript_1/1_Conf_1.000	1017	20	7.66E-116	NP_493356.2	82	421.394	288	238	hypothetical protein C01A2.3
Locus_24741_Transcript_1/1_Conf_1.000	154	3	3.81E-09	XP_002639439.1	74	64.6994	51	38	Hypothetical protein CBG04032
Locus_24742_Transcript_1/1_Conf_1.000	288	0							
Locus_24743_Transcript_1/1_Conf_1.000	130	0							
Locus_24744_Transcript_1/1_Conf_1.000	150	5	1.00E-17	XP_001893254.1	92	93.2041	50	46	hypothetical protein Bm1_08915
Locus_24745_Transcript_1/1_Conf_1.000	358	0							
Locus_24746_Transcript_1/1_Conf_1.000	153	0							
Locus_24747_Transcript_1/1_Conf_1.000	154	0							
Locus_24748_Transcript_1/1_Conf_1.000	182	20	9.14E-27	A8WL06.2	100	123.25	59	59	Homeobox protein unc-62
Locus_24749_Transcript_1/1_Conf_1.000	143	20	2.24E-14	NP_001021183.1	89	82.0333	47	42	hypothetical protein C24A1.3
Locus_2475_Transcript_1/1_Conf_1.000	763	20	8.27E-49	XP_002631218.1	61	197.978	254	157	Hypothetical protein CBG03015
Locus_24750_Transcript_1/1_Conf_1.000	185	20	7.47E-21	XP_002641474.1	92	103.605	56	52	C. briggsae CBR-PTP-1 protein
Locus_24751_Transcript_1/1_Conf_1.000	340	20	1.45E-29	NP_501968.2	74	132.494	110	82	Flavin-containing MonoOxygenase family member (fmo-1)

Locus_24752_Transcript_1/1_Conf_1.000	136	13	5.21E-11	XP_519221.2	100	70.8626	45	45	PREDICTED: similar to I3 protein
Locus_24753_Transcript_1/1_Conf_1.000	267	2	2.99E-06	NP_508991.1	75	55.0694	53	40	hypothetical protein Y23B4A.2
Locus_24754_Transcript_1/1_Conf_1.000	140	4	3.48E-07	AAA96224.2	74	58.151	39	29	Hypothetical protein T07H6.4
Locus_24755_Transcript_1/1_Conf_1.000	372	20	3.65E-36	NP_492763.1	70	154.451	124	88	hypothetical protein F25H2.7
Locus_24756_Transcript_1/1_Conf_1.000	172	0							
Locus_24757_Transcript_1/1_Conf_1.000	227	0							
Locus_24758_Transcript_1/1_Conf_1.000	209	6	1.24E-20	NP_001024545.1	93	102.834	49	46	hypothetical protein F09E10.7
Locus_24759_Transcript_1/1_Conf_1.000	248	0							
Locus_2476_Transcript_1/2_Conf_1.000	2134	20	0	NP_001040799.1	91	1153.27	712	653	hypothetical protein T04B8.5
Locus_2476_Transcript_2/2_Conf_1.000	1458	20	0	NP_001040799.1	92	774.622	487	449	hypothetical protein T04B8.5
Locus_24760_Transcript_1/1_Conf_1.000	139	0							
Locus_24761_Transcript_1/1_Conf_1.000	136	0							
Locus_24762_Transcript_1/1_Conf_1.000	131	0							
Locus_24763_Transcript_1/1_Conf_1.000	159	0							
Locus_24764_Transcript_1/1_Conf_1.000	251	20	2.73E-36	XP_002647008.1	93	154.836	86	80	Hypothetical protein CBG23794
Locus_24765_Transcript_1/1_Conf_1.000	136	0							
Locus_24766_Transcript_1/1_Conf_1.000	291	0							
Locus_24767_Transcript_1/1_Conf_1.000	250	20	7.21E-21	XP_002631054.1	80	103.605	82	66	C. briggsae CBR-BTF-1 protein
Locus_24768_Transcript_1/1_Conf_1.000	135	0							
Locus_24769_Transcript_1/1_Conf_1.000	146	20	1.56E-10	XP_002759913.1	100	69.3218	45	45	PREDICTED: 28S ribosomal protein S21, mitochondrial-like
Locus_2477_Transcript_1/1_Conf_1.000	471	20	2.51E-29	NP_509186.3	55	131.724	161	90	Carbonic AnHydrase family member (cah-5)
Locus_24770_Transcript_1/1_Conf_1.000	175	20	3.04E-27	XP_002825949.1	100	124.79	58	58	PREDICTED: DNA-3-methyladenine glycosylase-like, partial
Locus_24771_Transcript_1/1_Conf_1.000	141	0							
Locus_24772_Transcript_1/1_Conf_1.000	237	20	9.24E-16	EFO16624.1	78	86.6557	61	48	hypothetical protein LOAG_11880
Locus_24773_Transcript_1/1_Conf_1.000	159	0							

Locus_24774_Transcript_1/1_Conf_1.000	149	20	7.73E-10	XP_002638989.1	78	67.0106	46	36	C. briggsae CBR-RPL-4 protein
Locus_24775_Transcript_1/1_Conf_1.000	156	0							
Locus_24776_Transcript_1/1_Conf_1.000	239	0							
Locus_24777_Transcript_1/1_Conf_1.000	760	11	1.73E-06	XP_002648923.1	51	57.3806	154	79	Hypothetical protein CBG17840
Locus_24778_Transcript_1/1_Conf_1.000	136	0							
Locus_24779_Transcript_1/1_Conf_1.000	165	0							
Locus_2478_Transcript_1/2_Conf_1.000	4143	20	9.75E-123	XP_001891725.1	57	446.817	695	400	hypothetical protein
Locus_2478_Transcript_2/2_Conf_1.000	4143	20	7.47E-123	XP_001891725.1	57	447.203	697	401	hypothetical protein
Locus_24780_Transcript_1/1_Conf_1.000	145	0							
Locus_24781_Transcript_1/1_Conf_1.000	212	0							
Locus_24782_Transcript_1/1_Conf_1.000	203	20	3.63E-20	XP_002632923.1	89	101.293	66	59	C. briggsae CBR-HIM-6 protein
Locus_24783_Transcript_1/1_Conf_1.000	181	0							
Locus_24784_Transcript_1/1_Conf_1.000	270	0							
Locus_24785_Transcript_1/1_Conf_1.000	279	20	8.26E-17	NP_001166985.1	100	90.1225	43	43	TYRO protein tyrosine kinase-binding protein isoform 3 precursor
Locus_24786_Transcript_1/1_Conf_1.000	158	20	9.67E-13	NP_496723.2	82	76.6406	52	43	hypothetical protein Y46G5A.19
Locus_24787_Transcript_1/1_Conf_1.000	411	0							
Locus_24788_Transcript_1/1_Conf_1.000	723	15	4.43E-09	NP_001076729.1	45	65.855	139	63	hypothetical protein Y41E3.19
Locus_24789_Transcript_1/1_Conf_1.000	297	0							

Locus_2479_Transcript_1/3_Conf_0.333	1313	20	1.28E-87	ACY40014.1	64	328.176	344	223	C. elegans FLN-1 protein, isoform a, partially confirmed by transcript evidence
Locus_2479_Transcript_2/3_Conf_0.667	3520	20	0	ACY40014.1	61	917.146	1187	730	C. elegans FLN-1 protein, isoform a, partially confirmed by transcript evidence
Locus_2479_Transcript_3/3_Conf_0.667	3520	20	0	ACY40014.1	61	915.99	1187	730	C. elegans FLN-1 protein, isoform a, partially confirmed by transcript evidence
Locus_24790_Transcript_1/1_Conf_1.000	319	20	2.30E-22	NP_001022192.1	77	108.612	81	63	BCS1 (mitochondrial chaperone) homolog family member (bcs-1)
Locus_24791_Transcript_1/1_Conf_1.000	420	0							
Locus_24792_Transcript_1/1_Conf_1.000	238	4	2.88E-09	NP_001021653.1	67	65.0846	56	38	FANCI (Fanconi anemia complex component I) homolog family member (fnci-1)
Locus_24793_Transcript_1/1_Conf_1.000	261	20	2.53E-29	XP_002630251.1	83	131.724	86	72	Hypothetical protein CBG00670
Locus_24794_Transcript_1/1_Conf_1.000	359	0							
Locus_24795_Transcript_1/1_Conf_1.000	203	0							
Locus_24796_Transcript_1/1_Conf_1.000	222	0							
Locus_24797_Transcript_1/1_Conf_1.000	133	0							
Locus_24798_Transcript_1/1_Conf_1.000	284	0							
Locus_24799_Transcript_1/1_Conf_1.000	193	20	2.91E-17	NP_505967.1	80	91.6633	62	50	hypothetical protein F55A11.1
Locus_248_Transcript_1/2_Conf_1.000	1922	20	0	XP_002641003.1	86	956.822	641	554	C. briggsae CBR-TAT-1 protein

Locus_248_Transcript_2/2_Conf_1.000	1922	20	0	XP_002641003.1	86	958.748	641	554	C. briggsae CBR-TAT-1 protein
Locus_2480_Transcript_1/4_Conf_0.500	1152	10	2.01E-62	AAM22693.1	65	244.202	398	259	AF504312_1adaptor protein UNC-53
Locus_2480_Transcript_2/4_Conf_0.250	1513	20	1.11E-101	CBB16173.1	75	375.17	490	371	C. elegans protein F45E10.1f, partially confirmed by transcript evidence
Locus_2480_Transcript_3/4_Conf_0.625	2518	20	1.72E-164	NP_741045.1	70	584.719	856	606	UNCoordinated family member (unc-53)
Locus_2480_Transcript_4/4_Conf_0.500	1164	10	2.67E-62	AAM22693.1	64	243.817	402	260	AF504312_1adaptor protein UNC-53
Locus_24800_Transcript_1/1_Conf_1.000	224	0							
Locus_24801_Transcript_1/1_Conf_1.000	250	0							
Locus_24802_Transcript_1/1_Conf_1.000	168	0							
Locus_24803_Transcript_1/1_Conf_1.000	206	0							
Locus_24804_Transcript_1/1_Conf_1.000	382	0							
Locus_24805_Transcript_1/1_Conf_1.000	149	0							
Locus_24806_Transcript_1/1_Conf_1.000	136	0							
Locus_24807_Transcript_1/1_Conf_1.000	143	17	2.48E-13	NP_001022373.1	87	78.5666	47	41	CLC-type chloride cHannel family member (clh-1)
Locus_24808_Transcript_1/1_Conf_1.000	172	0							
Locus_24809_Transcript_1/1_Conf_1.000	241	0							
Locus_2481_Transcript_1/1_Conf_1.000	367	0							
Locus_24810_Transcript_1/1_Conf_1.000	286	20	9.67E-37	XP_002633562.1	77	156.377	93	72	Hypothetical protein CBG05433
Locus_24811_Transcript_1/1_Conf_1.000	234	20	4.13E-40	BAH12664.1	100	167.548	78	78	unnamed protein product
Locus_24812_Transcript_1/1_Conf_1.000	180	0							
Locus_24813_Transcript_1/1_Conf_1.000	175	2	2.50E-05	XP_002648434.1	58	51.9878	53	31	Hypothetical protein CBG24703
Locus_24814_Transcript_1/1_Conf_1.000	356	0							

Locus_24815_Transcript_1/1_Conf_1.000	180	20	1.19E-26	XP_001095809.2	100	122.865	60	60	PREDICTED: biogenesis of lysosome-related organelles complex 1 subunit 1
Locus_24816_Transcript_1/1_Conf_1.000	134	0							
Locus_24817_Transcript_1/1_Conf_1.000	195	2	4.64E-07	NP_505267.1	86	57.7658	61	53	Regulator of Presynaptic Morphology family member (rpm-1)
Locus_24818_Transcript_1/1_Conf_1.000	145	4	3.37E-05	CAA16382.5	73	51.6026	46	34	C. elegans protein Y45F10D.7, partially confirmed by transcript evidence
Locus_24819_Transcript_1/1_Conf_1.000	352	20	3.09E-19	XP_002641620.1	60	98.2117	110	67	C. briggsae CBR-BUB-1 protein
Locus_2482_Transcript_1/1_Conf_1.000	572	20	1.47E-41	NP_498339.1	81	172.94	131	107	ABC transporter, class F family member (abcf-3)
Locus_24820_Transcript_1/1_Conf_1.000	131	20	2.20E-09	ADM47606.1	95	65.4698	43	41	MHC class I antigen
Locus_24821_Transcript_1/1_Conf_1.000	301	2	9.26E-08	XP_002633755.1	63	60.077	58	37	Hypothetical protein CBG03442
Locus_24822_Transcript_1/1_Conf_1.000	150	0							
Locus_24823_Transcript_1/1_Conf_1.000	366	0							
Locus_24824_Transcript_1/1_Conf_1.000	293	0							
Locus_24825_Transcript_1/1_Conf_1.000	143	0							
Locus_24826_Transcript_1/1_Conf_1.000	196	0							

Locus_24827_Transcript_1/1_Conf_1.000	142	20	4.22E-21	EFN76814.1	100	104.375	47	47	Ras-like GTP-binding protein Rho1
Locus_24828_Transcript_1/1_Conf_1.000	254	0							
Locus_24829_Transcript_1/1_Conf_1.000	147	0							
Locus_2483_Transcript_1/2_Conf_1.000	1174	0							
Locus_2483_Transcript_2/2_Conf_1.000	1174	0							
Locus_24830_Transcript_1/1_Conf_1.000	129	0							
Locus_24831_Transcript_1/1_Conf_1.000	334	0							
Locus_24832_Transcript_1/1_Conf_1.000	262	20	4.77E-28	XP_002631558.1	77	127.487	92	71	Hypothetical protein CBG20734
Locus_24833_Transcript_1/1_Conf_1.000	237	0							
Locus_24834_Transcript_1/1_Conf_1.000	478	20	3.04E-19	XP_001894846.1	66	98.2117	103	69	hypothetical protein
Locus_24835_Transcript_1/1_Conf_1.000	193	1	3.69E-04	XP_001901807.1	60	48.1358	64	39	F-box domain containing protein
Locus_24836_Transcript_1/1_Conf_1.000	163	0							
Locus_24837_Transcript_1/1_Conf_1.000	184	20	4.69E-15	XP_002647686.1	80	84.3445	57	46	Hypothetical protein CBG17874

Locus_24838_Transcript_1/1_Conf_1.000	198	20	1.26E-12	CBJ28140.1	72	76.2554	66	48	hypothetical protein
Locus_24839_Transcript_1/1_Conf_1.000	170	0							
Locus_2484_Transcript_1/1_Conf_1.000	1554	20	2.55E-101	XP_002641142.1	57	374.015	509	293	Hypothetical protein CBG08994
Locus_24840_Transcript_1/1_Conf_1.000	162	0							
Locus_24841_Transcript_1/1_Conf_1.000	169	20	1.42E-24	NP_001182041.1	100	115.931	56	56	protein disulfide-isomerase A3
Locus_24842_Transcript_1/1_Conf_1.000	177	0							
Locus_24843_Transcript_1/1_Conf_1.000	184	0							
Locus_24844_Transcript_1/1_Conf_1.000	228	20	1.30E-25	NP_495863.1	90	119.398	75	68	PhenylAlanine Hydroxylase family member (pah-1)
Locus_24845_Transcript_1/1_Conf_1.000	284	7	1.56E-10	EFO24689.1	57	69.3218	90	52	hypothetical protein LOAG_03797
Locus_24846_Transcript_1/1_Conf_1.000	144	0							

Locus_24847_Transcript_1/1_Conf_1.000	310	20	7.70E-31	EFO19136.1	83	136.732	101	84	TKL/STKR/TYPE1 protein kinase
Locus_24848_Transcript_1/1_Conf_1.000	174	0							
Locus_24849_Transcript_1/1_Conf_1.000	360	20	7.77E-15	NP_001021785.2	56	83.5741	110	62	hypothetical protein Y52B11A.3
Locus_2485_Transcript_1/1_Conf_1.000	304	20	1.42E-24	AAI67646.1	100	115.931	88	88	Unknown (protein for MGC:185319)
Locus_24850_Transcript_1/1_Conf_1.000	158	0							
Locus_24851_Transcript_1/1_Conf_1.000	155	2	5.16E-06	XP_002639255.1	68	54.299	51	35	C. briggsae CBR-OCRL-1 protein
Locus_24852_Transcript_1/1_Conf_1.000	128	0							
Locus_24853_Transcript_1/1_Conf_1.000	144	0							
Locus_24854_Transcript_1/1_Conf_1.000	168	20	2.78E-12	NP_505810.2	78	75.0998	55	43	P21-Activated Kinase family member (pak-2)
Locus_24855_Transcript_1/1_Conf_1.000	398	1	2.07E-31	NP_501548.2	69	138.658	131	91	hypothetical protein C27B7.7
Locus_24856_Transcript_1/1_Conf_1.000	184	0							
Locus_24857_Transcript_1/1_Conf_1.000	206	0							
Locus_24858_Transcript_1/1_Conf_1.000	149	0							
Locus_24859_Transcript_1/1_Conf_1.000	138	0							
Locus_2486_Transcript_1/1_Conf_1.000	816	2	8.61E-10	EFO27866.1	52	68.5514	109	57	GTPase activating protein and VPS9 domains 1
Locus_24860_Transcript_1/1_Conf_1.000	378	8	1.99E-34	NP_492398.1	75	148.673	115	87	hypothetical protein F55H12.4
Locus_24861_Transcript_1/1_Conf_1.000	142	0							

Locus_24862_Transcript_1/1_Conf_1.000	203	0							
Locus_24863_Transcript_1/1_Conf_1.000	269	0							
Locus_24864_Transcript_1/1_Conf_1.000	140	20	2.84E-17	XP_002824717.1	100	91.6633	44	44	PREDICTED: proteasome subunit alpha type-6-like
Locus_24865_Transcript_1/1_Conf_1.000	282	20	5.36E-11	EFN81965.1	73	70.8626	63	46	Putative methyltransferase KIAA0859-like protein
Locus_24866_Transcript_1/1_Conf_1.000	300	20	5.24E-11	AAN08883.1	60	70.8626	89	54	MSP-domain protein 5
Locus_24867_Transcript_1/1_Conf_1.000	191	2	2.24E-09	NP_499962.2	78	65.4698	66	52	hypothetical protein K11H12.9
Locus_24868_Transcript_1/1_Conf_1.000	156	1	6.28E-04	NP_505689.1	65	47.3654	46	30	hypothetical protein Y32F6B.1
Locus_24869_Transcript_1/1_Conf_1.000	440	20	1.78E-11	NP_741839.2	48	72.4034	125	60	hypothetical protein F48E3.8
Locus_2487_Transcript_1/1_Conf_1.000	749	20	1.36E-64	NP_741200.1	73	250.366	187	137	DIsplaced Gonad family member (dig-1)
Locus_24870_Transcript_1/1_Conf_1.000	275	20	2.77E-12	XP_002647178.1	66	75.0998	72	48	Hypothetical protein CBG22337
Locus_24871_Transcript_1/1_Conf_1.000	323	0							
Locus_24872_Transcript_1/1_Conf_1.000	130	8	4.15E-08	XP_002630422.1	72	61.2326	37	27	C. briggsae CBR-AGR-1 protein
Locus_24873_Transcript_1/1_Conf_1.000	172	3	1.37E-11	XP_002637786.1	94	72.7886	38	36	Hypothetical protein CBG04571
Locus_24874_Transcript_1/1_Conf_1.000	155	4	8.75E-22	NP_497769.3	100	106.686	51	51	TOllisH (Tolloid and BMP-1 family) family member (toh-1)
Locus_24875_Transcript_1/1_Conf_1.000	267	0							
Locus_24876_Transcript_1/1_Conf_1.000	695	20	8.74E-28	XP_002630011.1	71	127.872	130	93	Hypothetical protein CBG13376
Locus_24877_Transcript_1/1_Conf_1.000	133	0							
Locus_24878_Transcript_1/1_Conf_1.000	312	20	1.45E-16	EFO23358.1	63	89.3521	101	64	hypothetical protein LOAG_05127
Locus_24879_Transcript_1/1_Conf_1.000	137	2	3.61E-12	XP_002633220.1	84	74.7146	45	38	C. briggsae CBR-FLP-13 protein
Locus_2488_Transcript_1/1_Conf_1.000	740	20	8.08E-54	NP_496457.1	83	214.542	172	143	hypothetical protein B0334.4

Locus_24880_Transcript_1/1_Conf_1.000	165	20	2.78E-20	NP_493616.1	92	101.679	54	50	hypothetical protein F33H2.5
Locus_24881_Transcript_1/1_Conf_1.000	128	0							
Locus_24882_Transcript_1/1_Conf_1.000	412	0							
Locus_24883_Transcript_1/1_Conf_1.000	160	0							
Locus_24884_Transcript_1/1_Conf_1.000	366	3	3.84E-06	NP_001040833.1	56	54.6842	114	64	hypothetical protein ZK669.5
Locus_24885_Transcript_1/1_Conf_1.000	282	0							
Locus_24886_Transcript_1/1_Conf_1.000	162	0							
Locus_24887_Transcript_1/1_Conf_1.000	172	2	2.86E-17	NP_503543.1	87	91.6633	56	49	hypothetical protein T08B1.1
Locus_24888_Transcript_1/1_Conf_1.000	201	0							
Locus_24889_Transcript_1/1_Conf_1.000	265	2	6.90E-11	XP_001895635.1	73	70.4774	86	63	hypothetical protein Bm1_20905
Locus_2489_Transcript_1/1_Conf_1.000	339	20	1.60E-36	NP_505349.1	89	155.606	87	78	hypothetical protein C25E10.12
Locus_24890_Transcript_1/1_Conf_1.000	129	0							
Locus_24891_Transcript_1/1_Conf_1.000	240	20	8.58E-30	NP_510155.3	82	133.265	79	65	PIP Kinase family member (ppk-3)
Locus_24892_Transcript_1/1_Conf_1.000	265	4	1.64E-12	NP_001020992.1	77	75.8702	66	51	hypothetical protein C09D4.1
Locus_24893_Transcript_1/1_Conf_1.000	132	4	9.52E-13	NP_495984.2	90	76.6406	43	39	RAB family member (rab-39)
Locus_24894_Transcript_1/1_Conf_1.000	128	0							

Locus_24895_Transcript_1/1_Conf_1.000	174	20	4.39E-26	XP_002634414.1	94	120.939	58	55	C. briggsae CBR-EPI-1 protein
Locus_24896_Transcript_1/1_Conf_1.000	159	0							
Locus_24897_Transcript_1/1_Conf_1.000	146	0							
Locus_24898_Transcript_1/1_Conf_1.000	223	0							
Locus_24899_Transcript_1/1_Conf_1.000	603	20	6.71E-46	NP_510155.3	64	187.578	196	127	PIP Kinase family member (ppk-3)
Locus_249_Transcript_1/1_Conf_1.000	337	7	3.98E-11	XP_002644052.1	57	71.2478	82	47	C. briggsae CBR-EGL-15 protein
Locus_2490_Transcript_1/1_Conf_1.000	808	10	1.81E-52	NP_508890.2	61	210.305	223	137	hypothetical protein Y34B4A.6
Locus_24900_Transcript_1/1_Conf_1.000	138	0							
Locus_24901_Transcript_1/1_Conf_1.000	204	0							
Locus_24902_Transcript_1/1_Conf_1.000	135	3	3.27E-05	NP_504660.1	63	51.6026	41	26	hypothetical protein F46E10.11
Locus_24903_Transcript_1/1_Conf_1.000	316	0							
Locus_24904_Transcript_1/1_Conf_1.000	163	3	7.37E-05	CAA84706.3	65	50.447	52	34	C. elegans protein C38H2.1, partially confirmed by transcript evidence
Locus_24905_Transcript_1/2_Conf_1.000	271	0							
Locus_24905_Transcript_2/2_Conf_1.000	298	0							
Locus_24906_Transcript_1/1_Conf_1.000	287	1	1.78E-06	XP_002638498.1	70	55.8398	60	42	Hypothetical protein CBG12930
Locus_24907_Transcript_1/1_Conf_1.000	171	0							
Locus_24908_Transcript_1/1_Conf_1.000	233	20	3.29E-29	EFO18171.1	89	131.339	76	68	hypothetical protein LOAG_10325
Locus_24909_Transcript_1/1_Conf_1.000	267	2	1.48E-05	XP_001892578.1	63	52.7582	79	50	hypothetical protein Bm1_05520

Locus_2491_Transcript_1/1_Conf_1.000	760	20	7.77E-07	EFN60440.1	42	58.5362	228	97	hypothetical protein EAG_01913
Locus_24910_Transcript_1/1_Conf_1.000	136	0							
Locus_24911_Transcript_1/1_Conf_1.000	128	0							
Locus_24912_Transcript_1/1_Conf_1.000	148	0							
Locus_24913_Transcript_1/1_Conf_1.000	163	0							
Locus_24914_Transcript_1/1_Conf_1.000	219	4	1.55E-26	XP_002646617.1	84	122.479	72	61	Hypothetical protein CBG20503
Locus_24915_Transcript_1/1_Conf_1.000	243	0							
Locus_24916_Transcript_1/1_Conf_1.000	274	0							
Locus_24917_Transcript_1/1_Conf_1.000	234	0							
Locus_24918_Transcript_1/1_Conf_1.000	268	20	2.52E-13	EFO23036.1	81	78.5666	54	44	CBP-B

Locus_24919_Transcript_1/1_Conf_1.000	133	17	9.54E-05	XP_002637396.1	83	50.0618	42	35	Hypothetical protein CBG19103
Locus_2492_Transcript_1/1_Conf_1.000	934	20	5.42E-134	AAW02892.1	98	481.485	250	247	goa-1
Locus_24920_Transcript_1/1_Conf_1.000	155	20	1.60E-15	XP_002632893.1	86	85.8853	51	44	Hypothetical protein CBG15101
Locus_24921_Transcript_1/1_Conf_1.000	133	0							
Locus_24922_Transcript_1/1_Conf_1.000	318	20	1.26E-20	EFO22577.1	61	102.834	105	65	hypothetical protein LOAG_05911
Locus_24923_Transcript_1/1_Conf_1.000	220	20	2.10E-15	NP_510249.2	70	85.5001	71	50	TREhalase family member (tre-4)

Locus_24924_Transcript_1/1_Conf_1.000	522	20	5.67E-33	NP_490796.2	61	144.05	184	113	abnormal cell MIGration family member (mig-1)
Locus_24925_Transcript_1/1_Conf_1.000	276	7	4.71E-12	NP_497641.2	66	74.3294	92	61	CaDHerin family member (cdh-1)
Locus_24926_Transcript_1/1_Conf_1.000	171	0							
Locus_24927_Transcript_1/1_Conf_1.000	276	20	2.10E-36	XP_002921690.1	100	155.221	75	75	PREDICTED: 26S protease regulatory subunit 6A-like
Locus_24928_Transcript_1/1_Conf_1.000	131	13	3.75E-09	EFO15717.1	81	64.6994	43	35	hypothetical protein LOAG_12793
Locus_24929_Transcript_1/1_Conf_1.000	201	0							
Locus_2493_Transcript_1/1_Conf_1.000	350	0							
Locus_24930_Transcript_1/1_Conf_1.000	126	0							
Locus_24931_Transcript_1/1_Conf_1.000	174	0							
Locus_24932_Transcript_1/1_Conf_1.000	223	4	1.77E-22	NP_001041206.1	79	108.997	74	59	hypothetical protein ZC487.1
Locus_24933_Transcript_1/1_Conf_1.000	130	0							
Locus_24934_Transcript_1/1_Conf_1.000	135	0							
Locus_24935_Transcript_1/1_Conf_1.000	150	0							
Locus_24936_Transcript_1/1_Conf_1.000	301	0							
Locus_24937_Transcript_1/1_Conf_1.000	348	20	1.25E-28	NP_506047.5	75	129.413	114	86	abnormal CHEmotaxis family member (che-11)

Locus_24938_Transcript_1/1_Conf_1.000	178	20	3.15E-08	XP_001237683.2	75	61.6178	52	39	AGAP005567-PA
Locus_24939_Transcript_1/1_Conf_1.000	194	0							
Locus_2494_Transcript_1/1_Conf_1.000	204	4	2.98E-06	EFO23863.1	58	55.0694	70	41	hypothetical protein LOAG_04618
Locus_24940_Transcript_1/1_Conf_1.000	174	20	7.76E-15	NP_504416.1	71	83.5741	53	38	hypothetical protein C10G8.4
Locus_24941_Transcript_1/1_Conf_1.000	169	20	5.57E-29	3K6S	100	130.568	56	56	Structure Of Integrin Alphaxbeta2 Ectodomain
Locus_24942_Transcript_1/1_Conf_1.000	173	0							
Locus_24943_Transcript_1/1_Conf_1.000	159	0							
Locus_24944_Transcript_1/1_Conf_1.000	185	0							
Locus_24945_Transcript_1/1_Conf_1.000	267	2	3.65E-04	EFO22882.1	72	48.1358	37	27	TK/FER protein kinase
Locus_24946_Transcript_1/1_Conf_1.000	159	0							
Locus_24947_Transcript_1/1_Conf_1.000	159	0							

Locus_24948_Transcript_1/1_Conf_1.000	215	20	2.93E-22	XP_002130881.1	85	108.227	63	54	PREDICTED: similar to glucosamine-6-phosphate deaminase 1
Locus_24949_Transcript_1/1_Conf_1.000	230	3	8.47E-09	XP_002632822.1	68	63.5438	70	48	C. briggsae CBR-NHR-97 protein
Locus_2495_Transcript_1/3_Conf_0.667	2889	4	9.44E-21	XP_002639685.1	39	107.457	822	328	C. briggsae CBR-SPD-2 protein
Locus_2495_Transcript_2/3_Conf_0.667	2934	6	3.77E-25	XP_002639685.1	40	122.094	823	336	C. briggsae CBR-SPD-2 protein
Locus_2495_Transcript_3/3_Conf_0.667	2934	6	3.77E-25	XP_002639685.1	40	122.094	823	336	C. briggsae CBR-SPD-2 protein
Locus_24950_Transcript_1/1_Conf_1.000	128	20	6.41E-17	XP_002821745.1	100	90.5077	42	42	PREDICTED: LOW QUALITY PROTEIN: solute carrier family 15 member 3-like
Locus_24951_Transcript_1/1_Conf_1.000	153	20	1.40E-11	CBK19469.1	87	72.7886	47	41	C. elegans protein T04B2.2b, partially confirmed by transcript evidence
Locus_24952_Transcript_1/1_Conf_1.000	201	4	1.34E-06	XP_002641616.1	66	56.225	66	44	C. briggsae CBR-ALX-1 protein
Locus_24953_Transcript_1/1_Conf_1.000	129	0							
Locus_24954_Transcript_1/1_Conf_1.000	142	0							
Locus_24955_Transcript_1/1_Conf_1.000	154	0							
Locus_24956_Transcript_1/1_Conf_1.000	187	0							
Locus_24957_Transcript_1/1_Conf_1.000	141	0							
Locus_24958_Transcript_1/1_Conf_1.000	502	0							
Locus_24959_Transcript_1/1_Conf_1.000	264	0							
Locus_2496_Transcript_1/1_Conf_1.000	355	0							
Locus_24960_Transcript_1/1_Conf_1.000	135	0							
Locus_24961_Transcript_1/1_Conf_1.000	129	5	1.21E-07	XP_002407980.1	81	59.6918	38	31	conserved hypothetical protein

Locus_24962_Transcript_1/1_Conf_1.000	188	20	4.99E-17	EFO14883.1	82	90.8929	62	51	TK/FER protein kinase
Locus_24963_Transcript_1/1_Conf_1.000	170	0							
Locus_24964_Transcript_1/1_Conf_1.000	226	20	1.49E-29	XP_002634978.1	95	132.494	74	71	C. briggsae CBR-PGP-1 protein
Locus_24965_Transcript_1/1_Conf_1.000	230	2	3.93E-06	XP_002631113.1	59	54.6842	66	39	C. briggsae CBR-ARS-1 protein
Locus_24966_Transcript_1/1_Conf_1.000	243	0							
Locus_24967_Transcript_1/1_Conf_1.000	183	1	3.05E-06	XP_002636321.1	70	55.0694	40	28	Hypothetical protein CBG08614
Locus_24968_Transcript_1/1_Conf_1.000	149	0							
Locus_24969_Transcript_1/1_Conf_1.000	200	0							
Locus_2497_Transcript_1/1_Conf_1.000	1368	0							
Locus_24970_Transcript_1/1_Conf_1.000	153	0							
Locus_24971_Transcript_1/1_Conf_1.000	235	20	2.77E-36	XP_002631558.1	98	154.836	77	76	Hypothetical protein CBG20734
Locus_24972_Transcript_1/1_Conf_1.000	137	3	3.37E-10	NP_497769.3	84	68.1662	46	39	TOllisH (Tolloid and BMP-1 family) family member (toh-1)
Locus_24973_Transcript_1/1_Conf_1.000	149	0							
Locus_24974_Transcript_1/1_Conf_1.000	145	0							
Locus_24975_Transcript_1/1_Conf_1.000	212	17	1.02E-06	EFO17895.1	60	56.6102	55	33	hypothetical protein LOAG_10603
Locus_24976_Transcript_1/1_Conf_1.000	164	0							
Locus_24977_Transcript_1/1_Conf_1.000	255	0							
Locus_24978_Transcript_1/1_Conf_1.000	274	0							
Locus_24979_Transcript_1/1_Conf_1.000	442	0							
Locus_2498_Transcript_1/1_Conf_1.000	1173	0							
Locus_24980_Transcript_1/1_Conf_1.000	188	4	1.78E-14	NP_495713.1	78	82.4185	61	48	RNA-dependent RNA polymerase Family family member (rrf-3)
Locus_24981_Transcript_1/1_Conf_1.000	165	0							

Locus_24982_Transcript_1/1_Conf_1.000	175	20	9.15E-24	EFN84489.1	100	113.235	58	58	Histone H2A.V
Locus_24983_Transcript_1/1_Conf_1.000	173	0							
Locus_24984_Transcript_1/1_Conf_1.000	212	0							
Locus_24985_Transcript_1/1_Conf_1.000	162	0							
Locus_24986_Transcript_1/1_Conf_1.000	172	0							
Locus_24987_Transcript_1/1_Conf_1.000	182	0							
Locus_24988_Transcript_1/1_Conf_1.000	131	0							
Locus_24989_Transcript_1/1_Conf_1.000	560	20	4.71E-50	CAB07368.3	72	201.06	180	130	C. elegans protein F22G12.4, confirmed by transcript evidence
Locus_2499_Transcript_1/1_Conf_1.000	144	0							
Locus_24990_Transcript_1/1_Conf_1.000	168	0							
Locus_24991_Transcript_1/1_Conf_1.000	129	0							
Locus_24992_Transcript_1/1_Conf_1.000	161	0							
Locus_24993_Transcript_1/1_Conf_1.000	198	6	3.30E-13	XP_001894136.1	69	78.1814	65	45	hypothetical protein
Locus_24994_Transcript_1/1_Conf_1.000	174	0							
Locus_24995_Transcript_1/1_Conf_1.000	534	4	1.82E-13	NP_497743.1	64	79.337	98	63	hypothetical protein C46F11.4
Locus_24996_Transcript_1/1_Conf_1.000	467	20	2.21E-25	XP_002632990.1	66	118.627	117	78	C. briggsae CBR-NHR-11 protein
Locus_24997_Transcript_1/1_Conf_1.000	268	2	4.31E-05	XP_001623877.1	72	51.2174	48	35	predicted protein
Locus_24998_Transcript_1/1_Conf_1.000	202	20	2.51E-29	XP_002644000.1	100	131.724	67	67	C. briggsae CBR-IFA-1 protein
Locus_24999_Transcript_1/1_Conf_1.000	245	10	7.74E-31	AAA64509.3	91	136.732	81	74	Hypothetical protein C09F5.1
Locus_25_Transcript_1/1_Conf_1.000	4623	20	9.79E-164	XP_001900720.1	53	583.178	967	518	Bromodomain containing protein
Locus_250_Transcript_1/1_Conf_1.000	1664	20	0	CAJ80808.3	83	772.311	563	471	C. elegans protein F36H1.2b, confirmed by transcript evidence
Locus_2500_Transcript_1/1_Conf_1.000	430	0							
Locus_25000_Transcript_1/1_Conf_1.000	140	5	2.41E-08	AAA81106.2	81	62.003	44	36	Hypothetical protein F41G3.5
Locus_25001_Transcript_1/1_Conf_1.000	133	0							
Locus_25002_Transcript_1/1_Conf_1.000	144	0							

Locus_25003_Transcript_1/1_Conf_1.000	144	20	1.97E-13	NP_500460.1	72	78.9518	47	34	hypothetical protein W02C12.1
Locus_25004_Transcript_1/1_Conf_1.000	286	2	2.84E-04	XP_001895815.1	52	48.521	76	40	Protein-tyrosine phosphatase containing protein
Locus_25005_Transcript_1/1_Conf_1.000	188	5	2.65E-10		70	68.5514	62	44	hypothetical protein F32B4.3a - Caenorhabditis elegans
Locus_25006_Transcript_1/1_Conf_1.000	180	0							
Locus_25007_Transcript_1/1_Conf_1.000	189	0							
Locus_25008_Transcript_1/1_Conf_1.000	358	20	7.79E-23	XP_002635009.1	69	110.153	84	58	C. briggsae CBR-ELT-6 protein
Locus_25009_Transcript_1/1_Conf_1.000	314	20	3.70E-20	NP_503109.1	74	101.293	87	65	beta-LACTamase domain containing family member (lact-6)
Locus_2501_Transcript_1/1_Conf_1.000	392	0							
Locus_25010_Transcript_1/1_Conf_1.000	178	0							
Locus_25011_Transcript_1/1_Conf_1.000	282	0							
Locus_25012_Transcript_1/1_Conf_1.000	169	10	8.66E-06	NP_001022158.1	66	53.5286	57	38	hypothetical protein F41G3.21
Locus_25013_Transcript_1/1_Conf_1.000	195	0							

Locus_25014_Transcript_1/1_Conf_1.000	133	20	3.16E-16	AAC47238.1	95	88.1965	44	42	non-muscle myosin heavy chain II
Locus_25015_Transcript_1/1_Conf_1.000	224	0							
Locus_25016_Transcript_1/1_Conf_1.000	222	0							
Locus_25017_Transcript_1/1_Conf_1.000	224	20	3.33E-29	XP_002642615.1	83	131.339	74	62	C. briggsae CBR-MUP-4 protein
Locus_25018_Transcript_1/1_Conf_1.000	134	0							
Locus_25019_Transcript_1/1_Conf_1.000	168	20	9.83E-26	XP_001105618.2	100	119.783	56	56	PREDICTED: poly(rC)-binding protein 2 isoform 2
Locus_2502_Transcript_1/2_Conf_1.000	2134	20	2.50E-169	NP_508849.3	67	600.512	621	420	hypothetical protein ZC8.6
Locus_2502_Transcript_2/2_Conf_1.000	2035	20	1.86E-174	NP_508849.3	71	617.461	588	420	hypothetical protein ZC8.6
Locus_25020_Transcript_1/1_Conf_1.000	362	2	5.72E-34	XP_002630907.1	71	147.132	119	85	Hypothetical protein CBG02631
Locus_25021_Transcript_1/1_Conf_1.000	138	0							
Locus_25022_Transcript_1/1_Conf_1.000	213	0							
Locus_25023_Transcript_1/1_Conf_1.000	285	20	2.46E-40	BAI81969.1	92	168.318	95	88	FKBP-binding protein fkb-3
Locus_25024_Transcript_1/1_Conf_1.000	132	0							

Locus_25025_Transcript_1/1_Conf_1.000	239	0							
Locus_25026_Transcript_1/1_Conf_1.000	183	20	2.57E-21	XP_002643286.1	89	105.145	59	53	Hypothetical protein CBG08162
Locus_25027_Transcript_1/1_Conf_1.000	312	0							
Locus_25028_Transcript_1/1_Conf_1.000	436	20	2.81E-57	NP_495437.2	85	224.557	145	124	hypothetical protein C52E12.4
Locus_25029_Transcript_1/1_Conf_1.000	217	0							
Locus_2503_Transcript_1/1_Conf_1.000	349	0							
Locus_25030_Transcript_1/1_Conf_1.000	143	0							
Locus_25031_Transcript_1/1_Conf_1.000	138	0							
Locus_25032_Transcript_1/1_Conf_1.000	166	0							
Locus_25033_Transcript_1/1_Conf_1.000	169	0							
Locus_25034_Transcript_1/1_Conf_1.000	245	0							
Locus_25035_Transcript_1/1_Conf_1.000	144	20	1.84E-19	XP_002914626.1	100	98.9821	47	47	PREDICTED: LOW QUALITY PROTEIN: probable ATP-dependent RNA helicase DDX17-like
Locus_25036_Transcript_1/1_Conf_1.000	161	0							
Locus_25037_Transcript_1/1_Conf_1.000	177	20	1.23E-20	NP_494711.1	89	102.834	58	52	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-48)
Locus_25038_Transcript_1/1_Conf_1.000	167	3	1.17E-18	EFO21620.1	87	96.2857	55	48	hypothetical protein LOAG_06866
Locus_25039_Transcript_1/1_Conf_1.000	205	0							
Locus_2504_Transcript_1/1_Conf_1.000	284	20	3.33E-37	XP_002642308.1	91	157.918	94	86	C. briggsae CBR-HEX-3 protein
Locus_25040_Transcript_1/1_Conf_1.000	188	0							
Locus_25041_Transcript_1/1_Conf_1.000	163	0							
Locus_25042_Transcript_1/1_Conf_1.000	133	0							
Locus_25043_Transcript_1/1_Conf_1.000	223	20	4.67E-15	EFO23870.1	72	84.3445	72	52	hypothetical protein LOAG_04614
Locus_25044_Transcript_1/1_Conf_1.000	138	0							
Locus_25045_Transcript_1/1_Conf_1.000	129	20	2.06E-15	XP_002643086.1	90	85.5001	43	39	C. briggsae CBR-ALH-1 protein
Locus_25046_Transcript_1/1_Conf_1.000	154	2	4.36E-05	NP_001076752.1	68	51.2174	50	34	hypothetical protein ZC15.10
Locus_25047_Transcript_1/1_Conf_1.000	238	8	1.52E-18	ADI24623.1	94	95.9005	78	74	Copine domain protein, atypical protein 2, isoform c, partially confirmed by transcript evidence
Locus_25048_Transcript_1/1_Conf_1.000	314	1	8.28E-04	XP_001898965.1	64	46.9802	54	35	Protein kinase domain containing protein
Locus_25049_Transcript_1/1_Conf_1.000	133	0							

Locus_2505_Transcript_1/1_Conf_1.000	366	0							
Locus_25050_Transcript_1/1_Conf_1.000	236	0							
Locus_25051_Transcript_1/1_Conf_1.000	175	0							
Locus_25052_Transcript_1/1_Conf_1.000	190	0							
Locus_25053_Transcript_1/1_Conf_1.000	392	0							
Locus_25054_Transcript_1/1_Conf_1.000	272	11	2.96E-30	XP_001899066.1	90	134.806	90	81	Clc-like
Locus_25055_Transcript_1/1_Conf_1.000	131	0							
Locus_25056_Transcript_1/1_Conf_1.000	392	20	2.47E-37	CAX65068.1	74	158.303	129	96	C. elegans protein K08C7.3d, confirmed by transcript evidence
Locus_25057_Transcript_1/1_Conf_1.000	210	8	1.51E-10	NP_001040671.1	64	69.3218	71	46	AXin-Like family member (axl-1)
Locus_25058_Transcript_1/1_Conf_1.000	198	20	2.21E-25	XP_002638487.1	90	118.627	65	59	Hypothetical protein CBG12917
Locus_25059_Transcript_1/1_Conf_1.000	263	0							
Locus_2506_Transcript_1/1_Conf_1.000	529	4	7.76E-17	NP_499212.1	56	90.5077	181	103	Masculinisation Of Germline family member (mog-1)
Locus_25060_Transcript_1/1_Conf_1.000	133	0							
Locus_25061_Transcript_1/1_Conf_1.000	154	0							
Locus_25062_Transcript_1/1_Conf_1.000	312	0							
Locus_25063_Transcript_1/1_Conf_1.000	278	20	3.72E-17	XP_002636218.1	78	91.2781	92	72	C. briggsae CBR-TNT-4 protein
Locus_25064_Transcript_1/1_Conf_1.000	208	0							
Locus_25065_Transcript_1/1_Conf_1.000	152	0							
Locus_25066_Transcript_1/1_Conf_1.000	278	20	3.71E-25	XP_002637122.1	71	117.857	92	66	C. briggsae CBR-UGT-49 protein
Locus_25067_Transcript_1/1_Conf_1.000	147	0							
Locus_25068_Transcript_1/1_Conf_1.000	136	1	6.59E-06	XP_002719154.1	75	53.9138	44	33	PREDICTED: alpha 1 type I collagen
Locus_25069_Transcript_1/1_Conf_1.000	191	0							
Locus_2507_Transcript_1/1_Conf_1.000	1346	20	2.90E-159	XP_002642829.1	97	566.229	295	289	Hypothetical protein CBG21228
Locus_25070_Transcript_1/1_Conf_1.000	198	18	4.47E-10	EFO23249.1	78	67.781	52	41	hypothetical protein LOAG_05238
Locus_25071_Transcript_1/1_Conf_1.000	459	20	1.45E-37	XP_002648400.1	69	159.073	152	105	C. briggsae CBR-DPF-1 protein

Locus_25072_Transcript_1/1_Conf_1.000	350	20	3.64E-36	XP_002120354.1	80	154.451	121	97	PREDICTED: similar to Methylglutaconyl-CoA hydratase, mitochondrial precursor (AU-specific RNA-binding enoyl-CoA hydratase) (AU-binding protein/enoyl-CoA hydratase)
Locus_25073_Transcript_1/1_Conf_1.000	235	0							
Locus_25074_Transcript_1/1_Conf_1.000	149	0							
Locus_25075_Transcript_1/1_Conf_1.000	377	5	1.59E-07	A8WRJ2.2	61	59.3066	75	46	GTPase-activating protein rrc-1
Locus_25076_Transcript_1/1_Conf_1.000	214	0							
Locus_25077_Transcript_1/1_Conf_1.000	136	20	1.56E-15	EFO17879.1	100	85.8853	41	41	hypothetical protein LOAG_10616
Locus_25078_Transcript_1/1_Conf_1.000	230	20	1.89E-08	XP_002646359.1	63	62.3882	72	46	Hypothetical protein CBG12076
Locus_25079_Transcript_1/1_Conf_1.000	150	0							
Locus_2508_Transcript_1/3_Conf_0.429	1197	20	2.69E-81	XP_002632934.1	68	306.99	348	239	Hypothetical protein CBG21689
Locus_2508_Transcript_2/3_Conf_0.571	2020	20	6.19E-146	CBH29652.1	61	522.702	707	438	C. elegans protein C10C5.1c, partially confirmed by transcript evidence
Locus_2508_Transcript_3/3_Conf_0.714	2128	20	2.43E-148	CBH29652.1	60	530.791	727	442	C. elegans protein C10C5.1c, partially confirmed by transcript evidence
Locus_25080_Transcript_1/1_Conf_1.000	163	20	1.21E-23	XP_001116282.2	100	112.849	54	54	PREDICTED: plexin-B2
Locus_25081_Transcript_1/1_Conf_1.000	198	0							
Locus_25082_Transcript_1/1_Conf_1.000	170	0							
Locus_25083_Transcript_1/1_Conf_1.000	175	7	4.25E-21	XP_002647789.1	86	104.375	58	50	Hypothetical protein CBG23555
Locus_25084_Transcript_1/1_Conf_1.000	223	0							
Locus_25085_Transcript_1/1_Conf_1.000	162								
Locus_25086_Transcript_1/1_Conf_1.000	531								

Locus_25087_Transcript_1/1_Conf_1.000	182	20	3.15E-19	NP_497809.1	86	98.2117	60	52	Heavy chain, Unconventional Myosin family member (hum-5)
Locus_25088_Transcript_1/1_Conf_1.000	208	20	1.37E-27	EFO23546.1	95	125.946	67	64	PDZ domain-containing protein
Locus_25089_Transcript_1/1_Conf_1.000	303	20	3.72E-33	XP_002641457.1	83	144.436	101	84	C. briggsae CBR-TOP-3 protein
Locus_2509_Transcript_1/1_Conf_1.000	920	20	5.02E-68	XP_002639645.1	74	262.307	225	168	C. briggsae CBR-IMP-1 protein
Locus_25090_Transcript_1/1_Conf_1.000	145	7	6.57E-09	XP_002641706.1	86	63.929	45	39	C. briggsae CBR-ROM-2 protein
Locus_25091_Transcript_1/1_Conf_1.000	247	0							
Locus_25092_Transcript_1/1_Conf_1.000	339	0							
Locus_25093_Transcript_1/1_Conf_1.000	326	16	5.11E-06	XP_002605049.1	51	54.299	82	42	hypothetical protein BRAFLDRAFT_85195
Locus_25094_Transcript_1/1_Conf_1.000	357	0							
Locus_25095_Transcript_1/1_Conf_1.000	164	0							
Locus_25096_Transcript_1/1_Conf_1.000	169	20	1.25E-12	BAE78960.1	80	76.2554	52	42	aspartate racemase
Locus_25097_Transcript_1/1_Conf_1.000	151	0							
Locus_25098_Transcript_1/1_Conf_1.000	155	20	2.30E-22	EFO23668.1	96	108.612	51	49	hypothetical protein LOAG_04821
Locus_25099_Transcript_1/1_Conf_1.000	156	0							
Locus_251_Transcript_1/1_Conf_1.000	795	20	3.65E-66	XP_002634865.1	66	255.758	256	170	C. briggsae CBR-PLX-1 protein
Locus_2510_Transcript_1/1_Conf_1.000	849	20	2.55E-100	AAG29105.1	85	369.392	223	190	AF273705_1zinc metallopeptidase 2 MEP2
Locus_25100_Transcript_1/1_Conf_1.000	144	0							

Locus_25101_Transcript_1/1_Conf_1.000	190	4	2.56E-05	NP_501343.1	64	51.9878	51	33	ELongator complex Protein Component family member (elpc-4)
Locus_25102_Transcript_1/1_Conf_1.000	169	0							
Locus_25103_Transcript_1/1_Conf_1.000	141	0							
Locus_25104_Transcript_1/1_Conf_1.000	443	20	2.30E-22	NP_503178.1	62	108.612	140	88	AuTophaGy (yeast Atg homolog) family member (atg-9)
Locus_25105_Transcript_1/1_Conf_1.000	163	0							
Locus_25106_Transcript_1/1_Conf_1.000	332	20	4.39E-42	EFO17747.1	97	174.096	87	85	STE/STE20/MSN protein kinase
Locus_25107_Transcript_1/1_Conf_1.000	133	0							
Locus_25108_Transcript_1/1_Conf_1.000	132	0							
Locus_25109_Transcript_1/1_Conf_1.000	257	0							
Locus_2511_Transcript_1/2_Conf_1.000	2147	20	1.15E-121	NP_001040884.2	90	442.195	349	315	hypothetical protein Y53G8B.4
Locus_2511_Transcript_2/2_Conf_1.000	2214	20	1.19E-121	NP_001040884.2	90	442.195	349	315	hypothetical protein Y53G8B.4
Locus_25110_Transcript_1/1_Conf_1.000	164	20	1.81E-11	XP_001902281.1	73	72.4034	53	39	Protein-tyrosine phosphatase containing protein
Locus_25111_Transcript_1/1_Conf_1.000	210	0							
Locus_25112_Transcript_1/1_Conf_1.000	215	0							
Locus_25113_Transcript_1/1_Conf_1.000	186	0							

Locus_25114_Transcript_1/1_Conf_1.000	275	20	8.06E-12	NP_508409.1	65	73.559	89	58	HEXosaminidase family member (hex-1)
Locus_25115_Transcript_1/1_Conf_1.000	136	20	5.19E-19	XP_002634414.1	93	97.4413	45	42	C. briggsae CBR-EPI-1 protein
Locus_25116_Transcript_1/1_Conf_1.000	149	0							
Locus_25117_Transcript_1/1_Conf_1.000	129	0							
Locus_25118_Transcript_1/1_Conf_1.000	132	0							
Locus_25119_Transcript_1/1_Conf_1.000	466	2	2.30E-06	NP_501321.1	58	55.4546	97	57	hypothetical protein C49H3.3
Locus_2512_Transcript_1/1_Conf_1.000	544	20	2.95E-46	XP_001901466.1	71	188.348	184	131	Paired amphipathic helix repeat family protein
Locus_25120_Transcript_1/1_Conf_1.000	227	0							
Locus_25121_Transcript_1/1_Conf_1.000	161	2	8.74E-06	XP_002646257.1	71	53.5286	52	37	Hypothetical protein CBG11961
Locus_25122_Transcript_1/1_Conf_1.000	548	20	1.04E-22	XP_001900186.1	65	110.153	145	95	hypothetical protein
Locus_25123_Transcript_1/1_Conf_1.000	156	20	1.03E-22	EFN85419.1	100	109.768	51	51	Serine/threonine-protein phosphatase 4 catalytic subunit
Locus_25124_Transcript_1/1_Conf_1.000	139	0							
Locus_25125_Transcript_1/1_Conf_1.000	154	0							
Locus_25126_Transcript_1/1_Conf_1.000	106	0							
Locus_25127_Transcript_1/1_Conf_1.000	204	0							
Locus_25128_Transcript_1/1_Conf_1.000	138	0							

Locus_25129_Transcript_1/1_Conf_1.000	146	20	5.93E-18	NP_001024588.1	100	93.9745	48	48	abnormal cell LINeage family member (lin-2)
Locus_2513_Transcript_1/1_Conf_1.000	233	0							
Locus_25130_Transcript_1/1_Conf_1.000	333	0							
Locus_25131_Transcript_1/1_Conf_1.000	224	20	3.57E-15	EFO20785.1	89	84.7297	48	43	TKL/MLK/HH498 protein kinase
Locus_25132_Transcript_1/1_Conf_1.000	173	0							
Locus_25133_Transcript_1/1_Conf_1.000	162	20	4.30E-21	XP_002759851.1	98	104.375	53	52	PREDICTED: rho-related GTP-binding protein RhoC-like
Locus_25134_Transcript_1/1_Conf_1.000	151	0							
Locus_25135_Transcript_1/1_Conf_1.000	149	0							
Locus_25136_Transcript_1/1_Conf_1.000	294	0							
Locus_25137_Transcript_1/1_Conf_1.000	261	0							
Locus_25138_Transcript_1/1_Conf_1.000	316	14	1.40E-19	EFO19841.1	69	99.3673	105	73	hypothetical protein LOAG_08651
Locus_25139_Transcript_1/1_Conf_1.000	260	0							
Locus_2514_Transcript_1/2_Conf_1.000	670	0							
Locus_2514_Transcript_2/2_Conf_1.000	670	0							
Locus_25140_Transcript_1/1_Conf_1.000	155	0							

Locus_25141_Transcript_1/1_Conf_1.000	156	6	4.97E-09	NP_491776.1	71	64.3142	52	37	hypothetical protein T09B4.7
Locus_25142_Transcript_1/1_Conf_1.000	297	20	4.92E-17	NP_495815.1	61	90.8929	99	61	hypothetical protein F54C9.9
Locus_25143_Transcript_1/1_Conf_1.000	137	20	1.79E-19	EFO27232.1	100	98.9821	45	45	voltage-gated potassium channel
Locus_25144_Transcript_1/1_Conf_1.000	322	0							
Locus_25145_Transcript_1/1_Conf_1.000	261	0							
Locus_25146_Transcript_1/1_Conf_1.000	169	20	1.47E-29	XP_002805655.1	100	132.494	55	55	PREDICTED: integrin beta-1
Locus_25147_Transcript_1/1_Conf_1.000	243	20	5.19E-27	NP_001122835.1	85	124.02	80	68	UNCoordinated family member (unc-22)
Locus_25148_Transcript_1/1_Conf_1.000	157	0							
Locus_25149_Transcript_1/1_Conf_1.000	365	0							
Locus_2515_Transcript_1/1_Conf_1.000	1649	20	5.30E-153	XP_002643132.1	67	545.814	517	348	C. briggsae CBR-POD-1 protein
Locus_25150_Transcript_1/1_Conf_1.000	354	2	8.09E-20	XP_002648027.1	73	100.138	112	82	Hypothetical protein CBG23996
Locus_25151_Transcript_1/1_Conf_1.000	132	4	3.28E-05	NP_741744.2	74	51.6026	43	32	hypothetical protein C15C7.7
Locus_25152_Transcript_1/1_Conf_1.000	168	2	5.42E-08	XP_002644454.1	75	60.8474	56	42	Hypothetical protein CBG14320

Locus_25153_Transcript_1/1_Conf_1.000	250	0							
Locus_25154_Transcript_1/1_Conf_1.000	169	0							
Locus_25155_Transcript_1/1_Conf_1.000	321	3	2.91E-09	XP_002637263.1	58	65.0846	113	66	Hypothetical protein CBG18943
Locus_25156_Transcript_1/1_Conf_1.000	326								
Locus_25157_Transcript_1/1_Conf_1.000	121	3	1.35E-06	XP_002639673.1	84	56.225	39	33	Hypothetical protein CBG12391
Locus_25158_Transcript_1/1_Conf_1.000	199	6	4.77E-12	NP_001022673.1	86	74.3294	66	57	NADC (Na+-coupled dicarboxylate transporter) family member (nac-3)
Locus_25159_Transcript_1/1_Conf_1.000	144	0							
Locus_2516_Transcript_1/1_Conf_1.000	316	7	1.03E-46	CAB04449.3	91	189.504	105	96	C. elegans protein F53A2.1, partially confirmed by transcript evidence
Locus_25160_Transcript_1/1_Conf_1.000	153	0							
Locus_25161_Transcript_1/1_Conf_1.000	263	20	1.75E-38	NP_497733.1	89	162.155	87	78	Protein Tyrosine Phosphatase family member (ptp-1)
Locus_25162_Transcript_1/1_Conf_1.000	168	20	8.06E-20	CAC10528.1	94	100.138	55	52	putative inositol 1,4,5-trisphosphate receptor
Locus_25163_Transcript_1/1_Conf_1.000	128	17	7.85E-07	NP_502225.1	80	56.9954	40	32	Gon-2 Extragenic Modifier family member (gem-4)
Locus_25164_Transcript_1/1_Conf_1.000	140	0							
Locus_25165_Transcript_1/1_Conf_1.000	219	5	1.72E-17	EFO21092.1	72	92.4337	72	52	hypothetical protein LOAG_07396
Locus_25166_Transcript_1/1_Conf_1.000	357	4	1.12E-29	XP_002641257.1	67	132.88	118	80	Hypothetical protein CBG05168
Locus_25167_Transcript_1/1_Conf_1.000	217	20	3.58E-12	XP_001898472.1	68	74.7146	64	44	Trehalase family protein
Locus_25168_Transcript_1/1_Conf_1.000	470	20	7.49E-66	NP_490828.3	87	253.062	156	136	HAlF transporter (PGP related) family member (haf-6)
Locus_25169_Transcript_1/1_Conf_1.000	167	20	9.26E-16	NP_498923.1	87	86.6557	54	47	hypothetical protein B0303.15
Locus_2517_Transcript_1/1_Conf_1.000	1635	20	3.40E-160	NP_740981.1	71	569.696	565	406	hypothetical protein R05F9.1

Locus_25170_Transcript_1/1_Conf_1.000	391	20	2.71E-60	XP_002819557.1	99	234.572	115	114	PREDICTED: hypothetical protein LOC100461873
Locus_25171_Transcript_1/1_Conf_1.000	165	4	7.55E-26	XP_002345197.1	100	120.168	54	54	PREDICTED: hypothetical protein XP_002345197
Locus_25172_Transcript_1/1_Conf_1.000	238	0							
Locus_25173_Transcript_1/1_Conf_1.000	155	0							
Locus_25174_Transcript_1/1_Conf_1.000	215	2	2.25E-14	NP_741941.1	88	82.0333	54	48	MEChanosensory abnormality family member (mec-5)
Locus_25175_Transcript_1/1_Conf_1.000	504	4	3.40E-29	NP_497751.1	75	131.339	101	76	hypothetical protein C14B1.10
Locus_25176_Transcript_1/1_Conf_1.000	292	7	4.03E-35	XP_002630272.1	86	150.984	96	83	C. briggsae CBR-EFF-1 protein
Locus_25177_Transcript_1/1_Conf_1.000	269	0							
Locus_25178_Transcript_1/1_Conf_1.000	140	18	1.01E-14	XP_002645243.1	97	83.1889	46	45	C. briggsae CBR-MYO-2 protein
Locus_25179_Transcript_1/1_Conf_1.000	186	0							

Locus_2518_Transcript_1/2_Conf_1.000	1213	20	3.12E-85	NP_001021274.1	80	320.087	232	186	EXOSome (multiexonuclease complex) component family member (exos-4.1)
Locus_2518_Transcript_2/2_Conf_1.000	1162	20	2.92E-85	NP_001021274.1	80	320.087	232	186	EXOSome (multiexonuclease complex) component family member (exos-4.1)
Locus_25180_Transcript_1/1_Conf_1.000	144	0							
Locus_25181_Transcript_1/1_Conf_1.000	159	20	1.34E-22	3ML6	100	109.383	52	52	A Complex Between Dishevlled2 And Clathrin Adaptor Ap-2
Locus_25182_Transcript_1/1_Conf_1.000	148	0							
Locus_25183_Transcript_1/1_Conf_1.000	286	20	1.23E-07	XP_002634977.1	64	59.6918	57	37	Hypothetical protein CBG13513
Locus_25184_Transcript_1/1_Conf_1.000	130	0							
Locus_25185_Transcript_1/1_Conf_1.000	162	0							

Locus_25186_Transcript_1/1_Conf_1.000	149	20	1.41E-11	EFO25550.1	82	72.7886	46	38	nucleolar protein 10
Locus_25187_Transcript_1/1_Conf_1.000	455	6	2.12E-20	XP_001892878.1	63	102.064	110	70	hypothetical protein Bm1_07045
Locus_25188_Transcript_1/1_Conf_1.000	278	20	2.75E-20	XP_001898597.1	75	101.679	96	72	Steroid receptor seven-up type 2
Locus_25189_Transcript_1/1_Conf_1.000	152	0							
Locus_2519_Transcript_1/2_Conf_1.000	914	0							
Locus_2519_Transcript_2/2_Conf_1.000	927	0							
Locus_25190_Transcript_1/1_Conf_1.000	191	0							
Locus_25191_Transcript_1/1_Conf_1.000	373	0							
Locus_25192_Transcript_1/1_Conf_1.000	259	11	1.40E-19	ADN00780.1	89	99.3673	59	53	class 3 lipase protein
Locus_25193_Transcript_1/1_Conf_1.000	343	0							
Locus_25194_Transcript_1/1_Conf_1.000	185	0							
Locus_25195_Transcript_1/1_Conf_1.000	139	0							
Locus_25196_Transcript_1/1_Conf_1.000	270	2	1.92E-21	XP_002634505.1	71	105.531	89	64	Hypothetical protein CBG08295
Locus_25197_Transcript_1/1_Conf_1.000	376	20	1.88E-08	EFO23604.1	59	62.3882	79	47	hypothetical protein LOAG_04880
Locus_25198_Transcript_1/1_Conf_1.000	244	0							
Locus_25199_Transcript_1/1_Conf_1.000	1268	20	7.93E-180	AAC47722.1	85	634.41	417	358	Native 66kDa protein
Locus_252_Transcript_1/1_Conf_1.000	186	0							
Locus_2520_Transcript_1/1_Conf_1.000	522	3	4.52E-06	EFO28201.1	55	54.6842	85	47	hypothetical protein LOAG_00283
Locus_25200_Transcript_1/1_Conf_1.000	211	0							
Locus_25201_Transcript_1/1_Conf_1.000	226	0							
Locus_25202_Transcript_1/1_Conf_1.000	245	20	1.56E-23	XP_002646299.1	78	112.464	80	63	Hypothetical protein CBG12006

Locus_25203_Transcript_1/1_Conf_1.000	128	20	3.76E-17	EFN84506.1	100	91.2781	42	42	GTP-binding nuclear protein Ran
Locus_25204_Transcript_1/1_Conf_1.000	655	4	9.45E-18	NP_501302.1	55	94.3597	152	84	MVB (yeast MultiVesicular Body sorting factor) related family member (mvb-12)
Locus_25205_Transcript_1/1_Conf_1.000	219	0							
Locus_25206_Transcript_1/1_Conf_1.000	187	2	1.23E-07	NP_497231.1	58	59.6918	68	40	hypothetical protein W06E11.7
Locus_25207_Transcript_1/1_Conf_1.000	191	0							
Locus_25208_Transcript_1/1_Conf_1.000	282	1	1.61E-07	XP_001898279.1	56	59.3066	86	49	hypothetical protein Bm1_34160
Locus_25209_Transcript_1/1_Conf_1.000	201	0							
Locus_2521_Transcript_1/1_Conf_1.000	266	20	1.81E-27	XP_002639700.1	83	125.561	87	73	Hypothetical protein CBG12421
Locus_25210_Transcript_1/1_Conf_1.000	139	0							
Locus_25211_Transcript_1/1_Conf_1.000	237	0							
Locus_25212_Transcript_1/1_Conf_1.000	146	17	5.56E-08	CAI42467.1	100	60.8474	44	44	TIMP metallopeptidase inhibitor 1
Locus_25213_Transcript_1/1_Conf_1.000	242	20	1.05E-27	XP_002826795.1	100	126.331	69	69	PREDICTED: protein FAM38A-like, partial
Locus_25214_Transcript_1/1_Conf_1.000	603	0							
Locus_25215_Transcript_1/1_Conf_1.000	182	0							
Locus_25216_Transcript_1/1_Conf_1.000	381	20	5.02E-46	XP_002629656.1	83	187.193	126	105	Hypothetical protein CBG00863
Locus_25217_Transcript_1/1_Conf_1.000	405	0							

Locus_25218_Transcript_1/1_Conf_1.000	203	4	2.29E-06	NP_506256.3	64	55.4546	51	33	CaDHerin family member (cdh-6)
Locus_25219_Transcript_1/1_Conf_1.000	140	0							
Locus_2522_Transcript_1/2_Conf_1.000	772	0							
Locus_2522_Transcript_2/2_Conf_1.000	778	0							
Locus_25220_Transcript_1/1_Conf_1.000	129	2	1.25E-04	NP_499780.1	75	49.6766	41	31	Temporarily Assigned Gene name family member (tag-164)
Locus_25221_Transcript_1/1_Conf_1.000	433	0							
Locus_25222_Transcript_1/1_Conf_1.000	128	20	2.28E-14	ADK09905.1	100	82.0333	42	42	non-muscle myosin IIA
Locus_25223_Transcript_1/1_Conf_1.000	226	0							

Locus_25224_Transcript_1/1_Conf_1.000	228	20	1.14E-21	XP_002930443.1	78	106.301	75	59	PREDICTED: dynein light chain 1, cytoplasmic-like
Locus_25225_Transcript_1/1_Conf_1.000	336	3	4.21E-45	NP_001022280.1	90	184.111	110	99	Serpentine Receptor, class AB (class A-like) family member (srab-14)
Locus_25226_Transcript_1/1_Conf_1.000	149	0							
Locus_25227_Transcript_1/1_Conf_1.000	174	0							
Locus_25228_Transcript_1/1_Conf_1.000	146	0							
Locus_25229_Transcript_1/1_Conf_1.000	211	20	3.37E-18	XP_002763951.1	100	94.7449	61	61	PREDICTED: NHP2-like protein 1-like
Locus_2523_Transcript_1/1_Conf_1.000	1244	3	1.26E-12	ADI24666.1	52	78.9518	172	90	Hypothetical protein Y59E9AL.36
Locus_25230_Transcript_1/1_Conf_1.000	389	0							
Locus_25231_Transcript_1/1_Conf_1.000	143	0							
Locus_25232_Transcript_1/1_Conf_1.000	899	20	1.43E-120	XP_002638375.1	79	436.802	298	238	Hypothetical protein CBG18580
Locus_25233_Transcript_1/1_Conf_1.000	242	0							

Locus_25234_Transcript_1/1_Conf_1.000	175	20	5.36E-24	NP_499922.1	96	114.005	58	56	Kinase, GLH-Binding family member (kgb-1)
Locus_25235_Transcript_1/1_Conf_1.000	217	5	4.51E-23	XP_002638527.1	91	110.923	69	63	C. briggsae CBR-UNC-80 protein
Locus_25236_Transcript_1/1_Conf_1.000	163	0							
Locus_25237_Transcript_1/1_Conf_1.000	216	0							
Locus_25238_Transcript_1/1_Conf_1.000	149	0							
Locus_25239_Transcript_1/1_Conf_1.000	210	0							
Locus_2524_Transcript_1/1_Conf_1.000	3186	20	6.02E-101	NP_497703.1	53	374.015	744	397	Nuclear Pore complex Protein family member (npp-9)
Locus_25240_Transcript_1/1_Conf_1.000	153	0							
Locus_25241_Transcript_1/1_Conf_1.000	136	0							
Locus_25242_Transcript_1/1_Conf_1.000	399	0							
Locus_25243_Transcript_1/1_Conf_1.000	258	0							
Locus_25244_Transcript_1/1_Conf_1.000	228	0							
Locus_25245_Transcript_1/1_Conf_1.000	138	0							
Locus_25246_Transcript_1/1_Conf_1.000	169	2	1.25E-04	XP_002642995.1	52	49.6766	68	36	Hypothetical protein CBG15282
Locus_25247_Transcript_1/1_Conf_1.000	140	0							
Locus_25248_Transcript_1/1_Conf_1.000	133	0							
Locus_25249_Transcript_1/1_Conf_1.000	264	0							
Locus_2525_Transcript_1/2_Conf_1.000	2931	20	1.57E-164	XP_001897294.1	63	585.104	691	441	DZF family protein
Locus_2525_Transcript_2/2_Conf_1.000	2898	20	1.55E-164	XP_001897294.1	63	585.104	691	441	DZF family protein
Locus_25250_Transcript_1/1_Conf_1.000	299	20	2.51E-29	NP_001022438.1	82	131.724	99	82	Ligand-Gated ion Channel family member (lgc-35)
Locus_25251_Transcript_1/1_Conf_1.000	143	0							
Locus_25252_Transcript_1/1_Conf_1.000	153	0							
Locus_25253_Transcript_1/1_Conf_1.000	419	0							
Locus_25254_Transcript_1/1_Conf_1.000	161	0							
Locus_25255_Transcript_1/1_Conf_1.000	194	1	1.77E-06	XP_002629926.1	67	55.8398	62	42	C. briggsae CBR-TAG-149 protein

Locus_25256_Transcript_1/1_Conf_1.000	225	20	6.47E-25	XP_002644368.1	81	117.087	74	60	C. briggsae CBR-CHT-1 protein
Locus_25257_Transcript_1/1_Conf_1.000	452	0							
Locus_25258_Transcript_1/1_Conf_1.000	134	0							
Locus_25259_Transcript_1/1_Conf_1.000	236	20	4.92E-17	NP_500737.1	77	90.8929	72	56	hypothetical protein W03F8.3
Locus_2526_Transcript_1/1_Conf_1.000	2791	20	0	XP_002644295.1	79	951.429	736	582	Hypothetical protein CBG14081
Locus_25260_Transcript_1/1_Conf_1.000	131	0							
Locus_25261_Transcript_1/1_Conf_1.000	281	20	2.17E-17	EFO24654.1	78	92.0485	66	52	RNA polymerase Rpb1
Locus_25262_Transcript_1/1_Conf_1.000	283	20	5.34E-27	NP_001021098.1	87	124.02	82	72	hypothetical protein F10G8.9
Locus_25263_Transcript_1/1_Conf_1.000	159	0							
Locus_25264_Transcript_1/1_Conf_1.000	387	2	5.95E-07	EFO17840.1	59	57.3806	77	46	hypothetical protein LOAG_10658
Locus_25265_Transcript_1/1_Conf_1.000	281	20	5.18E-19	NP_001023531.1	70	97.4413	93	66	Pyrazinamidase and NiCotinamidase family member (pnc-2)
Locus_25266_Transcript_1/1_Conf_1.000	421	0							
Locus_25267_Transcript_1/1_Conf_1.000	277	0							
Locus_25268_Transcript_1/1_Conf_1.000	236	0							
Locus_25269_Transcript_1/1_Conf_1.000	144	0							
Locus_2527_Transcript_1/2_Conf_1.000	1157	20	3.73E-141	NP_492635.1	72	505.753	397	286	More Of MS family member (mom-5)
Locus_2527_Transcript_2/2_Conf_1.000	258	20	3.32E-21	XP_001901058.1	70	104.76	88	62	Frizzled/Smoothened family membrane region containing protein
Locus_25270_Transcript_1/1_Conf_1.000	138	0							
Locus_25271_Transcript_1/1_Conf_1.000	136	10	6.57E-14	NP_492266.2	93	80.4925	45	42	hypothetical protein C34B7.2
Locus_25272_Transcript_1/1_Conf_1.000	241	0							
Locus_25273_Transcript_1/1_Conf_1.000	133	0							
Locus_25274_Transcript_1/1_Conf_1.000	128	20	1.06E-11	NP_505135.1	95	73.1738	41	39	ASpartyl Protease family member (asp-5)
Locus_25275_Transcript_1/1_Conf_1.000	159	20	4.47E-18	XP_002644419.1	96	94.3597	52	50	Hypothetical protein CBG14273
Locus_25276_Transcript_1/1_Conf_1.000	202	0							
Locus_25277_Transcript_1/1_Conf_1.000	141	0							

Locus_25278_Transcript_1/1_Conf_1.000	388	20	3.37E-10	NP_491657.1	63	68.1662	95	60	hypothetical protein F55F8.7
Locus_25279_Transcript_1/1_Conf_1.000	143	0							
Locus_2528_Transcript_1/2_Conf_1.000	1018	4	2.99E-19	AAF39779.2	48	100.523	291	142	Hypothetical protein C51G7.4
Locus_2528_Transcript_2/2_Conf_1.000	1015	4	2.98E-19	AAF39779.2	48	100.523	291	142	Hypothetical protein C51G7.4
Locus_25280_Transcript_1/1_Conf_1.000	129	0							
Locus_25281_Transcript_1/1_Conf_1.000	156	1	1.27E-04	XP_002643480.1	76	49.6766	42	32	Hypothetical protein CBG16145
Locus_25282_Transcript_1/1_Conf_1.000	253	20	3.97E-06	XP_002642807.1	84	54.6842	51	43	C. briggsae CBR-KEL-3 protein
Locus_25283_Transcript_1/1_Conf_1.000	285	20	7.93E-31	XP_001901053.1	79	136.732	93	74	Frizzled/Smoothened family membrane region containing protein
Locus_25284_Transcript_1/1_Conf_1.000	282	0							
Locus_25285_Transcript_1/1_Conf_1.000	162	0							
Locus_25286_Transcript_1/1_Conf_1.000	280	0							
Locus_25287_Transcript_1/1_Conf_1.000	359	20	4.88E-25	EFO27858.1	67	117.472	122	82	hypothetical protein LOAG_00620
Locus_25288_Transcript_1/1_Conf_1.000	338	0							
Locus_25289_Transcript_1/1_Conf_1.000	153	1	3.02E-06	XP_002635871.1	74	55.0694	51	38	Hypothetical protein CBG01087
Locus_2529_Transcript_1/1_Conf_1.000	688	20	5.49E-67	CAA96571.1	69	258.07	221	154	parasite pepsinogen
Locus_25290_Transcript_1/1_Conf_1.000	330	0							
Locus_25291_Transcript_1/1_Conf_1.000	311	0							
Locus_25292_Transcript_1/1_Conf_1.000	209	0							
Locus_25293_Transcript_1/1_Conf_1.000	136	0							
Locus_25294_Transcript_1/1_Conf_1.000	140	2	7.01E-08	XP_002633940.1	77	60.4622	40	31	Hypothetical protein CBG20015
Locus_25295_Transcript_1/1_Conf_1.000	233	0							
Locus_25296_Transcript_1/1_Conf_1.000	425	20	1.37E-51	XP_002647010.1	90	205.682	143	129	C. briggsae CBR-COR-1 protein
Locus_25297_Transcript_1/1_Conf_1.000	128	0							
Locus_25298_Transcript_1/1_Conf_1.000	550	17	2.24E-81	NP_001022641.1	89	305.064	183	163	LEThal family member (let-805)
Locus_25299_Transcript_1/1_Conf_1.000	186	13	3.57E-23	AAC27893.1	90	111.309	61	55	ornithine decarboxylase
Locus_253_Transcript_1/1_Conf_1.000	472	0							

Locus_2530_Transcript_1/7_Conf_0.409	1049	20	6.69E-139	AAN11401.1	77	498.049	348	270	metalloprotease 1 precursor
Locus_2530_Transcript_2/7_Conf_0.091	172	11	3.27E-13	AAN11401.1	78	78.1814	56	44	metalloprotease 1 precursor
Locus_2530_Transcript_3/7_Conf_0.409	931	20	1.92E-123	AAN11401.1	78	446.432	308	242	metalloprotease 1 precursor
Locus_2530_Transcript_4/7_Conf_0.364	931	20	8.63E-124	AAN11401.1	78	447.588	308	242	metalloprotease 1 precursor
Locus_2530_Transcript_5/7_Conf_0.545	1049	20	1.76E-139	AAN11401.1	77	499.975	348	270	metalloprotease 1 precursor
Locus_2530_Transcript_6/7_Conf_0.091	259	12	4.96E-17	AAN11401.1	70	90.8929	78	55	metalloprotease 1 precursor
Locus_2530_Transcript_7/7_Conf_0.409	931	20	8.63E-124	AAN11401.1	78	447.588	308	242	metalloprotease 1 precursor
Locus_25300_Transcript_1/1_Conf_1.000	222	20	9.73E-13	XP_002630063.1	66	76.6406	69	46	Hypothetical protein CBG13437
Locus_25301_Transcript_1/1_Conf_1.000	131	0							
Locus_25302_Transcript_1/1_Conf_1.000	251	0							
Locus_25303_Transcript_1/1_Conf_1.000	209	0							

Locus_25304_Transcript_1/1_Conf_1.000	174	20	8.84E-27	NP_937818.1	100	123.25	57	57	nucleoside diphosphate kinase A isoform a
Locus_25305_Transcript_1/1_Conf_1.000	294	0							
Locus_25306_Transcript_1/1_Conf_1.000	171	0							
Locus_25307_Transcript_1/1_Conf_1.000	516	13	2.99E-15	XP_002632584.1	47	85.1149	144	69	Hypothetical protein CBG13848
Locus_25308_Transcript_1/1_Conf_1.000	365	0							
Locus_25309_Transcript_1/1_Conf_1.000	145	0							
Locus_2531_Transcript_1/1_Conf_1.000	1130	20	2.45E-105	NP_504635.1	70	386.726	352	247	GAstrulation Defective family member (gad-1)
Locus_25310_Transcript_1/1_Conf_1.000	130	7	6.19E-12	ACT34056.1	97	73.9442	42	41	glutamate dehydrogenase
Locus_25311_Transcript_1/1_Conf_1.000	128	0							
Locus_25312_Transcript_1/1_Conf_1.000	249	0							
Locus_25313_Transcript_1/1_Conf_1.000	168	5	1.57E-15	NP_495951.2	85	85.8853	55	47	hypothetical protein W07A12.4
Locus_25314_Transcript_1/1_Conf_1.000	133	0							
Locus_25315_Transcript_1/1_Conf_1.000	138	0							
Locus_25316_Transcript_1/1_Conf_1.000	134	5	2.50E-13	EFO24258.1	93	78.5666	44	41	DNA-directed RNA polymerase
Locus_25317_Transcript_1/1_Conf_1.000	129	0							

Locus_25318_Transcript_1/1_Conf_1.000	169	13	1.24E-20	EFO25169.1	100	102.834	55	55	trehalose 6-phosphate synthase 1
Locus_25319_Transcript_1/1_Conf_1.000	205	0							
Locus_2532_Transcript_1/2_Conf_1.000	967	0							
Locus_2532_Transcript_2/2_Conf_1.000	846	0							
Locus_25320_Transcript_1/1_Conf_1.000	214	1	3.60E-04	AAB47739.1	56	48.1358	74	42	transposase
Locus_25321_Transcript_1/1_Conf_1.000	287	1	9.76E-05	NP_498936.1	50	50.0618	72	36	hypothetical protein K02D10.1
Locus_25322_Transcript_1/1_Conf_1.000	328	2	2.21E-09	XP_002635372.1	55	65.4698	99	55	C. briggsae CBR-RPM-1 protein
Locus_25323_Transcript_1/1_Conf_1.000	183	0							
Locus_25324_Transcript_1/1_Conf_1.000	199	20	1.13E-29	NP_001024855.1	95	132.88	66	63	Nuclear Hormone Receptor family member (nhr-1)
Locus_25325_Transcript_1/1_Conf_1.000	148	20	2.17E-20	XP_002751090.1	97	102.064	49	48	PREDICTED: 60S ribosomal protein L21-like
Locus_25326_Transcript_1/1_Conf_1.000	174	0							
Locus_25327_Transcript_1/1_Conf_1.000	130	0							
Locus_25328_Transcript_1/2_Conf_1.000	191	0							
Locus_25328_Transcript_2/2_Conf_1.000	301	0							
Locus_25329_Transcript_1/1_Conf_1.000	293	20	7.17E-08	XP_002646105.1	61	60.4622	81	50	Hypothetical protein CBG07981
Locus_2533_Transcript_1/1_Conf_1.000	464	2	4.07E-11	XP_002639234.1	70	71.2478	68	48	Hypothetical protein CBG03790
Locus_25330_Transcript_1/1_Conf_1.000	134	0							
Locus_25331_Transcript_1/1_Conf_1.000	316	0							
Locus_25332_Transcript_1/1_Conf_1.000	227	0							
Locus_25333_Transcript_1/1_Conf_1.000	284	0							
Locus_25334_Transcript_1/1_Conf_1.000	235	20	2.87E-33	XP_002630488.1	96	144.821	78	75	C. briggsae CBR-RPY-1 protein
Locus_25335_Transcript_1/1_Conf_1.000	153	0							
Locus_25336_Transcript_1/1_Conf_1.000	230	1	8.20E-04	NP_509643.1	65	46.9802	40	26	hypothetical protein F36G3.2
Locus_25337_Transcript_1/1_Conf_1.000	185	0							
Locus_25338_Transcript_1/1_Conf_1.000	175	0							

Locus_25339_Transcript_1/1_Conf_1.000	230	20	5.49E-08	NP_503298.1	67	60.8474	53	36	UDP-GlucuronosylTransferase family member (ugt-29)
Locus_2534_Transcript_1/1_Conf_1.000	613	0							
Locus_25340_Transcript_1/1_Conf_1.000	164	5	2.71E-07	XP_002998319.1	77	58.5362	48	37	copine-like protein
Locus_25341_Transcript_1/1_Conf_1.000	149	0							
Locus_25342_Transcript_1/1_Conf_1.000	137	0							
Locus_25343_Transcript_1/1_Conf_1.000	187	0							
Locus_25344_Transcript_1/1_Conf_1.000	150	0							
Locus_25345_Transcript_1/1_Conf_1.000	216	5	4.07E-32	NP_490803.1	94	140.969	71	67	hypothetical protein F54A5.1
Locus_25346_Transcript_1/1_Conf_1.000	212	20	2.25E-22	NP_501957.1	75	108.612	70	53	hypothetical protein C43F9.5
Locus_25347_Transcript_1/1_Conf_1.000	170	0							
Locus_25348_Transcript_1/1_Conf_1.000	140	3	3.47E-15	EFO21620.1	82	84.7297	46	38	hypothetical protein LOAG_06866
Locus_25349_Transcript_1/1_Conf_1.000	546	20	5.11E-54	NP_491761.3	70	214.157	184	129	hypothetical protein T27A3.5
Locus_2535_Transcript_1/1_Conf_1.000	2132	20	0	XP_002631588.1	69	706.827	656	457	Hypothetical protein CBG20766
Locus_25350_Transcript_1/1_Conf_1.000	272	0							
Locus_25351_Transcript_1/1_Conf_1.000	134	0							
Locus_25352_Transcript_1/1_Conf_1.000	241	20	1.85E-32	NP_496500.1	92	142.124	79	73	hypothetical protein VF13D12L.3
Locus_25353_Transcript_1/1_Conf_1.000	429	20	3.58E-60	CAR63575.1	87	234.187	142	124	hypothetical protein
Locus_25354_Transcript_1/1_Conf_1.000	297	0							
Locus_25355_Transcript_1/1_Conf_1.000	452	20	8.55E-54	EFO24754.1	79	213.001	150	119	hypothetical protein LOAG_03725
Locus_25356_Transcript_1/1_Conf_1.000	169	4	8.66E-06	NP_505743.1	71	53.5286	39	28	hypothetical protein F28H7.3
Locus_25357_Transcript_1/1_Conf_1.000	246	0							
Locus_25358_Transcript_1/1_Conf_1.000	186	1	5.71E-13	XP_001141034.1	100	77.411	51	51	PREDICTED: hypothetical protein
Locus_25359_Transcript_1/1_Conf_1.000	250	20	3.67E-49	EAW82235.1	100	197.593	83	83	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein), isoform CRA_f

Locus_2536_Transcript_1/1_Conf_1.000	1849	20	1.49E-82	XP_001899827.1	79	311.997	253	202	TBP-like factor
Locus_25360_Transcript_1/1_Conf_1.000	129	0							
Locus_25361_Transcript_1/1_Conf_1.000	271	0							
Locus_25362_Transcript_1/1_Conf_1.000	245	0							
Locus_25363_Transcript_1/1_Conf_1.000	295	0							
Locus_25364_Transcript_1/1_Conf_1.000	166	0							
Locus_25365_Transcript_1/1_Conf_1.000	145	0							
Locus_25366_Transcript_1/1_Conf_1.000	219	0							
Locus_25367_Transcript_1/1_Conf_1.000	390	0							
Locus_25368_Transcript_1/1_Conf_1.000	217	0							
Locus_25369_Transcript_1/1_Conf_1.000	130	0							
Locus_2537_Transcript_1/3_Conf_0.714	3098	20	0	NP_001076724.1	79	1119.76	872	689	Na-K-Cl Cotransporter homolog family member (nkcc-1)
Locus_2537_Transcript_2/3_Conf_0.286	859	20	1.23E-41	NP_001076724.1	85	174.481	118	101	Na-K-Cl Cotransporter homolog family member (nkcc-1)
Locus_2537_Transcript_3/3_Conf_0.714	3098	20	0	NP_001076724.1	79	1119.76	872	689	Na-K-Cl Cotransporter homolog family member (nkcc-1)
Locus_25370_Transcript_1/1_Conf_1.000	231	20	3.64E-28	NP_492593.2	80	127.872	77	62	hypothetical protein F26E4.3
Locus_25371_Transcript_1/1_Conf_1.000	133	0							
Locus_25372_Transcript_1/1_Conf_1.000	143	12	5.92E-07	NP_501598.2	73	57.3806	45	33	Prolyl Carboxy Peptidase like family member (pcp-3)
Locus_25373_Transcript_1/1_Conf_1.000	151	0							
Locus_25374_Transcript_1/1_Conf_1.000	408	0							
Locus_25375_Transcript_1/1_Conf_1.000	357	20	9.11E-56	NP_001123162.1	95	219.55	118	113	UNCoordinated family member (unc-1)
Locus_25376_Transcript_1/1_Conf_1.000	131	1	1.63E-04	CAR63718.1	69	49.2914	42	29	hypothetical protein
Locus_25377_Transcript_1/1_Conf_1.000	159	13	8.72E-14	CBA11992.1	87	80.1073	47	41	endonuclease-reverse transcriptase HmRTE-e01
Locus_25378_Transcript_1/1_Conf_1.000	159	0							
Locus_25379_Transcript_1/1_Conf_1.000	245	3	2.41E-24	XP_002631142.1	81	115.161	81	66	C. briggsae CBR-TAG-180 protein

Locus_2538_Transcript_1/1_Conf_1.000	1332	20	0	EFO25501.1	97	706.442	393	385	26S protease regulatory subunit 8
Locus_25380_Transcript_1/1_Conf_1.000	242	0							
Locus_25381_Transcript_1/1_Conf_1.000	134	0							
Locus_25382_Transcript_1/1_Conf_1.000	242	2	1.09E-08	NP_001022338.1	59	63.1586	79	47	hypothetical protein T09F3.5
Locus_25383_Transcript_1/1_Conf_1.000	229	0							
Locus_25384_Transcript_1/1_Conf_1.000	195	0							
Locus_25385_Transcript_1/1_Conf_1.000	206	0							
Locus_25386_Transcript_1/1_Conf_1.000	160	0							
Locus_25387_Transcript_1/1_Conf_1.000	137	0							
Locus_25388_Transcript_1/1_Conf_1.000	231	0							
Locus_25389_Transcript_1/1_Conf_1.000	224	0							
Locus_2539_Transcript_1/1_Conf_1.000	267	0							
Locus_25390_Transcript_1/1_Conf_1.000	230	20	1.70E-25	CAI95512.1	86	119.013	72	62	cytochrome b
Locus_25391_Transcript_1/1_Conf_1.000	194	0							
Locus_25392_Transcript_1/1_Conf_1.000	115	0							
Locus_25393_Transcript_1/1_Conf_1.000	193	0							
Locus_25394_Transcript_1/1_Conf_1.000	134	0							
Locus_25395_Transcript_1/1_Conf_1.000	305	5	9.81E-26	EFO19679.1	90	119.783	102	92	hypothetical protein LOAG_08814
Locus_25396_Transcript_1/1_Conf_1.000	144	20	1.28E-20	ADM47830.1	100	102.834	48	48	immunoglobulin heavy chain variable region
Locus_25397_Transcript_1/1_Conf_1.000	147	0							

Locus_25398_Transcript_1/1_Conf_1.000	149	0							
Locus_25399_Transcript_1/1_Conf_1.000	151	20	2.92E-17	ABE66949.1	92	91.6633	50	46	immunoglobulin heavy chain variable region
Locus_254_Transcript_1/1_Conf_1.000	666	20	8.59E-99	NP_495707.1	94	363.614	188	178	Ribosomal Protein, Large subunit family member (rpl-10)
Locus_2540_Transcript_1/1_Conf_1.000	568	20	1.10E-65	NP_496503.1	87	253.062	174	152	Lactate DeHydrogenase family member (ldh-1)
Locus_25400_Transcript_1/1_Conf_1.000	156	11	2.38E-11	XP_002636807.1	81	72.0182	53	43	Hypothetical protein CBG09249
Locus_25401_Transcript_1/1_Conf_1.000	135	0							
Locus_25402_Transcript_1/1_Conf_1.000	166	0							
Locus_25403_Transcript_1/1_Conf_1.000	508	0							
Locus_25404_Transcript_1/1_Conf_1.000	177	20	9.14E-16	EFO23663.1	83	86.6557	56	47	myosin xviiia
Locus_25405_Transcript_1/1_Conf_1.000	160	0							
Locus_25406_Transcript_1/1_Conf_1.000	325	5	1.39E-11	CAA88959.2	59	72.7886	114	68	C. elegans protein M03C11.2, partially confirmed by transcript evidence
Locus_25407_Transcript_1/1_Conf_1.000	170	0							
Locus_25408_Transcript_1/1_Conf_1.000	189	20	2.23E-25	XP_002634588.1	92	118.627	63	58	Hypothetical protein CBG08399
Locus_25409_Transcript_1/1_Conf_1.000	272	0							
Locus_2541_Transcript_1/2_Conf_1.000	1732	20	6.62E-53	XP_002647206.1	62	213.386	247	155	Hypothetical protein CBG22384
Locus_2541_Transcript_2/2_Conf_1.000	966	20	2.29E-58	XP_002647206.1	62	230.335	284	178	Hypothetical protein CBG22384
Locus_25410_Transcript_1/1_Conf_1.000	163	0							
Locus_25411_Transcript_1/1_Conf_1.000	134	0							
Locus_25412_Transcript_1/1_Conf_1.000	359	2	1.17E-10	EFO26102.1	55	69.707	119	66	hypothetical protein LOAG_02385
Locus_25413_Transcript_1/1_Conf_1.000	149	0							

Locus_25414_Transcript_1/1_Conf_1.000	249	20	1.50E-18	XP_002631710.1	75	95.9005	77	58	Hypothetical protein CBG20910
Locus_25415_Transcript_1/1_Conf_1.000	187	20	6.95E-27	XP_002630446.1	96	123.635	62	60	Hypothetical protein CBG11179
Locus_25416_Transcript_1/1_Conf_1.000	132	0							
Locus_25417_Transcript_1/1_Conf_1.000	153	20	5.48E-24	XP_002759549.1	100	114.005	50	50	PREDICTED: transmembrane 4 L6 family member 1-like
Locus_25418_Transcript_1/1_Conf_1.000	328	20	3.62E-28	XP_002629844.1	71	127.872	103	74	C. briggsae CBR-SCP-1 protein
Locus_25419_Transcript_1/1_Conf_1.000	156	3	6.27E-12	NP_001022489.1	76	73.9442	51	39	Homolog of Hedgehog AcylTransferase family member (hhat-1)
Locus_2542_Transcript_1/1_Conf_1.000	1472	20	1.13E-127	NP_493796.2	67	461.455	499	335	THO Complex (transcription factor/nuclear export) subunit family member (thoc-1)
Locus_25420_Transcript_1/1_Conf_1.000	211	0							
Locus_25421_Transcript_1/1_Conf_1.000	146	0							
Locus_25422_Transcript_1/1_Conf_1.000	258	4	2.45E-32	NP_508470.1	80	141.739	86	69	hypothetical protein T03G6.3
Locus_25423_Transcript_1/1_Conf_1.000	215	20	1.56E-15	NP_001020987.1	71	85.8853	71	51	UNCoordinated family member (unc-89)
Locus_25424_Transcript_1/1_Conf_1.000	255	9	2.31E-14	CAL49442.3	72	82.0333	87	63	C. elegans protein F36H1.2c, partially confirmed by transcript evidence
Locus_25425_Transcript_1/1_Conf_1.000	180	0							
Locus_25426_Transcript_1/1_Conf_1.000	213	4	2.49E-05	CBM41222.1	64	51.9878	56	36	C. elegans protein T10G3.3b, partially confirmed by transcript evidence
Locus_25427_Transcript_1/1_Conf_1.000	135	0							
Locus_25428_Transcript_1/1_Conf_1.000	209	0							
Locus_25429_Transcript_1/1_Conf_1.000	271	0							
Locus_2543_Transcript_1/1_Conf_1.000	1420	20	3.54E-171	XP_001900407.1	91	605.905	367	336	Nucleolar protein K01G5.5
Locus_25430_Transcript_1/1_Conf_1.000	209	20	7.01E-32	NP_497769.3	92	140.198	69	64	TOllisH (Tolloid and BMP-1 family) family member (toh-1)

Locus_25431_Transcript_1/1_Conf_1.000	145	3	6.35E-12	XP_002637017.1	88	73.9442	44	39	Hypothetical protein CBG09510
Locus_25432_Transcript_1/1_Conf_1.000	180	6	1.12E-16	NP_001021110.1	86	89.7373	59	51	CAlSYntenin/Alcadein homolog family member (casy-1)
Locus_25433_Transcript_1/1_Conf_1.000	171	0							
Locus_25434_Transcript_1/1_Conf_1.000	419	0							
Locus_25435_Transcript_1/1_Conf_1.000	196	0							
Locus_25436_Transcript_1/1_Conf_1.000	211	0							
Locus_25437_Transcript_1/1_Conf_1.000	400	20	3.31E-13	XP_001902061.1	47	78.1814	154	73	ancient conserved domain protein 2
Locus_25438_Transcript_1/1_Conf_1.000	222	2	1.19E-10	NP_495978.1	70	69.707	62	44	Temporarily Assigned Gene name family member (tag-165)
Locus_25439_Transcript_1/1_Conf_1.000	165	0							
Locus_2544_Transcript_1/1_Conf_1.000	1273	20	3.89E-09	XP_001892980.1	45	67.3958	210	95	Kelch motif family protein
Locus_25440_Transcript_1/1_Conf_1.000	141	0							
Locus_25441_Transcript_1/1_Conf_1.000	1035	0							
Locus_25442_Transcript_1/1_Conf_1.000	477	2	4.87E-09	EFO19385.1	60	64.3142	102	62	hypothetical protein LOAG_09109
Locus_25443_Transcript_1/1_Conf_1.000	261	0							
Locus_25444_Transcript_1/1_Conf_1.000	169	0							
Locus_25445_Transcript_1/1_Conf_1.000	129	20	7.31E-13	XP_002914987.1	97	77.0258	40	39	PREDICTED: mitochondrial import receptor subunit TOM5 homolog
Locus_25446_Transcript_1/1_Conf_1.000	139	0							
Locus_25447_Transcript_1/1_Conf_1.000	311	0							
Locus_25448_Transcript_1/1_Conf_1.000	205	0							
Locus_25449_Transcript_1/1_Conf_1.000	147	0							

Locus_2545_Transcript_1/1_Conf_1.000	1441	20	2.29E-24	NP_499947.1	44	118.242	360	160	Eph(F)riN family member (efn-4)
Locus_25450_Transcript_1/1_Conf_1.000	392	0							
Locus_25451_Transcript_1/1_Conf_1.000	446	0							
Locus_25452_Transcript_1/1_Conf_1.000	203	0							
Locus_25453_Transcript_1/1_Conf_1.000	233	20	8.12E-28	XP_001899774.1	87	126.716	77	67	Guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif family protein
Locus_25454_Transcript_1/1_Conf_1.000	291	0							
Locus_25455_Transcript_1/1_Conf_1.000	359	0							
Locus_25456_Transcript_1/1_Conf_1.000	261	20	2.37E-19	XP_002629783.1	77	98.5969	72	56	Hypothetical protein CBG01025
Locus_25457_Transcript_1/1_Conf_1.000	134	0							
Locus_25458_Transcript_1/1_Conf_1.000	143	20	2.10E-20	BAG51482.1	100	102.064	47	47	unnamed protein product
Locus_25459_Transcript_1/1_Conf_1.000	335	20	6.33E-33	NP_001024306.1	75	143.665	112	85	Poly(ADP-ribose) Metabolism Enzyme family member (pme-5)

Locus_2546_Transcript_1/2_Conf_1.000	3052	20	3.46E-138	EFO26461.1	82	497.664	331	274	brahma associated protein
Locus_2546_Transcript_2/2_Conf_1.000	1613	20	1.76E-177	NP_499250.1	81	627.091	459	375	Temporarily Assigned Gene name family member (tag-246)
Locus_25460_Transcript_1/1_Conf_1.000	296	0							
Locus_25461_Transcript_1/1_Conf_1.000	250	0							
Locus_25462_Transcript_1/1_Conf_1.000	283	0							
Locus_25463_Transcript_1/1_Conf_1.000	345	0							
Locus_25464_Transcript_1/1_Conf_1.000	200	0							
Locus_25465_Transcript_1/1_Conf_1.000	140	20	1.72E-14	NP_001021183.1	93	82.4185	45	42	hypothetical protein C24A1.3
Locus_25466_Transcript_1/1_Conf_1.000	555	10	2.88E-31	XP_002647560.1	60	138.658	184	111	Hypothetical protein CBG06646
Locus_25467_Transcript_1/1_Conf_1.000	129	5	5.99E-07	XP_002635249.1	77	57.3806	40	31	Hypothetical protein CBG11493
Locus_25468_Transcript_1/1_Conf_1.000	372	0							
Locus_25469_Transcript_1/1_Conf_1.000	144	20	5.03E-09	XP_001441628.1	80	64.3142	46	37	hypothetical protein
Locus_2547_Transcript_1/1_Conf_1.000	187	0							

Locus_25470_Transcript_1/1_Conf_1.000	1235	20	1.56E-156	NP_506599.1	91	556.984	316	289	Histone DeAcetylase family member (hda-1)
Locus_25471_Transcript_1/1_Conf_1.000	129	0							
Locus_25472_Transcript_1/1_Conf_1.000	157	0							
Locus_25473_Transcript_1/1_Conf_1.000	168	0							
Locus_25474_Transcript_1/1_Conf_1.000	236	20	5.07E-30	NP_504697.2	91	134.035	78	71	hypothetical protein W02F12.2
Locus_25475_Transcript_1/1_Conf_1.000	155	5	1.50E-13	ACI49151.1	94	79.337	39	37	hypothetical protein Cbre_JD20.006
Locus_25476_Transcript_1/1_Conf_1.000	417	20	6.62E-70	XP_001894250.1	91	266.544	138	126	Low-density lipoprotein receptor-related protein
Locus_25477_Transcript_1/1_Conf_1.000	141	0							

Locus_25478_Transcript_1/1_Conf_1.000	378	20	2.69E-31	CAX65068.1	76	138.272	126	97	C. elegans protein K08C7.3d, confirmed by transcript evidence
Locus_25479_Transcript_1/1_Conf_1.000	204	0							
Locus_2548_Transcript_1/1_Conf_1.000	2240	20	4.11E-138	NP_501455.1	62	496.893	635	397	Temporarily Assigned Gene name family member (tag-77)
Locus_25480_Transcript_1/1_Conf_1.000	205	0							
Locus_25481_Transcript_1/1_Conf_1.000	164	7	4.17E-16	ACJ65168.1	85	87.8113	57	49	Uncoordinated protein 68, isoform b, partially confirmed by transcript evidence
Locus_25482_Transcript_1/1_Conf_1.000	386	6	9.50E-21	NP_502119.2	54	103.219	151	82	hypothetical protein F54D1.6
Locus_25483_Transcript_1/1_Conf_1.000	178	0							
Locus_25484_Transcript_1/1_Conf_1.000	201	0							
Locus_25485_Transcript_1/1_Conf_1.000	134	0							
Locus_25486_Transcript_1/2_Conf_1.000	705	20	2.07E-24	A8WQT4.2	89	116.701	96	86	Calcium uptake protein 1 homolog
Locus_25486_Transcript_2/2_Conf_1.000	701	20	2.06E-24	A8WQT4.2	89	116.701	96	86	Calcium uptake protein 1 homolog
Locus_25487_Transcript_1/1_Conf_1.000	374	5	4.96E-17	NP_001129770.1	65	90.8929	120	78	hypothetical protein F33H2.8
Locus_25488_Transcript_1/1_Conf_1.000	269	20	1.05E-43	XP_002821429.1	96	179.489	89	86	PREDICTED: CD81 antigen-like
Locus_25489_Transcript_1/1_Conf_1.000	180	0							
Locus_2549_Transcript_1/1_Conf_1.000	1299	4	1.67E-39	XP_002634600.1	52	168.318	353	184	Hypothetical protein CBG08415
Locus_25490_Transcript_1/1_Conf_1.000	231	0							
Locus_25491_Transcript_1/1_Conf_1.000	287	20	2.31E-30	XP_001901457.1	87	135.191	94	82	Hypothetical UPF0202 protein F55A12.8 in chromosome I
Locus_25492_Transcript_1/1_Conf_1.000	420	0							
Locus_25493_Transcript_1/1_Conf_1.000	148	0							
Locus_25494_Transcript_1/1_Conf_1.000	217	0							

Locus_25495_Transcript_1/1_Conf_1.000	258	15	1.65E-12	XP_001896436.1	72	75.8702	73	53	hypothetical protein Bm1_24880
Locus_25496_Transcript_1/1_Conf_1.000	199	6	2.54E-05	NP_502296.1	53	51.9878	65	35	hypothetical protein M18.3
Locus_25497_Transcript_1/1_Conf_1.000	129	0							
Locus_25498_Transcript_1/1_Conf_1.000	171	3	5.96E-15	NP_001129860.1	92	83.9593	42	39	hypothetical protein H01G02.3
Locus_25499_Transcript_1/1_Conf_1.000	278	20	2.75E-28	XP_002646518.1	81	128.257	92	75	Hypothetical protein CBG20357
Locus_255_Transcript_1/5_Conf_0.400	832	20	2.08E-75	XP_002633038.1	71	286.574	260	186	Hypothetical protein CBG05717
Locus_255_Transcript_2/5_Conf_0.533	1679	20	1.13E-150	NP_501065.2	78	538.11	463	362	hypothetical protein T22D1.4
Locus_255_Transcript_3/5_Conf_0.667	2045	20	2.00E-176	NP_501065.2	75	624.009	569	429	hypothetical protein T22D1.4
Locus_255_Transcript_4/5_Conf_0.667	2051	20	2.01E-176	NP_501065.2	75	624.009	569	429	hypothetical protein T22D1.4
Locus_255_Transcript_5/5_Conf_0.667	2051	20	2.01E-176	NP_501065.2	75	624.009	569	429	hypothetical protein T22D1.4
Locus_2550_Transcript_1/1_Conf_1.000	953	20	6.67E-79	NP_505112.1	72	298.516	315	229	hypothetical protein F20D6.11
Locus_25500_Transcript_1/1_Conf_1.000	169	0							
Locus_25501_Transcript_1/1_Conf_1.000	195	20	1.49E-13	NP_497632.1	94	79.337	37	35	Kruppel-Like Factor (zinc finger protein) family member (klf-1)
Locus_25502_Transcript_1/1_Conf_1.000	190	0							
Locus_25503_Transcript_1/1_Conf_1.000	171	20	1.85E-24	CAQ10285.1	100	115.546	54	54	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)
Locus_25504_Transcript_1/1_Conf_1.000	237	20	3.08E-11	XP_001959417.1	67	71.633	79	53	GF12865

Locus_25505_Transcript_1/1_Conf_1.000	157	0							
Locus_25506_Transcript_1/1_Conf_1.000	176	0							
Locus_25507_Transcript_1/1_Conf_1.000	210	0							
Locus_25508_Transcript_1/1_Conf_1.000	372	20	1.99E-50	NP_498645.1	91	201.83	122	112	MUscle Positioning family member (mup-4)
Locus_25509_Transcript_1/1_Conf_1.000	420	0							
Locus_2551_Transcript_1/1_Conf_1.000	880	0							
Locus_25510_Transcript_1/1_Conf_1.000	215	3	4.55E-07	XP_001895050.1	55	57.7658	70	39	hypothetical protein Bm1_17960
Locus_25511_Transcript_1/1_Conf_1.000	257	20	4.64E-31	XP_001138884.1	100	137.502	64	64	PREDICTED: similar to F1Fo-ATPase synthase f subunit isoform 4
Locus_25512_Transcript_1/1_Conf_1.000	255	4	1.08E-11	NP_495713.1	68	73.1738	83	57	RNA-dependent RNA polymerase Family family member (rrf-3)
Locus_25513_Transcript_1/1_Conf_1.000	218	20	1.27E-17	CAX65068.1	76	92.8189	71	54	C. elegans protein K08C7.3d, confirmed by transcript evidence
Locus_25514_Transcript_1/1_Conf_1.000	144	20	1.01E-17	XP_002923631.1	100	93.2041	47	47	PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like isoform 2
Locus_25515_Transcript_1/1_Conf_1.000	243	3	2.11E-20	NP_495801.1	74	102.064	81	60	hypothetical protein T13H5.6
Locus_25516_Transcript_1/1_Conf_1.000	297	0							
Locus_25517_Transcript_1/1_Conf_1.000	203	0							
Locus_25518_Transcript_1/1_Conf_1.000	126	0							
Locus_25519_Transcript_1/1_Conf_1.000	153	11	1.35E-14	CBW44370.1	79	82.8037	49	39	C. elegans protein F14D7.6c, confirmed by transcript evidence
Locus_2552_Transcript_1/1_Conf_1.000	353	0							
Locus_25520_Transcript_1/1_Conf_1.000	197	20	3.78E-17	EFO27545.1	77	91.2781	68	53	hypothetical protein LOAG_00943
Locus_25521_Transcript_1/1_Conf_1.000	130	0							
Locus_25522_Transcript_1/1_Conf_1.000	137	0							

Locus_25523_Transcript_1/1_Conf_1.000	132	0							
Locus_25524_Transcript_1/1_Conf_1.000	187	9	2.65E-10	CAD44516.1	75	68.5514	61	46	VAB-10B protein
Locus_25525_Transcript_1/1_Conf_1.000	185	0							
Locus_25526_Transcript_1/1_Conf_1.000	386	20	5.21E-19	ADI61822.1	63	97.4413	93	59	endonuclease-reverse transcriptase
Locus_25527_Transcript_1/1_Conf_1.000	266	0							
Locus_25528_Transcript_1/1_Conf_1.000	261	5	2.08E-07	EFO26811.1	62	58.9214	70	44	hypothetical protein LOAG_01665
Locus_25529_Transcript_1/1_Conf_1.000	134	0							
Locus_2553_Transcript_1/1_Conf_1.000	409	0							
Locus_25530_Transcript_1/1_Conf_1.000	154	0							
Locus_25531_Transcript_1/1_Conf_1.000	130	2	1.34E-06	XP_001900715.1	79	56.225	39	31	hypothetical protein
Locus_25532_Transcript_1/1_Conf_1.000	349	2	3.32E-05	NP_001021613.1	73	51.6026	41	30	hypothetical protein T06G6.12
Locus_25533_Transcript_1/1_Conf_1.000	128	0							
Locus_25534_Transcript_1/1_Conf_1.000	163	20	2.06E-23	NP_001171941.1	100	112.079	54	54	NADH dehydrogenase ubiquinone 1 alpha subcomplex subunit 2 isoform 2
Locus_25535_Transcript_1/1_Conf_1.000	219	0							
Locus_25536_Transcript_1/1_Conf_1.000	188	0							
Locus_25537_Transcript_1/1_Conf_1.000	203	20	4.92E-09	EFO24868.1	66	64.3142	68	45	hypothetical protein LOAG_03617
Locus_25538_Transcript_1/1_Conf_1.000	215	0							
Locus_25539_Transcript_1/1_Conf_1.000	139	0							

Locus_2554_Transcript_1/1_Conf_1.000	280	20	7.71E-23	CAR63555.1	80	110.153	85	68	putative 15 kDa selenoprotein precursor
Locus_25540_Transcript_1/1_Conf_1.000	568	20	8.51E-34	EFO22877.1	80	147.132	111	89	kelch domain-containing protein family protein
Locus_25541_Transcript_1/1_Conf_1.000	198	1	3.20E-08	EAW55278.1	77	61.6178	36	28	transmembrane protein 14B, isoform CRA_c
Locus_25542_Transcript_1/1_Conf_1.000	285	0							
Locus_25543_Transcript_1/1_Conf_1.000	151	0							
Locus_25544_Transcript_1/1_Conf_1.000	195	0							
Locus_25545_Transcript_1/1_Conf_1.000	377	2	1.25E-28	NP_492185.2	73	129.413	119	87	SMG-associated and Lethal family member (smgl-1)
Locus_25546_Transcript_1/1_Conf_1.000	266	0							
Locus_25547_Transcript_1/1_Conf_1.000	153	0							
Locus_25548_Transcript_1/1_Conf_1.000	144	20	2.50E-08	EFN73236.1	82	62.003	47	39	BTB/POZ domain-containing protein 9
Locus_25549_Transcript_1/1_Conf_1.000	149	0							
Locus_2555_Transcript_1/1_Conf_1.000	720	20	6.01E-75	EFO24268.1	77	284.648	239	186	hypothetical protein LOAG_04219
Locus_25550_Transcript_1/1_Conf_1.000	139	0							

Locus_25551_Transcript_1/1_Conf_1.000	261	20	2.80E-28	ADK09905.1	100	128.257	86	86	non-muscle myosin IIA
Locus_25552_Transcript_1/1_Conf_1.000	257	20	3.00E-38	XP_002629730.1	95	161.384	85	81	Hypothetical protein CBG00961
Locus_25553_Transcript_1/1_Conf_1.000	153	0							
Locus_25554_Transcript_1/1_Conf_1.000	196	2	1.88E-08	NP_502201.2	69	62.3882	63	44	PeRoXisome assembly factor family member (prx-2)
Locus_25555_Transcript_1/1_Conf_1.000	299	2	1.64E-04	EFO22952.1	59	49.2914	83	49	hypothetical protein LOAG_05535
Locus_25556_Transcript_1/1_Conf_1.000	167	3	6.42E-09	EFO26002.1	78	63.929	52	41	bromodomain containing protein
Locus_25557_Transcript_1/1_Conf_1.000	277	0							
Locus_25558_Transcript_1/1_Conf_1.000	234	20	1.99E-34	NP_497027.1	98	148.673	78	77	Masculinisation Of Germline family member (mog-4)
Locus_25559_Transcript_1/1_Conf_1.000	150	3	1.97E-05	XP_002641487.1	67	52.373	49	33	Hypothetical protein CBG09778
Locus_2556_Transcript_1/1_Conf_1.000	811	0							
Locus_25560_Transcript_1/1_Conf_1.000	204	0							
Locus_25561_Transcript_1/1_Conf_1.000	216	1	6.12E-04	NP_502067.2	63	47.3654	60	38	BiCaudal C (Drosophila) homolog family member (bcc-1)
Locus_25562_Transcript_1/1_Conf_1.000	209	0							
Locus_25563_Transcript_1/1_Conf_1.000	272	4	1.17E-10	NP_506157.3	57	69.707	89	51	hypothetical protein ZC116.3
Locus_25564_Transcript_1/1_Conf_1.000	146	0							
Locus_25565_Transcript_1/1_Conf_1.000	333	0							
Locus_25566_Transcript_1/1_Conf_1.000	177	0							
Locus_25567_Transcript_1/1_Conf_1.000	172	7	2.05E-15	XP_001892790.1	85	85.5001	54	46	SH2 domain containing protein
Locus_25568_Transcript_1/1_Conf_1.000	243	0							

Locus_25569_Transcript_1/1_Conf_1.000	589	2	2.28E-64	XP_002641621.1	76	248.825	198	152	Hypothetical protein CBG09941
Locus_2557_Transcript_1/1_Conf_1.000	1442	2	3.66E-14	XP_002636404.1	46	84.3445	273	128	Hypothetical protein CBG23056
Locus_25570_Transcript_1/1_Conf_1.000	198	0							
Locus_25571_Transcript_1/1_Conf_1.000	199	0							
Locus_25572_Transcript_1/1_Conf_1.000	139	5	1.20E-07	XP_002639618.1	67	59.6918	46	31	Hypothetical protein CBG12331
Locus_25573_Transcript_1/1_Conf_1.000	141	1	4.69E-04	NP_508435.2	69	47.7506	43	30	hypothetical protein C43H6.7
Locus_25574_Transcript_1/1_Conf_1.000	260	0							
Locus_25575_Transcript_1/1_Conf_1.000	134	20	1.47E-13	XP_002648986.1	93	79.337	44	41	C. briggsae CBR-SAX-2 protein
Locus_25576_Transcript_1/1_Conf_1.000	167	0							
Locus_25577_Transcript_1/1_Conf_1.000	170	0							
Locus_25578_Transcript_1/1_Conf_1.000	168	20	1.57E-15	NP_001076764.1	95	85.8853	44	42	Intermediate Filament, A family member (ifa-1)
Locus_25579_Transcript_1/1_Conf_1.000	136	0							
Locus_2558_Transcript_1/1_Conf_1.000	1141	20	3.16E-60	EFO28288.1	59	236.884	347	207	hypothetical protein LOAG_00181
Locus_25580_Transcript_1/1_Conf_1.000	139	0							
Locus_25581_Transcript_1/1_Conf_1.000	137	0							
Locus_25582_Transcript_1/1_Conf_1.000	142	0							
Locus_25583_Transcript_1/1_Conf_1.000	158	0							
Locus_25584_Transcript_1/1_Conf_1.000	506	0							
Locus_25585_Transcript_1/1_Conf_1.000	181	3	3.38E-05	NP_499313.2	65	51.6026	60	39	hypothetical protein F43D9.1
Locus_25586_Transcript_1/1_Conf_1.000	142	3	1.08E-08	XP_002633114.1	74	63.1586	47	35	C. briggsae CBR-UNC-8 protein
Locus_25587_Transcript_1/1_Conf_1.000	134	0							
Locus_25588_Transcript_1/1_Conf_1.000	133	0							
Locus_25589_Transcript_1/1_Conf_1.000	190	0							
Locus_2559_Transcript_1/8_Conf_0.200	259	20	1.72E-30	CAA51334.1	98	130.568	66	65	Immunoglobulin kappa light chain variable region L16

Locus_2559_Transcript_2/8_Conf_0.100	211	20	9.13E-32	ACJ71716.1	98	139.813	70	69	immunoglobulin kappa light chain variable region
Locus_2559_Transcript_3/8_Conf_0.300	889	20	9.12E-104	BAF64543.1	98	380.948	210	207	immunoglobulin light chain
Locus_2559_Transcript_4/8_Conf_0.150	306	20	7.21E-37	AAA16949.1	96	156.762	82	79	immunoglobulin kappa chain
Locus_2559_Transcript_5/8_Conf_0.100	384	20	1.65E-65	CAA51135.1	98	251.906	127	125	Ig kappa light chain (VJC)
Locus_2559_Transcript_6/8_Conf_0.250	383	20	4.16E-52	CAA29935.1	99	204.527	105	104	unnamed protein product
Locus_2559_Transcript_7/8_Conf_0.100	483	20	2.86E-73	AAA72132.1	96	277.715	144	139	immunoglobulin kappa chain variable region
Locus_2559_Transcript_8/8_Conf_0.450	892	20	1.05E-107	BAC01759.1	99	394.045	210	209	immunoglobulin kappa light chain VLJ region
Locus_25590_Transcript_1/1_Conf_1.000	246	5	2.04E-15	ACI49128.1	86	85.5001	51	44	hypothetical protein Cbre_JD15.003
Locus_25591_Transcript_1/1_Conf_1.000	144	0							
Locus_25592_Transcript_1/1_Conf_1.000	140	0							
Locus_25593_Transcript_1/1_Conf_1.000	165	0							
Locus_25594_Transcript_1/1_Conf_1.000	344	20	8.23E-12	ACC44276.1	66	73.559	112	75	SLO-2
Locus_25595_Transcript_1/1_Conf_1.000	226	0							
Locus_25596_Transcript_1/1_Conf_1.000	174	0							
Locus_25597_Transcript_1/1_Conf_1.000	175	0							
Locus_25598_Transcript_1/1_Conf_1.000	186	0							
Locus_25599_Transcript_1/1_Conf_1.000	309	20	6.10E-28	XP_001893904.1	73	127.102	101	74	Protein-tyrosine phosphatase containing protein
Locus_256_Transcript_1/1_Conf_1.000	274	20	2.95E-22	XP_002633330.1	79	108.227	81	64	C. briggsae CBR-DNJ-2 protein

Locus_2560_Transcript_1/1_Conf_1.000	404	20	5.75E-21	NP_495537.1	86	103.99	75	65	HAlF transporter (PGP related) family member (haf-2)
Locus_25600_Transcript_1/1_Conf_1.000	357	0							
Locus_25601_Transcript_1/1_Conf_1.000	163	0							
Locus_25602_Transcript_1/1_Conf_1.000	123	0							
Locus_25603_Transcript_1/1_Conf_1.000	198	2	5.11E-06	XP_002642154.1	74	54.299	66	49	Hypothetical protein CBG18111
Locus_25604_Transcript_1/1_Conf_1.000	132	20	4.58E-07	NP_497182.2	73	57.7658	42	31	hypothetical protein Y50D7A.2
Locus_25605_Transcript_1/1_Conf_1.000	184	0							
Locus_25606_Transcript_1/1_Conf_1.000	134	20	2.05E-15	NP_114107.1	100	85.5001	42	42	28S ribosomal protein S21, mitochondrial
Locus_25607_Transcript_1/1_Conf_1.000	321	12	9.28E-32	XP_002642296.1	87	139.813	107	94	Hypothetical protein CBG18288
Locus_25608_Transcript_1/1_Conf_1.000	147	0							
Locus_25609_Transcript_1/1_Conf_1.000	169	0							
Locus_2561_Transcript_1/1_Conf_1.000	215	20	2.25E-06	EFO23536.1	56	55.4546	71	40	hypothetical protein LOAG_04951
Locus_25610_Transcript_1/1_Conf_1.000	175	0							
Locus_25611_Transcript_1/1_Conf_1.000	161	0							
Locus_25612_Transcript_1/1_Conf_1.000	159	0							
Locus_25613_Transcript_1/1_Conf_1.000	345	3	5.30E-19	XP_002631142.1	59	97.4413	118	70	C. briggsae CBR-TAG-180 protein
Locus_25614_Transcript_1/1_Conf_1.000	132	4	4.42E-10	XP_002639744.1	74	67.781	43	32	C. briggsae CBR-LAM-3 protein
Locus_25615_Transcript_1/1_Conf_1.000	198	2	1.49E-05	EFO20174.1	67	52.7582	43	29	hypothetical protein LOAG_08316
Locus_25616_Transcript_1/1_Conf_1.000	170	0							
Locus_25617_Transcript_1/1_Conf_1.000	188	2	3.36E-05	ACO15789.1	63	51.6026	63	40	Hypothetical protein Y55F3BL.4
Locus_25618_Transcript_1/1_Conf_1.000	228	0							
Locus_25619_Transcript_1/1_Conf_1.000	156	2	2.55E-05	NP_501669.1	68	51.9878	50	34	CyPIN (guanine aminohydrolase) homolog) family member (cpin-1)
Locus_2562_Transcript_1/1_Conf_1.000	2136	20	0	NP_491363.1	87	1036.94	698	608	Dynein Heavy Chain family member (dhc-1)
Locus_25620_Transcript_1/1_Conf_1.000	154	0							
Locus_25621_Transcript_1/1_Conf_1.000	254	4	8.83E-14	XP_002633836.1	68	80.1073	74	51	Hypothetical protein CBG19874
Locus_25622_Transcript_1/1_Conf_1.000	349	0							

Locus_25623_Transcript_1/1_Conf_1.000	147	20	1.04E-22	XP_001146702.1	100	109.768	48	48	PREDICTED: similar to Cystatin C precursor (Neuroendocrine basic polypeptide) (Gamma-trace) (Post-gamma-globulin)
Locus_25624_Transcript_1/1_Conf_1.000	316	20	1.39E-35	XP_002648005.1	81	152.525	102	83	C. briggsae CBR-PQN-48 protein
Locus_25625_Transcript_1/1_Conf_1.000	168	0							
Locus_25626_Transcript_1/1_Conf_1.000	284	2	3.37E-05	XP_002634820.1	64	51.6026	67	43	Hypothetical protein CBG13928
Locus_25627_Transcript_1/1_Conf_1.000	210	0							
Locus_25628_Transcript_1/1_Conf_1.000	257	20	8.50E-17	XP_002633353.1	68	90.1225	83	57	Hypothetical protein CBG06097
Locus_25629_Transcript_1/1_Conf_1.000	224	20	6.74E-14	NP_490693.2	66	80.4925	74	49	ATM (ataxia telangectasia mutated) family member (atm-1)
Locus_2563_Transcript_1/1_Conf_1.000	641	8	4.73E-11	ACI49177.1	81	72.0182	71	58	hypothetical protein Csp3_JD02.005
Locus_25630_Transcript_1/1_Conf_1.000	336	20	3.70E-33	NP_001122445.1	78	144.436	110	86	hypothetical protein F08A10.1
Locus_25631_Transcript_1/1_Conf_1.000	169	0							
Locus_25632_Transcript_1/1_Conf_1.000	218	0							
Locus_25633_Transcript_1/1_Conf_1.000	272	0							
Locus_25634_Transcript_1/1_Conf_1.000	162	1	9.63E-05	NP_497480.2	77	50.0618	36	28	POLH (DNA polymerase eta) homolog family member (polh-1)
Locus_25635_Transcript_1/1_Conf_1.000	221	0							
Locus_25636_Transcript_1/1_Conf_1.000	147	0							
Locus_25637_Transcript_1/1_Conf_1.000	198	0							

Locus_25638_Transcript_1/1_Conf_1.000	380	20	5.97E-39	AAF99087.1	80	163.696	125	100	AF149288_1KRP85
Locus_25639_Transcript_1/1_Conf_1.000	263	0							
Locus_2564_Transcript_1/1_Conf_1.000	1333	20	1.15E-83	XP_002636916.1	62	315.079	361	227	C. briggsae CBR-NHR-47 protein
Locus_25640_Transcript_1/1_Conf_1.000	143	0							
Locus_25641_Transcript_1/1_Conf_1.000	194	0							
Locus_25642_Transcript_1/1_Conf_1.000	212	20	3.97E-27	XP_002750805.1	100	124.405	58	58	PREDICTED: peroxiredoxin-1-like
Locus_25643_Transcript_1/1_Conf_1.000	305	20	2.10E-44	AAM82167.1	91	181.8	101	92	gamma-butyrobetaine,2-oxoglutarate dioxygenase
Locus_25644_Transcript_1/1_Conf_1.000	129	20	5.41E-16	NP_001021172.1	100	87.4261	43	43	PDF Receptor homolog family member (pdfr-1)
Locus_25645_Transcript_1/1_Conf_1.000	222	0							
Locus_25646_Transcript_1/1_Conf_1.000	148	0							
Locus_25647_Transcript_1/1_Conf_1.000	369	0							
Locus_25648_Transcript_1/1_Conf_1.000	164	0							
Locus_25649_Transcript_1/1_Conf_1.000	130	0							
Locus_2565_Transcript_1/1_Conf_1.000	335	0							

Locus_25650_Transcript_1/1_Conf_1.000	147	20	3.24E-16	NP_001020988.1	89	88.1965	48	43	UNCoordinated family member (unc-89)
Locus_25651_Transcript_1/1_Conf_1.000	253	0							
Locus_25652_Transcript_1/1_Conf_1.000	304	4	4.28E-05	NP_498124.2	54	51.2174	74	40	Zinc finger Transcription Factor family member (ztf-8)
Locus_25653_Transcript_1/1_Conf_1.000	194	0							
Locus_25654_Transcript_1/1_Conf_1.000	204	20	1.02E-22	XP_002912987.1	100	109.768	54	54	PREDICTED: protein disulfide-isomerase-like
Locus_25655_Transcript_1/1_Conf_1.000	356	0							
Locus_25656_Transcript_1/1_Conf_1.000	544	20	1.85E-48	NP_001024728.1	72	195.667	183	132	SERotonin/octopamine receptor family member (ser-1)
Locus_25657_Transcript_1/1_Conf_1.000	171	0							
Locus_25658_Transcript_1/1_Conf_1.000	286	3	1.11E-32	NP_001022363.1	85	142.895	95	81	Temporarily Assigned Gene name family member (tag-180)
Locus_25659_Transcript_1/1_Conf_1.000	359	16	1.25E-12	XP_002629787.1	68	76.2554	95	65	Hypothetical protein CBG01029
Locus_2566_Transcript_1/3_Conf_0.750	2466	20	0	XP_002633285.1	88	1071.61	731	650	Hypothetical protein CBG06014

Locus_2566_Transcript_2/3_Conf_0.750	2466	20	0	XP_002633285.1	88	1071.61	731	650	Hypothetical protein CBG06014
Locus_2566_Transcript_3/3_Conf_0.750	2466	20	0	XP_002633285.1	88	1071.61	731	650	Hypothetical protein CBG06014
Locus_25660_Transcript_1/1_Conf_1.000	135	20	3.15E-16	NP_499865.1	97	88.1965	44	43	hypothetical protein F29C4.6
Locus_25661_Transcript_1/1_Conf_1.000	238	0							
Locus_25662_Transcript_1/1_Conf_1.000	207	2	3.06E-11	EFO25474.1	68	71.633	66	45	acyltransferase
Locus_25663_Transcript_1/1_Conf_1.000	163	0							
Locus_25664_Transcript_1/1_Conf_1.000	163	4	2.71E-07	NP_502613.2	68	58.5362	51	35	QUInine non-avoider family member (qui-1)
Locus_25665_Transcript_1/1_Conf_1.000	147	0							
Locus_25666_Transcript_1/1_Conf_1.000	222	0							
Locus_25667_Transcript_1/1_Conf_1.000	137	1	2.50E-05	NP_495884.2	78	51.9878	41	32	hypothetical protein F46C5.6
Locus_25668_Transcript_1/1_Conf_1.000	179	0							
Locus_25669_Transcript_1/1_Conf_1.000	367	1	3.84E-06	XP_002641244.1	53	54.6842	121	65	Hypothetical protein CBG09112

Locus_2567_Transcript_1/1_Conf_1.000	810	20	1.11E-126	XP_002646709.1	91	456.833	269	246	Hypothetical protein CBG13088
Locus_25670_Transcript_1/1_Conf_1.000	220	2	7.00E-11	XP_002644637.1	85	70.4774	49	42	C. briggsae CBR-ACN-1 protein
Locus_25671_Transcript_1/1_Conf_1.000	137	20	2.58E-18	XP_002824940.1	100	95.1301	44	44	PREDICTED: alpha-actinin-1-like
Locus_25672_Transcript_1/1_Conf_1.000	263	0							
Locus_25673_Transcript_1/1_Conf_1.000	212	0							
Locus_25674_Transcript_1/1_Conf_1.000	170	0							
Locus_25675_Transcript_1/1_Conf_1.000	384	5	4.56E-23	CAR63715.1	98	110.923	55	54	putative NHL (ring finger b-box coiled coil) domain containing family member
Locus_25676_Transcript_1/1_Conf_1.000	266	2	9.65E-05	Q6E3C7.1	50	50.0618	59	30	Cytoplasmic polyadenylation element-binding protein 1
Locus_25677_Transcript_1/1_Conf_1.000	132	0							
Locus_25678_Transcript_1/1_Conf_1.000	138	0							
Locus_25679_Transcript_1/1_Conf_1.000	273	0							
Locus_2568_Transcript_1/1_Conf_1.000	576	20	1.23E-67	XP_001900416.1	78	259.61	187	147	DNA primase, eukaryotic-type, small subunit family protein

Locus_25680_Transcript_1/1_Conf_1.000	253	20	2.73E-31	EFO21762.1	96	138.272	63	61	hypothetical protein LOAG_06724
Locus_25681_Transcript_1/1_Conf_1.000	145	0							
Locus_25682_Transcript_1/1_Conf_1.000	170	0							
Locus_25683_Transcript_1/1_Conf_1.000	152	0							
Locus_25684_Transcript_1/1_Conf_1.000	134	0							
Locus_25685_Transcript_1/1_Conf_1.000	143	0							
Locus_25686_Transcript_1/1_Conf_1.000	132	1	5.77E-10	ADD49663.1	88	67.3958	43	38	ecdysone receptor isoform +9.1_B
Locus_25687_Transcript_1/1_Conf_1.000	284	18	3.94E-38	NP_503107.2	89	160.999	94	84	hypothetical protein T02D1.6
Locus_25688_Transcript_1/1_Conf_1.000	305	20	5.38E-24	XP_002640523.1	81	114.005	81	66	Hypothetical protein CBG18685
Locus_25689_Transcript_1/1_Conf_1.000	331	2	5.98E-15	EFO16157.1	63	83.9593	112	71	ribonuclease P/MRP protein subunit POP1 containing protein
Locus_2569_Transcript_1/1_Conf_1.000	132	0							
Locus_25690_Transcript_1/1_Conf_1.000	155	4	3.69E-12	XP_002641218.1	78	74.7146	50	39	Hypothetical protein CBG09082
Locus_25691_Transcript_1/1_Conf_1.000	151	0							
Locus_25692_Transcript_1/1_Conf_1.000	206	4	3.76E-09	XP_001900733.1	61	64.6994	70	43	hypothetical protein Bm1_46355
Locus_25693_Transcript_1/1_Conf_1.000	230	0							
Locus_25694_Transcript_1/1_Conf_1.000	307	0							
Locus_25695_Transcript_1/1_Conf_1.000	130	0							
Locus_25696_Transcript_1/1_Conf_1.000	133	0							
Locus_25697_Transcript_1/1_Conf_1.000	213	4	2.49E-05	CBM41222.1	64	51.9878	56	36	C. elegans protein T10G3.3b, partially confirmed by transcript evidence
Locus_25698_Transcript_1/1_Conf_1.000	189	0							
Locus_25699_Transcript_1/1_Conf_1.000	614	0							
Locus_257_Transcript_1/1_Conf_1.000	304	2	3.61E-20	XP_002639243.1	75	101.293	84	63	Hypothetical protein CBG03801
Locus_2570_Transcript_1/1_Conf_1.000	320	0							
Locus_25700_Transcript_1/1_Conf_1.000	276	0							
Locus_25701_Transcript_1/1_Conf_1.000	132	20	5.05E-14	XP_002634119.1	97	80.8777	44	43	Hypothetical protein CBG01673

Locus_25702_Transcript_1/1_Conf_1.000	496	20	6.57E-22	CAA84693.3	59	107.071	166	99	C. elegans protein D2045.2, partially confirmed by transcript evidence
Locus_25703_Transcript_1/1_Conf_1.000	160	0							
Locus_25704_Transcript_1/1_Conf_1.000	131	0							
Locus_25705_Transcript_1/1_Conf_1.000	212	0							
Locus_25706_Transcript_1/1_Conf_1.000	145	0							
Locus_25707_Transcript_1/1_Conf_1.000	136	0							
Locus_25708_Transcript_1/1_Conf_1.000	135	9	1.12E-05	XP_002826360.1	100	53.1434	44	44	PREDICTED: transmembrane protein 219-like
Locus_25709_Transcript_1/1_Conf_1.000	296	0							
Locus_2571_Transcript_1/1_Conf_1.000	735	1	3.30E-07	NP_490789.3	42	59.6918	191	81	hypothetical protein Y95B8A.11
Locus_25710_Transcript_1/1_Conf_1.000	284	2	2.51E-06	XP_002631327.1	72	53.5286	48	35	Hypothetical protein CBG03149
Locus_25711_Transcript_1/1_Conf_1.000	141	2	5.35E-08	XP_002631501.1	73	60.8474	45	33	Hypothetical protein CBG20665
Locus_25712_Transcript_1/1_Conf_1.000	149	0							
Locus_25713_Transcript_1/1_Conf_1.000	171	20	7.29E-13	AAB62695.1	78	77.0258	57	45	P-type ATPase
Locus_25714_Transcript_1/1_Conf_1.000	450	0							
Locus_25715_Transcript_1/1_Conf_1.000	203	0							
Locus_25716_Transcript_1/1_Conf_1.000	151	0							
Locus_25717_Transcript_1/1_Conf_1.000	258	0							
Locus_25718_Transcript_1/1_Conf_1.000	150	5	1.00E-17	NP_001024333.1	97	93.2041	49	48	Olfactory LeaRNing defective family member (olrn-1)
Locus_25719_Transcript_1/1_Conf_1.000	288	2	1.04E-14	XP_002646895.1	60	83.1889	107	65	Hypothetical protein CBG19593
Locus_2572_Transcript_1/4_Conf_0.556	914	20	5.04E-129	XP_002646784.1	87	464.922	300	261	Hypothetical protein CBG18435
Locus_2572_Transcript_2/4_Conf_0.667	1253	20	9.11E-128	XP_002646784.1	92	461.455	264	243	Hypothetical protein CBG18435
Locus_2572_Transcript_3/4_Conf_0.556	1253	20	9.11E-128	XP_002646784.1	92	461.455	264	243	Hypothetical protein CBG18435
Locus_2572_Transcript_4/4_Conf_0.667	1253	20	9.11E-128	XP_002646784.1	92	461.455	264	243	Hypothetical protein CBG18435
Locus_25720_Transcript_1/1_Conf_1.000	270	20	8.35E-17	NP_001022450.1	65	90.1225	89	58	hypothetical protein Y48E1A.1
Locus_25721_Transcript_1/1_Conf_1.000	219	0							
Locus_25722_Transcript_1/1_Conf_1.000	166	9	4.30E-13	NP_492132.1	76	77.7962	55	42	Enhancer of Glp-One (glp-1) family member (ego-1)
Locus_25723_Transcript_1/1_Conf_1.000	189	5	1.45E-08	XP_002631434.1	65	62.7734	60	39	Hypothetical protein CBG03294
Locus_25724_Transcript_1/1_Conf_1.000	148	3	6.55E-09	NP_505978.1	76	63.929	47	36	hypothetical protein D2023.4

Locus_25725_Transcript_1/1_Conf_1.000	140	0							
Locus_25726_Transcript_1/1_Conf_1.000	236	20	4.58E-31	EFO15620.1	96	137.502	77	74	hypothetical protein LOAG_12889
Locus_25727_Transcript_1/1_Conf_1.000	649	4	8.08E-14	NP_498323.2	53	81.2629	210	113	hypothetical protein C05D10.4
Locus_25728_Transcript_1/1_Conf_1.000	152	20	1.77E-14	XP_002645100.1	74	82.4185	50	37	C. briggsae CBR-DEG-1 protein
Locus_25729_Transcript_1/1_Conf_1.000	188	3	5.53E-08	XP_002642594.1	75	60.8474	52	39	Hypothetical protein CBG09147
Locus_2573_Transcript_1/1_Conf_1.000	1094	20	3.43E-149	NP_001024806.1	96	532.332	269	260	CALUmenin (calcium-binding protein) homolog family member (calu-1)
Locus_25730_Transcript_1/1_Conf_1.000	203	1	2.79E-04	XP_001897289.1	52	48.521	63	33	Regulator of G protein signaling domain containing protein
Locus_25731_Transcript_1/1_Conf_1.000	246	2	8.00E-20	XP_002647842.1	82	100.138	82	68	C. briggsae CBR-ACC-1 protein
Locus_25732_Transcript_1/1_Conf_1.000	387	5	2.92E-46	XP_002643956.1	80	187.963	127	102	Hypothetical protein CBG17315
Locus_25733_Transcript_1/1_Conf_1.000	146	0							
Locus_25734_Transcript_1/1_Conf_1.000	139	0							
Locus_25735_Transcript_1/1_Conf_1.000	312	4	1.08E-11	XP_002637547.1	65	73.1738	92	60	Hypothetical protein CBG19279
Locus_25736_Transcript_1/1_Conf_1.000	218	20	1.01E-14	EFO22696.1	88	83.1889	72	64	hypothetical protein LOAG_05790
Locus_25737_Transcript_1/1_Conf_1.000	279	4	6.31E-25	XP_002631133.1	91	117.087	81	74	C. briggsae CBR-CLH-2 protein
Locus_25738_Transcript_1/1_Conf_1.000	367	0							
Locus_25739_Transcript_1/1_Conf_1.000	133	0							

Locus_2574_Transcript_1/1_Conf_1.000	1106	20	1.35E-84	XP_002630638.1	68	317.775	274	189	C. briggsae CBR-TRY-1 protein
Locus_25740_Transcript_1/1_Conf_1.000	160	0							
Locus_25742_Transcript_1/1_Conf_1.000	217	20	1.36E-19	XP_002637203.1	77	99.3673	72	56	Hypothetical protein CBG09729
Locus_25743_Transcript_1/1_Conf_1.000	154	0							
Locus_25744_Transcript_1/1_Conf_1.000	134	0							
Locus_25745_Transcript_1/1_Conf_1.000	236	9	3.20E-08	XP_002633427.1	61	61.6178	80	49	C. briggsae CBR-NHX-9 protein
Locus_25746_Transcript_1/1_Conf_1.000	137	0							
Locus_25747_Transcript_1/1_Conf_1.000	281	20	8.53E-22	XP_002646299.1	73	106.686	91	67	Hypothetical protein CBG12006
Locus_25748_Transcript_1/1_Conf_1.000	177	0							
Locus_25749_Transcript_1/1_Conf_1.000	166	0							
Locus_2575_Transcript_1/1_Conf_1.000	1930	20	7.91E-135	XP_002641309.1	86	485.723	323	281	C. briggsae CBR-NEX-2 protein
Locus_25750_Transcript_1/1_Conf_1.000	302	20	4.86E-41	NP_491529.2	97	170.629	100	97	hypothetical protein Y110A7A.6
Locus_25751_Transcript_1/1_Conf_1.000	175	0							
Locus_25752_Transcript_1/1_Conf_1.000	155	0							
Locus_25753_Transcript_1/1_Conf_1.000	258	0							
Locus_25754_Transcript_1/1_Conf_1.000	132	0							
Locus_25755_Transcript_1/1_Conf_1.000	141	20	3.03E-19	BAH14701.1	100	98.2117	45	45	unnamed protein product
Locus_25756_Transcript_1/1_Conf_1.000	561	0							
Locus_25757_Transcript_1/1_Conf_1.000	192	20	1.18E-10	XP_392546.3	77	69.707	53	41	PREDICTED: similar to Pantothenate kinase 4 (Pantothenic acid kinase 4) (hPanK4) isoform 1
Locus_25758_Transcript_1/1_Conf_1.000	136	0							

Locus_25759_Transcript_1/1_Conf_1.000	200	3	4.32E-13	NP_001024442.1	72	77.7962	62	45	hypothetical protein C35B8.3
Locus_2576_Transcript_1/1_Conf_1.000	565	20	1.74E-47	NP_741553.1	76	192.586	154	118	ALdehyde deHydrogenase family member (alh-4)
Locus_25760_Transcript_1/1_Conf_1.000	242	0							
Locus_25761_Transcript_1/1_Conf_1.000	159	0							
Locus_25762_Transcript_1/1_Conf_1.000	151	0							
Locus_25763_Transcript_1/1_Conf_1.000	210	0							
Locus_25764_Transcript_1/1_Conf_1.000	135	0							
Locus_25765_Transcript_1/1_Conf_1.000	233	0							
Locus_25766_Transcript_1/1_Conf_1.000	270	0							
Locus_25767_Transcript_1/1_Conf_1.000	179	0							
Locus_25768_Transcript_1/1_Conf_1.000	220	0							
Locus_25769_Transcript_1/1_Conf_1.000	310	0							
Locus_2577_Transcript_1/2_Conf_1.000	1647	20	1.15E-123	NP_508463.1	64	448.358	507	326	hypothetical protein F52H2.6
Locus_2577_Transcript_2/2_Conf_1.000	1301	20	1.26E-103	NP_508463.1	64	381.333	433	280	hypothetical protein F52H2.6
Locus_25770_Transcript_1/1_Conf_1.000	171	0							
Locus_25771_Transcript_1/1_Conf_1.000	134	0							
Locus_25772_Transcript_1/1_Conf_1.000	150	0							
Locus_25773_Transcript_1/1_Conf_1.000	165	0							
Locus_25774_Transcript_1/1_Conf_1.000	554	13	4.25E-11	XP_002631536.1	41	71.633	173	72	Hypothetical protein CBG20702
Locus_25775_Transcript_1/1_Conf_1.000	190	0							
Locus_25776_Transcript_1/1_Conf_1.000	221	0							
Locus_25777_Transcript_1/1_Conf_1.000	169	0							
Locus_25778_Transcript_1/1_Conf_1.000	148	0							
Locus_25779_Transcript_1/1_Conf_1.000	239	2	2.79E-04	XP_002648604.1	58	48.521	62	36	Hypothetical protein CBG24940
Locus_2578_Transcript_1/3_Conf_0.667	388	0							
Locus_2578_Transcript_2/3_Conf_0.333	377	0							
Locus_2578_Transcript_3/3_Conf_0.667	377	0							
Locus_25780_Transcript_1/1_Conf_1.000	314	12	2.56E-21	ACD02409.2	61	105.145	106	65	Delta and osm-11-like protein 3, partially confirmed by transcript evidence

Locus_25781_Transcript_1/1_Conf_1.000	130	20	1.16E-18	XP_002761817.1	100	96.2857	43	43	PREDICTED: lysosomal alpha-mannosidase isoform 2
Locus_25782_Transcript_1/1_Conf_1.000	202	0							
Locus_25783_Transcript_1/1_Conf_1.000	139	0							
Locus_25784_Transcript_1/1_Conf_1.000	298	0							
Locus_25785_Transcript_1/1_Conf_1.000	407	20	2.88E-09	XP_002112951.1	52	65.0846	128	67	hypothetical protein TRIADDRAFT_25152
Locus_25786_Transcript_1/1_Conf_1.000	242	13	3.39E-10	NP_505389.3	63	68.1662	74	47	GRounDhog (hedgehog-like family) family member (grd-6)
Locus_25787_Transcript_1/1_Conf_1.000	248	0							
Locus_25788_Transcript_1/1_Conf_1.000	131	1	4.30E-05	CBJ28140.1	72	51.2174	37	27	hypothetical protein
Locus_25789_Transcript_1/1_Conf_1.000	202	0							
Locus_2579_Transcript_1/1_Conf_1.000	296	3	9.62E-13	ACO15779.1	70	76.6406	68	48	Neuronal symmetry protein 7, isoform b
Locus_25790_Transcript_1/1_Conf_1.000	139	0							
Locus_25791_Transcript_1/1_Conf_1.000	142	0							
Locus_25792_Transcript_1/1_Conf_1.000	253	20	8.26E-12	XP_002629983.1	73	73.559	82	60	Hypothetical protein CBG13345
Locus_25793_Transcript_1/1_Conf_1.000	144	0							
Locus_25794_Transcript_1/1_Conf_1.000	173	0							
Locus_25795_Transcript_1/1_Conf_1.000	130	0							
Locus_25796_Transcript_1/1_Conf_1.000	139	20	2.41E-08	XP_002641457.1	82	62.003	46	38	C. briggsae CBR-TOP-3 protein
Locus_25797_Transcript_1/1_Conf_1.000	152	0							
Locus_25798_Transcript_1/1_Conf_1.000	447	2	5.65E-05	XP_001603548.1	61	50.8322	86	53	PREDICTED: similar to ENSANGP00000010363
Locus_25799_Transcript_1/1_Conf_1.000	197	0							
Locus_258_Transcript_1/1_Conf_1.000	1339	20	2.15E-130	XP_002634773.1	75	470.315	416	315	Hypothetical protein CBG13872
Locus_2580_Transcript_1/1_Conf_1.000	516	20	2.26E-55	XP_002647771.1	83	218.394	156	130	C. briggsae CBR-PPH-5 protein
Locus_25800_Transcript_1/1_Conf_1.000	157	0							
Locus_25801_Transcript_1/1_Conf_1.000	163	2	1.88E-08	NP_500240.1	69	62.3882	52	36	hypothetical protein Y69A2AR.31

Locus_25802_Transcript_1/1_Conf_1.000	142	0							
Locus_25803_Transcript_1/1_Conf_1.000	185	0							
Locus_25804_Transcript_1/1_Conf_1.000	168	5	2.27E-22	NP_492127.1	96	108.612	55	53	Low-density lipoprotein Receptor Related family member (lrp-1)
Locus_25805_Transcript_1/1_Conf_1.000	205	18	1.09E-08	NP_498071.1	84	63.1586	44	37	hypothetical protein C45G9.7
Locus_25806_Transcript_1/1_Conf_1.000	163	3	3.66E-04	NP_001033381.1	60	48.1358	53	32	hypothetical protein Y71H2AM.15
Locus_25807_Transcript_1/1_Conf_1.000	228	0							
Locus_25808_Transcript_1/1_Conf_1.000	155	0							
Locus_25809_Transcript_1/1_Conf_1.000	146	0							
Locus_2581_Transcript_1/1_Conf_1.000	627	20	2.98E-47	NP_001022969.1	87	192.2	148	129	U2AF splicing factor family member (uaf-1)
Locus_25810_Transcript_1/1_Conf_1.000	189	20	1.31E-09	EFO18137.1	71	66.2402	46	33	zinc finger protein
Locus_25811_Transcript_1/1_Conf_1.000	191	0							
Locus_25812_Transcript_1/1_Conf_1.000	253	8	2.11E-07	EFO20293.1	65	58.9214	84	55	PDZ domain-containing protein
Locus_25813_Transcript_1/1_Conf_1.000	142	0							
Locus_25814_Transcript_1/1_Conf_1.000	180	2	1.52E-05	NP_497609.1	64	52.7582	54	35	hypothetical protein Y71H2AM.13
Locus_25815_Transcript_1/1_Conf_1.000	154	0							
Locus_25816_Transcript_1/1_Conf_1.000	152	0							
Locus_25817_Transcript_1/1_Conf_1.000	149	0							
Locus_25818_Transcript_1/1_Conf_1.000	143	0							
Locus_25819_Transcript_1/1_Conf_1.000	131	0							
Locus_2582_Transcript_1/1_Conf_1.000	440	20	2.46E-45	ABK80760.1	100	184.882	91	91	60S ribosomal protein L37a
Locus_25820_Transcript_1/1_Conf_1.000	622	20	8.68E-68	XP_002640264.1	72	260.381	206	150	Hypothetical protein CBG12789
Locus_25821_Transcript_1/1_Conf_1.000	153	0							
Locus_25822_Transcript_1/1_Conf_1.000	129	0							

Locus_25823_Transcript_1/1_Conf_1.000	370	19	3.45E-18	EFO26611.1	61	94.7449	124	76	hypothetical protein LOAG_01867
Locus_25824_Transcript_1/1_Conf_1.000	175	3	1.33E-06	XP_002642918.1	68	56.225	58	40	Hypothetical protein CBG15194
Locus_25825_Transcript_1/1_Conf_1.000	167	2	7.84E-15	XP_002646694.1	87	83.5741	55	48	C. briggsae CBR-SPON-1 protein
Locus_25826_Transcript_1/1_Conf_1.000	227	2	1.15E-05	XP_002631363.1	81	53.1434	37	30	Hypothetical protein CBG03199
Locus_25827_Transcript_1/1_Conf_1.000	270	4	1.86E-16	NP_001022058.1	85	88.9669	55	47	hypothetical protein E02H1.8
Locus_25828_Transcript_1/1_Conf_1.000	222	2	4.09E-11	XP_002640985.1	66	71.2478	69	46	C. briggsae CBR-CDH-12 protein
Locus_25829_Transcript_1/1_Conf_1.000	146	0							
Locus_2583_Transcript_1/1_Conf_1.000	498	20	1.40E-40	XP_001897955.1	70	169.088	165	117	membrin
Locus_25830_Transcript_1/1_Conf_1.000	133	0							
Locus_25831_Transcript_1/1_Conf_1.000	209	4	7.81E-07	XP_002633255.1	57	56.9954	89	51	Hypothetical protein CBG05980
Locus_25832_Transcript_1/1_Conf_1.000	260	0							
Locus_25833_Transcript_1/1_Conf_1.000	333	0							
Locus_25834_Transcript_1/1_Conf_1.000	216	0							
Locus_25835_Transcript_1/1_Conf_1.000	298	0							
Locus_25836_Transcript_1/1_Conf_1.000	142	0							
Locus_25837_Transcript_1/1_Conf_1.000	185	0							
Locus_25838_Transcript_1/1_Conf_1.000	158	20	2.54E-21	XP_002927123.1	100	105.145	52	52	PREDICTED: transcription intermediary factor 1-beta-like
Locus_25839_Transcript_1/1_Conf_1.000	206	20	2.35E-19	XP_001893904.1	77	98.5969	68	53	Protein-tyrosine phosphatase containing protein
Locus_2584_Transcript_1/1_Conf_1.000	240	9	2.27E-06	NP_491127.1	78	55.4546	37	29	hypothetical protein Y54E10A.3
Locus_25840_Transcript_1/1_Conf_1.000	166	0							
Locus_25841_Transcript_1/1_Conf_1.000	355	12	4.73E-28	CAC39009.1	76	127.487	120	92	membrane aminopeptidase H11-4, isoform 4
Locus_25842_Transcript_1/1_Conf_1.000	164	0							

Locus_25843_Transcript_1/1_Conf_1.000	343	20	2.08E-31	NP_499594.2	77	138.658	114	88	TIMeless (Drosophila/mammal) related family member (tim-1)
Locus_25844_Transcript_1/1_Conf_1.000	135	20	8.29E-17	XP_001139169.1	97	90.1225	45	44	PREDICTED: alpha-2-macroglobulin isoform 1
Locus_25845_Transcript_1/1_Conf_1.000	153	0							
Locus_25846_Transcript_1/1_Conf_1.000	160	0							
Locus_25847_Transcript_1/1_Conf_1.000	224	0							
Locus_25848_Transcript_1/1_Conf_1.000	240	0							
Locus_25849_Transcript_1/1_Conf_1.000	135	0							
Locus_2585_Transcript_1/2_Conf_1.000	737	20	4.38E-60	XP_002643190.1	83	235.343	170	142	C. briggsae CBR-TSP-9 protein
Locus_2585_Transcript_2/2_Conf_1.000	749	20	3.34E-87	NP_508232.1	84	325.479	231	195	TetraSPanin family member (tsp-9)
Locus_25850_Transcript_1/1_Conf_1.000	323	2	3.53E-23	NP_500282.2	73	111.309	91	67	hypothetical protein Y54G2A.29
Locus_25851_Transcript_1/1_Conf_1.000	142	0							
Locus_25852_Transcript_1/1_Conf_1.000	409	11	3.06E-19	XP_002632455.1	55	98.2117	122	68	Hypothetical protein CBG13677
Locus_25853_Transcript_1/1_Conf_1.000	385	0							
Locus_25854_Transcript_1/1_Conf_1.000	150	0							
Locus_25855_Transcript_1/1_Conf_1.000	229	2	5.68E-05	XP_002571369.1	63	50.8322	69	44	inhibitor of growth family member 5
Locus_25856_Transcript_1/1_Conf_1.000	307	0							
Locus_25857_Transcript_1/1_Conf_1.000	155	0							
Locus_25858_Transcript_1/1_Conf_1.000	128	5	1.21E-07	NP_004537.1	100	59.6918	42	42	NADH dehydrogenase ubiquinone 1 beta subcomplex subunit 2, mitochondrial precursor
Locus_25859_Transcript_1/1_Conf_1.000	138	0							
Locus_2586_Transcript_1/1_Conf_1.000	1145	20	3.84E-98	XP_001899156.1	68	362.844	373	255	Nuclear hormone receptor family member nhr-41

Locus_25860_Transcript_1/1_Conf_1.000	242	0							
Locus_25861_Transcript_1/1_Conf_1.000	160	0							
Locus_25862_Transcript_1/1_Conf_1.000	199	0							
Locus_25863_Transcript_1/1_Conf_1.000	209	0							
Locus_25864_Transcript_1/1_Conf_1.000	147	20	5.00E-17	NP_505445.2	93	90.8929	47	44	Nematode AStacin protease family member (nas-3)
Locus_25865_Transcript_1/1_Conf_1.000	141	0							
Locus_25866_Transcript_1/1_Conf_1.000	174	0							
Locus_25867_Transcript_1/1_Conf_1.000	452	20	5.54E-53	NP_499482.1	80	210.305	148	119	defective SPErmatogenesis family member (spe-6)
Locus_25868_Transcript_1/1_Conf_1.000	238	0							
Locus_25869_Transcript_1/1_Conf_1.000	333	0							
Locus_2587_Transcript_1/2_Conf_1.000	928	20	2.17E-34	XP_001899299.1	61	150.599	260	160	hypothetical protein Bm1_39225
Locus_2587_Transcript_2/2_Conf_1.000	915	20	2.12E-34	XP_001899299.1	61	150.599	260	160	hypothetical protein Bm1_39225
Locus_25870_Transcript_1/1_Conf_1.000	142	0							
Locus_25871_Transcript_1/1_Conf_1.000	137	0							
Locus_25872_Transcript_1/1_Conf_1.000	284	20	2.56E-29	NP_505512.3	84	131.724	94	79	AQuaPorin or aquaglyceroporin related family member (aqp-4)
Locus_25873_Transcript_1/1_Conf_1.000	561	4	7.96E-29	XP_002638567.1	60	130.568	179	108	Hypothetical protein CBG05609
Locus_25874_Transcript_1/1_Conf_1.000	237	5	3.18E-16	NP_001021110.1	91	88.1965	49	45	CAlSYntenin/Alcadein homolog family member (casy-1)
Locus_25875_Transcript_1/1_Conf_1.000	248	0							
Locus_25876_Transcript_1/1_Conf_1.000	190	0							
Locus_25877_Transcript_1/1_Conf_1.000	217	19	1.32E-14	XP_001902377.1	68	82.8037	69	47	Adducin-related protein 1
Locus_25878_Transcript_1/1_Conf_1.000	217	0							
Locus_25879_Transcript_1/1_Conf_1.000	200	1	1.26E-04	NP_491362.1	62	49.6766	61	38	hypothetical protein ZK973.1

Locus_2588_Transcript_1/1_Conf_1.000	1099	20	4.16E-94	AAC79672.3	76	349.362	299	228	putative cdc2-related kinase
Locus_25880_Transcript_1/1_Conf_1.000	151	0							
Locus_25881_Transcript_1/1_Conf_1.000	145	20	2.41E-19	XP_002818132.1	100	98.5969	46	46	PREDICTED: tRNA methyltransferase 112 homolog
Locus_25882_Transcript_1/1_Conf_1.000	372	0							
Locus_25883_Transcript_1/1_Conf_1.000	143	0							
Locus_25884_Transcript_1/1_Conf_1.000	237	0							
Locus_25885_Transcript_1/1_Conf_1.000	182	0							
Locus_25886_Transcript_1/1_Conf_1.000	218	0							
Locus_25887_Transcript_1/1_Conf_1.000	182	0							
Locus_25888_Transcript_1/1_Conf_1.000	130	0							
Locus_25889_Transcript_1/1_Conf_1.000	209	0							
Locus_2589_Transcript_1/1_Conf_1.000	147	0							
Locus_25890_Transcript_1/1_Conf_1.000	216	0							
Locus_25891_Transcript_1/1_Conf_1.000	168	0							
Locus_25892_Transcript_1/1_Conf_1.000	236	20	4.91E-25	XP_002634260.1	77	117.472	76	59	Hypothetical protein CBG01831
Locus_25893_Transcript_1/1_Conf_1.000	177	0							
Locus_25894_Transcript_1/1_Conf_1.000	264	0							
Locus_25895_Transcript_1/1_Conf_1.000	243	20	8.28E-25	NP_741684.2	89	116.701	73	65	PROximal proliferation in germline family member (pro-3)
Locus_25896_Transcript_1/1_Conf_1.000	192	0							
Locus_25897_Transcript_1/1_Conf_1.000	255	0							
Locus_25898_Transcript_1/1_Conf_1.000	166	0							
Locus_25899_Transcript_1/1_Conf_1.000	180	0							
Locus_259_Transcript_1/2_Conf_1.000	1451	20	1.73E-96	XP_002631411.1	76	357.836	303	232	Hypothetical protein CBG03263
Locus_259_Transcript_2/2_Conf_1.000	619	20	1.44E-70	P51535.1	90	269.626	153	138	Myoglobin
Locus_2590_Transcript_1/1_Conf_1.000	266	0							
Locus_25900_Transcript_1/1_Conf_1.000	143	0							
Locus_25901_Transcript_1/1_Conf_1.000	201	4	4.60E-15	Q20548.2	75	84.3445	66	50	Probable RING finger protein 207 homolog
Locus_25902_Transcript_1/1_Conf_1.000	148	0							
Locus_25903_Transcript_1/1_Conf_1.000	206	3	1.99E-10	CAH04706.3	63	68.9366	66	42	C. elegans protein K04H4.2c, partially confirmed by transcript evidence
Locus_25904_Transcript_1/1_Conf_1.000	141	0							

Locus_25905_Transcript_1/1_Conf_1.000	152	0							
Locus_25906_Transcript_1/1_Conf_1.000	251	0							
Locus_25907_Transcript_1/1_Conf_1.000	467	0							
Locus_25908_Transcript_1/1_Conf_1.000	276	20	1.23E-36	NP_507688.2	85	155.992	92	79	CYtochrome P450 family member (cyp-42A1)
Locus_25909_Transcript_1/1_Conf_1.000	138	20	6.13E-12	NP_001038776.1	84	73.9442	46	39	alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A
Locus_2591_Transcript_1/1_Conf_1.000	1908	20	3.88E-150	NP_492762.1	65	536.569	586	386	hypothetical protein F25H2.6
Locus_25910_Transcript_1/1_Conf_1.000	147	0							
Locus_25911_Transcript_1/1_Conf_1.000	153	0							
Locus_25912_Transcript_1/1_Conf_1.000	396	6	1.77E-06	XP_002577829.1	50	55.8398	79	40	hypothetical protein
Locus_25913_Transcript_1/1_Conf_1.000	128	0							
Locus_25914_Transcript_1/1_Conf_1.000	152	0							
Locus_25915_Transcript_1/1_Conf_1.000	137	20	2.19E-09	XP_002629772.1	79	65.4698	44	35	Hypothetical protein CBG01012
Locus_25916_Transcript_1/1_Conf_1.000	129	20	4.14E-16	3IYG	100	87.8113	43	43	Ca Model Of Bovine TricCCT DERIVED FROM A 4.0 ANGSTROM Cryo-Em Map
Locus_25917_Transcript_1/1_Conf_1.000	189	1	6.96E-11	NP_506678.2	72	70.4774	58	42	hypothetical protein W09D12.1
Locus_25918_Transcript_1/1_Conf_1.000	321	20	6.21E-36	ACI49180.1	82	153.68	98	81	hypothetical protein Csp3_JD02.008
Locus_25919_Transcript_1/1_Conf_1.000	156	0							
Locus_2592_Transcript_1/1_Conf_1.000	1021	11	2.97E-59	AAD32265.1	71	233.417	220	157	AF133832_1NIP3
Locus_25920_Transcript_1/1_Conf_1.000	192	4	4.35E-05	EFO16147.1	62	51.2174	62	39	major facilitator superfamily transporter
Locus_25921_Transcript_1/1_Conf_1.000	140	0							
Locus_25922_Transcript_1/1_Conf_1.000	141	0							

Locus_25923_Transcript_1/1_Conf_1.000	140	2	1.28E-09	NP_496764.1	80	66.2402	46	37	hypothetical protein Y38F1A.6
Locus_25924_Transcript_1/1_Conf_1.000	220	17	4.69E-07	XP_520983.2	100	57.7658	73	73	PREDICTED: similar to elongation factor-1-beta
Locus_25925_Transcript_1/1_Conf_1.000	259	20	3.20E-32	XP_002631100.1	82	141.354	86	71	Hypothetical protein CBG02874
Locus_25926_Transcript_1/1_Conf_1.000	183	0							
Locus_25927_Transcript_1/1_Conf_1.000	217	15	9.09E-24	XP_001896231.1	86	113.235	68	59	SEC14-like protein 4
Locus_25928_Transcript_1/1_Conf_1.000	178	0							
Locus_25929_Transcript_1/1_Conf_1.000	243	0							
Locus_2593_Transcript_1/1_Conf_1.000	2047	20	0	NP_501914.1	82	898.656	626	515	Isoleucyl tRNA Synthetase family member (irs-1)
Locus_25930_Transcript_1/1_Conf_1.000	620	0							
Locus_25931_Transcript_1/1_Conf_1.000	332	0							
Locus_25932_Transcript_1/1_Conf_1.000	145	0							
Locus_25933_Transcript_1/1_Conf_1.000	167	2	1.13E-05	NP_496725.2	64	53.1434	54	35	ACyLtransferase-like family member (acl-7)
Locus_25934_Transcript_1/1_Conf_1.000	197	0							
Locus_25935_Transcript_1/1_Conf_1.000	162	0							
Locus_25936_Transcript_1/1_Conf_1.000	493	4	1.37E-27	NP_001022619.1	60	125.946	166	100	NorDiHydroGuaiaretic acid resistant family member (ndg-4)
Locus_25937_Transcript_1/1_Conf_1.000	244	9	2.57E-34	NP_741755.1	92	148.288	81	75	hypothetical protein C01C4.3
Locus_25938_Transcript_1/1_Conf_1.000	181	0							
Locus_25939_Transcript_1/1_Conf_1.000	142	0							
Locus_2594_Transcript_1/1_Conf_1.000	664	20	3.59E-81	XP_002646512.1	89	305.064	221	198	C. briggsae CBR-TOP-1 protein

Locus_25940_Transcript_1/1_Conf_1.000	155	0							
Locus_25941_Transcript_1/1_Conf_1.000	235	20	1.34E-14	NP_001122528.1	65	82.8037	70	46	Cation transporting ATPase family member (catp-1)
Locus_25942_Transcript_1/1_Conf_1.000	393	2	5.90E-10	XP_002643618.1	62	67.3958	100	62	Hypothetical protein CBG16356
Locus_25943_Transcript_1/1_Conf_1.000	239	0							
Locus_25944_Transcript_1/1_Conf_1.000	401	20	4.86E-73	XP_002762104.1	100	276.944	125	125	PREDICTED: DNA-directed RNA polymerase II subunit RPB9-like
Locus_25945_Transcript_1/1_Conf_1.000	184	0							
Locus_25946_Transcript_1/1_Conf_1.000	194	20	1.22E-07	XP_533290.2	80	59.6918	57	46	PREDICTED: similar to Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8)
Locus_25947_Transcript_1/1_Conf_1.000	139	20	1.97E-18	XP_002819230.1	100	95.5153	45	45	PREDICTED: transcription elongation factor B polypeptide 1-like
Locus_25948_Transcript_1/1_Conf_1.000	245	0							
Locus_25949_Transcript_1/1_Conf_1.000	246	2	1.12E-05	NP_498014.2	67	53.1434	53	36	COenzyme Q (ubiquinone) biosynthesis family member (coq-8)
Locus_2595_Transcript_1/3_Conf_0.667	1170	20	5.26E-58	NP_492860.1	78	229.565	201	157	hypothetical protein Y52B11A.9

Locus_2595_Transcript_2/3_Conf_0.667	1170	20	5.26E-58	NP_492860.1	78	229.565	201	157	hypothetical protein Y52B11A.9
Locus_2595_Transcript_3/3_Conf_0.667	1170	20	5.26E-58	NP_492860.1	78	229.565	201	157	hypothetical protein Y52B11A.9
Locus_25950_Transcript_1/1_Conf_1.000	144	0							
Locus_25951_Transcript_1/1_Conf_1.000	161	0							
Locus_25952_Transcript_1/1_Conf_1.000	135	0							
Locus_25953_Transcript_1/1_Conf_1.000	274	6	4.28E-05	XP_313869.4	71	51.2174	39	28	AGAP004566-PA
Locus_25954_Transcript_1/1_Conf_1.000	584								
Locus_25955_Transcript_1/1_Conf_1.000	129	0							
Locus_25956_Transcript_1/1_Conf_1.000	151	0							
Locus_25957_Transcript_1/1_Conf_1.000	184	0							
Locus_25958_Transcript_1/1_Conf_1.000	181	0							
Locus_25959_Transcript_1/1_Conf_1.000	163	4	2.71E-07	EFO28302.1	78	58.5362	51	40	hypothetical protein LOAG_00195
Locus_2596_Transcript_1/1_Conf_1.000	1084	2	1.25E-10	XP_002630692.1	52	72.0182	143	75	Hypothetical protein CBG02374
Locus_25960_Transcript_1/1_Conf_1.000	388	20	5.17E-35	XP_002914611.1	71	150.599	121	87	PREDICTED: cytohesin-4-like
Locus_25961_Transcript_1/1_Conf_1.000	377	20	2.67E-63	XP_002641621.1	93	244.588	125	117	Hypothetical protein CBG09941
Locus_25962_Transcript_1/1_Conf_1.000	183	0							
Locus_25963_Transcript_1/1_Conf_1.000	231	0							
Locus_25964_Transcript_1/1_Conf_1.000	169	1	2.43E-08	NP_500905.2	67	62.003	55	37	hypothetical protein C46G7.1
Locus_25965_Transcript_1/1_Conf_1.000	153	1	2.86E-14	XP_002826351.1	91	75.485	36	33	PREDICTED: hypothetical protein LOC100437226

Locus_25966_Transcript_1/1_Conf_1.000	133	5	5.06E-06	NP_501743.1	67	54.299	43	29	CAVeolin family member (cav-1)
Locus_25967_Transcript_1/1_Conf_1.000	175	6	4.27E-05	XP_002405738.1	65	51.2174	43	28	hexosaminidase domain-containing protein, putative
Locus_25968_Transcript_1/1_Conf_1.000	179	20	4.84E-17	NP_493694.2	83	90.8929	59	49	MItochondrial Solute Carrier family member (misc-1)
Locus_25969_Transcript_1/1_Conf_1.000	174	0							
Locus_2597_Transcript_1/2_Conf_1.000	1277	3	2.88E-28	XP_002630689.1	45	130.954	378	172	Hypothetical protein CBG02369
Locus_2597_Transcript_2/2_Conf_1.000	620	3	1.51E-19		48	100.138	223	109	hypothetical protein F08B1.2
Locus_25970_Transcript_1/1_Conf_1.000	320	3	3.43E-26	XP_002639499.1	73	121.324	97	71	C. briggsae CBR-ITX-1 protein
Locus_25971_Transcript_1/1_Conf_1.000	209	0							
Locus_25972_Transcript_1/1_Conf_1.000	158	0							
Locus_25973_Transcript_1/1_Conf_1.000	151	4	1.11E-16	NP_495365.1	93	89.7373	47	44	RaPsYn family member (rpy-1)
Locus_25974_Transcript_1/1_Conf_1.000	1667	20	0	XP_002644337.1	79	661.374	512	407	C. briggsae CBR-KLP-4 protein
Locus_25975_Transcript_1/1_Conf_1.000	240	0							
Locus_25976_Transcript_1/1_Conf_1.000	173	20	4.87E-25	ACH45822.1	100	117.472	57	57	putative nef1 variant 1
Locus_25977_Transcript_1/1_Conf_1.000	167	0							

Locus_25978_Transcript_1/1_Conf_1.000	164	20	3.76E-25	XP_002760341.1	100	117.857	54	54	PREDICTED: glutamine synthetase
Locus_25979_Transcript_1/1_Conf_1.000	157	0							
Locus_2598_Transcript_1/1_Conf_1.000	1320	20	1.52E-104	AAC98796.1	88	384.415	234	208	dolichol monophosphate mannose synthase
Locus_25980_Transcript_1/1_Conf_1.000	161	20	3.79E-09	XP_002630623.1	71	64.6994	56	40	C. briggsae CBR-NDX-3 protein
Locus_25981_Transcript_1/1_Conf_1.000	247	0							
Locus_25982_Transcript_1/1_Conf_1.000	152	20	2.40E-11	EFO26471.1	75	72.0182	49	37	hypothetical protein LOAG_02007
Locus_25983_Transcript_1/1_Conf_1.000	130	0							
Locus_25984_Transcript_1/1_Conf_1.000	175	0							
Locus_25985_Transcript_1/1_Conf_1.000	240	0							
Locus_25986_Transcript_1/1_Conf_1.000	268	20	3.52E-15	XP_002633325.1	59	84.7297	94	56	Hypothetical protein CBG06062
Locus_25987_Transcript_1/1_Conf_1.000	175	0							
Locus_25988_Transcript_1/1_Conf_1.000	181	20	1.41E-19	XP_002630203.1	86	99.3673	60	52	Hypothetical protein CBG00613
Locus_25989_Transcript_1/1_Conf_1.000	170	0							
Locus_2599_Transcript_1/1_Conf_1.000	1009	20	2.22E-83	EFO26496.1	67	313.538	336	226	hypothetical protein LOAG_01982
Locus_25990_Transcript_1/1_Conf_1.000	156	0							
Locus_25991_Transcript_1/1_Conf_1.000	147	0							

Locus_25992_Transcript_1/1_Conf_1.000	166	1	1.25E-04	XP_002641244.1	66	49.6766	48	32	Hypothetical protein CBG09112
Locus_25993_Transcript_1/1_Conf_1.000	129	0							
Locus_25994_Transcript_1/1_Conf_1.000	129	1	3.64E-04	XP_002642305.1	77	48.1358	36	28	Hypothetical protein CBG18297
Locus_25995_Transcript_1/1_Conf_1.000	259	20	1.14E-29	NP_001023792.1	98	132.88	85	84	EXPulsion defective (defecation) family member (exp-2)
Locus_25996_Transcript_1/1_Conf_1.000	346	4	7.94E-07	XP_002638551.1	74	56.9954	43	32	Hypothetical protein CBG05587
Locus_25997_Transcript_1/1_Conf_1.000	284	20	8.46E-49	BAG65408.1	100	196.438	94	94	unnamed protein product
Locus_25998_Transcript_1/1_Conf_1.000	159	0							
Locus_25999_Transcript_1/1_Conf_1.000	288	20	2.02E-10	XP_002630318.1	73	68.9366	63	46	Hypothetical protein CBG04241
Locus_26_Transcript_1/3_Conf_0.636	314	0							
Locus_26_Transcript_3/3_Conf_0.727	279	0							
Locus_260_Transcript_1/2_Conf_1.000	1541	20	9.44E-56	NP_501053.2	63	222.631	305	194	Lateral-signal-Induced Phosphatase family member (lip-1)
Locus_260_Transcript_2/2_Conf_1.000	1502	20	1.19E-55	NP_501053.2	63	222.246	304	193	Lateral-signal-Induced Phosphatase family member (lip-1)
Locus_2600_Transcript_1/1_Conf_1.000	373	4	1.95E-13	XP_002643098.1	76	78.9518	59	45	Hypothetical protein CBG23022
Locus_26000_Transcript_1/1_Conf_1.000	180	0							
Locus_26001_Transcript_1/1_Conf_1.000	193	0							
Locus_26002_Transcript_1/1_Conf_1.000	154	0							

Locus_26003_Transcript_1/1_Conf_1.000	219	0							
Locus_26004_Transcript_1/1_Conf_1.000	168	20	1.42E-16	NP_491363.1	89	89.3521	55	49	Dynein Heavy Chain family member (dhc-1)
Locus_26005_Transcript_1/1_Conf_1.000	148	0							
Locus_26006_Transcript_1/1_Conf_1.000	178	0							
Locus_26007_Transcript_1/1_Conf_1.000	231	6	4.95E-09	XP_002637804.1	64	64.3142	76	49	Hypothetical protein CBG04590
Locus_26008_Transcript_1/1_Conf_1.000	142	0							
Locus_26009_Transcript_1/1_Conf_1.000	267	20	1.21E-23	XP_002647993.1	92	112.849	82	76	C. briggsae CBR-ACR-6 protein
Locus_2601_Transcript_1/1_Conf_1.000	1438	6	1.67E-67	NP_491128.4	56	261.536	478	272	Conserved Oligomeric Golgi (COG) Component family member (cogc-1)
Locus_26010_Transcript_1/1_Conf_1.000	135	20	2.33E-19	XP_002927413.1	100	98.5969	44	44	PREDICTED: eukaryotic translation initiation factor 3 subunit C-like
Locus_26011_Transcript_1/1_Conf_1.000	270	1	5.05E-22	NP_001023862.1	72	107.457	86	62	hypothetical protein F26F2.8
Locus_26012_Transcript_1/1_Conf_1.000	129	0							
Locus_26013_Transcript_1/1_Conf_1.000	166	0							
Locus_26014_Transcript_1/1_Conf_1.000	204	0							
Locus_26015_Transcript_1/1_Conf_1.000	138	0							
Locus_26016_Transcript_1/1_Conf_1.000	248	20	6.77E-19		100	97.0561	73	73	Orn decarboxylase antizyme
Locus_26017_Transcript_1/1_Conf_1.000	139	0							
Locus_26018_Transcript_1/1_Conf_1.000	178	0							
Locus_26019_Transcript_1/1_Conf_1.000	222	5	3.33E-29	ABS45067.1	92	131.339	67	62	latrophilin-like protein 2
Locus_2602_Transcript_1/1_Conf_1.000	317	20	4.20E-24	NP_501767.1	74	114.39	99	74	Sperm-Specific family, class P family member (ssp-10)
Locus_26020_Transcript_1/1_Conf_1.000	166	0							

Locus_26021_Transcript_1/1_Conf_1.000	140	0							
Locus_26022_Transcript_1/1_Conf_1.000	128	0							
Locus_26023_Transcript_1/1_Conf_1.000	147	0							
Locus_26024_Transcript_1/1_Conf_1.000	173	0							
Locus_26025_Transcript_1/1_Conf_1.000	222	0							
Locus_26026_Transcript_1/1_Conf_1.000	405	0							
Locus_26027_Transcript_1/1_Conf_1.000	461	20	3.77E-70	CAJ98743.1	92	267.314	147	136	serine/threonine phosphatase
Locus_26028_Transcript_1/1_Conf_1.000	137	0							
Locus_26029_Transcript_1/1_Conf_1.000	212	20	4.12E-16	EFO26456.1	76	87.8113	64	49	hypothetical protein LOAG_02027
Locus_2603_Transcript_1/1_Conf_1.000	1909	20	0	AAC48152.3	85	1069.69	623	534	Laminin related. see also lmb- protein 2, partially confirmed by transcript evidence
Locus_26030_Transcript_1/1_Conf_1.000	189	0							
Locus_26031_Transcript_1/1_Conf_1.000	142	0							
Locus_26032_Transcript_1/1_Conf_1.000	266	0							
Locus_26033_Transcript_1/1_Conf_1.000	369	0							
Locus_26034_Transcript_1/1_Conf_1.000	298	0							
Locus_26035_Transcript_1/1_Conf_1.000	184	4	1.23E-15	EFO19152.1	79	86.2705	59	47	hypothetical protein LOAG_09340
Locus_26036_Transcript_1/1_Conf_1.000	308	20	3.60E-20	XP_002640994.1	69	101.293	101	70	C. briggsae CBR-POLH-1 protein
Locus_26037_Transcript_1/1_Conf_1.000	371	4	8.81E-06	XP_002646250.1	54	53.5286	108	59	C. briggsae CBR-AEX-1 protein
Locus_26038_Transcript_1/1_Conf_1.000	419	3	1.45E-16	NP_492183.2	64	89.3521	91	59	hypothetical protein F55D12.5
Locus_26039_Transcript_1/1_Conf_1.000	128	0							
Locus_2604_Transcript_1/1_Conf_1.000	226	0							
Locus_26040_Transcript_1/1_Conf_1.000	150	0							
Locus_26041_Transcript_1/1_Conf_1.000	131	0							
Locus_26042_Transcript_1/1_Conf_1.000	148	0							
Locus_26043_Transcript_1/1_Conf_1.000	301	0							
Locus_26044_Transcript_1/1_Conf_1.000	196	17	2.07E-23	XP_002640347.1	90	112.079	65	59	C. briggsae CBR-HAF-9 protein
Locus_26045_Transcript_1/1_Conf_1.000	175	0							
Locus_26046_Transcript_1/1_Conf_1.000	176	3	8.60E-06	EFO27601.1	64	53.5286	53	34	hypothetical protein LOAG_00885
Locus_26047_Transcript_1/1_Conf_1.000	273	1	6.61E-06	EFO15824.1	83	53.9138	36	30	hypothetical protein LOAG_12685

Locus_26048_Transcript_1/1_Conf_1.000	344	20	3.81E-25	NP_498951.1	71	117.857	106	76	hypothetical protein F44E2.10
Locus_26049_Transcript_1/1_Conf_1.000	129	0							
Locus_2605_Transcript_1/1_Conf_1.000	908	20	6.92E-147	YP_002725710.1	96	524.242	302	291	cytochrome c oxidase subunit I
Locus_26050_Transcript_1/1_Conf_1.000	345	0							
Locus_26051_Transcript_1/1_Conf_1.000	183	0							
Locus_26052_Transcript_1/1_Conf_1.000	311	0							
Locus_26053_Transcript_1/1_Conf_1.000	226	0							
Locus_26054_Transcript_1/1_Conf_1.000	178	0							
Locus_26055_Transcript_1/1_Conf_1.000	150	0							
Locus_26056_Transcript_1/1_Conf_1.000	316	0							
Locus_26057_Transcript_1/1_Conf_1.000	344	0							
Locus_26058_Transcript_1/1_Conf_1.000	365	20	7.99E-20	NP_491864.2	65	100.138	93	61	hypothetical protein K06A5.8
Locus_26059_Transcript_1/1_Conf_1.000	132	0							
Locus_2606_Transcript_1/1_Conf_1.000	685	20	2.66E-106	NP_001022450.1	90	388.652	228	207	hypothetical protein Y48E1A.1
Locus_26060_Transcript_1/1_Conf_1.000	212	0							
Locus_26061_Transcript_1/1_Conf_1.000	154	14	7.95E-07	XP_002111941.1	72	56.9954	47	34	expressed hypothetical protein
Locus_26062_Transcript_1/1_Conf_1.000	340	0							
Locus_26063_Transcript_1/1_Conf_1.000	215	0							
Locus_26064_Transcript_1/1_Conf_1.000	192	0							
Locus_26065_Transcript_1/1_Conf_1.000	447	7	1.59E-07	XP_001894326.1	65	59.3066	70	46	DEK protein
Locus_26066_Transcript_1/1_Conf_1.000	136	20	2.50E-13	NP_492053.1	91	78.5666	45	41	LEThal family member (let-75)
Locus_26067_Transcript_1/1_Conf_1.000	487	20	1.22E-15	XP_969725.1	77	86.2705	70	54	PREDICTED: similar to Nuclear transcription factor Y subunit beta (Nuclear transcription factor Y subunit B) (NF-YB) (CAAT-box DNA-binding protein subunit B)
Locus_26068_Transcript_1/1_Conf_1.000	291	0							
Locus_26069_Transcript_1/1_Conf_1.000	423	20	1.14E-21		59	106.301	142	84	hypothetical protein T28B8.4
Locus_2607_Transcript_1/1_Conf_1.000	619	1	3.61E-05	XP_001894276.1	63	52.373	47	30	ShTK domain containing protein
Locus_26070_Transcript_1/1_Conf_1.000	130	0							

Locus_26071_Transcript_1/1_Conf_1.000	159	20	4.32E-21	XP_002823301.1	100	104.375	52	52	PREDICTED: keratin, type II cytoskeletal 7-like
Locus_26072_Transcript_1/1_Conf_1.000	229	20	1.05E-18	ACO14409.1	76	90.1225	65	50	Oligoribonuclease, mitochondrial precursor
Locus_26073_Transcript_1/1_Conf_1.000	213	0							
Locus_26074_Transcript_1/1_Conf_1.000	158	11	7.64E-18	ACM46025.1	94	93.5893	50	47	Let-23 fertility effector/regulator protein 2, isoform d
Locus_26075_Transcript_1/1_Conf_1.000	238	0							
Locus_26076_Transcript_1/1_Conf_1.000	130	3	5.24E-11	XP_002631617.1	79	70.8626	43	34	Hypothetical protein CBG20802
Locus_26077_Transcript_1/1_Conf_1.000	256	0							
Locus_26078_Transcript_1/1_Conf_1.000	142	0							
Locus_26079_Transcript_1/1_Conf_1.000	235	0							
Locus_2608_Transcript_1/1_Conf_1.000	512	20	7.02E-14	XP_001601037.1	53	80.4925	142	76	PREDICTED: similar to n-acetylgalactosaminyltransferase
Locus_26080_Transcript_1/1_Conf_1.000	422	7	1.65E-12	XP_002640486.1	54	75.8702	142	77	Hypothetical protein CBG13622
Locus_26081_Transcript_1/1_Conf_1.000	188	0							
Locus_26082_Transcript_1/2_Conf_1.000	413	20	6.95E-48	AAC46543.2	81	193.356	137	112	Hypothetical protein F48E8.6
Locus_26082_Transcript_2/2_Conf_1.000	365	20	7.43E-42	AAC46543.2	82	173.326	121	100	Hypothetical protein F48E8.6
Locus_26083_Transcript_1/1_Conf_1.000	217	4	1.01E-06	EFO17148.1	78	56.6102	41	32	hypothetical protein LOAG_11354
Locus_26084_Transcript_1/1_Conf_1.000	131	0							
Locus_26085_Transcript_1/1_Conf_1.000	161	1	6.68E-14	AAM45145.1	88	80.4925	52	46	AF278680_1L3B25
Locus_26086_Transcript_1/1_Conf_1.000	187	4	4.38E-05	XP_002637648.1	56	51.2174	55	31	C. briggsae CBR-FSHR-1 protein
Locus_26087_Transcript_1/1_Conf_1.000	157	0							
Locus_26088_Transcript_1/1_Conf_1.000	255	2	7.45E-13	XP_002635599.1	75	77.0258	69	52	Hypothetical protein CBG20588
Locus_26089_Transcript_1/1_Conf_1.000	168	0							

Locus_2609_Transcript_1/1_Conf_1.000	540	20	2.13E-65	XP_002630326.1	81	251.906	181	147	Hypothetical protein CBG04253
Locus_26090_Transcript_1/1_Conf_1.000	146	1	8.31E-04	NP_497771.1	68	46.9802	45	31	DumPY : shorter than wild-type family member (dpy-27)
Locus_26091_Transcript_1/1_Conf_1.000	228	0							
Locus_26092_Transcript_1/1_Conf_1.000	141	0							
Locus_26093_Transcript_1/1_Conf_1.000	171	10	6.35E-25	NP_504628.1	92	117.087	55	51	hypothetical protein T05H4.7
Locus_26094_Transcript_1/1_Conf_1.000	387	0							
Locus_26095_Transcript_1/1_Conf_1.000	174	0							
Locus_26096_Transcript_1/1_Conf_1.000	342	0							
Locus_26097_Transcript_1/1_Conf_1.000	225	0							
Locus_26098_Transcript_1/1_Conf_1.000	207	0							
Locus_26099_Transcript_1/1_Conf_1.000	139	0							
Locus_261_Transcript_1/1_Conf_1.000	1670	20	0	CAB07859.3	81	760.755	572	465	C. elegans protein W09D10.2, partially confirmed by transcript evidence
Locus_2610_Transcript_1/1_Conf_1.000	1003	20	7.12E-50	XP_001896958.1	69	202.216	222	154	Uncharacterized protein family UPF0005 containing protein
Locus_26100_Transcript_1/1_Conf_1.000	129	0							
Locus_26101_Transcript_1/1_Conf_1.000	357	0							
Locus_26102_Transcript_1/1_Conf_1.000	141	0							
Locus_26103_Transcript_1/1_Conf_1.000	247	20	5.36E-16	XP_002646583.1	82	87.4261	57	47	Hypothetical protein CBG20465
Locus_26104_Transcript_1/1_Conf_1.000	391	0							
Locus_26105_Transcript_1/1_Conf_1.000	217	1	2.75E-04	NP_509316.1	64	48.521	42	27	hypothetical protein ZK154.5
Locus_26106_Transcript_1/1_Conf_1.000	157	0							
Locus_26107_Transcript_1/1_Conf_1.000	233	0							
Locus_26108_Transcript_1/1_Conf_1.000	165	0							
Locus_26109_Transcript_1/1_Conf_1.000	182	0							
Locus_2611_Transcript_1/1_Conf_1.000	193	0							
Locus_26110_Transcript_1/1_Conf_1.000	285	4	2.39E-19	EAW74503.1	100	98.5969	42	42	phosphofurin acidic cluster sorting protein 1, isoform CRA_b
Locus_26111_Transcript_1/1_Conf_1.000	155	0							
Locus_26112_Transcript_1/1_Conf_1.000	528	0							
Locus_26113_Transcript_1/1_Conf_1.000	175	0							

Locus_26114_Transcript_1/1_Conf_1.000	138	20	2.84E-17	NP_510672.2	95	91.6633	46	44	Nematode AStacin protease family member (nas-39)
Locus_26115_Transcript_1/1_Conf_1.000	152	1	1.66E-04	CBA11992.1	68	49.2914	48	33	endonuclease-reverse transcriptase HmRTE-e01
Locus_26116_Transcript_1/1_Conf_1.000	141	0							
Locus_26117_Transcript_1/1_Conf_1.000	207	20	1.24E-20	NP_493275.1	86	102.834	73	63	SELB (SelB homolog) translation factor for selenocysteine incorporation family member (selb-1)
Locus_26118_Transcript_1/1_Conf_1.000	478	20	2.03E-39	XP_001900095.1	83	165.236	142	119	ABC transporter family protein
Locus_26119_Transcript_1/1_Conf_1.000	172	0							
Locus_2612_Transcript_1/1_Conf_1.000	491	20	1.05E-35	XP_002645442.1	78	152.91	141	110	C. briggsae CBR-TAG-241 protein
Locus_26120_Transcript_1/1_Conf_1.000	241	20	1.12E-45	BAG58844.1	100	186.037	80	80	unnamed protein product
Locus_26121_Transcript_1/1_Conf_1.000	157	0							
Locus_26122_Transcript_1/1_Conf_1.000	167	20	1.53E-18	ADI24623.1	85	95.9005	55	47	Copine domain protein, atypical protein 2, isoform c, partially confirmed by transcript evidence
Locus_26123_Transcript_1/1_Conf_1.000	243	18	1.85E-08	XP_001898275.1	53	62.3882	93	50	GRIP domain containing protein
Locus_26124_Transcript_1/1_Conf_1.000	291	0							
Locus_26125_Transcript_1/1_Conf_1.000	526	20	1.67E-64	XP_002634423.1	85	248.825	172	147	C. briggsae CBR-PTR-14 protein
Locus_26126_Transcript_1/1_Conf_1.000	152	20	3.24E-08	NP_495354.1	70	61.6178	50	35	hypothetical protein T19D12.10

Locus_26127_Transcript_1/1_Conf_1.000	138	7	3.85E-06	XP_002639419.1	76	54.6842	43	33	Hypothetical protein CBG04011
Locus_26128_Transcript_1/1_Conf_1.000	215	0							
Locus_26129_Transcript_1/1_Conf_1.000	269	0							
Locus_2613_Transcript_1/1_Conf_1.000	681	20	2.77E-55	EFO27544.1	64	219.164	226	145	hypothetical protein LOAG_00942
Locus_26130_Transcript_1/1_Conf_1.000	128	0							
Locus_26131_Transcript_1/1_Conf_1.000	243	0							
Locus_26132_Transcript_1/1_Conf_1.000	177	0							
Locus_26133_Transcript_1/1_Conf_1.000	128	0							
Locus_26134_Transcript_1/1_Conf_1.000	172	0							
Locus_26135_Transcript_1/1_Conf_1.000	239	0							
Locus_26136_Transcript_1/1_Conf_1.000	149	20	3.59E-07	XP_001898117.1	75	58.151	49	37	FYVE zinc finger family protein
Locus_26137_Transcript_1/1_Conf_1.000	463	2	6.95E-11	NP_498895.1	63	70.4774	107	68	RNA HelicAse family member (rha-2)
Locus_26138_Transcript_1/1_Conf_1.000	188	20	2.32E-06	EFN81468.1	72	55.4546	47	34	Histone-lysine N-methyltransferase SETMAR
Locus_26139_Transcript_1/1_Conf_1.000	152	0							

Locus_2614_Transcript_1/3_Conf_0.333	2028	20	0	EFO27896.1	75	726.472	595	452	PLK/PLK1 protein kinase
Locus_2614_Transcript_2/3_Conf_0.333	184	0							
Locus_2614_Transcript_3/3_Conf_0.500	1986	20	0	EFO27896.1	75	726.472	595	452	PLK/PLK1 protein kinase
Locus_26140_Transcript_1/1_Conf_1.000	133	0							
Locus_26141_Transcript_1/1_Conf_1.000	172	0							
Locus_26142_Transcript_1/1_Conf_1.000	177	9	9.76E-18	XP_002631132.1	84	93.2041	58	49	Hypothetical protein CBG02915

Locus_26143_Transcript_1/1_Conf_1.000	168	20	2.59E-18	EFO17467.1	87	95.1301	54	47	hypothetical protein LOAG_11032
Locus_26144_Transcript_1/1_Conf_1.000	131	0							
Locus_26145_Transcript_1/1_Conf_1.000	189	0							
Locus_26146_Transcript_1/1_Conf_1.000	150	0							
Locus_26147_Transcript_1/1_Conf_1.000	402	20	3.64E-20	NP_495206.2	76	101.293	113	86	hypothetical protein R12C12.5
Locus_26148_Transcript_1/1_Conf_1.000	254	0							
Locus_26149_Transcript_1/1_Conf_1.000	161	20	1.10E-16	NP_494491.3	92	89.7373	53	49	Guanylyl CYclase family member (gcy-19)
Locus_2615_Transcript_1/1_Conf_1.000	735	20	4.73E-30	XP_001897810.1	67	135.576	143	97	dehydrogenases, short chain protein 9
Locus_26150_Transcript_1/1_Conf_1.000	308	0							
Locus_26151_Transcript_1/1_Conf_1.000	132	0							
Locus_26152_Transcript_1/1_Conf_1.000	147	0							
Locus_26153_Transcript_1/1_Conf_1.000	229	0							
Locus_26154_Transcript_1/1_Conf_1.000	254	0							
Locus_26155_Transcript_1/1_Conf_1.000	141	6	8.26E-09	CAX65068.1	82	63.5438	46	38	C. elegans protein K08C7.3d, confirmed by transcript evidence
Locus_26156_Transcript_1/1_Conf_1.000	238	0							

Locus_26157_Transcript_1/1_Conf_1.000	167	20	5.99E-23	ACZ06864.1	100	110.538	55	55	nucleophosmin
Locus_26158_Transcript_1/1_Conf_1.000	166	0							
Locus_26159_Transcript_1/1_Conf_1.000	1092	20	1.31E-23	XP_001894303.1	47	115.161	363	173	hypothetical protein Bm1_14190
Locus_2616_Transcript_1/2_Conf_1.000	2344	20	1.00E-25	NP_495784.1	43	123.635	486	212	ZYGote defective: embryonic lethal family member (zyg-9)
Locus_2616_Transcript_2/2_Conf_1.000	2343	20	1.00E-25	NP_495784.1	43	123.635	486	212	ZYGote defective: embryonic lethal family member (zyg-9)
Locus_26160_Transcript_1/1_Conf_1.000	499	20	9.40E-37	XP_002634598.1	79	156.377	133	106	Hypothetical protein CBG08413
Locus_26161_Transcript_1/1_Conf_1.000	235	4	1.29E-33	NP_499479.2	96	145.976	78	75	hypothetical protein Y66D12A.24
Locus_26162_Transcript_1/1_Conf_1.000	285	1	3.03E-14	CAR63594.1	66	81.6481	84	56	hypothetical protein
Locus_26163_Transcript_1/1_Conf_1.000	152	0							
Locus_26164_Transcript_1/1_Conf_1.000	324	0							
Locus_26165_Transcript_1/1_Conf_1.000	214	0							
Locus_26166_Transcript_1/1_Conf_1.000	297	0							
Locus_26167_Transcript_1/1_Conf_1.000	242	0							
Locus_26168_Transcript_1/1_Conf_1.000	139	0							
Locus_26169_Transcript_1/1_Conf_1.000	260	20	3.09E-43	NP_057578.1	100	177.948	86	86	E3 ubiquitin-protein ligase RNF181

Locus_2617_Transcript_1/1_Conf_1.000	728	20	3.77E-24	XP_002648620.1	62	115.931	154	97	Hypothetical protein CBG24963
Locus_26170_Transcript_1/1_Conf_1.000	156	0							
Locus_26171_Transcript_1/1_Conf_1.000	148	0							
Locus_26172_Transcript_1/1_Conf_1.000	141	0							
Locus_26173_Transcript_1/1_Conf_1.000	154	0							
Locus_26174_Transcript_1/1_Conf_1.000	350	0							
Locus_26175_Transcript_1/1_Conf_1.000	136	0							
Locus_26176_Transcript_1/1_Conf_1.000	152	0							
Locus_26177_Transcript_1/1_Conf_1.000	314	3	2.74E-15	XP_002631142.1	64	85.1149	102	66	C. briggsae CBR-TAG-180 protein
Locus_26178_Transcript_1/1_Conf_1.000	166	9	1.13E-13	NP_001021638.1	85	79.7221	54	46	hypothetical protein T23G11.6
Locus_26179_Transcript_1/1_Conf_1.000	159	3	9.34E-08	XP_002641147.1	78	60.077	52	41	C. briggsae CBR-RGS-5 protein
Locus_2618_Transcript_1/2_Conf_1.000	886	20	1.69E-134	XP_002639887.1	92	483.026	270	251	C. briggsae CBR-RSKN-2 protein
Locus_2618_Transcript_2/2_Conf_1.000	1076	20	2.91E-161	NP_001040645.1	90	572.392	333	301	RSK-pNinety (RSK-p90 kinase) homolog family member (rskn-2)
Locus_26180_Transcript_1/1_Conf_1.000	150	0							
Locus_26181_Transcript_1/1_Conf_1.000	182	0							

Locus_26182_Transcript_1/1_Conf_1.000	211	0							
Locus_26183_Transcript_1/1_Conf_1.000	193	2	6.08E-07	AAV28323.2	56	57.3806	60	34	Hypothetical protein T15B7.1
Locus_26184_Transcript_1/1_Conf_1.000	137	20	3.99E-11	NP_492907.2	100	71.2478	36	36	Cyclin-Dependent Kinase family member (cdk-9)
Locus_26185_Transcript_1/1_Conf_1.000	555	14	1.88E-14	CBW48338.1	59	82.8037	121	72	Hypothetical protein C27A7.1d
Locus_26186_Transcript_1/1_Conf_1.000	166	0							
Locus_26187_Transcript_1/1_Conf_1.000	161	0							
Locus_26188_Transcript_1/1_Conf_1.000	153	0							
Locus_26189_Transcript_1/1_Conf_1.000	336	2	1.85E-08	XP_002641514.1	54	62.3882	116	63	Hypothetical protein CBG09809
Locus_2619_Transcript_1/1_Conf_1.000	696	20	2.24E-39	NP_497896.1	71	166.392	146	105	PDCD (mammalian ProgrammeD Cell Death protein) homolog family member (pdcd-2)
Locus_26190_Transcript_1/1_Conf_1.000	343	20	2.22E-41	XP_002629896.1	77	171.785	113	88	Hypothetical protein CBG21934
Locus_26191_Transcript_1/1_Conf_1.000	144	6	1.16E-05	XP_002603196.1	67	53.1434	43	29	hypothetical protein BRAFLDRAFT_226530
Locus_26192_Transcript_1/1_Conf_1.000	378	20	2.67E-47	NP_498062.2	84	191.43	126	106	hypothetical protein R144.6
Locus_26193_Transcript_1/1_Conf_1.000	178	0							
Locus_26194_Transcript_1/1_Conf_1.000	164	0							
Locus_26195_Transcript_1/1_Conf_1.000	215	0							
Locus_26196_Transcript_1/1_Conf_1.000	294	2	1.59E-07	NP_509975.1	66	59.3066	98	65	Temporarily Assigned Gene name family member (tag-241)
Locus_26197_Transcript_1/1_Conf_1.000	217	0							

Locus_26198_Transcript_1/1_Conf_1.000	169	20	1.68E-25	XP_520842.1	100	119.013	56	56	PREDICTED: interferon, alpha-inducible protein (clone IFI-15K)
Locus_26199_Transcript_1/1_Conf_1.000	169	0							
Locus_262_Transcript_1/1_Conf_1.000	347	0							
Locus_2620_Transcript_1/2_Conf_1.000	2085	20	0	XP_002648832.1	90	856.67	551	497	Hypothetical protein CBG16947
Locus_2620_Transcript_2/2_Conf_1.000	2086	20	0	XP_002648832.1	90	857.825	551	497	Hypothetical protein CBG16947
Locus_26200_Transcript_1/1_Conf_1.000	139	0							
Locus_26201_Transcript_1/1_Conf_1.000	368	0							
Locus_26202_Transcript_1/1_Conf_1.000	134	20	6.82E-11	NP_001041125.1	92	70.4774	38	35	hypothetical protein F55C5.11
Locus_26203_Transcript_1/1_Conf_1.000	159	0							
Locus_26204_Transcript_1/1_Conf_1.000	142	0							
Locus_26205_Transcript_1/1_Conf_1.000	194	0							
Locus_26206_Transcript_1/1_Conf_1.000	135	0							
Locus_26207_Transcript_1/1_Conf_1.000	137	0							
Locus_26208_Transcript_1/1_Conf_1.000	199	0							
Locus_26209_Transcript_1/1_Conf_1.000	142	0							
Locus_2621_Transcript_1/1_Conf_1.000	843	0							
Locus_26210_Transcript_1/1_Conf_1.000	170	0							
Locus_26211_Transcript_1/1_Conf_1.000	276	20	2.17E-33	CAR63560.1	84	145.206	91	77	hypothetical protein
Locus_26212_Transcript_1/1_Conf_1.000	273	20	3.13E-48	ADN38247.1	100	194.512	90	90	MHC class I antigen
Locus_26213_Transcript_1/1_Conf_1.000	155	0							

Locus_26214_Transcript_1/1_Conf_1.000	188	20	2.65E-18	XP_002632123.1	85	95.1301	62	53	C. briggsae CBR-CWN-1 protein
Locus_26215_Transcript_1/1_Conf_1.000	213	0							
Locus_26216_Transcript_1/1_Conf_1.000	334	0							
Locus_26217_Transcript_1/1_Conf_1.000	137	0							
Locus_26218_Transcript_1/1_Conf_1.000	269	0							
Locus_26219_Transcript_1/1_Conf_1.000	133	0							
Locus_2622_Transcript_1/2_Conf_1.000	1092	20	2.52E-67	XP_001895980.1	59	260.381	367	220	RNA pol II accessory factor, Cdc73 family protein
Locus_2622_Transcript_2/2_Conf_1.000	1092	20	2.52E-67	XP_001895980.1	59	260.381	367	220	RNA pol II accessory factor, Cdc73 family protein
Locus_26220_Transcript_1/1_Conf_1.000	193	20	4.63E-23	XP_001636325.1	93	110.923	63	59	predicted protein
Locus_26221_Transcript_1/1_Conf_1.000	389	20	3.13E-32	XP_001897373.1	65	141.354	135	89	B-box zinc finger family protein
Locus_26222_Transcript_1/1_Conf_1.000	271	20	1.42E-16	XP_002641225.1	80	89.3521	62	50	C. briggsae CBR-SMA-4 protein
Locus_26223_Transcript_1/1_Conf_1.000	148	0							
Locus_26224_Transcript_1/1_Conf_1.000	249	1	3.59E-04	CAD56659.1	55	48.1358	78	43	ancyclostoma-secreted protein-like protein

Locus_26225_Transcript_1/1_Conf_1.000	255	11	5.52E-08	NP_492051.1	65	60.8474	70	46	yeast BUB homolog family member (bub-1)
Locus_26226_Transcript_1/1_Conf_1.000	398	20	6.64E-46	ACQ44114.1	82	186.808	132	109	multidrug resistance-associated protein 2
Locus_26227_Transcript_1/1_Conf_1.000	180	16	2.59E-05	XP_002631000.1	53	51.9878	64	34	Hypothetical protein CBG02746
Locus_26228_Transcript_1/1_Conf_1.000	147	0							
Locus_26229_Transcript_1/1_Conf_1.000	142	0							
Locus_2623_Transcript_1/1_Conf_1.000	240	0							
Locus_26230_Transcript_1/1_Conf_1.000	144	0							
Locus_26231_Transcript_1/1_Conf_1.000	267	20	3.50E-31	XP_002632463.1	86	137.887	88	76	Hypothetical protein CBG13687
Locus_26232_Transcript_1/1_Conf_1.000	170	0							
Locus_26233_Transcript_1/1_Conf_1.000	272	7	3.07E-11	NP_001023197.1	61	71.633	86	53	hypothetical protein F38E11.6
Locus_26234_Transcript_1/1_Conf_1.000	235	0							
Locus_26235_Transcript_1/1_Conf_1.000	238	0							
Locus_26236_Transcript_1/1_Conf_1.000	241	0							
Locus_26237_Transcript_1/1_Conf_1.000	218	12	2.55E-26	AAV41897.1	84	121.709	72	61	SAX-2
Locus_26238_Transcript_1/1_Conf_1.000	145	0							
Locus_26239_Transcript_1/1_Conf_1.000	154	0							
Locus_2624_Transcript_1/1_Conf_1.000	361	20	2.85E-17	XP_002639922.1	65	91.6633	92	60	Hypothetical protein CBG08254
Locus_26240_Transcript_1/1_Conf_1.000	130	0							
Locus_26241_Transcript_1/1_Conf_1.000	238	2	2.52E-05	EFO27157.1	70	51.9878	50	35	hypothetical protein LOAG_01331
Locus_26242_Transcript_1/1_Conf_1.000	149	9	2.25E-09	NP_495746.1	72	65.4698	48	35	hypothetical protein K01C8.7
Locus_26243_Transcript_1/1_Conf_1.000	225	0							

Locus_26244_Transcript_1/1_Conf_1.000	200	20	1.39E-19	NP_491529.2	89	99.3673	64	57	hypothetical protein Y110A7A.6
Locus_26245_Transcript_1/1_Conf_1.000	180	20	6.56E-17	AAA18259.1	93	90.5077	47	44	protein kinase C
Locus_26246_Transcript_1/1_Conf_1.000	244	20	1.33E-06	NP_504102.2	62	56.225	72	45	CYtochrome P450 family member (cyp-34A8)
Locus_26247_Transcript_1/1_Conf_1.000	141	0							
Locus_26248_Transcript_1/1_Conf_1.000	138	0							
Locus_26249_Transcript_1/1_Conf_1.000	284	1	8.29E-04	XP_001898167.1	66	46.9802	42	28	hypothetical protein Bm1_33605
Locus_2625_Transcript_1/1_Conf_1.000	630	20	2.87E-106	NP_496787.1	94	388.267	209	197	hypothetical protein F29C12.4
Locus_26250_Transcript_1/1_Conf_1.000	170	20	6.37E-25	EDL19700.1	98	117.087	54	53	mCG129661, isoform CRA_d
Locus_26251_Transcript_1/1_Conf_1.000	153	0							
Locus_26252_Transcript_1/1_Conf_1.000	167	0							
Locus_26253_Transcript_1/1_Conf_1.000	161	0							

Locus_26254_Transcript_1/1_Conf_1.000	208	20	3.87E-06	XP_002643160.1	62	54.6842	72	45	Hypothetical protein CBG15341
Locus_26255_Transcript_1/1_Conf_1.000	205	20	5.42E-08	XP_001926555.1	66	60.8474	54	36	PREDICTED: similar to protein tyrosine phosphatase, non-receptor type 20
Locus_26256_Transcript_1/1_Conf_1.000	157	0							
Locus_26257_Transcript_1/1_Conf_1.000	165	0							
Locus_26258_Transcript_1/1_Conf_1.000	237	20	2.77E-28	XP_002634167.1	87	128.257	78	68	Hypothetical protein CBG01734
Locus_26259_Transcript_1/1_Conf_1.000	265	0							
Locus_2626_Transcript_1/2_Conf_0.600	1533	20	2.30E-78	XP_001899238.1	57	297.745	526	301	Low-density lipoprotein receptor repeat class B containing protein
Locus_2626_Transcript_2/2_Conf_0.400	1581	20	1.86E-115	XP_002640024.1	65	421.009	513	337	Hypothetical protein CBG12496
Locus_26260_Transcript_1/1_Conf_1.000	166	0							
Locus_26261_Transcript_1/1_Conf_1.000	197	20	2.01E-18	XP_002640668.1	95	95.5153	65	62	C. briggsae CBR-UNC-54 protein
Locus_26262_Transcript_1/1_Conf_1.000	243	0							
Locus_26263_Transcript_1/1_Conf_1.000	280	0							
Locus_26264_Transcript_1/1_Conf_1.000	128	0							
Locus_26265_Transcript_1/1_Conf_1.000	141	0							
Locus_26266_Transcript_1/1_Conf_1.000	185	0							

Locus_26267_Transcript_1/1_Conf_1.000	308	20	1.12E-13	XP_002642390.1	61	79.7221	97	60	Hypothetical protein CBG18394
Locus_26268_Transcript_1/1_Conf_1.000	255	9	8.18E-36	NP_496430.1	92	153.295	83	77	hypothetical protein C33B4.2
Locus_26269_Transcript_1/1_Conf_1.000	146	9	2.33E-14	NP_504648.1	81	82.0333	48	39	Carnitine Palmitoyl Transferase family member (cpt-6)
Locus_2627_Transcript_1/1_Conf_1.000	386	20	1.04E-67	XP_002640454.1	100	259.225	128	128	C. briggsae CBR-APS-3 protein
Locus_26270_Transcript_1/2_Conf_1.000	301	0							
Locus_26270_Transcript_2/2_Conf_1.000	346	0							
Locus_26271_Transcript_1/1_Conf_1.000	141	0							
Locus_26272_Transcript_1/1_Conf_1.000	136	7	1.42E-08	NP_872018.1	84	62.7734	38	32	Anion/Bicarbonate TranSporter family member (abts-3)
Locus_26273_Transcript_1/1_Conf_1.000	350	20	1.70E-17	EFO27552.1	56	92.4337	109	62	G-patch domain-containing protein
Locus_26274_Transcript_1/1_Conf_1.000	170	4	1.63E-12	XP_001140303.1	100	75.8702	46	46	PREDICTED: hypothetical protein
Locus_26275_Transcript_1/1_Conf_1.000	186	15	1.45E-16	XP_002811847.1	98	89.3521	61	60	PREDICTED: midkine-like
Locus_26276_Transcript_1/2_Conf_1.000	253	20	1.31E-25	NP_001023126.1	73	119.398	84	62	Cleavage and Polyadenylation Specificity Factor family member (cpsf-4)
Locus_26276_Transcript_2/2_Conf_1.000	259	20	2.22E-25	NP_001023126.1	72	118.627	86	62	Cleavage and Polyadenylation Specificity Factor family member (cpsf-4)
Locus_26277_Transcript_1/1_Conf_1.000	384	0							
Locus_26278_Transcript_1/1_Conf_1.000	124	0							
Locus_26279_Transcript_1/1_Conf_1.000	251	20	9.07E-32	XP_002644858.1	83	139.813	83	69	Hypothetical protein CBG05031
Locus_2628_Transcript_1/2_Conf_1.000	430	0							

Locus_2628_Transcript_2/2_Conf_1.000	436	0							
Locus_26280_Transcript_1/1_Conf_1.000	200	10	5.10E-14	NP_502380.1	86	80.8777	52	45	hypothetical protein C25G4.6
Locus_26281_Transcript_1/1_Conf_1.000	183	3	2.66E-10	XP_002638520.1	72	68.5514	59	43	C. briggsae CBR-LGC-2 protein
Locus_26282_Transcript_1/1_Conf_1.000	303	0							
Locus_26283_Transcript_1/1_Conf_1.000	187	0							
Locus_26284_Transcript_1/1_Conf_1.000	242	2	1.80E-11	XP_002641160.1	76	72.4034	50	38	Hypothetical protein CBG09017
Locus_26285_Transcript_1/1_Conf_1.000	192	0							
Locus_26286_Transcript_1/1_Conf_1.000	131	6	1.33E-14	BAD93059.1	100	82.8037	43	43	ADP,ATP carrier protein, liver isoform T2 variant
Locus_26287_Transcript_1/1_Conf_1.000	268	0							
Locus_26288_Transcript_1/1_Conf_1.000	211	0							
Locus_26289_Transcript_1/1_Conf_1.000	203	19	1.53E-10	AAN34967.1	66	69.3218	66	44	thioredoxin 2
Locus_2629_Transcript_1/1_Conf_1.000	283	2	8.27E-12	XP_002646505.1	66	73.559	81	54	Hypothetical protein CBG20338
Locus_26290_Transcript_1/1_Conf_1.000	200	0							
Locus_26291_Transcript_1/1_Conf_1.000	152	20	1.96E-13	ZP_02865662.1	77	78.9518	49	38	conserved hypothetical protein
Locus_26292_Transcript_1/1_Conf_1.000	193	0							
Locus_26293_Transcript_1/1_Conf_1.000	143	0							
Locus_26294_Transcript_1/1_Conf_1.000	181	20	3.47E-26	3O3T	100	121.324	60	60	CrystalStructure Analysis Of M32a Mutant Of Human Clic1

Locus_26295_Transcript_1/1_Conf_1.000	154	20	4.80E-20	XP_002920111.1	100	100.908	51	51	PREDICTED: amyloid beta A4 protein-like isoform 4
Locus_26296_Transcript_1/1_Conf_1.000	534	0							
Locus_26297_Transcript_1/1_Conf_1.000	319	20	1.44E-24	XP_970656.1	71	115.931	106	76	PREDICTED: similar to Histone deacetylase 11 (HD11)
Locus_26298_Transcript_1/1_Conf_1.000	146	0							
Locus_26299_Transcript_1/1_Conf_1.000	203	0							
Locus_263_Transcript_1/1_Conf_1.000	296	0							
Locus_2630_Transcript_1/1_Conf_1.000	1463	20	2.65E-44	XP_001897852.1	54	184.496	348	191	notch-like transmembrane receptor
Locus_26300_Transcript_1/1_Conf_1.000	130	20	5.78E-18	NP_497235.2	100	93.9745	43	43	G-protein-coupled Receptor Kinase family member (grk-2)
Locus_26301_Transcript_1/1_Conf_1.000	132	0							
Locus_26302_Transcript_1/1_Conf_1.000	133	0							
Locus_26303_Transcript_1/1_Conf_1.000	230	4	1.76E-14	NP_503353.2	70	82.4185	77	54	hypothetical protein H24K24.4
Locus_26304_Transcript_1/1_Conf_1.000	163	0							
Locus_26305_Transcript_1/1_Conf_1.000	189	20	2.39E-19	NP_001122539.1	87	98.5969	62	54	hypothetical protein Y47G6A.19
Locus_26306_Transcript_1/1_Conf_1.000	470	20	8.34E-41	XP_002642877.1	74	169.859	146	109	Hypothetical protein CBG15147
Locus_26307_Transcript_1/1_Conf_1.000	138	0							
Locus_26308_Transcript_1/1_Conf_1.000	190	1	1.15E-05	AAA68328.2	54	53.1434	62	34	Hypothetical protein F35D2.4

Locus_26309_Transcript_1/1_Conf_1.000	187	0							
Locus_2631_Transcript_1/2_Conf_1.000	856	0							
Locus_2631_Transcript_2/2_Conf_1.000	436	1	6.15E-04	ZP_05975603.1	48	47.3654	121	59	conserved hypothetical protein
Locus_26310_Transcript_1/1_Conf_1.000	355	5	1.57E-39	XP_002642902.1	81	165.622	116	94	Hypothetical protein CBG15176
Locus_26311_Transcript_1/1_Conf_1.000	164	0							
Locus_26312_Transcript_1/1_Conf_1.000	415	0							
Locus_26313_Transcript_1/1_Conf_1.000	558	1	1.10E-06	XP_001895331.1	43	56.9954	158	68	hypothetical protein Bm1_19380
Locus_26314_Transcript_1/1_Conf_1.000	188	3	1.31E-17	NP_504623.1	86	92.8189	60	52	hypothetical protein F13H6.5
Locus_26315_Transcript_1/1_Conf_1.000	139	0							
Locus_26316_Transcript_1/1_Conf_1.000	129	0							
Locus_26317_Transcript_1/1_Conf_1.000	167	0							
Locus_26318_Transcript_1/1_Conf_1.000	130	0							
Locus_26319_Transcript_1/1_Conf_1.000	146	0							
Locus_2632_Transcript_1/1_Conf_1.000	415	4	4.84E-17	XP_002645042.1	69	90.8929	106	74	C. briggsae CBR-ACL-12 protein
Locus_26320_Transcript_1/1_Conf_1.000	346	20	5.81E-50	EFO21680.1	92	200.29	115	106	hypothetical protein LOAG_06808
Locus_26321_Transcript_1/1_Conf_1.000	190	0							
Locus_26322_Transcript_1/1_Conf_1.000	199	6	1.64E-12	NP_491802.1	75	75.8702	66	50	hypothetical protein C48E7.6
Locus_26323_Transcript_1/1_Conf_1.000	253	20	2.92E-25	CAA21622.4	81	118.242	83	68	C. elegans protein Y43F8C.12, partially confirmed by transcript evidence
Locus_26324_Transcript_1/1_Conf_1.000	182	0							
Locus_26325_Transcript_1/1_Conf_1.000	179	11	1.23E-12	AAN11401.1	75	76.2554	57	43	metalloprotease 1 precursor
Locus_26326_Transcript_1/1_Conf_1.000	181	9	1.91E-16	NP_001020988.1	82	88.9669	57	47	UNCoordinated family member (unc-89)
Locus_26327_Transcript_1/1_Conf_1.000	155	12	2.09E-07	XP_001897657.1	70	58.9214	51	36	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase
Locus_26328_Transcript_1/1_Conf_1.000	412	0							
Locus_26329_Transcript_1/1_Conf_1.000	213	0							
Locus_2633_Transcript_1/1_Conf_1.000	398	20	5.58E-69	AAH51205.1	100	263.462	131	131	Rps15a protein
Locus_26330_Transcript_1/1_Conf_1.000	253	3	2.11E-07	XP_002638396.1	59	58.9214	84	50	Hypothetical protein CBG18605
Locus_26331_Transcript_1/1_Conf_1.000	144	0							
Locus_26332_Transcript_1/1_Conf_1.000	171	0							

Locus_26333_Transcript_1/1_Conf_1.000	150	20	4.36E-21	BAD96849.1	100	104.375	49	49	defender against cell death 1 variant
Locus_26334_Transcript_1/1_Conf_1.000	136	0							
Locus_26335_Transcript_1/1_Conf_1.000	505	20	3.09E-14	XP_783768.2	56	81.6481	161	91	PREDICTED: similar to Sec14l1 protein
Locus_26336_Transcript_1/1_Conf_1.000	145	8	2.66E-18	XP_002637345.1	97	95.1301	48	47	C. briggsae CBR-UNC-68 protein
Locus_26337_Transcript_1/1_Conf_1.000	155	0							
Locus_26338_Transcript_1/1_Conf_1.000	462	0							
Locus_26339_Transcript_1/1_Conf_1.000	224	2	4.09E-11	XP_002637395.1	68	71.2478	72	49	Hypothetical protein CBG19102
Locus_2634_Transcript_1/1_Conf_1.000	651	20	1.52E-60	EFO21579.1	86	236.498	189	164	RiNg Finger protein family member
Locus_26340_Transcript_1/1_Conf_1.000	255	14	2.82E-20	XP_002633446.1	74	101.679	87	65	Hypothetical protein CBG06214
Locus_26341_Transcript_1/1_Conf_1.000	133	0							
Locus_26342_Transcript_1/1_Conf_1.000	273	0							
Locus_26343_Transcript_1/1_Conf_1.000	203	1	3.65E-04	NP_001076618.1	70	48.1358	40	28	hypothetical protein Y110A7A.21
Locus_26344_Transcript_1/1_Conf_1.000	273	0							
Locus_26345_Transcript_1/1_Conf_1.000	238	0							
Locus_26346_Transcript_1/1_Conf_1.000	138	0							
Locus_26347_Transcript_1/1_Conf_1.000	334	0							
Locus_26348_Transcript_1/1_Conf_1.000	314	0							
Locus_26349_Transcript_1/1_Conf_1.000	446	20	2.00E-26	XP_001902022.1	65	122.094	148	97	hypothetical protein Bm1_52770
Locus_2635_Transcript_1/1_Conf_1.000	670	0							

Locus_26350_Transcript_1/1_Conf_1.000	151	20	6.09E-15	XP_510220.2	100	83.9593	50	50	PREDICTED: similar to Ig H-chain (C-D-JH4) precursor
Locus_26351_Transcript_1/1_Conf_1.000	149	0							
Locus_26352_Transcript_1/1_Conf_1.000	341	20	8.26E-09	EFO21921.1	50	63.5438	108	55	hypothetical protein LOAG_06561
Locus_26353_Transcript_1/1_Conf_1.000	214	2	4.39E-10	XP_002643263.1	80	67.781	71	57	Hypothetical protein CBG08133
Locus_26354_Transcript_1/1_Conf_1.000	166	0							
Locus_26355_Transcript_1/1_Conf_1.000	169	0							
Locus_26356_Transcript_1/1_Conf_1.000	240	20	8.92E-11	XP_002410853.1	63	70.0922	60	38	cysteine-rich secretory protein-buccal gland secretion, putative
Locus_26357_Transcript_1/1_Conf_1.000	157	0							
Locus_26358_Transcript_1/1_Conf_1.000	182	0							
Locus_26359_Transcript_1/1_Conf_1.000	196	0							
Locus_2636_Transcript_1/1_Conf_1.000	518	3	2.98E-23	ADI24662.1	65	111.694	155	101	Hypothetical protein Y110A2AL.12a
Locus_26360_Transcript_1/1_Conf_1.000	186	0							
Locus_26361_Transcript_1/1_Conf_1.000	135	0							
Locus_26362_Transcript_1/1_Conf_1.000	144	0							
Locus_26363_Transcript_1/1_Conf_1.000	228	0							
Locus_26364_Transcript_1/1_Conf_1.000	281	0							
Locus_26365_Transcript_1/1_Conf_1.000	256	16	5.52E-08	NP_510810.3	66	60.8474	56	37	PaTched Related family member (ptr-5)
Locus_26366_Transcript_1/1_Conf_1.000	150	20	1.23E-15	XP_002636676.1	87	86.2705	49	43	Hypothetical protein CBG23390
Locus_26367_Transcript_1/1_Conf_1.000	359	0							
Locus_26368_Transcript_1/1_Conf_1.000	227	2	4.49E-18	NP_499205.1	76	94.3597	72	55	hypothetical protein K03H1.5
Locus_26369_Transcript_1/1_Conf_1.000	215	0							
Locus_2637_Transcript_1/1_Conf_1.000	976	20	2.03E-62	XP_002631377.1	82	243.817	240	197	Hypothetical protein CBG03219
Locus_26370_Transcript_1/1_Conf_1.000	131	0							
Locus_26371_Transcript_1/1_Conf_1.000	153	0							
Locus_26372_Transcript_1/1_Conf_1.000	282	0							
Locus_26373_Transcript_1/1_Conf_1.000	154	0							
Locus_26374_Transcript_1/1_Conf_1.000	132	0							
Locus_26375_Transcript_1/1_Conf_1.000	133	0							
Locus_26376_Transcript_1/1_Conf_1.000	271	20	3.99E-35	XP_001892290.1	76	150.984	89	68	EGF-like domain containing protein
Locus_26377_Transcript_1/1_Conf_1.000	145	0							

Locus_26378_Transcript_1/1_Conf_1.000	241	20	1.42E-16	P41755.1	75	89.3521	81	61	NAD-specific glutamate dehydrogenase
Locus_26379_Transcript_1/1_Conf_1.000	187	0							
Locus_2638_Transcript_1/1_Conf_1.000	255	0							
Locus_26380_Transcript_1/1_Conf_1.000	162	0							
Locus_26381_Transcript_1/1_Conf_1.000	130	20	1.13E-13	NP_493247.2	88	79.7221	43	38	hypothetical protein Y18D10A.9
Locus_26382_Transcript_1/1_Conf_1.000	209	20	9.81E-26	EFO23768.1	86	119.783	68	59	hypothetical protein LOAG_04713
Locus_26383_Transcript_1/1_Conf_1.000	133	0							
Locus_26384_Transcript_1/1_Conf_1.000	124	0							
Locus_26385_Transcript_1/1_Conf_1.000	195	0							
Locus_26386_Transcript_1/1_Conf_1.000	139	20	1.12E-13	XP_001849399.1	86	79.7221	46	40	multidrug resistance protein 2
Locus_26387_Transcript_1/1_Conf_1.000	284	0							
Locus_26388_Transcript_1/1_Conf_1.000	204	3	2.28E-06	AAK84608.3	81	55.4546	65	53	AC024790_6Hypothetical protein Y47D7A.14a
Locus_26389_Transcript_1/1_Conf_1.000	357	20	1.73E-30	NP_500803.1	73	135.576	101	74	hypothetical protein ZK616.3
Locus_2639_Transcript_1/1_Conf_1.000	846	20	2.08E-86	XP_001894717.1	76	323.168	250	192	SPRY domain containing protein
Locus_26390_Transcript_1/1_Conf_1.000	162	20	2.52E-21	EFO15057.1	100	105.145	53	53	DNA polymerase epsilon catalytic subunit
Locus_26391_Transcript_1/1_Conf_1.000	129	0							

Locus_26392_Transcript_1/1_Conf_1.000	131	0							
Locus_26393_Transcript_1/1_Conf_1.000	268	20	3.99E-43	NP_001020988.1	97	177.563	88	86	UNCoordinated family member (unc-89)
Locus_26394_Transcript_1/1_Conf_1.000	159	0							
Locus_26395_Transcript_1/1_Conf_1.000	143	0							
Locus_26396_Transcript_1/1_Conf_1.000	175	3	6.36E-09	NP_741731.1	86	63.929	37	32	SERotonin/octopamine receptor family member (ser-7)
Locus_26397_Transcript_1/1_Conf_1.000	129	0							
Locus_26398_Transcript_1/1_Conf_1.000	157	20	3.32E-21	XP_002828837.1	100	104.76	52	52	PREDICTED: PDZ domain-containing protein GIPC1-like isoform 1
Locus_26399_Transcript_1/1_Conf_1.000	171	0							
Locus_264_Transcript_1/1_Conf_1.000	628	20	2.41E-89	XP_002630255.1	93	332.028	195	182	C. briggsae CBR-CCT-4 protein
Locus_2640_Transcript_1/1_Conf_1.000	541	20	5.62E-58	NP_501688.1	84	227.254	149	126	hypothetical protein C33A12.1

Locus_26400_Transcript_1/1_Conf_1.000	150	20	1.96E-13	ABB02455.1	93	78.9518	43	40	anti-anthrax monoclonal antibody A63-6
Locus_26401_Transcript_1/1_Conf_1.000	153	0							
Locus_26402_Transcript_1/1_Conf_1.000	152	0							
Locus_26403_Transcript_1/1_Conf_1.000	139	5	7.49E-10	CAA88959.2	84	67.0106	44	37	C. elegans protein M03C11.2, partially confirmed by transcript evidence
Locus_26404_Transcript_1/1_Conf_1.000	161	1	4.79E-04	NP_493077.1	65	47.7506	52	34	hypothetical protein R05D7.4
Locus_26405_Transcript_1/1_Conf_1.000	467	0							
Locus_26406_Transcript_1/1_Conf_1.000	170	0							
Locus_26407_Transcript_1/1_Conf_1.000	155	20	2.73E-07	XP_002933280.1	79	58.5362	49	39	PREDICTED: protein phosphatase 1L
Locus_26408_Transcript_1/1_Conf_1.000	283	20	3.80E-49	ACJ65168.1	100	197.593	94	94	Uncoordinated protein 68, isoform b, partially confirmed by transcript evidence
Locus_26409_Transcript_1/1_Conf_1.000	174	0							
Locus_2641_Transcript_1/1_Conf_1.000	1343	20	7.05E-73	XP_001894296.1	55	279.256	459	255	hypothetical protein
Locus_26410_Transcript_1/1_Conf_1.000	146	4	7.76E-10	NP_505445.2	76	67.0106	46	35	Nematode AStacin protease family member (nas-3)
Locus_26411_Transcript_1/1_Conf_1.000	289	20	4.48E-26	XP_002634104.1	76	120.939	91	70	Hypothetical protein CBG01656
Locus_26412_Transcript_1/1_Conf_1.000	352	20	1.62E-44	XP_002637101.1	84	182.185	116	98	Hypothetical protein CBG09600
Locus_26413_Transcript_1/1_Conf_1.000	130	0							
Locus_26414_Transcript_1/1_Conf_1.000	186	0							
Locus_26415_Transcript_1/1_Conf_1.000	249	0							
Locus_26416_Transcript_1/1_Conf_1.000	140	0							
Locus_26417_Transcript_1/1_Conf_1.000	167	0							
Locus_26418_Transcript_1/1_Conf_1.000	128	0							

Locus_26419_Transcript_1/1_Conf_1.000	225	0							
Locus_2642_Transcript_1/1_Conf_1.000	2537	20	0	NP_001041024.1	70	737.643	688	487	hypothetical protein Y41E3.1
Locus_26420_Transcript_1/1_Conf_1.000	155	0							
Locus_26421_Transcript_1/1_Conf_1.000	140	3	2.49E-05	NP_492193.2	71	51.9878	45	32	JunctoPHilin family member (jph-1)
Locus_26422_Transcript_1/1_Conf_1.000	144	20	3.98E-14	NP_507487.1	89	81.2629	48	43	P-GlycoProtein related family member (pgp-9)
Locus_26423_Transcript_1/1_Conf_1.000	401	20	1.34E-30	XP_002630350.1	70	135.961	137	96	Hypothetical protein CBG04280
Locus_26424_Transcript_1/1_Conf_1.000	145	0							
Locus_26425_Transcript_1/1_Conf_1.000	208	0							
Locus_26426_Transcript_1/1_Conf_1.000	175	0							
Locus_26427_Transcript_1/1_Conf_1.000	214	3	5.74E-10	NP_504373.2	65	67.3958	69	45	hypothetical protein F14F9.5
Locus_26428_Transcript_1/1_Conf_1.000	135	2	3.73E-09	NP_510616.2	75	64.6994	44	33	Multidrug Resistance Protein family member (mrp-3)
Locus_26429_Transcript_1/1_Conf_1.000	379	20	3.41E-18	XP_002630819.1	59	94.7449	125	74	Hypothetical protein CBG02521
Locus_2643_Transcript_1/1_Conf_1.000	569	20	1.63E-85	XP_001895824.1	92	318.931	189	174	SH2 domain containing protein
Locus_26430_Transcript_1/1_Conf_1.000	143	0							
Locus_26431_Transcript_1/1_Conf_1.000	147	20	3.70E-20	3N3G	100	101.293	48	48	4-(3-Trifluoromethylphenyl)-Pyrimidine-2-Carbonitrile As Cathepsin S Inhibitors: N3
Locus_26432_Transcript_1/1_Conf_1.000	216	0							
Locus_26433_Transcript_1/1_Conf_1.000	133	0							
Locus_26434_Transcript_1/1_Conf_1.000	333	20	2.95E-14	CBL43415.1	65	81.6481	81	53	C. elegans protein C32C4.2b, partially confirmed by transcript evidence
Locus_26435_Transcript_1/1_Conf_1.000	133	0							
Locus_26436_Transcript_1/1_Conf_1.000	195	4	1.03E-06	XP_002634339.1	63	56.6102	65	41	C. briggsae CBR-RIC-3 protein

Locus_26437_Transcript_1/1_Conf_1.000	373	20	1.02E-46	XP_002636748.1	87	189.504	124	109	Hypothetical protein CBG23475
Locus_26438_Transcript_1/1_Conf_1.000	184	20	3.71E-12	EFO26419.1	70	74.7146	55	39	hypothetical protein LOAG_02064
Locus_26439_Transcript_1/1_Conf_1.000	153	4	9.70E-13	NP_491050.3	87	76.6406	47	41	InTestinal Neurexin-like family member (itx-1)
Locus_2644_Transcript_1/1_Conf_1.000	1443	14	1.40E-05	XP_001478231.1	47	55.8398	193	92	PREDICTED: hypothetical protein
Locus_26440_Transcript_1/1_Conf_1.000	138	20	3.96E-19	XP_002810977.1	100	97.8265	45	45	PREDICTED: v-type proton ATPase 21 kDa proteolipid subunit-like
Locus_26441_Transcript_1/1_Conf_1.000	318	0							
Locus_26442_Transcript_1/1_Conf_1.000	284	20	2.47E-40	XP_002637017.1	89	168.318	94	84	Hypothetical protein CBG09510
Locus_26443_Transcript_1/1_Conf_1.000	168	1	4.75E-04	EFO23545.1	64	47.7506	48	31	hypothetical protein LOAG_04940
Locus_26444_Transcript_1/1_Conf_1.000	193	0							
Locus_26445_Transcript_1/1_Conf_1.000	176	0							
Locus_26446_Transcript_1/1_Conf_1.000	227	4	4.81E-12	XP_002636929.1	81	74.3294	75	61	Hypothetical protein CBG09397
Locus_26447_Transcript_1/1_Conf_1.000	130	20	3.17E-16	NP_500379.1	95	88.1965	43	41	hypothetical protein Y37E11B.5
Locus_26448_Transcript_1/1_Conf_1.000	144	0							
Locus_26449_Transcript_1/1_Conf_1.000	191	0							
Locus_2645_Transcript_1/1_Conf_1.000	288	0							
Locus_26450_Transcript_1/1_Conf_1.000	167	12	4.44E-18	ACI49219.1	87	94.3597	54	47	hypothetical protein Csp3_JD05.004
Locus_26451_Transcript_1/1_Conf_1.000	140	0							
Locus_26452_Transcript_1/1_Conf_1.000	130	20	6.61E-14	AAL14108.1	93	80.4925	43	40	GOP-1

Locus_26453_Transcript_1/1_Conf_1.000	208	20	5.05E-14	ACU83597.1	75	80.8777	66	50	poly-(ADP-ribose) polymerase I
Locus_26454_Transcript_1/1_Conf_1.000	137	1	5.58E-05	XP_001390210.1	75	50.8322	45	34	hypothetical protein An03g03270
Locus_26455_Transcript_1/1_Conf_1.000	370	0							
Locus_26456_Transcript_1/1_Conf_1.000	191	0							
Locus_26457_Transcript_1/1_Conf_1.000	279	0							
Locus_26458_Transcript_1/1_Conf_1.000	146	0							
Locus_26459_Transcript_1/1_Conf_1.000	143	0							
Locus_2646_Transcript_1/1_Conf_1.000	1574	20	1.20E-114	XP_002642100.1	70	418.313	422	298	Hypothetical protein CBG18041
Locus_26460_Transcript_1/1_Conf_1.000	181	4	3.15E-11	XP_002637396.1	79	71.633	63	50	Hypothetical protein CBG19103
Locus_26461_Transcript_1/1_Conf_1.000	241	0							
Locus_26462_Transcript_1/1_Conf_1.000	138	0							
Locus_26463_Transcript_1/1_Conf_1.000	151	0							
Locus_26464_Transcript_1/1_Conf_1.000	768								
Locus_26465_Transcript_1/1_Conf_1.000	200	12	1.76E-06	NP_498265.1	64	55.8398	56	36	hypothetical protein F01F1.9
Locus_26466_Transcript_1/1_Conf_1.000	137	0							
Locus_26467_Transcript_1/1_Conf_1.000	137	0							
Locus_26468_Transcript_1/1_Conf_1.000	129	0							
Locus_26469_Transcript_1/1_Conf_1.000	198	0							
Locus_2647_Transcript_1/1_Conf_1.000	265	8	5.46E-08	XP_002639256.1	79	60.8474	48	38	Hypothetical protein CBG03816
Locus_26470_Transcript_1/1_Conf_1.000	346	1	7.94E-07	EFO24319.1	52	56.9954	94	49	hypothetical protein LOAG_04165
Locus_26471_Transcript_1/1_Conf_1.000	163	20	1.94E-13	XP_001900186.1	79	78.9518	53	42	hypothetical protein
Locus_26472_Transcript_1/1_Conf_1.000	131	2	1.02E-06	XP_002643817.1	65	56.6102	46	30	Hypothetical protein CBG02032

Locus_26473_Transcript_1/1_Conf_1.000	388	20	3.13E-32	XP_002642446.1	76	141.354	130	99	Hypothetical protein CBG06851
Locus_26474_Transcript_1/1_Conf_1.000	219	12	3.04E-06	XP_002629716.1	56	55.0694	74	42	Hypothetical protein CBG00946
Locus_26475_Transcript_1/1_Conf_1.000	286	0							
Locus_26476_Transcript_1/1_Conf_1.000	211	3	2.96E-06	XP_002637522.1	81	55.0694	71	58	Hypothetical protein CBG19245
Locus_26477_Transcript_1/1_Conf_1.000	142	0							
Locus_26478_Transcript_1/1_Conf_1.000	209	0							
Locus_26479_Transcript_1/1_Conf_1.000	151	0							
Locus_2648_Transcript_1/1_Conf_1.000	156	2	7.93E-07	NP_498636.2	70	56.9954	51	36	hypothetical protein T20B12.1
Locus_26480_Transcript_1/1_Conf_1.000	324	6	1.69E-25	XP_002641872.1	63	119.013	122	78	C. briggsae CBR-LIM-8 protein
Locus_26481_Transcript_1/1_Conf_1.000	256	0							
Locus_26482_Transcript_1/1_Conf_1.000	154	0							
Locus_26483_Transcript_1/1_Conf_1.000	130	0							
Locus_26484_Transcript_1/1_Conf_1.000	389	20	3.47E-31	NP_491716.1	66	137.887	124	83	hypothetical protein B0207.7
Locus_26485_Transcript_1/1_Conf_1.000	160	0							
Locus_26486_Transcript_1/1_Conf_1.000	159	0							
Locus_26487_Transcript_1/1_Conf_1.000	347								
Locus_26488_Transcript_1/1_Conf_1.000	153	20	4.07E-19	YP_003433734.1	94	97.8265	51	48	ATP synthase F0 subunit 6
Locus_26489_Transcript_1/1_Conf_1.000	220	0							
Locus_2649_Transcript_1/1_Conf_1.000	310	0							
Locus_26490_Transcript_1/1_Conf_1.000	247	20	9.44E-21	XP_002646475.1	75	103.219	82	62	Hypothetical protein CBG19448
Locus_26491_Transcript_1/1_Conf_1.000	223	0							
Locus_26492_Transcript_1/1_Conf_1.000	175	0							
Locus_26493_Transcript_1/1_Conf_1.000	375	3	3.19E-24	XP_002642192.1	63	114.775	123	78	Hypothetical protein CBG18160
Locus_26494_Transcript_1/1_Conf_1.000	206	0							
Locus_26495_Transcript_1/1_Conf_1.000	260	20	1.49E-21	NP_502245.1	75	105.916	84	63	hypothetical protein F38H4.5
Locus_26496_Transcript_1/1_Conf_1.000	158	0							
Locus_26497_Transcript_1/1_Conf_1.000	134	0							
Locus_26498_Transcript_1/1_Conf_1.000	341	0							
Locus_26499_Transcript_1/1_Conf_1.000	281	0							

Locus_265_Transcript_1/1_Conf_1.000	1118	20	1.90E-118	NP_509362.1	85	430.254	301	258	Dauer or Aging adult Overexpression family member (dao-3)
Locus_2650_Transcript_1/1_Conf_1.000	592	20	4.52E-52	NP_001171651.1	100	207.994	102	102	glucose-6-phosphate isomerase isoform 1
Locus_26500_Transcript_1/1_Conf_1.000	147	1	4.53E-10	NP_497796.1	86	67.781	37	32	hypothetical protein F37A8.5
Locus_26501_Transcript_1/1_Conf_1.000	297	0							
Locus_26502_Transcript_1/1_Conf_1.000	237	0							
Locus_26503_Transcript_1/1_Conf_1.000	134	0							
Locus_26504_Transcript_1/1_Conf_1.000	159	0							
Locus_26505_Transcript_1/1_Conf_1.000	186	5	8.51E-17	NP_001122868.1	85	90.1225	61	52	GLIoTactin (Drosophila neuroligin-like) homolog family member (nrx-1)
Locus_26506_Transcript_1/1_Conf_1.000	170	0							
Locus_26507_Transcript_1/1_Conf_1.000	132	20	1.98E-10	EFO23808.1	86	68.9366	43	37	hypothetical protein LOAG_04674
Locus_26508_Transcript_1/1_Conf_1.000	143	0							
Locus_26509_Transcript_1/1_Conf_1.000	149	0							
Locus_2651_Transcript_1/2_Conf_1.000	1422	20	7.72E-25	XP_002641168.1	56	119.783	167	95	Hypothetical protein CBG09025
Locus_2651_Transcript_2/2_Conf_1.000	1251	20	2.31E-30	NP_498306.3	74	137.887	110	82	hypothetical protein T04C9.1
Locus_26510_Transcript_1/1_Conf_1.000	144	0							
Locus_26511_Transcript_1/1_Conf_1.000	134	17	7.04E-16	XP_521343.2	97	87.0409	44	43	PREDICTED: similar to L antigen family, member 3
Locus_26512_Transcript_1/1_Conf_1.000	158	0							
Locus_26513_Transcript_1/1_Conf_1.000	179	0							
Locus_26514_Transcript_1/1_Conf_1.000	140	6	1.20E-07	NP_001129925.1	79	59.6918	44	35	High Incidence of Males (increased X chromosome loss) family member (him-4)
Locus_26515_Transcript_1/1_Conf_1.000	168	0							
Locus_26516_Transcript_1/1_Conf_1.000	213	0							
Locus_26517_Transcript_1/1_Conf_1.000	219	20	3.03E-22	NP_505548.1	81	108.227	69	56	FSHR (mammalian follicle stimulating hormone receptor) homolog family member (fshr-1)
Locus_26518_Transcript_1/1_Conf_1.000	145	0							

Locus_26519_Transcript_1/1_Conf_1.000	165	0							
Locus_2652_Transcript_1/1_Conf_1.000	759	0							
Locus_26520_Transcript_1/1_Conf_1.000	133	0							
Locus_26521_Transcript_1/1_Conf_1.000	361	8	2.85E-25	XP_002640492.1	71	118.242	119	85	Hypothetical protein CBG13628
Locus_26522_Transcript_1/1_Conf_1.000	159	0							
Locus_26523_Transcript_1/1_Conf_1.000	239	0							
Locus_26524_Transcript_1/1_Conf_1.000	325	20	1.17E-34	XP_002636068.1	78	149.443	107	84	Hypothetical protein CBG01308
Locus_26525_Transcript_1/1_Conf_1.000	261	0							
Locus_26526_Transcript_1/1_Conf_1.000	358	3	5.93E-39	XP_001900400.1	79	163.696	120	95	Zinc finger, C2H2 type family protein
Locus_26527_Transcript_1/1_Conf_1.000	197	20	6.46E-17	EFO26573.1	79	90.5077	64	51	O-glycosyl hydrolase family 30 protein
Locus_26528_Transcript_1/1_Conf_1.000	185	0							
Locus_26529_Transcript_1/1_Conf_1.000	364	0							
Locus_2653_Transcript_1/1_Conf_1.000	865	20	3.79E-115	XP_002646059.1	91	418.698	289	263	C. briggsae CBR-PMR-1 protein
Locus_26530_Transcript_1/1_Conf_1.000	171	20	5.95E-23	AAY14814.1	96	110.538	56	54	unknown
Locus_26531_Transcript_1/1_Conf_1.000	181	0							

Locus_26532_Transcript_1/1_Conf_1.000	253	20	1.27E-12	EDM01692.1	78	76.2554	56	44	cold shock domain protein A, isoform CRA_a
Locus_26533_Transcript_1/1_Conf_1.000	135	20	1.41E-16	XP_002916718.1	100	89.3521	44	44	PREDICTED: stress-induced-phosphoprotein 1-like
Locus_26534_Transcript_1/1_Conf_1.000	133	2	6.18E-04	XP_002629723.1	80	47.3654	40	32	C. briggsae CBR-UGT-58 protein
Locus_26535_Transcript_1/1_Conf_1.000	141	4	1.41E-08	XP_002637554.1	73	62.7734	46	34	Hypothetical protein CBG19286
Locus_26536_Transcript_1/1_Conf_1.000	188	20	1.90E-08	NP_001022736.1	71	62.3882	46	33	hypothetical protein R155.1
Locus_26537_Transcript_1/1_Conf_1.000	184	8	6.34E-12	ABC69942.1	71	73.9442	60	43	STIP
Locus_26538_Transcript_1/1_Conf_1.000	427	20	4.02E-19	XP_002637195.1	72	97.8265	87	63	C. briggsae CBR-LIG-1 protein
Locus_26539_Transcript_1/1_Conf_1.000	150	2	3.24E-08	XP_002634886.1	79	61.6178	48	38	Hypothetical protein CBG10557
Locus_2654_Transcript_1/1_Conf_1.000	1199	20	1.10E-159	XP_002633720.1	84	567.385	376	316	C. briggsae CBR-PPS-1 protein
Locus_26540_Transcript_1/1_Conf_1.000	213	0							
Locus_26541_Transcript_1/1_Conf_1.000	140	0							
Locus_26542_Transcript_1/1_Conf_1.000	134	0							
Locus_26543_Transcript_1/1_Conf_1.000	183	0							

Locus_26544_Transcript_1/1_Conf_1.000	267	1	2.99E-06	NP_508765.1	69	55.0694	56	39	hypothetical protein F25F6.1
Locus_26545_Transcript_1/1_Conf_1.000	197	0							
Locus_26546_Transcript_1/1_Conf_1.000	184	0							
Locus_26547_Transcript_1/1_Conf_1.000	325	20	2.07E-15	XP_002644902.1	62	85.5001	93	58	Hypothetical protein CBG10839
Locus_26548_Transcript_1/1_Conf_1.000	177	0							
Locus_26549_Transcript_1/1_Conf_1.000	148	0							
Locus_2655_Transcript_1/2_Conf_1.000	1256	20	1.02E-70	NP_001033411.1	78	271.937	277	217	hypothetical protein F53H1.1
Locus_2655_Transcript_2/2_Conf_1.000	1186	20	9.43E-71	NP_001033411.1	78	271.937	277	217	hypothetical protein F53H1.1
Locus_26550_Transcript_1/1_Conf_1.000	208	2	3.06E-11	NP_492839.4	73	71.633	71	52	Leucine-rich repeats, Ras-like domain, Kinase family member (lrk-1)
Locus_26551_Transcript_1/1_Conf_1.000	140	0							
Locus_26552_Transcript_1/1_Conf_1.000	220	2	1.19E-10	XP_002642371.1	72	69.707	68	49	Hypothetical protein CBG18375
Locus_26553_Transcript_1/1_Conf_1.000	178	0							
Locus_26554_Transcript_1/1_Conf_1.000	165	0							
Locus_26555_Transcript_1/1_Conf_1.000	454	18	2.49E-29	NP_490848.2	62	131.724	157	98	hypothetical protein Y92H12BR.7
Locus_26556_Transcript_1/1_Conf_1.000	131	0							
Locus_26557_Transcript_1/1_Conf_1.000	138	0							
Locus_26558_Transcript_1/1_Conf_1.000	367	0							
Locus_26559_Transcript_1/1_Conf_1.000	178	0							
Locus_2656_Transcript_1/4_Conf_0.625	1790	20	3.93E-157	AAO62949.1	69	559.681	551	384	neuronal acetylcholinesterase precursor
Locus_2656_Transcript_2/4_Conf_0.625	1819	20	5.25E-157	AAO62949.1	69	559.296	558	386	neuronal acetylcholinesterase precursor
Locus_2656_Transcript_3/4_Conf_0.625	1801	20	1.23E-158	AAO62949.1	70	564.688	551	386	neuronal acetylcholinesterase precursor
Locus_2656_Transcript_4/4_Conf_0.625	1801	20	6.77E-157	AAO62949.1	69	558.91	551	383	neuronal acetylcholinesterase precursor
Locus_26560_Transcript_1/1_Conf_1.000	244	20	2.49E-29	NP_001021650.1	85	131.724	81	69	HaMmeRhead embryonic lethal family member (hmr-1)
Locus_26561_Transcript_1/1_Conf_1.000	134	1	1.57E-07	XP_853076.1	94	59.3066	34	32	PREDICTED: similar to Actin-related protein 2/3 complex subunit 1B (ARP2/3 complex 41 kDa subunit) (p41-ARC)

Locus_26562_Transcript_1/1_Conf_1.000	145	0							
Locus_26563_Transcript_1/1_Conf_1.000	259	0							
Locus_26564_Transcript_1/1_Conf_1.000	294	20	8.40E-25	EFO22954.1	100	116.701	57	57	Mef2c protein
Locus_26565_Transcript_1/1_Conf_1.000	178	0							
Locus_26566_Transcript_1/1_Conf_1.000	130	0							
Locus_26567_Transcript_1/1_Conf_1.000	179	0							
Locus_26568_Transcript_1/1_Conf_1.000	216	20	3.69E-25	NP_001024175.1	90	117.857	70	63	UNCoordinated family member (unc-62)
Locus_26569_Transcript_1/1_Conf_1.000	131	0							
Locus_2657_Transcript_1/1_Conf_1.000	501	20	3.21E-32	XP_002644479.1	72	141.354	165	119	C. briggsae CBR-MRP-6 protein
Locus_26570_Transcript_1/1_Conf_1.000	155	0							
Locus_26571_Transcript_1/1_Conf_1.000	129	0							
Locus_26572_Transcript_1/1_Conf_1.000	383	0							
Locus_26573_Transcript_1/1_Conf_1.000	355	0							
Locus_26574_Transcript_1/1_Conf_1.000	161	0							

Locus_26575_Transcript_1/1_Conf_1.000	166	20	1.02E-14	XP_002640693.1	85	83.1889	54	46	Hypothetical protein CBG19758
Locus_26576_Transcript_1/1_Conf_1.000	181	20	3.86E-09	EFO26660.1	78	64.6994	47	37	ELC-1 protein
Locus_26577_Transcript_1/1_Conf_1.000	171	0							
Locus_26578_Transcript_1/1_Conf_1.000	197	0							
Locus_26579_Transcript_1/1_Conf_1.000	301	0							
Locus_2658_Transcript_1/2_Conf_1.000	551	20	1.16E-45	NP_504455.1	72	186.422	179	129	Nuclear Hormone Receptor family member (nhr-47)
Locus_2658_Transcript_2/2_Conf_1.000	543	20	1.09E-24	NP_504455.1	88	116.701	60	53	Nuclear Hormone Receptor family member (nhr-47)
Locus_26580_Transcript_1/1_Conf_1.000	174	0							
Locus_26581_Transcript_1/1_Conf_1.000	135	0							
Locus_26582_Transcript_1/1_Conf_1.000	235	0							
Locus_26583_Transcript_1/1_Conf_1.000	308	0							
Locus_26584_Transcript_1/1_Conf_1.000	147	0							
Locus_26585_Transcript_1/1_Conf_1.000	164	0							
Locus_26586_Transcript_1/1_Conf_1.000	138	0							
Locus_26587_Transcript_1/1_Conf_1.000	149	20	4.38E-13	NP_494777.1	87	77.7962	49	43	MoLTing defective family member (mlt-7)
Locus_26588_Transcript_1/1_Conf_1.000	764	20	7.78E-31	NP_508889.1	57	138.272	184	105	hypothetical protein Y34B4A.7
Locus_26589_Transcript_1/1_Conf_1.000	182	0							

Locus_2659_Transcript_1/1_Conf_1.000	666	20	5.40E-93	XP_001897209.1	87	344.354	220	192	adaptor-related protein complex 2, beta 1 subunit
Locus_26590_Transcript_1/1_Conf_1.000	173	0							
Locus_26591_Transcript_1/1_Conf_1.000	172	20	9.80E-26	3F8U	100	119.783	57	57	TapasinERP57 HETERODIMER
Locus_26592_Transcript_1/1_Conf_1.000	242	5	1.24E-20	NP_001024499.1	75	102.834	77	58	Calcium Channel, Alpha subunit family member (cca-1)
Locus_26593_Transcript_1/1_Conf_1.000	128	0							
Locus_26594_Transcript_1/1_Conf_1.000	265	0							
Locus_26595_Transcript_1/1_Conf_1.000	197	0							
Locus_26596_Transcript_1/1_Conf_1.000	243	20	2.33E-19	XP_002635088.1	70	98.5969	81	57	C. briggsae CBR-ASP-6 protein
Locus_26597_Transcript_1/1_Conf_1.000	207	0							
Locus_26598_Transcript_1/1_Conf_1.000	231	0							
Locus_26599_Transcript_1/1_Conf_1.000	154	0							
Locus_266_Transcript_1/5_Conf_0.500	1644	20	1.79E-100	XP_002640720.1	53	371.318	579	310	C. briggsae CBR-TAG-301 protein
Locus_266_Transcript_2/5_Conf_0.600	2140	20	2.48E-100	XP_002640720.1	53	371.318	579	310	C. briggsae CBR-TAG-301 protein
Locus_266_Transcript_3/5_Conf_0.600	2136	20	2.47E-100	XP_002640720.1	53	371.318	579	310	C. briggsae CBR-TAG-301 protein

Locus_266_Transcript_4/5_Conf_0.200	620	20	6.30E-34	XP_002640720.1	72	147.902	127	92	C. briggsae CBR-TAG-301 protein
Locus_266_Transcript_5/5_Conf_0.600	2140	20	2.48E-100	XP_002640720.1	53	371.318	579	310	C. briggsae CBR-TAG-301 protein
Locus_2660_Transcript_1/1_Conf_1.000	457	0							
Locus_26600_Transcript_1/1_Conf_1.000	157	0							
Locus_26601_Transcript_1/1_Conf_1.000	141	0							
Locus_26602_Transcript_1/1_Conf_1.000	167	0							
Locus_26603_Transcript_1/1_Conf_1.000	139	20	2.41E-08	CAR94311.1	80	62.003	45	36	CG3603-PA
Locus_26604_Transcript_1/1_Conf_1.000	211	20	4.71E-12	XP_002647146.1	75	74.3294	62	47	Hypothetical protein CBG16450
Locus_26605_Transcript_1/1_Conf_1.000	215	20	5.90E-31	CAX51641.1	98	137.117	71	70	C. elegans protein F11E6.8b, partially confirmed by transcript evidence
Locus_26606_Transcript_1/1_Conf_1.000	157	0							
Locus_26607_Transcript_1/1_Conf_1.000	133	0							
Locus_26608_Transcript_1/1_Conf_1.000	200	20	9.62E-13	NP_493608.2	85	76.6406	48	41	hypothetical protein ZK909.3

Locus_26609_Transcript_1/1_Conf_1.000	208	0							
Locus_2661_Transcript_1/1_Conf_1.000	1657	20	1.34E-95	XP_001899995.1	91	355.14	212	195	fizzy-related protein
Locus_26610_Transcript_1/1_Conf_1.000	181	9	1.52E-05	XP_001197720.1	57	52.7582	57	33	PREDICTED: similar to mannose receptor, C type 1-like 1
Locus_26611_Transcript_1/1_Conf_1.000	208	0							
Locus_26612_Transcript_1/1_Conf_1.000	176	2	9.19E-08	NP_496234.3	78	60.077	42	33	hypothetical protein C07E3.6
Locus_26613_Transcript_1/1_Conf_1.000	222	0							
Locus_26614_Transcript_1/2_Conf_1.000	264	20	2.22E-09	XP_002809164.1	100	65.4698	54	54	PREDICTED: HLA class II histocompatibility antigen, DQ alpha 1 chain-like
Locus_26614_Transcript_2/2_Conf_1.000	290	20	2.24E-09	XP_002809164.1	100	65.4698	54	54	PREDICTED: HLA class II histocompatibility antigen, DQ alpha 1 chain-like
Locus_26615_Transcript_1/1_Conf_1.000	318	0							
Locus_26616_Transcript_1/1_Conf_1.000	220	0							
Locus_26617_Transcript_1/1_Conf_1.000	167	0							
Locus_26618_Transcript_1/1_Conf_1.000	208	0							
Locus_26619_Transcript_1/1_Conf_1.000	282	2	3.60E-07	NP_496803.1	66	58.151	66	44	hypothetical protein F15D4.2
Locus_2662_Transcript_1/1_Conf_1.000	1548	20	0	NP_497939.2	81	761.525	516	422	Suppressor/Enhancer of Lin-12 family member (sel-2)
Locus_26620_Transcript_1/1_Conf_1.000	138	0							

Locus_26621_Transcript_1/1_Conf_1.000	215	20	6.52E-30	NP_492438.1	92	133.65	71	66	RADiation sensitivity abnormal/yeast RAD-related family member (rad-54)
Locus_26622_Transcript_1/1_Conf_1.000	222	0							
Locus_26623_Transcript_1/1_Conf_1.000	165	3	5.44E-08	NP_872190.1	69	60.8474	53	37	hypothetical protein C37C3.12
Locus_26624_Transcript_1/1_Conf_1.000	232	20	3.89E-30	XP_002633760.1	82	134.42	76	63	C. briggsae CBR-GON-1 protein
Locus_26625_Transcript_1/1_Conf_1.000	133	0							
Locus_26626_Transcript_1/1_Conf_1.000	146	20	3.98E-14	Q5RD44.2	100	81.2629	37	37	Anion exchange protein 2
Locus_26627_Transcript_1/1_Conf_1.000	133	0							
Locus_26628_Transcript_1/1_Conf_1.000	185	1	8.86E-06	XP_002645934.1	55	53.5286	58	32	Hypothetical protein CBG07699
Locus_26629_Transcript_1/1_Conf_1.000	159	0							
Locus_2663_Transcript_1/1_Conf_1.000	693	20	2.90E-31	NP_500617.1	83	139.428	87	73	hypothetical protein T22B11.5

Locus_26630_Transcript_1/1_Conf_1.000	151	20	1.66E-12	XP_001901686.1	87	75.8702	47	41	Cohesin subunit SA-1
Locus_26631_Transcript_1/1_Conf_1.000	259	2	2.72E-23	NP_001022254.1	74	111.694	77	57	hypothetical protein M05D6.9
Locus_26632_Transcript_1/1_Conf_1.000	395	20	2.78E-68	XP_002637927.1	97	261.151	131	128	Hypothetical protein CBG04739
Locus_26633_Transcript_1/1_Conf_1.000	141	0							
Locus_26634_Transcript_1/1_Conf_1.000	163	0							
Locus_26635_Transcript_1/1_Conf_1.000	191	8	2.39E-19	NP_493603.1	88	98.5969	59	52	PaTched Related family member (ptr-23)
Locus_26636_Transcript_1/1_Conf_1.000	178	0							

Locus_26637_Transcript_1/1_Conf_1.000	184	20	4.68E-23	XP_002931287.1	98	110.923	60	59	PREDICTED: filamin-A-like, partial
Locus_26638_Transcript_1/1_Conf_1.000	219	20	7.24E-08	EFO19578.1	63	60.4622	72	46	hypothetical protein LOAG_08912
Locus_26639_Transcript_1/1_Conf_1.000	259	20	1.14E-37	EFO21255.1	94	159.458	85	80	hypothetical protein LOAG_07233
Locus_2664_Transcript_1/1_Conf_1.000	813	20	2.61E-75	NP_496593.1	91	286.189	182	167	hypothetical protein Y57A10A.16
Locus_26640_Transcript_1/1_Conf_1.000	288	20	8.99E-43	XP_002753346.1	98	176.407	89	88	PREDICTED: pyruvate kinase isozymes M1/M2-like isoform 1
Locus_26641_Transcript_1/1_Conf_1.000	166	2	7.59E-10	NP_499157.2	84	67.0106	44	37	hypothetical protein T05G5.8
Locus_26642_Transcript_1/1_Conf_1.000	255	20	2.24E-09	XP_002634553.1	70	65.4698	82	58	Hypothetical protein CBG08354
Locus_26643_Transcript_1/1_Conf_1.000	200	0							
Locus_26644_Transcript_1/1_Conf_1.000	190	0							
Locus_26645_Transcript_1/1_Conf_1.000	334	0							
Locus_26646_Transcript_1/1_Conf_1.000	179	0							
Locus_26647_Transcript_1/1_Conf_1.000	186	0							

Locus_26648_Transcript_1/1_Conf_1.000	289	7	2.64E-10	NP_498653.2	54	68.5514	109	59	LIGase family member (lig-4)
Locus_26649_Transcript_1/1_Conf_1.000	186	3	1.46E-08	NP_495925.1	61	62.7734	65	40	hypothetical protein F44G4.8
Locus_2665_Transcript_1/1_Conf_1.000	733	20	2.71E-70	XP_002644989.1	72	269.24	232	168	Hypothetical protein CBG10971
Locus_26650_Transcript_1/1_Conf_1.000	149	0							
Locus_26651_Transcript_1/1_Conf_1.000	237	0							
Locus_26652_Transcript_1/1_Conf_1.000	446	20	5.62E-37	NP_506406.1	74	157.147	148	110	hypothetical protein F20G2.1
Locus_26653_Transcript_1/1_Conf_1.000	181	8	5.76E-05	XP_002585537.1	70	50.8322	60	42	hypothetical protein BRAFLDRAFT_111890
Locus_26654_Transcript_1/1_Conf_1.000	247	20	7.23E-21	XP_002631425.1	83	103.605	68	57	Hypothetical protein CBG03281
Locus_26655_Transcript_1/1_Conf_1.000	306	0							
Locus_26656_Transcript_1/1_Conf_1.000	173	0							
Locus_26657_Transcript_1/1_Conf_1.000	269	20	2.79E-12	NP_490693.2	55	75.0998	89	49	ATM (ataxia telangectasia mutated) family member (atm-1)
Locus_26658_Transcript_1/1_Conf_1.000	225	0							
Locus_26659_Transcript_1/1_Conf_1.000	162	0							
Locus_2666_Transcript_1/1_Conf_1.000	323	20	2.29E-30	NP_001023663.1	79	135.191	107	85	Kinesin Light Chain family member (klc-2)
Locus_26660_Transcript_1/1_Conf_1.000	236	0							
Locus_26661_Transcript_1/1_Conf_1.000	281	0							
Locus_26662_Transcript_1/1_Conf_1.000	345	4	1.14E-13	NP_509618.1	92	79.7221	40	37	hypothetical protein C11E4.4
Locus_26663_Transcript_1/1_Conf_1.000	154	0							
Locus_26664_Transcript_1/1_Conf_1.000	158	0							
Locus_26665_Transcript_1/1_Conf_1.000	391	0							

Locus_26666_Transcript_1/1_Conf_1.000	237	0							
Locus_26667_Transcript_1/1_Conf_1.000	144	20	5.02E-17	NP_492907.2	93	90.8929	44	41	Cyclin-Dependent Kinase family member (cdk-9)
Locus_26668_Transcript_1/1_Conf_1.000	307	0							
Locus_26669_Transcript_1/1_Conf_1.000	213	0							
Locus_2667_Transcript_1/1_Conf_1.000	325	0							
Locus_26670_Transcript_1/1_Conf_1.000	267	0							
Locus_26671_Transcript_1/1_Conf_1.000	202	0							
Locus_26672_Transcript_1/1_Conf_1.000	141	0							
Locus_26673_Transcript_1/1_Conf_1.000	134	0							
Locus_26674_Transcript_1/1_Conf_1.000	142	3	1.01E-14	AAM82167.1	87	83.1889	47	41	gamma-butyrobetaine,2-oxoglutarate dioxygenase
Locus_26675_Transcript_1/1_Conf_1.000	267	20	8.32E-41	XP_002644403.1	97	169.859	88	86	Hypothetical protein CBG14248
Locus_26676_Transcript_1/1_Conf_1.000	161	1	2.54E-05	EFO23475.1	68	51.9878	51	35	hypothetical protein LOAG_05011
Locus_26677_Transcript_1/1_Conf_1.000	216	20	1.72E-06	XP_002641616.1	75	55.8398	48	36	C. briggsae CBR-ALX-1 protein
Locus_26678_Transcript_1/1_Conf_1.000	129	4	6.84E-11	XP_002632353.1	88	70.4774	43	38	Hypothetical protein CBG00367
Locus_26679_Transcript_1/1_Conf_1.000	178	0							
Locus_2668_Transcript_1/1_Conf_1.000	523	20	3.54E-43	NP_491888.2	86	177.948	172	149	hypothetical protein F57B10.9
Locus_26680_Transcript_1/1_Conf_1.000	328	1	2.14E-04	EFO17852.1	70	48.9062	37	26	ACL-8 protein
Locus_26681_Transcript_1/1_Conf_1.000	138	2	1.37E-11	NP_491291.3	80	72.7886	47	38	C-type LECtin family member (clec-89)
Locus_26682_Transcript_1/1_Conf_1.000	221	3	1.05E-06	NP_501320.2	61	56.6102	73	45	eXPOrtin (nuclear export receptor) family member (xpo-3)
Locus_26683_Transcript_1/1_Conf_1.000	200	20	4.94E-09	ADD13547.1	79	64.3142	58	46	Inositol triphosphate receptor protein 1, isoform h
Locus_26684_Transcript_1/1_Conf_1.000	132	0							
Locus_26685_Transcript_1/1_Conf_1.000	132	0							

Locus_26686_Transcript_1/1_Conf_1.000	323	20	1.03E-06	NP_508806.1	55	56.6102	87	48	DNaJ domain (prokaryotic heat shock protein) family member (dnj-14)
Locus_26687_Transcript_1/1_Conf_1.000	280	20	9.14E-16	XP_002190367.1	66	86.6557	95	63	PREDICTED: similar to ATP-binding cassette transporter
Locus_26688_Transcript_1/1_Conf_1.000	165	0							
Locus_26689_Transcript_1/1_Conf_1.000	202	0							
Locus_2669_Transcript_1/2_Conf_1.000	479	4	1.51E-18	NP_503408.1	65	95.9005	101	66	hypothetical protein Y75B7AR.1
Locus_2669_Transcript_2/2_Conf_1.000	479	4	1.51E-18	NP_503408.1	65	95.9005	101	66	hypothetical protein Y75B7AR.1
Locus_26690_Transcript_1/1_Conf_1.000	288	20	1.44E-24	NP_496170.1	80	115.931	87	70	LEThal family member (let-268)
Locus_26691_Transcript_1/1_Conf_1.000	268	20	1.68E-41	ADN33424.1	100	172.17	88	88	ACR-17-like protein
Locus_26692_Transcript_1/1_Conf_1.000	220	0							
Locus_26693_Transcript_1/1_Conf_1.000	300	0							
Locus_26694_Transcript_1/1_Conf_1.000	190	2	1.96E-05	CBA11992.1	64	52.373	45	29	endonuclease-reverse transcriptase HmRTE-e01
Locus_26695_Transcript_1/1_Conf_1.000	171	0							
Locus_26696_Transcript_1/1_Conf_1.000	134	0							
Locus_26697_Transcript_1/1_Conf_1.000	257	5	5.34E-11	CBX25206.1	77	70.8626	57	44	Hypothetical protein Y17G7B.6c
Locus_26698_Transcript_1/1_Conf_1.000	146	0							
Locus_26699_Transcript_1/1_Conf_1.000	175	0							
Locus_267_Transcript_1/1_Conf_1.000	2400	20	0	NP_508537.1	92	1337.01	769	714	SPeCtrin family member (spc-1)
Locus_2670_Transcript_1/1_Conf_1.000	394	20	5.48E-32	XP_002646170.1	68	140.584	131	90	C. briggsae CBR-TAF-5 protein
Locus_26700_Transcript_1/1_Conf_1.000	278	3	7.04E-08	NP_001123075.1	57	60.4622	100	57	hypothetical protein ZC455.1

Locus_26701_Transcript_1/1_Conf_1.000	190	2	1.15E-05	NP_505506.2	73	53.1434	63	46	hypothetical protein F40F9.5
Locus_26702_Transcript_1/1_Conf_1.000	129	0							
Locus_26703_Transcript_1/1_Conf_1.000	149	0							
Locus_26704_Transcript_1/1_Conf_1.000	137	20	1.85E-08	CBN79579.1	83	62.3882	43	36	conserved unknown protein
Locus_26705_Transcript_1/1_Conf_1.000	140	0							
Locus_26706_Transcript_1/1_Conf_1.000	259	0							
Locus_26707_Transcript_1/1_Conf_1.000	350	20	8.95E-43	NP_509839.1	86	176.407	115	100	TransThyretin-Related family domain family member (ttr-31)
Locus_26708_Transcript_1/1_Conf_1.000	150	20	2.39E-19	3GQY	100	98.5969	49	49	Activator-BoundStructure Of Human Pyruvate Kinase M2
Locus_26709_Transcript_1/1_Conf_1.000	167	0							
Locus_2671_Transcript_1/1_Conf_1.000	377	20	8.42E-17	XP_002632730.1	67	90.1225	84	57	C. briggsae CBR-LST-3 protein
Locus_26710_Transcript_1/1_Conf_1.000	182	0							
Locus_26711_Transcript_1/1_Conf_1.000	230	20	1.17E-34	NP_509311.1	97	149.443	75	73	DEGeneration of certain neurons family member (deg-1)
Locus_26712_Transcript_1/1_Conf_1.000	230	20	1.93E-37	DAA27776.1	100	158.688	76	76	amino-terminal enhancer of split
Locus_26713_Transcript_1/1_Conf_1.000	348	0							
Locus_26714_Transcript_1/1_Conf_1.000	129	0							
Locus_26715_Transcript_1/1_Conf_1.000	189	7	1.27E-12	EFO19841.1	77	76.2554	62	48	hypothetical protein LOAG_08651
Locus_26716_Transcript_1/1_Conf_1.000	170	0							
Locus_26717_Transcript_1/1_Conf_1.000	163	2	4.18E-08	NP_508379.1	75	61.2326	56	42	ACyLtransferase-like family member (acl-4)
Locus_26718_Transcript_1/1_Conf_1.000	134	20	7.52E-18	NP_741763.1	97	93.5893	44	43	Homeodomain interacting Protein Kinase family member (hpk-1)
Locus_26719_Transcript_1/1_Conf_1.000	153	2	4.36E-05	NP_001123088.1	80	51.2174	50	40	hypothetical protein B0310.1

Locus_2672_Transcript_1/1_Conf_1.000	1215	20	3.54E-129	XP_002639872.1	84	466.077	311	262	Hypothetical protein CBG12227
Locus_26720_Transcript_1/1_Conf_1.000	134	0							
Locus_26721_Transcript_1/1_Conf_1.000	152	0							
Locus_26722_Transcript_1/1_Conf_1.000	140	0							
Locus_26723_Transcript_1/1_Conf_1.000	128	0							
Locus_26724_Transcript_1/1_Conf_1.000	212	17	1.16E-18	XP_002633939.1	77	96.2857	70	54	Hypothetical protein CBG20014
Locus_26725_Transcript_1/1_Conf_1.000	327	20	4.00E-27	XP_002631190.1	76	124.405	104	80	Hypothetical protein CBG02979
Locus_26726_Transcript_1/1_Conf_1.000	231	0							
Locus_26727_Transcript_1/1_Conf_1.000	232	0							
Locus_26728_Transcript_1/1_Conf_1.000	276	20	1.00E-46	ADF56009.1	98	189.504	91	90	nicotinic acetylcholine receptor alpha subunit 38
Locus_26729_Transcript_1/1_Conf_1.000	145	0							
Locus_2673_Transcript_1/2_Conf_1.000	737	4	1.08E-28	NP_500404.2	60	85.1149	117	71	hypothetical protein Y37E11AM.2
Locus_2673_Transcript_2/2_Conf_1.000	737	4	1.08E-28	NP_500404.2	60	85.1149	117	71	hypothetical protein Y37E11AM.2
Locus_26730_Transcript_1/1_Conf_1.000	195	0							
Locus_26731_Transcript_1/1_Conf_1.000	398	0							
Locus_26732_Transcript_1/1_Conf_1.000	181	0							
Locus_26733_Transcript_1/1_Conf_1.000	244	0							

Locus_26734_Transcript_1/1_Conf_1.000	148	20	3.71E-12	ADM18967.1	100	74.7146	36	36	glucose regulated protein 78
Locus_26735_Transcript_1/1_Conf_1.000	200	2	5.11E-06	NP_490861.3	60	54.299	63	38	hypothetical protein Y92H12A.5
Locus_26736_Transcript_1/1_Conf_1.000	143	0							
Locus_26737_Transcript_1/1_Conf_1.000	251	5	4.09E-16	NP_492157.2	63	87.8113	92	58	hypothetical protein D2005.6
Locus_26738_Transcript_1/1_Conf_1.000	172	20	3.38E-18	NP_001024333.1	80	94.7449	57	46	Olfactory LeaRNing defective family member (olrn-1)
Locus_26739_Transcript_1/1_Conf_1.000	196	20	5.13E-06	XP_001900094.1	60	54.299	63	38	Voltage gated chloride channel family protein
Locus_2674_Transcript_1/1_Conf_1.000	505	0							
Locus_26740_Transcript_1/1_Conf_1.000	133	0							
Locus_26741_Transcript_1/1_Conf_1.000	132	0							
Locus_26742_Transcript_1/1_Conf_1.000	156	0							
Locus_26743_Transcript_1/1_Conf_1.000	134	0							
Locus_26744_Transcript_1/1_Conf_1.000	149	0							
Locus_26745_Transcript_1/1_Conf_1.000	152	0							
Locus_26746_Transcript_1/1_Conf_1.000	149	0							
Locus_26747_Transcript_1/1_Conf_1.000	306	4	6.35E-17	NP_498273.1	79	90.5077	63	50	hypothetical protein F01F1.2
Locus_26748_Transcript_1/1_Conf_1.000	130	3	3.29E-05	NP_502249.3	80	51.6026	40	32	TRPA cation channel homolog family member (trpa-1)
Locus_26749_Transcript_1/1_Conf_1.000	241	0							
Locus_2675_Transcript_1/2_Conf_1.000	1413	7	7.16E-23	NP_505497.1	74	113.235	85	63	Zinc finger Transcription Factor family member (ztf-9)

Locus_2675_Transcript_2/2_Conf_1.000	1401	7	7.07E-23	NP_505497.1	74	113.235	85	63	Zinc finger Transcription Factor family member (ztf-9)
Locus_26750_Transcript_1/1_Conf_1.000	155	5	3.12E-11	AAA83446.5	85	71.633	49	42	Hypothetical protein F44A2.3
Locus_26751_Transcript_1/1_Conf_1.000	229	0							
Locus_26752_Transcript_1/1_Conf_1.000	385								
Locus_26753_Transcript_1/1_Conf_1.000	153	0							
Locus_26754_Transcript_1/1_Conf_1.000	153	8	1.45E-08	NP_510664.1	75	62.7734	45	34	LEThal family member (let-2)
Locus_26755_Transcript_1/1_Conf_1.000	165	0							
Locus_26756_Transcript_1/1_Conf_1.000	160	0							
Locus_26757_Transcript_1/1_Conf_1.000	245	0							
Locus_26758_Transcript_1/1_Conf_1.000	149	6	1.08E-11	XP_002644311.1	89	73.1738	46	41	C. briggsae CBR-AQP-7 protein
Locus_26759_Transcript_1/1_Conf_1.000	142	0							
Locus_2676_Transcript_1/1_Conf_1.000	1136	20	5.47E-12	CAA97782.4	51	76.6406	200	103	C. elegans protein C44B9.5, confirmed by transcript evidence
Locus_26760_Transcript_1/1_Conf_1.000	151	0							
Locus_26761_Transcript_1/1_Conf_1.000	397	0							
Locus_26762_Transcript_1/1_Conf_1.000	175	2	3.61E-04	AAD13339.1	60	48.1358	53	32	ancylostoma-secreted protein 1 precursor
Locus_26763_Transcript_1/1_Conf_1.000	164	0							
Locus_26764_Transcript_1/1_Conf_1.000	521	20	5.70E-54	NP_508523.1	85	213.772	173	148	Temporarily Assigned Gene name family member (tag-312)
Locus_26765_Transcript_1/1_Conf_1.000	255	0							
Locus_26766_Transcript_1/1_Conf_1.000	131	0							
Locus_26767_Transcript_1/1_Conf_1.000	176	9	8.03E-12	XP_002637952.1	88	73.559	54	48	Hypothetical protein CBG04769
Locus_26768_Transcript_1/1_Conf_1.000	175	4	7.50E-18	ABS50363.1	91	93.5893	57	52	LIM domain protein variant
Locus_26769_Transcript_1/1_Conf_1.000	164	0							

Locus_2677_Transcript_1/1_Conf_1.000	618	9	1.01E-07	NP_501074.1	48	60.8474	95	46	hypothetical protein B0478.3
Locus_26770_Transcript_1/1_Conf_1.000	170	0							
Locus_26771_Transcript_1/1_Conf_1.000	165	4	1.69E-09	NP_510156.2	77	65.855	53	41	hypothetical protein F11C1.4
Locus_26772_Transcript_1/1_Conf_1.000	181	0							
Locus_26773_Transcript_1/1_Conf_1.000	204	20	1.74E-14	NP_491496.1	78	82.4185	57	45	Downstream Of Mes (in same operon) family member (dom-3)
Locus_26774_Transcript_1/1_Conf_1.000	134	20	8.89E-19	XP_002921250.1	100	96.6709	44	44	PREDICTED: 6-phosphofructokinase type C-like
Locus_26775_Transcript_1/1_Conf_1.000	270	4	2.35E-11	XP_002641216.1	81	72.0182	48	39	Hypothetical protein CBG09080
Locus_26776_Transcript_1/1_Conf_1.000	138	0							
Locus_26777_Transcript_1/1_Conf_1.000	566	0							
Locus_26778_Transcript_1/1_Conf_1.000	174	0							
Locus_26779_Transcript_1/1_Conf_1.000	170	20	8.08E-12	XP_002760891.1	100	73.559	38	38	PREDICTED: 40S ribosomal protein S25-like
Locus_2678_Transcript_1/1_Conf_1.000	1405	20	4.70E-59	NP_492743.3	50	233.417	472	239	MUS (Drosophila mutagen sensitive) related family member (mus-101)
Locus_26780_Transcript_1/1_Conf_1.000	190	0							
Locus_26781_Transcript_1/1_Conf_1.000	201	0							
Locus_26782_Transcript_1/1_Conf_1.000	361	0							
Locus_26783_Transcript_1/1_Conf_1.000	206	1	6.63E-06	NP_510520.4	71	53.9138	53	38	Osm-9 and Capsaicin receptor-Related family member (ocr-3)
Locus_26784_Transcript_1/1_Conf_1.000	306	2	9.51E-05	CAD20812.1	45	50.0618	106	48	SXC2 protein
Locus_26785_Transcript_1/1_Conf_1.000	188	0							
Locus_26786_Transcript_1/1_Conf_1.000	165	0							
Locus_26787_Transcript_1/1_Conf_1.000	157	0							
Locus_26788_Transcript_1/1_Conf_1.000	197	0							

Locus_26789_Transcript_1/1_Conf_1.000	163	20	5.44E-16	XP_002639418.1	86	87.4261	53	46	C. briggsae CBR-LIM-7 protein
Locus_2679_Transcript_1/1_Conf_1.000	659	20	1.27E-70	ADN20761.1	98	270.011	174	171	cytochrome c oxidase subunit II
Locus_26790_Transcript_1/1_Conf_1.000	213	0							
Locus_26791_Transcript_1/1_Conf_1.000	240	20	4.13E-24	1AV5	100	114.39	51	51	Pkci-Substrate Analog
Locus_26792_Transcript_1/1_Conf_1.000	231	20	3.20E-16	NP_001021871.1	88	88.1965	52	46	UNCoordinated family member (unc-13)
Locus_26793_Transcript_1/1_Conf_1.000	166	0							
Locus_26794_Transcript_1/1_Conf_1.000	140	0							

Locus_26795_Transcript_1/1_Conf_1.000	215	20	5.70E-34	XP_001135927.1	100	147.132	71	71	PREDICTED: similar to elongation factor-1-beta
Locus_26796_Transcript_1/1_Conf_1.000	226	0							
Locus_26797_Transcript_1/1_Conf_1.000	218	0							
Locus_26798_Transcript_1/1_Conf_1.000	223	0							
Locus_26799_Transcript_1/1_Conf_1.000	226	12	2.46E-24	XP_002638736.1	86	115.161	75	65	C. briggsae CBR-EGO-1 protein
Locus_268_Transcript_1/1_Conf_1.000	1373	20	4.28E-65	ADK24111.1	59	253.447	396	236	Hypothetical protein ZK1248.7
Locus_2680_Transcript_1/1_Conf_1.000	598	0							
Locus_26800_Transcript_1/1_Conf_1.000	147	0							
Locus_26801_Transcript_1/1_Conf_1.000	179	0							
Locus_26802_Transcript_1/1_Conf_1.000	335	20	2.50E-21	XP_002982216.1	65	105.145	106	69	hypothetical protein SELMODRAFT_421595
Locus_26803_Transcript_1/1_Conf_1.000	217	0							
Locus_26804_Transcript_1/1_Conf_1.000	143	20	1.51E-10	XP_002708655.1	100	69.3218	47	47	PREDICTED: tropomyosin 4
Locus_26805_Transcript_1/1_Conf_1.000	452	0							
Locus_26806_Transcript_1/1_Conf_1.000	384	2	2.41E-32	XP_002630907.1	81	141.739	92	75	Hypothetical protein CBG02631
Locus_26807_Transcript_1/1_Conf_1.000	161	0							
Locus_26808_Transcript_1/1_Conf_1.000	274	20	9.48E-29	XP_002636773.1	79	129.798	91	72	C. briggsae CBR-INX-11 protein
Locus_26809_Transcript_1/1_Conf_1.000	338	15	1.55E-31	XP_002638625.1	75	139.043	108	82	Hypothetical protein CBG05678
Locus_2681_Transcript_1/2_Conf_1.000	1581	20	0	NP_741452.2	88	768.459	519	458	hypothetical protein C55F2.1
Locus_2681_Transcript_2/2_Conf_1.000	1581	20	0	NP_741452.2	88	768.459	519	458	hypothetical protein C55F2.1
Locus_26810_Transcript_1/1_Conf_1.000	133	19	3.49E-15	XP_002630579.1	97	84.7297	44	43	C. briggsae CBR-NHX-2 protein
Locus_26811_Transcript_1/1_Conf_1.000	163	0							

Locus_26812_Transcript_1/1_Conf_1.000	289	20	2.09E-15	XP_001607227.1	62	85.5001	96	60	PREDICTED: hypothetical protein
Locus_26813_Transcript_1/1_Conf_1.000	143	20	6.74E-19	XP_002931287.1	100	97.0561	47	47	PREDICTED: filamin-A-like, partial
Locus_26814_Transcript_1/1_Conf_1.000	226	2	1.26E-28	NP_499205.1	89	129.413	75	67	hypothetical protein K03H1.5
Locus_26815_Transcript_1/1_Conf_1.000	135	10	2.19E-09	XP_002631278.1	81	65.4698	43	35	C. briggsae CBR-PQN-47 protein
Locus_26816_Transcript_1/1_Conf_1.000	221	0							
Locus_26817_Transcript_1/1_Conf_1.000	132	0							
Locus_26818_Transcript_1/1_Conf_1.000	334	20	6.12E-36	XP_002631690.1	91	153.68	85	78	C. briggsae CBR-PDE-3 protein
Locus_26819_Transcript_1/1_Conf_1.000	166	10	3.07E-19	NP_001122601.1	94	98.2117	54	51	Multiple PDZ domain protein family member (mpz-1)

Locus_2682_Transcript_1/1_Conf_1.000	473	20	2.32E-59	XP_001902067.1	95	231.491	117	112	DNA-directed RNA polymerase II 15.1 kDa polypeptide
Locus_26820_Transcript_1/1_Conf_1.000	151	5	7.45E-13	NP_001021650.1	82	77.0258	50	41	HaMmeRhead embryonic lethal family member (hmr-1)
Locus_26821_Transcript_1/1_Conf_1.000	200	0							
Locus_26822_Transcript_1/1_Conf_1.000	142	0							
Locus_26823_Transcript_1/1_Conf_1.000	146	0							
Locus_26824_Transcript_1/1_Conf_1.000	194	0							
Locus_26825_Transcript_1/1_Conf_1.000	150	0							
Locus_26826_Transcript_1/1_Conf_1.000	174	8	3.26E-13	NP_001021991.1	76	78.1814	55	42	hypothetical protein C26D10.6
Locus_26827_Transcript_1/1_Conf_1.000	164	2	5.46E-08	NP_499445.2	80	60.8474	36	29	hypothetical protein Y47D3A.14
Locus_26828_Transcript_1/1_Conf_1.000	230	20	1.59E-15	XP_002637122.1	80	85.8853	61	49	C. briggsae CBR-UGT-49 protein
Locus_26829_Transcript_1/1_Conf_1.000	202	2	7.36E-05	NP_500870.2	58	50.447	67	39	hypothetical protein C06E7.2
Locus_2683_Transcript_1/1_Conf_1.000	1369	20	1.16E-171	XP_002630814.1	81	607.446	456	372	C. briggsae CBR-FZO-1 protein
Locus_26830_Transcript_1/1_Conf_1.000	315	4	7.19E-16	NP_491962.1	82	87.0409	67	55	hypothetical protein H27M09.1
Locus_26831_Transcript_1/1_Conf_1.000	158	0							
Locus_26832_Transcript_1/1_Conf_1.000	166	6	6.41E-17	NP_001021110.1	96	90.5077	51	49	CAlSYntenin/Alcadein homolog family member (casy-1)
Locus_26833_Transcript_1/1_Conf_1.000	149	0							
Locus_26834_Transcript_1/1_Conf_1.000	128	20	8.68E-06	NP_502174.2	69	53.5286	36	25	hypothetical protein M04B2.2
Locus_26835_Transcript_1/1_Conf_1.000	229	0							
Locus_26836_Transcript_1/1_Conf_1.000	220	2	6.13E-07	XP_002631025.1	59	57.3806	69	41	Hypothetical protein CBG02782
Locus_26837_Transcript_1/1_Conf_1.000	162	0							
Locus_26838_Transcript_1/1_Conf_1.000	132	0							
Locus_26839_Transcript_1/1_Conf_1.000	191	0							
Locus_2684_Transcript_1/2_Conf_1.000	504	0							

Locus_2684_Transcript_2/2_Conf_1.000	1824	20	2.38E-133	AAN11402.1	72	480.715	400	289	secreted-protein 1 precursor
Locus_26840_Transcript_1/1_Conf_1.000	155	0							
Locus_26841_Transcript_1/1_Conf_1.000	131	20	6.83E-19	XP_002923583.1	100	97.0561	43	43	PREDICTED: calponin-2-like
Locus_26842_Transcript_1/1_Conf_1.000	160	0							
Locus_26843_Transcript_1/1_Conf_1.000	132	0							
Locus_26844_Transcript_1/1_Conf_1.000	132	0							
Locus_26845_Transcript_1/1_Conf_1.000	138	20	1.41E-16	XP_002833724.1	100	89.3521	45	45	PREDICTED: keratin, type II cytoskeletal 5-like
Locus_26846_Transcript_1/1_Conf_1.000	368	0							
Locus_26847_Transcript_1/1_Conf_1.000	147	0							
Locus_26848_Transcript_1/1_Conf_1.000	247	0							
Locus_26849_Transcript_1/1_Conf_1.000	286	0							
Locus_2685_Transcript_1/1_Conf_1.000	434	20	7.48E-34	NP_508706.2	75	146.747	135	102	NCK (Non-Catalytic region of tyrosine Kinase) adaptor protein family member (nck-1)
Locus_26850_Transcript_1/1_Conf_1.000	152	0							
Locus_26851_Transcript_1/1_Conf_1.000	329	0							
Locus_26852_Transcript_1/1_Conf_1.000	234	0							
Locus_26853_Transcript_1/1_Conf_1.000	195	20	5.64E-21	XP_002634571.1	100	103.99	48	48	C. briggsae CBR-GPA-7 protein
Locus_26854_Transcript_1/1_Conf_1.000	238	12	5.80E-10	NP_499376.1	68	67.3958	79	54	hypothetical protein K01G5.10
Locus_26855_Transcript_1/1_Conf_1.000	251	20	7.41E-42	EFO21218.1	98	173.326	83	82	CAMK/CAMKL/NUAK protein kinase
Locus_26856_Transcript_1/1_Conf_1.000	161	0							

Locus_26857_Transcript_1/1_Conf_1.000	137	0							
Locus_26858_Transcript_1/1_Conf_1.000	151	0							
Locus_26859_Transcript_1/1_Conf_1.000	165	20	5.62E-13	XP_002732167.1	82	77.411	52	43	PREDICTED: hypothetical protein, partial
Locus_2686_Transcript_1/1_Conf_1.000	381	0							
Locus_26860_Transcript_1/1_Conf_1.000	836	20	3.45E-86	NP_495615.2	70	322.398	281	197	hypothetical protein B0495.5
Locus_26861_Transcript_1/1_Conf_1.000	175	6	1.85E-08	XP_002644672.1	68	62.3882	57	39	C. briggsae CBR-VPS-41 protein
Locus_26862_Transcript_1/1_Conf_1.000	198	20	4.76E-20	XP_002629862.1	89	100.908	65	58	Hypothetical protein CBG21896
Locus_26863_Transcript_1/1_Conf_1.000	230	20	6.23E-28	CBK19482.1	86	127.102	76	66	C. elegans protein Y116A8C.13b, partially confirmed by transcript evidence
Locus_26864_Transcript_1/1_Conf_1.000	213	0							
Locus_26865_Transcript_1/1_Conf_1.000	323	0							
Locus_26866_Transcript_1/1_Conf_1.000	183	18	2.25E-17	Q24702.1	83	92.0485	60	50	DVA-1 polyprotein
Locus_26867_Transcript_1/1_Conf_1.000	254	0							
Locus_26868_Transcript_1/1_Conf_1.000	197	20	6.22E-28	XP_002641359.1	98	127.102	65	64	C. briggsae CBR-RSKS-1 protein
Locus_26869_Transcript_1/1_Conf_1.000	220	0							

Locus_2687_Transcript_1/2_Conf_1.000	1302	20	1.19E-61	XP_001892903.1	68	241.891	216	147	cytokine inducible SH2-containing protein 5
Locus_2687_Transcript_2/2_Conf_1.000	1254	20	5.60E-61	XP_001892903.1	79	239.58	168	133	cytokine inducible SH2-containing protein 5
Locus_26870_Transcript_1/1_Conf_1.000	157	1	8.20E-04	NP_493078.2	67	46.9802	37	25	hypothetical protein R05D7.5
Locus_26871_Transcript_1/1_Conf_1.000	159	0							
Locus_26872_Transcript_1/1_Conf_1.000	131	0							
Locus_26873_Transcript_1/1_Conf_1.000	183	0							
Locus_26874_Transcript_1/1_Conf_1.000	202	20	2.29E-06	EFO22266.1	63	55.4546	58	37	hypothetical protein LOAG_06220
Locus_26875_Transcript_1/1_Conf_1.000	254	20	1.32E-09	EFO26172.1	75	66.2402	60	45	Ulp1 protease
Locus_26876_Transcript_1/1_Conf_1.000	164	0							
Locus_26877_Transcript_1/1_Conf_1.000	207	20	7.77E-23	EFO21255.1	95	110.153	68	65	hypothetical protein LOAG_07233
Locus_26878_Transcript_1/1_Conf_1.000	145	0							
Locus_26879_Transcript_1/1_Conf_1.000	222	0							
Locus_2688_Transcript_1/1_Conf_1.000	530	0							
Locus_26880_Transcript_1/1_Conf_1.000	157	0							
Locus_26881_Transcript_1/1_Conf_1.000	271	20	2.95E-38	EFO24540.1	88	161.384	90	80	hypothetical protein LOAG_03946
Locus_26882_Transcript_1/1_Conf_1.000	378	8	1.74E-30	NP_001022643.1	69	135.576	126	88	LEThal family member (let-805)
Locus_26883_Transcript_1/1_Conf_1.000	492	0							
Locus_26884_Transcript_1/1_Conf_1.000	130	0							
Locus_26885_Transcript_1/1_Conf_1.000	196	3	7.89E-15	XP_002642115.1	89	83.5741	56	50	C. briggsae CBR-NDG-4 protein
Locus_26886_Transcript_1/1_Conf_1.000	132	0							
Locus_26887_Transcript_1/1_Conf_1.000	152	0							
Locus_26888_Transcript_1/1_Conf_1.000	338	20	3.56E-52	XP_002631304.1	94	207.608	112	106	Hypothetical protein CBG03118

Locus_26889_Transcript_1/1_Conf_1.000	165	2	9.89E-18	NP_001122963.1	90	93.2041	54	49	hypothetical protein F58E6.1
Locus_2689_Transcript_1/1_Conf_1.000	605	20	6.87E-75	CAR63569.1	91	283.878	168	153	putative elongation factor 1-beta/1-delta 1
Locus_26890_Transcript_1/1_Conf_1.000	129	0							
Locus_26891_Transcript_1/1_Conf_1.000	188	0							
Locus_26892_Transcript_1/1_Conf_1.000	205	0							
Locus_26893_Transcript_1/1_Conf_1.000	204	0							
Locus_26894_Transcript_1/1_Conf_1.000	179	20	1.97E-18	NP_492839.4	89	95.5153	57	51	Leucine-rich repeats, Ras-like domain, Kinase family member (lrk-1)
Locus_26895_Transcript_1/1_Conf_1.000	173	0							
Locus_26896_Transcript_1/1_Conf_1.000	145	20	3.72E-12	XP_002636452.1	91	74.7146	47	43	C. briggsae CBR-FOLT-1 protein
Locus_26897_Transcript_1/1_Conf_1.000	165	20	2.52E-13	XP_002809331.1	100	78.5666	38	38	PREDICTED: LOW QUALITY PROTEIN: interferon regulatory factor 2-binding protein 2-like
Locus_26898_Transcript_1/1_Conf_1.000	221	0							
Locus_26899_Transcript_1/1_Conf_1.000	149	0							
Locus_269_Transcript_1/1_Conf_1.000	1291	0							
Locus_2690_Transcript_1/1_Conf_1.000	136	3	3.27E-05	NP_510725.1	86	51.6026	36	31	hypothetical protein T20F7.6
Locus_26900_Transcript_1/1_Conf_1.000	250	0							
Locus_26901_Transcript_1/1_Conf_1.000	211	0							
Locus_26902_Transcript_1/1_Conf_1.000	220	2	5.74E-05	XP_002639815.1	56	50.8322	69	39	Hypothetical protein CBG21340
Locus_26903_Transcript_1/1_Conf_1.000	207	0							
Locus_26904_Transcript_1/1_Conf_1.000	144	0							
Locus_26905_Transcript_1/1_Conf_1.000	145	0							

Locus_26906_Transcript_1/1_Conf_1.000	257	20	1.30E-41	P02751.4	100	172.555	85	85	Fibronectin
Locus_26907_Transcript_1/1_Conf_1.000	139	0							
Locus_26908_Transcript_1/1_Conf_1.000	138	0							
Locus_26909_Transcript_1/1_Conf_1.000	312	0							
Locus_2691_Transcript_1/1_Conf_1.000	716	20	1.71E-90	NP_495445.2	83	336.265	238	198	hypothetical protein ZK1127.5
Locus_26910_Transcript_1/1_Conf_1.000	148	2	8.53E-17	NP_501866.1	93	90.1225	48	45	hypothetical protein C24F3.4
Locus_26911_Transcript_1/1_Conf_1.000	179	0							
Locus_26912_Transcript_1/1_Conf_1.000	148	0							
Locus_26913_Transcript_1/1_Conf_1.000	347	20	4.94E-33	XP_002642963.1	85	144.05	99	85	Hypothetical protein CBG15247
Locus_26914_Transcript_1/1_Conf_1.000	282	0							
Locus_26915_Transcript_1/1_Conf_1.000	283	0							
Locus_26916_Transcript_1/1_Conf_1.000	140	0							
Locus_26917_Transcript_1/1_Conf_1.000	203	20	4.58E-31	ABY48069.1	100	137.502	67	67	beta-tubulin
Locus_26918_Transcript_1/1_Conf_1.000	210	20	1.01E-22	CAB57358.1	85	109.768	69	59	microsomal aminopeptidase

Locus_26919_Transcript_1/1_Conf_1.000	398	3	4.21E-08	NP_491118.2	72	61.2326	65	47	hypothetical protein Y54E10A.11
Locus_2692_Transcript_1/1_Conf_1.000	671	20	3.48E-31	XP_002642923.1	63	139.043	168	107	Hypothetical protein CBG15199
Locus_26920_Transcript_1/1_Conf_1.000	190	3	6.29E-12	XP_002632467.1	82	73.9442	50	41	C. briggsae CBR-GNRR-8 protein
Locus_26921_Transcript_1/1_Conf_1.000	253	0							
Locus_26922_Transcript_1/1_Conf_1.000	133	0							
Locus_26923_Transcript_1/1_Conf_1.000	328	20	2.12E-36	AAH17408.1	100	155.221	81	81	Enoyl Coenzyme A hydratase 1, peroxisomal
Locus_26924_Transcript_1/1_Conf_1.000	174	3	7.78E-07	XP_002636378.1	70	56.9954	57	40	C. briggsae CBR-UGT-63 protein
Locus_26925_Transcript_1/1_Conf_1.000	248	0							
Locus_26926_Transcript_1/1_Conf_1.000	130	4	9.86E-18	XP_002645998.1	97	93.2041	42	41	Hypothetical protein CBG07786
Locus_26927_Transcript_1/1_Conf_1.000	161	0							
Locus_26928_Transcript_1/1_Conf_1.000	257	2	6.05E-39	XP_002636673.1	92	163.696	83	77	Hypothetical protein CBG23386
Locus_26929_Transcript_1/1_Conf_1.000	135	0							
Locus_2693_Transcript_1/1_Conf_1.000	329	0							
Locus_26930_Transcript_1/1_Conf_1.000	168	10	1.47E-13	NP_499472.1	78	79.337	56	44	Sterol regulatory element Binding Protein family member (sbp-1)
Locus_26931_Transcript_1/1_Conf_1.000	149	20	2.56E-21	XP_002821635.1	100	105.145	49	49	PREDICTED: stress-induced-phosphoprotein 1-like
Locus_26932_Transcript_1/1_Conf_1.000	282	0							

Locus_26933_Transcript_1/1_Conf_1.000	254	20	5.34E-19	NP_497632.1	100	97.4413	44	44	Kruppel-Like Factor (zinc finger protein) family member (klf-1)
Locus_26934_Transcript_1/1_Conf_1.000	173	0							
Locus_26935_Transcript_1/1_Conf_1.000	303	20	7.21E-53	XP_002812714.1	100	209.92	99	99	PREDICTED: collagen alpha-1(III) chain-like isoform 2
Locus_26936_Transcript_1/1_Conf_1.000	197	8	1.44E-16	NP_001022643.1	78	89.3521	65	51	LEThal family member (let-805)
Locus_26937_Transcript_1/1_Conf_1.000	267	0							

Locus_26938_Transcript_1/1_Conf_1.000	134	3	8.34E-09	NP_001021350.1	82	63.5438	41	34	C-type LECtin family member (clec-225)
Locus_26939_Transcript_1/1_Conf_1.000	197	0							
Locus_2694_Transcript_1/1_Conf_1.000	1688	20	7.64E-155	XP_002631800.1	80	551.977	457	370	Hypothetical protein CBG21019
Locus_26940_Transcript_1/1_Conf_1.000	184	0							
Locus_26941_Transcript_1/1_Conf_1.000	146	0							
Locus_26942_Transcript_1/1_Conf_1.000	138	20	8.27E-17	DAA16569.1	100	90.1225	45	45	heat shock protein HSP 90-beta
Locus_26943_Transcript_1/1_Conf_1.000	173	0							
Locus_26944_Transcript_1/1_Conf_1.000	206	0							
Locus_26945_Transcript_1/1_Conf_1.000	152	20	2.65E-10	NP_491761.3	78	68.5514	50	39	hypothetical protein T27A3.5
Locus_26946_Transcript_1/1_Conf_1.000	173	0							
Locus_26947_Transcript_1/1_Conf_1.000	140	20	1.32E-22	XP_002807463.1	100	109.383	46	46	PREDICTED: LOW QUALITY PROTEIN: kinesin-like protein KIF22-like
Locus_26948_Transcript_1/1_Conf_1.000	378	20	4.43E-34	XP_002633255.1	79	147.517	121	96	Hypothetical protein CBG05980
Locus_26949_Transcript_1/1_Conf_1.000	257	0							

Locus_2695_Transcript_1/1_Conf_1.000	396	20	1.65E-12	XP_002065721.1	61	75.8702	122	75	GK19967
Locus_26950_Transcript_1/1_Conf_1.000	266	0							
Locus_26951_Transcript_1/1_Conf_1.000	140	3	1.20E-07	XP_002643051.1	75	59.6918	45	34	C. briggsae CBR-DPF-6 protein
Locus_26952_Transcript_1/1_Conf_1.000	175	0							
Locus_26953_Transcript_1/1_Conf_1.000	152	0							
Locus_26954_Transcript_1/1_Conf_1.000	239	0							
Locus_26955_Transcript_1/1_Conf_1.000	148	0							
Locus_26956_Transcript_1/1_Conf_1.000	205	0							
Locus_26957_Transcript_1/1_Conf_1.000	142	0							
Locus_26958_Transcript_1/1_Conf_1.000	200	20	2.21E-25	NP_495675.1	89	118.627	66	59	hypothetical protein DH11.1
Locus_26959_Transcript_1/1_Conf_1.000	142	0							
Locus_2696_Transcript_1/1_Conf_1.000	7915	0							
Locus_26960_Transcript_1/1_Conf_1.000	167	0							
Locus_26961_Transcript_1/1_Conf_1.000	167	0							
Locus_26962_Transcript_1/1_Conf_1.000	148	20	3.46E-18	XP_519221.2	100	94.7449	42	42	PREDICTED: similar to I3 protein
Locus_26963_Transcript_1/1_Conf_1.000	223	0							
Locus_26964_Transcript_1/1_Conf_1.000	169	0							
Locus_26965_Transcript_1/1_Conf_1.000	135	0							

Locus_26966_Transcript_1/1_Conf_1.000	268	20	3.30E-13	CAA96571.1	60	78.1814	91	55	parasite pepsinogen
Locus_26967_Transcript_1/1_Conf_1.000	154	0							
Locus_26968_Transcript_1/1_Conf_1.000	209	20	1.74E-14	EFO23598.1	89	82.4185	49	44	hypothetical protein LOAG_04888
Locus_26969_Transcript_1/1_Conf_1.000	174	0							
Locus_2697_Transcript_1/1_Conf_1.000	596	20	1.62E-65	NP_500188.1	98	252.677	161	158	Vacuolar H ATPase family member (vha-3)
Locus_26970_Transcript_1/1_Conf_1.000	158	4	2.02E-10	XP_001896931.1	70	68.9366	51	36	Cadherin domain containing protein
Locus_26971_Transcript_1/1_Conf_1.000	311	0							
Locus_26972_Transcript_1/1_Conf_1.000	432	0							
Locus_26973_Transcript_1/1_Conf_1.000	149	7	8.00E-07	XP_002631522.1	70	56.9954	48	34	Hypothetical protein CBG20688
Locus_26974_Transcript_1/1_Conf_1.000	147	0							
Locus_26975_Transcript_1/1_Conf_1.000	139	0							
Locus_26976_Transcript_1/1_Conf_1.000	141	0							
Locus_26977_Transcript_1/1_Conf_1.000	242	0							
Locus_26978_Transcript_1/1_Conf_1.000	223	0							
Locus_26979_Transcript_1/1_Conf_1.000	235	4	2.36E-19	NP_497665.2	76	98.5969	82	63	hypothetical protein R148.5
Locus_2698_Transcript_1/1_Conf_1.000	132	0							
Locus_26980_Transcript_1/1_Conf_1.000	161	20	6.23E-20	XP_002633968.1	96	100.523	52	50	C. briggsae CBR-MCA-1 protein
Locus_26981_Transcript_1/1_Conf_1.000	132	0							
Locus_26982_Transcript_1/1_Conf_1.000	159	0							
Locus_26983_Transcript_1/1_Conf_1.000	249	0							
Locus_26984_Transcript_1/1_Conf_1.000	179	0							
Locus_26985_Transcript_1/1_Conf_1.000	224	0							
Locus_26986_Transcript_1/1_Conf_1.000	347	20	2.46E-16	NP_495984.2	76	88.5817	69	53	RAB family member (rab-39)
Locus_26987_Transcript_1/1_Conf_1.000	174	0							
Locus_26988_Transcript_1/1_Conf_1.000	270	2	1.13E-05	NP_492201.1	72	53.1434	43	31	hypothetical protein C54G4.4
Locus_26989_Transcript_1/1_Conf_1.000	175	0							
Locus_2699_Transcript_1/1_Conf_1.000	817	0							
Locus_26990_Transcript_1/1_Conf_1.000	167	0							
Locus_26991_Transcript_1/1_Conf_1.000	169	10	2.87E-09	XP_002636377.1	74	65.0846	55	41	Hypothetical protein CBG08678
Locus_26992_Transcript_1/1_Conf_1.000	102	0							
Locus_26993_Transcript_1/1_Conf_1.000	152	0							

Locus_26994_Transcript_1/1_Conf_1.000	349	20	4.01E-51	NP_509205.2	93	204.142	115	108	P-GlycoProtein related family member (pgp-10)
Locus_26995_Transcript_1/1_Conf_1.000	145	0							
Locus_26996_Transcript_1/1_Conf_1.000	422	19	4.15E-56	XP_002637249.1	79	220.705	141	112	Hypothetical protein CBG18928
Locus_26997_Transcript_1/1_Conf_1.000	145	3	1.32E-09	NP_500870.2	81	66.2402	44	36	hypothetical protein C06E7.2
Locus_26998_Transcript_1/1_Conf_1.000	151	0							
Locus_26999_Transcript_1/1_Conf_1.000	174	0							
Locus_27_Transcript_1/1_Conf_1.000	1156	20	4.63E-83	NP_493177.2	81	312.768	238	194	hypothetical protein W02D9.2
Locus_270_Transcript_1/8_Conf_0.267	425	3	5.12E-06	EFO25531.1	58	54.299	41	24	hypothetical protein LOAG_02955
Locus_270_Transcript_2/8_Conf_0.267	467	3	5.13E-06	EFO25531.1	58	54.299	41	24	hypothetical protein LOAG_02955
Locus_270_Transcript_3/8_Conf_0.367	738	6	9.96E-20	EFO25531.1	62	101.293	85	53	hypothetical protein LOAG_02955
Locus_270_Transcript_4/8_Conf_0.300	558	6	9.91E-16	EFO25531.1	64	87.0409	68	44	hypothetical protein LOAG_02955
Locus_270_Transcript_5/8_Conf_0.400	646	6	1.45E-15	EFO25531.1	64	87.0409	68	44	hypothetical protein LOAG_02955
Locus_270_Transcript_6/8_Conf_0.133	348	0							
Locus_270_Transcript_7/8_Conf_0.367	559	7	5.08E-20	EFO25531.1	62	101.293	85	53	hypothetical protein LOAG_02955
Locus_270_Transcript_8/8_Conf_0.367	517	6	7.86E-16	EFO25531.1	64	87.0409	68	44	hypothetical protein LOAG_02955
Locus_2700_Transcript_1/1_Conf_1.000	755	20	9.88E-39	NP_001129785.1	60	164.466	197	119	hypothetical protein M04C9.3
Locus_27000_Transcript_1/1_Conf_1.000	155	0							
Locus_27001_Transcript_1/1_Conf_1.000	340	0							
Locus_27002_Transcript_1/1_Conf_1.000	184	20	2.33E-14	XP_002820242.1	100	82.0333	40	40	PREDICTED: proteasome subunit beta type-7-like
Locus_27003_Transcript_1/1_Conf_1.000	129	0							
Locus_27004_Transcript_1/1_Conf_1.000	149	0							
Locus_27005_Transcript_1/1_Conf_1.000	214	0							
Locus_27006_Transcript_1/1_Conf_1.000	197	3	1.59E-07	XP_002631270.1	64	59.3066	67	43	C. briggsae CBR-MAB-10 protein
Locus_27007_Transcript_1/1_Conf_1.000	167	0							
Locus_27008_Transcript_1/1_Conf_1.000	162	0							
Locus_27009_Transcript_1/1_Conf_1.000	140	0							

Locus_2701_Transcript_1/1_Conf_1.000	2452	20	0	XP_002642168.1	78	986.482	747	588	Hypothetical protein CBG18133
Locus_27010_Transcript_1/1_Conf_1.000	144	0							
Locus_27011_Transcript_1/1_Conf_1.000	266	0							
Locus_27012_Transcript_1/1_Conf_1.000	355	4	1.33E-30	NP_741200.1	86	135.961	114	99	DIsplaced Gonad family member (dig-1)
Locus_27013_Transcript_1/1_Conf_1.000	128	20	6.86E-11	NP_502513.1	88	70.4774	42	37	hypothetical protein C39E9.10
Locus_27014_Transcript_1/1_Conf_1.000	147	0							
Locus_27015_Transcript_1/1_Conf_1.000	155	20	6.09E-07	BAG60121.1	100	57.3806	51	51	unnamed protein product
Locus_27016_Transcript_1/1_Conf_1.000	221	0							
Locus_27017_Transcript_1/1_Conf_1.000	140	0							
Locus_27018_Transcript_1/1_Conf_1.000	268	0							
Locus_27019_Transcript_1/1_Conf_1.000	156	1	8.20E-04	YP_480243.1	62	46.9802	51	32	NUDIX hydrolase

Locus_2702_Transcript_1/2_Conf_1.000	1395	20	0	NP_494846.1	87	785.793	464	408	hypothetical protein F41C3.5
Locus_2702_Transcript_2/2_Conf_1.000	1266	20	0	NP_494846.1	87	708.368	423	369	hypothetical protein F41C3.5
Locus_27020_Transcript_1/1_Conf_1.000	161	20	6.45E-17	EFO22677.1	86	90.5077	52	45	derlin-2
Locus_27021_Transcript_1/1_Conf_1.000	239	1	1.86E-16	NP_505520.2	86	88.9669	50	43	hypothetical protein F46B6.2
Locus_27022_Transcript_1/1_Conf_1.000	219	8	2.33E-06	NP_492198.1	71	55.4546	45	32	hypothetical protein H05L14.1
Locus_27023_Transcript_1/1_Conf_1.000	157	0							
Locus_27024_Transcript_1/1_Conf_1.000	312	20	3.92E-46	XP_002914802.1	100	187.578	104	104	PREDICTED: high mobility group protein B1-like
Locus_27025_Transcript_1/1_Conf_1.000	203	0							
Locus_27026_Transcript_1/1_Conf_1.000	190	11	6.94E-19	NP_493718.1	85	97.0561	63	54	PaTched Related family member (ptr-3)

Locus_27027_Transcript_1/1_Conf_1.000	169	15	3.27E-21	NP_001129927.1	90	104.76	55	50	PhosphoLipase C family member (plc-1)
Locus_27028_Transcript_1/1_Conf_1.000	136	0							
Locus_27029_Transcript_1/1_Conf_1.000	145	0							
Locus_2703_Transcript_1/1_Conf_1.000	619	20	9.27E-86	XP_002648990.1	86	320.087	209	180	Hypothetical protein CBG21322
Locus_27030_Transcript_1/1_Conf_1.000	603	20	5.16E-30	EFO17504.1	70	134.806	134	95	hypothetical protein LOAG_10996
Locus_27031_Transcript_1/1_Conf_1.000	490	3	1.87E-08	AAT06310.2	81	62.3882	44	36	putative calcium-independent phospholipase A2 isoform a
Locus_27032_Transcript_1/1_Conf_1.000	249	20	1.31E-30	NP_499308.1	82	135.961	82	68	hypothetical protein D2045.5
Locus_27033_Transcript_1/1_Conf_1.000	242	0							
Locus_27034_Transcript_1/1_Conf_1.000	419	0							
Locus_27035_Transcript_1/1_Conf_1.000	143	0							
Locus_27036_Transcript_1/1_Conf_1.000	239	0							
Locus_27037_Transcript_1/1_Conf_1.000	221	3	5.19E-06	XP_002633417.1	58	54.299	70	41	C. briggsae CBR-TRPA-1 protein
Locus_27038_Transcript_1/1_Conf_1.000	184	20	1.01E-09	XP_001898132.1	73	66.6254	60	44	Utp21 specific WD40 associated domain containing protein
Locus_27039_Transcript_1/1_Conf_1.000	211	20	1.01E-30	XP_002644104.1	98	136.346	65	64	C. briggsae CBR-PLC-1 protein

Locus_2704_Transcript_1/4_Conf_0.667	1106	20	8.94E-129	XP_002643552.1	86	464.537	296	255	Hypothetical protein CBG16248
Locus_2704_Transcript_2/4_Conf_0.667	1110	20	3.10E-129	XP_002643552.1	86	466.077	297	256	Hypothetical protein CBG16248
Locus_2704_Transcript_3/4_Conf_0.667	1109	20	8.98E-129	XP_002643552.1	86	464.537	296	255	Hypothetical protein CBG16248
Locus_2704_Transcript_4/4_Conf_0.667	1106	20	8.94E-129	XP_002643552.1	86	464.537	296	255	Hypothetical protein CBG16248
Locus_27040_Transcript_1/1_Conf_1.000	144	0							
Locus_27041_Transcript_1/1_Conf_1.000	511	20	2.17E-39	XP_002636125.1	63	165.236	176	112	Hypothetical protein CBG01375
Locus_27042_Transcript_1/1_Conf_1.000	156	0							
Locus_27043_Transcript_1/1_Conf_1.000	248	0							
Locus_27044_Transcript_1/1_Conf_1.000	180	2	4.88E-04	XP_002638587.1	68	47.7506	44	30	Hypothetical protein CBG05635
Locus_27045_Transcript_1/1_Conf_1.000	1308	20	4.19E-131	NP_502420.2	76	472.626	443	339	hypothetical protein C26H9A.2
Locus_27046_Transcript_1/1_Conf_1.000	137	0							
Locus_27047_Transcript_1/1_Conf_1.000	345	20	9.93E-42	NP_499056.1	86	172.94	109	94	fatty acid ELOngation family member (elo-4)
Locus_27048_Transcript_1/1_Conf_1.000	315	0							
Locus_27049_Transcript_1/1_Conf_1.000	142	0							
Locus_2705_Transcript_1/1_Conf_1.000	195	0							
Locus_27050_Transcript_1/1_Conf_1.000	131	0							
Locus_27051_Transcript_1/1_Conf_1.000	166	0							
Locus_27052_Transcript_1/1_Conf_1.000	213	20	2.39E-32	XP_002825867.1	100	141.739	70	70	PREDICTED: calcium and integrin-binding protein 1-like
Locus_27053_Transcript_1/1_Conf_1.000	136	0							
Locus_27054_Transcript_1/1_Conf_1.000	156	0							
Locus_27055_Transcript_1/1_Conf_1.000	128	0							
Locus_27056_Transcript_1/1_Conf_1.000	160	8	2.62E-10	NP_501419.2	66	68.5514	51	34	hypothetical protein D2096.3

Locus_27057_Transcript_1/1_Conf_1.000	138	0							
Locus_27058_Transcript_1/1_Conf_1.000	224	0							
Locus_27059_Transcript_1/1_Conf_1.000	147	3	1.32E-09	EFO18230.1	82	66.2402	46	38	CTG-2 protein
Locus_2706_Transcript_1/1_Conf_1.000	555	20	2.78E-42	CAR63630.1	81	175.252	120	98	hypothetical protein
Locus_27060_Transcript_1/1_Conf_1.000	144	4	3.05E-06	XP_002634052.1	72	55.0694	47	34	C. briggsae CBR-VHA-5 protein
Locus_27061_Transcript_1/1_Conf_1.000	133	0							
Locus_27062_Transcript_1/1_Conf_1.000	221	0							
Locus_27063_Transcript_1/1_Conf_1.000	137	0							
Locus_27064_Transcript_1/1_Conf_1.000	144	0							
Locus_27065_Transcript_1/1_Conf_1.000	206	0							
Locus_27066_Transcript_1/1_Conf_1.000	231	0							
Locus_27067_Transcript_1/1_Conf_1.000	137	0							
Locus_27068_Transcript_1/1_Conf_1.000	229	0							
Locus_27069_Transcript_1/1_Conf_1.000	164	2	3.09E-11	XP_002639255.1	84	71.633	52	44	C. briggsae CBR-OCRL-1 protein
Locus_2707_Transcript_1/1_Conf_1.000	386	20	7.98E-44	ABD75715.1	87	179.874	129	113	vacuolar protein sorting factor
Locus_27070_Transcript_1/1_Conf_1.000	238	20	3.87E-30	NP_741809.1	88	134.42	78	69	Beta Carbonic Anhydrase family member (bca-1)
Locus_27071_Transcript_1/1_Conf_1.000	172	20	4.88E-17	XP_002633255.1	86	90.8929	53	46	Hypothetical protein CBG05980
Locus_27072_Transcript_1/1_Conf_1.000	198	0							
Locus_27073_Transcript_1/1_Conf_1.000	182	0							
Locus_27074_Transcript_1/1_Conf_1.000	195	1	2.22E-17	CAR63594.1	79	92.0485	64	51	hypothetical protein
Locus_27075_Transcript_1/1_Conf_1.000	132	0							
Locus_27076_Transcript_1/1_Conf_1.000	131	0							
Locus_27077_Transcript_1/1_Conf_1.000	179	20	1.23E-20	XP_002810153.1	100	102.834	48	48	PREDICTED: LOW QUALITY PROTEIN: HCLS1-associated protein X-1-like
Locus_27078_Transcript_1/1_Conf_1.000	128	0							

Locus_27079_Transcript_1/1_Conf_1.000	172	20	2.27E-06	XP_001897983.1	70	55.4546	54	38	RIKEN cDNA 2700097O09
Locus_2708_Transcript_1/1_Conf_1.000	1651	20	0	NP_504038.1	80	638.647	496	400	MTM (myotubularin) family member (mtm-9)
Locus_27080_Transcript_1/1_Conf_1.000	133	0							
Locus_27081_Transcript_1/1_Conf_1.000	155	0							
Locus_27082_Transcript_1/1_Conf_1.000	157	0							
Locus_27083_Transcript_1/1_Conf_1.000	730	20	2.87E-80	XP_001900598.1	84	302.368	205	173	probable DNA helicase ERCC2/XPD - southern platyfish
Locus_27084_Transcript_1/1_Conf_1.000	202	0							
Locus_27085_Transcript_1/1_Conf_1.000	346	5	7.19E-08	NP_502803.3	83	60.4622	43	36	EPS (human endocytosis) related family member (eps-8)
Locus_27086_Transcript_1/1_Conf_1.000	243	0							
Locus_27087_Transcript_1/1_Conf_1.000	191	0							
Locus_27088_Transcript_1/1_Conf_1.000	203	20	1.68E-25	NP_501861.1	92	119.013	67	62	Mitochondrial Sorting of Proteins (yeast MSP) in Nematode family member (mspn-1)
Locus_27089_Transcript_1/1_Conf_1.000	163	0							

Locus_2709_Transcript_1/1_Conf_1.000	726	20	4.32E-12	AAD13339.1	46	75.8702	228	107	ancylostoma-secreted protein 1 precursor
Locus_27090_Transcript_1/1_Conf_1.000	185	4	5.73E-13	NP_495292.1	90	77.411	50	45	hypothetical protein T25D10.4
Locus_27091_Transcript_1/1_Conf_1.000	154	0							
Locus_27092_Transcript_1/1_Conf_1.000	144	0							
Locus_27093_Transcript_1/1_Conf_1.000	194	0							
Locus_27094_Transcript_1/1_Conf_1.000	238	0							
Locus_27095_Transcript_1/1_Conf_1.000	222	2	7.71E-10	NP_497795.1	75	67.0106	48	36	Neuropeptide-Like Protein family member (nlp-10)
Locus_27096_Transcript_1/1_Conf_1.000	192	0							
Locus_27097_Transcript_1/1_Conf_1.000	139	0							
Locus_27098_Transcript_1/1_Conf_1.000	151	0							
Locus_27099_Transcript_1/1_Conf_1.000	183	20	2.65E-26	CAR63533.1	98	121.709	61	60	putative Vitellogenin-linked Transcript family member
Locus_271_Transcript_1/1_Conf_1.000	2079	20	0	NP_496968.1	84	865.529	620	525	hypothetical protein Y48B6A.12
Locus_2710_Transcript_1/2_Conf_1.000	2499	0							
Locus_2710_Transcript_2/2_Conf_1.000	2499	0							
Locus_27100_Transcript_1/1_Conf_1.000	155	2	4.66E-07	NP_499790.1	77	57.7658	45	35	TWiK family of potassium channels family member (twk-40)
Locus_27101_Transcript_1/1_Conf_1.000	249	0							
Locus_27102_Transcript_1/1_Conf_1.000	184	0							
Locus_27103_Transcript_1/1_Conf_1.000	140	0							
Locus_27104_Transcript_1/1_Conf_1.000	128	0							
Locus_27105_Transcript_1/1_Conf_1.000	277	20	3.60E-20	XP_001186243.1	69	101.293	92	64	PREDICTED: hypothetical protein
Locus_27106_Transcript_1/1_Conf_1.000	158	20	5.13E-14	XP_002636662.1	85	80.8777	42	36	C. briggsae CBR-GANA-1 protein
Locus_27107_Transcript_1/1_Conf_1.000	162	0							
Locus_27108_Transcript_1/1_Conf_1.000	139	2	2.26E-06	NP_495695.2	74	55.4546	47	35	hypothetical protein K02C4.5
Locus_27109_Transcript_1/1_Conf_1.000	159	1	6.26E-04	XP_002630560.1	68	47.3654	48	33	C. briggsae CBR-NPP-21 protein
Locus_2711_Transcript_1/1_Conf_1.000	225	20	1.31E-09	EFO17291.1	56	66.2402	74	42	hypothetical protein LOAG_11208
Locus_27110_Transcript_1/1_Conf_1.000	136	0							

Locus_27111_Transcript_1/1_Conf_1.000	184	20	9.73E-29	NP_001137152.1	100	129.798	61	61	glutathione S-transferase kappa 1 isoform c
Locus_27112_Transcript_1/1_Conf_1.000	155	0							
Locus_27113_Transcript_1/1_Conf_1.000	243	0							
Locus_27114_Transcript_1/1_Conf_1.000	211	0							
Locus_27115_Transcript_1/1_Conf_1.000	167	20	8.35E-25	XP_002761262.1	100	116.701	55	55	PREDICTED: coactosin-like protein-like
Locus_27116_Transcript_1/1_Conf_1.000	308	2	5.96E-07	NP_508809.1	86	57.3806	36	31	hypothetical protein F55D10.4
Locus_27117_Transcript_1/1_Conf_1.000	273	0							
Locus_27118_Transcript_1/1_Conf_1.000	148	0							
Locus_27119_Transcript_1/1_Conf_1.000	145	3	1.51E-13	NP_495697.2	93	79.337	48	45	Lim and Transglutaminase Domain family member (ltd-1)
Locus_2712_Transcript_1/1_Conf_1.000	767	20	9.76E-82	XP_002635274.1	86	307.375	227	197	Hypothetical protein CBG11518
Locus_27120_Transcript_1/1_Conf_1.000	170	0							
Locus_27121_Transcript_1/1_Conf_1.000	132	0							
Locus_27122_Transcript_1/1_Conf_1.000	214	0							
Locus_27123_Transcript_1/1_Conf_1.000	195	5	4.78E-20	XP_002634857.1	89	100.908	64	57	C. briggsae CBR-LGC-30 protein
Locus_27124_Transcript_1/1_Conf_1.000	256	0							
Locus_27125_Transcript_1/1_Conf_1.000	173	0							
Locus_27126_Transcript_1/1_Conf_1.000	212	0							
Locus_27127_Transcript_1/1_Conf_1.000	145	0							
Locus_27128_Transcript_1/1_Conf_1.000	136	0							
Locus_27129_Transcript_1/1_Conf_1.000	215	0							
Locus_2713_Transcript_1/2_Conf_1.000	1809	0							
Locus_2713_Transcript_2/2_Conf_1.000	1908	0							
Locus_27130_Transcript_1/1_Conf_1.000	258	0							
Locus_27131_Transcript_1/1_Conf_1.000	130	0							
Locus_27132_Transcript_1/1_Conf_1.000	117	0							
Locus_27133_Transcript_1/1_Conf_1.000	387	0							
Locus_27134_Transcript_1/1_Conf_1.000	305	3	1.98E-26	XP_002630047.1	74	122.094	101	75	Hypothetical protein CBG13418
Locus_27135_Transcript_1/1_Conf_1.000	175	1	4.72E-04	XP_002631859.1	54	47.7506	57	31	Hypothetical protein CBG07809
Locus_27136_Transcript_1/1_Conf_1.000	138	0							
Locus_27137_Transcript_1/1_Conf_1.000	200	0							

Locus_27138_Transcript_1/1_Conf_1.000	174	16	7.76E-15	XP_002644219.1	76	83.5741	63	48	Hypothetical protein CBG17217
Locus_27139_Transcript_1/1_Conf_1.000	158	5	3.80E-09	XP_002647112.1	88	64.6994	42	37	C. briggsae CBR-FRM-8 protein
Locus_2714_Transcript_1/1_Conf_1.000	2140	4	6.41E-48	CAZ39159.1	47	197.208	576	274	C. elegans protein C01C7.1b, partially confirmed by transcript evidence
Locus_27140_Transcript_1/1_Conf_1.000	176	20	1.41E-24	NP_495614.3	96	115.931	58	56	Na/H eXchanger family member (nhx-2)
Locus_27141_Transcript_1/1_Conf_1.000	144	5	1.24E-15	XP_002647501.1	91	86.2705	48	44	Hypothetical protein CBG06575
Locus_27142_Transcript_1/1_Conf_1.000	160	20	1.49E-05	XP_002647042.1	69	52.7582	46	32	Hypothetical protein CBG03560
Locus_27143_Transcript_1/1_Conf_1.000	264	7	9.01E-11	NP_492477.2	66	70.0922	83	55	PRogression Of Meiosis family member (prom-1)
Locus_27144_Transcript_1/1_Conf_1.000	167	0							
Locus_27145_Transcript_1/1_Conf_1.000	133	0							
Locus_27146_Transcript_1/1_Conf_1.000	177	4	1.67E-09	NP_510249.2	71	65.855	57	41	TREhalase family member (tre-4)
Locus_27147_Transcript_1/1_Conf_1.000	316	20	1.19E-18	XP_002644672.1	64	96.2857	107	69	C. briggsae CBR-VPS-41 protein
Locus_27148_Transcript_1/1_Conf_1.000	133	6	6.38E-09	XP_002636925.1	83	63.929	43	36	C. briggsae CBR-RHR-1 protein
Locus_27149_Transcript_1/1_Conf_1.000	132	0							
Locus_2715_Transcript_1/1_Conf_1.000	851	7	3.31E-07	XP_002631036.1	48	60.077	187	90	Hypothetical protein CBG02793

Locus_27150_Transcript_1/1_Conf_1.000	206	0							
Locus_27151_Transcript_1/1_Conf_1.000	131	0							
Locus_27152_Transcript_1/1_Conf_1.000	259	0							
Locus_27153_Transcript_1/1_Conf_1.000	139	0							
Locus_27154_Transcript_1/1_Conf_1.000	175	0							
Locus_27155_Transcript_1/1_Conf_1.000	190	20	1.77E-22	A8X4H1.2	87	108.997	63	55	Dual specificity tyrosine-phosphorylation-regulated kinase mbk-1
Locus_27156_Transcript_1/1_Conf_1.000	135	0							
Locus_27157_Transcript_1/1_Conf_1.000	238	20	6.81E-35	XP_002644000.1	97	150.214	79	77	C. briggsae CBR-IFA-1 protein
Locus_27158_Transcript_1/1_Conf_1.000	128	0							
Locus_27159_Transcript_1/1_Conf_1.000	161	20	5.10E-22	NP_001022571.1	94	107.457	53	50	NeuroFibroMatosis homolog family member (nfm-1)
Locus_2716_Transcript_1/1_Conf_1.000	182	0							
Locus_27160_Transcript_1/1_Conf_1.000	141	0							
Locus_27161_Transcript_1/1_Conf_1.000	352	0							
Locus_27162_Transcript_1/1_Conf_1.000	143	0							
Locus_27163_Transcript_1/1_Conf_1.000	142	0							
Locus_27164_Transcript_1/1_Conf_1.000	142	20	2.65E-15	EFO21255.1	87	85.1149	47	41	hypothetical protein LOAG_07233
Locus_27165_Transcript_1/1_Conf_1.000	134	0							
Locus_27166_Transcript_1/1_Conf_1.000	134	0							
Locus_27167_Transcript_1/1_Conf_1.000	230	0							
Locus_27168_Transcript_1/1_Conf_1.000	172	0							
Locus_27169_Transcript_1/1_Conf_1.000	129	0							
Locus_2717_Transcript_1/1_Conf_1.000	502	20	2.92E-17	CAD28559.2	49	91.6633	146	72	metalloprotease I
Locus_27170_Transcript_1/1_Conf_1.000	216	5	2.32E-11	NP_507813.1	67	72.0182	71	48	hypothetical protein Y43F8C.13
Locus_27171_Transcript_1/1_Conf_1.000	167	0							
Locus_27172_Transcript_1/1_Conf_1.000	138	0							
Locus_27173_Transcript_1/1_Conf_1.000	161	0							
Locus_27174_Transcript_1/1_Conf_1.000	131	0							
Locus_27175_Transcript_1/1_Conf_1.000	154	0							
Locus_27176_Transcript_1/1_Conf_1.000	266	20	2.51E-45	AAH04358.1	100	184.882	88	88	Transmembrane protein 176B

Locus_27177_Transcript_1/1_Conf_1.000	255	20	1.88E-32	XP_002634414.1	75	142.124	85	64	C. briggsae CBR-EPI-1 protein
Locus_27178_Transcript_1/1_Conf_1.000	193	0							
Locus_27179_Transcript_1/1_Conf_1.000	149	0							
Locus_2718_Transcript_1/1_Conf_1.000	343	20	2.44E-56	ACN93882.1	95	221.476	114	109	putative glutamate-cysteine ligase catalytic subunit
Locus_27180_Transcript_1/1_Conf_1.000	138	0							
Locus_27181_Transcript_1/1_Conf_1.000	174	0							
Locus_27182_Transcript_1/1_Conf_1.000	159	0							
Locus_27183_Transcript_1/1_Conf_1.000	150	0							
Locus_27184_Transcript_1/1_Conf_1.000	158	20	4.06E-11	EFO23046.1	75	71.2478	52	39	TK/FER protein kinase
Locus_27185_Transcript_1/1_Conf_1.000	146	20	2.76E-07	NP_495409.3	75	58.5362	49	37	hypothetical protein C44B7.10
Locus_27186_Transcript_1/1_Conf_1.000	149	0							

Locus_27187_Transcript_1/1_Conf_1.000	146	20	3.14E-19	XP_002913731.1	100	98.2117	48	48	PREDICTED: fibronectin-like isoform 4
Locus_27188_Transcript_1/1_Conf_1.000	140	0							
Locus_27189_Transcript_1/1_Conf_1.000	198	0							
Locus_2719_Transcript_1/1_Conf_1.000	285	1	4.84E-04	XP_002641754.1	57	47.7506	80	46	C. briggsae CBR-EMB-30 protein
Locus_27190_Transcript_1/1_Conf_1.000	570	18	5.08E-26	NP_001023369.1	63	121.324	153	97	Nuclear Hormone Receptor family member (nhr-66)
Locus_27191_Transcript_1/1_Conf_1.000	439	0							
Locus_27192_Transcript_1/1_Conf_1.000	155	20	9.68E-21	AAZ91344.1	98	103.219	51	50	Synaptotagmin protein 2
Locus_27193_Transcript_1/1_Conf_1.000	239	20	3.74E-25	EFO23834.1	79	117.857	79	63	hypothetical protein LOAG_04651
Locus_27194_Transcript_1/1_Conf_1.000	132	0							
Locus_27195_Transcript_1/1_Conf_1.000	232	18	1.14E-21	XP_002644475.1	76	106.301	77	59	Hypothetical protein CBG14354
Locus_27196_Transcript_1/1_Conf_1.000	287	20	1.10E-40	XP_002634234.1	89	169.474	95	85	Hypothetical protein CBG01804
Locus_27197_Transcript_1/1_Conf_1.000	306	0							
Locus_27198_Transcript_1/1_Conf_1.000	234	0							
Locus_27199_Transcript_1/1_Conf_1.000	239	0							

Locus_272_Transcript_1/4_Conf_0.400	897	20	1.15E-61	CAO00417.1	62	241.121	261	163	two-domain activation associated secreted protein ASP4 precursor
Locus_272_Transcript_2/4_Conf_0.200	185	0							
Locus_272_Transcript_3/4_Conf_0.300	253	9	1.32E-09	CAO00417.1	60	66.2402	70	42	two-domain activation associated secreted protein ASP4 precursor
Locus_272_Transcript_4/4_Conf_0.700	1404	20	1.96E-89	CAO00417.1	57	334.339	444	254	two-domain activation associated secreted protein ASP4 precursor
Locus_2720_Transcript_1/1_Conf_1.000	1925	20	1.30E-28	XP_002129449.1	47	132.88	310	146	PREDICTED: hypothetical protein
Locus_27200_Transcript_1/1_Conf_1.000	142	0							
Locus_27201_Transcript_1/1_Conf_1.000	176	20	5.55E-21	NP_001021871.1	93	103.99	58	54	UNCoordinated family member (unc-13)
Locus_27202_Transcript_1/1_Conf_1.000	130	0							
Locus_27203_Transcript_1/1_Conf_1.000	163	0							
Locus_27204_Transcript_1/1_Conf_1.000	137	7	2.12E-04	XP_002636031.1	71	48.9062	46	33	Hypothetical protein CBG01269
Locus_27205_Transcript_1/1_Conf_1.000	197	0							
Locus_27206_Transcript_1/1_Conf_1.000	217	6	7.94E-28	XP_002639744.1	90	126.716	72	65	C. briggsae CBR-LAM-3 protein
Locus_27207_Transcript_1/1_Conf_1.000	162	0							
Locus_27208_Transcript_1/1_Conf_1.000	128	20	2.88E-09	NP_505070.2	92	65.0846	39	36	Valyl tRNA Synthetase family member (vrs-1)
Locus_27209_Transcript_1/1_Conf_1.000	143	0							

Locus_2721_Transcript_1/1_Conf_1.000	823	20	1.10E-121	NP_492765.1	95	440.269	248	238	Proteasome Alpha Subunit family member (pas-5)
Locus_27210_Transcript_1/1_Conf_1.000	251	1	1.61E-04	XP_002639744.1	61	49.2914	83	51	C. briggsae CBR-LAM-3 protein
Locus_27211_Transcript_1/1_Conf_1.000	172	20	4.41E-18	XP_002811661.1	100	94.3597	44	44	PREDICTED: cyclin-L2-like
Locus_27212_Transcript_1/1_Conf_1.000	132	2	7.29E-13	NP_493603.1	93	77.0258	43	40	PaTched Related family member (ptr-23)
Locus_27213_Transcript_1/1_Conf_1.000	209	1	4.89E-09	NP_497674.3	68	64.3142	66	45	hypothetical protein Y53G8AL.1
Locus_27214_Transcript_1/1_Conf_1.000	210	0							
Locus_27215_Transcript_1/1_Conf_1.000	157	1	3.43E-18	XP_002634588.1	98	94.7449	50	49	Hypothetical protein CBG08399
Locus_27216_Transcript_1/1_Conf_1.000	148	2	7.24E-08	NP_504489.3	74	60.4622	50	37	HEXosaminidase family member (hex-2)
Locus_27217_Transcript_1/1_Conf_1.000	200	0							
Locus_27218_Transcript_1/1_Conf_1.000	226	9	2.08E-23	XP_002646356.1	81	112.079	76	62	Hypothetical protein CBG12070
Locus_27219_Transcript_1/1_Conf_1.000	213	0							
Locus_2722_Transcript_1/1_Conf_1.000	237	15	3.74E-25	XP_001902374.1	91	117.857	78	71	MYND finger family protein
Locus_27220_Transcript_1/1_Conf_1.000	282	20	8.50E-33	2WS2	86	143.28	93	80	The 2 AngstromStructure Of A Nu-Class Gst From Haemonchus Contortus
Locus_27221_Transcript_1/1_Conf_1.000	128	0							

Locus_27222_Transcript_1/1_Conf_1.000	163	17	1.70E-09	AAA28106.1	95	65.855	46	44	DNA-binding protein mab5
Locus_27223_Transcript_1/1_Conf_1.000	254	9	3.58E-15	AAO18224.1	91	84.7297	47	43	FMRFamide-like prepropeptide
Locus_27224_Transcript_1/1_Conf_1.000	211	0							
Locus_27225_Transcript_1/1_Conf_1.000	137	0							
Locus_27226_Transcript_1/1_Conf_1.000	229	0							
Locus_27227_Transcript_1/1_Conf_1.000	131	0							
Locus_27228_Transcript_1/1_Conf_1.000	164	20	6.65E-14	EFO24191.1	75	80.4925	53	40	hypothetical protein LOAG_04290
Locus_27229_Transcript_1/1_Conf_1.000	289	0							
Locus_2723_Transcript_1/2_Conf_1.000	325	0							
Locus_2723_Transcript_2/2_Conf_1.000	244	0							
Locus_27230_Transcript_1/1_Conf_1.000	158	7	2.38E-19	NP_504415.2	98	98.5969	52	51	Na/Ca eXchangers family member (ncx-2)
Locus_27231_Transcript_1/1_Conf_1.000	281	20	2.24E-22	XP_002644607.1	70	108.612	92	65	Hypothetical protein CBG14563
Locus_27232_Transcript_1/1_Conf_1.000	179	0							
Locus_27233_Transcript_1/1_Conf_1.000	297	20	1.37E-51	XP_002805211.1	100	205.682	98	98	PREDICTED: epididymal secretory protein E1 isoform 2
Locus_27234_Transcript_1/1_Conf_1.000	235	20	3.29E-21	NP_490828.3	81	104.76	77	63	HAlF transporter (PGP related) family member (haf-6)
Locus_27235_Transcript_1/1_Conf_1.000	275	0							
Locus_27236_Transcript_1/1_Conf_1.000	141	20	1.90E-13	XP_002637557.1	86	78.9518	45	39	Hypothetical protein CBG19289
Locus_27237_Transcript_1/1_Conf_1.000	240	3	2.97E-06	CAA91482.3	71	55.0694	80	57	C. elegans protein T04F8.6, partially confirmed by transcript evidence
Locus_27238_Transcript_1/1_Conf_1.000	192	20	3.43E-18	XP_002647771.1	82	94.7449	63	52	C. briggsae CBR-PPH-5 protein

Locus_27239_Transcript_1/1_Conf_1.000	506								
Locus_2724_Transcript_1/2_Conf_1.000	1453	1	5.70E-23	CAR63643.1	55	113.62	171	95	hypothetical protein
Locus_2724_Transcript_2/2_Conf_1.000	1453	1	5.69E-23	CAR63643.1	55	113.62	171	95	hypothetical protein
Locus_27240_Transcript_1/1_Conf_1.000	128	0							
Locus_27241_Transcript_1/1_Conf_1.000	177	0							
Locus_27242_Transcript_1/1_Conf_1.000	235	0							
Locus_27243_Transcript_1/1_Conf_1.000	251	0							
Locus_27244_Transcript_1/1_Conf_1.000	309	0							
Locus_27245_Transcript_1/1_Conf_1.000	202	5	1.69E-09	XP_002640146.1	64	65.855	68	44	C. briggsae CBR-GLY-2 protein
Locus_27246_Transcript_1/1_Conf_1.000	172	0							
Locus_27247_Transcript_1/1_Conf_1.000	132	0							
Locus_27248_Transcript_1/1_Conf_1.000	330	4	1.20E-31	XP_002637246.1	86	139.428	109	94	Hypothetical protein CBG18923
Locus_27249_Transcript_1/1_Conf_1.000	381	0							
Locus_2725_Transcript_1/2_Conf_1.000	339	0							
Locus_2725_Transcript_2/2_Conf_1.000	335	0							
Locus_27250_Transcript_1/1_Conf_1.000	189	0							
Locus_27251_Transcript_1/1_Conf_1.000	151	4	7.20E-16	NP_001033432.1	89	87.0409	49	44	hypothetical protein T19E7.6
Locus_27252_Transcript_1/1_Conf_1.000	201	0							
Locus_27253_Transcript_1/1_Conf_1.000	193	0							
Locus_27254_Transcript_1/1_Conf_1.000	317	0							
Locus_27255_Transcript_1/1_Conf_1.000	156	0							
Locus_27256_Transcript_1/1_Conf_1.000	135	0							
Locus_27257_Transcript_1/1_Conf_1.000	146	0							
Locus_27258_Transcript_1/1_Conf_1.000	629	20	1.47E-62	NP_492775.2	74	243.047	209	155	LAMinin related. See also lmb- family member (lam-3)
Locus_27259_Transcript_1/1_Conf_1.000	220	20	4.68E-15	XP_002631639.1	69	84.3445	72	50	Hypothetical protein CBG20828
Locus_2726_Transcript_1/1_Conf_1.000	1240	20	1.22E-92	NP_499642.2	72	344.739	314	228	Enhancer of PolyComb-like family member (epc-1)
Locus_27260_Transcript_1/1_Conf_1.000	150	0							
Locus_27261_Transcript_1/1_Conf_1.000	129	0							
Locus_27262_Transcript_1/1_Conf_1.000	204	20	1.16E-18	XP_002636748.1	76	96.2857	67	51	Hypothetical protein CBG23475
Locus_27263_Transcript_1/1_Conf_1.000	252	0							
Locus_27264_Transcript_1/1_Conf_1.000	287	0							
Locus_27265_Transcript_1/1_Conf_1.000	478	0							
Locus_27266_Transcript_1/1_Conf_1.000	151	0							
Locus_27267_Transcript_1/1_Conf_1.000	164	0							
Locus_27268_Transcript_1/1_Conf_1.000	199	20	1.21E-31	EFO12308.1	100	139.428	66	66	MYO-2

Locus_27269_Transcript_1/1_Conf_1.000	132	0							
Locus_2727_Transcript_1/4_Conf_0.600	1214	7	2.23E-91	XP_002647070.1	84	340.502	224	189	Hypothetical protein CBG03596
Locus_2727_Transcript_2/4_Conf_0.700	1357	7	2.62E-91	XP_002647070.1	84	340.502	224	189	Hypothetical protein CBG03596
Locus_2727_Transcript_3/4_Conf_0.700	1357	7	3.42E-91	XP_002647070.1	84	340.117	224	189	Hypothetical protein CBG03596
Locus_2727_Transcript_4/4_Conf_0.700	1357	7	2.62E-91	XP_002647070.1	84	340.502	224	189	Hypothetical protein CBG03596
Locus_27270_Transcript_1/1_Conf_1.000	144	0							
Locus_27271_Transcript_1/1_Conf_1.000	176	20	5.54E-29	BAG59028.1	100	130.568	58	58	unnamed protein product
Locus_27272_Transcript_1/1_Conf_1.000	296	20	2.60E-34	NP_501792.2	77	148.288	94	73	abnormal GONad development family member (gon-1)
Locus_27273_Transcript_1/1_Conf_1.000	148	0							
Locus_27274_Transcript_1/1_Conf_1.000	188	0							
Locus_27275_Transcript_1/1_Conf_1.000	129	0							
Locus_27276_Transcript_1/1_Conf_1.000	150	0							
Locus_27277_Transcript_1/1_Conf_1.000	146	0							
Locus_27278_Transcript_1/1_Conf_1.000	245	5	6.14E-20	XP_002638957.1	75	100.523	81	61	Hypothetical protein CBG22193
Locus_27279_Transcript_1/1_Conf_1.000	238	0							
Locus_2728_Transcript_1/2_Conf_1.000	641	20	1.78E-50	BAB59011.1	86	202.986	129	111	nippocystatin
Locus_2728_Transcript_2/2_Conf_1.000	641	20	1.78E-50	BAB59011.1	86	202.986	129	111	nippocystatin
Locus_27280_Transcript_1/1_Conf_1.000	177	5	8.85E-11	NP_501388.1	67	70.0922	61	41	hypothetical protein K07H8.5
Locus_27281_Transcript_1/1_Conf_1.000	140	4	2.26E-06	XP_002633417.1	76	55.4546	43	33	C. briggsae CBR-TRPA-1 protein
Locus_27282_Transcript_1/1_Conf_1.000	148	0							

Locus_27283_Transcript_1/1_Conf_1.000	138	20	3.72E-09	XP_002923775.1	100	64.6994	46	46	PREDICTED: hypothetical protein LOC100476237
Locus_27284_Transcript_1/1_Conf_1.000	250	0							
Locus_27285_Transcript_1/1_Conf_1.000	140	4	4.86E-09	EFO27124.1	79	64.3142	44	35	laminin alpha 1 chain
Locus_27286_Transcript_1/1_Conf_1.000	145	0							
Locus_27287_Transcript_1/1_Conf_1.000	198	0							
Locus_27288_Transcript_1/1_Conf_1.000	187	0							
Locus_27289_Transcript_1/1_Conf_1.000	241	0							
Locus_2729_Transcript_1/2_Conf_1.000	1373	20	7.33E-49	XP_002631067.1	49	199.519	426	209	C. briggsae CBR-TRR-1 protein
Locus_2729_Transcript_2/2_Conf_1.000	1240	20	7.30E-37	XP_002631067.1	47	159.458	388	184	C. briggsae CBR-TRR-1 protein
Locus_27290_Transcript_1/1_Conf_1.000	214	0							
Locus_27291_Transcript_1/1_Conf_1.000	197	0							
Locus_27292_Transcript_1/1_Conf_1.000	148	0							
Locus_27293_Transcript_1/1_Conf_1.000	215	0							
Locus_27294_Transcript_1/1_Conf_1.000	161	0							
Locus_27295_Transcript_1/1_Conf_1.000	191	0							
Locus_27296_Transcript_1/1_Conf_1.000	587	20	8.46E-43	NP_741631.2	64	177.178	196	126	hypothetical protein C55A6.10
Locus_27297_Transcript_1/1_Conf_1.000	145	20	9.14E-19	Q2VIR3.2	100	96.6709	47	47	Eukaryotic translation initiation factor 2 subunit 3-like protein
Locus_27298_Transcript_1/1_Conf_1.000	120	0							

Locus_27299_Transcript_1/1_Conf_1.000	322	20	4.62E-23	XP_002643824.1	64	110.923	99	64	Hypothetical protein CBG02040
Locus_273_Transcript_1/2_Conf_1.000	2670	20	0	ACI49199.1	78	1068.91	885	696	hypothetical protein Csp3_JD03.008
Locus_273_Transcript_2/2_Conf_1.000	1053	20	3.19E-80	ACI49199.1	73	303.138	288	211	hypothetical protein Csp3_JD03.008
Locus_2730_Transcript_1/2_Conf_0.833	542	0							
Locus_2730_Transcript_2/2_Conf_0.833	536	0							
Locus_27300_Transcript_1/1_Conf_1.000	144	0							
Locus_27301_Transcript_1/1_Conf_1.000	132	0							
Locus_27302_Transcript_1/1_Conf_1.000	160	20	1.48E-21	2XND	100	105.916	53	53	CrystalStructure Of Bovine F1-C8 Sub-Complex Of Atp Synthase
Locus_27303_Transcript_1/1_Conf_1.000	138	4	2.58E-10	NP_503353.2	84	68.5514	45	38	hypothetical protein H24K24.4
Locus_27304_Transcript_1/1_Conf_1.000	148	0							
Locus_27305_Transcript_1/1_Conf_1.000	162	0							
Locus_27306_Transcript_1/1_Conf_1.000	316	20	4.47E-42	NP_001022681.1	98	174.096	104	102	hypothetical protein K11H3.7
Locus_27307_Transcript_1/1_Conf_1.000	164	4	6.23E-12	NP_491646.3	80	73.9442	45	36	hypothetical protein F46F11.7
Locus_27308_Transcript_1/1_Conf_1.000	308	20	7.48E-26	NP_500551.2	76	120.168	100	76	hypothetical protein F55F10.1
Locus_27309_Transcript_1/1_Conf_1.000	398	20	7.83E-55	XP_002643352.1	87	216.468	132	115	C. briggsae CBR-KIN-25 protein
Locus_2731_Transcript_1/2_Conf_1.000	3499	20	6.78E-178	NP_494796.2	55	629.787	1101	607	hypothetical protein T05C1.4

Locus_2731_Transcript_2/2_Conf_1.000	3455	20	6.68E-178	NP_494796.2	55	629.787	1101	607	hypothetical protein T05C1.4
Locus_27310_Transcript_1/1_Conf_1.000	213	0							
Locus_27311_Transcript_1/1_Conf_1.000	368	0							
Locus_27312_Transcript_1/1_Conf_1.000	130	2	2.69E-07	NP_492590.1	76	58.5362	42	32	hypothetical protein K02A11.3
Locus_27313_Transcript_1/1_Conf_1.000	157	0							
Locus_27314_Transcript_1/1_Conf_1.000	207	4	1.62E-12	XP_002632143.1	77	75.8702	66	51	Hypothetical protein CBG07002
Locus_27315_Transcript_1/1_Conf_1.000	300	20	3.15E-40	NP_492177.2	89	167.933	99	89	hypothetical protein R11A5.7
Locus_27316_Transcript_1/1_Conf_1.000	133	0							
Locus_27317_Transcript_1/1_Conf_1.000	135	0							
Locus_27318_Transcript_1/1_Conf_1.000	340	5	2.91E-38	NP_494711.1	84	161.384	98	83	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-48)
Locus_27319_Transcript_1/1_Conf_1.000	495	2	5.36E-32	NP_500987.3	78	140.584	99	78	hypothetical protein Y73B6BL.1
Locus_2732_Transcript_1/2_Conf_1.000	639	20	4.49E-56	XP_002643222.1	79	217.624	180	143	Hypothetical protein CBG08087
Locus_2732_Transcript_2/2_Conf_1.000	1317	20	5.69E-144	XP_002643222.1	81	515.383	420	342	Hypothetical protein CBG08087
Locus_27320_Transcript_1/1_Conf_1.000	175	0							
Locus_27321_Transcript_1/1_Conf_1.000	218	7	2.02E-23	XP_002643289.1	88	112.079	72	64	C. briggsae CBR-DVE-1 protein
Locus_27322_Transcript_1/1_Conf_1.000	160	0							
Locus_27323_Transcript_1/1_Conf_1.000	147	0							

Locus_27324_Transcript_1/1_Conf_1.000	199	3	3.20E-08	XP_002638395.1	72	61.6178	50	36	Hypothetical protein CBG18604
Locus_27325_Transcript_1/1_Conf_1.000	268	7	3.38E-42	NP_495495.1	93	174.481	88	82	hypothetical protein E04F6.6
Locus_27326_Transcript_1/1_Conf_1.000	157	0							
Locus_27327_Transcript_1/1_Conf_1.000	164	0							
Locus_27328_Transcript_1/1_Conf_1.000	220	0							
Locus_27329_Transcript_1/1_Conf_1.000	204	0							
Locus_2733_Transcript_1/1_Conf_1.000	647	20	4.94E-56	P27613.1	79	221.476	164	130	Globin-like host-protective antigen
Locus_27330_Transcript_1/1_Conf_1.000	300	0							
Locus_27331_Transcript_1/1_Conf_1.000	128	0							
Locus_27332_Transcript_1/1_Conf_1.000	228	0							
Locus_27333_Transcript_1/1_Conf_1.000	224	0							
Locus_27334_Transcript_1/1_Conf_1.000	268	20	5.78E-34	NP_503052.1	93	147.132	88	82	hypothetical protein C52D10.12
Locus_27335_Transcript_1/1_Conf_1.000	152	0							
Locus_27336_Transcript_1/1_Conf_1.000	302	0							
Locus_27337_Transcript_1/1_Conf_1.000	173	20	1.47E-13	EFO26082.1	78	79.337	57	45	hypothetical protein LOAG_02394
Locus_27338_Transcript_1/1_Conf_1.000	251	20	5.15E-27	XP_002632128.1	86	124.02	83	72	Hypothetical protein CBG06984
Locus_27339_Transcript_1/1_Conf_1.000	173	4	5.97E-07	EFO17910.1	72	57.3806	54	39	hypothetical protein LOAG_10588
Locus_2734_Transcript_1/1_Conf_1.000	704	0							
Locus_27340_Transcript_1/1_Conf_1.000	177	6	7.49E-10	CAX65068.1	75	67.0106	54	41	C. elegans protein K08C7.3d, confirmed by transcript evidence
Locus_27341_Transcript_1/1_Conf_1.000	133	0							
Locus_27342_Transcript_1/1_Conf_1.000	257	0							
Locus_27343_Transcript_1/1_Conf_1.000	212	6	8.86E-19	ADI99915.1	81	96.6709	70	57	hammerhead protein
Locus_27344_Transcript_1/1_Conf_1.000	147	0							
Locus_27345_Transcript_1/1_Conf_1.000	164	0							
Locus_27346_Transcript_1/1_Conf_1.000	181	9	9.48E-16	NP_498645.1	78	86.6557	60	47	MUscle Positioning family member (mup-4)
Locus_27347_Transcript_1/1_Conf_1.000	131	0							
Locus_27348_Transcript_1/1_Conf_1.000	142	0							
Locus_27349_Transcript_1/1_Conf_1.000	173	0							
Locus_2735_Transcript_1/2_Conf_1.000	539	0							
Locus_2735_Transcript_2/2_Conf_1.000	557	0							
Locus_27350_Transcript_1/1_Conf_1.000	130	0							

Locus_27351_Transcript_1/1_Conf_1.000	183	20	1.56E-18	NP_493616.1	87	95.9005	55	48	hypothetical protein F33H2.5
Locus_27352_Transcript_1/1_Conf_1.000	162	0							
Locus_27353_Transcript_1/1_Conf_1.000	134	0							
Locus_27354_Transcript_1/1_Conf_1.000	168	0							
Locus_27355_Transcript_1/1_Conf_1.000	189	0							
Locus_27356_Transcript_1/1_Conf_1.000	151	0							
Locus_27357_Transcript_1/1_Conf_1.000	204	0							
Locus_27358_Transcript_1/1_Conf_1.000	152	20	2.40E-11	XP_002799163.1	100	72.0182	34	34	PREDICTED: vigilin-like
Locus_27359_Transcript_1/1_Conf_1.000	271	0							
Locus_2736_Transcript_1/1_Conf_1.000	455	0							
Locus_27360_Transcript_1/1_Conf_1.000	403	0							
Locus_27361_Transcript_1/1_Conf_1.000	197	0							
Locus_27362_Transcript_1/1_Conf_1.000	503	20	1.02E-86	AAM54172.2	99	322.398	167	166	AF077541_9Alpha-catulin (catenin/vinculin related) protein 1, isoform d, confirmed by transcript evidence
Locus_27363_Transcript_1/1_Conf_1.000	527	9	5.08E-21	XP_002643964.1	57	104.375	180	104	C. briggsae CBR-HUM-4 protein
Locus_27364_Transcript_1/1_Conf_1.000	243	0							
Locus_27365_Transcript_1/1_Conf_1.000	374	0							
Locus_27366_Transcript_1/1_Conf_1.000	167	0							
Locus_27367_Transcript_1/1_Conf_1.000	287	3	1.55E-10	XP_002634616.1	56	69.3218	94	53	Hypothetical protein CBG18470
Locus_27368_Transcript_1/1_Conf_1.000	235	20	7.10E-16	NP_502118.4	76	87.0409	77	59	Gon-Two Like (TRP subfamily) family member (gtl-2)

Locus_27369_Transcript_1/1_Conf_1.000	142	20	1.36E-19	XP_001714126.2	100	99.3673	47	47	PREDICTED: similar to major histocompatibility complex, class II, DR beta 5 isoform 2
Locus_2737_Transcript_1/1_Conf_1.000	1354	0							
Locus_27370_Transcript_1/1_Conf_1.000	157	0							
Locus_27371_Transcript_1/1_Conf_1.000	148	0							
Locus_27372_Transcript_1/1_Conf_1.000	301	4	2.96E-22	EFO24933.1	83	108.227	80	67	AGC/PKN protein kinase
Locus_27373_Transcript_1/1_Conf_1.000	216	20	4.81E-33	2WII	100	144.05	72	72	Complement C3b In Complex With Factor H Domains 1-4
Locus_27374_Transcript_1/1_Conf_1.000	179	19	9.43E-21	EAW95274.1	100	103.219	59	59	hCG2040005
Locus_27375_Transcript_1/1_Conf_1.000	178	0							

Locus_27376_Transcript_1/1_Conf_1.000	327	20	7.52E-42	XP_002631558.1	82	173.326	106	87	Hypothetical protein CBG20734
Locus_27377_Transcript_1/1_Conf_1.000	142	20	3.46E-15	XP_002646726.1	93	84.7297	44	41	Hypothetical protein CBG13109
Locus_27378_Transcript_1/1_Conf_1.000	188	0							
Locus_27379_Transcript_1/1_Conf_1.000	155	0							
Locus_2738_Transcript_1/1_Conf_1.000	264	20	4.58E-39	NP_001022488.1	92	164.081	88	81	UNCoordinated family member (unc-52)
Locus_27380_Transcript_1/1_Conf_1.000	216	0							
Locus_27381_Transcript_1/1_Conf_1.000	147	0							
Locus_27382_Transcript_1/1_Conf_1.000	205	0							
Locus_27383_Transcript_1/1_Conf_1.000	187	0							
Locus_27384_Transcript_1/1_Conf_1.000	205	0							
Locus_27385_Transcript_1/1_Conf_1.000	153	20	1.65E-20	NP_937758.1	100	102.449	51	51	TYRO protein tyrosine kinase-binding protein isoform 2 precursor
Locus_27386_Transcript_1/1_Conf_1.000	149	0							
Locus_27387_Transcript_1/1_Conf_1.000	141	9	1.27E-09	XP_002643629.1	97	66.2402	47	46	C. briggsae CBR-LET-2 protein
Locus_27388_Transcript_1/1_Conf_1.000	139	0							
Locus_27389_Transcript_1/1_Conf_1.000	129	0							
Locus_2739_Transcript_1/1_Conf_1.000	493	0							
Locus_27390_Transcript_1/1_Conf_1.000	189	20	1.00E-09	XP_002641412.1	70	66.6254	64	45	Hypothetical protein CBG13278
Locus_27391_Transcript_1/1_Conf_1.000	223								
Locus_27392_Transcript_1/1_Conf_1.000	147	20	2.10E-15	BAH12126.1	100	85.5001	37	37	unnamed protein product
Locus_27393_Transcript_1/1_Conf_1.000	227	0							
Locus_27394_Transcript_1/1_Conf_1.000	180	0							
Locus_27395_Transcript_1/1_Conf_1.000	141	0							

Locus_27396_Transcript_1/1_Conf_1.000	136	20	1.85E-08	ADJ19295.1	77	62.3882	44	34	carbamoyl phosphate synthetase-aspartate transcarbamoylase-dihydroorotase
Locus_27397_Transcript_1/1_Conf_1.000	213	20	1.55E-31	XP_002921123.1	100	139.043	70	70	PREDICTED: proteasome activator complex subunit 2-like
Locus_27398_Transcript_1/1_Conf_1.000	207	0							
Locus_27399_Transcript_1/1_Conf_1.000	417	20	3.43E-34	XP_002815693.1	70	147.902	129	91	PREDICTED: LOW QUALITY PROTEIN: beta-hexosaminidase subunit beta-like
Locus_274_Transcript_1/1_Conf_1.000	488	12	1.34E-30	ACE79378.1	88	135.961	120	106	surface-associated antigen 2
Locus_2740_Transcript_1/4_Conf_0.625	1869	20	1.02E-62		47	246.128	631	298	protein F20H11.2
Locus_2740_Transcript_2/4_Conf_0.625	3390	20	0	ADF27719.1	60	841.262	1180	718	notch signaling pathway homolog-1
Locus_2740_Transcript_3/4_Conf_0.625	3591	20	0		59	841.262	1252	742	protein F20H11.2
Locus_2740_Transcript_4/4_Conf_0.625	3597	20	0		59	841.647	1259	744	protein F20H11.2
Locus_27400_Transcript_1/1_Conf_1.000	207	0							
Locus_27401_Transcript_1/1_Conf_1.000	279	0							
Locus_27402_Transcript_1/1_Conf_1.000	130	0							
Locus_27403_Transcript_1/1_Conf_1.000	133	0							
Locus_27404_Transcript_1/1_Conf_1.000	232	2	1.44E-08	NP_495202.1	69	62.7734	65	45	hypothetical protein ZK84.1

Locus_27405_Transcript_1/1_Conf_1.000	135	20	1.62E-12	XP_002643996.1	91	75.8702	45	41	Hypothetical protein CBG17377
Locus_27406_Transcript_1/1_Conf_1.000	173	19	1.68E-17	NP_490744.1	83	92.4337	56	47	fatty Acid CoA Synthetase family member (acs-13)
Locus_27407_Transcript_1/1_Conf_1.000	300	0							
Locus_27408_Transcript_1/1_Conf_1.000	157	0							
Locus_27409_Transcript_1/1_Conf_1.000	203	0							
Locus_2741_Transcript_1/1_Conf_1.000	4302	20	0	NP_001023390.1	80	1392.87	1134	909	PDZ eXchange Factor family member (pxf-1)
Locus_27410_Transcript_1/1_Conf_1.000	268	20	1.57E-31	XP_001896231.1	80	139.043	88	71	SEC14-like protein 4
Locus_27411_Transcript_1/1_Conf_1.000	205	5	5.41E-16	NP_500551.2	77	87.4261	63	49	hypothetical protein F55F10.1
Locus_27412_Transcript_1/1_Conf_1.000	237	0							
Locus_27413_Transcript_1/1_Conf_1.000	171	20	5.39E-16	XP_001893633.1	84	87.4261	57	48	protein F10G7.1
Locus_27414_Transcript_1/1_Conf_1.000	304	0							
Locus_27415_Transcript_1/1_Conf_1.000	187	3	1.04E-06	NP_497814.3	79	56.6102	43	34	UNCoordinated family member (unc-79)
Locus_27416_Transcript_1/1_Conf_1.000	450	20	5.74E-50	NP_506358.3	78	200.29	150	118	hypothetical protein C56A3.8
Locus_27417_Transcript_1/1_Conf_1.000	199	0							
Locus_27418_Transcript_1/1_Conf_1.000	168	0							
Locus_27419_Transcript_1/1_Conf_1.000	178	3	9.14E-16	XP_002639748.1	88	86.6557	51	45	Hypothetical protein CBG24342
Locus_2742_Transcript_1/1_Conf_1.000	150	0							
Locus_27420_Transcript_1/1_Conf_1.000	166	0							
Locus_27421_Transcript_1/1_Conf_1.000	217	1	5.54E-05	XP_001899466.1	54	50.8322	92	50	Hypothetical 84.0 kDa protein T23G5.2 in chromosome III, putative
Locus_27422_Transcript_1/1_Conf_1.000	166	0							

Locus_27423_Transcript_1/1_Conf_1.000	525	20	1.72E-69	AAD01960.1	90	265.388	175	159	UNC-45
Locus_27424_Transcript_1/1_Conf_1.000	375	20	2.28E-38	XP_002645548.1	77	161.77	108	84	Hypothetical protein CBG05229
Locus_27425_Transcript_1/1_Conf_1.000	162	0							
Locus_27426_Transcript_1/1_Conf_1.000	144	0							
Locus_27427_Transcript_1/1_Conf_1.000	301	20	8.28E-49	ADF56005.1	97	196.438	99	97	nicotinic acetylcholine receptor non-alpha subunit 29.1
Locus_27428_Transcript_1/1_Conf_1.000	139	0							
Locus_27429_Transcript_1/1_Conf_1.000	246	7	1.51E-18	NP_501963.1	69	95.9005	69	48	PaTched Related family member (ptr-14)
Locus_2743_Transcript_1/1_Conf_1.000	1333	3	4.55E-48	NP_509147.2	75	196.823	181	137	GEX Interacting protein family member (gei-15)
Locus_27430_Transcript_1/1_Conf_1.000	333	2	1.98E-10	EFO22933.1	70	68.9366	88	62	hypothetical protein LOAG_05552
Locus_27431_Transcript_1/1_Conf_1.000	143	0							
Locus_27432_Transcript_1/1_Conf_1.000	263	0							
Locus_27433_Transcript_1/1_Conf_1.000	145	20	1.56E-18	EFO20921.1	91	95.9005	48	44	NEK/NEK6 protein kinase
Locus_27434_Transcript_1/1_Conf_1.000	162	2	2.00E-10	NP_498385.2	80	68.9366	51	41	hypothetical protein C56G2.4
Locus_27435_Transcript_1/1_Conf_1.000	157	0							
Locus_27436_Transcript_1/1_Conf_1.000	236	8	2.20E-25	XP_002642996.1	85	118.627	77	66	C. briggsae CBR-UNC-45 protein
Locus_27437_Transcript_1/1_Conf_1.000	248	20	3.14E-24	NP_001073331.1	100	114.775	55	55	acyl-CoA-binding protein isoform 3
Locus_27438_Transcript_1/1_Conf_1.000	222	0							
Locus_27439_Transcript_1/1_Conf_1.000	129	0							
Locus_2744_Transcript_1/1_Conf_1.000	396	0							
Locus_27440_Transcript_1/1_Conf_1.000	225	5	1.65E-12	NP_001022641.1	54	75.8702	109	59	LEThal family member (let-805)
Locus_27441_Transcript_1/1_Conf_1.000	260	20	1.95E-13	XP_002630378.1	70	78.9518	77	54	Hypothetical protein CBG04317
Locus_27442_Transcript_1/1_Conf_1.000	154	2	5.88E-10	NP_001123185.1	76	67.3958	51	39	hypothetical protein T21H8.1

Locus_27443_Transcript_1/1_Conf_1.000	174	0							
Locus_27444_Transcript_1/1_Conf_1.000	136	0							
Locus_27445_Transcript_1/1_Conf_1.000	158	5	5.48E-16	XP_002631013.1	86	87.4261	52	45	C. briggsae CBR-PTR-18 protein
Locus_27446_Transcript_1/1_Conf_1.000	207	0							
Locus_27447_Transcript_1/1_Conf_1.000	163	3	1.39E-11	NP_001129849.1	77	72.7886	53	41	Choline Kinase A family member (cka-1)
Locus_27448_Transcript_1/1_Conf_1.000	199	0							
Locus_27449_Transcript_1/1_Conf_1.000	376	20	4.29E-45	CAA84706.3	82	184.111	123	101	C. elegans protein C38H2.1, partially confirmed by transcript evidence
Locus_2745_Transcript_1/2_Conf_0.500	1262	20	1.44E-157	NP_507859.2	78	560.451	419	330	hypothetical protein Y60A3A.14
Locus_2745_Transcript_2/2_Conf_0.500	941	20	2.80E-154	NP_001123113.1	91	548.895	300	273	Cysteine PRotease related family member (cpr-6)
Locus_27450_Transcript_1/1_Conf_1.000	233	9	7.13E-16	NP_495675.1	77	87.0409	77	60	hypothetical protein DH11.1
Locus_27451_Transcript_1/1_Conf_1.000	129	0							
Locus_27452_Transcript_1/1_Conf_1.000	139	0							
Locus_27453_Transcript_1/1_Conf_1.000	129	8	1.47E-13	NP_001020988.1	90	79.337	42	38	UNCoordinated family member (unc-89)
Locus_27454_Transcript_1/1_Conf_1.000	163	20	1.06E-19	NP_501709.2	92	99.7525	53	49	Membrane Calcium ATPase family member (mca-1)
Locus_27455_Transcript_1/1_Conf_1.000	156	4	7.93E-07	NP_497607.3	75	56.9954	52	39	hypothetical protein Y71H2AM.7
Locus_27456_Transcript_1/1_Conf_1.000	185	20	1.51E-13	AAP36473.1	100	79.337	38	38	Homo sapiens defender against cell death 1
Locus_27457_Transcript_1/1_Conf_1.000	131	0							
Locus_27458_Transcript_1/1_Conf_1.000	171	0							
Locus_27459_Transcript_1/1_Conf_1.000	201	0							
Locus_2746_Transcript_1/1_Conf_1.000	927	20	2.87E-103	NP_001021125.1	75	379.407	313	235	hypothetical protein B0361.2
Locus_27460_Transcript_1/1_Conf_1.000	156	1	8.20E-04	EFO23386.1	59	46.9802	54	32	hypothetical protein LOAG_05100

Locus_27461_Transcript_1/1_Conf_1.000	158	0							
Locus_27462_Transcript_1/1_Conf_1.000	186	20	8.81E-14	NP_001039751.1	78	80.1073	60	47	estradiol 17-beta-dehydrogenase 11
Locus_27463_Transcript_1/1_Conf_1.000	171	2	4.89E-09	NP_493493.2	72	64.3142	55	40	hypothetical protein F09C3.2
Locus_27464_Transcript_1/1_Conf_1.000	129	20	9.55E-13	XP_002634501.1	95	76.6406	42	40	C. briggsae CBR-SMGL-2 protein
Locus_27465_Transcript_1/1_Conf_1.000	199	20	1.81E-19	XP_002633481.1	88	98.9821	63	56	C. briggsae CBR-PHY-2 protein
Locus_27466_Transcript_1/1_Conf_1.000	367	20	1.11E-29	XP_002630906.1	82	132.88	101	83	Hypothetical protein CBG02630
Locus_27467_Transcript_1/1_Conf_1.000	268	20	2.13E-28	XP_001896987.1	77	128.642	89	69	Zinc finger, C2H2 type family protein
Locus_27468_Transcript_1/1_Conf_1.000	271	0							
Locus_27469_Transcript_1/1_Conf_1.000	172	0							
Locus_2747_Transcript_1/1_Conf_1.000	1404	20	1.63E-35	XP_002636192.1	46	155.221	417	192	Hypothetical protein CBG12107
Locus_27470_Transcript_1/1_Conf_1.000	227	0							
Locus_27471_Transcript_1/1_Conf_1.000	155	0							
Locus_27472_Transcript_1/1_Conf_1.000	143	20	3.46E-15	EAW53398.1	100	84.7297	39	39	S100 calcium binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)), isoform CRA_b
Locus_27473_Transcript_1/1_Conf_1.000	131	0							
Locus_27474_Transcript_1/1_Conf_1.000	397	0							
Locus_27475_Transcript_1/1_Conf_1.000	204	13	5.41E-16	XP_002639706.1	84	87.4261	64	54	Hypothetical protein CBG12427
Locus_27476_Transcript_1/1_Conf_1.000	269	0							
Locus_27477_Transcript_1/1_Conf_1.000	188	0							
Locus_27478_Transcript_1/1_Conf_1.000	191	0							
Locus_27479_Transcript_1/1_Conf_1.000	166	0							
Locus_2748_Transcript_1/3_Conf_0.500	328	0							
Locus_2748_Transcript_2/3_Conf_0.667	850	0							
Locus_2748_Transcript_3/3_Conf_0.667	853	0							
Locus_27480_Transcript_1/1_Conf_1.000	233	0							
Locus_27481_Transcript_1/1_Conf_1.000	185	0							

Locus_27482_Transcript_1/1_Conf_1.000	151	20	1.07E-19	XP_002815470.1	100	99.7525	50	50	PREDICTED: t-complex protein 1 subunit epsilon-like
Locus_27483_Transcript_1/1_Conf_1.000	150	0							
Locus_27484_Transcript_1/1_Conf_1.000	145	0							
Locus_27485_Transcript_1/1_Conf_1.000	179	11	7.49E-10	NP_505966.1	83	67.0106	53	44	hypothetical protein T04F3.4
Locus_27486_Transcript_1/1_Conf_1.000	182	20	3.26E-16	XP_001101279.2	98	88.1965	56	55	PREDICTED: transforming acidic coiled-coil-containing protein 3 isoform 2
Locus_27487_Transcript_1/1_Conf_1.000	138	0							
Locus_27488_Transcript_1/1_Conf_1.000	147	8	1.72E-09	XP_002631607.1	94	65.855	35	33	Hypothetical protein CBG20788
Locus_27489_Transcript_1/1_Conf_1.000	277	0							
Locus_2749_Transcript_1/1_Conf_1.000	476	20	1.73E-14	NP_506514.1	64	82.4185	119	77	hypothetical protein ZC376.6
Locus_27490_Transcript_1/1_Conf_1.000	138	20	2.84E-17	XP_002812010.1	100	91.6633	46	46	PREDICTED: ras-related protein Rab-1A-like
Locus_27491_Transcript_1/1_Conf_1.000	143	0							
Locus_27492_Transcript_1/1_Conf_1.000	336	0							
Locus_27493_Transcript_1/1_Conf_1.000	146	0							
Locus_27494_Transcript_1/1_Conf_1.000	195	0							
Locus_27495_Transcript_1/1_Conf_1.000	196	5	2.00E-26	CAR63717.1	90	122.094	65	59	hypothetical protein
Locus_27496_Transcript_1/1_Conf_1.000	151	20	2.17E-12	NP_500644.2	84	75.485	50	42	hypothetical protein R11E3.1

Locus_27497_Transcript_1/1_Conf_1.000	146	0							
Locus_27498_Transcript_1/1_Conf_1.000	187	20	7.99E-07	EFO16346.1	72	56.9954	47	34	hypothetical protein LOAG_12158
Locus_27499_Transcript_1/1_Conf_1.000	193	0							
Locus_275_Transcript_1/1_Conf_1.000	1071	20	1.50E-141	XP_002646059.1	82	506.908	360	298	C. briggsae CBR-PMR-1 protein
Locus_2750_Transcript_1/1_Conf_1.000	850	20	6.17E-46	XP_001898424.1	61	188.734	231	141	DEAD/H
Locus_27500_Transcript_1/1_Conf_1.000	152	0							
Locus_27501_Transcript_1/1_Conf_1.000	174	0							
Locus_27502_Transcript_1/1_Conf_1.000	142	0							
Locus_27503_Transcript_1/1_Conf_1.000	195	0							
Locus_27504_Transcript_1/1_Conf_1.000	160	0							
Locus_27505_Transcript_1/1_Conf_1.000	327	0							
Locus_27506_Transcript_1/1_Conf_1.000	128	0							
Locus_27507_Transcript_1/1_Conf_1.000	193	12	1.60E-07	EFO24873.1	65	59.3066	63	41	hypothetical protein LOAG_03612
Locus_27508_Transcript_1/1_Conf_1.000	347	20	8.72E-30	XP_002642454.1	59	133.265	122	72	Hypothetical protein CBG06864
Locus_27509_Transcript_1/1_Conf_1.000	130	0							
Locus_2751_Transcript_1/1_Conf_1.000	324	0							
Locus_27510_Transcript_1/1_Conf_1.000	132	0							
Locus_27511_Transcript_1/1_Conf_1.000	219	20	6.96E-27	NP_001022949.1	89	123.635	73	65	GLYcosylation related family member (gly-11)
Locus_27512_Transcript_1/1_Conf_1.000	181	0							
Locus_27513_Transcript_1/1_Conf_1.000	164	0							
Locus_27514_Transcript_1/1_Conf_1.000	148	0							

Locus_27515_Transcript_1/1_Conf_1.000	215	20	7.22E-21	NP_501545.1	85	103.605	70	60	RADiation sensitivity abnormal/yeast RAD-related family member (rad-26)
Locus_27516_Transcript_1/1_Conf_1.000	173	0							
Locus_27517_Transcript_1/1_Conf_1.000	167	0							
Locus_27518_Transcript_1/1_Conf_1.000	316	0							
Locus_27519_Transcript_1/1_Conf_1.000	133	20	2.34E-19	2AI6	100	98.5969	44	44	SolutionStructure Of Human Phosphohistidine Phosphatase 1
Locus_2752_Transcript_1/2_Conf_1.000	251	0							
Locus_2752_Transcript_2/2_Conf_1.000	228	0							
Locus_27520_Transcript_1/1_Conf_1.000	144	0							
Locus_27521_Transcript_1/1_Conf_1.000	202	0							
Locus_27522_Transcript_1/1_Conf_1.000	388	20	2.84E-25	XP_002639805.1	63	118.242	126	80	C. briggsae CBR-BCH-1 protein
Locus_27523_Transcript_1/1_Conf_1.000	138	0							
Locus_27524_Transcript_1/1_Conf_1.000	129	0							
Locus_27525_Transcript_1/1_Conf_1.000	411	20	3.83E-30	EFO20785.1	66	134.42	139	93	TKL/MLK/HH498 protein kinase
Locus_27526_Transcript_1/1_Conf_1.000	131	0							
Locus_27527_Transcript_1/1_Conf_1.000	144	0							
Locus_27528_Transcript_1/1_Conf_1.000	136	0							
Locus_27529_Transcript_1/1_Conf_1.000	175	0							
Locus_2753_Transcript_1/2_Conf_1.000	946	0							
Locus_2753_Transcript_2/2_Conf_1.000	857	0							
Locus_27530_Transcript_1/1_Conf_1.000	150	0							
Locus_27531_Transcript_1/1_Conf_1.000	138	0							
Locus_27532_Transcript_1/1_Conf_1.000	229	4	1.07E-19	NP_001040774.1	81	99.7525	76	62	hypothetical protein F40H3.1
Locus_27533_Transcript_1/1_Conf_1.000	137	0							
Locus_27534_Transcript_1/1_Conf_1.000	160	20	5.46E-16	NP_741109.1	86	87.4261	53	46	FERM domain (protein4.1-ezrin-radixin-moesin) family member (frm-8)
Locus_27535_Transcript_1/1_Conf_1.000	334	0							
Locus_27536_Transcript_1/1_Conf_1.000	145	4	4.71E-07	XP_002631433.1	68	57.7658	48	33	C. briggsae CBR-REV-1 protein
Locus_27537_Transcript_1/1_Conf_1.000	138	0							
Locus_27538_Transcript_1/1_Conf_1.000	140	20	5.74E-10	XP_001096533.2	100	67.3958	46	46	PREDICTED: heterogeneous nuclear ribonucleoprotein A3-like isoform 3
Locus_27539_Transcript_1/1_Conf_1.000	273	20	1.28E-33	XP_002632193.1	83	145.976	90	75	Hypothetical protein CBG07059

Locus_2754_Transcript_1/1_Conf_1.000	1523	20	1.44E-32	EFO17966.1	63	145.591	202	128	hypothetical protein LOAG_10533
Locus_27540_Transcript_1/1_Conf_1.000	148	0							
Locus_27541_Transcript_1/1_Conf_1.000	178	11	8.85E-11	ADD13547.1	80	70.0922	57	46	Inositol triphosphate receptor protein 1, isoform h
Locus_27542_Transcript_1/1_Conf_1.000	172	20	9.85E-10	XP_001899819.1	71	66.6254	56	40	protein ZK524.3
Locus_27543_Transcript_1/1_Conf_1.000	322	0							
Locus_27544_Transcript_1/1_Conf_1.000	153	0							
Locus_27545_Transcript_1/1_Conf_1.000	228	0							
Locus_27546_Transcript_1/1_Conf_1.000	175	0							
Locus_27547_Transcript_1/1_Conf_1.000	145	0							
Locus_27548_Transcript_1/1_Conf_1.000	209	0							
Locus_27549_Transcript_1/1_Conf_1.000	147	20	1.01E-17	XP_002934764.1	100	93.2041	48	48	PREDICTED: LOW QUALITY PROTEIN: myosin 9-like

Locus_2755_Transcript_1/1_Conf_1.000	891	20	1.15E-13	XP_002639934.1	49	81.6481	184	91	C. briggsae CBR-DRH-3 protein
Locus_27550_Transcript_1/1_Conf_1.000	148	20	3.13E-19	XP_001114645.2	100	98.2117	49	49	PREDICTED: ras GTPase-activating protein 4
Locus_27551_Transcript_1/1_Conf_1.000	201	0							
Locus_27552_Transcript_1/1_Conf_1.000	270	0							
Locus_27553_Transcript_1/1_Conf_1.000	152	0							
Locus_27554_Transcript_1/1_Conf_1.000	307	0							
Locus_27555_Transcript_1/1_Conf_1.000	146	0							
Locus_27556_Transcript_1/1_Conf_1.000	219	0							
Locus_27557_Transcript_1/1_Conf_1.000	188	20	6.29E-28	BAG61003.1	100	127.102	62	62	unnamed protein product
Locus_27558_Transcript_1/1_Conf_1.000	315	20	7.90E-39	NP_001022703.1	90	163.31	93	84	TRP (transient receptor potential) channel family member (trp-2)
Locus_27559_Transcript_1/1_Conf_1.000	134	0							
Locus_2756_Transcript_1/1_Conf_1.000	392	8	7.15E-53	NP_505622.1	90	209.92	121	110	hypothetical protein ZK856.7

Locus_27560_Transcript_1/1_Conf_1.000	147	0							
Locus_27561_Transcript_1/1_Conf_1.000	199	0							
Locus_27562_Transcript_1/1_Conf_1.000	145	0							
Locus_27563_Transcript_1/1_Conf_1.000	353	20	2.28E-22	XP_002646732.1	70	108.612	117	82	Hypothetical protein CBG13117
Locus_27564_Transcript_1/1_Conf_1.000	258	0							
Locus_27565_Transcript_1/1_Conf_1.000	243	0							
Locus_27566_Transcript_1/1_Conf_1.000	157	0							
Locus_27567_Transcript_1/1_Conf_1.000	135	0							
Locus_27568_Transcript_1/1_Conf_1.000	129	0							
Locus_27569_Transcript_1/1_Conf_1.000	147	13	2.49E-08	NP_492438.1	78	62.003	47	37	RADiation sensitivity abnormal/yeast RAD-related family member (rad-54)
Locus_2757_Transcript_1/1_Conf_1.000	507	0							
Locus_27570_Transcript_1/1_Conf_1.000	217	0							
Locus_27571_Transcript_1/1_Conf_1.000	151	0							
Locus_27572_Transcript_1/1_Conf_1.000	308	20	3.47E-31	XP_002636973.1	84	137.887	102	86	Hypothetical protein CBG09454
Locus_27573_Transcript_1/1_Conf_1.000	136	1	6.16E-04	NP_505768.1	70	47.3654	40	28	hypothetical protein C29A12.6
Locus_27574_Transcript_1/1_Conf_1.000	136	0							
Locus_27575_Transcript_1/1_Conf_1.000	260	20	4.46E-42	3O78	100	174.096	86	86	TheStructure Of Ca2+ Sensor (Case-12)
Locus_27576_Transcript_1/1_Conf_1.000	139	0							
Locus_27577_Transcript_1/1_Conf_1.000	164	0							
Locus_27578_Transcript_1/1_Conf_1.000	246	6	1.36E-19	XP_002634682.1	78	99.3673	71	56	Hypothetical protein CBG19668

Locus_27579_Transcript_1/1_Conf_1.000	150	0							
Locus_2758_Transcript_1/1_Conf_1.000	713	2	1.09E-04	NP_510325.1	42	51.2174	183	78	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-39)
Locus_27580_Transcript_1/1_Conf_1.000	139	20	4.38E-18	XP_002343109.1	100	94.3597	45	45	PREDICTED: hypothetical protein XP_002343109
Locus_27581_Transcript_1/1_Conf_1.000	216	0							
Locus_27582_Transcript_1/1_Conf_1.000	219	5	2.65E-18	NP_001022683.1	83	95.1301	73	61	hypothetical protein M01A8.2
Locus_27583_Transcript_1/1_Conf_1.000	134	0							
Locus_27584_Transcript_1/1_Conf_1.000	199	0							
Locus_27585_Transcript_1/1_Conf_1.000	153	0							
Locus_27586_Transcript_1/1_Conf_1.000	137	0							
Locus_27587_Transcript_1/1_Conf_1.000	168	0							
Locus_27588_Transcript_1/1_Conf_1.000	139	0							
Locus_27589_Transcript_1/1_Conf_1.000	130	0							
Locus_2759_Transcript_1/1_Conf_1.000	432	20	1.37E-27	NP_493029.1	84	125.946	79	67	hypothetical protein R06C1.4
Locus_27590_Transcript_1/1_Conf_1.000	134	0							
Locus_27591_Transcript_1/1_Conf_1.000	138	0							
Locus_27592_Transcript_1/1_Conf_1.000	132	0							
Locus_27593_Transcript_1/1_Conf_1.000	134	0							
Locus_27594_Transcript_1/1_Conf_1.000	173	0							
Locus_27595_Transcript_1/1_Conf_1.000	136	0							
Locus_27596_Transcript_1/1_Conf_1.000	201	2	4.17E-08	NP_492188.1	62	61.2326	62	39	GLoBin family member (glb-26)
Locus_27597_Transcript_1/1_Conf_1.000	191	0							
Locus_27598_Transcript_1/1_Conf_1.000	143	20	2.56E-18	P01023.3	100	95.1301	47	47	Alpha-2-macroglobulin
Locus_27599_Transcript_1/1_Conf_1.000	150	0							
Locus_276_Transcript_1/2_Conf_1.000	1459	20	6.72E-48	NP_502125.1	88	196.438	107	95	hypothetical protein B0035.1

Locus_276_Transcript_2/2_Conf_1.000	1426	20	6.50E-48	NP_502125.1	88	196.438	107	95	hypothetical protein B0035.1
Locus_2760_Transcript_1/1_Conf_1.000	1130	20	5.46E-105	NP_498407.1	74	385.571	327	244	hypothetical protein C05D11.8
Locus_27600_Transcript_1/1_Conf_1.000	157	0							
Locus_27601_Transcript_1/1_Conf_1.000	145	2	5.75E-05	XP_001895662.1	66	50.8322	48	32	ImpB/MucB/SamB family protein
Locus_27602_Transcript_1/1_Conf_1.000	239	0							
Locus_27603_Transcript_1/1_Conf_1.000	135	20	1.05E-11	NP_503758.4	81	73.1738	44	36	KETtiN (Drosophila actin-binding) homolog family member (ketn-1)
Locus_27604_Transcript_1/1_Conf_1.000	177	0							
Locus_27605_Transcript_1/1_Conf_1.000	137	0							
Locus_27606_Transcript_1/1_Conf_1.000	128	20	1.29E-09	XP_002633255.1	80	66.2402	42	34	Hypothetical protein CBG05980
Locus_27607_Transcript_1/1_Conf_1.000	130	0							
Locus_27608_Transcript_1/1_Conf_1.000	162	0							
Locus_27609_Transcript_1/1_Conf_1.000	143	0							
Locus_2761_Transcript_1/1_Conf_1.000	2952	20	0	CBB16332.1	65	812.757	1009	659	C. elegans protein Y47D3A.29b, partially confirmed by transcript evidence
Locus_27610_Transcript_1/1_Conf_1.000	130	0							
Locus_27611_Transcript_1/1_Conf_1.000	165	0							
Locus_27612_Transcript_1/1_Conf_1.000	195	0							
Locus_27613_Transcript_1/1_Conf_1.000	164	20	2.21E-17	XP_002633437.1	87	92.0485	54	47	C. briggsae CBR-UNC-22 protein
Locus_27614_Transcript_1/1_Conf_1.000	316	0							
Locus_27615_Transcript_1/1_Conf_1.000	151	14	2.74E-07	NP_001032513.1	86	58.5362	37	32	selenocysteine-specific elongation factor
Locus_27616_Transcript_1/1_Conf_1.000	178	20	1.77E-27	NP_758844.1	100	125.561	58	58	gamma-secretase subunit PEN-2

Locus_27617_Transcript_1/1_Conf_1.000	156	20	7.40E-13	EFO25007.1	76	77.0258	51	39	hypothetical protein LOAG_03480
Locus_27618_Transcript_1/1_Conf_1.000	167	0							
Locus_27619_Transcript_1/1_Conf_1.000	204	20	8.60E-30	XP_002819585.1	100	133.265	67	67	glutamate [NMDA] receptor-associated protein 1-like, partial
Locus_2762_Transcript_1/1_Conf_1.000	1252	20	2.09E-31	NP_508788.1	50	141.354	356	179	LuNaPark (membrane protein) homolog family member (lnp-1)
Locus_27620_Transcript_1/1_Conf_1.000	183	0							
Locus_27621_Transcript_1/1_Conf_1.000	203	0							
Locus_27622_Transcript_1/1_Conf_1.000	188	0							
Locus_27623_Transcript_1/1_Conf_1.000	208	0							
Locus_27624_Transcript_1/1_Conf_1.000	232	4	8.42E-17	XP_001899484.1	68	90.1225	80	55	Leucine Rich Repeat family protein
Locus_27625_Transcript_1/1_Conf_1.000	299	0							
Locus_27626_Transcript_1/1_Conf_1.000	206	0							
Locus_27627_Transcript_1/1_Conf_1.000	212	0							
Locus_27628_Transcript_1/1_Conf_1.000	132	0							
Locus_27629_Transcript_1/1_Conf_1.000	241	20	7.30E-13	ZP_02025538.1	84	77.0258	51	43	hypothetical protein EUBVEN_00788
Locus_2763_Transcript_1/1_Conf_1.000	419	20	3.88E-70	XP_001159171.1	100	267.314	134	134	PREDICTED: cytoplasmic polyadenylation element binding protein 1 isoform 3
Locus_27630_Transcript_1/1_Conf_1.000	271	5	1.38E-11	ADI24623.1	60	72.7886	89	54	Copine domain protein, atypical protein 2, isoform c, partially confirmed by transcript evidence
Locus_27631_Transcript_1/1_Conf_1.000	293	3	1.00E-09	XP_002489033.1	75	66.6254	45	34	hypothetical protein SORBIDRAFT_0351s002020
Locus_27632_Transcript_1/1_Conf_1.000	132	0							
Locus_27633_Transcript_1/1_Conf_1.000	243	0							
Locus_27634_Transcript_1/1_Conf_1.000	163	0							

Locus_27635_Transcript_1/1_Conf_1.000	228	20	9.27E-40	AAH14504.2	100	166.392	75	75	P4HB protein
Locus_27636_Transcript_1/1_Conf_1.000	188	20	1.60E-23	XP_002631108.1	91	112.464	62	57	Hypothetical protein CBG02883
Locus_27637_Transcript_1/1_Conf_1.000	195	0							
Locus_27638_Transcript_1/1_Conf_1.000	139	20	7.48E-18	XP_002802342.1	100	93.5893	46	46	PREDICTED: adenylate kinase 2, mitochondrial
Locus_27639_Transcript_1/2_Conf_1.000	285	0							
Locus_27639_Transcript_2/2_Conf_1.000	285	0							
Locus_2764_Transcript_1/1_Conf_1.000	597	20	1.08E-40	P31732.1	66	170.244	202	135	Muscle cell intermediate filament protein OV71
Locus_27640_Transcript_1/1_Conf_1.000	302	5	4.27E-29	XP_002634479.1	81	130.954	106	86	Hypothetical protein CBG10738
Locus_27641_Transcript_1/1_Conf_1.000	139	0							
Locus_27642_Transcript_1/1_Conf_1.000	245	0							
Locus_27643_Transcript_1/1_Conf_1.000	148	20	3.58E-23	BAG64777.1	100	111.309	49	49	unnamed protein product
Locus_27644_Transcript_1/1_Conf_1.000	148	0							
Locus_27645_Transcript_1/1_Conf_1.000	196	3	7.39E-13	NP_497641.2	73	77.0258	65	48	CaDHerin family member (cdh-1)
Locus_27646_Transcript_1/1_Conf_1.000	144	0							
Locus_27647_Transcript_1/1_Conf_1.000	132	0							

Locus_27648_Transcript_1/1_Conf_1.000	142	20	1.04E-11	NP_001023062.1	82	73.1738	46	38	Ligand-Gated ion Channel family member (lgc-43)
Locus_27649_Transcript_1/1_Conf_1.000	135	20	5.38E-16	ADD13547.1	95	87.4261	45	43	Inositol triphosphate receptor protein 1, isoform h
Locus_2765_Transcript_1/1_Conf_1.000	682	20	8.34E-44	NP_501998.1	87	181.03	109	95	hypothetical protein T25B9.9
Locus_27650_Transcript_1/1_Conf_1.000	153	0							
Locus_27651_Transcript_1/1_Conf_1.000	139	0							
Locus_27652_Transcript_1/1_Conf_1.000	160	0							
Locus_27653_Transcript_1/1_Conf_1.000	303	0							
Locus_27654_Transcript_1/1_Conf_1.000	150	0							
Locus_27655_Transcript_1/1_Conf_1.000	257	20	4.79E-36	AAC32864.1	92	154.066	85	79	putative potassium channel subunit n2P26
Locus_27656_Transcript_1/1_Conf_1.000	172	0							
Locus_27657_Transcript_1/1_Conf_1.000	189	12	4.65E-23	XP_001894402.1	88	110.923	62	55	PDZ domain containing protein
Locus_27658_Transcript_1/1_Conf_1.000	233	2	2.80E-12	NP_497765.2	87	75.0998	77	67	Adenylyl CYclase family member (acy-3)

Locus_27659_Transcript_1/1_Conf_1.000	185	20	9.73E-29	XP_001098702.2	100	129.798	61	61	PREDICTED: transcription intermediary factor 1-beta isoform 4
Locus_2766_Transcript_1/1_Conf_1.000	1423	20	7.73E-134	EFO24850.1	95	481.871	269	256	hypothetical protein LOAG_03629
Locus_27660_Transcript_1/1_Conf_1.000	136	0							
Locus_27661_Transcript_1/1_Conf_1.000	228	0							
Locus_27662_Transcript_1/1_Conf_1.000	134	0							
Locus_27663_Transcript_1/1_Conf_1.000	226	3	1.65E-28	NP_506242.2	89	129.028	75	67	hypothetical protein R186.6
Locus_27664_Transcript_1/1_Conf_1.000	265	20	9.94E-18	NP_001021940.1	73	93.2041	94	69	hypothetical protein C08H9.3
Locus_27665_Transcript_1/1_Conf_1.000	253	19	6.98E-19	XP_002644127.1	76	97.0561	84	64	C. briggsae CBR-TAG-289 protein
Locus_27666_Transcript_1/1_Conf_1.000	195	0							
Locus_27667_Transcript_1/1_Conf_1.000	137	0							
Locus_27668_Transcript_1/1_Conf_1.000	144	0							
Locus_27669_Transcript_1/1_Conf_1.000	179	20	1.19E-15	CAA22108.2	82	86.2705	58	48	C. elegans protein Y75B8A.24, partially confirmed by transcript evidence
Locus_2767_Transcript_1/3_Conf_0.600	487	0							
Locus_2767_Transcript_2/3_Conf_0.700	1114	0							
Locus_2767_Transcript_3/3_Conf_0.800	491	0							
Locus_27670_Transcript_1/1_Conf_1.000	149	0							
Locus_27671_Transcript_1/1_Conf_1.000	260	0							
Locus_27672_Transcript_1/1_Conf_1.000	132	4	3.28E-05	NP_741744.2	74	51.6026	43	32	hypothetical protein C15C7.7
Locus_27673_Transcript_1/1_Conf_1.000	144	0							
Locus_27674_Transcript_1/1_Conf_1.000	309	0							
Locus_27675_Transcript_1/1_Conf_1.000	228	0							
Locus_27676_Transcript_1/1_Conf_1.000	130	0							

Locus_27677_Transcript_1/1_Conf_1.000	166	0							
Locus_27678_Transcript_1/1_Conf_1.000	154	0							
Locus_27679_Transcript_1/1_Conf_1.000	157	0							
Locus_2768_Transcript_1/2_Conf_1.000	220	20	2.17E-20	ACI49170.1	98	102.064	53	52	hypothetical protein Csp3_JD01.002
Locus_2768_Transcript_2/2_Conf_1.000	393	20	9.28E-56	NP_524709.1	94	219.55	122	115	ribosomal protein S15Aa, isoform D
Locus_27680_Transcript_1/1_Conf_1.000	160	0							
Locus_27681_Transcript_1/1_Conf_1.000	401	20	2.22E-17	XP_002638474.1	56	92.0485	111	63	C. briggsae CBR-TTR-26 protein
Locus_27682_Transcript_1/1_Conf_1.000	137	2	7.78E-07	NP_505688.1	73	56.9954	45	33	Cdc-42 Related Protein family member (crp-1)
Locus_27683_Transcript_1/1_Conf_1.000	174	0							
Locus_27684_Transcript_1/1_Conf_1.000	169	0							
Locus_27685_Transcript_1/1_Conf_1.000	229	0							
Locus_27686_Transcript_1/1_Conf_1.000	240	20	5.04E-22	XP_002647231.1	83	107.457	81	68	C. briggsae CBR-SOS-1 protein
Locus_27687_Transcript_1/1_Conf_1.000	128	0							
Locus_27688_Transcript_1/1_Conf_1.000	136	0							
Locus_27689_Transcript_1/1_Conf_1.000	283	5	6.33E-12	NP_497699.1	61	73.9442	92	57	hypothetical protein C56G7.3
Locus_2769_Transcript_1/2_Conf_1.000	337	0							
Locus_2769_Transcript_2/2_Conf_1.000	360	0							
Locus_27690_Transcript_1/1_Conf_1.000	143	7	9.11E-16	NP_495434.1	97	86.6557	43	42	hypothetical protein C15F1.1
Locus_27691_Transcript_1/1_Conf_1.000	146	5	2.11E-15	EFO16550.1	91	85.5001	47	43	hypothetical protein LOAG_11955
Locus_27692_Transcript_1/1_Conf_1.000	216	20	2.02E-31	XP_002937574.1	100	138.658	71	71	PREDICTED: heat shock cognate 71 kDa protein-like
Locus_27693_Transcript_1/1_Conf_1.000	206	10	4.91E-09	XP_002633479.1	71	64.3142	57	41	Hypothetical protein CBG06250
Locus_27694_Transcript_1/1_Conf_1.000	198	7	6.63E-30	XP_002636804.1	98	133.65	65	64	C. briggsae CBR-EXP-2 protein

Locus_27695_Transcript_1/1_Conf_1.000	155	0							
Locus_27696_Transcript_1/1_Conf_1.000	175	0							
Locus_27697_Transcript_1/1_Conf_1.000	178	0							
Locus_27698_Transcript_1/1_Conf_1.000	238	0							
Locus_27699_Transcript_1/1_Conf_1.000	155	4	7.18E-16	XP_002637927.1	90	87.0409	51	46	Hypothetical protein CBG04739
Locus_277_Transcript_1/1_Conf_1.000	1057	0							
Locus_2770_Transcript_1/1_Conf_1.000	1456	20	7.05E-106	NP_499694.2	74	389.037	348	259	hypothetical protein ZK1010.2
Locus_27700_Transcript_1/1_Conf_1.000	136	0							
Locus_27701_Transcript_1/1_Conf_1.000	149	20	1.51E-05	AAB61392.1	67	52.7582	49	33	transposase
Locus_27702_Transcript_1/1_Conf_1.000	174	0							
Locus_27703_Transcript_1/1_Conf_1.000	217	0							
Locus_27704_Transcript_1/1_Conf_1.000	128	0							
Locus_27705_Transcript_1/1_Conf_1.000	180	1	4.88E-04	XP_002639032.1	73	47.7506	45	33	Hypothetical protein CBG22281
Locus_27706_Transcript_1/1_Conf_1.000	275	20	5.20E-27	AAC08430.1	89	124.02	68	61	unknown
Locus_27707_Transcript_1/1_Conf_1.000	257	0							
Locus_27708_Transcript_1/1_Conf_1.000	151	0							
Locus_27709_Transcript_1/1_Conf_1.000	225	20	4.64E-23	XP_002632693.1	83	110.923	73	61	Hypothetical protein CBG21624
Locus_2771_Transcript_1/1_Conf_1.000	308	0							
Locus_27710_Transcript_1/1_Conf_1.000	128	0							
Locus_27711_Transcript_1/1_Conf_1.000	136	0							
Locus_27712_Transcript_1/1_Conf_1.000	157	0							
Locus_27713_Transcript_1/1_Conf_1.000	130	0							
Locus_27714_Transcript_1/1_Conf_1.000	174	5	3.48E-15	NP_741242.1	81	84.7297	58	47	Dipeptidyl Peptidase Four (IV) family member (dpf-6)
Locus_27715_Transcript_1/1_Conf_1.000	191	20	3.33E-21	XP_001084759.2	98	104.76	63	62	PREDICTED: myosin regulatory light polypeptide 9-like isoform 4
Locus_27716_Transcript_1/1_Conf_1.000	251	0							

Locus_27717_Transcript_1/1_Conf_1.000	135	18	2.96E-06	XP_002756512.1	78	55.0694	38	30	PREDICTED: cytochrome P450 2C20-like isoform 3
Locus_27718_Transcript_1/1_Conf_1.000	166	20	4.58E-23	XP_002919748.1	100	110.923	55	55	PREDICTED: pyruvate kinase isozymes M1/M2-like
Locus_27719_Transcript_1/1_Conf_1.000	159	0							
Locus_2772_Transcript_1/1_Conf_1.000	735	0							
Locus_27720_Transcript_1/1_Conf_1.000	251	14	7.41E-42	NP_510548.2	97	173.326	83	81	hypothetical protein F39D8.3
Locus_27721_Transcript_1/1_Conf_1.000	141	0							
Locus_27722_Transcript_1/1_Conf_1.000	152	0							
Locus_27723_Transcript_1/1_Conf_1.000	262	0							
Locus_27724_Transcript_1/1_Conf_1.000	162	0							
Locus_27725_Transcript_1/1_Conf_1.000	189	0							
Locus_27726_Transcript_1/1_Conf_1.000	361	20	4.84E-41	CAR63592.1	81	170.629	122	100	hypothetical protein
Locus_27727_Transcript_1/1_Conf_1.000	156	0							
Locus_27728_Transcript_1/1_Conf_1.000	198	20	4.30E-29	NP_001022190.1	98	130.954	66	65	hypothetical protein F53A10.2
Locus_27729_Transcript_1/1_Conf_1.000	172	0							
Locus_2773_Transcript_1/1_Conf_1.000	273	20	1.28E-33	ABP52060.1	96	145.976	79	76	ribosomal protein L36

Locus_27730_Transcript_1/1_Conf_1.000	309	20	3.94E-35	XP_001902583.1	88	150.984	100	88	Patched family protein
Locus_27731_Transcript_1/1_Conf_1.000	133	0							
Locus_27732_Transcript_1/1_Conf_1.000	211	0							
Locus_27733_Transcript_1/1_Conf_1.000	175	0							
Locus_27734_Transcript_1/1_Conf_1.000	156	0							
Locus_27735_Transcript_1/1_Conf_1.000	147	0							
Locus_27736_Transcript_1/1_Conf_1.000	279	20	2.83E-33	NP_001076680.1	82	144.821	93	77	hypothetical protein F13H10.3
Locus_27737_Transcript_1/1_Conf_1.000	211	0							
Locus_27738_Transcript_1/1_Conf_1.000	150	0							
Locus_27739_Transcript_1/1_Conf_1.000	162	0							
Locus_2774_Transcript_1/2_Conf_1.000	372	11	3.22E-08	NP_490938.3	73	61.6178	80	59	AFaDin (actin filament binding protein) homolog family member (afd-1)
Locus_2774_Transcript_2/2_Conf_1.000	383	11	3.18E-08	NP_490938.3	73	61.6178	80	59	AFaDin (actin filament binding protein) homolog family member (afd-1)
Locus_27740_Transcript_1/1_Conf_1.000	220	0							
Locus_27741_Transcript_1/1_Conf_1.000	270	20	5.96E-31	EFO13452.1	78	137.117	90	71	hypothetical protein LOAG_15077
Locus_27742_Transcript_1/1_Conf_1.000	190	0							
Locus_27743_Transcript_1/1_Conf_1.000	162	5	8.69E-14	XP_002631453.1	85	80.1073	54	46	C. briggsae CBR-RIG-6 protein
Locus_27744_Transcript_1/1_Conf_1.000	224	0							
Locus_27745_Transcript_1/1_Conf_1.000	539	4	5.02E-35	NP_001024306.1	64	150.984	174	112	Poly(ADP-ribose) Metabolism Enzyme family member (pme-5)
Locus_27746_Transcript_1/1_Conf_1.000	191	0							
Locus_27747_Transcript_1/1_Conf_1.000	177	0							
Locus_27748_Transcript_1/1_Conf_1.000	156	20	2.22E-17	NP_001022373.1	94	92.0485	51	48	CLC-type chloride cHannel family member (clh-1)

Locus_27749_Transcript_1/1_Conf_1.000	174	20	2.67E-15	XP_002635372.1	80	85.1149	57	46	C. briggsae CBR-RPM-1 protein
Locus_2775_Transcript_1/1_Conf_1.000	964	20	4.64E-136	AAK28335.1	84	488.419	322	273	glycogen synthase
Locus_27750_Transcript_1/1_Conf_1.000	235	12	5.61E-21	XP_002633387.1	84	103.99	76	64	C. briggsae CBR-TWK-25 protein
Locus_27751_Transcript_1/1_Conf_1.000	311	20	2.55E-42	AAC38987.1	89	174.866	103	92	P-glycoprotein
Locus_27752_Transcript_1/1_Conf_1.000	360	20	4.11E-24	XP_001899665.1	75	114.39	93	70	LD41395p
Locus_27753_Transcript_1/1_Conf_1.000	132	0							
Locus_27754_Transcript_1/1_Conf_1.000	132	0							
Locus_27755_Transcript_1/1_Conf_1.000	130	0							
Locus_27756_Transcript_1/1_Conf_1.000	144	3	5.94E-10	XP_002634455.1	75	67.3958	48	36	Hypothetical protein CBG10706
Locus_27757_Transcript_1/1_Conf_1.000	142	0							
Locus_27758_Transcript_1/1_Conf_1.000	151	20	1.50E-21	XP_002811111.1	100	105.916	49	49	PREDICTED: proteasome subunit beta type-2-like
Locus_27759_Transcript_1/1_Conf_1.000	375	0							
Locus_2776_Transcript_1/1_Conf_1.000	1022	20	5.28E-149	NP_491023.2	91	531.561	276	253	CathePsin Z family member (cpz-1)
Locus_27760_Transcript_1/1_Conf_1.000	134	0							

Locus_27761_Transcript_1/1_Conf_1.000	147	20	5.19E-06	XP_002406495.1	70	54.299	47	33	protein tyrosine phosphatase, putative
Locus_27762_Transcript_1/1_Conf_1.000	290	2	2.92E-09	XP_002635623.1	58	65.0846	91	53	Hypothetical protein CBG21816
Locus_27763_Transcript_1/1_Conf_1.000	128	0							
Locus_27764_Transcript_1/1_Conf_1.000	158	0							
Locus_27765_Transcript_1/1_Conf_1.000	180	0							
Locus_27766_Transcript_1/1_Conf_1.000	273	0							
Locus_27767_Transcript_1/1_Conf_1.000	135	20	1.16E-18	XP_002756078.1	100	96.2857	44	44	PREDICTED: coronin-1A isoform 1
Locus_27768_Transcript_1/1_Conf_1.000	288	0							
Locus_27769_Transcript_1/1_Conf_1.000	191	0							
Locus_2777_Transcript_1/1_Conf_1.000	181	19	2.85E-12	XP_001514349.1	80	75.0998	47	38	PREDICTED: similar to F1Fo-ATPase subunit e
Locus_27770_Transcript_1/1_Conf_1.000	182	20	1.56E-18	NP_509517.2	86	95.9005	59	51	hypothetical protein C24A3.4
Locus_27771_Transcript_1/1_Conf_1.000	169	0							
Locus_27772_Transcript_1/1_Conf_1.000	130	0							

Locus_27773_Transcript_1/1_Conf_1.000	152	20	9.71E-21	NP_509032.1	92	103.219	50	46	Drosophila ODD-skipped-like family member (odd-2)
Locus_27774_Transcript_1/1_Conf_1.000	179	0							
Locus_27775_Transcript_1/1_Conf_1.000	196	0							
Locus_27776_Transcript_1/1_Conf_1.000	147	0							
Locus_27777_Transcript_1/1_Conf_1.000	132	0							
Locus_27778_Transcript_1/1_Conf_1.000	261	20	7.13E-24	NP_493247.2	78	113.62	84	66	hypothetical protein Y18D10A.9
Locus_27779_Transcript_1/1_Conf_1.000	129	0							
Locus_2778_Transcript_1/1_Conf_1.000	471	20	7.19E-77	EFO26349.1	96	289.656	157	151	hypothetical protein LOAG_02130
Locus_27780_Transcript_1/1_Conf_1.000	160	4	1.26E-12	EFO17909.1	83	76.2554	53	44	hypothetical protein LOAG_10587
Locus_27781_Transcript_1/1_Conf_1.000	164	0							
Locus_27782_Transcript_1/1_Conf_1.000	129	0							
Locus_27783_Transcript_1/1_Conf_1.000	138	0							
Locus_27784_Transcript_1/1_Conf_1.000	232	0							
Locus_27785_Transcript_1/2_Conf_1.000	256	6	1.40E-11	NP_495914.1	68	72.7886	85	58	hypothetical protein C18E9.8
Locus_27785_Transcript_2/2_Conf_1.000	256	6	2.17E-12	NP_495914.1	69	75.485	85	59	hypothetical protein C18E9.8
Locus_27786_Transcript_1/1_Conf_1.000	239	0							
Locus_27787_Transcript_1/1_Conf_1.000	177	0							
Locus_27788_Transcript_1/1_Conf_1.000	177	5	1.12E-13	XP_001897130.1	84	79.7221	58	49	DNA-directed RNA polymerase, beta subunit family protein
Locus_27789_Transcript_1/1_Conf_1.000	170	0							
Locus_2779_Transcript_1/2_Conf_1.000	1145	20	6.81E-79	EFO19779.1	90	298.901	173	156	ubiquitin-conjugating enzyme E2 H
Locus_2779_Transcript_2/2_Conf_1.000	1145	20	6.80E-79	EFO19779.1	90	298.901	173	156	ubiquitin-conjugating enzyme E2 H

Locus_27790_Transcript_1/1_Conf_1.000	188	4	7.46E-13	XP_002636973.1	77	77.0258	62	48	Hypothetical protein CBG09454
Locus_27791_Transcript_1/1_Conf_1.000	247	1	1.91E-05	XP_001965764.1	57	52.373	59	34	GF22278
Locus_27792_Transcript_1/1_Conf_1.000	146	0							
Locus_27793_Transcript_1/1_Conf_1.000	166	0							
Locus_27794_Transcript_1/1_Conf_1.000	136	20	1.28E-09	XP_002110106.1	82	66.2402	46	38	hypothetical protein TRIADDRAFT_53727
Locus_27795_Transcript_1/1_Conf_1.000	139	20	1.28E-17	EAX02335.1	97	92.8189	45	44	ribonuclease/angiogenin inhibitor 1, isoform CRA_c
Locus_27796_Transcript_1/1_Conf_1.000	215	20	2.17E-25	XP_002634229.1	91	118.627	69	63	C. briggsae CBR-UNC-26 protein
Locus_27797_Transcript_1/1_Conf_1.000	134	0							
Locus_27798_Transcript_1/1_Conf_1.000	181	1	3.49E-10	EDL90203.1	71	68.1662	52	37	ATPase, H+ transporting, V0 subunit B (predicted), isoform CRA_c
Locus_27799_Transcript_1/1_Conf_1.000	146	0							
Locus_278_Transcript_1/1_Conf_1.000	322	0							
Locus_2780_Transcript_1/1_Conf_1.000	833	20	3.39E-09	XP_001640075.1	50	66.6254	125	63	predicted protein
Locus_27800_Transcript_1/1_Conf_1.000	251	0							
Locus_27801_Transcript_1/1_Conf_1.000	224	0							
Locus_27802_Transcript_1/1_Conf_1.000	175	0							
Locus_27803_Transcript_1/1_Conf_1.000	131	0							
Locus_27804_Transcript_1/1_Conf_1.000	142	0							

Locus_27805_Transcript_1/1_Conf_1.000	211	20	5.94E-15	EFO23287.1	71	83.9593	67	48	hypothetical protein LOAG_05194
Locus_27806_Transcript_1/1_Conf_1.000	185	0							
Locus_27807_Transcript_1/1_Conf_1.000	178	0							
Locus_27808_Transcript_1/1_Conf_1.000	135	0							
Locus_27809_Transcript_1/1_Conf_1.000	144	0							
Locus_2781_Transcript_1/1_Conf_1.000	2375	20	0	CAR63713.1	93	848.195	492	458	putative ZYGote defective: embryonic lethal family member
Locus_27810_Transcript_1/1_Conf_1.000	285	0							
Locus_27811_Transcript_1/1_Conf_1.000	217	0							
Locus_27812_Transcript_1/1_Conf_1.000	138	0							
Locus_27813_Transcript_1/1_Conf_1.000	175	0							
Locus_27814_Transcript_1/1_Conf_1.000	150	0							
Locus_27815_Transcript_1/1_Conf_1.000	177	0							
Locus_27816_Transcript_1/1_Conf_1.000	158	0							
Locus_27817_Transcript_1/1_Conf_1.000	147	0							
Locus_27818_Transcript_1/1_Conf_1.000	215	20	2.17E-33	XP_002821617.1	100	145.206	71	71	PREDICTED: peroxiredoxin-5, mitochondrial-like isoform 2
Locus_27819_Transcript_1/1_Conf_1.000	154	2	3.02E-06	NP_499757.2	63	55.0694	52	33	hypothetical protein T03F6.4
Locus_2782_Transcript_1/1_Conf_1.000	534	20	1.22E-09	CAB04203.2	84	66.6254	44	37	C. elegans protein F26H9.2, confirmed by transcript evidence
Locus_27820_Transcript_1/1_Conf_1.000	172	0							
Locus_27821_Transcript_1/1_Conf_1.000	137	0							
Locus_27822_Transcript_1/1_Conf_1.000	145	2	1.79E-06	XP_002639197.1	72	55.8398	44	32	Hypothetical protein CBG03740
Locus_27823_Transcript_1/1_Conf_1.000	160	0							
Locus_27824_Transcript_1/1_Conf_1.000	233	20	4.92E-25	NP_494721.1	88	117.472	72	64	hypothetical protein R11F4.1
Locus_27825_Transcript_1/1_Conf_1.000	187	0							
Locus_27826_Transcript_1/1_Conf_1.000	148	0							

Locus_27827_Transcript_1/1_Conf_1.000	255	2	9.08E-19	XP_002643107.1	70	96.6709	82	58	Hypothetical protein CBG23034
Locus_27828_Transcript_1/1_Conf_1.000	505	0							
Locus_27829_Transcript_1/1_Conf_1.000	223	0							
Locus_2783_Transcript_1/1_Conf_1.000	150	0							
Locus_27830_Transcript_1/1_Conf_1.000	180	0							
Locus_27831_Transcript_1/1_Conf_1.000	286	0							
Locus_27832_Transcript_1/1_Conf_1.000	131	2	1.63E-04	NP_492594.2	75	49.2914	44	33	hypothetical protein F26E4.5
Locus_27833_Transcript_1/1_Conf_1.000	225	0							
Locus_27834_Transcript_1/1_Conf_1.000	248	0							
Locus_27835_Transcript_1/1_Conf_1.000	148	0							
Locus_27836_Transcript_1/1_Conf_1.000	219	0							
Locus_27837_Transcript_1/1_Conf_1.000	159	20	3.54E-15	NP_492003.2	88	84.7297	53	47	hypothetical protein W01A8.6
Locus_27838_Transcript_1/1_Conf_1.000	195	0							
Locus_27839_Transcript_1/1_Conf_1.000	134	0							
Locus_2784_Transcript_1/1_Conf_1.000	225	0							
Locus_27840_Transcript_1/1_Conf_1.000	221	0							
Locus_27841_Transcript_1/1_Conf_1.000	285	2	1.36E-14	XP_002635263.1	85	82.8037	69	59	Hypothetical protein CBG11507
Locus_27842_Transcript_1/1_Conf_1.000	170	20	2.51E-13	XP_002155655.1	73	78.5666	56	41	PREDICTED: similar to transposase homolog
Locus_27843_Transcript_1/1_Conf_1.000	151	0							
Locus_27844_Transcript_1/1_Conf_1.000	447	8	1.06E-11	EFO14501.1	56	73.1738	121	68	hypothetical protein LOAG_14017
Locus_27845_Transcript_1/1_Conf_1.000	414	8	6.75E-19	AAT76297.1	85	97.0561	62	53	FMRFamide-related peptide FLP-16 precursor
Locus_27846_Transcript_1/1_Conf_1.000	174	0							
Locus_27847_Transcript_1/1_Conf_1.000	161	0							
Locus_27848_Transcript_1/1_Conf_1.000	129	0							
Locus_27849_Transcript_1/1_Conf_1.000	300	20	1.43E-08	NP_496176.1	64	62.7734	73	47	beta-LACTamase domain containing family member (lact-2)
Locus_2785_Transcript_1/1_Conf_1.000	1271	20	2.05E-135	XP_002636781.1	75	486.878	390	293	Hypothetical protein CBG23516
Locus_27850_Transcript_1/1_Conf_1.000	143	20	4.83E-17	XP_002912971.1	100	90.8929	47	47	PREDICTED: core histone macro-H2A.1-like isoform 2

Locus_27851_Transcript_1/1_Conf_1.000	227	0							
Locus_27852_Transcript_1/1_Conf_1.000	189	0							
Locus_27853_Transcript_1/1_Conf_1.000	140	0							
Locus_27854_Transcript_1/1_Conf_1.000	205	0							
Locus_27855_Transcript_1/1_Conf_1.000	167	20	2.61E-10	XP_002921983.1	80	68.5514	56	45	PREDICTED: dual specificity mitogen-activated protein kinase kinase 7-like
Locus_27856_Transcript_1/1_Conf_1.000	149	2	2.49E-08	XP_001891640.1	79	62.003	49	39	zgc:55839
Locus_27857_Transcript_1/1_Conf_1.000	151	0							
Locus_27858_Transcript_1/1_Conf_1.000	169	0							
Locus_27859_Transcript_1/1_Conf_1.000	186	0							
Locus_2786_Transcript_1/1_Conf_1.000	657	20	1.32E-51	NP_505373.1	61	206.838	217	134	hypothetical protein B0222.5
Locus_27860_Transcript_1/1_Conf_1.000	174	0							
Locus_27861_Transcript_1/1_Conf_1.000	159	0							
Locus_27862_Transcript_1/1_Conf_1.000	217	6	1.50E-10	NP_495280.1	69	69.3218	71	49	hypothetical protein C32D5.12
Locus_27863_Transcript_1/1_Conf_1.000	131	8	1.52E-10	CAX65068.1	88	69.3218	43	38	C. elegans protein K08C7.3d, confirmed by transcript evidence
Locus_27864_Transcript_1/1_Conf_1.000	292	4	2.46E-16	ACI49095.1	80	88.5817	65	52	hypothetical protein Cbre_JD12.003
Locus_27865_Transcript_1/1_Conf_1.000	237	13	5.41E-24	NP_500282.2	80	114.005	77	62	hypothetical protein Y54G2A.29
Locus_27866_Transcript_1/1_Conf_1.000	213	3	1.16E-10	XP_002644341.1	64	69.707	71	46	Hypothetical protein CBG14163
Locus_27867_Transcript_1/1_Conf_1.000	177	0							
Locus_27868_Transcript_1/1_Conf_1.000	234	9	3.52E-15	EFO27462.1	77	84.7297	71	55	hypothetical protein LOAG_01021
Locus_27869_Transcript_1/1_Conf_1.000	329	0							
Locus_2787_Transcript_1/1_Conf_1.000	180	20	1.36E-22	ACY40018.1	93	109.383	59	55	C. elegans FLN-1 protein, isoform g
Locus_27870_Transcript_1/1_Conf_1.000	263	20	3.90E-30	NP_495674.2	87	134.42	87	76	P-GlycoProtein related family member (pgp-11)
Locus_27871_Transcript_1/1_Conf_1.000	220	20	1.19E-10	XP_002629878.1	69	69.707	72	50	Hypothetical protein CBG21915

Locus_27872_Transcript_1/1_Conf_1.000	254	20	1.97E-05	EFN75741.1	62	52.373	58	36	Serine protease easter
Locus_27873_Transcript_1/1_Conf_1.000	142	20	2.94E-06	NP_503278.2	68	55.0694	45	31	UDP-GlucuronosylTransferase family member (ugt-42)
Locus_27874_Transcript_1/1_Conf_1.000	239	2	3.38E-34	XP_002630454.1	93	147.902	79	74	Hypothetical protein CBG11187
Locus_27875_Transcript_1/1_Conf_1.000	176	3	6.58E-06	XP_002631424.1	74	53.9138	47	35	Hypothetical protein CBG03280
Locus_27876_Transcript_1/1_Conf_1.000	142	0							
Locus_27877_Transcript_1/1_Conf_1.000	133	0							
Locus_27878_Transcript_1/1_Conf_1.000	128	19	9.25E-16	XP_002807855.1	100	86.6557	42	42	PREDICTED: LOW QUALITY PROTEIN: uncharacterized protein C19orf43-like
Locus_27879_Transcript_1/1_Conf_1.000	249	0							
Locus_2788_Transcript_1/1_Conf_1.000	878	0							
Locus_27880_Transcript_1/1_Conf_1.000	138	0							
Locus_27881_Transcript_1/1_Conf_1.000	139	0							
Locus_27882_Transcript_1/1_Conf_1.000	152	0							
Locus_27883_Transcript_1/1_Conf_1.000	328	0							
Locus_27884_Transcript_1/1_Conf_1.000	272	20	1.79E-27	XP_002637669.1	82	125.561	90	74	Hypothetical protein CBG19425
Locus_27885_Transcript_1/1_Conf_1.000	316	20	1.76E-46	XP_002746160.1	100	188.734	90	90	PREDICTED: H/ACA ribonucleoprotein complex subunit 2-like
Locus_27886_Transcript_1/1_Conf_1.000	145	0							
Locus_27887_Transcript_1/1_Conf_1.000	230	0							

Locus_27888_Transcript_1/1_Conf_1.000	270	20	1.34E-06	XP_002597580.1	47	56.225	88	42	hypothetical protein BRAFLDRAFT_82314
Locus_27889_Transcript_1/1_Conf_1.000	226	0							
Locus_2789_Transcript_1/1_Conf_1.000	680	5	2.11E-31	NP_001021610.1	56	139.813	194	110	hypothetical protein T05F1.6
Locus_27890_Transcript_1/1_Conf_1.000	144	0							
Locus_27891_Transcript_1/1_Conf_1.000	178	0							
Locus_27892_Transcript_1/1_Conf_1.000	173	0							
Locus_27893_Transcript_1/1_Conf_1.000	159	20	4.17E-24	XP_002747286.1	100	114.39	53	53	PREDICTED: endoplasmic reticulum-Golgi intermediate compartment protein 3 isoform 2
Locus_27894_Transcript_1/1_Conf_1.000	210	0							
Locus_27895_Transcript_1/1_Conf_1.000	164	0							
Locus_27896_Transcript_1/1_Conf_1.000	226	0							
Locus_27897_Transcript_1/1_Conf_1.000	126	0							
Locus_27898_Transcript_1/1_Conf_1.000	176	2	1.79E-11	NP_510441.1	67	72.4034	53	36	hypothetical protein F40E10.5
Locus_27899_Transcript_1/1_Conf_1.000	171	0							
Locus_279_Transcript_1/1_Conf_1.000	780	20	3.66E-39	NP_498519.1	55	166.007	221	123	hypothetical protein F31E3.4
Locus_2790_Transcript_1/1_Conf_1.000	1104	20	1.12E-54	XP_002639433.1	57	218.394	331	189	C. briggsae CBR-PQN-19 protein

Locus_27900_Transcript_1/1_Conf_1.000	227	1	8.23E-04	NP_497908.1	57	46.9802	68	39	hypothetical protein F56F3.4
Locus_27901_Transcript_1/1_Conf_1.000	290	0							
Locus_27902_Transcript_1/1_Conf_1.000	133	0							
Locus_27903_Transcript_1/1_Conf_1.000	129	0							
Locus_27904_Transcript_1/1_Conf_1.000	176	20	5.56E-13	XP_002643114.1	78	77.411	56	44	C. briggsae CBR-OSM-12 protein
Locus_27905_Transcript_1/1_Conf_1.000	148	0							
Locus_27906_Transcript_1/1_Conf_1.000	155	0							
Locus_27907_Transcript_1/1_Conf_1.000	204	20	6.83E-19	ZP_04861996.1	83	97.0561	67	56	pyrroline-5-carboxylate reductase
Locus_27908_Transcript_1/1_Conf_1.000	179	0							
Locus_27909_Transcript_1/1_Conf_1.000	145	0							
Locus_2791_Transcript_1/1_Conf_1.000	763	20	1.20E-23	NP_498874.2	98	114.39	54	53	hypothetical protein F42H10.3
Locus_27910_Transcript_1/1_Conf_1.000	130	20	1.09E-16	CBK19358.1	100	89.7373	43	43	C. elegans protein 4R79.2b, partially confirmed by transcript evidence
Locus_27911_Transcript_1/1_Conf_1.000	153	13	1.27E-12	CBA11992.1	83	76.2554	49	41	endonuclease-reverse transcriptase HmRTE-e01
Locus_27912_Transcript_1/1_Conf_1.000	285	20	6.25E-44	NP_001129826.1	93	180.259	94	88	hypothetical protein T13H5.1
Locus_27913_Transcript_1/1_Conf_1.000	162	0							
Locus_27914_Transcript_1/1_Conf_1.000	140	0							
Locus_27915_Transcript_1/1_Conf_1.000	145	16	1.08E-11	XP_001894688.1	81	73.1738	43	35	Protein-tyrosine phosphatase containing protein
Locus_27916_Transcript_1/1_Conf_1.000	134	0							
Locus_27917_Transcript_1/1_Conf_1.000	128	0							
Locus_27918_Transcript_1/1_Conf_1.000	198	2	6.02E-15	NP_001023516.1	77	83.9593	61	47	Temporarily Assigned Gene name family member (tag-273)
Locus_27919_Transcript_1/1_Conf_1.000	259	0							
Locus_2792_Transcript_1/1_Conf_1.000	2274	20	0	XP_002642200.1	69	691.804	692	484	C. briggsae CBR-ZYG-8 protein
Locus_27920_Transcript_1/1_Conf_1.000	182	4	3.06E-06	NP_001021463.1	59	55.0694	66	39	SUppressor of activated let-60 Ras family member (sur-2)
Locus_27921_Transcript_1/1_Conf_1.000	132	3	9.52E-13	XP_002640727.1	86	76.6406	44	38	C. briggsae CBR-EXOC-8 protein
Locus_27922_Transcript_1/1_Conf_1.000	339	0							

Locus_27923_Transcript_1/1_Conf_1.000	143	0							
Locus_27924_Transcript_1/1_Conf_1.000	131	0							
Locus_27925_Transcript_1/1_Conf_1.000	128	0							
Locus_27926_Transcript_1/1_Conf_1.000	135	0							
Locus_27927_Transcript_1/1_Conf_1.000	221	0							
Locus_27928_Transcript_1/1_Conf_1.000	436	20	1.60E-36	NP_501999.2	75	155.606	124	94	hypothetical protein T25B9.10
Locus_27929_Transcript_1/1_Conf_1.000	215	20	5.01E-14	XP_001377095.1	67	80.8777	73	49	PREDICTED: similar to NGEP long
Locus_2793_Transcript_1/1_Conf_1.000	825	4	8.22E-16	ACO15786.1	67	88.5817	119	80	Hypothetical protein W10D9.6
Locus_27930_Transcript_1/1_Conf_1.000	315	4	5.71E-05	NP_496947.2	85	50.8322	35	30	GUstatory Receptor family member (gur-4)
Locus_27931_Transcript_1/1_Conf_1.000	135	2	5.96E-07	NP_001022528.1	84	57.3806	39	33	hypothetical protein ZK669.7
Locus_27932_Transcript_1/1_Conf_1.000	133	0							
Locus_27933_Transcript_1/1_Conf_1.000	170	0							
Locus_27934_Transcript_1/1_Conf_1.000	149	20	1.77E-22	3FBY	100	108.997	49	49	The Signature Domain Of Cartilage Oligomeric Matrix Protein.
Locus_27935_Transcript_1/1_Conf_1.000	163	0							
Locus_27936_Transcript_1/1_Conf_1.000	260	0							
Locus_27937_Transcript_1/1_Conf_1.000	158	1	8.20E-04	ADI61822.1	69	46.9802	42	29	endonuclease-reverse transcriptase
Locus_27938_Transcript_1/1_Conf_1.000	137	0							
Locus_27939_Transcript_1/1_Conf_1.000	279	0							
Locus_2794_Transcript_1/1_Conf_1.000	781	20	1.78E-110	NP_491004.1	87	402.905	260	228	Fructose-1,6-BiPhosphatase family member (fbp-1)
Locus_27940_Transcript_1/1_Conf_1.000	140	0							
Locus_27941_Transcript_1/1_Conf_1.000	172	5	4.00E-11	NP_509643.1	73	71.2478	57	42	hypothetical protein F36G3.2
Locus_27942_Transcript_1/1_Conf_1.000	132	0							
Locus_27943_Transcript_1/1_Conf_1.000	139	0							
Locus_27944_Transcript_1/1_Conf_1.000	144	0							
Locus_27945_Transcript_1/1_Conf_1.000	198	0							
Locus_27946_Transcript_1/1_Conf_1.000	132	0							
Locus_27947_Transcript_1/1_Conf_1.000	184	0							
Locus_27948_Transcript_1/1_Conf_1.000	141	0							
Locus_27949_Transcript_1/1_Conf_1.000	260	0							

Locus_2795_Transcript_1/1_Conf_1.000	804	20	7.53E-67	XP_002639210.1	84	258.07	172	146	C. briggsae CBR-SKR-1 protein
Locus_27950_Transcript_1/1_Conf_1.000	155	20	5.16E-06	XP_002123114.1	79	54.299	44	35	PREDICTED: similar to solute carrier family 15 (H+/peptide transporter), member 2
Locus_27951_Transcript_1/1_Conf_1.000	149	0							
Locus_27952_Transcript_1/1_Conf_1.000	155	15	6.08E-15	NP_500082.1	82	83.9593	51	42	CaLPain family member (clp-7)
Locus_27953_Transcript_1/1_Conf_1.000	192	0							
Locus_27954_Transcript_1/1_Conf_1.000	289	0							
Locus_27955_Transcript_1/1_Conf_1.000	474	20	1.56E-31	XP_002599666.1	66	139.043	159	105	hypothetical protein BRAFLDRAFT_70346
Locus_27956_Transcript_1/1_Conf_1.000	186	0							
Locus_27957_Transcript_1/1_Conf_1.000	204	0							
Locus_27958_Transcript_1/1_Conf_1.000	177	0							
Locus_27959_Transcript_1/1_Conf_1.000	147	19	3.97E-06	NP_510616.2	76	54.6842	46	35	Multidrug Resistance Protein family member (mrp-3)
Locus_2796_Transcript_1/2_Conf_1.000	920	20	4.26E-59	XP_002634340.1	80	232.646	161	129	Hypothetical protein CBG17684

Locus_2796_Transcript_2/2_Conf_1.000	920	20	4.26E-59	XP_002634340.1	80	232.646	161	129	Hypothetical protein CBG17684
Locus_27960_Transcript_1/1_Conf_1.000	134	0							
Locus_27961_Transcript_1/1_Conf_1.000	231	0							
Locus_27962_Transcript_1/1_Conf_1.000	164	0							
Locus_27963_Transcript_1/1_Conf_1.000	150	20	1.23E-15	1TW9	84	86.2705	50	42	Glutathione Transferase-2
Locus_27964_Transcript_1/1_Conf_1.000	128	0							
Locus_27965_Transcript_1/1_Conf_1.000	144	0							
Locus_27966_Transcript_1/1_Conf_1.000	307	0							
Locus_27967_Transcript_1/1_Conf_1.000	159	0							
Locus_27968_Transcript_1/1_Conf_1.000	184	0							
Locus_27969_Transcript_1/1_Conf_1.000	265	0							
Locus_2797_Transcript_1/1_Conf_1.000	879	20	3.65E-89	NP_491475.2	78	332.413	252	199	hypothetical protein F21F3.1

Locus_27970_Transcript_1/1_Conf_1.000	137	20	1.79E-19	XP_002810390.1	100	98.9821	43	43	PREDICTED: LOW QUALITY PROTEIN: neurogenic locus notch homolog protein 2-like
Locus_27971_Transcript_1/1_Conf_1.000	161	0							
Locus_27972_Transcript_1/1_Conf_1.000	166	20	9.23E-24	BAG63567.1	100	113.235	54	54	unnamed protein product
Locus_27973_Transcript_1/1_Conf_1.000	170	0							
Locus_27974_Transcript_1/1_Conf_1.000	245	0							

Locus_27975_Transcript_1/1_Conf_1.000	149	20	6.33E-12	NP_498081.2	81	73.9442	49	40	ALdehyde deHydrogenase family member (alh-1)
Locus_27976_Transcript_1/1_Conf_1.000	138	0							
Locus_27977_Transcript_1/1_Conf_1.000	158	0							
Locus_27978_Transcript_1/1_Conf_1.000	220	20	1.91E-08	XP_002637730.1	62	62.3882	72	45	Hypothetical protein CBG11596
Locus_27979_Transcript_1/1_Conf_1.000	171	0							

Locus_2798_Transcript_1/2_Conf_1.000	1060	5	4.71E-31	NP_492588.1	74	139.813	143	106	GEI-4(Four) Interacting protein family member (gfi-2)
Locus_2798_Transcript_2/2_Conf_1.000	1045	5	4.60E-31	NP_492588.1	74	139.813	143	106	GEI-4(Four) Interacting protein family member (gfi-2)
Locus_27980_Transcript_1/1_Conf_1.000	221	0							
Locus_27981_Transcript_1/1_Conf_1.000	355	0							
Locus_27982_Transcript_1/1_Conf_1.000	144	0							
Locus_27983_Transcript_1/1_Conf_1.000	147	0							
Locus_27984_Transcript_1/1_Conf_1.000	129	0							
Locus_27985_Transcript_1/1_Conf_1.000	160	20	2.90E-17	XP_002633729.1	100	91.6633	52	52	C. briggsae CBR-GLT-3 protein
Locus_27986_Transcript_1/1_Conf_1.000	393	20	2.09E-23	XP_002640985.1	64	112.079	127	82	C. briggsae CBR-CDH-12 protein
Locus_27987_Transcript_1/1_Conf_1.000	754	20	4.79E-118	XP_002643750.1	92	427.943	251	233	C. briggsae CBR-GRK-1 protein
Locus_27988_Transcript_1/1_Conf_1.000	161	2	9.34E-08	NP_506285.1	67	60.077	49	33	hypothetical protein F57B1.5
Locus_27989_Transcript_1/1_Conf_1.000	165	0							
Locus_2799_Transcript_1/1_Conf_1.000	610	20	9.51E-88	XP_002643349.1	88	326.635	203	180	Hypothetical protein CBG15946
Locus_27990_Transcript_1/1_Conf_1.000	174	0							
Locus_27991_Transcript_1/1_Conf_1.000	170	0							
Locus_27992_Transcript_1/1_Conf_1.000	217	0							
Locus_27993_Transcript_1/1_Conf_1.000	285	0							
Locus_27994_Transcript_1/1_Conf_1.000	195	4	3.01E-06	NP_001021463.1	59	55.0694	66	39	SUppressor of activated let-60 Ras family member (sur-2)

Locus_27995_Transcript_1/1_Conf_1.000	406	20	3.87E-22	EFO20018.1	83	107.842	73	61	negative elongation factor C/D
Locus_27996_Transcript_1/1_Conf_1.000	144	2	7.51E-05	XP_002638650.1	72	50.447	43	31	C. briggsae CBR-TGT-2 protein
Locus_27997_Transcript_1/1_Conf_1.000	158	20	4.49E-10	NP_496490.2	76	67.781	51	39	NEPrilysin metallopeptidase family member (nep-1)
Locus_27998_Transcript_1/1_Conf_1.000	142	0							
Locus_27999_Transcript_1/1_Conf_1.000	155	0							
Locus_28_Transcript_1/5_Conf_0.125	624	20	1.57E-24	XP_002639761.1	95	116.701	66	63	C. briggsae CBR-PAB-1 protein
Locus_28_Transcript_2/5_Conf_0.250	1096	20	3.68E-34	XP_002639761.1	92	150.214	90	83	C. briggsae CBR-PAB-1 protein
Locus_28_Transcript_3/5_Conf_0.312	2043	20	2.03E-128	NP_001021710.1	72	464.537	437	317	PolyA Binding protein family member (pab-1)
Locus_28_Transcript_4/5_Conf_0.375	2049	20	1.67E-130	NP_001021710.1	72	471.47	437	318	PolyA Binding protein family member (pab-1)
Locus_28_Transcript_5/5_Conf_0.500	1576	20	0	DAA05868.1	97	903.664	464	452	TPA_inf: eukaryotic translation elongation factor 1A
Locus_280_Transcript_1/4_Conf_0.700	2020	20	9.79E-59	NP_492467.1	61	233.032	316	195	mammalian ASPM (Abnormal SPindles and primary Microcephaly) homolog family member (aspm-1)
Locus_280_Transcript_2/4_Conf_0.700	2149	20	1.06E-58	NP_492467.1	61	233.032	316	195	mammalian ASPM (Abnormal SPindles and primary Microcephaly) homolog family member (aspm-1)
Locus_280_Transcript_3/4_Conf_0.700	2125	20	1.04E-58	NP_492467.1	61	233.032	316	195	mammalian ASPM (Abnormal SPindles and primary Microcephaly) homolog family member (aspm-1)
Locus_280_Transcript_4/4_Conf_0.700	2125	20	1.04E-58	NP_492467.1	61	233.032	316	195	mammalian ASPM (Abnormal SPindles and primary Microcephaly) homolog family member (aspm-1)
Locus_2800_Transcript_1/1_Conf_1.000	143	0							
Locus_28000_Transcript_1/1_Conf_1.000	265	0							
Locus_28001_Transcript_1/1_Conf_1.000	149	0							
Locus_28002_Transcript_1/1_Conf_1.000	204	0							
Locus_28003_Transcript_1/1_Conf_1.000	181	0							
Locus_28004_Transcript_1/1_Conf_1.000	141	3	9.45E-05	ABF57453.1	71	50.0618	38	27	ZIM-3
Locus_28005_Transcript_1/1_Conf_1.000	135	2	2.50E-05	EFO26456.1	69	51.9878	46	32	hypothetical protein LOAG_02027

Locus_28006_Transcript_1/1_Conf_1.000	140	20	3.47E-15	CBJ33591.1	88	84.7297	45	40	conserved unknown protein
Locus_28007_Transcript_1/1_Conf_1.000	159	0							
Locus_28008_Transcript_1/1_Conf_1.000	128	0							
Locus_28009_Transcript_1/1_Conf_1.000	233	4	1.03E-06	XP_002630482.1	66	56.6102	80	53	Hypothetical protein CBG11218
Locus_2801_Transcript_1/1_Conf_1.000	193	0							
Locus_28010_Transcript_1/1_Conf_1.000	158	2	1.14E-05	XP_002635599.1	78	53.1434	47	37	Hypothetical protein CBG20588
Locus_28011_Transcript_1/1_Conf_1.000	179	0							
Locus_28012_Transcript_1/1_Conf_1.000	182	0							
Locus_28013_Transcript_1/1_Conf_1.000	260	0							
Locus_28014_Transcript_1/1_Conf_1.000	143	0							
Locus_28015_Transcript_1/1_Conf_1.000	160	1	4.18E-16	XP_002804850.1	93	87.8113	45	42	PREDICTED: hypothetical protein LOC100427666
Locus_28016_Transcript_1/1_Conf_1.000	322	20	4.73E-52	XP_002644419.1	94	207.223	107	101	Hypothetical protein CBG14273
Locus_28017_Transcript_1/1_Conf_1.000	144	0							
Locus_28018_Transcript_1/1_Conf_1.000	177	0							
Locus_28019_Transcript_1/1_Conf_1.000	261	20	3.40E-42	EFO21455.1	97	174.481	86	84	voltage-gated calcium channel
Locus_2802_Transcript_2/2_Conf_0.964	106	0							
Locus_28020_Transcript_1/1_Conf_1.000	142	0							
Locus_28021_Transcript_1/1_Conf_1.000	181	0							
Locus_28022_Transcript_1/1_Conf_1.000	135	1	6.59E-06	NP_492131.1	77	53.9138	36	28	RNA-dependent RNA polymerase Family family member (rrf-1)
Locus_28023_Transcript_1/1_Conf_1.000	135	20	1.12E-13	XP_002630557.1	93	79.7221	44	41	Hypothetical protein CBG13002
Locus_28024_Transcript_1/1_Conf_1.000	259	20	7.91E-23	NP_510810.3	80	110.153	86	69	PaTched Related family member (ptr-5)
Locus_28025_Transcript_1/1_Conf_1.000	388	20	9.77E-26	XP_002646790.1	65	119.783	127	83	Hypothetical protein CBG18441
Locus_28026_Transcript_1/1_Conf_1.000	245	0							

Locus_28027_Transcript_1/1_Conf_1.000	152	0							
Locus_28028_Transcript_1/1_Conf_1.000	261	20	1.03E-22	CAD11605.1	70	109.768	85	60	metalloprotease
Locus_28029_Transcript_1/1_Conf_1.000	139	0							
Locus_2803_Transcript_1/1_Conf_1.000	1171	20	2.50E-92	NP_508654.1	67	343.584	364	246	hypothetical protein F47B7.2
Locus_28030_Transcript_1/1_Conf_1.000	138	20	4.54E-15	NP_001165131.1	100	84.3445	45	45	NADH-cytochrome b5 reductase 3 isoform 3
Locus_28031_Transcript_1/1_Conf_1.000	183	0							
Locus_28032_Transcript_1/1_Conf_1.000	214	2	4.70E-04	XP_002639738.1	82	47.7506	34	28	Hypothetical protein CBG12466
Locus_28033_Transcript_1/1_Conf_1.000	152	0							
Locus_28034_Transcript_1/1_Conf_1.000	134	20	1.33E-06	CBL43415.1	72	56.225	43	31	C. elegans protein C32C4.2b, partially confirmed by transcript evidence
Locus_28035_Transcript_1/1_Conf_1.000	153	0							
Locus_28036_Transcript_1/1_Conf_1.000	137	0							
Locus_28037_Transcript_1/1_Conf_1.000	164	20	2.52E-21	NP_494880.1	92	105.145	54	50	COLlagen family member (col-73)
Locus_28038_Transcript_1/1_Conf_1.000	222	3	1.96E-05	XP_002634967.1	70	52.373	58	41	Hypothetical protein CBG13503
Locus_28039_Transcript_1/1_Conf_1.000	136	0							
Locus_2804_Transcript_1/1_Conf_1.000	647	20	8.73E-53	XP_002634755.1	72	210.69	204	147	Hypothetical protein CBG05349
Locus_28040_Transcript_1/1_Conf_1.000	190	0							
Locus_28041_Transcript_1/1_Conf_1.000	224	0							
Locus_28042_Transcript_1/1_Conf_1.000	263	20	7.13E-24	NP_001021097.1	77	113.62	86	67	hypothetical protein F10G8.9
Locus_28043_Transcript_1/1_Conf_1.000	169	2	7.83E-07	NP_001022489.1	64	56.9954	56	36	Homolog of Hedgehog AcylTransferase family member (hhat-1)
Locus_28044_Transcript_1/1_Conf_1.000	170	0							

Locus_28045_Transcript_1/1_Conf_1.000	221	20	6.76E-14	XP_001902718.1	68	80.4925	73	50	leucyl aminopeptidase
Locus_28046_Transcript_1/1_Conf_1.000	200	0							
Locus_28047_Transcript_1/1_Conf_1.000	177	20	9.74E-26	XP_002633391.1	98	119.783	58	57	Hypothetical protein CBG06150
Locus_28048_Transcript_1/1_Conf_1.000	216	4	5.54E-05	NP_508464.2	58	50.8322	72	42	hypothetical protein F52H2.7
Locus_28049_Transcript_1/1_Conf_1.000	161	0							
Locus_2805_Transcript_1/1_Conf_1.000	255	0							
Locus_28050_Transcript_1/1_Conf_1.000	142	0							
Locus_28051_Transcript_1/1_Conf_1.000	148	0							
Locus_28052_Transcript_1/1_Conf_1.000	277	20	1.51E-26	XP_002642928.1	71	122.479	92	66	Hypothetical protein CBG15204
Locus_28053_Transcript_1/1_Conf_1.000	173	0							
Locus_28054_Transcript_1/1_Conf_1.000	187	20	3.83E-17	EFP02977.1	86	91.2781	61	53	hypothetical protein CRE_28037
Locus_28055_Transcript_1/1_Conf_1.000	312	0							
Locus_28056_Transcript_1/1_Conf_1.000	128	0							
Locus_28057_Transcript_1/1_Conf_1.000	172	3	2.59E-18	NP_505390.2	83	95.1301	56	47	hypothetical protein F07C3.2
Locus_28058_Transcript_1/1_Conf_1.000	152	0							
Locus_28059_Transcript_1/1_Conf_1.000	164	0							
Locus_2806_Transcript_1/2_Conf_1.000	1320	20	0	NP_493349.1	89	652.129	385	345	Temporarily Assigned Gene name family member (tag-210)
Locus_2806_Transcript_2/2_Conf_1.000	1311	20	0	NP_493349.1	89	652.129	385	345	Temporarily Assigned Gene name family member (tag-210)
Locus_28060_Transcript_1/1_Conf_1.000	152	0							
Locus_28061_Transcript_1/1_Conf_1.000	130	0							

Locus_28062_Transcript_1/1_Conf_1.000	190	3	3.82E-09	NP_497222.1	65	64.6994	60	39	hypothetical protein T19C3.5
Locus_28063_Transcript_1/1_Conf_1.000	144	0							
Locus_28064_Transcript_1/1_Conf_1.000	171	0							
Locus_28065_Transcript_1/1_Conf_1.000	184	0							
Locus_28066_Transcript_1/1_Conf_1.000	145	0							
Locus_28067_Transcript_1/1_Conf_1.000	172	0							
Locus_28068_Transcript_1/1_Conf_1.000	209	0							
Locus_28069_Transcript_1/1_Conf_1.000	129	20	3.51E-15	XP_002800892.1	100	84.7297	42	42	PREDICTED: transcription factor Dp-1-like
Locus_2807_Transcript_1/1_Conf_1.000	282	0							
Locus_28070_Transcript_1/1_Conf_1.000	215	3	8.57E-06	NP_492337.1	64	53.5286	48	31	FERtilization defective (abnormal sperm) family member (fer-1)
Locus_28071_Transcript_1/1_Conf_1.000	252	14	1.01E-17	NP_492132.1	72	93.2041	81	59	Enhancer of Glp-One (glp-1) family member (ego-1)
Locus_28072_Transcript_1/1_Conf_1.000	154	0							
Locus_28073_Transcript_1/1_Conf_1.000	134	0							
Locus_28074_Transcript_1/1_Conf_1.000	143	2	5.56E-05	XP_002647069.1	71	50.8322	45	32	C. briggsae CBR-TIM-1 protein
Locus_28075_Transcript_1/1_Conf_1.000	218	0							
Locus_28076_Transcript_1/1_Conf_1.000	161	0							
Locus_28077_Transcript_1/1_Conf_1.000	176	0							
Locus_28078_Transcript_1/1_Conf_1.000	280	20	1.08E-16	EFP11552.1	67	89.7373	83	56	CRE-TAG-151 protein
Locus_28079_Transcript_1/1_Conf_1.000	217	2	5.35E-08	EFO24359.1	63	60.8474	71	45	hypothetical protein LOAG_04123
Locus_2808_Transcript_1/1_Conf_1.000	2039	20	0	NP_001021772.1	68	852.432	662	454	CEll Death abnormality family member (ced-1)
Locus_28080_Transcript_1/1_Conf_1.000	216	0							
Locus_28081_Transcript_1/1_Conf_1.000	507	0							

Locus_28082_Transcript_1/1_Conf_1.000	227	20	1.11E-08	XP_002966539.1	67	63.1586	74	50	hypothetical protein SELMODRAFT_407541
Locus_28083_Transcript_1/1_Conf_1.000	139	0							
Locus_28084_Transcript_1/1_Conf_1.000	326	0							
Locus_28085_Transcript_1/1_Conf_1.000	132	9	9.22E-08	EFO15922.1	78	60.077	42	33	hypothetical protein LOAG_12585
Locus_28086_Transcript_1/1_Conf_1.000	149	0							
Locus_28087_Transcript_1/1_Conf_1.000	300	20	5.58E-29	XP_001894414.1	81	130.568	100	81	Sodium:neurotransmitter symporter family protein
Locus_28088_Transcript_1/1_Conf_1.000	167								
Locus_28089_Transcript_1/1_Conf_1.000	140	0							
Locus_2809_Transcript_1/2_Conf_1.000	1107	20	9.84E-43	XP_002641513.1	87	178.718	119	104	Hypothetical protein CBG09808
Locus_2809_Transcript_2/2_Conf_1.000	899	20	9.84E-21	XP_002641512.1	70	105.145	98	69	Hypothetical protein CBG09807
Locus_28090_Transcript_1/1_Conf_1.000	191	0							
Locus_28091_Transcript_1/1_Conf_1.000	173	0							
Locus_28092_Transcript_1/1_Conf_1.000	247	0							
Locus_28093_Transcript_1/1_Conf_1.000	152	20	4.66E-23	XP_001892850.1	98	110.923	50	49	Zinc finger, ZZ type family protein
Locus_28094_Transcript_1/1_Conf_1.000	219	0							
Locus_28095_Transcript_1/1_Conf_1.000	388	20	2.11E-20	XP_001193594.1	70	102.064	118	83	PREDICTED: similar to endonuclease-reverse transcriptase
Locus_28096_Transcript_1/1_Conf_1.000	161	2	7.15E-08	NP_496972.1	68	60.4622	50	34	hypothetical protein Y54G11A.1
Locus_28097_Transcript_1/1_Conf_1.000	153	3	5.70E-13	NP_503388.1	85	77.411	48	41	PaTched Related family member (ptr-16)
Locus_28098_Transcript_1/1_Conf_1.000	133	0							
Locus_28099_Transcript_1/1_Conf_1.000	188	0							

Locus_281_Transcript_1/1_Conf_1.000	412	0							
Locus_2810_Transcript_1/1_Conf_1.000	412	0							
Locus_28100_Transcript_1/1_Conf_1.000	214	0							
Locus_28101_Transcript_1/1_Conf_1.000	131	0							
Locus_28102_Transcript_1/1_Conf_1.000	187	0							
Locus_28103_Transcript_1/1_Conf_1.000	135	0							
Locus_28104_Transcript_1/1_Conf_1.000	137	0							
Locus_28105_Transcript_1/1_Conf_1.000	158	20	3.01E-14	XP_002641552.1	84	81.6481	52	44	C. briggsae CBR-RBC-2 protein
Locus_28106_Transcript_1/1_Conf_1.000	211	20	9.16E-32	EFO86768.1	100	139.813	69	69	hypothetical protein CRE_04506
Locus_28107_Transcript_1/1_Conf_1.000	143	0							
Locus_28108_Transcript_1/1_Conf_1.000	148	3	5.20E-06	NP_506157.3	73	54.299	38	28	hypothetical protein ZC116.3
Locus_28109_Transcript_1/1_Conf_1.000	371	0							
Locus_2811_Transcript_1/3_Conf_0.571	1121	4	1.07E-28	NP_502516.2	51	132.109	240	124	hypothetical protein C39E9.12
Locus_2811_Transcript_2/3_Conf_0.714	1658	4	1.84E-28	NP_502516.2	51	132.109	240	124	hypothetical protein C39E9.12
Locus_2811_Transcript_3/3_Conf_0.714	1631	4	1.80E-28	NP_502516.2	51	132.109	240	124	hypothetical protein C39E9.12
Locus_28110_Transcript_1/1_Conf_1.000	165	0							
Locus_28111_Transcript_1/1_Conf_1.000	136	0							
Locus_28112_Transcript_1/1_Conf_1.000	134	0							
Locus_28113_Transcript_1/1_Conf_1.000	203	0							
Locus_28114_Transcript_1/1_Conf_1.000	137	0							
Locus_28115_Transcript_1/1_Conf_1.000	215	1	8.02E-04	AAA50740.2	54	46.9802	55	30	Hypothetical protein R12B2.2
Locus_28116_Transcript_1/1_Conf_1.000	256	20	2.24E-17	EFO25929.1	71	92.0485	80	57	hypothetical protein LOAG_02551
Locus_28117_Transcript_1/1_Conf_1.000	179	0							

Locus_28118_Transcript_1/1_Conf_1.000	284	0							
Locus_28119_Transcript_1/1_Conf_1.000	172	7	1.20E-15	NP_506408.1	92	86.2705	56	52	hypothetical protein F20G2.3
Locus_2812_Transcript_1/2_Conf_1.000	621	0							
Locus_2812_Transcript_2/2_Conf_1.000	568	0							
Locus_28120_Transcript_1/1_Conf_1.000	344	0							
Locus_28121_Transcript_1/1_Conf_1.000	147	0							
Locus_28123_Transcript_1/1_Conf_1.000	151	1	6.32E-04	XP_002631617.1	64	47.3654	48	31	Hypothetical protein CBG20802
Locus_28124_Transcript_1/1_Conf_1.000	182	0							
Locus_28125_Transcript_1/1_Conf_1.000	154	0							
Locus_28126_Transcript_1/1_Conf_1.000	163	0							
Locus_28127_Transcript_1/1_Conf_1.000	345	0							
Locus_28128_Transcript_1/1_Conf_1.000	153	10	1.22E-15	XP_002647008.1	84	86.2705	50	42	Hypothetical protein CBG23794
Locus_28129_Transcript_1/1_Conf_1.000	387	20	5.38E-08	XP_002071418.1	48	60.8474	124	60	GK25144
Locus_2813_Transcript_1/3_Conf_0.600	1462	20	0	EFO28255.1	83	680.248	480	403	hypothetical protein LOAG_00212
Locus_2813_Transcript_2/3_Conf_0.600	1714	20	0	EFO28255.1	83	679.863	481	403	hypothetical protein LOAG_00212
Locus_2813_Transcript_3/3_Conf_0.600	1714	20	0	EFO28255.1	83	679.863	481	403	hypothetical protein LOAG_00212
Locus_28130_Transcript_1/1_Conf_1.000	447	0							
Locus_28131_Transcript_1/1_Conf_1.000	147	0							
Locus_28132_Transcript_1/1_Conf_1.000	138	0							
Locus_28133_Transcript_1/1_Conf_1.000	164	0							
Locus_28134_Transcript_1/1_Conf_1.000	348	0							
Locus_28135_Transcript_1/1_Conf_1.000	163	0							
Locus_28136_Transcript_1/1_Conf_1.000	160	0							

Locus_28137_Transcript_1/1_Conf_1.000	134	0							
Locus_28138_Transcript_1/1_Conf_1.000	133	20	1.33E-06	XP_002730593.1	85	56.225	40	34	PREDICTED: aspartylglucosaminidase-like
Locus_28139_Transcript_1/1_Conf_1.000	154	0							
Locus_2814_Transcript_1/3_Conf_0.400	1167	7	1.31E-16	XP_002646437.1	53	92.0485	199	106	C. briggsae CBR-TFG-1 protein
Locus_2814_Transcript_2/3_Conf_0.400	615	20	5.66E-19	NP_498248.2	85	98.2117	62	53	hypothetical protein Y37B11A.2
Locus_2814_Transcript_3/3_Conf_0.600	1570	4	1.96E-16	XP_002646437.1	53	92.0485	199	106	C. briggsae CBR-TFG-1 protein
Locus_28140_Transcript_1/1_Conf_1.000	144	0							
Locus_28141_Transcript_1/1_Conf_1.000	490	20	1.86E-48	EFO85679.1	88	195.282	125	110	CRE-PYR-1 protein
Locus_28142_Transcript_1/1_Conf_1.000	222	20	7.17E-32	NP_001076639.1	94	140.198	74	70	TWiK family of potassium channels family member (twk-39)
Locus_28143_Transcript_1/1_Conf_1.000	142	0							
Locus_28144_Transcript_1/1_Conf_1.000	137	0							
Locus_28145_Transcript_1/1_Conf_1.000	387	20	7.96E-52	EFO15775.1	89	206.453	129	116	hypothetical protein LOAG_12734
Locus_28146_Transcript_1/1_Conf_1.000	162	2	1.64E-04	NP_495350.4	63	49.2914	52	33	hypothetical protein T19D12.6
Locus_28147_Transcript_1/1_Conf_1.000	147	20	3.47E-10	ACI49239.1	75	68.1662	48	36	hypothetical protein Csp3_JD06.005
Locus_28148_Transcript_1/1_Conf_1.000	154	0							
Locus_28149_Transcript_1/1_Conf_1.000	143	0							
Locus_2815_Transcript_1/1_Conf_1.000	726	0							
Locus_28150_Transcript_1/1_Conf_1.000	250	0							
Locus_28151_Transcript_1/1_Conf_1.000	270	0							
Locus_28152_Transcript_1/1_Conf_1.000	133	0							
Locus_28153_Transcript_1/1_Conf_1.000	148	0							
Locus_28154_Transcript_1/1_Conf_1.000	185	0							

Locus_28155_Transcript_1/1_Conf_1.000	142	0							
Locus_28156_Transcript_1/1_Conf_1.000	173	20	8.63E-14	EFO21654.1	80	80.1073	56	45	hypothetical protein LOAG_06832
Locus_28157_Transcript_1/1_Conf_1.000	275	0							
Locus_28158_Transcript_1/1_Conf_1.000	136	0							
Locus_28159_Transcript_1/1_Conf_1.000	144	0							
Locus_2816_Transcript_1/2_Conf_1.000	1999	20	1.21E-77	XP_002640488.1	50	295.819	667	338	Hypothetical protein CBG13624
Locus_2816_Transcript_2/2_Conf_1.000	2005	20	9.33E-78	XP_002640488.1	50	296.204	667	339	Hypothetical protein CBG13624
Locus_28160_Transcript_1/1_Conf_1.000	147	20	2.56E-21	XP_002812491.1	100	105.145	48	48	PREDICTED: c-X-C chemokine receptor type 4-like
Locus_28161_Transcript_1/1_Conf_1.000	182	0							
Locus_28162_Transcript_1/1_Conf_1.000	182	0							
Locus_28163_Transcript_1/1_Conf_1.000	150	0							
Locus_28164_Transcript_1/1_Conf_1.000	193	0							
Locus_28165_Transcript_1/1_Conf_1.000	184	0							
Locus_28166_Transcript_1/1_Conf_1.000	130	0							
Locus_28167_Transcript_1/1_Conf_1.000	303	2	1.63E-04	XP_002629805.1	64	49.2914	50	32	Hypothetical protein CBG01049
Locus_28168_Transcript_1/1_Conf_1.000	169	0							
Locus_28169_Transcript_1/1_Conf_1.000	313	4	2.49E-08	NP_506187.2	66	62.003	62	41	hypothetical protein C15C8.4
Locus_2817_Transcript_1/1_Conf_1.000	838	6	1.11E-07	NP_001041121.1	47	61.6178	111	53	hypothetical protein F53C11.5
Locus_28170_Transcript_1/1_Conf_1.000	160	0							
Locus_28171_Transcript_1/1_Conf_1.000	146	0							
Locus_28172_Transcript_1/1_Conf_1.000	149	0							

Locus_28173_Transcript_1/1_Conf_1.000	177	20	2.10E-28	XP_002927413.1	100	128.642	58	58	PREDICTED: eukaryotic translation initiation factor 3 subunit C-like
Locus_28174_Transcript_1/1_Conf_1.000	441	0							
Locus_28175_Transcript_1/1_Conf_1.000	353	20	7.59E-34	EFO23183.1	77	146.747	114	88	acetyltransferase
Locus_28176_Transcript_1/1_Conf_1.000	232	20	2.63E-18	NP_494983.1	77	95.1301	67	52	intestinal acid PHOsphatase family member (pho-1)
Locus_28177_Transcript_1/1_Conf_1.000	152	7	7.73E-10	NP_504512.1	86	67.0106	51	44	hypothetical protein F44E7.2
Locus_28178_Transcript_1/1_Conf_1.000	322	0							
Locus_28179_Transcript_1/1_Conf_1.000	152	0							
Locus_2818_Transcript_1/1_Conf_1.000	541	0							
Locus_28180_Transcript_1/1_Conf_1.000	166	0							
Locus_28181_Transcript_1/1_Conf_1.000	178	0							
Locus_28182_Transcript_1/1_Conf_1.000	169	20	2.27E-22	EFO92254.1	96	108.612	56	54	hypothetical protein CRE_10947
Locus_28183_Transcript_1/1_Conf_1.000	254	0							
Locus_28184_Transcript_1/1_Conf_1.000	226	0							
Locus_28185_Transcript_1/1_Conf_1.000	202	0							
Locus_28186_Transcript_1/1_Conf_1.000	142	0							
Locus_28187_Transcript_1/1_Conf_1.000	200	0							
Locus_28188_Transcript_1/1_Conf_1.000	132	2	2.13E-04	EFO23475.1	69	48.9062	46	32	hypothetical protein LOAG_05011
Locus_28189_Transcript_1/1_Conf_1.000	217	2	1.56E-07	NP_501398.1	67	59.3066	68	46	hypothetical protein F35H10.5
Locus_2819_Transcript_1/1_Conf_1.000	457	20	4.65E-52	NP_001021667.1	86	207.223	128	111	Nuclear Hormone Receptor family member (nhr-85)
Locus_28190_Transcript_1/1_Conf_1.000	179	0							
Locus_28191_Transcript_1/1_Conf_1.000	128	0							
Locus_28192_Transcript_1/1_Conf_1.000	154	0							
Locus_28193_Transcript_1/1_Conf_1.000	152	0							
Locus_28194_Transcript_1/1_Conf_1.000	129	0							
Locus_28195_Transcript_1/1_Conf_1.000	132	0							

Locus_28196_Transcript_1/1_Conf_1.000	157	0							
Locus_28197_Transcript_1/1_Conf_1.000	247	0							
Locus_28198_Transcript_1/1_Conf_1.000	168	20	1.09E-16	EDM07288.1	100	89.7373	55	55	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1, isoform CRA_b
Locus_28199_Transcript_1/1_Conf_1.000	147	0							
Locus_282_Transcript_1/2_Conf_1.000	756	4	1.94E-50	XP_002631619.1	58	203.371	248	146	Hypothetical protein CBG20804
Locus_282_Transcript_2/2_Conf_1.000	738	6	5.60E-47	XP_002631619.1	58	191.815	248	144	Hypothetical protein CBG20804
Locus_2820_Transcript_1/1_Conf_1.000	819	0							
Locus_28200_Transcript_1/1_Conf_1.000	134	0							
Locus_28201_Transcript_1/1_Conf_1.000	445	0							
Locus_28202_Transcript_1/1_Conf_1.000	142	0							
Locus_28203_Transcript_1/1_Conf_1.000	149	0							
Locus_28204_Transcript_1/1_Conf_1.000	241	20	4.60E-07	XP_002813545.1	72	57.7658	47	34	PREDICTED: histone-lysine N-methyltransferase SETMAR-like
Locus_28205_Transcript_1/1_Conf_1.000	260	0							
Locus_28206_Transcript_1/1_Conf_1.000	189	11	1.36E-14	NP_001040760.1	82	82.8037	62	51	hypothetical protein F10G7.5
Locus_28207_Transcript_1/1_Conf_1.000	138	0							
Locus_28208_Transcript_1/1_Conf_1.000	139	0							
Locus_28209_Transcript_1/1_Conf_1.000	130	0							
Locus_2821_Transcript_1/1_Conf_1.000	1192	20	1.97E-92	NP_498105.1	75	343.969	323	245	SYNtaxin family member (syn-16)
Locus_28210_Transcript_1/1_Conf_1.000	128	0							
Locus_28211_Transcript_1/1_Conf_1.000	216	20	1.27E-25	EFO82830.1	93	119.398	72	67	CRE-KLP-4 protein
Locus_28212_Transcript_1/1_Conf_1.000	183	0							
Locus_28213_Transcript_1/1_Conf_1.000	182	12	1.15E-18	XP_002631133.1	88	96.2857	59	52	C. briggsae CBR-CLH-2 protein

Locus_28214_Transcript_1/1_Conf_1.000	196	20	4.80E-12	EFO86757.1	71	74.3294	64	46	CRE-RPS-12 protein
Locus_28215_Transcript_1/1_Conf_1.000	133	0							
Locus_28216_Transcript_1/1_Conf_1.000	176	0							
Locus_28217_Transcript_1/1_Conf_1.000	190	0							
Locus_28218_Transcript_1/1_Conf_1.000	143	20	1.01E-14	NP_001026997.1	100	83.1889	38	38	BolA-like protein 2
Locus_28219_Transcript_1/1_Conf_1.000	134	0							
Locus_2822_Transcript_1/1_Conf_1.000	927	8	1.71E-55	XP_002630572.1	66	220.705	215	142	Hypothetical protein CBG13025
Locus_28220_Transcript_1/1_Conf_1.000	168	0							
Locus_28221_Transcript_1/1_Conf_1.000	142	11	1.32E-06	EFO19307.1	72	56.225	47	34	hypothetical protein LOAG_09187
Locus_28222_Transcript_1/1_Conf_1.000	133	1	1.13E-05	CAJ43277.1	65	53.1434	35	23	hypothetical protein
Locus_28223_Transcript_1/1_Conf_1.000	272	20	9.87E-26	NP_001024619.1	83	119.783	85	71	PhosphoLipase C family member (plc-1)

Locus_28224_Transcript_1/1_Conf_1.000	139	20	9.77E-18	DAA24281.1	100	93.2041	45	45	78 kDa glucose-regulated protein precursor
Locus_28225_Transcript_1/1_Conf_1.000	284	20	6.51E-41	EFO26082.1	94	170.244	92	87	hypothetical protein LOAG_02394
Locus_28226_Transcript_1/1_Conf_1.000	259	0							
Locus_28227_Transcript_1/1_Conf_1.000	167	2	4.91E-17	NP_490820.1	85	90.8929	55	47	hypothetical protein R06A10.4
Locus_28228_Transcript_1/1_Conf_1.000	333	2	1.98E-18	EFO19525.1	76	95.5153	86	66	hypothetical protein LOAG_08965
Locus_28229_Transcript_1/1_Conf_1.000	153	0							
Locus_2823_Transcript_1/2_Conf_1.000	564	20	1.02E-39	NP_500183.2	69	166.777	165	114	hypothetical protein M70.4
Locus_2823_Transcript_2/2_Conf_1.000	564	20	1.02E-39	NP_500183.2	69	166.777	165	114	hypothetical protein M70.4
Locus_28230_Transcript_1/1_Conf_1.000	146	2	2.94E-17	NP_502231.1	89	91.6633	48	43	LiPocalin-Related protein family member (lpr-2)
Locus_28231_Transcript_1/1_Conf_1.000	183	0							
Locus_28232_Transcript_1/1_Conf_1.000	191	0							
Locus_28233_Transcript_1/1_Conf_1.000	278	3	7.30E-05	XP_002639451.1	54	50.447	86	47	C. briggsae CBR-SMG-5 protein
Locus_28234_Transcript_1/1_Conf_1.000	172	0							
Locus_28235_Transcript_1/1_Conf_1.000	152	0							
Locus_28236_Transcript_1/1_Conf_1.000	133	0							
Locus_28237_Transcript_1/1_Conf_1.000	213	20	2.95E-14	EFP03780.1	65	81.6481	70	46	CRE-SNF-9 protein
Locus_28238_Transcript_1/1_Conf_1.000	242	0							

Locus_28239_Transcript_1/1_Conf_1.000	128	20	1.21E-15	XP_002743098.1	100	86.2705	42	42	PREDICTED: transitional endoplasmic reticulum ATPase-like
Locus_2824_Transcript_1/1_Conf_1.000	384	0							
Locus_28240_Transcript_1/1_Conf_1.000	158	20	1.95E-21	XP_002647993.1	92	105.531	52	48	C. briggsae CBR-ACR-6 protein
Locus_28241_Transcript_1/1_Conf_1.000	129	0							
Locus_28242_Transcript_1/1_Conf_1.000	242	3	7.80E-23	EFP09464.1	80	110.153	71	57	hypothetical protein CRE_25481
Locus_28243_Transcript_1/1_Conf_1.000	216	20	1.77E-27	XP_002920069.1	100	125.561	72	72	PREDICTED: 10 kDa heat shock protein, mitochondrial-like isoform 1
Locus_28244_Transcript_1/1_Conf_1.000	395	4	1.65E-20	NP_497665.2	72	102.449	115	83	hypothetical protein R148.5
Locus_28245_Transcript_1/1_Conf_1.000	210	7	2.27E-06	EFO90845.1	67	55.4546	59	40	hypothetical protein CRE_09760
Locus_28246_Transcript_1/1_Conf_1.000	195	20	7.39E-21	XP_001103713.2	100	103.605	64	64	PREDICTED: polyglutamine-binding protein 1-like isoform 5
Locus_28247_Transcript_1/1_Conf_1.000	193	0							
Locus_28248_Transcript_1/1_Conf_1.000	260	5	1.61E-07	EFO16233.1	63	59.3066	85	54	variant SH3 domain-containing protein

Locus_28249_Transcript_1/1_Conf_1.000	177	8	1.47E-05	XP_002631188.1	87	52.7582	40	35	Hypothetical protein CBG02977
Locus_2825_Transcript_1/1_Conf_1.000	961	20	2.27E-50	XP_002641997.1	54	203.756	274	150	C. briggsae CBR-LEC-4 protein
Locus_28250_Transcript_1/1_Conf_1.000	169	0							
Locus_28251_Transcript_1/1_Conf_1.000	281	3	1.16E-10	EFP08940.1	61	69.707	90	55	hypothetical protein CRE_18077
Locus_28252_Transcript_1/1_Conf_1.000	130	0							
Locus_28253_Transcript_1/1_Conf_1.000	147	0							
Locus_28254_Transcript_1/1_Conf_1.000	135	0							
Locus_28255_Transcript_1/1_Conf_1.000	233	0							
Locus_28256_Transcript_1/1_Conf_1.000	136	0							
Locus_28257_Transcript_1/1_Conf_1.000	160	0							
Locus_28258_Transcript_1/1_Conf_1.000	185	0							
Locus_28259_Transcript_1/1_Conf_1.000	184	0							
Locus_2826_Transcript_1/1_Conf_1.000	603	6	1.01E-25	NP_001021203.1	57	120.553	185	107	CEll Death abnormality family member (ced-4)
Locus_28260_Transcript_1/1_Conf_1.000	163	0							
Locus_28261_Transcript_1/1_Conf_1.000	379	20	1.37E-43		83	179.104	116	97	DNA topoisomerase II
Locus_28262_Transcript_1/1_Conf_1.000	137	1	6.16E-04	EFO23183.1	62	47.3654	45	28	acetyltransferase
Locus_28263_Transcript_1/1_Conf_1.000	152	20	4.82E-20	XP_002827931.1	100	100.908	50	50	PREDICTED: transmembrane channel-like protein 6-like isoform 1
Locus_28264_Transcript_1/1_Conf_1.000	131	0							
Locus_28265_Transcript_1/1_Conf_1.000	138	0							
Locus_28266_Transcript_1/1_Conf_1.000	250	0							
Locus_28267_Transcript_1/1_Conf_1.000	135	0							
Locus_28268_Transcript_1/1_Conf_1.000	154	0							
Locus_28269_Transcript_1/1_Conf_1.000	140	0							

Locus_2827_Transcript_1/5_Conf_0.167	284	20	9.44E-16	EFN76148.1	81	86.6557	55	45	S-adenosylmethionine synthetase
Locus_2827_Transcript_2/5_Conf_0.667	999	20	8.12E-155	NP_500872.1	94	550.821	323	306	hypothetical protein C06E7.1
Locus_2827_Transcript_3/5_Conf_0.667	999	20	8.12E-155	NP_500872.1	94	550.821	323	306	hypothetical protein C06E7.1

Locus_2827_Transcript_4/5_Conf_0.667	999	20	8.12E-155	NP_500872.1	94	550.821	323	306	hypothetical protein C06E7.1
Locus_2827_Transcript_5/5_Conf_0.667	999	20	8.12E-155	NP_500872.1	94	550.821	323	306	hypothetical protein C06E7.1
Locus_28270_Transcript_1/1_Conf_1.000	135	0							
Locus_28271_Transcript_1/1_Conf_1.000	144	0							
Locus_28272_Transcript_1/1_Conf_1.000	159	0							
Locus_28273_Transcript_1/1_Conf_1.000	155	0							
Locus_28274_Transcript_1/1_Conf_1.000	131	2	7.35E-05	EFO86287.1	95	50.447	42	40	hypothetical protein CRE_01961
Locus_28275_Transcript_1/1_Conf_1.000	128	0							
Locus_28276_Transcript_1/1_Conf_1.000	179	0							
Locus_28277_Transcript_1/1_Conf_1.000	262	20	5.88E-10	CAQ48388.2	60	67.3958	90	54	C. elegans protein C26H9A.1b, confirmed by transcript evidence
Locus_28278_Transcript_1/2_Conf_1.000	160	0							
Locus_28278_Transcript_2/2_Conf_1.000	442	0							

Locus_28279_Transcript_1/1_Conf_1.000	130	20	7.55E-18	EAW74399.1	100	93.5893	43	43	SCY1-like 1 (S. cerevisiae), isoform CRA_e
Locus_2828_Transcript_1/1_Conf_1.000	1001	4	6.47E-19	XP_001900077.1	55	99.3673	163	90	hypothetical protein Bm1_43075
Locus_28280_Transcript_1/1_Conf_1.000	164	10	2.46E-08	EFP03890.1	92	62.003	42	39	hypothetical protein CRE_28780
Locus_28281_Transcript_1/1_Conf_1.000	158	0							
Locus_28282_Transcript_1/1_Conf_1.000	318	20	3.21E-24	NP_490666.2	70	114.775	104	73	hypothetical protein Y48G1C.4
Locus_28283_Transcript_1/1_Conf_1.000	185	0							
Locus_28284_Transcript_1/1_Conf_1.000	176	20	1.05E-19	EFO85683.1	92	99.7525	57	53	hypothetical protein CRE_01767
Locus_28285_Transcript_1/1_Conf_1.000	157	1	1.96E-05	EFO26145.1	68	52.373	47	32	ImpB/MucB/SamB family protein
Locus_28286_Transcript_1/1_Conf_1.000	141	0							
Locus_28287_Transcript_1/1_Conf_1.000	156	0							
Locus_28288_Transcript_1/1_Conf_1.000	152	0							
Locus_28289_Transcript_1/1_Conf_1.000	200	0							
Locus_2829_Transcript_1/1_Conf_1.000	464	4	1.45E-08	NP_491750.3	59	62.7734	118	70	hypothetical protein C27A12.9
Locus_28290_Transcript_1/1_Conf_1.000	128	0							
Locus_28291_Transcript_1/1_Conf_1.000	160	0							
Locus_28292_Transcript_1/1_Conf_1.000	128	0							
Locus_28293_Transcript_1/1_Conf_1.000	138	20	9.14E-16	XP_002641343.1	91	86.6557	46	42	C. briggsae CBR-DPY-18 protein
Locus_28294_Transcript_1/1_Conf_1.000	192	0							
Locus_28295_Transcript_1/1_Conf_1.000	141	0							
Locus_28296_Transcript_1/1_Conf_1.000	145	6	1.20E-10	XP_002637627.1	85	69.707	48	41	Hypothetical protein CBG19372
Locus_28297_Transcript_1/1_Conf_1.000	190	10	5.90E-18	EFO86305.1	81	93.9745	54	44	hypothetical protein CRE_01756
Locus_28298_Transcript_1/1_Conf_1.000	145	0							
Locus_28299_Transcript_1/1_Conf_1.000	145	5	1.52E-05	Q60P76.3	71	52.7582	45	32	Spindle assembly abnormal protein 6
Locus_283_Transcript_1/1_Conf_1.000	455	20	2.58E-26	CAR63555.1	97	121.709	78	76	putative 15 kDa selenoprotein precursor
Locus_2830_Transcript_1/1_Conf_1.000	549	19	9.74E-24	XP_001371696.1	77	109.383	79	61	PREDICTED: hypothetical protein, partial
Locus_28300_Transcript_1/1_Conf_1.000	141	0							
Locus_28301_Transcript_1/1_Conf_1.000	212	0							

Locus_28302_Transcript_1/1_Conf_1.000	196	20	2.63E-18	EFP04543.1	86	95.1301	59	51	hypothetical protein CRE_31199
Locus_28303_Transcript_1/1_Conf_1.000	297	20	2.44E-24	EFP05586.1	71	115.161	95	68	hypothetical protein CRE_27168
Locus_28304_Transcript_1/1_Conf_1.000	163	7	3.66E-12	XP_002629928.1	83	74.7146	53	44	Hypothetical protein CBG21976
Locus_28305_Transcript_1/1_Conf_1.000	168	4	2.44E-16	AAC47925.2	88	88.5817	53	47	Hypothetical protein C02H7.2
Locus_28306_Transcript_1/1_Conf_1.000	134	0							
Locus_28307_Transcript_1/1_Conf_1.000	168	0							
Locus_28308_Transcript_1/1_Conf_1.000	168	11	3.90E-06	XP_002629645.1	65	54.6842	55	36	Hypothetical protein CBG00850
Locus_28309_Transcript_1/1_Conf_1.000	325	1	6.27E-04	EFO85702.1	46	47.3654	106	49	hypothetical protein CRE_01591
Locus_2831_Transcript_1/2_Conf_1.000	569	20	9.90E-83	XP_002641838.1	94	309.686	168	159	C. briggsae CBR-GER-1 protein
Locus_2831_Transcript_2/2_Conf_1.000	569	20	8.38E-82	XP_002641838.1	94	306.605	168	158	C. briggsae CBR-GER-1 protein
Locus_28310_Transcript_1/1_Conf_1.000	150	0							
Locus_28311_Transcript_1/1_Conf_1.000	751	1	4.97E-06	XP_001895120.1	41	55.8398	201	84	IQ calmodulin-binding motif family protein
Locus_28312_Transcript_1/1_Conf_1.000	188	0							
Locus_28313_Transcript_1/1_Conf_1.000	135	0							
Locus_28314_Transcript_1/1_Conf_1.000	156	1	2.46E-08	NP_001022279.1	94	62.003	38	36	Serpentine Receptor, class AB (class A-like) family member (srab-14)
Locus_28315_Transcript_1/1_Conf_1.000	222	7	1.04E-30	NP_510476.2	95	136.346	73	70	hypothetical protein Y70D2A.1

Locus_28316_Transcript_1/1_Conf_1.000	237	1	3.62E-36	ABC55426.1	100	154.451	71	71	mutant truncated midkine B
Locus_28317_Transcript_1/1_Conf_1.000	208	20	7.01E-32	NP_498717.1	98	140.198	69	68	hypothetical protein ZK688.2
Locus_28318_Transcript_1/1_Conf_1.000	131	2	7.33E-05	XP_001893489.1	70	50.447	41	29	Hepatocellular carcinoma-associated antigen 66
Locus_28319_Transcript_1/1_Conf_1.000	166	0							
Locus_2832_Transcript_1/1_Conf_1.000	447	20	7.80E-39	NP_502549.2	82	163.31	133	110	TransThyretin-Related family domain family member (ttr-51)
Locus_28320_Transcript_1/1_Conf_1.000	249	0							
Locus_28321_Transcript_1/1_Conf_1.000	152	0							
Locus_28322_Transcript_1/1_Conf_1.000	132	0							
Locus_28323_Transcript_1/1_Conf_1.000	132	0							
Locus_28324_Transcript_1/1_Conf_1.000	133	0							
Locus_28325_Transcript_1/1_Conf_1.000	180	0							
Locus_28326_Transcript_1/1_Conf_1.000	221	0							
Locus_28327_Transcript_1/1_Conf_1.000	261	8	1.50E-05	EFP07920.1	63	52.7582	80	51	hypothetical protein CRE_14096
Locus_28328_Transcript_1/1_Conf_1.000	176	0							
Locus_28329_Transcript_1/1_Conf_1.000	257	1	8.26E-12	CAR63604.1	67	73.559	83	56	hypothetical protein
Locus_2833_Transcript_1/1_Conf_1.000	1388	20	5.11E-82	XP_002632328.1	98	309.686	175	172	C. briggsae CBR-ARF-6 protein
Locus_28330_Transcript_1/1_Conf_1.000	243	0							

Locus_28331_Transcript_1/1_Conf_1.000	150	0							
Locus_28332_Transcript_1/1_Conf_1.000	133	3	4.43E-10	EFO89666.1	83	67.781	43	36	hypothetical protein CRE_07374
Locus_28333_Transcript_1/1_Conf_1.000	519	0							
Locus_28334_Transcript_1/1_Conf_1.000	244	0							
Locus_28335_Transcript_1/1_Conf_1.000	153	0							
Locus_28336_Transcript_1/1_Conf_1.000	283	20	5.35E-27	XP_002635104.1	75	124.02	94	71	Hypothetical protein CBG11324
Locus_28337_Transcript_1/1_Conf_1.000	215	0							
Locus_28338_Transcript_1/1_Conf_1.000	130	0							
Locus_28339_Transcript_1/1_Conf_1.000	240	20	2.87E-17	NP_001041183.1	75	91.6633	78	59	Na/Ca eXchangers family member (ncx-1)
Locus_2834_Transcript_1/1_Conf_1.000	589	20	3.32E-31	XP_002633524.1	62	138.658	182	114	Hypothetical protein CBG05389
Locus_28340_Transcript_1/1_Conf_1.000	195	0							
Locus_28341_Transcript_1/1_Conf_1.000	130	0							
Locus_28342_Transcript_1/1_Conf_1.000	225	9	1.04E-06	EFO86810.1	54	56.6102	75	41	hypothetical protein CRE_04697
Locus_28343_Transcript_1/1_Conf_1.000	246	0							
Locus_28344_Transcript_1/1_Conf_1.000	168	20	1.74E-22	BAD92875.1	98	108.997	54	53	MHC class II antigen variant
Locus_28345_Transcript_1/1_Conf_1.000	231	20	1.64E-20	XP_002647214.1	80	102.449	76	61	Hypothetical protein CBG22398

Locus_28346_Transcript_1/1_Conf_1.000	243	20	2.04E-23	NP_491653.2	79	112.079	79	63	hypothetical protein F55F8.3
Locus_28347_Transcript_1/1_Conf_1.000	168	0							
Locus_28348_Transcript_1/1_Conf_1.000	135	6	5.06E-06	AAK62032.1	77	54.299	36	28	metalloprotease 1 precursor
Locus_28349_Transcript_1/1_Conf_1.000	151	0							
Locus_2835_Transcript_1/1_Conf_1.000	278	8	1.24E-20	XP_698903.4	84	102.834	64	54	PREDICTED: hypothetical protein
Locus_28350_Transcript_1/1_Conf_1.000	148	0							
Locus_28351_Transcript_1/1_Conf_1.000	130	0							
Locus_28352_Transcript_1/1_Conf_1.000	181	5	1.32E-14	NP_502573.1	78	82.8037	60	47	hypothetical protein Y62E10A.6
Locus_28353_Transcript_1/1_Conf_1.000	223	20	1.55E-34	EFP12687.1	95	149.058	73	70	CRE-LAM-3 protein
Locus_28354_Transcript_1/1_Conf_1.000	144	6	1.16E-05	XP_002641536.1	80	53.1434	47	38	C. briggsae CBR-LET-805 protein
Locus_28355_Transcript_1/1_Conf_1.000	175	0							
Locus_28356_Transcript_1/1_Conf_1.000	166	1	1.81E-11	NP_507678.2	79	72.4034	54	43	hypothetical protein C54E10.2
Locus_28357_Transcript_1/1_Conf_1.000	152	0							
Locus_28358_Transcript_1/1_Conf_1.000	143	0							
Locus_28359_Transcript_1/1_Conf_1.000	555	13	5.00E-100	XP_002633317.1	97	367.081	185	180	Hypothetical protein CBG06054
Locus_2836_Transcript_1/1_Conf_1.000	522	4	4.03E-55	NP_001033504.1	91	217.624	125	114	hypothetical protein T23B12.11
Locus_28360_Transcript_1/1_Conf_1.000	130	2	2.78E-04	XP_002638523.1	70	48.521	41	29	Hypothetical protein CBG05551

Locus_28361_Transcript_1/1_Conf_1.000	211	14	1.20E-07	XP_001898113.1	53	59.6918	69	37	EB module family protein
Locus_28362_Transcript_1/1_Conf_1.000	204	0							
Locus_28363_Transcript_1/1_Conf_1.000	184	0							
Locus_28364_Transcript_1/1_Conf_1.000	175	0							
Locus_28365_Transcript_1/1_Conf_1.000	162	20	8.40E-25	EAW59542.1	100	116.701	53	53	hCG2040023
Locus_28366_Transcript_1/1_Conf_1.000	190	20	7.70E-18	NP_495838.2	84	93.5893	64	54	PYRimidine biosynthesis family member (pyr-1)
Locus_28367_Transcript_1/1_Conf_1.000	186	0							
Locus_28368_Transcript_1/1_Conf_1.000	181	4	4.70E-15	XP_002637525.1	86	84.3445	59	51	Hypothetical protein CBG19248
Locus_28369_Transcript_1/1_Conf_1.000	135	20	3.72E-17	NP_001165131.1	100	91.2781	45	45	NADH-cytochrome b5 reductase 3 isoform 3
Locus_2837_Transcript_1/1_Conf_1.000	660	0							
Locus_28370_Transcript_1/1_Conf_1.000	172	17	4.00E-11	XP_002645256.1	92	71.2478	38	35	Hypothetical protein CBG00135
Locus_28371_Transcript_1/1_Conf_1.000	187	0							
Locus_28372_Transcript_1/1_Conf_1.000	174	20	1.72E-30	AAD32452.1	100	135.576	58	58	AF067168_1NADH-ubiquinone oxidoreductase B22 subunit homolog
Locus_28373_Transcript_1/1_Conf_1.000	162	0							
Locus_28374_Transcript_1/1_Conf_1.000	325	0							
Locus_28375_Transcript_1/1_Conf_1.000	130	0							
Locus_28376_Transcript_1/1_Conf_1.000	296	0							

Locus_28377_Transcript_1/1_Conf_1.000	129	4	7.83E-07	EFO19582.1	76	56.9954	43	33	hypothetical protein LOAG_08910
Locus_28378_Transcript_1/1_Conf_1.000	143	0							
Locus_28379_Transcript_1/1_Conf_1.000	136	0							
Locus_2838_Transcript_1/1_Conf_1.000	1288	20	2.30E-158	XP_002643018.1	86	563.148	361	312	C. briggsae CBR-DNJ-10 protein
Locus_28380_Transcript_1/1_Conf_1.000	134	0							
Locus_28381_Transcript_1/1_Conf_1.000	176	0							
Locus_28382_Transcript_1/1_Conf_1.000	144	20	9.17E-19	XP_001150353.1	100	96.6709	48	48	PREDICTED: similar to S863-3 isoform 5
Locus_28383_Transcript_1/1_Conf_1.000	226	0							
Locus_28384_Transcript_1/1_Conf_1.000	156	0							
Locus_28385_Transcript_1/1_Conf_1.000	161	0							
Locus_28386_Transcript_1/1_Conf_1.000	156	0							
Locus_28387_Transcript_1/1_Conf_1.000	132	4	8.66E-06	NP_506407.1	72	53.5286	37	27	hypothetical protein F20G2.2
Locus_28388_Transcript_1/1_Conf_1.000	185	0							
Locus_28389_Transcript_1/1_Conf_1.000	168	5	1.13E-05	NP_510170.2	62	53.1434	56	35	hypothetical protein K03A11.4
Locus_2839_Transcript_1/3_Conf_0.400	479	0							
Locus_2839_Transcript_2/3_Conf_0.600	1360	20	3.38E-30	XP_002638693.1	77	137.502	131	101	Hypothetical protein CBG11890
Locus_2839_Transcript_3/3_Conf_0.600	1309	20	3.19E-30	XP_002638693.1	77	137.502	131	101	Hypothetical protein CBG11890
Locus_28390_Transcript_1/1_Conf_1.000	128	0							
Locus_28391_Transcript_1/1_Conf_1.000	166	0							
Locus_28392_Transcript_1/1_Conf_1.000	165	20	1.59E-07	XP_001900461.1	80	59.3066	52	42	Mast C-terminus family protein
Locus_28393_Transcript_1/1_Conf_1.000	135	0							
Locus_28394_Transcript_1/1_Conf_1.000	161	0							
Locus_28395_Transcript_1/1_Conf_1.000	266	20	5.63E-29	EFP05198.1	80	130.568	88	71	CRE-NHX-2 protein

Locus_28396_Transcript_1/1_Conf_1.000	211	20	3.37E-18	NP_496500.1	75	94.7449	68	51	hypothetical protein VF13D12L.3
Locus_28397_Transcript_1/1_Conf_1.000	179	1	2.77E-04	AAO63576.1	56	48.521	48	27	secreted protein 4 precursor
Locus_28398_Transcript_1/1_Conf_1.000	159	20	8.43E-25	NP_001012983.1	100	116.701	52	52	kallikrein-6 isoform B
Locus_28399_Transcript_1/1_Conf_1.000	252	0							
Locus_284_Transcript_1/1_Conf_1.000	660	20	1.19E-60	EFO22689.1	89	236.884	136	122	hypothetical protein LOAG_05794

Locus_2840_Transcript_1/1_Conf_1.000	231	13	1.17E-18	EFO17816.1	69	96.2857	76	53	hypothetical protein LOAG_10682
Locus_28400_Transcript_1/1_Conf_1.000	218	20	5.19E-11	NP_001033571.1	76	70.8626	72	55	SULfate Permease family member (sulp-7)
Locus_28401_Transcript_1/1_Conf_1.000	149	0							
Locus_28402_Transcript_1/1_Conf_1.000	138	0							
Locus_28403_Transcript_1/1_Conf_1.000	154	20	6.11E-07	EFP13149.1	76	57.3806	51	39	CRE-CYP-13A6 protein
Locus_28404_Transcript_1/1_Conf_1.000	283	0							
Locus_28405_Transcript_1/1_Conf_1.000	250	0							
Locus_28406_Transcript_1/1_Conf_1.000	148	0							
Locus_28407_Transcript_1/1_Conf_1.000	341	3	4.83E-33	NP_498314.2	77	144.05	111	86	hypothetical protein ZK328.6
Locus_28408_Transcript_1/1_Conf_1.000	194	0							
Locus_28409_Transcript_1/1_Conf_1.000	341	20	9.07E-32	XP_002643868.1	79	139.813	110	87	Hypothetical protein CBG02104
Locus_2841_Transcript_1/1_Conf_1.000	1116	0							
Locus_28410_Transcript_1/1_Conf_1.000	226	1	3.69E-04	AAK35187.1	59	48.1358	79	47	AF352702_1activation associated secreted protein-like protein
Locus_28411_Transcript_1/1_Conf_1.000	143	0							
Locus_28412_Transcript_1/1_Conf_1.000	189	0							
Locus_28413_Transcript_1/1_Conf_1.000	218	20	1.04E-19	XP_001200410.1	77	99.7525	70	54	PREDICTED: similar to MGC53562 protein, partial
Locus_28414_Transcript_1/1_Conf_1.000	150	0							
Locus_28415_Transcript_1/1_Conf_1.000	184	0							
Locus_28416_Transcript_1/1_Conf_1.000	144	0							

Locus_28417_Transcript_1/1_Conf_1.000	271	20	9.24E-24	EFO98755.1	82	113.235	90	74	hypothetical protein CRE_25911
Locus_28418_Transcript_1/1_Conf_1.000	182	20	4.37E-26	BAH13421.1	100	120.939	60	60	unnamed protein product
Locus_28419_Transcript_1/1_Conf_1.000	420	20	1.34E-30	NP_500551.2	65	135.961	145	95	hypothetical protein F55F10.1
Locus_2842_Transcript_1/4_Conf_0.500	742	0							
Locus_2842_Transcript_2/4_Conf_0.625	808	1	9.13E-04	XP_002130630.1	34	48.521	171	59	PREDICTED: similar to eukaryotic translation initiation factor 3, subunit 10 (theta)
Locus_2842_Transcript_3/4_Conf_0.250	565	0							
Locus_2842_Transcript_4/4_Conf_0.625	758	0							
Locus_28420_Transcript_1/1_Conf_1.000	207	0							
Locus_28421_Transcript_1/1_Conf_1.000	157	0							
Locus_28422_Transcript_1/1_Conf_1.000	144	0							
Locus_28423_Transcript_1/1_Conf_1.000	195	5	7.18E-08	EFO19074.1	60	60.4622	61	37	hypothetical protein LOAG_09420
Locus_28424_Transcript_1/1_Conf_1.000	227	0							
Locus_28425_Transcript_1/1_Conf_1.000	364	6	4.54E-23	EFO21083.1	68	110.923	122	84	hypothetical protein LOAG_07407
Locus_28426_Transcript_1/1_Conf_1.000	143	2	1.46E-05	ADI61822.1	63	52.7582	47	30	endonuclease-reverse transcriptase

Locus_28427_Transcript_1/1_Conf_1.000	223	20	1.27E-36	P00736.2	100	155.992	73	73	Complement C1r subcomponent
Locus_28428_Transcript_1/1_Conf_1.000	175	20	3.05E-19	NP_500129.1	91	98.2117	57	52	hypothetical protein Y41D4A.6
Locus_28429_Transcript_1/1_Conf_1.000	131	0							
Locus_2843_Transcript_1/1_Conf_1.000	215	0							
Locus_28430_Transcript_1/1_Conf_1.000	160	0							
Locus_28431_Transcript_1/1_Conf_1.000	142	4	7.71E-15	EFO23136.1	89	83.5741	46	41	hypothetical protein LOAG_05358
Locus_28432_Transcript_1/1_Conf_1.000	196	2	5.69E-05	XP_001899991.1	70	50.8322	51	36	Hypothetical 48.3 kDa protein F07F6.1 in chromosome III, putative
Locus_28433_Transcript_1/1_Conf_1.000	143	0							
Locus_28434_Transcript_1/1_Conf_1.000	145	5	1.24E-07	NP_510427.1	81	59.6918	37	30	hypothetical protein C44H4.4
Locus_28435_Transcript_1/1_Conf_1.000	169	0							
Locus_28436_Transcript_1/1_Conf_1.000	156	0							
Locus_28437_Transcript_1/1_Conf_1.000	342	20	5.45E-56	NP_497970.1	95	220.32	113	108	Adenylyl CYclase family member (acy-1)
Locus_28438_Transcript_1/1_Conf_1.000	138	4	8.57E-06	XP_002636925.1	89	53.5286	46	41	C. briggsae CBR-RHR-1 protein
Locus_28439_Transcript_1/1_Conf_1.000	135	3	9.51E-05	XP_002636379.1	67	50.0618	40	27	Hypothetical protein CBG08681
Locus_2844_Transcript_1/1_Conf_1.000	625	20	3.59E-53	NP_001123142.1	72	211.846	196	143	related to yeast Vacuolar Protein Sorting factor family member (vps-41)
Locus_28440_Transcript_1/1_Conf_1.000	147	0							
Locus_28441_Transcript_1/1_Conf_1.000	241	0							

Locus_28442_Transcript_1/1_Conf_1.000	228	2	5.30E-11	XP_002643649.1	83	70.8626	62	52	Hypothetical protein CBG16398
Locus_28443_Transcript_1/1_Conf_1.000	235	20	7.61E-18	BAH12043.1	100	93.5893	78	78	unnamed protein product
Locus_28444_Transcript_1/1_Conf_1.000	154	0							
Locus_28445_Transcript_1/1_Conf_1.000	178	0							
Locus_28446_Transcript_1/1_Conf_1.000	383	0							
Locus_28447_Transcript_1/1_Conf_1.000	148	20	1.41E-19	XP_002829227.1	100	99.3673	49	49	PREDICTED: heterogeneous nuclear ribonucleoprotein L-like isoform 2
Locus_28448_Transcript_1/1_Conf_1.000	400	0							
Locus_28449_Transcript_1/1_Conf_1.000	224	0							
Locus_2845_Transcript_1/2_Conf_1.000	631	3	1.16E-06	NP_493591.2	54	57.3806	153	83	Enhancer of unc-40 Ventral Axon guidance defects family member (eva-1)
Locus_2845_Transcript_2/2_Conf_1.000	631	3	1.16E-06	NP_493591.2	54	57.3806	153	83	Enhancer of unc-40 Ventral Axon guidance defects family member (eva-1)
Locus_28450_Transcript_1/1_Conf_1.000	184	20	3.26E-16	EFP13302.1	83	88.1965	60	50	CRE-PAT-2 protein
Locus_28451_Transcript_1/1_Conf_1.000	152	0							
Locus_28452_Transcript_1/1_Conf_1.000	140	20	3.26E-13	NP_001024060.1	89	78.1814	46	41	PAPS (adenosine 3'-phosphate 5'-phosphosulfate) Transporter family member (pst-1)
Locus_28453_Transcript_1/1_Conf_1.000	140	0							
Locus_28454_Transcript_1/1_Conf_1.000	137	0							
Locus_28455_Transcript_1/1_Conf_1.000	174	0							
Locus_28456_Transcript_1/1_Conf_1.000	138	0							
Locus_28457_Transcript_1/1_Conf_1.000	201	0							
Locus_28458_Transcript_1/1_Conf_1.000	173	20	4.88E-25	BAA07643.1	100	117.472	57	57	KIAA0085
Locus_28459_Transcript_1/1_Conf_1.000	129	0							
Locus_2846_Transcript_1/1_Conf_1.000	195	0							
Locus_28460_Transcript_1/1_Conf_1.000	156	0							
Locus_28461_Transcript_1/1_Conf_1.000	245	0							
Locus_28462_Transcript_1/1_Conf_1.000	192	0							
Locus_28463_Transcript_1/1_Conf_1.000	169	0							
Locus_28464_Transcript_1/1_Conf_1.000	145	0							
Locus_28465_Transcript_1/1_Conf_1.000	197	3	9.00E-35	NP_492020.1	100	149.828	65	65	hypothetical protein K10D3.4
Locus_28466_Transcript_1/1_Conf_1.000	135	2	4.87E-09	NP_001022489.1	78	64.3142	47	37	Homolog of Hedgehog AcylTransferase family member (hhat-1)
Locus_28467_Transcript_1/1_Conf_1.000	259	0							
Locus_28468_Transcript_1/1_Conf_1.000	171	4	3.63E-12	NP_499313.2	87	74.7146	56	49	hypothetical protein F43D9.1
Locus_28469_Transcript_1/1_Conf_1.000	131	0							

Locus_2847_Transcript_1/1_Conf_1.000	611	20	9.58E-64	AAL06642.1	80	246.899	169	136	serine-threonine protein kinase
Locus_28470_Transcript_1/1_Conf_1.000	148	0							
Locus_28471_Transcript_1/1_Conf_1.000	140	0							
Locus_28472_Transcript_1/1_Conf_1.000	275	20	1.98E-34	EFO94520.1	85	148.673	84	72	CRE-NHR-105 protein
Locus_28473_Transcript_1/1_Conf_1.000	136	0							
Locus_28474_Transcript_1/1_Conf_1.000	270	0							
Locus_28475_Transcript_1/1_Conf_1.000	156	0							
Locus_28476_Transcript_1/1_Conf_1.000	241	0							
Locus_28477_Transcript_1/1_Conf_1.000	131	18	3.51E-15	XP_003064997.1	97	84.7297	37	36	predicted protein
Locus_28478_Transcript_1/1_Conf_1.000	179	2	2.58E-10	XP_002630273.1	76	68.5514	56	43	Hypothetical protein CBG00701
Locus_28479_Transcript_1/1_Conf_1.000	191	4	8.22E-12	XP_001896262.1	72	73.559	62	45	3'5'-cyclic nucleotide phosphodiesterase family protein
Locus_2848_Transcript_1/1_Conf_1.000	733	20	5.53E-31	NP_001041056.1	63	138.658	165	104	hypothetical protein Y67H2A.2

Locus_28480_Transcript_1/1_Conf_1.000	278	20	8.83E-43	XP_002634414.1	87	176.407	91	80	C. briggsae CBR-EPI-1 protein
Locus_28481_Transcript_1/1_Conf_1.000	133	0							
Locus_28482_Transcript_1/1_Conf_1.000	136	0							
Locus_28483_Transcript_1/1_Conf_1.000	155	0							
Locus_28484_Transcript_1/1_Conf_1.000	227	0							
Locus_28485_Transcript_1/1_Conf_1.000	134	20	9.85E-10	XP_002640443.1	86	66.6254	44	38	C. briggsae CBR-HAF-6 protein
Locus_28486_Transcript_1/1_Conf_1.000	170	0							
Locus_28487_Transcript_1/1_Conf_1.000	463	20	5.13E-22	EFO21647.1	59	107.457	139	83	cpsf3-prov protein
Locus_28488_Transcript_1/1_Conf_1.000	175	0							
Locus_28489_Transcript_1/1_Conf_1.000	164	0							
Locus_2849_Transcript_1/1_Conf_1.000	415	20	7.88E-60	XP_002636570.1	91	233.032	136	125	C. briggsae CBR-PYC-1 protein
Locus_28490_Transcript_1/1_Conf_1.000	166	0							
Locus_28491_Transcript_1/1_Conf_1.000	144	0							
Locus_28492_Transcript_1/1_Conf_1.000	165	0							
Locus_28493_Transcript_1/1_Conf_1.000	133	0							
Locus_28494_Transcript_1/1_Conf_1.000	155	20	4.08E-11	XP_002643853.1	78	71.2478	51	40	Hypothetical protein CBG02083
Locus_28495_Transcript_1/1_Conf_1.000	209	0							
Locus_28496_Transcript_1/1_Conf_1.000	192	0							
Locus_28497_Transcript_1/1_Conf_1.000	194	0							
Locus_28498_Transcript_1/1_Conf_1.000	159	1	2.92E-09	YP_001152214.1	79	56.6102	44	35	ORF124
Locus_28499_Transcript_1/1_Conf_1.000	165	0							
Locus_285_Transcript_1/5_Conf_0.545	989	1	7.74E-17	CAR63661.1	97	92.4337	41	40	hypothetical protein
Locus_285_Transcript_2/5_Conf_0.455	881	0							
Locus_285_Transcript_3/5_Conf_0.455	989	1	7.74E-17	CAR63661.1	97	92.4337	41	40	hypothetical protein
Locus_285_Transcript_4/5_Conf_0.182	720	7	3.82E-29	CAR63661.1	78	132.494	103	81	hypothetical protein
Locus_285_Transcript_5/5_Conf_0.455	881	0							

Locus_2850_Transcript_1/1_Conf_1.000	541	20	4.34E-26	XP_002647009.1	63	121.324	173	110	C. briggsae CBR-DIV-1 protein
Locus_28500_Transcript_1/1_Conf_1.000	300	0							
Locus_28501_Transcript_1/1_Conf_1.000	192	3	1.55E-10	NP_505451.1	68	69.3218	63	43	hypothetical protein F11A3.1
Locus_28502_Transcript_1/1_Conf_1.000	141	0							
Locus_28503_Transcript_1/1_Conf_1.000	349	0							
Locus_28504_Transcript_1/1_Conf_1.000	164	0							
Locus_28505_Transcript_1/1_Conf_1.000	170	0							
Locus_28506_Transcript_1/1_Conf_1.000	163	0							
Locus_28507_Transcript_1/1_Conf_1.000	129	20	9.58E-13	EFO92677.1	95	76.6406	42	40	hypothetical protein CRE_16357
Locus_28508_Transcript_1/1_Conf_1.000	224	7	3.25E-08	NP_001122650.1	78	61.6178	74	58	PaTChed family member (ptc-3)
Locus_28509_Transcript_1/1_Conf_1.000	178	0							
Locus_2851_Transcript_1/1_Conf_1.000	442	20	3.55E-23	ACD88894.1	75	111.309	106	80	transthyretin-like protein
Locus_28510_Transcript_1/1_Conf_1.000	186	20	2.49E-08	XP_002171686.1	81	62.003	48	39	chaperone protein dnaJ 3
Locus_28511_Transcript_1/1_Conf_1.000	367	7	5.18E-19	XP_002631002.1	56	97.4413	139	78	Hypothetical protein CBG02749
Locus_28512_Transcript_1/1_Conf_1.000	162	10	2.99E-06	XP_002631054.1	67	55.0694	49	33	C. briggsae CBR-BTF-1 protein
Locus_28513_Transcript_1/1_Conf_1.000	166	20	1.25E-12	EFP05438.1	75	76.2554	54	41	hypothetical protein CRE_27247
Locus_28514_Transcript_1/1_Conf_1.000	332	0							
Locus_28515_Transcript_1/1_Conf_1.000	186	4	6.78E-06	EFO91751.1	62	53.9138	59	37	CRE-SQV-8 protein

Locus_28516_Transcript_1/1_Conf_1.000	135	20	3.38E-18	BAG54183.1	100	94.7449	45	45	unnamed protein product
Locus_28517_Transcript_1/1_Conf_1.000	138	0							
Locus_28518_Transcript_1/1_Conf_1.000	128	0							
Locus_28519_Transcript_1/1_Conf_1.000	327	0							
Locus_2852_Transcript_1/1_Conf_1.000	758	2	1.72E-06	XP_001896845.1	46	57.3806	156	72	hypothetical protein Bm1_26975
Locus_28520_Transcript_1/1_Conf_1.000	175	18	1.62E-12	NP_491778.2	83	75.8702	48	40	hypothetical protein T09B4.4
Locus_28521_Transcript_1/1_Conf_1.000	130	0							
Locus_28522_Transcript_1/1_Conf_1.000	203	0							
Locus_28523_Transcript_1/1_Conf_1.000	140	0							
Locus_28524_Transcript_1/1_Conf_1.000	159	0							
Locus_28525_Transcript_1/1_Conf_1.000	227	6	4.81E-12	XP_002638684.1	69	74.3294	75	52	C. briggsae CBR-LRS-2 protein
Locus_28526_Transcript_1/1_Conf_1.000	159	0							
Locus_28527_Transcript_1/1_Conf_1.000	169	0							
Locus_28528_Transcript_1/1_Conf_1.000	138	0							
Locus_28529_Transcript_1/1_Conf_1.000	256	0							
Locus_2853_Transcript_1/1_Conf_1.000	639	20	8.01E-35	XP_002638640.1	80	150.984	115	92	Hypothetical protein CBG05694
Locus_28530_Transcript_1/1_Conf_1.000	249	0							
Locus_28531_Transcript_1/1_Conf_1.000	233	4	7.17E-08	NP_499273.3	61	60.4622	83	51	hypothetical protein R01H10.7
Locus_28532_Transcript_1/1_Conf_1.000	224	0							
Locus_28533_Transcript_1/1_Conf_1.000	200	0							
Locus_28534_Transcript_1/1_Conf_1.000	315	0							
Locus_28535_Transcript_1/1_Conf_1.000	231	0							
Locus_28536_Transcript_1/1_Conf_1.000	130	0							
Locus_28537_Transcript_1/1_Conf_1.000	155	0							
Locus_28538_Transcript_1/1_Conf_1.000	148	20	2.75E-15	EFP08562.1	93	85.1149	49	46	hypothetical protein CRE_15512
Locus_28539_Transcript_1/1_Conf_1.000	177	2	8.28E-09	NP_500216.1	73	63.5438	57	42	hypothetical protein Y69A2AR.16

Locus_2854_Transcript_1/2_Conf_1.000	1237	15	8.02E-44	XP_001894670.1	51	182.57	397	204	hypothetical protein Bm1_16065
Locus_2854_Transcript_2/2_Conf_1.000	1237	15	8.02E-44	XP_001894670.1	51	182.57	397	204	hypothetical protein Bm1_16065
Locus_28540_Transcript_1/1_Conf_1.000	140	0							
Locus_28541_Transcript_1/1_Conf_1.000	259	3	1.50E-05	XP_002640312.1	67	52.7582	46	31	Hypothetical protein CBG12852
Locus_28542_Transcript_1/1_Conf_1.000	225	20	6.29E-12	XP_002640011.1	90	73.9442	74	67	Hypothetical protein CBG12481
Locus_28543_Transcript_1/1_Conf_1.000	162	0							
Locus_28544_Transcript_1/1_Conf_1.000	140	3	1.47E-05	EFP00055.1	69	52.7582	49	34	hypothetical protein CRE_18594
Locus_28545_Transcript_1/1_Conf_1.000	136	20	4.89E-09	AAM97610.1	78	64.3142	41	32	AF480920_1ADP/ATP carrier
Locus_28546_Transcript_1/1_Conf_1.000	165	20	5.80E-18	NP_492053.1	92	93.9745	54	50	LEThal family member (let-75)
Locus_28547_Transcript_1/1_Conf_1.000	148	0							
Locus_28548_Transcript_1/1_Conf_1.000	161	0							
Locus_28549_Transcript_1/1_Conf_1.000	268								
Locus_2855_Transcript_1/1_Conf_1.000	332	0							
Locus_28550_Transcript_1/1_Conf_1.000	132	20	3.39E-18	XP_002804983.1	100	94.7449	43	43	PREDICTED: isocitrate dehydrogenase
Locus_28551_Transcript_1/1_Conf_1.000	151	0							

Locus_28552_Transcript_1/1_Conf_1.000	131	0							
Locus_28553_Transcript_1/1_Conf_1.000	130	0							
Locus_28554_Transcript_1/1_Conf_1.000	130	0							
Locus_28555_Transcript_1/1_Conf_1.000	147	0							
Locus_28556_Transcript_1/1_Conf_1.000	255	1	5.19E-06	EFO17857.1	64	54.299	71	46	CK1/TTBK protein kinase
Locus_28557_Transcript_1/1_Conf_1.000	137	0							
Locus_28558_Transcript_1/1_Conf_1.000	236	20	1.06E-19	BAG63075.1	100	99.7525	76	76	unnamed protein product
Locus_28559_Transcript_1/1_Conf_1.000	183	20	1.15E-21	XP_002642021.1	86	106.301	60	52	C. briggsae CBR-COQ-8 protein
Locus_2856_Transcript_1/1_Conf_1.000	314	20	3.12E-35	XP_002641973.1	84	151.369	101	85	C. briggsae CBR-HSP-12.2 protein
Locus_28560_Transcript_1/1_Conf_1.000	175	0							
Locus_28561_Transcript_1/1_Conf_1.000	131	0							
Locus_28562_Transcript_1/1_Conf_1.000	595	20	5.46E-29	XP_001899696.1	60	131.339	170	103	CCR4-Not complex component, Not1 family protein
Locus_28563_Transcript_1/1_Conf_1.000	132	0							
Locus_28564_Transcript_1/1_Conf_1.000	210	20	3.72E-17	NP_001024318.1	79	91.2781	67	53	hypothetical protein ZK697.14

Locus_28565_Transcript_1/1_Conf_1.000	206	20	8.91E-35	BAG65408.1	100	149.828	68	68	unnamed protein product
Locus_28566_Transcript_1/1_Conf_1.000	286	20	2.84E-12	XP_001894871.1	64	75.0998	77	50	Leucine Rich Repeat family protein
Locus_28567_Transcript_1/1_Conf_1.000	160	20	6.91E-11	XP_002632976.1	76	70.4774	52	40	Hypothetical protein CBG21736
Locus_28568_Transcript_1/1_Conf_1.000	181	20	1.46E-13	EFO87295.1	85	79.337	60	51	hypothetical protein CRE_25800
Locus_28569_Transcript_1/1_Conf_1.000	208	0							
Locus_2857_Transcript_1/1_Conf_1.000	737	20	1.09E-34	NP_501636.2	91	150.984	84	77	Vacuolar H ATPase family member (vha-17)
Locus_28570_Transcript_1/1_Conf_1.000	252								
Locus_28571_Transcript_1/1_Conf_1.000	282	0							
Locus_28572_Transcript_1/1_Conf_1.000	198	0							
Locus_28573_Transcript_1/1_Conf_1.000	163	20	4.62E-15	XP_002638818.1	83	84.3445	54	45	Hypothetical protein CBG22021
Locus_28574_Transcript_1/1_Conf_1.000	154	0							
Locus_28575_Transcript_1/1_Conf_1.000	129	0							
Locus_28576_Transcript_1/1_Conf_1.000	269	12	1.57E-39	CAR63715.1	98	165.622	89	88	putative NHL (ring finger b-box coiled coil) domain containing family member
Locus_28577_Transcript_1/1_Conf_1.000	147	0							

Locus_28578_Transcript_1/1_Conf_1.000	210	20	1.20E-15	Q0MQ98.1	100	86.2705	42	42	NDUA4_GORGORecName: Full=NADH dehydrogenase
Locus_28579_Transcript_1/1_Conf_1.000	259	0							
Locus_2858_Transcript_1/1_Conf_1.000	758	20	6.99E-109	BAC06575.1	95	397.512	216	206	As37
Locus_28580_Transcript_1/1_Conf_1.000	235	0							
Locus_28581_Transcript_1/1_Conf_1.000	216	0							
Locus_28582_Transcript_1/1_Conf_1.000	203	3	5.80E-18	XP_002637648.1	85	93.9745	62	53	C. briggsae CBR-FSHR-1 protein
Locus_28583_Transcript_1/1_Conf_1.000	150	20	1.27E-12	XP_002644330.1	89	76.2554	48	43	C. briggsae CBR-SPC-1 protein
Locus_28584_Transcript_1/1_Conf_1.000	176	0							
Locus_28585_Transcript_1/1_Conf_1.000	133	0							
Locus_28586_Transcript_1/1_Conf_1.000	142	0							
Locus_28587_Transcript_1/1_Conf_1.000	204	20	2.68E-31	EFP07753.1	100	138.272	67	67	CRE-EGL-44 protein
Locus_28588_Transcript_1/1_Conf_1.000	293	20	2.20E-49	XP_002926989.1	100	198.364	97	97	PREDICTED: t-complex protein 1 subunit gamma-like isoform 2
Locus_28589_Transcript_1/1_Conf_1.000	139	0							
Locus_2859_Transcript_1/1_Conf_1.000	1038	20	3.26E-69	NP_498947.1	73	266.544	267	195	PeRoXisome assembly factor family member (prx-19)
Locus_28590_Transcript_1/1_Conf_1.000	195	20	3.66E-28	BAH13680.1	100	127.872	65	65	unnamed protein product

Locus_28591_Transcript_1/1_Conf_1.000	174	20	1.12E-21	EFO24540.1	92	106.301	57	53	hypothetical protein LOAG_03946
Locus_28592_Transcript_1/1_Conf_1.000	210	0							
Locus_28593_Transcript_1/1_Conf_1.000	396	0							
Locus_28594_Transcript_1/1_Conf_1.000	183	12	5.01E-17	NP_001040770.1	75	90.8929	58	44	hypothetical protein F26G1.9
Locus_28595_Transcript_1/1_Conf_1.000	182	20	1.11E-21	XP_002634423.1	91	106.301	59	54	C. briggsae CBR-PTR-14 protein
Locus_28596_Transcript_1/1_Conf_1.000	219	20	5.52E-32	XP_002639929.1	91	140.584	73	67	Hypothetical protein CBG08265
Locus_28597_Transcript_1/1_Conf_1.000	131	0							
Locus_28598_Transcript_1/1_Conf_1.000	143	0							
Locus_28599_Transcript_1/1_Conf_1.000	148	0							
Locus_286_Transcript_1/2_Conf_1.000	1154	20	2.55E-174	CAL30086.1	100	615.92	331	331	calreticulin precursor
Locus_286_Transcript_2/2_Conf_1.000	328	20	8.58E-46	CAL30086.1	100	186.422	84	84	calreticulin precursor
Locus_2860_Transcript_1/2_Conf_1.000	1581	20	2.56E-56	NP_501842.2	51	224.557	438	226	hypothetical protein K08F4.2
Locus_2860_Transcript_2/2_Conf_1.000	630	4	2.03E-27	NP_501842.2	75	126.331	104	78	hypothetical protein K08F4.2
Locus_28600_Transcript_1/1_Conf_1.000	169	4	3.40E-10	XP_002643114.1	73	68.1662	56	41	C. briggsae CBR-OSM-12 protein
Locus_28601_Transcript_1/1_Conf_1.000	186	0							
Locus_28602_Transcript_1/1_Conf_1.000	176	0							
Locus_28603_Transcript_1/1_Conf_1.000	131	0							
Locus_28604_Transcript_1/1_Conf_1.000	147	0							
Locus_28605_Transcript_1/1_Conf_1.000	138	0							
Locus_28606_Transcript_1/1_Conf_1.000	183	0							
Locus_28607_Transcript_1/1_Conf_1.000	147	0							
Locus_28608_Transcript_1/1_Conf_1.000	147	0							
Locus_28609_Transcript_1/1_Conf_1.000	167	0							

Locus_2861_Transcript_1/1_Conf_1.000	1246	20	5.89E-111	XP_001894436.1	84	405.601	272	229	heparan 6-O sulfotransferase HST-6
Locus_28610_Transcript_1/1_Conf_1.000	151	0							
Locus_28611_Transcript_1/1_Conf_1.000	191	7	1.45E-08	XP_002631564.1	80	62.7734	42	34	Hypothetical protein CBG20740
Locus_28612_Transcript_1/1_Conf_1.000	173	20	3.38E-18	3MTL	100	94.7449	57	57	CrystalStructure OfThe Pctaire1 Kinase In Complex With Ind E804
Locus_28613_Transcript_1/1_Conf_1.000	135	10	1.62E-12	EFP02763.1	90	75.8702	44	40	hypothetical protein CRE_28516
Locus_28614_Transcript_1/1_Conf_1.000	160	0							
Locus_28615_Transcript_1/1_Conf_1.000	147	0							
Locus_28616_Transcript_1/1_Conf_1.000	142	0							
Locus_28617_Transcript_1/1_Conf_1.000	316	0							
Locus_28618_Transcript_1/1_Conf_1.000	139	20	4.68E-20	EFB20679.1	100	100.908	46	46	hypothetical protein PANDA_013768
Locus_28619_Transcript_1/1_Conf_1.000	141	0							
Locus_2862_Transcript_1/1_Conf_1.000	925	20	1.60E-29	XP_001897636.1	55	134.42	259	145	hypothetical protein Bm1_30970
Locus_28620_Transcript_1/1_Conf_1.000	199	0							
Locus_28621_Transcript_1/1_Conf_1.000	245	20	1.91E-29	CAV31817.1	97	132.109	81	79	C. elegans protein Y54G9A.3b, partially confirmed by transcript evidence
Locus_28622_Transcript_1/1_Conf_1.000	152	0							
Locus_28623_Transcript_1/1_Conf_1.000	226	5	2.24E-17	XP_002633271.1	70	92.0485	75	53	Hypothetical protein CBG06000
Locus_28624_Transcript_1/1_Conf_1.000	276	20	2.25E-30	XP_002631304.1	82	135.191	89	73	Hypothetical protein CBG03118
Locus_28625_Transcript_1/1_Conf_1.000	151	11	1.77E-14	XP_002630350.1	86	82.4185	50	43	Hypothetical protein CBG04280
Locus_28626_Transcript_1/1_Conf_1.000	184	0							
Locus_28627_Transcript_1/1_Conf_1.000	155	20	1.41E-11	XP_002637173.1	84	72.7886	51	43	Hypothetical protein CBG09691
Locus_28628_Transcript_1/1_Conf_1.000	185	20	9.77E-13	NP_741217.1	77	76.6406	59	46	EXOSome (multiexonuclease complex) component family member (exos-9)
Locus_28629_Transcript_1/1_Conf_1.000	191	0							

Locus_2863_Transcript_1/1_Conf_1.000	1367	20	5.39E-169	NP_001022138.1	82	598.586	451	374	hypothetical protein F33G12.6
Locus_28630_Transcript_1/1_Conf_1.000	134	8	1.63E-04	XP_146277.8	66	49.2914	39	26	PREDICTED: hypothetical protein
Locus_28631_Transcript_1/1_Conf_1.000	279	0							
Locus_28632_Transcript_1/1_Conf_1.000	194	20	8.47E-25	BAD96354.1	98	116.701	56	55	HSPC163 protein variant
Locus_28633_Transcript_1/1_Conf_1.000	138	20	8.55E-14	2KN6	100	80.1073	37	37	Structure Of Full-Length Human Asc (Apoptosis-Associated Speck-Like Protein Containing A Card)
Locus_28634_Transcript_1/1_Conf_1.000	208	0							
Locus_28635_Transcript_1/1_Conf_1.000	152	20	9.74E-21	XP_002810367.1	100	103.219	50	50	PREDICTED: e3 SUMO-protein ligase PIAS3-like isoform 2
Locus_28636_Transcript_1/1_Conf_1.000	149	11	1.51E-05	EFP07704.1	72	52.7582	44	32	CRE-NHR-22 protein

Locus_28637_Transcript_1/1_Conf_1.000	207	20	4.14E-16	ZP_06274641.1	76	87.8113	68	52	Aldehyde Dehydrogenase
Locus_28638_Transcript_1/1_Conf_1.000	155	0							
Locus_28639_Transcript_1/1_Conf_1.000	139	0							
Locus_2864_Transcript_1/1_Conf_1.000	465	0							
Locus_28640_Transcript_1/1_Conf_1.000	479	20	1.91E-29	XP_001898731.1	61	132.109	167	102	Tyrosyl-DNA phosphodiesterase family protein
Locus_28641_Transcript_1/1_Conf_1.000	140	0							
Locus_28642_Transcript_1/1_Conf_1.000	151	0							
Locus_28643_Transcript_1/1_Conf_1.000	133	0							
Locus_28644_Transcript_1/1_Conf_1.000	142	20	1.78E-19	XP_002824720.1	100	98.9821	46	46	PREDICTED: NF-kappa-B inhibitor alpha-like

Locus_28645_Transcript_1/1_Conf_1.000	251	19	1.72E-06	EFO21404.1	60	55.8398	90	54	hypothetical protein LOAG_07083
Locus_28646_Transcript_1/1_Conf_1.000	187	5	2.49E-16	NP_504243.2	81	88.5817	61	50	hypothetical protein Y61A9LA.1
Locus_28647_Transcript_1/1_Conf_1.000	253	20	2.56E-37	EFO86864.1	98	158.303	84	83	CRE-PST-2 protein
Locus_28648_Transcript_1/1_Conf_1.000	160	0							
Locus_28649_Transcript_1/1_Conf_1.000	180	3	1.12E-05	XP_002632187.1	83	53.1434	36	30	Hypothetical protein CBG07050
Locus_2865_Transcript_1/1_Conf_1.000	1353	20	9.65E-70	NP_504235.2	54	268.855	476	261	Drosophila SOS homolog family member (sos-1)
Locus_28650_Transcript_1/1_Conf_1.000	235	20	2.99E-14	AAC05749.1	91	81.6481	78	71	putative peroxisome microbody protein 175.1
Locus_28651_Transcript_1/1_Conf_1.000	237	3	9.93E-10	XP_002639815.1	79	66.6254	68	54	Hypothetical protein CBG21340
Locus_28652_Transcript_1/1_Conf_1.000	140	0							
Locus_28653_Transcript_1/1_Conf_1.000	128	0							

Locus_28654_Transcript_1/1_Conf_1.000	167	20	2.53E-05	EDL08051.1	55	51.9878	54	30	mCG113993
Locus_28655_Transcript_1/1_Conf_1.000	199	20	3.90E-14	XP_002634566.1	75	81.2629	66	50	Hypothetical protein CBG08372
Locus_28656_Transcript_1/1_Conf_1.000	162	0							
Locus_28657_Transcript_1/1_Conf_1.000	145	0							
Locus_28658_Transcript_1/1_Conf_1.000	144	0							
Locus_28659_Transcript_1/1_Conf_1.000	153	0							
Locus_2866_Transcript_1/1_Conf_1.000	645	3	1.07E-34	XP_002633659.1	79	150.599	129	102	Hypothetical protein CBG03332
Locus_28660_Transcript_1/1_Conf_1.000	184	0							
Locus_28661_Transcript_1/1_Conf_1.000	189	0							
Locus_28662_Transcript_1/1_Conf_1.000	128	20	7.37E-05	XP_783686.2	72	50.447	36	26	PREDICTED: similar to BTB (POZ) domain containing 9
Locus_28663_Transcript_1/1_Conf_1.000	179	7	7.99E-20	XP_002638768.1	90	100.138	54	49	Hypothetical protein CBG05111
Locus_28664_Transcript_1/1_Conf_1.000	141	0							
Locus_28665_Transcript_1/1_Conf_1.000	165	0							
Locus_28666_Transcript_1/1_Conf_1.000	133	0							
Locus_28667_Transcript_1/1_Conf_1.000	186	20	1.84E-11	XP_002644034.1	77	72.4034	58	45	C. briggsae CBR-SULP-7 protein
Locus_28668_Transcript_1/1_Conf_1.000	158	0							
Locus_28669_Transcript_1/1_Conf_1.000	189	0							
Locus_2867_Transcript_1/1_Conf_1.000	570	0							
Locus_28670_Transcript_1/1_Conf_1.000	232	0							
Locus_28671_Transcript_1/1_Conf_1.000	267	0							
Locus_28672_Transcript_1/1_Conf_1.000	140	0							
Locus_28673_Transcript_1/1_Conf_1.000	129	0							
Locus_28674_Transcript_1/1_Conf_1.000	174	0							
Locus_28675_Transcript_1/1_Conf_1.000	191	0							
Locus_28676_Transcript_1/1_Conf_1.000	134	0							
Locus_28677_Transcript_1/1_Conf_1.000	150	0							
Locus_28678_Transcript_1/1_Conf_1.000	145	0							

Locus_28679_Transcript_1/1_Conf_1.000	195	0							
Locus_2868_Transcript_1/1_Conf_1.000	918	20	1.81E-25	ABD85013.1	47	120.939	255	121	OGA-1d
Locus_28680_Transcript_1/1_Conf_1.000	131	0							
Locus_28681_Transcript_1/1_Conf_1.000	202	0							
Locus_28682_Transcript_1/1_Conf_1.000	167	20	1.21E-23	EFP07527.1	100	112.849	55	55	CRE-SNT-1 protein
Locus_28683_Transcript_1/1_Conf_1.000	139	20	1.12E-13	AAL14108.1	88	79.7221	45	40	GOP-1
Locus_28684_Transcript_1/1_Conf_1.000	231	2	4.18E-16	EFO22577.1	73	87.8113	76	56	hypothetical protein LOAG_05911
Locus_28685_Transcript_1/1_Conf_1.000	138	1	2.49E-05	XP_001137788.1	100	51.9878	46	46	PREDICTED: similar to put. HMG-17 protein
Locus_28686_Transcript_1/1_Conf_1.000	159	0							
Locus_28687_Transcript_1/1_Conf_1.000	147	0							
Locus_28688_Transcript_1/1_Conf_1.000	169	17	2.97E-06	XP_002629645.1	68	55.0694	54	37	Hypothetical protein CBG00850
Locus_28689_Transcript_1/1_Conf_1.000	144	20	1.24E-07	XP_002644714.1	80	59.6918	47	38	C. briggsae CBR-SULP-2 protein

Locus_2869_Transcript_1/1_Conf_1.000	396	20	1.74E-70	AAA51433.1	99	268.47	131	130	guanine nucleotide regulatory protein
Locus_28690_Transcript_1/1_Conf_1.000	159	20	1.18E-18	XP_002633760.1	85	96.2857	49	42	C. briggsae CBR-GON-1 protein
Locus_28691_Transcript_1/1_Conf_1.000	248	20	2.49E-21	NP_491610.1	85	105.145	78	67	hypothetical protein C09D4.3
Locus_28692_Transcript_1/1_Conf_1.000	142	0							
Locus_28693_Transcript_1/1_Conf_1.000	180	1	8.02E-04	XP_002639005.1	53	46.9802	66	35	Hypothetical protein CBG22251
Locus_28694_Transcript_1/1_Conf_1.000	156	0							
Locus_28695_Transcript_1/1_Conf_1.000	148	10	3.24E-16	XP_002631213.1	97	88.1965	48	47	Hypothetical protein CBG03010
Locus_28696_Transcript_1/1_Conf_1.000	139	0							

Locus_28697_Transcript_1/1_Conf_1.000	157	20	1.70E-25	P02751.4	100	119.013	51	51	Fibronectin
Locus_28698_Transcript_1/1_Conf_1.000	153	0							
Locus_28699_Transcript_1/1_Conf_1.000	190	0							
Locus_287_Transcript_1/1_Conf_1.000	562	20	5.62E-75	XP_002639641.1	87	283.878	185	161	C. briggsae CBR-PRP-4 protein
Locus_2870_Transcript_1/1_Conf_1.000	466	3	7.65E-10	XP_002347210.1	86	67.0106	60	52	PREDICTED: similar to hCG2040253
Locus_28700_Transcript_1/1_Conf_1.000	318	0							
Locus_28701_Transcript_1/1_Conf_1.000	233	0							
Locus_28702_Transcript_1/1_Conf_1.000	168	8	7.85E-07	EFP05191.1	69	56.9954	49	34	CRE-CPNA-2 protein
Locus_28703_Transcript_1/1_Conf_1.000	168	20	2.27E-14	NP_496465.1	86	82.0333	50	43	hypothetical protein F54D5.12
Locus_28704_Transcript_1/1_Conf_1.000	138	0							
Locus_28705_Transcript_1/1_Conf_1.000	145	12	2.34E-14	EFP10814.1	93	82.0333	48	45	hypothetical protein CRE_06204
Locus_28706_Transcript_1/1_Conf_1.000	174	5	1.24E-20	EFP13291.1	94	102.834	56	53	hypothetical protein CRE_12211
Locus_28707_Transcript_1/1_Conf_1.000	153	0							
Locus_28708_Transcript_1/1_Conf_1.000	128	0							
Locus_28709_Transcript_1/1_Conf_1.000	153	20	1.23E-07	XP_002408840.1	73	59.6918	49	36	snf2 histone linker PHD ring helicase, putative
Locus_2871_Transcript_1/3_Conf_0.333	234	15	5.81E-18	NP_491221.1	92	93.9745	69	64	PaTched Related family member (ptr-2)

Locus_2871_Transcript_2/3_Conf_0.500	1845	20	0	NP_491221.1	82	796.579	608	503	PaTched Related family member (ptr-2)
Locus_2871_Transcript_3/3_Conf_0.667	2664	20	0	XP_002646298.1	83	1181.01	868	722	Hypothetical protein CBG12004
Locus_28710_Transcript_1/1_Conf_1.000	208	0							
Locus_28711_Transcript_1/1_Conf_1.000	215	5	5.19E-11	CAV31765.1	74	70.8626	62	46	C. elegans protein C33B4.3c, partially confirmed by transcript evidence
Locus_28712_Transcript_1/1_Conf_1.000	145	0							
Locus_28713_Transcript_1/1_Conf_1.000	133	0							
Locus_28714_Transcript_1/1_Conf_1.000	154	0							
Locus_28715_Transcript_1/1_Conf_1.000	189	0							
Locus_28716_Transcript_1/1_Conf_1.000	214	0							
Locus_28717_Transcript_1/1_Conf_1.000	162	4	7.15E-08	EFP09199.1	79	60.4622	43	34	CRE-CED-11 protein
Locus_28718_Transcript_1/1_Conf_1.000	273	20	4.10E-40	NP_497665.2	94	167.548	91	86	hypothetical protein R148.5
Locus_28719_Transcript_1/1_Conf_1.000	164	0							
Locus_2872_Transcript_1/2_Conf_1.000	943	0							
Locus_2872_Transcript_2/2_Conf_1.000	766	8	2.14E-20	NP_492047.1	55	103.605	106	59	Chondroitin ProteoGlycan family member (cpg-3)
Locus_28720_Transcript_1/1_Conf_1.000	169	0							
Locus_28721_Transcript_1/1_Conf_1.000	158	3	3.01E-06	EFO24692.1	67	55.0694	52	35	protein-tyrosine phosphatase
Locus_28722_Transcript_1/1_Conf_1.000	129	0							
Locus_28723_Transcript_1/1_Conf_1.000	174	2	2.78E-04	NP_001024371.2	58	48.521	56	33	hypothetical protein C07B5.4
Locus_28724_Transcript_1/1_Conf_1.000	148	6	9.79E-13	EFO23711.1	76	76.6406	47	36	hypothetical protein LOAG_04772
Locus_28725_Transcript_1/1_Conf_1.000	266	20	1.95E-13	XP_001897825.1	73	78.9518	75	55	Major Facilitator Superfamily protein

Locus_28726_Transcript_1/1_Conf_1.000	296	20	4.93E-33	EFP10194.1	95	144.05	72	69	CRE-PPK-3 protein
Locus_28727_Transcript_1/1_Conf_1.000	137	2	9.22E-08	EFO88960.1	77	60.077	45	35	hypothetical protein CRE_06660
Locus_28728_Transcript_1/1_Conf_1.000	144	1	8.31E-04	EFO13394.1	93	46.9802	44	41	hypothetical protein LOAG_15135
Locus_28729_Transcript_1/1_Conf_1.000	304	0							
Locus_2873_Transcript_1/1_Conf_1.000	1249	20	2.10E-116	EFO24882.1	69	423.705	409	284	hypothetical protein LOAG_03599
Locus_28730_Transcript_1/1_Conf_1.000	158	0							
Locus_28731_Transcript_1/1_Conf_1.000	140	0							
Locus_28732_Transcript_1/1_Conf_1.000	152	20	7.46E-21	XP_002832350.1	100	103.605	50	50	PREDICTED: LOW QUALITY PROTEIN: filamin-A-like
Locus_28733_Transcript_1/1_Conf_1.000	232	0							
Locus_28734_Transcript_1/1_Conf_1.000	234	20	2.36E-35	NP_505641.2	98	151.754	77	76	Resistance to Inhibitors of Cholinesterase family member (ric-4)

Locus_28735_Transcript_1/1_Conf_1.000	207	20	5.04E-22	NP_001040658.2	86	107.457	68	59	High Incidence of Males (increased X chromosome loss) family member (him-1)
Locus_28736_Transcript_1/1_Conf_1.000	135	0							
Locus_28737_Transcript_1/1_Conf_1.000	178	10	2.18E-17	EFP01431.1	86	92.0485	58	50	CRE-UNC-89 protein
Locus_28738_Transcript_1/1_Conf_1.000	139	0							
Locus_28739_Transcript_1/1_Conf_1.000	332	20	3.28E-21	ACI49074.1	72	104.76	93	67	hypothetical protein Cbre_JD10.006
Locus_2874_Transcript_1/1_Conf_1.000	3102	20	1.79E-49	EFO22988.1	58	202.986	322	189	hypothetical protein LOAG_05497
Locus_28740_Transcript_1/1_Conf_1.000	349	3	2.31E-06	XP_002646097.1	50	55.4546	118	59	C. briggsae CBR-AMX-2 protein
Locus_28741_Transcript_1/1_Conf_1.000	161	0							
Locus_28742_Transcript_1/1_Conf_1.000	135	0							
Locus_28743_Transcript_1/1_Conf_1.000	175	4	1.09E-16	NP_508451.2	89	89.7373	49	44	hypothetical protein K02E10.6
Locus_28744_Transcript_1/1_Conf_1.000	191	0							
Locus_28745_Transcript_1/1_Conf_1.000	348	0							
Locus_28746_Transcript_1/1_Conf_1.000	200	0							
Locus_28747_Transcript_1/1_Conf_1.000	179	4	2.67E-15	NP_501709.2	77	85.1149	59	46	Membrane Calcium ATPase family member (mca-1)
Locus_28748_Transcript_1/1_Conf_1.000	385	0							
Locus_28749_Transcript_1/1_Conf_1.000	161	5	1.30E-17	EFP06805.1	90	92.8189	53	48	hypothetical protein CRE_11195
Locus_2875_Transcript_1/1_Conf_1.000	300	0							
Locus_28750_Transcript_1/1_Conf_1.000	141	0							
Locus_28751_Transcript_1/1_Conf_1.000	137	0							
Locus_28752_Transcript_1/1_Conf_1.000	269	20	5.25E-19	NP_493135.2	67	97.4413	89	60	GLYcosylation related family member (gly-16)
Locus_28753_Transcript_1/1_Conf_1.000	139	0							
Locus_28754_Transcript_1/1_Conf_1.000	174	0							
Locus_28755_Transcript_1/1_Conf_1.000	137	3	7.04E-08	XP_002646095.1	77	60.4622	44	34	C. briggsae CBR-HMR-1 protein
Locus_28756_Transcript_1/1_Conf_1.000	207	0							

Locus_28757_Transcript_1/1_Conf_1.000	231	20	9.34E-16	EFO96466.1	73	86.6557	80	59	hypothetical protein CRE_13856
Locus_28758_Transcript_1/1_Conf_1.000	141	0							
Locus_28759_Transcript_1/1_Conf_1.000	136	0							
Locus_2876_Transcript_1/1_Conf_1.000	909	20	5.71E-24	XP_002641337.1	51	115.931	245	127	C. briggsae CBR-CKU-70 protein
Locus_28760_Transcript_1/1_Conf_1.000	187	20	1.15E-29	XP_002759346.1	100	132.88	62	62	PREDICTED: eukaryotic translation initiation factor 3 subunit E
Locus_28761_Transcript_1/1_Conf_1.000	136	20	4.28E-05	EFO27420.1	69	51.2174	42	29	TK/FER protein kinase
Locus_28762_Transcript_1/1_Conf_1.000	181	0							
Locus_28763_Transcript_1/1_Conf_1.000	135	0							
Locus_28764_Transcript_1/1_Conf_1.000	395	3	1.27E-12	NP_001041053.1	65	76.2554	79	52	hypothetical protein Y62E10A.20
Locus_28765_Transcript_1/1_Conf_1.000	128	0							
Locus_28766_Transcript_1/1_Conf_1.000	132	20	1.52E-18	1LYA	100	95.9005	44	44	CrystalStructures Of Native And Inhibited Forms Of Human Cathepsin D: Implications For Lysosomal Targeting And Drug Design
Locus_28767_Transcript_1/1_Conf_1.000	178	0							
Locus_28768_Transcript_1/1_Conf_1.000	218	0							
Locus_28769_Transcript_1/1_Conf_1.000	182	0							

Locus_2877_Transcript_1/1_Conf_1.000	1549	20	0	NP_495011.1	85	783.097	518	441	Protein Kinase C family member (pkc-3)
Locus_28770_Transcript_1/1_Conf_1.000	151	0							
Locus_28771_Transcript_1/1_Conf_1.000	159	3	1.59E-15	XP_002632481.1	88	85.8853	53	47	Hypothetical protein CBG13716
Locus_28772_Transcript_1/1_Conf_1.000	174	3	3.50E-07	XP_002633353.1	72	58.151	55	40	Hypothetical protein CBG06097
Locus_28773_Transcript_1/1_Conf_1.000	146	14	3.16E-11	EFO89614.1	80	71.633	46	37	CRE-NAS-10 protein
Locus_28774_Transcript_1/1_Conf_1.000	190	0							
Locus_28775_Transcript_1/1_Conf_1.000	175	0							
Locus_28776_Transcript_1/1_Conf_1.000	130	0							
Locus_28777_Transcript_1/1_Conf_1.000	161	0							
Locus_28778_Transcript_1/1_Conf_1.000	131	0							
Locus_28779_Transcript_1/1_Conf_1.000	245	0							
Locus_2878_Transcript_1/1_Conf_1.000	438	0							
Locus_28780_Transcript_1/1_Conf_1.000	129	0							
Locus_28781_Transcript_1/1_Conf_1.000	186	0							
Locus_28782_Transcript_1/1_Conf_1.000	178	0							
Locus_28783_Transcript_1/1_Conf_1.000	154	0							
Locus_28784_Transcript_1/1_Conf_1.000	154	0							

Locus_28785_Transcript_1/1_Conf_1.000	296	20	4.62E-15	XP_002815150.1	100	84.3445	40	40	PREDICTED: annexin A5-like
Locus_28786_Transcript_1/1_Conf_1.000	159	0							
Locus_28787_Transcript_1/1_Conf_1.000	135	0							
Locus_28788_Transcript_1/1_Conf_1.000	162	0							
Locus_28789_Transcript_1/1_Conf_1.000	183	0							
Locus_2879_Transcript_1/1_Conf_1.000	549	0							
Locus_28790_Transcript_1/1_Conf_1.000	145	0							
Locus_28791_Transcript_1/1_Conf_1.000	365	0							
Locus_28792_Transcript_1/1_Conf_1.000	255	4	3.82E-09	XP_002639125.1	66	64.6994	72	48	C. briggsae CBR-FER-1 protein
Locus_28793_Transcript_1/1_Conf_1.000	158	0							
Locus_28794_Transcript_1/1_Conf_1.000	189	20	4.50E-18	NP_001134686.1	79	94.3597	63	50	3-oxo-5-alpha-steroid 4-dehydrogenase 2
Locus_28795_Transcript_1/1_Conf_1.000	175	20	2.59E-10	XP_002806309.1	100	68.5514	35	35	PREDICTED: moesin isoform 3
Locus_28796_Transcript_1/1_Conf_1.000	251	0							
Locus_28797_Transcript_1/1_Conf_1.000	138	20	1.20E-07	XP_002441471.1	94	59.6918	36	34	hypothetical protein SORBIDRAFT_09g027400

Locus_28798_Transcript_1/1_Conf_1.000	174	3	6.18E-04	XP_001511870.1	68	47.3654	47	32	PREDICTED: similar to TMPRSS11A protein
Locus_28799_Transcript_1/1_Conf_1.000	136	0							
Locus_288_Transcript_1/1_Conf_1.000	991	20	2.84E-43	EFO18804.1	58	180.259	253	147	hypothetical protein LOAG_09689
Locus_2880_Transcript_1/1_Conf_1.000	382	20	2.32E-67	AAU87984.1	100	258.07	127	127	MHC class II antigen
Locus_28800_Transcript_1/1_Conf_1.000	154	0							
Locus_28801_Transcript_1/1_Conf_1.000	206	0							
Locus_28802_Transcript_1/1_Conf_1.000	129	20	2.20E-17	XP_002916749.1	100	92.0485	43	43	PREDICTED: LOW QUALITY PROTEIN: protein fat-free homolog
Locus_28803_Transcript_1/1_Conf_1.000	258	0							
Locus_28804_Transcript_1/1_Conf_1.000	212	0							
Locus_28805_Transcript_1/1_Conf_1.000	130	0							
Locus_28806_Transcript_1/1_Conf_1.000	267	0							
Locus_28807_Transcript_1/1_Conf_1.000	209	0							
Locus_28808_Transcript_1/1_Conf_1.000	140	0							
Locus_28809_Transcript_1/1_Conf_1.000	298	20	7.55E-34	NP_500274.2	84	146.747	93	79	hypothetical protein Y54G2A.4
Locus_2881_Transcript_1/1_Conf_1.000	729	20	1.37E-106	NP_500005.1	91	389.808	225	205	MAP kinase Activated protein Kinase family member (mak-2)
Locus_28810_Transcript_1/1_Conf_1.000	137	15	1.24E-12	NP_004853.2	100	76.2554	45	45	lipopolysaccharide-induced tumor necrosis factor-alpha factor isoform 1
Locus_28811_Transcript_1/1_Conf_1.000	169	0							
Locus_28812_Transcript_1/1_Conf_1.000	172	0							
Locus_28813_Transcript_1/1_Conf_1.000	151	0							
Locus_28814_Transcript_1/1_Conf_1.000	139	3	2.49E-13	NP_001021694.1	90	78.5666	43	39	EATing: abnormal pharyngeal pumping family member (eat-18)
Locus_28815_Transcript_1/1_Conf_1.000	128	0							
Locus_28816_Transcript_1/1_Conf_1.000	159	20	7.89E-15	ACF07996.1	100	83.5741	40	40	splicing regulator SRrp37-2

Locus_28817_Transcript_1/1_Conf_1.000	146	0							
Locus_28818_Transcript_1/1_Conf_1.000	181	20	1.56E-15	XP_002637502.1	80	85.8853	51	41	Hypothetical protein CBG19223
Locus_28819_Transcript_1/1_Conf_1.000	137	0							
Locus_2882_Transcript_1/1_Conf_1.000	1158	20	1.20E-38	XP_001893474.1	50	165.236	398	199	Rap/ran-GAP family protein
Locus_28820_Transcript_1/1_Conf_1.000	151	0							
Locus_28821_Transcript_1/1_Conf_1.000	178	0							
Locus_28822_Transcript_1/1_Conf_1.000	151	0							
Locus_28823_Transcript_1/1_Conf_1.000	207	0							
Locus_28824_Transcript_1/1_Conf_1.000	221	7	2.25E-17	EFO99378.1	84	92.0485	73	62	hypothetical protein CRE_18274
Locus_28825_Transcript_1/1_Conf_1.000	142	0							
Locus_28826_Transcript_1/1_Conf_1.000	154	0							
Locus_28827_Transcript_1/1_Conf_1.000	169	0							
Locus_28828_Transcript_1/1_Conf_1.000	167	0							
Locus_28829_Transcript_1/1_Conf_1.000	139	0							
Locus_2883_Transcript_1/1_Conf_1.000	2420	20	3.36E-133	XP_001902902.1	62	480.715	653	405	Src substrate cortactin
Locus_28830_Transcript_1/1_Conf_1.000	200	20	1.30E-09	XP_969753.1	65	66.2402	66	43	PREDICTED: similar to xylulokinase homolog
Locus_28831_Transcript_1/1_Conf_1.000	139	0							
Locus_28832_Transcript_1/1_Conf_1.000	128	0							
Locus_28833_Transcript_1/1_Conf_1.000	181	0							
Locus_28834_Transcript_1/1_Conf_1.000	149	20	3.95E-22	XP_002749824.1	100	107.842	49	49	PREDICTED: angio-associated migratory cell protein-like
Locus_28835_Transcript_1/1_Conf_1.000	776	20	1.35E-78	NP_494394.1	70	296.975	258	182	SQuashed Vulva family member (sqv-2)

Locus_28836_Transcript_1/1_Conf_1.000	135	9	9.52E-13	AAH73141.1	100	76.6406	45	45	YWHAZ protein
Locus_28837_Transcript_1/1_Conf_1.000	154	0							
Locus_28838_Transcript_1/1_Conf_1.000	141	0							
Locus_28839_Transcript_1/1_Conf_1.000	135	0							
Locus_2884_Transcript_1/1_Conf_1.000	381	2	7.34E-05	NP_505735.1	53	50.447	97	52	hypothetical protein T28B11.1
Locus_28840_Transcript_1/1_Conf_1.000	204	20	3.82E-18	XP_002644311.1	81	83.9593	53	43	C. briggsae CBR-AQP-7 protein
Locus_28841_Transcript_1/1_Conf_1.000	133	4	6.17E-20	AAF67640.1	100	100.523	43	43	AF220047_1uncharacterized hematopoietic stem/progenitor cells protein MDS027
Locus_28842_Transcript_1/1_Conf_1.000	214	20	6.11E-36	XP_002753109.1	100	153.68	71	71	PREDICTED: phosphatidylethanolamine-binding protein 1-like

Locus_28843_Transcript_1/1_Conf_1.000	239	20	6.84E-19	XP_001902900.1	86	97.0561	61	53	Zinc finger, C2H2 type family protein
Locus_28844_Transcript_1/1_Conf_1.000	245	2	9.55E-05	EFO92535.1	61	50.0618	80	49	CRE-KLF-1 protein
Locus_28845_Transcript_1/1_Conf_1.000	140	0							
Locus_28846_Transcript_1/1_Conf_1.000	128	0							
Locus_28847_Transcript_1/1_Conf_1.000	143	0							
Locus_28848_Transcript_1/1_Conf_1.000	156	0							
Locus_28849_Transcript_1/1_Conf_1.000	174	0							
Locus_2885_Transcript_1/1_Conf_1.000	1284	20	1.55E-05	XP_002407762.1	62	55.4546	51	32	hypothetical protein IscW_ISCW000169
Locus_28850_Transcript_1/1_Conf_1.000	140	2	8.03E-12	EFO28433.1	88	73.559	45	40	hypothetical protein LOAG_00029
Locus_28851_Transcript_1/1_Conf_1.000	148	0							
Locus_28852_Transcript_1/1_Conf_1.000	147	0							
Locus_28853_Transcript_1/1_Conf_1.000	151	0							
Locus_28854_Transcript_1/1_Conf_1.000	156	0							
Locus_28855_Transcript_1/1_Conf_1.000	196	0							

Locus_28856_Transcript_1/1_Conf_1.000	227	20	5.86E-34	EFO82668.1	94	147.132	75	71	CRE-CCA-1 protein
Locus_28857_Transcript_1/1_Conf_1.000	154	3	1.50E-05	XP_002641380.1	82	52.7582	40	33	Hypothetical protein CBG13237
Locus_28858_Transcript_1/1_Conf_1.000	196	0							
Locus_28859_Transcript_1/1_Conf_1.000	137	10	2.05E-15	XP_002633437.1	91	85.5001	45	41	C. briggsae CBR-UNC-22 protein
Locus_2886_Transcript_1/2_Conf_1.000	1223	20	1.13E-58	XP_001897804.1	59	231.876	302	180	LEM domain containing protein
Locus_2886_Transcript_2/2_Conf_1.000	780	20	1.82E-38	XP_002631646.1	64	163.696	181	116	C. briggsae CBR-LEM-2 protein
Locus_28860_Transcript_1/1_Conf_1.000	134	0							
Locus_28861_Transcript_1/1_Conf_1.000	128	20	1.43E-16	XP_001897649.1	100	89.3521	39	39	Probable G protein-coupled receptor kinase F19C6.1
Locus_28862_Transcript_1/1_Conf_1.000	211	0							
Locus_28863_Transcript_1/1_Conf_1.000	162	0							
Locus_28864_Transcript_1/1_Conf_1.000	162	0							
Locus_28865_Transcript_1/1_Conf_1.000	145	6	2.42E-11	EFO97329.1	86	72.0182	46	40	hypothetical protein CRE_16676
Locus_28866_Transcript_1/1_Conf_1.000	129	0							
Locus_28867_Transcript_1/1_Conf_1.000	145	10	3.38E-13	CAX65068.1	85	78.1814	48	41	C. elegans protein K08C7.3d, confirmed by transcript evidence
Locus_28868_Transcript_1/1_Conf_1.000	158	0							
Locus_28869_Transcript_1/1_Conf_1.000	128	0							
Locus_2887_Transcript_1/1_Conf_1.000	1547	20	3.04E-46	AAF59653.4	45	191.045	529	239	Hypothetical protein Y50D7A.1
Locus_28870_Transcript_1/1_Conf_1.000	165	0							
Locus_28871_Transcript_1/1_Conf_1.000	133	5	9.25E-08	NP_495875.2	75	60.077	44	33	hypothetical protein F07H5.9
Locus_28872_Transcript_1/1_Conf_1.000	238	6	2.98E-22	NP_001021650.1	81	108.227	79	64	HaMmeRhead embryonic lethal family member (hmr-1)
Locus_28873_Transcript_1/1_Conf_1.000	164	0							
Locus_28874_Transcript_1/1_Conf_1.000	135	0							
Locus_28875_Transcript_1/1_Conf_1.000	316	20	4.52E-18	XP_001122229.1	67	94.3597	96	65	PREDICTED: similar to Autophagy-specific gene 2 CG1241-PA

Locus_28876_Transcript_1/1_Conf_1.000	129	0							
Locus_28877_Transcript_1/1_Conf_1.000	217	4	1.97E-18	NP_001021339.1	76	95.5153	71	54	defective SPErmatogenesis family member (spe-10)
Locus_28878_Transcript_1/1_Conf_1.000	197	20	2.29E-30	BAG62970.1	100	135.191	65	65	unnamed protein product
Locus_28879_Transcript_1/1_Conf_1.000	139	20	1.79E-19	XP_002826207.1	100	98.9821	45	45	PREDICTED: nodal modulator 1
Locus_2888_Transcript_1/1_Conf_1.000	464	3	1.00E-09	XP_001845923.1	58	66.6254	74	43	conserved hypothetical protein
Locus_28880_Transcript_1/1_Conf_1.000	168	0							
Locus_28881_Transcript_1/1_Conf_1.000	262	3	1.07E-11	CAB00874.2	63	73.1738	84	53	C. elegans protein R09H10.5, partially confirmed by transcript evidence
Locus_28882_Transcript_1/1_Conf_1.000	189	0							
Locus_28883_Transcript_1/1_Conf_1.000	128	20	2.20E-17	ADN42857.1	100	92.0485	42	42	CD5L-OKT3scFv-CD14 protein
Locus_28884_Transcript_1/1_Conf_1.000	211	0							
Locus_28885_Transcript_1/1_Conf_1.000	143	0							
Locus_28886_Transcript_1/1_Conf_1.000	263	20	3.78E-25	NP_001122835.1	83	117.857	87	73	UNCoordinated family member (unc-22)
Locus_28887_Transcript_1/1_Conf_1.000	175	0							
Locus_28888_Transcript_1/1_Conf_1.000	195	20	4.63E-23	XP_001902120.1	86	110.923	65	56	NAD-dependent malic enzyme, mitochondrial precursor

Locus_28889_Transcript_1/1_Conf_1.000	151	0							
Locus_2889_Transcript_1/1_Conf_1.000	275	0							
Locus_28890_Transcript_1/1_Conf_1.000	130	0							
Locus_28891_Transcript_1/1_Conf_1.000	155	0							
Locus_28892_Transcript_1/1_Conf_1.000	143	0							
Locus_28893_Transcript_1/1_Conf_1.000	151	0							
Locus_28894_Transcript_1/1_Conf_1.000	133	13	7.06E-08	CAM84574.1	83	60.4622	43	36	intestinal prolyl carboxypeptidase 2
Locus_28895_Transcript_1/1_Conf_1.000	139	0							
Locus_28896_Transcript_1/1_Conf_1.000	143	4	5.94E-07	XP_002643980.1	84	57.3806	45	38	C. briggsae CBR-OCT-2 protein
Locus_28897_Transcript_1/1_Conf_1.000	172	0							
Locus_28898_Transcript_1/1_Conf_1.000	189	0							
Locus_28899_Transcript_1/1_Conf_1.000	158	0							
Locus_289_Transcript_1/1_Conf_1.000	607	0							
Locus_2890_Transcript_1/4_Conf_0.375	777	20	6.48E-113	NP_508412.1	91	410.994	257	234	Vacuolar H ATPase family member (vha-15)
Locus_2890_Transcript_2/4_Conf_0.625	1113	20	1.29E-167	NP_508412.1	91	593.578	370	339	Vacuolar H ATPase family member (vha-15)

Locus_2890_Transcript_3/4_Conf_0.625	1113	20	1.29E-167	NP_508412.1	91	593.578	370	339	Vacuolar H ATPase family member (vha-15)
Locus_2890_Transcript_4/4_Conf_0.625	1113	20	1.29E-167	NP_508412.1	91	593.578	370	339	Vacuolar H ATPase family member (vha-15)
Locus_28900_Transcript_1/1_Conf_1.000	296	20	2.45E-24	NP_510445.1	80	115.161	98	79	TetraSPanin family member (tsp-8)
Locus_28901_Transcript_1/1_Conf_1.000	531	4	8.51E-11	EFP00646.1	57	70.4774	118	68	hypothetical protein CRE_21280
Locus_28902_Transcript_1/1_Conf_1.000	137	0							
Locus_28903_Transcript_1/1_Conf_1.000	178	7	3.85E-14	NP_505448.1	80	81.2629	60	48	GelSoliN-Like family member (gsnl-1)
Locus_28904_Transcript_1/1_Conf_1.000	207	0							
Locus_28905_Transcript_1/1_Conf_1.000	128	0							
Locus_28906_Transcript_1/1_Conf_1.000	132	1	2.52E-05	EAW64647.1	82	51.9878	35	29	hCG2042149
Locus_28907_Transcript_1/1_Conf_1.000	193	8	1.27E-12	XP_002640991.1	69	76.2554	63	44	Hypothetical protein CBG11740
Locus_28908_Transcript_1/1_Conf_1.000	230	0							
Locus_28909_Transcript_1/1_Conf_1.000	149	0							
Locus_2891_Transcript_1/1_Conf_1.000	392	20	4.38E-18	XP_002635517.1	69	94.3597	91	63	Hypothetical protein CBG08821
Locus_28910_Transcript_1/1_Conf_1.000	197	6	3.81E-09	XP_001892850.1	73	64.6994	61	45	Zinc finger, ZZ type family protein

Locus_28911_Transcript_1/1_Conf_1.000	280	6	2.26E-06	NP_505688.1	75	55.4546	45	34	Cdc-42 Related Protein family member (crp-1)
Locus_28912_Transcript_1/1_Conf_1.000	163	0							
Locus_28913_Transcript_1/1_Conf_1.000	482	0							
Locus_28914_Transcript_1/1_Conf_1.000	186	3	3.60E-07	NP_509571.1	73	58.151	52	38	hypothetical protein T20B5.2
Locus_28915_Transcript_1/1_Conf_1.000	148	0							
Locus_28916_Transcript_1/1_Conf_1.000	139	0							
Locus_28917_Transcript_1/1_Conf_1.000	148	20	6.33E-20	XP_002922750.1	100	100.523	48	48	PREDICTED: FACT complex subunit SSRP1-like
Locus_28918_Transcript_1/1_Conf_1.000	171	0							
Locus_28919_Transcript_1/1_Conf_1.000	198	0							
Locus_2892_Transcript_1/1_Conf_1.000	873	20	1.75E-83	NP_502775.2	85	313.538	198	169	hypothetical protein Y57G11C.31
Locus_28920_Transcript_1/1_Conf_1.000	149	0							
Locus_28921_Transcript_1/1_Conf_1.000	147	0							
Locus_28922_Transcript_1/1_Conf_1.000	210	0							
Locus_28923_Transcript_1/1_Conf_1.000	151	20	7.72E-18	EFO98196.1	89	93.5893	49	44	CRE-OCR-3 protein
Locus_28924_Transcript_1/1_Conf_1.000	128	0							
Locus_28925_Transcript_1/1_Conf_1.000	133	0							
Locus_28926_Transcript_1/1_Conf_1.000	366	4	2.56E-18	XP_002634375.1	73	95.1301	79	58	C. briggsae CBR-UNC-24 protein
Locus_28927_Transcript_1/1_Conf_1.000	136	0							
Locus_28928_Transcript_1/1_Conf_1.000	158	0							
Locus_28929_Transcript_1/1_Conf_1.000	207	0							
Locus_2893_Transcript_1/1_Conf_1.000	2625	20	0	AAK31453.4	80	995.342	822	661	Hypothetical protein C25H3.8
Locus_28930_Transcript_1/1_Conf_1.000	186	0							
Locus_28931_Transcript_1/1_Conf_1.000	142	0							
Locus_28932_Transcript_1/1_Conf_1.000	223	0							
Locus_28933_Transcript_1/1_Conf_1.000	220	3	1.67E-04	XP_002603962.1	61	49.2914	57	35	hypothetical protein BRAFLDRAFT_71750
Locus_28934_Transcript_1/1_Conf_1.000	262	20	2.91E-17	XP_002647628.1	67	91.6633	86	58	Hypothetical protein CBG06721
Locus_28935_Transcript_1/1_Conf_1.000	177	0							
Locus_28936_Transcript_1/1_Conf_1.000	131	0							
Locus_28937_Transcript_1/1_Conf_1.000	146	5	1.98E-05	ACV31094.1	95	52.373	48	46	Glutamate receptor family (ampa) protein 4, isoform b
Locus_28938_Transcript_1/1_Conf_1.000	162	0							

Locus_28939_Transcript_1/1_Conf_1.000	249	0							
Locus_2894_Transcript_1/1_Conf_1.000	219	0							
Locus_28940_Transcript_1/1_Conf_1.000	165	2	1.93E-05	XP_002635372.1	66	52.373	54	36	C. briggsae CBR-RPM-1 protein
Locus_28941_Transcript_1/1_Conf_1.000	128	20	2.06E-15	XP_002912859.1	100	85.5001	41	41	PREDICTED: homer protein homolog 3-like
Locus_28942_Transcript_1/1_Conf_1.000	201	12	1.48E-13	XP_002647861.1	75	79.337	66	50	Hypothetical protein CBG23659
Locus_28943_Transcript_1/1_Conf_1.000	210	0							
Locus_28944_Transcript_1/1_Conf_1.000	171	20	7.06E-08	XP_002647283.1	92	60.4622	39	36	Hypothetical protein CBG06323
Locus_28945_Transcript_1/1_Conf_1.000	339	0							
Locus_28946_Transcript_1/1_Conf_1.000	397	14	3.57E-15	EFO27653.1	64	84.7297	104	67	hypothetical protein LOAG_00832
Locus_28947_Transcript_1/1_Conf_1.000	178	0							
Locus_28948_Transcript_1/1_Conf_1.000	135	0							
Locus_28949_Transcript_1/1_Conf_1.000	139	0							
Locus_2895_Transcript_1/1_Conf_1.000	537	20	9.76E-39	AAF08341.1	93	163.31	89	83	AF064240_1peptidyl-prolyl cis-trans isomerase
Locus_28950_Transcript_1/1_Conf_1.000	168	0							
Locus_28951_Transcript_1/1_Conf_1.000	134	0							
Locus_28952_Transcript_1/1_Conf_1.000	185	20	1.12E-24	NP_495675.1	95	116.316	61	58	hypothetical protein DH11.1
Locus_28953_Transcript_1/1_Conf_1.000	262	20	2.89E-33	CAZ65495.1	87	144.821	87	76	C. elegans protein F34D10.6a, partially confirmed by transcript evidence

Locus_28954_Transcript_1/1_Conf_1.000	184	20	1.32E-17	EFO91911.1	83	92.8189	61	51	hypothetical protein CRE_12268
Locus_28955_Transcript_1/1_Conf_1.000	155	0							
Locus_28956_Transcript_1/1_Conf_1.000	138	0							
Locus_28957_Transcript_1/1_Conf_1.000	231	3	4.49E-10	NP_492438.1	77	67.781	53	41	RADiation sensitivity abnormal/yeast RAD-related family member (rad-54)
Locus_28958_Transcript_1/1_Conf_1.000	347	7	3.57E-15	EFO92670.1	62	84.7297	115	72	hypothetical protein CRE_16359
Locus_28959_Transcript_1/1_Conf_1.000	174	0							
Locus_2896_Transcript_1/1_Conf_1.000	173	0							
Locus_28960_Transcript_1/1_Conf_1.000	144	20	2.26E-17	EFP05547.1	100	92.0485	47	47	CRE-UNC-68 protein
Locus_28961_Transcript_1/1_Conf_1.000	131	0							
Locus_28962_Transcript_1/1_Conf_1.000	135	16	1.80E-11	ADN00780.1	86	72.4034	44	38	class 3 lipase protein
Locus_28963_Transcript_1/1_Conf_1.000	130	0							
Locus_28964_Transcript_1/1_Conf_1.000	149	0							
Locus_28965_Transcript_1/1_Conf_1.000	166	0							
Locus_28966_Transcript_1/1_Conf_1.000	154	0							
Locus_28967_Transcript_1/1_Conf_1.000	141	0							
Locus_28968_Transcript_1/1_Conf_1.000	224	0							
Locus_28969_Transcript_1/1_Conf_1.000	179	0							
Locus_2897_Transcript_1/1_Conf_1.000	413	4	3.70E-33	CAR63680.1	75	144.436	113	85	hypothetical protein
Locus_28970_Transcript_1/1_Conf_1.000	194	20	4.34E-29	XP_002931630.1	100	130.954	64	64	PREDICTED: receptor-type tyrosine-protein phosphatase F-like
Locus_28971_Transcript_1/1_Conf_1.000	132	0							
Locus_28972_Transcript_1/1_Conf_1.000	142	0							
Locus_28973_Transcript_1/1_Conf_1.000	160	0							
Locus_28974_Transcript_1/1_Conf_1.000	143	12	2.41E-08	EFO93074.1	80	62.003	47	38	hypothetical protein CRE_10237

Locus_28975_Transcript_1/1_Conf_1.000	152	0							
Locus_28976_Transcript_1/1_Conf_1.000	215	0							
Locus_28977_Transcript_1/1_Conf_1.000	128	0							
Locus_28978_Transcript_1/1_Conf_1.000	135	0							
Locus_28979_Transcript_1/1_Conf_1.000	214	20	2.10E-28	NP_504415.2	97	128.642	70	68	Na/Ca eXchangers family member (ncx-2)
Locus_2898_Transcript_1/1_Conf_1.000	600	5	6.39E-49	NP_497742.2	71	197.593	184	132	hypothetical protein C46F11.5
Locus_28980_Transcript_1/1_Conf_1.000	164	0							
Locus_28981_Transcript_1/1_Conf_1.000	141	1	4.71E-04	XP_002639233.1	74	47.7506	43	32	Hypothetical protein CBG03789
Locus_28982_Transcript_1/1_Conf_1.000	134	0							
Locus_28983_Transcript_1/1_Conf_1.000	140	0							
Locus_28984_Transcript_1/1_Conf_1.000	134	0							
Locus_28985_Transcript_1/1_Conf_1.000	247	0							
Locus_28986_Transcript_1/1_Conf_1.000	138	0							
Locus_28987_Transcript_1/1_Conf_1.000	209	0							
Locus_28988_Transcript_1/1_Conf_1.000	134	20	6.39E-17	XP_002810085.1	100	90.5077	44	44	PREDICTED: lamin-A/C-like
Locus_28989_Transcript_1/1_Conf_1.000	144	20	2.58E-21	XP_002814804.1	100	105.145	47	47	PREDICTED: insulin-like growth factor-binding protein 7-like

Locus_2899_Transcript_1/2_Conf_1.000	2237	20	3.55E-65	XP_002634092.1	68	254.603	272	187	Hypothetical protein CBG01639
Locus_2899_Transcript_2/2_Conf_1.000	2237	20	3.55E-65	XP_002634092.1	68	254.603	272	187	Hypothetical protein CBG01639
Locus_28990_Transcript_1/1_Conf_1.000	135	0							
Locus_28991_Transcript_1/1_Conf_1.000	153	20	1.27E-12	XP_002819585.1	100	76.2554	50	50	glutamate [NMDA] receptor-associated protein 1-like, partial
Locus_28992_Transcript_1/1_Conf_1.000	168	20	1.03E-06	XP_001946020.1	68	56.6102	54	37	PREDICTED: similar to CG8129 CG8129-PB
Locus_28993_Transcript_1/1_Conf_1.000	138	0							
Locus_28994_Transcript_1/1_Conf_1.000	137	20	2.04E-15	XP_002643681.1	95	85.5001	44	42	Hypothetical protein CBG01860
Locus_28995_Transcript_1/1_Conf_1.000	142	0							
Locus_28996_Transcript_1/1_Conf_1.000	129	1	1.11E-12	AAA36776.1	100	76.2554	35	35	transformation-related protein
Locus_28997_Transcript_1/1_Conf_1.000	149	0							
Locus_28998_Transcript_1/1_Conf_1.000	139	0							
Locus_28999_Transcript_1/1_Conf_1.000	135	0							
Locus_29_Transcript_1/1_Conf_1.000	641	0							
Locus_290_Transcript_1/3_Conf_0.500	341	14	6.10E-20	CAA26849.1	64	100.523	101	65	put. vitellogenin
Locus_290_Transcript_2/3_Conf_0.750	1196	20	1.21E-57	XP_002632391.1	83	228.409	156	130	C. briggsae CBR-LACT-6 protein
Locus_290_Transcript_3/3_Conf_0.833	453	20	4.11E-32	XP_002644638.1	64	140.969	150	97	C. briggsae CBR-VIT-2 protein
Locus_2900_Transcript_1/1_Conf_1.000	957	7	7.02E-52	XP_002635230.1	59	208.764	324	192	C. briggsae CBR-NRF-5 protein
Locus_29000_Transcript_1/1_Conf_1.000	150	20	9.14E-11	NP_499784.2	83	70.0922	49	41	KELch-repeat containing protein family member (kel-3)
Locus_29001_Transcript_1/1_Conf_1.000	142	0							
Locus_29002_Transcript_1/1_Conf_1.000	189	0							
Locus_29003_Transcript_1/1_Conf_1.000	302	0							

Locus_29004_Transcript_1/1_Conf_1.000	135	4	1.28E-17	EFO98604.1	95	92.8189	45	43	CRE-ACY-1 protein
Locus_29005_Transcript_1/1_Conf_1.000	217	0							
Locus_29006_Transcript_1/1_Conf_1.000	135	2	1.25E-04	NP_504545.2	68	49.6766	44	30	hypothetical protein M03F8.4
Locus_29007_Transcript_1/1_Conf_1.000	146	20	3.15E-19	XP_002821888.1	100	98.2117	47	47	PREDICTED: glycosyltransferase-like protein LARGE2-like
Locus_29008_Transcript_1/1_Conf_1.000	145	17	2.05E-10	XP_001901223.1	81	68.9366	48	39	CLN3 protein
Locus_29009_Transcript_1/1_Conf_1.000	164	6	9.63E-05	AAB17945.1	62	50.0618	54	34	mariner transposase
Locus_2901_Transcript_1/1_Conf_1.000	547	20	2.43E-88	XP_002643684.1	93	328.176	178	166	C. briggsae CBR-NHR-1 protein
Locus_29010_Transcript_1/1_Conf_1.000	144	20	3.15E-19	XP_002753706.1	100	98.2117	48	48	PREDICTED: proteasome activator complex subunit 2-like
Locus_29011_Transcript_1/1_Conf_1.000	132	0							
Locus_29012_Transcript_1/1_Conf_1.000	130	0							
Locus_29013_Transcript_1/1_Conf_1.000	132	0							
Locus_29014_Transcript_1/1_Conf_1.000	156	20	2.22E-17	XP_001161193.1	100	92.0485	42	42	PREDICTED: similar to 16.7Kd protein isoform 1
Locus_29015_Transcript_1/1_Conf_1.000	228	0							
Locus_29016_Transcript_1/1_Conf_1.000	151	1	3.72E-04	XP_002640228.1	85	48.1358	35	30	C. briggsae CBR-ASD-2 protein
Locus_29017_Transcript_1/1_Conf_1.000	147	0							
Locus_29018_Transcript_1/1_Conf_1.000	129	20	7.57E-18	XP_002345467.1	100	93.5893	42	42	PREDICTED: hypothetical protein

Locus_29019_Transcript_1/1_Conf_1.000	190	3	1.96E-05	XP_002646129.1	70	52.373	41	29	Hypothetical protein CBG08008
Locus_2902_Transcript_1/3_Conf_0.667	860	20	1.01E-19	AAO63576.1	51	101.679	172	88	secreted protein 4 precursor
Locus_2902_Transcript_2/3_Conf_0.667	904	20	5.46E-19	AAO63576.1	52	99.3673	157	83	secreted protein 4 precursor
Locus_2902_Transcript_3/3_Conf_0.667	860	20	4.54E-20	AAO63576.1	51	102.834	172	89	secreted protein 4 precursor
Locus_29020_Transcript_1/1_Conf_1.000	256	20	6.73E-30	XP_002591083.1	84	133.65	83	70	hypothetical protein BRAFLDRAFT_119067
Locus_29021_Transcript_1/1_Conf_1.000	156	20	1.35E-14	XP_002633417.1	86	82.8037	51	44	C. briggsae CBR-TRPA-1 protein
Locus_29022_Transcript_1/1_Conf_1.000	305	0							
Locus_29023_Transcript_1/2_Conf_1.000	222	0							
Locus_29023_Transcript_2/2_Conf_1.000	228	0							
Locus_29024_Transcript_1/1_Conf_1.000	162	5	5.47E-08	XP_002639199.1	73	60.8474	52	38	Hypothetical protein CBG03742
Locus_29025_Transcript_1/1_Conf_1.000	162	20	5.29E-11	EFP08914.1	84	70.8626	46	39	hypothetical protein CRE_18067
Locus_29026_Transcript_1/1_Conf_1.000	138	0							
Locus_29027_Transcript_1/1_Conf_1.000	131	0							
Locus_29028_Transcript_1/1_Conf_1.000	405	0							
Locus_29029_Transcript_1/1_Conf_1.000	160	0							
Locus_2903_Transcript_1/1_Conf_1.000	624	5	1.52E-11	CAC35853.2	66	73.559	74	49	C. elegans protein Y111B2A.24, partially confirmed by transcript evidence
Locus_29030_Transcript_1/1_Conf_1.000	151	0							
Locus_29031_Transcript_1/1_Conf_1.000	204	20	8.69E-06	EFP13372.1	84	53.5286	38	32	hypothetical protein CRE_11299
Locus_29032_Transcript_1/1_Conf_1.000	200	20	3.52E-23	NP_499198.1	87	111.309	66	58	TransThyretin-Related family domain family member (ttr-4)
Locus_29033_Transcript_1/1_Conf_1.000	154	0							
Locus_29034_Transcript_1/1_Conf_1.000	152	0							
Locus_29035_Transcript_1/1_Conf_1.000	138	0							
Locus_29036_Transcript_1/1_Conf_1.000	173	0							
Locus_29037_Transcript_1/1_Conf_1.000	137	5	8.58E-14	CAR97828.1	91	80.1073	45	41	C. elegans protein F44G4.8b, confirmed by transcript evidence

Locus_29038_Transcript_1/1_Conf_1.000	143	0							
Locus_29039_Transcript_1/1_Conf_1.000	141	0							
Locus_2904_Transcript_1/1_Conf_1.000	974	20	7.59E-110	XP_002643063.1	75	401.364	330	249	Hypothetical protein CBG22980
Locus_29040_Transcript_1/1_Conf_1.000	209	0							
Locus_29041_Transcript_1/1_Conf_1.000	136	0							
Locus_29042_Transcript_1/1_Conf_1.000	195	7	1.54E-26	EFO89638.1	87	122.479	63	55	CRE-RHGF-1 protein
Locus_29043_Transcript_1/1_Conf_1.000	305	20	1.09E-08	XP_388657.1	58	63.1586	77	45	hypothetical protein FG08481.1
Locus_29044_Transcript_1/1_Conf_1.000	141	0							
Locus_29045_Transcript_1/1_Conf_1.000	131	0							
Locus_29046_Transcript_1/1_Conf_1.000	180	0							
Locus_29047_Transcript_1/1_Conf_1.000	168	0							
Locus_29048_Transcript_1/1_Conf_1.000	175	0							
Locus_29049_Transcript_1/1_Conf_1.000	480	20	3.02E-43	BAF30979.1	90	177.948	100	90	mitochondrial elongation factor Tu2 precursor
Locus_2905_Transcript_1/1_Conf_1.000	164	0							
Locus_29050_Transcript_1/1_Conf_1.000	177	3	9.82E-10	NP_001021087.1	72	66.6254	51	37	hypothetical protein F08A10.1
Locus_29051_Transcript_1/1_Conf_1.000	173	0							
Locus_29052_Transcript_1/1_Conf_1.000	151	20	1.96E-21	BAG60558.1	100	105.531	50	50	unnamed protein product

Locus_29053_Transcript_1/1_Conf_1.000	165	20	1.76E-06	XP_002731196.1	69	55.8398	53	37	PREDICTED: sphingosine kinase A, B, putative-like
Locus_29054_Transcript_1/1_Conf_1.000	133	2	2.97E-06	NP_001022698.3	75	55.0694	45	34	hypothetical protein R01H2.7
Locus_29055_Transcript_1/1_Conf_1.000	141	1	1.24E-04	XP_002126093.1	62	49.6766	37	23	PREDICTED: similar to sp4 protein
Locus_29056_Transcript_1/1_Conf_1.000	131	20	6.86E-11	NP_741553.1	83	70.4774	42	35	ALdehyde deHydrogenase family member (alh-4)
Locus_29057_Transcript_1/1_Conf_1.000	148	0							
Locus_29058_Transcript_1/1_Conf_1.000	196	0							
Locus_29059_Transcript_1/1_Conf_1.000	149	0							
Locus_2906_Transcript_1/1_Conf_1.000	731	20	1.47E-92	XP_002641003.1	86	343.199	222	192	C. briggsae CBR-TAT-1 protein
Locus_29060_Transcript_1/1_Conf_1.000	254	0							
Locus_29061_Transcript_1/1_Conf_1.000	145	0							
Locus_29062_Transcript_1/1_Conf_1.000	175	2	8.59E-22	AAG43143.1	97	106.686	46	45	AF061732_1My029 protein
Locus_29063_Transcript_1/1_Conf_1.000	146	0							
Locus_29064_Transcript_1/1_Conf_1.000	144	0							
Locus_29065_Transcript_1/1_Conf_1.000	166	20	1.64E-12	AAK68292.3	76	75.8702	55	42	U28943_4Clc-type chloride channel protein 3, isoform b, confirmed by transcript evidence
Locus_29066_Transcript_1/1_Conf_1.000	209	0							
Locus_29067_Transcript_1/1_Conf_1.000	185	20	2.50E-08	EFP07235.1	91	62.003	61	56	hypothetical protein CRE_13472
Locus_29068_Transcript_1/1_Conf_1.000	129	0							
Locus_29069_Transcript_1/1_Conf_1.000	155	2	4.36E-05	NP_508964.2	68	51.2174	45	31	Regulator of G protein Signaling family member (rgs-6)
Locus_2907_Transcript_1/1_Conf_1.000	805	20	1.90E-86	NP_502016.2	79	323.168	270	214	hypothetical protein F13E9.1
Locus_29070_Transcript_1/1_Conf_1.000	177	0							
Locus_29071_Transcript_1/1_Conf_1.000	137	0							
Locus_29072_Transcript_1/1_Conf_1.000	158	20	9.05E-11	XP_002636118.1	78	70.0922	50	39	Hypothetical protein CBG01364
Locus_29073_Transcript_1/1_Conf_1.000	169	0							

Locus_29074_Transcript_1/1_Conf_1.000	237	20	2.78E-28	XP_001897168.1	84	128.257	79	67	hypothetical protein
Locus_29075_Transcript_1/1_Conf_1.000	142	0							
Locus_29076_Transcript_1/1_Conf_1.000	146	2	6.82E-06	NP_492081.1	70	53.9138	48	34	hypothetical protein F07A5.3
Locus_29077_Transcript_1/1_Conf_1.000	148	2	1.05E-06	NP_001021200.1	67	56.6102	49	33	tryptophanyl (W) tRNA Synthetase family member (wrs-2)
Locus_29078_Transcript_1/1_Conf_1.000	133	3	5.40E-08	XP_002640308.1	70	60.8474	48	34	Hypothetical protein CBG12847
Locus_29079_Transcript_1/1_Conf_1.000	135	1	8.08E-04	EFO90747.1	66	46.9802	51	34	CRE-NHR-62 protein
Locus_2908_Transcript_1/1_Conf_1.000	879	20	2.97E-107	XP_002640012.1	80	392.504	278	224	Hypothetical protein CBG12482
Locus_29080_Transcript_1/1_Conf_1.000	213	0							
Locus_29081_Transcript_1/1_Conf_1.000	154	20	1.00E-17	NP_001122835.1	88	93.2041	51	45	UNCoordinated family member (unc-22)
Locus_29082_Transcript_1/1_Conf_1.000	210	20	6.80E-11	ABD04163.1	85	70.4774	42	36	plasma glutamate carboxypeptidase-like protein
Locus_29083_Transcript_1/1_Conf_1.000	169	0							
Locus_29084_Transcript_1/1_Conf_1.000	132	0							
Locus_29086_Transcript_1/1_Conf_1.000	362	0							
Locus_29087_Transcript_1/1_Conf_1.000	139	0							
Locus_29088_Transcript_1/1_Conf_1.000	186	0							
Locus_29089_Transcript_1/1_Conf_1.000	148	0							
Locus_2909_Transcript_1/1_Conf_1.000	1760	20	4.06E-82	XP_002637428.1	58	310.457	446	262	C. briggsae CBR-GCK-1 protein
Locus_29090_Transcript_1/1_Conf_1.000	248								
Locus_29091_Transcript_1/1_Conf_1.000	159	0							

Locus_29092_Transcript_1/1_Conf_1.000	135	1	2.78E-04	XP_001366578.1	65	48.521	47	31	PREDICTED: similar to CHKB protein
Locus_29093_Transcript_1/1_Conf_1.000	159	0							
Locus_29094_Transcript_1/1_Conf_1.000	224	20	1.78E-14	XP_002729522.1	98	82.4185	50	49	PREDICTED: heterogeneous nuclear ribonucleoprotein K
Locus_29095_Transcript_1/1_Conf_1.000	159	20	3.80E-09	NP_496938.1	67	64.6994	53	36	hypothetical protein F01D5.8
Locus_29096_Transcript_1/1_Conf_1.000	443	20	2.13E-52	XP_001894880.1	80	208.379	147	119	hypothetical protein
Locus_29097_Transcript_1/1_Conf_1.000	240	0							
Locus_29098_Transcript_1/1_Conf_1.000	132	0							
Locus_29099_Transcript_1/1_Conf_1.000	165	0							
Locus_291_Transcript_1/2_Conf_1.000	158	7	4.96E-09	NP_505384.2	75	64.3142	45	34	ASpartyl Protease family member (asp-2)
Locus_291_Transcript_2/2_Conf_1.000	345	20	2.44E-21	ADJ94115.1	80	82.4185	55	44	aspartic protease
Locus_2910_Transcript_1/1_Conf_1.000	479	0							
Locus_29100_Transcript_1/1_Conf_1.000	163	0							
Locus_29101_Transcript_1/1_Conf_1.000	153	20	1.23E-07	ADI24637.1	66	59.6918	45	30	Lin-12 and glp-1 x-hybridizing protein 1, isoform a, partially confirmed by transcript evidence
Locus_29102_Transcript_1/1_Conf_1.000	569	5	4.25E-25	XP_002633543.1	58	118.242	191	111	Hypothetical protein CBG05410
Locus_29103_Transcript_1/1_Conf_1.000	189	20	2.39E-19	EFO14883.1	87	98.5969	62	54	TK/FER protein kinase

Locus_29104_Transcript_1/1_Conf_1.000	146	5	1.47E-08	EFO93838.1	72	62.7734	48	35	CRE-SPO-11 protein
Locus_29105_Transcript_1/1_Conf_1.000	171	0							
Locus_29106_Transcript_1/1_Conf_1.000	132	4	3.63E-04	CAA84706.3	71	48.1358	42	30	C. elegans protein C38H2.1, partially confirmed by transcript evidence
Locus_29107_Transcript_1/1_Conf_1.000	130	0							
Locus_29108_Transcript_1/1_Conf_1.000	149	0							
Locus_29109_Transcript_1/1_Conf_1.000	138	18	1.09E-08	P30646.4	80	63.1586	45	36	Uncharacterized sugar kinase R08D7.7
Locus_2911_Transcript_1/1_Conf_1.000	531	20	1.86E-66	NP_001164609.1	100	255.373	129	129	clusterin isoform 3
Locus_29110_Transcript_1/1_Conf_1.000	372	4	8.46E-17	Q60WT2.2	97	90.1225	47	46	Alkaline ceramidase
Locus_29111_Transcript_1/1_Conf_1.000	144	0							
Locus_29112_Transcript_1/1_Conf_1.000	164	20	1.43E-24	BAF83813.1	100	115.931	54	54	unnamed protein product
Locus_29113_Transcript_1/1_Conf_1.000	231	20	1.54E-26	XP_002630880.1	85	122.479	77	66	C. briggsae CBR-TAT-4.1 protein
Locus_29114_Transcript_1/1_Conf_1.000	156	0							
Locus_29115_Transcript_1/1_Conf_1.000	205	0							
Locus_29116_Transcript_1/1_Conf_1.000	130	0							

Locus_29117_Transcript_1/1_Conf_1.000	134	20	1.09E-16	XP_002743762.1	100	89.7373	44	44	PREDICTED: 60S ribosomal protein L9-like isoform 1
Locus_29118_Transcript_1/1_Conf_1.000	171	0							
Locus_29119_Transcript_1/1_Conf_1.000	129	4	3.64E-12	EFP12691.1	88	74.7146	44	39	hypothetical protein CRE_29767
Locus_2912_Transcript_1/2_Conf_1.000	436	20	8.48E-46	NP_001021536.1	89	186.422	115	103	hypothetical protein K03E5.2
Locus_2912_Transcript_2/2_Conf_1.000	708	20	1.44E-33	ACO15785.1	89	147.132	87	78	Hypothetical protein K03E5.2d
Locus_29120_Transcript_1/1_Conf_1.000	148	0							
Locus_29121_Transcript_1/1_Conf_1.000	139	0							
Locus_29122_Transcript_1/1_Conf_1.000	152	0							
Locus_29123_Transcript_1/1_Conf_1.000	175	0							
Locus_29124_Transcript_1/1_Conf_1.000	164	0							
Locus_29125_Transcript_1/1_Conf_1.000	134	0							
Locus_29126_Transcript_1/1_Conf_1.000	238	0							
Locus_29127_Transcript_1/1_Conf_1.000	132	0							
Locus_29128_Transcript_1/1_Conf_1.000	152	7	8.53E-17	EFO91579.1	87	90.1225	48	42	hypothetical protein CRE_11978
Locus_29129_Transcript_1/1_Conf_1.000	191	0							
Locus_2913_Transcript_1/2_Conf_1.000	870	20	2.71E-52	NP_502816.2	63	209.92	274	173	hypothetical protein Y41E3.10
Locus_2913_Transcript_2/2_Conf_1.000	741	20	5.84E-52	CAR63569.1	92	208.379	119	110	putative elongation factor 1-beta/1-delta 1
Locus_29130_Transcript_1/1_Conf_1.000	137	20	3.61E-20	XP_002810126.1	100	101.293	45	45	PREDICTED: LOW QUALITY PROTEIN: disintegrin and metalloproteinase domain-containing protein 15-like
Locus_29131_Transcript_1/1_Conf_1.000	138	2	2.77E-04	EFO19238.1	69	48.521	43	30	hypothetical protein LOAG_09255
Locus_29132_Transcript_1/1_Conf_1.000	163	1	7.86E-15	BAG60904.1	100	83.5741	39	39	unnamed protein product
Locus_29133_Transcript_1/1_Conf_1.000	194	0							
Locus_29134_Transcript_1/1_Conf_1.000	148	0							
Locus_29135_Transcript_1/1_Conf_1.000	328	0							
Locus_29136_Transcript_1/1_Conf_1.000	169	0							
Locus_29137_Transcript_1/1_Conf_1.000	142	0							
Locus_29138_Transcript_1/1_Conf_1.000	137	0							
Locus_29139_Transcript_1/1_Conf_1.000	173	0							
Locus_2914_Transcript_1/1_Conf_1.000	139	0							

Locus_29140_Transcript_1/1_Conf_1.000	152	3	1.51E-05	NP_499028.1	77	52.7582	54	42	NHL (ring finger b-box coiled coil) domain containing family member (nhl-1)
Locus_29141_Transcript_1/1_Conf_1.000	218	16	1.27E-09	XP_002639681.1	63	66.2402	72	46	Hypothetical protein CBG12400
Locus_29142_Transcript_1/1_Conf_1.000	209	4	2.28E-06	XP_002640308.1	69	55.4546	71	49	Hypothetical protein CBG12847
Locus_29143_Transcript_1/1_Conf_1.000	131	0							
Locus_29144_Transcript_1/1_Conf_1.000	142	8	1.01E-06	EFO82374.1	79	56.6102	44	35	CRE-MUP-2 protein
Locus_29145_Transcript_1/1_Conf_1.000	174	0							
Locus_29146_Transcript_1/1_Conf_1.000	147	0							
Locus_29147_Transcript_1/1_Conf_1.000	148	0							
Locus_29148_Transcript_1/1_Conf_1.000	136	19	2.27E-06	XP_002933205.1	78	55.4546	41	32	PREDICTED: TP53-regulating kinase
Locus_29149_Transcript_1/1_Conf_1.000	169	0							
Locus_2915_Transcript_1/1_Conf_1.000	1437	20	1.20E-158	NP_503730.1	82	564.303	388	319	hypothetical protein Y45G12B.3
Locus_29150_Transcript_1/1_Conf_1.000	185	0							
Locus_29151_Transcript_1/1_Conf_1.000	146	0							
Locus_29152_Transcript_1/1_Conf_1.000	206	2	7.57E-10	NP_491490.1	61	67.0106	67	41	hypothetical protein W03G9.5
Locus_29153_Transcript_1/1_Conf_1.000	162	0							
Locus_29154_Transcript_1/1_Conf_1.000	181	2	7.53E-05	XP_002633201.1	75	50.447	40	30	C. briggsae CBR-NOL-10 protein
Locus_29155_Transcript_1/1_Conf_1.000	155	20	5.00E-09	EFO15925.1	70	64.3142	51	36	amino acid permease
Locus_29156_Transcript_1/1_Conf_1.000	198	0							
Locus_29157_Transcript_1/1_Conf_1.000	166	20	1.21E-23	EFO82569.1	100	112.849	55	55	CRE-TBA-9 protein

Locus_29158_Transcript_1/1_Conf_1.000	165	20	2.14E-12	XP_002645894.1	81	75.485	55	45	Hypothetical protein CBG07647
Locus_29159_Transcript_1/1_Conf_1.000	255	0							
Locus_2916_Transcript_1/1_Conf_1.000	1703	20	9.45E-153	NP_498854.1	72	545.043	491	354	Leucine AminoPeptidase family member (lap-1)
Locus_29160_Transcript_1/1_Conf_1.000	131	9	4.30E-13	EFO82561.1	93	77.7962	43	40	CRE-ACS-17 protein
Locus_29161_Transcript_1/1_Conf_1.000	128	20	3.53E-15	3MCE	100	84.7297	42	42	CrystalStructure OfThe Nac Domain Of Alpha Subunit Of Nascent Polypeptide-Associated Complex(Nac)
Locus_29162_Transcript_1/1_Conf_1.000	201	0							
Locus_29163_Transcript_1/1_Conf_1.000	134	2	4.75E-04	EFO87316.1	70	47.7506	44	31	CRE-DSC-4 protein
Locus_29164_Transcript_1/1_Conf_1.000	181	0							
Locus_29165_Transcript_1/1_Conf_1.000	138	0							
Locus_29166_Transcript_1/1_Conf_1.000	176	0							
Locus_29167_Transcript_1/1_Conf_1.000	129	20	1.58E-15	XP_002745917.1	100	85.8853	42	42	PREDICTED: heterogeneous nuclear ribonucleoproteins A2/B1-like
Locus_29168_Transcript_1/1_Conf_1.000	173	0							
Locus_29169_Transcript_1/1_Conf_1.000	157	0							
Locus_2917_Transcript_1/1_Conf_1.000	316	20	8.52E-09	NP_495668.1	46	63.5438	102	47	hypothetical protein ZK669.2
Locus_29170_Transcript_1/1_Conf_1.000	149	4	3.98E-06	EFO93055.1	71	54.6842	49	35	CRE-PSR-1 protein
Locus_29171_Transcript_1/1_Conf_1.000	163	0							

Locus_29172_Transcript_1/1_Conf_1.000	133	5	5.07E-06	EFO83717.1	78	54.299	37	29	CRE-CDH-1 protein
Locus_29173_Transcript_1/1_Conf_1.000	155	0							
Locus_29174_Transcript_1/1_Conf_1.000	159	10	6.91E-11	CAA72915.1	79	70.4774	49	39	serine protease inhibitor-like protein
Locus_29175_Transcript_1/1_Conf_1.000	156	0							
Locus_29176_Transcript_1/1_Conf_1.000	137	0							
Locus_29177_Transcript_1/1_Conf_1.000	168	0							
Locus_29178_Transcript_1/1_Conf_1.000	147	0							
Locus_29179_Transcript_1/1_Conf_1.000	134	0							
Locus_2918_Transcript_1/2_Conf_1.000	1316	20	9.10E-09	CAG01396.1	57	66.2402	115	66	unnamed protein product
Locus_2918_Transcript_2/2_Conf_1.000	1316	20	9.10E-09	CAG01396.1	57	66.2402	115	66	unnamed protein product
Locus_29180_Transcript_1/1_Conf_1.000	136	0							
Locus_29181_Transcript_1/1_Conf_1.000	139	0							
Locus_29182_Transcript_1/1_Conf_1.000	159	20	2.23E-09	EFO13528.1	69	65.4698	52	36	hypothetical protein LOAG_14998
Locus_29183_Transcript_1/1_Conf_1.000	131	0							
Locus_29184_Transcript_1/1_Conf_1.000	183	0							
Locus_29185_Transcript_1/1_Conf_1.000	136	0							
Locus_29186_Transcript_1/1_Conf_1.000	175	0							
Locus_29187_Transcript_1/1_Conf_1.000	171	0							
Locus_29188_Transcript_1/1_Conf_1.000	179	3	1.28E-09	XP_002640845.1	69	66.2402	59	41	C. briggsae CBR-CDH-1 protein
Locus_29189_Transcript_1/1_Conf_1.000	158	20	3.22E-16	NP_001040727.1	90	88.1965	52	47	hypothetical protein C01F1.3

Locus_2919_Transcript_1/1_Conf_1.000	1136	20	1.27E-109	NP_506579.1	92	400.979	233	216	hypothetical protein F23B12.5
Locus_29190_Transcript_1/1_Conf_1.000	135	2	1.79E-11	ABS45067.1	79	72.4034	44	35	latrophilin-like protein 2
Locus_29191_Transcript_1/1_Conf_1.000	140	20	5.02E-22	XP_002923042.1	100	107.457	46	46	PREDICTED: lysyl oxidase homolog 1-like
Locus_29192_Transcript_1/1_Conf_1.000	138	0							
Locus_29193_Transcript_1/1_Conf_1.000	138	20	6.13E-12	XP_002642560.1	84	73.9442	45	38	C. briggsae CBR-RCQ-5 protein
Locus_29194_Transcript_1/1_Conf_1.000	221	0							
Locus_29195_Transcript_1/1_Conf_1.000	176	0							
Locus_29196_Transcript_1/1_Conf_1.000	135	0							
Locus_29197_Transcript_1/1_Conf_1.000	171	0							
Locus_29198_Transcript_1/1_Conf_1.000	137	20	2.50E-13	NP_741756.1	93	78.5666	45	42	Endophilin-Related Protein family member (erp-1)
Locus_29199_Transcript_1/1_Conf_1.000	173	0							
Locus_292_Transcript_1/1_Conf_1.000	422	20	2.69E-47	XP_001901347.1	82	191.43	140	116	DNA excision repair protein ERCC-6
Locus_2920_Transcript_1/1_Conf_1.000	385	0							
Locus_29200_Transcript_1/1_Conf_1.000	166	5	1.13E-05	NP_001022014.1	63	53.1434	55	35	neuRonal IGCAM family member (rig-6)
Locus_29201_Transcript_1/1_Conf_1.000	187	20	4.84E-12	NP_510181.3	85	74.3294	62	53	hypothetical protein F09A5.1
Locus_29202_Transcript_1/1_Conf_1.000	182	20	7.01E-19	EFO24810.1	80	97.0561	60	48	hypothetical protein LOAG_03675

Locus_29203_Transcript_1/1_Conf_1.000	167	0							
Locus_29204_Transcript_1/1_Conf_1.000	150	0							
Locus_29205_Transcript_1/1_Conf_1.000	154	0							
Locus_29206_Transcript_1/1_Conf_1.000	157	20	3.33E-21	EFO89626.1	96	104.76	52	50	CRE-IFA-1 protein
Locus_29207_Transcript_1/1_Conf_1.000	136	0							
Locus_29208_Transcript_1/1_Conf_1.000	136	0							
Locus_29209_Transcript_1/1_Conf_1.000	177	0							
Locus_2921_Transcript_1/1_Conf_1.000	208	0							
Locus_29210_Transcript_1/1_Conf_1.000	224	12	2.25E-09	EFO87962.1	80	65.4698	46	37	hypothetical protein CRE_05718
Locus_29211_Transcript_1/1_Conf_1.000	270	0							
Locus_29212_Transcript_1/1_Conf_1.000	146	15	9.82E-13	EFP09685.1	89	76.6406	48	43	CRE-SULP-3 protein
Locus_29213_Transcript_1/1_Conf_1.000	137	0							
Locus_29214_Transcript_1/1_Conf_1.000	147	20	7.00E-11	NP_506684.3	81	70.4774	48	39	hypothetical protein F02D8.4
Locus_29215_Transcript_1/1_Conf_1.000	164	0							
Locus_29216_Transcript_1/1_Conf_1.000	225	0							
Locus_29217_Transcript_1/1_Conf_1.000	315	20	1.76E-38	NP_494846.1	83	162.155	104	87	hypothetical protein F41C3.5
Locus_29218_Transcript_1/1_Conf_1.000	142	20	1.37E-11	EFO91272.1	84	72.7886	46	39	hypothetical protein CRE_04285
Locus_29219_Transcript_1/1_Conf_1.000	208	20	1.05E-19	NP_495473.2	79	99.7525	69	55	SPONdin (extracellular matrix glycoprotein) family member (spon-1)
Locus_2922_Transcript_1/2_Conf_1.000	916	9	1.34E-04	XP_001475360.1	40	51.6026	193	78	PREDICTED: hypothetical protein
Locus_2922_Transcript_2/2_Conf_1.000	505	0							
Locus_29220_Transcript_1/1_Conf_1.000	187	0							
Locus_29221_Transcript_1/1_Conf_1.000	129	0							
Locus_29222_Transcript_1/1_Conf_1.000	168	0							
Locus_29223_Transcript_1/1_Conf_1.000	137	1	2.78E-04	EFO98227.1	68	48.521	45	31	hypothetical protein CRE_15394
Locus_29224_Transcript_1/1_Conf_1.000	152	0							

Locus_29225_Transcript_1/1_Conf_1.000	129	12	1.33E-14	NP_001023646.1	97	82.8037	42	41	AKT kinase family member (akt-1)
Locus_29226_Transcript_1/1_Conf_1.000	234	2	1.21E-15	NP_493709.1	79	86.2705	77	61	hypothetical protein K01A2.10
Locus_29227_Transcript_1/1_Conf_1.000	130	0							
Locus_29228_Transcript_1/1_Conf_1.000	150	2	4.39E-05	XP_001626861.1	72	51.2174	47	34	predicted protein
Locus_29229_Transcript_1/1_Conf_1.000	155	0							
Locus_2923_Transcript_1/1_Conf_1.000	140	0							
Locus_29230_Transcript_1/1_Conf_1.000	148	0							
Locus_29231_Transcript_1/1_Conf_1.000	129	3	3.90E-06	NP_493027.1	82	54.6842	39	32	hypothetical protein R06C1.2
Locus_29232_Transcript_1/1_Conf_1.000	133	20	4.89E-17	XP_002803107.1	100	90.8929	44	44	PREDICTED: programmed cell death 6-interacting protein
Locus_29233_Transcript_1/1_Conf_1.000	148	0							
Locus_29234_Transcript_1/1_Conf_1.000	141	0							
Locus_29235_Transcript_1/1_Conf_1.000	137	0							
Locus_29236_Transcript_1/1_Conf_1.000	130	20	2.61E-10	XP_002642977.1	90	68.5514	40	36	C. briggsae CBR-TTR-7 protein
Locus_29237_Transcript_1/1_Conf_1.000	133	0							
Locus_29238_Transcript_1/1_Conf_1.000	170	0							
Locus_29239_Transcript_1/1_Conf_1.000	270	1	1.21E-07	EFP12879.1	63	59.6918	71	45	hypothetical protein CRE_05993
Locus_2924_Transcript_1/2_Conf_1.000	307	20	1.51E-18	NP_001133519.1	63	95.9005	73	46	Granulins
Locus_2924_Transcript_2/2_Conf_1.000	303	20	2.34E-19	XP_002739994.1	62	98.5969	79	49	PREDICTED: granulin-like, partial
Locus_29240_Transcript_1/1_Conf_1.000	129	0							
Locus_29241_Transcript_1/1_Conf_1.000	180	0							
Locus_29242_Transcript_1/1_Conf_1.000	133	0							
Locus_29243_Transcript_1/1_Conf_1.000	133	0							
Locus_29244_Transcript_1/1_Conf_1.000	147	0							
Locus_29245_Transcript_1/1_Conf_1.000	340	0							
Locus_29246_Transcript_1/1_Conf_1.000	152	0							

Locus_29247_Transcript_1/1_Conf_1.000	141	20	7.99E-20	EFO82306.1	97	100.138	46	45	CRE-UBC-17 protein
Locus_29248_Transcript_1/1_Conf_1.000	176	5	3.73E-17	EFP07599.1	88	91.2781	52	46	hypothetical protein CRE_26355
Locus_29249_Transcript_1/1_Conf_1.000	181	19	2.85E-12	AAZ91344.1	100	75.0998	36	36	Synaptotagmin protein 2
Locus_2925_Transcript_1/1_Conf_1.000	1661	20	0	AAF00539.1	94	744.577	403	381	AF187690_1kinase JNK-1
Locus_29250_Transcript_1/1_Conf_1.000	203	0							
Locus_29251_Transcript_1/1_Conf_1.000	308	5	9.20E-16	CAA94853.5	68	86.6557	76	52	C. elegans protein ZK856.5, confirmed by transcript evidence
Locus_29252_Transcript_1/1_Conf_1.000	131	0							
Locus_29253_Transcript_1/1_Conf_1.000	170	0							
Locus_29254_Transcript_1/1_Conf_1.000	239	0							
Locus_29255_Transcript_1/1_Conf_1.000	130	0							
Locus_29256_Transcript_1/1_Conf_1.000	147	0							
Locus_29257_Transcript_1/1_Conf_1.000	154	0							
Locus_29258_Transcript_1/1_Conf_1.000	164	0							
Locus_29259_Transcript_1/1_Conf_1.000	128	0							
Locus_2926_Transcript_1/3_Conf_0.667	1135	2	3.22E-04	NP_491414.3	39	50.8322	209	83	hypothetical protein Y119C1A.1
Locus_2926_Transcript_2/3_Conf_0.667	1159	2	3.29E-04	NP_491414.3	39	50.8322	209	83	hypothetical protein Y119C1A.1
Locus_2926_Transcript_3/3_Conf_0.667	1165	2	3.32E-04	NP_491414.3	39	50.8322	209	83	hypothetical protein Y119C1A.1
Locus_29260_Transcript_1/1_Conf_1.000	136	0							
Locus_29261_Transcript_1/1_Conf_1.000	173	0							
Locus_29262_Transcript_1/1_Conf_1.000	189	20	2.02E-26	XP_002645698.1	98	122.094	62	61	Hypothetical protein CBG07358
Locus_29263_Transcript_1/1_Conf_1.000	230	0							
Locus_29264_Transcript_1/1_Conf_1.000	187	0							

Locus_29265_Transcript_1/1_Conf_1.000	159	20	5.46E-16	XP_002812714.1	100	87.4261	52	52	PREDICTED: collagen alpha-1(III) chain-like isoform 2
Locus_29266_Transcript_1/1_Conf_1.000	223	0							
Locus_29267_Transcript_1/1_Conf_1.000	128	0							
Locus_29268_Transcript_1/1_Conf_1.000	135	0							
Locus_29269_Transcript_1/1_Conf_1.000	228	0							
Locus_2927_Transcript_1/1_Conf_1.000	169	18	1.17E-10	Q94637.1	78	69.707	50	39	Vitellogenin-6
Locus_29270_Transcript_1/1_Conf_1.000	139	0							
Locus_29271_Transcript_1/1_Conf_1.000	157	20	2.30E-14	XP_002641185.1	84	82.0333	51	43	Hypothetical protein CBG09046
Locus_29272_Transcript_1/1_Conf_1.000	186	0							
Locus_29273_Transcript_1/1_Conf_1.000	146	0							
Locus_29274_Transcript_1/1_Conf_1.000	224	2	1.27E-04	NP_491075.2	60	49.6766	74	45	hypothetical protein Y71F9AL.1
Locus_29275_Transcript_1/1_Conf_1.000	137	0							
Locus_29276_Transcript_1/1_Conf_1.000	128	4	2.15E-04	XP_002633509.1	66	48.9062	36	24	Hypothetical protein CBG05371
Locus_29277_Transcript_1/1_Conf_1.000	164	20	6.04E-15	NP_491303.3	84	83.9593	53	45	hypothetical protein E01A2.5
Locus_29278_Transcript_1/1_Conf_1.000	169	0							

Locus_29279_Transcript_1/1_Conf_1.000	294	20	5.58E-53	BAG61199.1	100	210.305	98	98	unnamed protein product
Locus_2928_Transcript_1/2_Conf_1.000	3472	20	1.09E-135	EFO28277.1	54	489.574	909	491	piwi domain-containing protein
Locus_2928_Transcript_2/2_Conf_1.000	3282	20	1.02E-135	EFO28277.1	54	489.574	909	491	piwi domain-containing protein
Locus_29280_Transcript_1/1_Conf_1.000	160	4	1.26E-20	XP_002634606.1	96	102.834	52	50	Hypothetical protein CBG08423
Locus_29281_Transcript_1/1_Conf_1.000	159	20	1.34E-22	XP_002637337.1	98	109.383	53	52	Hypothetical protein CBG19032
Locus_29282_Transcript_1/1_Conf_1.000	143	0							
Locus_29283_Transcript_1/1_Conf_1.000	130	0							
Locus_29284_Transcript_1/1_Conf_1.000	148	0							
Locus_29285_Transcript_1/1_Conf_1.000	203	0							
Locus_29286_Transcript_1/1_Conf_1.000	128	0							
Locus_29287_Transcript_1/1_Conf_1.000	159	0							
Locus_29288_Transcript_1/1_Conf_1.000	139	0							
Locus_29289_Transcript_1/1_Conf_1.000	139	0							
Locus_2929_Transcript_1/1_Conf_1.000	990	20	8.46E-72	NP_501038.1	66	275.018	325	217	DYnein Chain, light Intermediate family member (dyci-1)
Locus_29290_Transcript_1/1_Conf_1.000	146	20	3.73E-12	NP_497268.1	87	74.7146	48	42	Caenorhabditis EpoxidE Hydrolase family member (ceeh-1)
Locus_29291_Transcript_1/1_Conf_1.000	144	0							
Locus_29292_Transcript_1/1_Conf_1.000	164	0							
Locus_29293_Transcript_1/1_Conf_1.000	210	0							
Locus_29294_Transcript_1/1_Conf_1.000	149	0							
Locus_29295_Transcript_1/1_Conf_1.000	283	0							
Locus_29296_Transcript_1/1_Conf_1.000	210	0							
Locus_29297_Transcript_1/1_Conf_1.000	189	5	1.15E-13	EFO26857.1	74	79.7221	59	44	leucine Rich Repeat family protein

Locus_29298_Transcript_1/1_Conf_1.000	347	20	3.43E-34	EFO20819.1	81	147.902	103	84	CK1/TTBKL protein kinase
Locus_29299_Transcript_1/1_Conf_1.000	135	20	4.41E-18	EAW99708.1	100	94.3597	44	44	hCG40733, isoform CRA_d
Locus_293_Transcript_10/21_Conf_1.000	156	0							
Locus_293_Transcript_11/21_Conf_1.000	198	20	7.88E-07	XP_001179362.1	60	56.9954	61	37	PREDICTED: similar to putative polyprotein, partial
Locus_293_Transcript_12/21_Conf_0.434	2010	8	2.87E-10	XP_002648426.1	48	72.0182	165	80	C. briggsae CBR-DCT-10 protein
Locus_293_Transcript_13/21_Conf_0.226	2911	20	4.86E-33	NP_496141.1	42	148.288	568	240	hypothetical protein C05C10.2
Locus_293_Transcript_14/21_Conf_0.151	2854	20	4.75E-33	NP_496141.1	42	148.288	568	240	hypothetical protein C05C10.2
Locus_293_Transcript_15/21_Conf_0.321	640	4	5.06E-05	EEQ88932.1	44	51.9878	93	41	conserved hypothetical protein
Locus_293_Transcript_16/21_Conf_0.491	4232	20	7.33E-33	NP_496141.1	42	148.288	568	240	hypothetical protein C05C10.2

Locus_293_Transcript_17/21_Conf_0.415	2066	8	2.97E-10	XP_002648426.1	48	72.0182	165	80	C. briggsae CBR-DCT-10 protein
Locus_293_Transcript_18/21_Conf_0.094	1213	0							
Locus_293_Transcript_19/21_Conf_0.321	3470	20	2.24E-48	XP_002648425.1	55	199.519	249	139	Hypothetical protein CBG24691
Locus_293_Transcript_20/21_Conf_0.151	2854	20	4.75E-33	NP_496141.1	42	148.288	568	240	hypothetical protein C05C10.2
Locus_293_Transcript_21/21_Conf_0.434	2010	8	2.87E-10	XP_002648426.1	48	72.0182	165	80	C. briggsae CBR-DCT-10 protein
Locus_293_Transcript_5/21_Conf_1.000	162	0							
Locus_293_Transcript_6/21_Conf_1.000	129	0							
Locus_293_Transcript_7/21_Conf_1.000	142	0							
Locus_293_Transcript_8/21_Conf_1.000	146	0							
Locus_293_Transcript_9/21_Conf_1.000	144	0							
Locus_2930_Transcript_1/1_Conf_1.000	1105	20	3.43E-96	NP_498556.1	83	356.295	242	203	hypothetical protein B0280.3
Locus_29300_Transcript_1/1_Conf_1.000	169	0							
Locus_29301_Transcript_1/1_Conf_1.000	194	0							
Locus_29302_Transcript_1/1_Conf_1.000	357	20	2.25E-38	XP_002645663.1	73	161.77	116	85	Hypothetical protein CBG07306
Locus_29303_Transcript_1/1_Conf_1.000	149	0							
Locus_29304_Transcript_1/1_Conf_1.000	148	5	1.08E-11	XP_002647777.1	75	73.1738	48	36	C. briggsae CBR-TSP-13 protein
Locus_29305_Transcript_1/1_Conf_1.000	133	2	1.86E-08	NP_492201.1	81	62.3882	43	35	hypothetical protein C54G4.4
Locus_29306_Transcript_1/1_Conf_1.000	238	11	1.80E-11	XP_002646356.1	69	72.4034	79	55	Hypothetical protein CBG12070
Locus_29307_Transcript_1/1_Conf_1.000	215	20	1.24E-12	XP_001902375.1	69	76.2554	72	50	Protein kinase domain containing protein
Locus_29308_Transcript_1/1_Conf_1.000	130	1	6.22E-04	NP_508551.1	65	47.3654	43	28	hypothetical protein F28B4.3
Locus_29309_Transcript_1/1_Conf_1.000	144	0							

Locus_2931_Transcript_1/1_Conf_1.000	488	20	2.51E-53	ABD39381.1	83	211.46	143	119	putative galectin protein 10
Locus_29310_Transcript_1/1_Conf_1.000	133	20	3.29E-05	XP_002923582.1	100	51.6026	43	43	PREDICTED: LOW QUALITY PROTEIN: membralin-like, partial
Locus_29311_Transcript_1/1_Conf_1.000	141	0							
Locus_29312_Transcript_1/1_Conf_1.000	135	0							
Locus_29313_Transcript_1/1_Conf_1.000	171	0							
Locus_29314_Transcript_1/1_Conf_1.000	136	14	7.30E-05	XP_002745176.1	70	50.447	34	24	PREDICTED: hypothetical protein LOC100415433
Locus_29315_Transcript_1/1_Conf_1.000	130	4	5.42E-08	ACI49212.1	83	60.8474	42	35	hypothetical protein Csp3_JD04.011
Locus_29316_Transcript_1/1_Conf_1.000	256	0							
Locus_29317_Transcript_1/1_Conf_1.000	133	0							
Locus_29318_Transcript_1/1_Conf_1.000	185	0							
Locus_29319_Transcript_1/1_Conf_1.000	130	4	1.64E-04	XP_002633829.1	63	49.2914	41	26	Hypothetical protein CBG19861
Locus_2932_Transcript_1/1_Conf_1.000	821	20	2.02E-83	NP_500363.1	96	313.153	189	183	CEll Death abnormality family member (ced-10)
Locus_29320_Transcript_1/1_Conf_1.000	298	2	3.52E-15	XP_002645173.1	67	84.7297	85	57	Hypothetical protein CBG16894
Locus_29321_Transcript_1/1_Conf_1.000	131	0							
Locus_29322_Transcript_1/1_Conf_1.000	142	0							

Locus_29323_Transcript_1/1_Conf_1.000	131	3	2.97E-06	AAZ82850.2	79	55.0694	43	34	Hypothetical protein C01B10.11
Locus_29324_Transcript_1/1_Conf_1.000	130	0							
Locus_29325_Transcript_1/1_Conf_1.000	133	0							
Locus_29326_Transcript_1/1_Conf_1.000	171	0							
Locus_29327_Transcript_1/1_Conf_1.000	144	0							
Locus_29328_Transcript_1/1_Conf_1.000	141	0							
Locus_29329_Transcript_1/1_Conf_1.000	138	0							
Locus_2933_Transcript_1/1_Conf_1.000	1170	2	1.31E-08	XP_001899586.1	60	65.4698	113	68	hypothetical protein
Locus_29330_Transcript_1/1_Conf_1.000	131	4	2.87E-17	NP_001022641.1	97	91.6633	43	42	LEThal family member (let-805)
Locus_29331_Transcript_1/1_Conf_1.000	133	20	2.27E-14	EFO24024.1	95	82.0333	44	42	CMGC/DYRK/HIPK protein kinase
Locus_29332_Transcript_1/1_Conf_1.000	311	20	2.48E-37	NP_001023265.1	81	158.303	103	84	UNCoordinated family member (unc-26)
Locus_29333_Transcript_1/1_Conf_1.000	140	0							
Locus_29334_Transcript_1/1_Conf_1.000	145	20	4.25E-16	CAF91420.1	95	87.8113	47	45	unnamed protein product
Locus_29335_Transcript_1/1_Conf_1.000	131	20	8.96E-11	EFO86831.1	86	70.0922	43	37	hypothetical protein CRE_04808
Locus_29336_Transcript_1/1_Conf_1.000	165	18	6.44E-09	EFP07603.1	79	63.929	54	43	hypothetical protein CRE_26305
Locus_29337_Transcript_1/1_Conf_1.000	195	0							

Locus_29338_Transcript_1/1_Conf_1.000	129	20	4.91E-17	XP_002913893.1	100	90.8929	42	42	PREDICTED: LOW QUALITY PROTEIN: secreted frizzled-related protein 2-like
Locus_29339_Transcript_1/1_Conf_1.000	171	5	9.52E-21	EFP08905.1	85	103.219	57	49	hypothetical protein CRE_18030
Locus_2934_Transcript_1/2_Conf_1.000	168	20	2.68E-23	EFO21508.1	100	111.694	55	55	ubiquitin C II
Locus_2934_Transcript_2/2_Conf_1.000	318	20	1.06E-51	EFO21508.1	100	206.068	105	105	ubiquitin C II
Locus_29340_Transcript_1/1_Conf_1.000	159	0							
Locus_29341_Transcript_1/1_Conf_1.000	134	20	7.83E-07	EFP05831.1	84	56.9954	44	37	CRE-PYC-1 protein
Locus_29342_Transcript_1/1_Conf_1.000	154	20	1.65E-20	EAW50472.1	100	102.449	51	51	hCG2042722
Locus_29343_Transcript_1/1_Conf_1.000	132	20	3.99E-19	XP_002929374.1	100	97.8265	43	43	PREDICTED: WD repeat-containing protein 1-like
Locus_29344_Transcript_1/1_Conf_1.000	134	0							
Locus_29345_Transcript_1/1_Conf_1.000	134	5	2.78E-12	EFP07387.1	90	75.0998	44	40	hypothetical protein CRE_26446

Locus_29346_Transcript_1/1_Conf_1.000	150	20	3.12E-19	BAG53122.1	100	98.2117	49	49	unnamed protein product
Locus_29347_Transcript_1/1_Conf_1.000	151	0							
Locus_29348_Transcript_1/1_Conf_1.000	131	0							
Locus_29349_Transcript_1/1_Conf_1.000	181	4	1.41E-08	NP_499313.2	63	62.7734	58	37	hypothetical protein F43D9.1
Locus_2935_Transcript_1/1_Conf_1.000	635	20	7.93E-96	NP_504202.1	95	353.599	187	179	hypothetical protein F32D1.5
Locus_29350_Transcript_1/1_Conf_1.000	136	20	3.37E-18	EFO21455.1	95	94.7449	45	43	voltage-gated calcium channel
Locus_29351_Transcript_1/1_Conf_1.000	128	0							
Locus_29352_Transcript_1/1_Conf_1.000	157	0							
Locus_29353_Transcript_1/1_Conf_1.000	158	13	3.79E-17	NP_501689.1	90	91.2781	52	47	fatty acid ELOngation family member (elo-1)
Locus_29354_Transcript_1/1_Conf_1.000	279	20	2.76E-12	EFO27955.1	72	75.0998	90	65	leucyl aminopeptidase
Locus_29355_Transcript_1/1_Conf_1.000	139	20	1.97E-18	XP_002826951.1	100	95.5153	45	45	PREDICTED: complement component 1 Q subcomponent-binding protein, mitochondrial-like
Locus_29356_Transcript_1/1_Conf_1.000	145	10	1.24E-07	NP_001022736.1	73	59.6918	45	33	hypothetical protein R155.1
Locus_29357_Transcript_1/1_Conf_1.000	140	0							
Locus_29358_Transcript_1/1_Conf_1.000	131	0							
Locus_29359_Transcript_1/1_Conf_1.000	143	0							
Locus_2936_Transcript_1/3_Conf_0.714	1036	2	3.53E-15	XP_002639470.1	64	87.0409	96	62	Hypothetical protein CBG04065
Locus_2936_Transcript_2/3_Conf_0.714	1033	2	3.51E-15	XP_002639470.1	64	87.0409	96	62	Hypothetical protein CBG04065
Locus_2936_Transcript_3/3_Conf_0.714	1033	2	3.51E-15	XP_002639470.1	64	87.0409	96	62	Hypothetical protein CBG04065
Locus_29360_Transcript_1/1_Conf_1.000	239	20	4.13E-32	XP_002634052.1	94	140.969	79	75	C. briggsae CBR-VHA-5 protein
Locus_29361_Transcript_1/1_Conf_1.000	130	0							

Locus_29362_Transcript_1/1_Conf_1.000	156	20	1.55E-18	XP_002629730.1	98	95.9005	52	51	Hypothetical protein CBG00961
Locus_29363_Transcript_1/1_Conf_1.000	443	4	1.96E-05	NP_496398.2	51	52.373	136	70	hypothetical protein T06D8.1
Locus_29364_Transcript_1/1_Conf_1.000	177	3	1.24E-04	EFO20410.1	73	49.6766	41	30	hypothetical protein LOAG_08081
Locus_29365_Transcript_1/1_Conf_1.000	134	0							
Locus_29366_Transcript_1/1_Conf_1.000	189	0							
Locus_29367_Transcript_1/1_Conf_1.000	205	0							
Locus_29368_Transcript_1/1_Conf_1.000	130	0							
Locus_29369_Transcript_1/1_Conf_1.000	172	0							
Locus_2937_Transcript_1/1_Conf_1.000	456	20	4.95E-70	XP_002641885.1	93	266.929	151	141	Hypothetical protein CBG16572
Locus_29370_Transcript_1/1_Conf_1.000	176	0							
Locus_29371_Transcript_1/1_Conf_1.000	323	4	1.26E-12	EFP11172.1	57	76.2554	106	61	hypothetical protein CRE_30769
Locus_29372_Transcript_1/1_Conf_1.000	182	5	3.58E-20	NP_508843.1	81	101.293	59	48	hypothetical protein M03F4.6
Locus_29373_Transcript_1/1_Conf_1.000	233	0							
Locus_29374_Transcript_1/1_Conf_1.000	128	0							
Locus_29375_Transcript_1/1_Conf_1.000	138	20	7.49E-10	XP_002744232.1	100	67.0106	45	45	PREDICTED: heterogeneous nuclear ribonucleoprotein A0-like
Locus_29376_Transcript_1/1_Conf_1.000	128	20	5.83E-10	EFO92321.1	86	67.3958	38	33	CRE-EPI-1 protein
Locus_29377_Transcript_1/1_Conf_1.000	141	20	2.57E-10	EFO17147.1	84	68.5514	45	38	TK/FER protein kinase
Locus_29378_Transcript_1/1_Conf_1.000	145	0							
Locus_29379_Transcript_1/1_Conf_1.000	284	20	3.45E-42	EFO23504.1	91	174.481	94	86	TK protein kinase
Locus_2938_Transcript_1/1_Conf_1.000	687	6	1.32E-28	CAD44516.1	52	130.568	228	119	VAB-10B protein
Locus_29380_Transcript_1/1_Conf_1.000	136	4	8.34E-09	EFO88465.1	88	63.5438	44	39	CRE-NRX-1 protein
Locus_29381_Transcript_1/1_Conf_1.000	203	0							
Locus_29382_Transcript_1/1_Conf_1.000	163	20	8.99E-11	EFO24804.1	75	70.0922	52	39	galactosyltransferase
Locus_29383_Transcript_1/1_Conf_1.000	217	20	2.95E-06	XP_313869.4	68	55.0694	47	32	AGAP004566-PA

Locus_29384_Transcript_1/1_Conf_1.000	185	0							
Locus_29385_Transcript_1/1_Conf_1.000	235	0							
Locus_29386_Transcript_1/1_Conf_1.000	164	0							
Locus_29387_Transcript_1/1_Conf_1.000	222	20	2.03E-26	ACJ65168.1	91	122.094	74	68	Uncoordinated protein 68, isoform b, partially confirmed by transcript evidence
Locus_29388_Transcript_1/1_Conf_1.000	238	20	1.33E-30	EFO24957.1	85	135.961	78	67	hypothetical protein LOAG_03532
Locus_29389_Transcript_1/1_Conf_1.000	136	0							
Locus_2939_Transcript_1/3_Conf_0.714	633	20	4.44E-33	XP_002156375.1	65	113.62	126	83	PREDICTED: similar to haloacid dehalogenase-like hydrolase domain containing 1A
Locus_2939_Transcript_2/3_Conf_0.714	633	20	7.52E-33	XP_002156375.1	64	113.235	125	81	PREDICTED: similar to haloacid dehalogenase-like hydrolase domain containing 1A
Locus_2939_Transcript_3/3_Conf_0.714	633	20	5.78E-33	XP_002156375.1	65	113.62	126	83	PREDICTED: similar to haloacid dehalogenase-like hydrolase domain containing 1A
Locus_29390_Transcript_1/1_Conf_1.000	183	20	2.66E-26	P02751.4	100	121.709	60	60	Fibronectin
Locus_29391_Transcript_1/1_Conf_1.000	143	0							
Locus_29392_Transcript_1/1_Conf_1.000	131	0							

Locus_29393_Transcript_1/1_Conf_1.000	239	20	4.14E-24	EFO24654.1	82	114.39	78	64	RNA polymerase Rpb1
Locus_29394_Transcript_1/1_Conf_1.000	132	3	2.06E-07	EFP09033.1	76	58.9214	38	29	hypothetical protein CRE_22505
Locus_29395_Transcript_1/1_Conf_1.000	162	20	1.21E-23	XP_001149698.1	100	112.849	53	53	PREDICTED: nicotinamide N-methyltransferase isoform 1
Locus_29396_Transcript_1/1_Conf_1.000	156	3	2.73E-15	EFP05940.1	88	85.1149	52	46	CRE-NPR-13 protein
Locus_29397_Transcript_1/1_Conf_1.000	200	0							
Locus_29398_Transcript_1/1_Conf_1.000	162	0							
Locus_29399_Transcript_1/1_Conf_1.000	202	20	1.30E-09	XP_002637502.1	65	66.2402	66	43	Hypothetical protein CBG19223
Locus_294_Transcript_1/2_Conf_1.000	2617	20	3.35E-102	NP_510521.1	68	377.867	412	283	Ubiquinol-Cytochrome c oxidoReductase complex family member (ucr-2.2)
Locus_294_Transcript_2/2_Conf_1.000	2617	20	4.37E-102	NP_510521.1	68	377.481	412	283	Ubiquinol-Cytochrome c oxidoReductase complex family member (ucr-2.2)
Locus_2940_Transcript_1/1_Conf_1.000	284	2	4.24E-16	XP_002639243.1	73	87.8113	71	52	Hypothetical protein CBG03801
Locus_29400_Transcript_1/1_Conf_1.000	196	20	1.70E-17	XP_512822.2	100	92.4337	43	43	PREDICTED: Fc fragment of IgG, receptor, transporter, alpha
Locus_29401_Transcript_1/1_Conf_1.000	137	20	9.17E-16	XP_002808339.1	100	86.6557	45	45	PREDICTED: LOW QUALITY PROTEIN: major vault protein-like
Locus_29402_Transcript_1/1_Conf_1.000	226	0							
Locus_29403_Transcript_1/1_Conf_1.000	145	6	1.47E-08	EFO97805.1	75	62.7734	48	36	hypothetical protein CRE_15976
Locus_29404_Transcript_1/1_Conf_1.000	139	0							
Locus_29405_Transcript_1/1_Conf_1.000	165	0							
Locus_29406_Transcript_1/1_Conf_1.000	174	0							
Locus_29407_Transcript_1/1_Conf_1.000	125	0							
Locus_29408_Transcript_1/1_Conf_1.000	297	2	1.22E-07	XP_001901263.1	70	59.6918	94	66	SEA domain containing protein

Locus_29409_Transcript_1/1_Conf_1.000	157	0							
Locus_2941_Transcript_1/2_Conf_1.000	944	20	5.30E-44	CAR63571.1	87	182.57	113	99	hypothetical protein
Locus_2941_Transcript_2/2_Conf_1.000	944	20	5.30E-44	CAR63571.1	87	182.57	113	99	hypothetical protein
Locus_29410_Transcript_1/1_Conf_1.000	197	5	2.08E-23	NP_001022641.1	92	112.079	65	60	LEThal family member (let-805)
Locus_29411_Transcript_1/1_Conf_1.000	130	0							
Locus_29412_Transcript_1/1_Conf_1.000	147	5	8.86E-14	EFO92682.1	83	80.1073	49	41	hypothetical protein CRE_16353
Locus_29413_Transcript_1/1_Conf_1.000	160	0							
Locus_29414_Transcript_1/1_Conf_1.000	163	20	6.43E-17	NP_001024837.1	88	90.5077	54	48	Gut granule LOss family member (glo-1)
Locus_29415_Transcript_1/1_Conf_1.000	158	0							
Locus_29416_Transcript_1/1_Conf_1.000	144	0							
Locus_29417_Transcript_1/1_Conf_1.000	141	0							
Locus_29418_Transcript_1/1_Conf_1.000	144	0							
Locus_29419_Transcript_1/1_Conf_1.000	128	9	3.90E-14	EFP02173.1	95	81.2629	42	40	CRE-MLT-7 protein
Locus_2942_Transcript_1/1_Conf_1.000	902	20	2.04E-58	NP_492120.1	86	230.335	146	126	Methylmalonyl-CoA Epimerase family member (mce-1)
Locus_29420_Transcript_1/1_Conf_1.000	146	20	1.67E-20	XP_002916766.1	100	102.449	48	48	PREDICTED: ubiquitin thioesterase OTUB1-like
Locus_29421_Transcript_1/1_Conf_1.000	263	20	1.59E-15	XP_001898877.1	69	85.8853	86	60	oxidoreductase, short chain dehydrogenase/reductase family protein
Locus_29422_Transcript_1/1_Conf_1.000	146	0							
Locus_29423_Transcript_1/1_Conf_1.000	149	0							
Locus_29424_Transcript_1/1_Conf_1.000	147	1	4.10E-19	XP_002825155.1	95	97.8265	48	46	PREDICTED: hypothetical protein LOC100447004
Locus_29425_Transcript_1/1_Conf_1.000	144	0							
Locus_29426_Transcript_1/1_Conf_1.000	133	0							
Locus_29427_Transcript_1/1_Conf_1.000	150	0							
Locus_29428_Transcript_1/1_Conf_1.000	198	0							
Locus_29429_Transcript_1/1_Conf_1.000	270	0							

Locus_2943_Transcript_1/1_Conf_1.000	1329	20	2.51E-131	NP_508509.3	76	473.396	417	320	hypothetical protein Y41G9A.3
Locus_29430_Transcript_1/1_Conf_1.000	131	0							
Locus_29431_Transcript_1/1_Conf_1.000	129	2	2.13E-04	NP_509266.1	73	48.9062	41	30	hypothetical protein F48E3.2
Locus_29432_Transcript_1/1_Conf_1.000	140	0							
Locus_29433_Transcript_1/1_Conf_1.000	133	0							
Locus_29434_Transcript_1/1_Conf_1.000	129	0							
Locus_29435_Transcript_1/1_Conf_1.000	136	0							
Locus_29436_Transcript_1/1_Conf_1.000	144	0							
Locus_29437_Transcript_1/1_Conf_1.000	128	0							
Locus_29438_Transcript_1/1_Conf_1.000	226	0							
Locus_29439_Transcript_1/1_Conf_1.000	151	20	3.71E-12	NP_492786.1	83	74.7146	49	41	Temporarily Assigned Gene name family member (tag-344)
Locus_2944_Transcript_1/2_Conf_1.000	1035	20	7.40E-106	XP_002631598.1	76	388.267	346	265	Hypothetical protein CBG20779
Locus_2944_Transcript_2/2_Conf_1.000	1035	20	7.40E-106	XP_002631598.1	76	388.267	346	265	Hypothetical protein CBG20779
Locus_29440_Transcript_1/1_Conf_1.000	136	0							
Locus_29441_Transcript_1/1_Conf_1.000	166	0							
Locus_29442_Transcript_1/1_Conf_1.000	159	0							
Locus_29443_Transcript_1/1_Conf_1.000	132	2	9.85E-10	XP_002637526.1	80	66.6254	42	34	Hypothetical protein CBG19249
Locus_29444_Transcript_1/1_Conf_1.000	146	0							
Locus_29445_Transcript_1/1_Conf_1.000	128	2	1.81E-11	NP_508818.1	100	72.4034	37	37	hypothetical protein F43C9.2
Locus_29446_Transcript_1/1_Conf_1.000	142	0							
Locus_29447_Transcript_1/1_Conf_1.000	150	0							
Locus_29448_Transcript_1/1_Conf_1.000	167	0							
Locus_29449_Transcript_1/1_Conf_1.000	173	20	5.21E-27	XP_002930168.1	100	124.02	57	57	PREDICTED: eukaryotic translation initiation factor 3 subunit B-like, partial
Locus_2945_Transcript_1/1_Conf_1.000	1586	20	1.85E-147	NP_001021972.1	80	527.324	405	327	DeHydrogenases, Short chain family member (dhs-6)
Locus_29450_Transcript_1/1_Conf_1.000	136	0							
Locus_29451_Transcript_1/1_Conf_1.000	173	0							

Locus_29452_Transcript_1/1_Conf_1.000	141	0							
Locus_29453_Transcript_1/1_Conf_1.000	144	0							
Locus_29454_Transcript_1/1_Conf_1.000	180	0							
Locus_29455_Transcript_1/1_Conf_1.000	168	0							
Locus_29456_Transcript_1/1_Conf_1.000	134	0							
Locus_29457_Transcript_1/1_Conf_1.000	141	0							
Locus_29458_Transcript_1/1_Conf_1.000	139	0							
Locus_29459_Transcript_1/1_Conf_1.000	395	20	2.93E-17	XP_002633547.1	54	91.6633	131	71	C. briggsae CBR-TRY-3 protein
Locus_2946_Transcript_1/1_Conf_1.000	1299	20	9.24E-131	XP_002634340.1	89	471.47	288	257	Hypothetical protein CBG17684
Locus_29460_Transcript_1/1_Conf_1.000	149	4	1.15E-13	XP_002630298.1	93	79.7221	49	46	C. briggsae CBR-LTD-1 protein
Locus_29461_Transcript_1/1_Conf_1.000	164	20	4.47E-18	XP_002636657.1	94	94.3597	54	51	Hypothetical protein CBG23368
Locus_29462_Transcript_1/1_Conf_1.000	211	0							
Locus_29463_Transcript_1/1_Conf_1.000	188	0							

Locus_29464_Transcript_1/1_Conf_1.000	167	20	4.14E-24	XP_001098693.2	100	114.39	55	55	PREDICTED: annexin A1 isoform 4
Locus_29465_Transcript_1/1_Conf_1.000	194	0							
Locus_29466_Transcript_1/1_Conf_1.000	164	0							
Locus_29467_Transcript_1/1_Conf_1.000	247	0							
Locus_29468_Transcript_1/1_Conf_1.000	149	0							
Locus_29469_Transcript_1/1_Conf_1.000	132	0							
Locus_2947_Transcript_1/1_Conf_1.000	822	20	6.39E-53	AAN11402.1	68	211.846	198	135	secreted-protein 1 precursor
Locus_29470_Transcript_1/1_Conf_1.000	149	13	1.01E-09	EFP10630.1	75	66.6254	48	36	hypothetical protein CRE_01169
Locus_29471_Transcript_1/1_Conf_1.000	143	0							
Locus_29472_Transcript_1/1_Conf_1.000	224	0							
Locus_29473_Transcript_1/1_Conf_1.000	136	12	8.34E-09	EFO86758.1	80	63.5438	45	36	hypothetical protein CRE_04840
Locus_29474_Transcript_1/1_Conf_1.000	190	0							
Locus_29475_Transcript_1/1_Conf_1.000	148	0							
Locus_29476_Transcript_1/1_Conf_1.000	178	0							
Locus_29477_Transcript_1/1_Conf_1.000	223	5	4.68E-15	XP_001899094.1	76	84.3445	59	45	hypothetical protein
Locus_29478_Transcript_1/1_Conf_1.000	134	20	3.06E-19	EFO28104.1	100	98.2117	44	44	hypothetical protein LOAG_00390
Locus_29479_Transcript_1/1_Conf_1.000	168	0							

Locus_2948_Transcript_1/1_Conf_1.000	915	20	1.49E-96	EFO19762.1	83	357.066	267	224	serologically defined breast cancer antigen NY-BR-99
Locus_29480_Transcript_1/1_Conf_1.000	170	0							
Locus_29481_Transcript_1/1_Conf_1.000	130	0							
Locus_29482_Transcript_1/1_Conf_1.000	134	0							
Locus_29483_Transcript_1/1_Conf_1.000	132	0							
Locus_29484_Transcript_1/1_Conf_1.000	219	5	1.32E-09	EFP06952.1	63	66.2402	71	45	CRE-RHGF-2 protein
Locus_29485_Transcript_1/1_Conf_1.000	266	0							
Locus_29486_Transcript_1/1_Conf_1.000	148	0							
Locus_29487_Transcript_1/1_Conf_1.000	136	0							
Locus_29488_Transcript_1/1_Conf_1.000	228	20	5.48E-24	EFO99702.1	86	114.005	73	63	hypothetical protein CRE_18564
Locus_29489_Transcript_1/1_Conf_1.000	286	7	1.40E-35	NP_001022641.1	84	152.525	93	79	LEThal family member (let-805)
Locus_2949_Transcript_1/1_Conf_1.000	655	20	2.88E-91	EFO24653.1	93	338.576	186	173	WD40 repeat protein
Locus_29490_Transcript_1/1_Conf_1.000	172	0							
Locus_29491_Transcript_1/1_Conf_1.000	132	0							
Locus_29492_Transcript_1/1_Conf_1.000	129	0							
Locus_29493_Transcript_1/1_Conf_1.000	142	1	6.13E-04	CAL57182.1	61	47.3654	47	29	unnamed protein product
Locus_29494_Transcript_1/1_Conf_1.000	141	0							
Locus_29495_Transcript_1/1_Conf_1.000	138	10	1.51E-10	NP_508761.3	86	69.3218	44	38	hypothetical protein F15A8.6
Locus_29496_Transcript_1/1_Conf_1.000	144	0							
Locus_29497_Transcript_1/1_Conf_1.000	152	0							
Locus_29498_Transcript_1/1_Conf_1.000	138	0							
Locus_29499_Transcript_1/1_Conf_1.000	135	0							
Locus_295_Transcript_1/1_Conf_1.000	2050	20	2.25E-127	XP_002633790.1	58	461.07	615	361	C. briggsae CBR-PIS-1 protein
Locus_2950_Transcript_1/1_Conf_1.000	129	0							
Locus_29500_Transcript_1/1_Conf_1.000	159	0							
Locus_29501_Transcript_1/1_Conf_1.000	139	0							
Locus_29502_Transcript_1/1_Conf_1.000	143	0							
Locus_29503_Transcript_1/1_Conf_1.000	156	0							
Locus_29504_Transcript_1/1_Conf_1.000	136	0							
Locus_29505_Transcript_1/1_Conf_1.000	128	0							
Locus_29506_Transcript_1/1_Conf_1.000	176	0							
Locus_29507_Transcript_1/1_Conf_1.000	153	4	7.95E-07	XP_002735800.1	62	56.9954	48	30	PREDICTED: matriptase-like

Locus_29508_Transcript_1/1_Conf_1.000	140	0							
Locus_29509_Transcript_1/1_Conf_1.000	142	0							
Locus_2951_Transcript_1/4_Conf_0.250	183	20	5.90E-26	AAG44787.1	100	120.553	60	60	AF271776_1DC48
Locus_2951_Transcript_2/4_Conf_0.250	225	20	4.33E-29	AAG44787.1	97	130.954	69	67	AF271776_1DC48
Locus_2951_Transcript_3/4_Conf_0.375	1476	20	2.39E-109	ACK55735.1	96	400.593	257	249	cytochrome c oxidase subunit III
Locus_2951_Transcript_4/4_Conf_0.375	1476	20	1.31E-107	ACK55735.1	96	394.815	257	249	cytochrome c oxidase subunit III
Locus_29510_Transcript_1/1_Conf_1.000	128	0							
Locus_29511_Transcript_1/1_Conf_1.000	232	20	2.71E-23	EFO87048.1	85	111.694	77	66	hypothetical protein CRE_19388
Locus_29512_Transcript_1/1_Conf_1.000	168	3	7.06E-16	NP_001023496.1	85	87.0409	55	47	L1 CAM ADhesion molecule homolog family member (lad-2)
Locus_29513_Transcript_1/1_Conf_1.000	222	6	2.81E-36	XP_002644616.1	97	154.836	73	71	Hypothetical protein CBG14575
Locus_29514_Transcript_1/1_Conf_1.000	138	0							
Locus_29515_Transcript_1/1_Conf_1.000	133	5	2.34E-11	CAR63575.1	88	72.0182	44	39	hypothetical protein
Locus_29516_Transcript_1/1_Conf_1.000	160	0							
Locus_29517_Transcript_1/1_Conf_1.000	141	0							
Locus_29518_Transcript_1/1_Conf_1.000	146	0							
Locus_29519_Transcript_1/1_Conf_1.000	139	0							
Locus_2952_Transcript_1/1_Conf_1.000	609	20	5.65E-40	2G64	88	167.933	108	96	Structure Of Caenorhabditis Elegans 6-Pyruvoyl Tetrahydropterin Synthase
Locus_29520_Transcript_1/1_Conf_1.000	159	5	1.07E-11	NP_496794.1	84	73.1738	50	42	hypothetical protein F32A11.1
Locus_29521_Transcript_1/1_Conf_1.000	138	1	6.59E-06	CAC51085.1	80	53.9138	35	28	hypothetical protein
Locus_29522_Transcript_1/1_Conf_1.000	132	0							
Locus_29523_Transcript_1/1_Conf_1.000	128	0							
Locus_29524_Transcript_1/1_Conf_1.000	129	0							
Locus_29525_Transcript_1/1_Conf_1.000	141	0							
Locus_29526_Transcript_1/1_Conf_1.000	153	0							

Locus_29527_Transcript_1/1_Conf_1.000	162	20	2.70E-23	NP_076869.1	100	111.694	53	53	vitamin K epoxide reductase complex subunit 1 isoform 1
Locus_29528_Transcript_1/1_Conf_1.000	159	20	2.30E-14	NP_501955.2	81	82.0333	53	43	Eph(F)riN family member (efn-2)
Locus_29529_Transcript_1/1_Conf_1.000	197	0							
Locus_2953_Transcript_1/1_Conf_1.000	504	0							
Locus_29530_Transcript_1/1_Conf_1.000	149	0							
Locus_29531_Transcript_1/1_Conf_1.000	141	0							
Locus_29532_Transcript_1/1_Conf_1.000	177	20	3.37E-18	NP_507242.1	84	94.7449	58	49	PseudoUridine Synthase family member (pus-1)
Locus_29533_Transcript_1/1_Conf_1.000	232	20	1.34E-22	NP_001021650.1	78	109.383	76	60	HaMmeRhead embryonic lethal family member (hmr-1)
Locus_29534_Transcript_1/1_Conf_1.000	146	6	2.42E-11	EFO84735.1	92	72.0182	39	36	CRE-DYB-1 protein
Locus_29535_Transcript_1/1_Conf_1.000	130	20	8.94E-19	EFO97377.1	100	96.6709	43	43	CRE-TBB-4 protein
Locus_29536_Transcript_1/1_Conf_1.000	261	2	4.33E-13	NP_493923.2	56	77.7962	102	58	hypothetical protein T23F4.2
Locus_29537_Transcript_1/1_Conf_1.000	138	7	3.25E-13	XP_002631460.1	86	78.1814	45	39	Hypothetical protein CBG20612
Locus_29538_Transcript_1/1_Conf_1.000	135	0							
Locus_29539_Transcript_1/1_Conf_1.000	246	0							
Locus_2954_Transcript_1/2_Conf_1.000	987	20	5.32E-42	EFO25643.1	59	176.022	271	162	3' exoribonuclease

Locus_2954_Transcript_2/2_Conf_1.000	987	20	5.32E-42	EFO25643.1	59	176.022	271	162	3' exoribonuclease
Locus_29540_Transcript_1/1_Conf_1.000	136	0							
Locus_29541_Transcript_1/1_Conf_1.000	202	20	3.64E-28	EFP06704.1	94	127.872	67	63	CRE-PLC-3 protein
Locus_29542_Transcript_1/1_Conf_1.000	166	20	4.43E-26	XP_002913893.1	100	120.939	55	55	PREDICTED: LOW QUALITY PROTEIN: secreted frizzled-related protein 2-like
Locus_29543_Transcript_1/1_Conf_1.000	193	3	1.36E-06	NP_505267.1	82	56.225	52	43	Regulator of Presynaptic Morphology family member (rpm-1)
Locus_29544_Transcript_1/1_Conf_1.000	156	0							
Locus_29545_Transcript_1/1_Conf_1.000	178	0							
Locus_29546_Transcript_1/1_Conf_1.000	202	0							
Locus_29547_Transcript_1/1_Conf_1.000	219	0							
Locus_29548_Transcript_1/1_Conf_1.000	133	0							
Locus_29549_Transcript_1/1_Conf_1.000	132	0							
Locus_2955_Transcript_1/1_Conf_1.000	271	0							
Locus_29550_Transcript_1/1_Conf_1.000	221	0							
Locus_29551_Transcript_1/1_Conf_1.000	160	20	3.78E-17	XP_002640668.1	95	91.2781	44	42	C. briggsae CBR-UNC-54 protein

Locus_29552_Transcript_1/1_Conf_1.000	157	0							
Locus_29553_Transcript_1/1_Conf_1.000	147	0							
Locus_29554_Transcript_1/1_Conf_1.000	135	0							
Locus_29555_Transcript_1/1_Conf_1.000	156	0							
Locus_29556_Transcript_1/1_Conf_1.000	193	20	2.32E-06	CAG06540.1	61	55.4546	62	38	unnamed protein product
Locus_29557_Transcript_1/1_Conf_1.000	130	0							
Locus_29558_Transcript_1/1_Conf_1.000	138	13	3.37E-10	ABN58658.1	78	68.1662	41	32	lysozyme 1
Locus_29559_Transcript_1/1_Conf_1.000	166	0							
Locus_2956_Transcript_1/1_Conf_1.000	199	0							
Locus_29560_Transcript_1/1_Conf_1.000	199	0							
Locus_29561_Transcript_1/1_Conf_1.000	146	0							
Locus_29562_Transcript_1/1_Conf_1.000	277	20	5.22E-11	XP_002750114.1	74	70.8626	58	43	PREDICTED: tRNA (cytosine-5-)-methyltransferase isoform 3
Locus_29563_Transcript_1/1_Conf_1.000	165	0							
Locus_29564_Transcript_1/1_Conf_1.000	155	0							
Locus_29565_Transcript_1/1_Conf_1.000	143	0							

Locus_29566_Transcript_1/1_Conf_1.000	356	20	1.92E-29	XP_002631218.1	73	132.109	113	83	Hypothetical protein CBG03015
Locus_29567_Transcript_1/1_Conf_1.000	150	0							
Locus_29568_Transcript_1/1_Conf_1.000	145	5	2.12E-07	NP_505312.1	80	58.9214	40	32	hypothetical protein T19A5.1
Locus_29569_Transcript_1/1_Conf_1.000	133	20	6.61E-14	XP_002786436.1	86	80.4925	44	38	DNA topoisomerase 2-alpha, putative
Locus_2957_Transcript_1/1_Conf_1.000	664	0							
Locus_29570_Transcript_1/1_Conf_1.000	199	20	1.86E-32	XP_002929659.1	100	142.124	66	66	PREDICTED: GTP-binding nuclear protein Ran-like, partial
Locus_29571_Transcript_1/1_Conf_1.000	138	0							
Locus_29572_Transcript_1/1_Conf_1.000	146	0							
Locus_29573_Transcript_1/1_Conf_1.000	154	0							
Locus_29574_Transcript_1/1_Conf_1.000	158	0							
Locus_29575_Transcript_1/1_Conf_1.000	203	4	1.44E-08	NP_871954.2	90	62.7734	43	39	hypothetical protein C50D2.9
Locus_29576_Transcript_1/1_Conf_1.000	143	0							
Locus_29577_Transcript_1/1_Conf_1.000	160	0							
Locus_29578_Transcript_1/1_Conf_1.000	195	0							
Locus_29579_Transcript_1/1_Conf_1.000	176	0							

Locus_2958_Transcript_1/1_Conf_1.000	1968	20	4.74E-151	NP_498626.2	73	539.65	491	362	hypothetical protein F08F8.2
Locus_29580_Transcript_1/1_Conf_1.000	188	4	4.25E-08	XP_002640372.1	74	61.2326	58	43	Hypothetical protein CBG20279
Locus_29581_Transcript_1/1_Conf_1.000	136	2	1.51E-10	XP_002633945.1	91	69.3218	37	34	C. briggsae CBR-ELO-1 protein
Locus_29582_Transcript_1/1_Conf_1.000	138	3	1.51E-10	EFO98925.1	76	69.3218	46	35	hypothetical protein CRE_19702
Locus_29583_Transcript_1/1_Conf_1.000	135	20	7.79E-15	XP_002642327.1	91	83.5741	45	41	C. briggsae CBR-TAT-3 protein
Locus_29584_Transcript_1/1_Conf_1.000	134	0							
Locus_29585_Transcript_1/1_Conf_1.000	147	4	1.72E-09	NP_491864.2	82	65.855	50	41	hypothetical protein K06A5.8
Locus_29586_Transcript_1/1_Conf_1.000	132	0							
Locus_29587_Transcript_1/1_Conf_1.000	171	5	3.29E-05	NP_001122986.1	63	51.6026	47	30	hypothetical protein R07B7.9
Locus_29588_Transcript_1/1_Conf_1.000	168	0							
Locus_29589_Transcript_1/1_Conf_1.000	172	20	8.32E-17	XP_002640829.1	89	90.1225	56	50	C. briggsae CBR-ADS-1 protein
Locus_2959_Transcript_1/1_Conf_1.000	1526	20	2.98E-70	NP_492634.1	59	270.781	393	235	Temporarily Assigned Gene name family member (tag-179)
Locus_29590_Transcript_1/1_Conf_1.000	136	0							
Locus_29591_Transcript_1/1_Conf_1.000	184	0							
Locus_29592_Transcript_1/1_Conf_1.000	184	20	3.14E-11	XP_002634427.1	62	71.633	61	38	Hypothetical protein CBG04438
Locus_29593_Transcript_1/1_Conf_1.000	121	0							
Locus_29594_Transcript_1/1_Conf_1.000	145	4	7.52E-13	EFP12451.1	86	77.0258	45	39	CRE-SET-18 protein
Locus_29595_Transcript_1/1_Conf_1.000	135	13	1.42E-16	EFP02173.1	97	89.3521	44	43	CRE-MLT-7 protein
Locus_29596_Transcript_1/1_Conf_1.000	200	0							
Locus_29597_Transcript_1/1_Conf_1.000	163	2	1.30E-09	NP_492348.1	75	66.2402	56	42	hypothetical protein K07A12.2
Locus_29598_Transcript_1/1_Conf_1.000	129	0							
Locus_29599_Transcript_1/1_Conf_1.000	175	0							

Locus_296_Transcript_1/2_Conf_1.000	2474	20	0	XP_002639316.1	83	1132.47	805	676	C. briggsae CBR-MCM-4 protein
Locus_296_Transcript_2/2_Conf_1.000	2162	20	0	XP_002639316.1	87	1090.1	722	631	C. briggsae CBR-MCM-4 protein
Locus_2960_Transcript_1/1_Conf_1.000	2106	20	2.91E-170	XP_002639569.1	64	603.594	721	466	Hypothetical protein CBG04200
Locus_29600_Transcript_1/1_Conf_1.000	132	2	1.33E-06	XP_002630033.1	79	56.225	43	34	C. briggsae CBR-PUF-12 protein
Locus_29601_Transcript_1/1_Conf_1.000	134	1	2.13E-04	NP_506714.1	68	48.9062	44	30	hypothetical protein C01G10.9
Locus_29602_Transcript_1/1_Conf_1.000	209	3	2.35E-11	AAY79430.1	90	72.0182	42	38	TGF-beta signaling molecule precursor
Locus_29603_Transcript_1/1_Conf_1.000	130	0							
Locus_29604_Transcript_1/1_Conf_1.000	244	0							
Locus_29605_Transcript_1/1_Conf_1.000	141	1	3.60E-04	CAX83711.1	65	48.1358	44	29	endonuclease-reverse transcriptase
Locus_29606_Transcript_1/1_Conf_1.000	142	20	1.23E-20	XP_001149559.1	100	102.834	46	46	PREDICTED: similar to Rer1 protein
Locus_29607_Transcript_1/1_Conf_1.000	179	0							

Locus_29608_Transcript_1/1_Conf_1.000	129	20	5.61E-13	EFO18101.1	95	77.411	42	40	KIF16B
Locus_29609_Transcript_1/1_Conf_1.000	143	0							
Locus_2961_Transcript_1/1_Conf_1.000	713	20	5.29E-76	XP_002642217.1	82	288.115	199	165	C. briggsae CBR-MMAB-1 protein
Locus_29610_Transcript_1/1_Conf_1.000	161	0							
Locus_29611_Transcript_1/1_Conf_1.000	135	0							
Locus_29612_Transcript_1/1_Conf_1.000	136	0							
Locus_29613_Transcript_1/1_Conf_1.000	167	0							
Locus_29614_Transcript_1/1_Conf_1.000	107	0							
Locus_29615_Transcript_1/1_Conf_1.000	354	20	1.33E-30	XP_002643095.1	71	135.961	117	84	C. briggsae CBR-GLY-11 protein
Locus_29616_Transcript_1/1_Conf_1.000	136	5	1.92E-13	XP_002645089.1	95	78.9518	44	42	Hypothetical protein CBG16766
Locus_29617_Transcript_1/1_Conf_1.000	137	0							
Locus_29618_Transcript_1/1_Conf_1.000	139	9	9.17E-16	XP_002633945.1	93	86.6557	45	42	C. briggsae CBR-ELO-1 protein
Locus_29619_Transcript_1/1_Conf_1.000	136	4	9.82E-10	NP_501127.2	88	66.6254	45	40	RNA Polymerase, Class III (C) family member (rpc-1)
Locus_2962_Transcript_1/1_Conf_1.000	1030	6	7.43E-58	NP_001023770.1	60	228.794	342	208	ACyLtransferase-like family member (acl-6)
Locus_29620_Transcript_1/1_Conf_1.000	189	0							
Locus_29621_Transcript_1/1_Conf_1.000	203	0							
Locus_29622_Transcript_1/1_Conf_1.000	167	20	4.44E-26	CAX65068.1	96	120.939	55	53	C. elegans protein K08C7.3d, confirmed by transcript evidence
Locus_29623_Transcript_1/1_Conf_1.000	143	0							
Locus_29624_Transcript_1/1_Conf_1.000	152	20	1.46E-08	EFO95751.1	77	62.7734	49	38	hypothetical protein CRE_13895
Locus_29625_Transcript_1/1_Conf_1.000	209	20	2.77E-20	EFP00995.1	84	101.679	69	58	CRE-PIF-1 protein
Locus_29626_Transcript_1/1_Conf_1.000	175	20	8.56E-22	NP_502367.2	91	106.686	58	53	hypothetical protein F28D1.9
Locus_29627_Transcript_1/1_Conf_1.000	174	0							
Locus_29628_Transcript_1/1_Conf_1.000	157	1	1.65E-04	EFO19094.1	73	49.2914	45	33	hypothetical protein LOAG_09400

Locus_29629_Transcript_1/1_Conf_1.000	150	0							
Locus_2963_Transcript_1/1_Conf_1.000	324	5	3.42E-10	XP_002642911.1	80	68.1662	82	66	Hypothetical protein CBG15186
Locus_29630_Transcript_1/1_Conf_1.000	130	0							
Locus_29631_Transcript_1/1_Conf_1.000	185	1	2.57E-21	XP_002805791.1	98	105.145	52	51	PREDICTED: hypothetical protein LOC100427250
Locus_29632_Transcript_1/1_Conf_1.000	132	0							
Locus_29633_Transcript_1/1_Conf_1.000	135	1	4.14E-08	EFO20077.1	73	61.2326	45	33	hypothetical protein LOAG_08413
Locus_29634_Transcript_1/1_Conf_1.000	177	0							
Locus_29635_Transcript_1/1_Conf_1.000	214	6	9.80E-18	XP_002636520.1	79	93.2041	67	53	Hypothetical protein CBG23201
Locus_29636_Transcript_1/1_Conf_1.000	135	0							
Locus_29637_Transcript_1/1_Conf_1.000	212	19	9.81E-26	EFO97239.1	86	119.783	68	59	hypothetical protein CRE_16805
Locus_29638_Transcript_1/1_Conf_1.000	190	0							
Locus_29639_Transcript_1/1_Conf_1.000	152	0							
Locus_2964_Transcript_1/1_Conf_1.000	742	20	4.66E-25	NP_501774.1	86	119.013	72	62	hypothetical protein K07F5.15
Locus_29640_Transcript_1/1_Conf_1.000	145	0							
Locus_29641_Transcript_1/1_Conf_1.000	213	0							
Locus_29642_Transcript_1/1_Conf_1.000	152	7	2.40E-11	NP_509417.2	74	72.0182	50	37	hypothetical protein F40B5.2
Locus_29643_Transcript_1/1_Conf_1.000	154	0							
Locus_29644_Transcript_1/1_Conf_1.000	149	0							
Locus_29645_Transcript_1/1_Conf_1.000	132	0							
Locus_29646_Transcript_1/1_Conf_1.000	194	20	5.32E-19	XP_002634345.1	85	97.4413	64	55	Hypothetical protein CBG17689
Locus_29647_Transcript_1/1_Conf_1.000	154	4	4.23E-08	EFO20018.1	68	61.2326	50	34	negative elongation factor C/D
Locus_29648_Transcript_1/1_Conf_1.000	133	7	4.59E-07	AAN11401.1	74	57.7658	43	32	metalloprotease 1 precursor
Locus_29649_Transcript_1/1_Conf_1.000	207	20	1.73E-30	XP_002924002.1	100	135.576	69	69	PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like
Locus_2965_Transcript_1/1_Conf_1.000	162	1	9.62E-05	AAO63576.1	61	50.0618	55	34	secreted protein 4 precursor
Locus_29650_Transcript_1/1_Conf_1.000	133	0							

Locus_29651_Transcript_1/1_Conf_1.000	208	20	2.04E-23	CAQ09841.1	100	112.079	69	69	major histocompatibility complex, class II, DM alpha
Locus_29652_Transcript_1/1_Conf_1.000	135	0							
Locus_29653_Transcript_1/1_Conf_1.000	143	8	4.23E-13	EFO24387.1	88	77.7962	44	39	hypothetical protein LOAG_04094
Locus_29654_Transcript_1/1_Conf_1.000	160	0							
Locus_29655_Transcript_1/1_Conf_1.000	136	3	8.63E-06	EFO24692.1	74	53.5286	39	29	protein-tyrosine phosphatase
Locus_29656_Transcript_1/1_Conf_1.000	154	1	4.84E-04	NP_495874.2	61	47.7506	49	30	hypothetical protein F07H5.8
Locus_29657_Transcript_1/1_Conf_1.000	142	0							
Locus_29658_Transcript_1/1_Conf_1.000	147	0							
Locus_29659_Transcript_1/1_Conf_1.000	130	0							
Locus_2966_Transcript_1/1_Conf_1.000	389	20	3.67E-65	ADF56000.1	96	250.751	129	125	nicotinic acetylcholine receptor non-alpha subunit 29.4
Locus_29660_Transcript_1/1_Conf_1.000	143	19	3.04E-11	EFO89653.1	86	71.633	46	40	CRE-SER-7 protein
Locus_29661_Transcript_1/1_Conf_1.000	191	0							
Locus_29662_Transcript_1/1_Conf_1.000	191	0							
Locus_29663_Transcript_1/1_Conf_1.000	154	0							
Locus_29664_Transcript_1/1_Conf_1.000	143	0							
Locus_29665_Transcript_1/1_Conf_1.000	138	0							
Locus_29666_Transcript_1/1_Conf_1.000	145	0							
Locus_29667_Transcript_1/1_Conf_1.000	149	0							
Locus_29668_Transcript_1/1_Conf_1.000	162	0							
Locus_29669_Transcript_1/1_Conf_1.000	153	5	8.79E-06	XP_002639840.1	69	53.5286	46	32	C. briggsae CBR-ANC-1 protein
Locus_2967_Transcript_1/1_Conf_1.000	2217	20	2.32E-109	XP_001895587.1	56	401.364	630	358	Bromodomain containing protein
Locus_29670_Transcript_1/1_Conf_1.000	190	20	2.02E-18	NP_001129835.1	82	95.5153	63	52	Novel Channel type/putative Nematode CAlcium channel family member (nca-2)
Locus_29671_Transcript_1/1_Conf_1.000	207	2	9.22E-08	NP_502746.1	71	60.077	69	49	hypothetical protein Y67A10A.9

Locus_29672_Transcript_1/1_Conf_1.000	187	20	1.01E-09	XP_001902366.1	64	66.6254	62	40	RIKEN cDNA 5730509K17 gene
Locus_29673_Transcript_1/1_Conf_1.000	132	0							
Locus_29674_Transcript_1/1_Conf_1.000	276	0							
Locus_29675_Transcript_1/1_Conf_1.000	132	0							
Locus_29676_Transcript_1/1_Conf_1.000	147	0							
Locus_29677_Transcript_1/1_Conf_1.000	138	20	1.16E-18	XP_002923578.1	100	96.2857	45	45	PREDICTED: polypyrimidine tract-binding protein 1-like
Locus_29678_Transcript_1/1_Conf_1.000	136	0							
Locus_29679_Transcript_1/1_Conf_1.000	175	0							
Locus_2968_Transcript_1/1_Conf_1.000	2001	20	0	XP_002632121.1	83	641.343	454	381	Hypothetical protein CBG06976
Locus_29680_Transcript_1/1_Conf_1.000	181	3	5.56E-05	XP_002633837.1	55	50.8322	59	33	Hypothetical protein CBG19875
Locus_29681_Transcript_1/1_Conf_1.000	141	0							
Locus_29682_Transcript_1/1_Conf_1.000	154	0							
Locus_29683_Transcript_1/1_Conf_1.000	140	14	1.05E-11	NP_001024131.1	92	73.1738	41	38	Peroxisomal Membrane Protein related family member (pmp-5)
Locus_29684_Transcript_1/1_Conf_1.000	132	0							
Locus_29685_Transcript_1/1_Conf_1.000	150	3	1.50E-05	NP_741539.2	83	52.7582	42	35	hypothetical protein C18C4.5
Locus_29686_Transcript_1/1_Conf_1.000	139	0							
Locus_29687_Transcript_1/1_Conf_1.000	144	0							
Locus_29688_Transcript_1/1_Conf_1.000	178	0							
Locus_29689_Transcript_1/1_Conf_1.000	149	0							
Locus_2969_Transcript_1/1_Conf_1.000	743	20	1.75E-56	XP_002634132.1	95	223.402	120	115	C. briggsae CBR-HTZ-1 protein

Locus_29690_Transcript_1/1_Conf_1.000	129	7	8.66E-14	XP_002640973.1	95	80.1073	43	41	C. briggsae CBR-SNF-6 protein
Locus_29691_Transcript_1/1_Conf_1.000	180	0							
Locus_29692_Transcript_1/1_Conf_1.000	140	0							
Locus_29693_Transcript_1/1_Conf_1.000	256	20	1.96E-21	XP_002636781.1	77	105.531	79	61	Hypothetical protein CBG23516
Locus_29694_Transcript_1/1_Conf_1.000	159	4	1.76E-22	EFO96815.1	96	108.997	51	49	CRE-NPR-19 protein
Locus_29695_Transcript_1/1_Conf_1.000	142	0							
Locus_29696_Transcript_1/1_Conf_1.000	220	0							
Locus_29697_Transcript_1/1_Conf_1.000	238	0							
Locus_29698_Transcript_1/1_Conf_1.000	153	0							
Locus_29699_Transcript_1/1_Conf_1.000	202	0							
Locus_297_Transcript_1/2_Conf_1.000	2730	20	0	NP_741403.2	86	1073.92	724	626	Dynamin Related Protein family member (drp-1)
Locus_297_Transcript_2/2_Conf_1.000	2718	20	0	NP_741403.2	86	1078.54	720	626	Dynamin Related Protein family member (drp-1)

Locus_2970_Transcript_1/1_Conf_1.000	797	20	5.69E-35	NP_504688.1	97	152.14	93	91	SyNaptoBrevin related family member (snb-1)
Locus_29700_Transcript_1/1_Conf_1.000	131	0							
Locus_29701_Transcript_1/1_Conf_1.000	131	0							
Locus_29702_Transcript_1/1_Conf_1.000	128	0							
Locus_29703_Transcript_1/1_Conf_1.000	176	0							
Locus_29704_Transcript_1/1_Conf_1.000	134	0							
Locus_29705_Transcript_1/1_Conf_1.000	142	0							
Locus_29706_Transcript_1/1_Conf_1.000	138	0							
Locus_29707_Transcript_1/1_Conf_1.000	148	0							
Locus_29708_Transcript_1/1_Conf_1.000	128	0							
Locus_29709_Transcript_1/1_Conf_1.000	146	20	7.50E-21	P02751.4	100	103.605	48	48	Fibronectin
Locus_2971_Transcript_1/1_Conf_1.000	814	5	1.78E-07	NP_495966.2	52	60.8474	84	44	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-95)
Locus_29710_Transcript_1/1_Conf_1.000	174	0							
Locus_29711_Transcript_1/1_Conf_1.000	180	9	2.40E-16	EFP10268.1	90	88.5817	55	50	hypothetical protein CRE_24096
Locus_29712_Transcript_1/1_Conf_1.000	128	0							
Locus_29713_Transcript_1/1_Conf_1.000	134	0							
Locus_29714_Transcript_1/1_Conf_1.000	211	8	3.38E-18	NP_001021988.1	82	94.7449	70	58	Epithelial Fusion Failure family member (eff-1)
Locus_29715_Transcript_1/1_Conf_1.000	129	0							

Locus_29716_Transcript_1/1_Conf_1.000	155	0							
Locus_29717_Transcript_1/1_Conf_1.000	270	20	9.22E-32	XP_002636599.1	89	139.813	89	80	Hypothetical protein CBG23298
Locus_29718_Transcript_1/1_Conf_1.000	157	0							
Locus_29719_Transcript_1/1_Conf_1.000	147	0							
Locus_2972_Transcript_1/1_Conf_1.000	992	20	9.30E-95	XP_001896907.1	99	351.288	172	171	RAS-like GTP-binding protein RhoA
Locus_29720_Transcript_1/1_Conf_1.000	133	0							
Locus_29721_Transcript_1/1_Conf_1.000	147	0							
Locus_29722_Transcript_1/1_Conf_1.000	134	0							
Locus_29723_Transcript_1/1_Conf_1.000	128	0							
Locus_29724_Transcript_1/1_Conf_1.000	133	0							
Locus_29725_Transcript_1/1_Conf_1.000	159	1	3.68E-04	XP_002634048.1	69	48.1358	52	36	Hypothetical protein CBG01587
Locus_29726_Transcript_1/1_Conf_1.000	185	3	6.36E-12	EFP11317.1	72	73.9442	61	44	hypothetical protein CRE_30788
Locus_29727_Transcript_1/1_Conf_1.000	166	0							
Locus_29728_Transcript_1/1_Conf_1.000	162	0							
Locus_29729_Transcript_1/1_Conf_1.000	146	0							
Locus_2973_Transcript_1/1_Conf_1.000	387	20	4.38E-26	NP_493029.1	84	120.939	82	69	hypothetical protein R06C1.4
Locus_29730_Transcript_1/1_Conf_1.000	196	20	3.91E-30	XP_002931287.1	100	134.42	64	64	PREDICTED: filamin-A-like, partial
Locus_29731_Transcript_1/1_Conf_1.000	178	0							
Locus_29732_Transcript_1/1_Conf_1.000	132	0							
Locus_29733_Transcript_1/1_Conf_1.000	163	0							
Locus_29734_Transcript_1/1_Conf_1.000	196	0							
Locus_29735_Transcript_1/1_Conf_1.000	335	0							

Locus_29736_Transcript_1/1_Conf_1.000	155	20	2.32E-14	CAI99629.1	86	82.0333	51	44	beta-1,3-glucuronosyltransferase
Locus_29737_Transcript_1/1_Conf_1.000	194	0							
Locus_29738_Transcript_1/1_Conf_1.000	206	0							
Locus_29739_Transcript_1/1_Conf_1.000	137	0							
Locus_2974_Transcript_1/1_Conf_1.000	1713	20	0	EFO23631.1	81	676.781	494	405	nuclear matrix protein SNEV
Locus_29740_Transcript_1/1_Conf_1.000	395	20	1.45E-24	CAV31765.1	61	115.931	132	81	C. elegans protein C33B4.3c, partially confirmed by transcript evidence
Locus_29741_Transcript_1/1_Conf_1.000	136	0							
Locus_29742_Transcript_1/1_Conf_1.000	146	6	4.89E-04	EFP05634.1	70	47.7506	47	33	CRE-UNC-70 protein
Locus_29743_Transcript_1/1_Conf_1.000	149	0							
Locus_29744_Transcript_1/1_Conf_1.000	161	20	1.31E-09	EFO20785.1	73	66.2402	53	39	TKL/MLK/HH498 protein kinase
Locus_29745_Transcript_1/1_Conf_1.000	165	0							
Locus_29746_Transcript_1/1_Conf_1.000	144	0							
Locus_29747_Transcript_1/1_Conf_1.000	355	15	2.21E-17	XP_001894784.1	72	92.0485	98	71	glutaminase DH11.1
Locus_29748_Transcript_1/1_Conf_1.000	273	0							
Locus_29749_Transcript_1/1_Conf_1.000	178	0							
Locus_2975_Transcript_1/1_Conf_1.000	1291	20	0	NP_509821.1	90	669.848	420	378	hypothetical protein F47B10.1
Locus_29750_Transcript_1/1_Conf_1.000	145	0							
Locus_29751_Transcript_1/1_Conf_1.000	173	0							
Locus_29752_Transcript_1/1_Conf_1.000	151	0							
Locus_29753_Transcript_1/1_Conf_1.000	139	0							
Locus_29754_Transcript_1/1_Conf_1.000	239	0							
Locus_29755_Transcript_1/1_Conf_1.000	212	5	3.39E-10	EFO19747.1	71	68.1662	70	50	hypothetical protein LOAG_08744
Locus_29756_Transcript_1/1_Conf_1.000	132	0							
Locus_29757_Transcript_1/1_Conf_1.000	155	5	5.70E-13	EFO85660.1	88	77.411	50	44	CRE-DEP-1 protein
Locus_29758_Transcript_1/1_Conf_1.000	199	3	3.32E-13	EFO85627.1	72	78.1814	66	48	hypothetical protein CRE_01589
Locus_29759_Transcript_1/1_Conf_1.000	131	0							

Locus_2976_Transcript_1/1_Conf_1.000	1670	20	2.18E-178	NP_495449.1	91	630.172	370	338	hypothetical protein ZK1127.10
Locus_29760_Transcript_1/1_Conf_1.000	130	2	4.14E-16	NP_495241.1	97	87.8113	43	42	hypothetical protein C30B5.5
Locus_29761_Transcript_1/1_Conf_1.000	162	3	1.94E-05	NP_001129867.1	84	52.373	51	43	hypothetical protein T05E11.2
Locus_29762_Transcript_1/1_Conf_1.000	233	0							
Locus_29763_Transcript_1/1_Conf_1.000	243	0							
Locus_29764_Transcript_1/1_Conf_1.000	130	0							
Locus_29765_Transcript_1/1_Conf_1.000	128	8	2.52E-13	NP_501548.2	90	78.5666	42	38	hypothetical protein C27B7.7
Locus_29766_Transcript_1/1_Conf_1.000	206	0							
Locus_29767_Transcript_1/1_Conf_1.000	158	3	4.22E-08	EFO86016.1	71	61.2326	49	35	CRE-SET-14 protein
Locus_29768_Transcript_1/1_Conf_1.000	143	0							
Locus_29769_Transcript_1/1_Conf_1.000	231	0							
Locus_2977_Transcript_1/1_Conf_1.000	1281	20	5.79E-61	XP_002405164.1	50	239.58	436	222	conserved hypothetical protein

Locus_29770_Transcript_1/1_Conf_1.000	179	20	1.32E-14	XP_002630011.1	77	82.8037	59	46	Hypothetical protein CBG13376
Locus_29771_Transcript_1/1_Conf_1.000	132	6	2.78E-04	EFP00800.1	74	48.521	43	32	CRE-UNC-80 protein
Locus_29772_Transcript_1/1_Conf_1.000	103	0							
Locus_29773_Transcript_1/1_Conf_1.000	145	0							
Locus_29774_Transcript_1/1_Conf_1.000	168	20	7.55E-26	P00736.2	100	120.168	56	56	Complement C1r subcomponent
Locus_29775_Transcript_1/1_Conf_1.000	213	0							
Locus_29776_Transcript_1/1_Conf_1.000	160	0							
Locus_29777_Transcript_1/1_Conf_1.000	135	20	2.34E-11	XP_002632693.1	84	72.0182	45	38	Hypothetical protein CBG21624
Locus_29778_Transcript_1/1_Conf_1.000	172	0							
Locus_29779_Transcript_1/1_Conf_1.000	144	0							
Locus_2978_Transcript_1/3_Conf_0.667	950	20	4.66E-64	NP_502575.1	95	249.21	133	127	hypothetical protein Y62E10A.10
Locus_2978_Transcript_2/3_Conf_0.667	1232	20	3.07E-112	NP_502575.1	94	409.838	227	214	hypothetical protein Y62E10A.10
Locus_2978_Transcript_3/3_Conf_0.667	1232	20	3.07E-112	NP_502575.1	94	409.838	227	214	hypothetical protein Y62E10A.10
Locus_29780_Transcript_1/1_Conf_1.000	128	20	1.43E-16	XP_002930057.1	100	89.3521	42	42	PREDICTED: spliceosome RNA helicase BAT1-like
Locus_29781_Transcript_1/1_Conf_1.000	133	0							
Locus_29782_Transcript_1/1_Conf_1.000	160	0							
Locus_29783_Transcript_1/1_Conf_1.000	142	0							

Locus_29784_Transcript_1/1_Conf_1.000	129	5	2.28E-14	XP_002644616.1	92	82.0333	40	37	Hypothetical protein CBG14575
Locus_29785_Transcript_1/1_Conf_1.000	142	0							
Locus_29786_Transcript_1/1_Conf_1.000	130	0							
Locus_29787_Transcript_1/1_Conf_1.000	158	20	7.15E-16	XP_002647072.1	88	87.0409	52	46	Hypothetical protein CBG03598
Locus_29788_Transcript_1/1_Conf_1.000	133	0							
Locus_29789_Transcript_1/1_Conf_1.000	146	0							
Locus_2979_Transcript_1/1_Conf_1.000	156	0							
Locus_29790_Transcript_1/1_Conf_1.000	102	0							
Locus_29791_Transcript_1/1_Conf_1.000	157	0							
Locus_29792_Transcript_1/1_Conf_1.000	151	0							
Locus_29793_Transcript_1/1_Conf_1.000	150	0							
Locus_29794_Transcript_1/1_Conf_1.000	137	0							
Locus_29795_Transcript_1/1_Conf_1.000	146	20	3.49E-10	XP_002640693.1	79	68.1662	48	38	Hypothetical protein CBG19758
Locus_29796_Transcript_1/1_Conf_1.000	130	0							
Locus_29797_Transcript_1/1_Conf_1.000	144	0							
Locus_29798_Transcript_1/1_Conf_1.000	209	20	1.79E-19	NP_499880.3	85	98.9821	68	58	hypothetical protein R02D3.3
Locus_29799_Transcript_1/1_Conf_1.000	134	20	2.34E-11	XP_002641945.1	81	72.0182	44	36	C. briggsae CBR-TAG-198 protein
Locus_298_Transcript_1/1_Conf_1.000	231	4	4.32E-13	XP_002635474.1	75	77.7962	68	51	Hypothetical protein CBG08769
Locus_2980_Transcript_1/1_Conf_1.000	455	20	4.67E-52	XP_002637604.1	84	207.223	117	99	C. briggsae CBR-RBX-1 protein
Locus_29800_Transcript_1/1_Conf_1.000	193	0							
Locus_29801_Transcript_1/1_Conf_1.000	132	0							
Locus_29802_Transcript_1/1_Conf_1.000	262	0							
Locus_29803_Transcript_1/1_Conf_1.000	229	0							
Locus_29804_Transcript_1/1_Conf_1.000	142	0							
Locus_29805_Transcript_1/1_Conf_1.000	134	20	1.05E-19	XP_002917845.1	100	99.7525	44	44	PREDICTED: cell division protein kinase 16-like
Locus_29806_Transcript_1/1_Conf_1.000	315	20	3.02E-22	NP_503682.1	70	108.227	102	72	hypothetical protein C01B4.8
Locus_29807_Transcript_1/1_Conf_1.000	134	0							

Locus_29808_Transcript_1/1_Conf_1.000	224	4	4.08E-19	NP_502312.2	77	97.8265	74	57	Neurexin Like receptor family member (nlr-1)
Locus_29809_Transcript_1/1_Conf_1.000	338	0							
Locus_2981_Transcript_1/3_Conf_0.571	433	0							
Locus_2981_Transcript_2/3_Conf_0.286	509	0							
Locus_2981_Transcript_3/3_Conf_0.714	481	0							
Locus_29810_Transcript_1/1_Conf_1.000	138	0							
Locus_29811_Transcript_1/1_Conf_1.000	162	20	1.34E-14	NP_497008.1	86	82.8037	53	46	hypothetical protein K10H10.2
Locus_29813_Transcript_1/1_Conf_1.000	134	4	7.06E-16	NP_502273.2	93	87.0409	44	41	UNCoordinated family member (unc-22)
Locus_29814_Transcript_1/1_Conf_1.000	164	0							
Locus_29815_Transcript_1/1_Conf_1.000	133	0							
Locus_29816_Transcript_1/1_Conf_1.000	128	0							
Locus_29817_Transcript_1/1_Conf_1.000	137	0							
Locus_29818_Transcript_1/1_Conf_1.000	152	20	5.69E-21	NP_499865.1	98	103.99	50	49	hypothetical protein F29C4.6
Locus_29819_Transcript_1/1_Conf_1.000	143	0							
Locus_2982_Transcript_1/1_Conf_1.000	1590	20	6.99E-70	EFO22014.1	63	269.626	327	207	actin
Locus_29820_Transcript_1/1_Conf_1.000	166	20	3.52E-23	XP_002760919.1	100	111.309	55	55	PREDICTED: fumarate hydratase, mitochondrial
Locus_29821_Transcript_1/1_Conf_1.000	145	0							
Locus_29822_Transcript_1/1_Conf_1.000	139	2	9.14E-16	NP_509421.2	91	86.6557	45	41	TBC (Tre-2/Bub2/Cdc16) domain family member (tbc-18)
Locus_29823_Transcript_1/1_Conf_1.000	140	0							
Locus_29824_Transcript_1/1_Conf_1.000	128	20	2.13E-12	2PBC	100	75.485	36	36	Fk506-Binding Protein 2
Locus_29825_Transcript_1/1_Conf_1.000	139	0							
Locus_29826_Transcript_1/1_Conf_1.000	129	0							
Locus_29827_Transcript_1/1_Conf_1.000	155	0							

Locus_29828_Transcript_1/1_Conf_1.000	158	0							
Locus_29829_Transcript_1/1_Conf_1.000	135	0							
Locus_2983_Transcript_1/1_Conf_1.000	1484	20	3.70E-110	NP_493229.1	74	403.29	321	238	hypothetical protein W02A11.1
Locus_29830_Transcript_1/1_Conf_1.000	135	0							
Locus_29831_Transcript_1/1_Conf_1.000	168	6	4.45E-10	NP_505281.1	76	67.781	51	39	hypothetical protein F07B7.12
Locus_29832_Transcript_1/1_Conf_1.000	222	1	2.85E-04	XP_002638606.1	76	48.521	34	26	Hypothetical protein CBG05657
Locus_29833_Transcript_1/1_Conf_1.000	172	20	8.32E-25	XP_002814671.1	100	116.701	57	57	PREDICTED: cytosol aminopeptidase-like
Locus_29834_Transcript_1/1_Conf_1.000	196	0							
Locus_29835_Transcript_1/1_Conf_1.000	180	0							
Locus_29836_Transcript_1/1_Conf_1.000	247	11	2.40E-32	EFP00800.1	90	141.739	82	74	CRE-UNC-80 protein
Locus_29837_Transcript_1/1_Conf_1.000	132	19	2.20E-09	XP_001893904.1	79	65.4698	43	34	Protein-tyrosine phosphatase containing protein
Locus_29838_Transcript_1/1_Conf_1.000	144	0							
Locus_29839_Transcript_1/1_Conf_1.000	164	20	2.80E-12	NP_504648.1	75	75.0998	54	41	Carnitine Palmitoyl Transferase family member (cpt-6)
Locus_2984_Transcript_1/1_Conf_1.000	1790	20	0	NP_001021021.1	84	704.516	479	407	hypothetical protein C32F10.8
Locus_29840_Transcript_1/1_Conf_1.000	128	0							
Locus_29841_Transcript_1/1_Conf_1.000	155	0							
Locus_29842_Transcript_1/1_Conf_1.000	168	0							
Locus_29843_Transcript_1/1_Conf_1.000	138	20	9.44E-21	XP_519230.2	100	103.219	45	45	PREDICTED: actin related protein 2/3 complex subunit 1B
Locus_29844_Transcript_1/1_Conf_1.000	216	3	8.83E-19	NP_509817.2	73	96.6709	67	49	hypothetical protein F47B10.5
Locus_29845_Transcript_1/1_Conf_1.000	198	20	4.17E-16	XP_002637730.1	72	87.8113	62	45	Hypothetical protein CBG11596
Locus_29846_Transcript_1/1_Conf_1.000	135	7	2.77E-12	XP_002630633.1	91	75.0998	45	41	C. briggsae CBR-NSY-1 protein
Locus_29847_Transcript_1/1_Conf_1.000	223	2	2.75E-07	AAY58318.1	63	58.5362	63	40	C-type lectin precursor

Locus_29848_Transcript_1/1_Conf_1.000	148	20	6.74E-22	XP_002818645.1	100	107.071	49	49	PREDICTED: glutathione S-transferase kappa 1-like
Locus_29849_Transcript_1/1_Conf_1.000	198	0							
Locus_2985_Transcript_1/2_Conf_1.000	2759	20	0	NP_496710.1	89	1379	921	827	hypothetical protein Y46G5A.4
Locus_2985_Transcript_2/2_Conf_1.000	2759	20	0	NP_496710.1	89	1379	921	827	hypothetical protein Y46G5A.4
Locus_29850_Transcript_1/1_Conf_1.000	128	0							
Locus_29851_Transcript_1/1_Conf_1.000	128	0							
Locus_29852_Transcript_1/1_Conf_1.000	177	4	2.85E-17	NP_001123075.1	85	91.6633	57	49	hypothetical protein ZC455.1
Locus_29853_Transcript_1/1_Conf_1.000	143	0							
Locus_29854_Transcript_1/1_Conf_1.000	610	20	1.76E-57	EFO85621.1	76	226.098	194	149	CRE-LET-268 protein
Locus_29855_Transcript_1/1_Conf_1.000	135	2	2.05E-07	NP_491888.2	80	58.9214	41	33	hypothetical protein F57B10.9
Locus_29856_Transcript_1/1_Conf_1.000	136	0							
Locus_29857_Transcript_1/1_Conf_1.000	140	5	3.26E-13	XP_002647091.1	93	78.1814	46	43	Hypothetical protein CBG03621
Locus_29858_Transcript_1/1_Conf_1.000	170	0							
Locus_29859_Transcript_1/1_Conf_1.000	161	0							
Locus_2986_Transcript_1/2_Conf_0.667	219	0							
Locus_2986_Transcript_2/2_Conf_0.667	219	0							
Locus_29860_Transcript_1/1_Conf_1.000	195	20	1.14E-13	NP_001129849.1	77	79.7221	62	48	Choline Kinase A family member (cka-1)

Locus_29861_Transcript_1/1_Conf_1.000	154	15	2.09E-07	XP_002643485.1	75	58.9214	48	36	C. briggsae CBR-PKC-2 protein
Locus_29862_Transcript_1/1_Conf_1.000	141	20	4.67E-20	XP_002830831.1	100	100.908	46	46	PREDICTED: integrin beta-2-like, partial
Locus_29863_Transcript_1/1_Conf_1.000	137	0							
Locus_29864_Transcript_1/1_Conf_1.000	130	0							
Locus_29865_Transcript_1/1_Conf_1.000	143	0							
Locus_29866_Transcript_1/1_Conf_1.000	215	0							
Locus_29867_Transcript_1/1_Conf_1.000	135	2	2.78E-04	EFO86810.1	53	48.521	45	24	hypothetical protein CRE_04697
Locus_29868_Transcript_1/1_Conf_1.000	145	0							
Locus_29869_Transcript_1/1_Conf_1.000	137	0							
Locus_2987_Transcript_1/1_Conf_1.000	2730	20	1.64E-99	NP_001024740.1	64	369.007	379	243	EATing: abnormal pharyngeal pumping family member (eat-20)
Locus_29870_Transcript_1/1_Conf_1.000	130	20	3.40E-18	EFO97249.1	100	94.7449	43	43	CRE-MEC-4 protein
Locus_29871_Transcript_1/1_Conf_1.000	345	2	4.98E-09	NP_496830.2	74	64.3142	55	41	hypothetical protein Y48E1C.4
Locus_29872_Transcript_1/1_Conf_1.000	188	0							
Locus_29873_Transcript_1/1_Conf_1.000	163	20	3.53E-23	NP_001611.1	100	111.309	54	54	neuroblast differentiation-associated protein AHNAK isoform 1
Locus_29874_Transcript_1/1_Conf_1.000	131	0							
Locus_29875_Transcript_1/1_Conf_1.000	134	14	5.42E-08	EFP04426.1	79	60.8474	43	34	CRE-TPST-2 protein
Locus_29876_Transcript_1/1_Conf_1.000	158	0							
Locus_29877_Transcript_1/1_Conf_1.000	132	0							
Locus_29878_Transcript_1/1_Conf_1.000	143	20	5.36E-16	EFP05547.1	93	87.4261	44	41	CRE-UNC-68 protein
Locus_29879_Transcript_1/1_Conf_1.000	130	0							
Locus_2988_Transcript_1/1_Conf_1.000	205	1	1.63E-04	XP_797470.2	69	49.2914	56	39	PREDICTED: similar to KIAA1636 protein

Locus_29880_Transcript_1/1_Conf_1.000	142	0							
Locus_29881_Transcript_1/1_Conf_1.000	136	0							
Locus_29882_Transcript_1/1_Conf_1.000	245	20	2.05E-23	XP_002736853.1	81	112.079	80	65	PREDICTED: sirtuin 6-like
Locus_29883_Transcript_1/1_Conf_1.000	162	0							
Locus_29884_Transcript_1/1_Conf_1.000	130	20	8.91E-19	XP_002819972.1	100	96.6709	43	43	PREDICTED: cathepsin L1-like
Locus_29885_Transcript_1/1_Conf_1.000	133	0							
Locus_29886_Transcript_1/1_Conf_1.000	179	0							
Locus_29887_Transcript_1/1_Conf_1.000	158	3	1.71E-09	NP_507813.1	76	65.855	50	38	hypothetical protein Y43F8C.13
Locus_29888_Transcript_1/1_Conf_1.000	146	2	1.85E-11	EAW97496.1	100	72.4034	48	48	hCG2015138, isoform CRA_c
Locus_29889_Transcript_1/1_Conf_1.000	150	0							
Locus_2989_Transcript_1/2_Conf_1.000	216	0							
Locus_2989_Transcript_2/2_Conf_1.000	915	20	8.31E-39	XP_002644874.1	55	165.236	229	128	C. briggsae CBR-LMP-1 protein
Locus_29890_Transcript_1/1_Conf_1.000	157	0							
Locus_29891_Transcript_1/1_Conf_1.000	139	20	1.32E-14	XP_002631109.1	95	82.8037	45	43	Hypothetical protein CBG02884
Locus_29892_Transcript_1/1_Conf_1.000	143	0							

Locus_29893_Transcript_1/1_Conf_1.000	153	20	7.41E-21	XP_002914092.1	100	103.605	51	51	PREDICTED: spectrin beta chain, brain 1-like isoform 1
Locus_29894_Transcript_1/1_Conf_1.000	155	0							
Locus_29895_Transcript_1/1_Conf_1.000	171	20	8.94E-11	XP_002639888.1	72	70.0922	55	40	C. briggsae CBR-DOD-18 protein
Locus_29896_Transcript_1/1_Conf_1.000	140	0							
Locus_29897_Transcript_1/1_Conf_1.000	158	0							
Locus_29898_Transcript_1/1_Conf_1.000	148	0							
Locus_29899_Transcript_1/1_Conf_1.000	135	0							
Locus_299_Transcript_1/1_Conf_1.000	2178	20	0	XP_002642384.1	83	753.051	535	449	Hypothetical protein CBG18388
Locus_2990_Transcript_1/2_Conf_1.000	3222	20	0	AAA82421.2	67	892.493	984	669	Far (factor arrest) like protein 11, partially confirmed by transcript evidence
Locus_2990_Transcript_2/2_Conf_1.000	3210	20	0	AAA82421.2	67	892.493	982	667	Far (factor arrest) like protein 11, partially confirmed by transcript evidence
Locus_29900_Transcript_1/1_Conf_1.000	128	0							
Locus_29901_Transcript_1/1_Conf_1.000	165	20	2.53E-13	EFP11117.1	86	78.5666	51	44	CRE-ACY-2 protein
Locus_29902_Transcript_1/1_Conf_1.000	145	20	5.19E-14	XP_002643080.1	89	80.8777	46	41	C. briggsae CBR-GLY-5 protein
Locus_29903_Transcript_1/1_Conf_1.000	171	0							
Locus_29904_Transcript_1/1_Conf_1.000	163	20	2.14E-12	XP_002599844.1	72	75.485	54	39	hypothetical protein BRAFLDRAFT_95534
Locus_29905_Transcript_1/1_Conf_1.000	156	0							
Locus_29906_Transcript_1/1_Conf_1.000	154	20	5.16E-14	EFP03107.1	90	80.8777	51	46	hypothetical protein CRE_28219
Locus_29907_Transcript_1/1_Conf_1.000	172	0							
Locus_29908_Transcript_1/1_Conf_1.000	228	20	7.91E-15	XP_001623132.1	61	83.5741	71	44	predicted protein

Locus_29909_Transcript_1/1_Conf_1.000	194	1	9.73E-05	XP_002634485.1	54	50.0618	64	35	C. briggsae CBR-UGT-45 protein
Locus_2991_Transcript_1/1_Conf_1.000	357	3	1.68E-17	NP_502746.1	62	92.4337	129	81	hypothetical protein Y67A10A.9
Locus_29910_Transcript_1/1_Conf_1.000	143	0							
Locus_29911_Transcript_1/1_Conf_1.000	201	0							
Locus_29912_Transcript_1/1_Conf_1.000	148	4	2.11E-07	XP_002638873.1	74	58.9214	47	35	Hypothetical protein CBG22091
Locus_29913_Transcript_1/1_Conf_1.000	137	0							
Locus_29914_Transcript_1/1_Conf_1.000	172	0							
Locus_29915_Transcript_1/1_Conf_1.000	135	20	1.20E-07	NP_496282.2	85	59.6918	42	36	hypothetical protein C14A4.3
Locus_29916_Transcript_1/1_Conf_1.000	203	0							
Locus_29917_Transcript_1/1_Conf_1.000	132	20	7.55E-18	XP_001503266.1	100	93.5893	43	43	PREDICTED: similar to N-ethylmaleimide sensitive fusion protein attachment protein alpha
Locus_29918_Transcript_1/1_Conf_1.000	146	20	3.37E-21	EFO82930.1	100	104.76	48	48	CRE-MEC-7 protein
Locus_29919_Transcript_1/1_Conf_1.000	139	8	7.76E-15	XP_002641231.1	93	83.5741	45	42	Hypothetical protein CBG09097
Locus_2992_Transcript_1/1_Conf_1.000	684	4	6.28E-23	NP_496534.1	59	111.694	157	93	Nuclear Pore complex Protein family member (npp-3)
Locus_29920_Transcript_1/1_Conf_1.000	163	0							
Locus_29921_Transcript_1/1_Conf_1.000	129	0							
Locus_29922_Transcript_1/1_Conf_1.000	148	0							
Locus_29923_Transcript_1/1_Conf_1.000	129	0							
Locus_29924_Transcript_1/1_Conf_1.000	143	13	1.01E-06	AAK94763.1	74	56.6102	47	35	GLY-19
Locus_29925_Transcript_1/1_Conf_1.000	224	5	5.34E-19	XP_002629656.1	75	97.4413	74	56	Hypothetical protein CBG00863
Locus_29926_Transcript_1/1_Conf_1.000	190	20	6.96E-11	EFO21603.1	69	70.4774	59	41	hypothetical protein LOAG_06885
Locus_29927_Transcript_1/1_Conf_1.000	142	0							
Locus_29928_Transcript_1/1_Conf_1.000	190	0							
Locus_29929_Transcript_1/1_Conf_1.000	129	0							

Locus_2993_Transcript_1/1_Conf_1.000	1985	20	0	XP_002638846.1	69	725.317	683	477	C. briggsae CBR-TOL-1 protein
Locus_29930_Transcript_1/1_Conf_1.000	141	5	2.67E-07	XP_002641291.1	78	58.5362	47	37	Hypothetical protein CBG05206
Locus_29931_Transcript_1/1_Conf_1.000	147	1	8.31E-04	NP_502174.2	68	46.9802	50	34	hypothetical protein M04B2.2
Locus_29932_Transcript_1/1_Conf_1.000	158	0							
Locus_29933_Transcript_1/1_Conf_1.000	135	0							
Locus_29934_Transcript_1/1_Conf_1.000	129	0							
Locus_29935_Transcript_1/1_Conf_1.000	207	7	5.05E-14	EFO24692.1	75	80.8777	58	44	protein-tyrosine phosphatase
Locus_29936_Transcript_1/1_Conf_1.000	202	20	2.29E-14	XP_002636250.1	67	82.0333	65	44	Hypothetical protein CBG08530
Locus_29937_Transcript_1/1_Conf_1.000	146	0							
Locus_29938_Transcript_1/1_Conf_1.000	134	20	1.13E-13	NP_001041244.1	84	79.7221	44	37	HunchBack Like (fly gap gene related) family member (hbl-1)
Locus_29939_Transcript_1/1_Conf_1.000	194	20	3.94E-14	XP_394424.2	73	81.2629	64	47	PREDICTED: similar to Tdc2 CG30446-PA

Locus_2994_Transcript_1/2_Conf_1.000	1692	20	1.51E-118	XP_002641709.1	70	431.409	437	310	C. briggsae CBR-CED-7 protein
Locus_2994_Transcript_2/2_Conf_1.000	799	20	2.57E-35	XP_002641709.1	73	153.295	132	97	C. briggsae CBR-CED-7 protein
Locus_29940_Transcript_1/1_Conf_1.000	164	20	4.91E-25	XP_002919104.1	100	117.472	54	54	PREDICTED: LOW QUALITY PROTEIN: collagen alpha-2(VI) chain-like
Locus_29941_Transcript_1/1_Conf_1.000	232	3	1.53E-18	CAA51991.1	90	95.9005	77	70	GABA A/glycine receptor subunit
Locus_29942_Transcript_1/1_Conf_1.000	128	0							
Locus_29943_Transcript_1/1_Conf_1.000	142	0							
Locus_29944_Transcript_1/1_Conf_1.000	140	5	5.94E-15	EFP07774.1	95	83.9593	46	44	CRE-RPY-1 protein
Locus_29945_Transcript_1/1_Conf_1.000	184	0							
Locus_29946_Transcript_1/1_Conf_1.000	202	0							
Locus_29947_Transcript_1/1_Conf_1.000	205	4	5.42E-08	NP_490909.2	57	60.8474	61	35	Temporarily Assigned Gene name family member (tag-96)
Locus_29948_Transcript_1/1_Conf_1.000	222	0							
Locus_29949_Transcript_1/1_Conf_1.000	148	0							

Locus_2995_Transcript_1/1_Conf_1.000	1667	20	3.49E-152	NP_507852.2	80	543.117	414	335	phenylalanyl (F) tRNA Synthetase family member (frs-3)
Locus_29950_Transcript_1/1_Conf_1.000	172	4	3.99E-19	NP_001122833.1	94	97.8265	56	53	hypothetical protein ZC518.1
Locus_29951_Transcript_1/1_Conf_1.000	140	4	1.98E-10	EFP07740.1	89	68.9366	38	34	CRE-SRO-1 protein
Locus_29952_Transcript_1/1_Conf_1.000	134	0							
Locus_29953_Transcript_1/1_Conf_1.000	151	3	1.19E-18	EFO83250.1	90	96.2857	50	45	hypothetical protein CRE_13579
Locus_29954_Transcript_1/1_Conf_1.000	175	0							
Locus_29955_Transcript_1/1_Conf_1.000	137	0							
Locus_29956_Transcript_1/1_Conf_1.000	138	20	2.19E-09	2WS2	78	65.4698	46	36	The 2 AngstromStructure Of A Nu-Class Gst From Haemonchus Contortus
Locus_29957_Transcript_1/1_Conf_1.000	187	0							
Locus_29958_Transcript_1/1_Conf_1.000	150	0							
Locus_29959_Transcript_1/1_Conf_1.000	135	0							
Locus_2996_Transcript_1/1_Conf_1.000	2077	20	0	XP_002639034.1	79	894.419	685	545	C. briggsae CBR-SPE-15 protein
Locus_29960_Transcript_1/1_Conf_1.000	128	0							
Locus_29961_Transcript_1/1_Conf_1.000	128	0							
Locus_29962_Transcript_1/1_Conf_1.000	177	20	1.51E-10	EFO83746.1	80	69.3218	47	38	hypothetical protein CRE_14220
Locus_29963_Transcript_1/1_Conf_1.000	131	3	5.07E-06	NP_001076772.1	74	54.299	43	32	GEX Interacting protein family member (gei-3)
Locus_29964_Transcript_1/1_Conf_1.000	275	0							
Locus_29965_Transcript_1/1_Conf_1.000	202	0							
Locus_29966_Transcript_1/1_Conf_1.000	129	5	1.53E-10	EFP00973.1	85	69.3218	42	36	CRE-UNC-122 protein
Locus_29967_Transcript_1/1_Conf_1.000	129	0							
Locus_29968_Transcript_1/1_Conf_1.000	129	3	2.98E-06	EFP05300.1	71	55.0694	42	30	CRE-DHS-20 protein
Locus_29969_Transcript_1/1_Conf_1.000	140	0							
Locus_2997_Transcript_1/1_Conf_1.000	1671	14	3.84E-66	NP_497136.2	51	257.299	580	297	hypothetical protein F54C4.3
Locus_29970_Transcript_1/1_Conf_1.000	140	0							
Locus_29971_Transcript_1/1_Conf_1.000	128	0							
Locus_29972_Transcript_1/1_Conf_1.000	154	20	2.93E-09	EFO88893.1	85	65.0846	42	36	CRE-WHT-4 protein
Locus_29973_Transcript_1/1_Conf_1.000	129	0							
Locus_29974_Transcript_1/1_Conf_1.000	139	0							

Locus_29975_Transcript_1/1_Conf_1.000	166	20	1.21E-15	CAA91463.2	85	86.2705	54	46	C. elegans protein F42E11.1a, partially confirmed by transcript evidence
Locus_29976_Transcript_1/1_Conf_1.000	130	0							
Locus_29977_Transcript_1/1_Conf_1.000	142	14	7.01E-08	EFP03255.1	73	60.4622	41	30	hypothetical protein CRE_28627
Locus_29978_Transcript_1/1_Conf_1.000	136	0							
Locus_29979_Transcript_1/1_Conf_1.000	175	0							
Locus_2998_Transcript_1/1_Conf_1.000	405	20	5.22E-27	XP_001894245.1	77	124.02	113	88	hypothetical protein Bm1_13905
Locus_29980_Transcript_1/1_Conf_1.000	134	0							
Locus_29981_Transcript_1/1_Conf_1.000	130	5	1.25E-04	NP_491872.1	67	49.6766	40	27	hypothetical protein C55B7.3
Locus_29982_Transcript_1/1_Conf_1.000	187	0							
Locus_29983_Transcript_1/1_Conf_1.000	174	4	1.62E-12	NP_490836.1	78	75.8702	57	45	hypothetical protein Y48G8AL.13
Locus_29984_Transcript_1/1_Conf_1.000	142	5	1.61E-12	EFO91467.1	86	75.8702	46	40	hypothetical protein CRE_11941
Locus_29985_Transcript_1/1_Conf_1.000	152	0							
Locus_29986_Transcript_1/1_Conf_1.000	165	0							
Locus_29987_Transcript_1/1_Conf_1.000	143	0							
Locus_29988_Transcript_1/1_Conf_1.000	322	0							
Locus_29989_Transcript_1/1_Conf_1.000	131	0							
Locus_2999_Transcript_1/1_Conf_1.000	253	0							
Locus_29990_Transcript_1/1_Conf_1.000	170	0							
Locus_29991_Transcript_1/1_Conf_1.000	144	0							
Locus_3_Transcript_1/3_Conf_0.625	223	18	7.45E-13	Q94637.1	77	77.0258	58	45	Vitellogenin-6
Locus_3_Transcript_3/3_Conf_0.875	468	20	5.99E-31	Q94637.1	70	137.117	141	100	Vitellogenin-6

Locus_30_Transcript_1/1_Conf_1.000	540	20	1.13E-58	NP_001040940.1	72	229.565	178	129	PhosphatidylSerine Receptor family member (psr-1)
Locus_300_Transcript_1/3_Conf_0.800	2284	20	0	XP_002631077.1	90	1134.78	714	645	Hypothetical protein CBG02850
Locus_300_Transcript_2/3_Conf_0.800	2317	20	0	XP_002631077.1	90	1149.81	717	652	Hypothetical protein CBG02850
Locus_300_Transcript_3/3_Conf_0.800	2317	20	0	XP_002631077.1	90	1149.81	717	652	Hypothetical protein CBG02850
Locus_3000_Transcript_1/1_Conf_1.000	702	20	2.42E-65	NP_500188.1	98	252.677	161	158	Vacuolar H ATPase family member (vha-3)
Locus_3001_Transcript_1/1_Conf_1.000	842	20	8.15E-51	XP_002630448.1	67	204.912	214	144	Hypothetical protein CBG11181
Locus_3002_Transcript_1/1_Conf_1.000	499	0							
Locus_3003_Transcript_1/1_Conf_1.000	638	20	3.52E-59	EFO18502.1	80	231.876	167	135	hypothetical protein LOAG_09992

Locus_3004_Transcript_1/1_Conf_1.000	727	20	2.16E-104	NP_001012649.1	100	382.489	184	184	interleukin-32 isoform B
Locus_3005_Transcript_1/1_Conf_1.000	378	0							
Locus_3006_Transcript_1/1_Conf_1.000	130	0							
Locus_3007_Transcript_1/3_Conf_0.500	568	3	7.42E-46	AAT64963.1	86	187.193	126	109	putative protein L3i10 isoform a
Locus_3007_Transcript_2/3_Conf_0.500	1201	4	7.52E-108	AAT64964.1	81	395.201	332	270	putative protein L3i10 isoform b
Locus_3007_Transcript_3/3_Conf_0.500	616	3	5.60E-51	AAT64963.1	86	204.527	142	123	putative protein L3i10 isoform a
Locus_3008_Transcript_1/1_Conf_1.000	1146	20	0	AAC48152.3	87	650.973	364	318	Laminin related. see also lmb- protein 2, partially confirmed by transcript evidence
Locus_3009_Transcript_1/2_Conf_1.000	761	20	1.82E-64	NP_508683.1	84	249.98	166	141	hypothetical protein T19D2.2
Locus_3009_Transcript_2/2_Conf_1.000	764	20	1.83E-64	NP_508683.1	84	249.98	166	141	hypothetical protein T19D2.2
Locus_301_Transcript_1/1_Conf_1.000	667	20	2.41E-109	ABC40752.1	99	398.667	222	221	myosin heavy chain
Locus_3010_Transcript_1/1_Conf_1.000	696	13	4.36E-43	NP_498762.2	73	178.718	200	146	Anaphase Promoting Complex; see also mat family member (apc-2)
Locus_3011_Transcript_1/1_Conf_1.000	488	20	3.06E-59	XP_002641482.1	88	231.106	154	136	Hypothetical protein CBG09773
Locus_3012_Transcript_1/2_Conf_1.000	512	19	1.40E-38	XP_003064993.1	95	162.54	82	78	predicted protein
Locus_3012_Transcript_2/2_Conf_1.000	330	12	2.34E-18	XP_002489102.1	88	92.8189	50	44	hypothetical protein SORBIDRAFT_0070s002020
Locus_3013_Transcript_1/2_Conf_1.000	1216	3	1.44E-05	NP_494766.1	38	55.4546	207	79	hypothetical protein H20J04.3
Locus_3013_Transcript_2/2_Conf_1.000	273	0							

Locus_3014_Transcript_1/2_Conf_1.000	1182	20	2.69E-153	NP_502812.1	85	534.258	346	296	glutamyl(E)/glutaminyl(Q) tRNA Synthetase family member (ers-1)
Locus_3014_Transcript_2/2_Conf_1.000	1192	20	3.40E-161	CBK19498.1	87	572.392	358	312	C. elegans protein Y41E3.4c, partially confirmed by transcript evidence
Locus_3015_Transcript_1/1_Conf_1.000	563	14	6.26E-50	NP_501856.2	87	200.675	116	102	TransThyretin-Related family domain family member (ttr-53)
Locus_3016_Transcript_1/1_Conf_1.000	2311	20	1.32E-163	NP_001022054.1	82	581.637	446	366	hypothetical protein D2085.5
Locus_3017_Transcript_1/1_Conf_1.000	456	0							
Locus_3018_Transcript_1/1_Conf_1.000	867	4	6.68E-27	XP_002642045.1	44	125.561	319	143	C. briggsae CBR-TAG-325 protein
Locus_3019_Transcript_1/1_Conf_1.000	583	20	5.03E-56	NP_001023346.1	86	221.09	145	126	hypothetical protein T01B11.2
Locus_302_Transcript_1/1_Conf_1.000	153	0							
Locus_3020_Transcript_1/1_Conf_1.000	810	20	1.41E-89	NP_510818.3	73	333.569	275	201	hypothetical protein F10D7.5
Locus_3021_Transcript_1/1_Conf_1.000	1596	20	1.38E-49	NP_491846.2	54	202.216	388	213	Suspended ANimation (anoxia-induced) defective family member (san-1)
Locus_3022_Transcript_1/1_Conf_1.000	330	0							
Locus_3023_Transcript_1/2_Conf_1.000	639	20	4.51E-62	XP_002631295.1	76	241.506	194	149	Hypothetical protein CBG03108
Locus_3023_Transcript_2/2_Conf_1.000	1736	20	0	XP_002631295.1	72	664.07	571	415	Hypothetical protein CBG03108
Locus_3024_Transcript_1/1_Conf_1.000	1502	20	5.91E-55	XP_001894000.1	54	219.935	377	205	Zinc finger in N-recognin family protein
Locus_3025_Transcript_1/1_Conf_1.000	1758	20	1.47E-140	NP_497989.1	72	504.597	486	354	Temporarily Assigned Gene name family member (tag-325)

Locus_3026_Transcript_1/1_Conf_1.000	572	20	3.39E-38	NP_079868.1	80	161.77	119	96	60S ribosomal protein L35
Locus_3027_Transcript_1/2_Conf_1.000	2232	20	2.39E-45	XP_002642470.1	47	188.734	567	270	Hypothetical protein CBG06886
Locus_3027_Transcript_2/2_Conf_1.000	2223	20	8.45E-43	XP_002642470.1	47	180.259	567	268	Hypothetical protein CBG06886
Locus_3028_Transcript_1/2_Conf_1.000	984	0							
Locus_3028_Transcript_2/2_Conf_1.000	548	0							
Locus_3029_Transcript_1/4_Conf_0.625	2076	20	1.03E-111	ABX10191.1	59	409.068	559	332	amine oxidase (flavin containing) domain 2 isoform b
Locus_3029_Transcript_2/4_Conf_0.500	2017	20	9.96E-112	ABX10191.1	59	409.068	559	332	amine oxidase (flavin containing) domain 2 isoform b

Locus_3029_Transcript_3/4_Conf_0.625	2076	20	1.03E-111	ABX10191.1	59	409.068	559	332	amine oxidase (flavin containing) domain 2 isoform b
Locus_3029_Transcript_4/4_Conf_0.625	2076	20	1.03E-111	ABX10191.1	59	409.068	559	332	amine oxidase (flavin containing) domain 2 isoform b
Locus_303_Transcript_1/1_Conf_1.000	407	6	5.80E-10	NP_694542.1	100	67.3958	85	85	follicular dendritic cell secreted peptide precursor
Locus_3030_Transcript_1/1_Conf_1.000	162	0							
Locus_3031_Transcript_1/3_Conf_0.500	1482	20	0	NP_499386.1	94	806.594	467	440	SERCA (Sarco-Endoplasmic Reticulum Calcium ATPase) family member (sca-1)

Locus_3031_Transcript_2/3_Conf_0.667	3251	20	0	NP_499385.3	95	1757.27	998	954	SERCA (Sarco-Endoplasmic Reticulum Calcium ATPase) family member (sca-1)
Locus_3031_Transcript_3/3_Conf_0.667	3664	20	0	NP_499386.1	93	1785.77	1040	976	SERCA (Sarco-Endoplasmic Reticulum Calcium ATPase) family member (sca-1)
Locus_3032_Transcript_1/1_Conf_1.000	1384	20	7.36E-81	NP_493466.2	68	305.834	295	202	hypothetical protein Y63D3A.8
Locus_3033_Transcript_1/1_Conf_1.000	1420	0							
Locus_3034_Transcript_1/1_Conf_1.000	322	0							
Locus_3035_Transcript_1/1_Conf_1.000	1308	20	8.67E-153	XP_002642393.1	80	544.658	379	304	Hypothetical protein CBG18398
Locus_3036_Transcript_1/1_Conf_1.000	238	20	1.01E-38	ADI60307.1	100	162.925	79	79	tubulin alpha 1
Locus_3037_Transcript_1/1_Conf_1.000	1405	7	1.45E-84	NP_001076750.1	65	318.161	436	286	UNCoordinated family member (unc-83)
Locus_3038_Transcript_1/1_Conf_1.000	246	9	7.96E-36	NP_741003.1	95	153.295	81	77	hypothetical protein C18A3.4
Locus_3039_Transcript_1/1_Conf_1.000	405	20	8.56E-46	NP_001022488.1	79	186.422	123	98	UNCoordinated family member (unc-52)
Locus_304_Transcript_1/1_Conf_1.000	806	20	3.07E-52	NP_499283.1	82	209.534	150	123	abnormal MEthyl Viologen sensitivity family member (mev-1)

Locus_3040_Transcript_1/1_Conf_1.000	945	20	8.53E-34	EFO18489.1	56	148.673	200	112	hypothetical protein LOAG_10003
Locus_3041_Transcript_1/1_Conf_1.000	509	2	1.74E-04	XP_001955271.1	44	49.2914	162	72	GF16318
Locus_3042_Transcript_1/7_Conf_0.111	792	20	1.04E-97	NP_001122748.1	80	360.533	272	220	UNCoordinated family member (unc-16)
Locus_3042_Transcript_2/7_Conf_0.222	1518	20	1.94E-146	CAX51690.1	75	523.857	483	364	C. elegans protein ZK1098.10e, partially confirmed by transcript evidence
Locus_3042_Transcript_3/7_Conf_0.556	3577	20	0	CAX51690.1	80	1428.69	1130	904	C. elegans protein ZK1098.10e, partially confirmed by transcript evidence
Locus_3042_Transcript_4/7_Conf_0.667	3577	20	0	XP_002641717.1	80	1411.74	1123	900	C. briggsae CBR-UNC-16 protein
Locus_3042_Transcript_5/7_Conf_0.556	3535	20	0	XP_002641717.1	80	1411.74	1123	900	C. briggsae CBR-UNC-16 protein
Locus_3042_Transcript_6/7_Conf_0.611	3577	20	0	XP_002641717.1	80	1411.74	1123	900	C. briggsae CBR-UNC-16 protein
Locus_3042_Transcript_7/7_Conf_0.556	3535	20	0	XP_002641717.1	80	1411.74	1123	900	C. briggsae CBR-UNC-16 protein
Locus_3043_Transcript_1/1_Conf_1.000	629	4	2.15E-21	XP_002641618.1	63	106.301	114	72	Hypothetical protein CBG09938

Locus_3044_Transcript_1/1_Conf_1.000	1051	20	2.81E-161	ADI24636.1	89	572.392	336	300	Hypothetical protein C34F11.3c
Locus_3045_Transcript_1/1_Conf_1.000	1314	20	4.44E-72	XP_001311491.1	47	276.559	444	211	hypothetical protein
Locus_3046_Transcript_1/2_Conf_1.000	3648	20	0	NP_001129776.1	85	1671.75	1132	970	Anion/Bicarbonate TranSporter family member (abts-1)
Locus_3046_Transcript_2/2_Conf_1.000	3689	20	0	XP_002639486.1	86	1671.75	1114	961	C. briggsae CBR-ABTS-1 protein
Locus_3047_Transcript_1/1_Conf_1.000	1321	20	5.53E-139	EFO23503.1	78	498.819	438	346	hypothetical protein LOAG_04985
Locus_3048_Transcript_1/1_Conf_1.000	498	20	2.02E-47	ACI49119.1	83	191.815	122	102	hypothetical protein Cbre_JD14.007
Locus_3049_Transcript_1/1_Conf_1.000	475	20	2.02E-71	XP_001506584.1	97	271.552	137	134	PREDICTED: similar to 40S ribosomal protein S12
Locus_305_Transcript_1/3_Conf_0.750	2022	20	5.12E-116	XP_001900703.1	67	423.32	453	305	ES2 protein
Locus_305_Transcript_2/3_Conf_0.750	2022	20	5.12E-116	XP_001900703.1	67	423.32	453	305	ES2 protein
Locus_305_Transcript_3/3_Conf_0.750	2022	20	5.12E-116	XP_001900703.1	67	423.32	453	305	ES2 protein

Locus_3050_Transcript_1/2_Conf_1.000	615	20	2.00E-32	XP_001902557.1	91	142.895	82	75	Sr protein
Locus_3050_Transcript_2/2_Conf_1.000	374	0							
Locus_3051_Transcript_1/1_Conf_1.000	1238	2	1.34E-06	XP_002633339.1	43	58.9214	210	92	Hypothetical protein CBG06078
Locus_3052_Transcript_1/1_Conf_1.000	1314	20	3.58E-122	EFO26697.1	85	442.965	328	280	Asna1 protein
Locus_3053_Transcript_1/1_Conf_1.000	1434	20	4.37E-68	NP_492567.3	83	263.462	180	150	ASF-Like family member (asfl-1)
Locus_3054_Transcript_1/1_Conf_1.000	862	20	7.04E-146	NP_506014.1	93	520.776	283	264	Protein Kinase C family member (pkc-1)
Locus_3055_Transcript_1/1_Conf_1.000	362	20	1.78E-27	XP_002642406.1	92	125.561	75	69	Hypothetical protein CBG06800
Locus_3056_Transcript_1/1_Conf_1.000	705	9	5.09E-23	XP_002634196.1	64	112.079	164	106	Hypothetical protein CBG01765
Locus_3057_Transcript_1/3_Conf_0.500	564	20	1.02E-31	NP_490730.2	58	140.198	220	128	hypothetical protein Y50C1A.1
Locus_3057_Transcript_2/3_Conf_0.333	1089	20	1.40E-118	NP_490730.2	80	430.639	320	257	hypothetical protein Y50C1A.1
Locus_3057_Transcript_3/3_Conf_0.500	570	20	2.97E-34	NP_490730.2	59	148.673	220	130	hypothetical protein Y50C1A.1
Locus_3058_Transcript_1/2_Conf_1.000	465	15	1.26E-12	EFO23679.1	56	76.2554	169	96	hypothetical protein LOAG_04806

Locus_3058_Transcript_2/2_Conf_1.000	933	20	1.15E-59	EFO23679.1	64	234.572	320	205	hypothetical protein LOAG_04806
Locus_3059_Transcript_1/1_Conf_1.000	1378	20	5.27E-172	XP_002636443.1	91	608.601	355	324	Hypothetical protein CBG23104
Locus_306_Transcript_1/1_Conf_1.000	1277	20	1.26E-100	NP_503397.1	98	371.318	205	201	RAB family member (rab-1)
Locus_3060_Transcript_1/1_Conf_1.000	1225	20	6.73E-136	XP_002634443.1	88	488.419	318	281	Hypothetical protein CBG04457
Locus_3061_Transcript_1/1_Conf_1.000	680	20	5.49E-72	XP_001900728.1	80	274.633	214	173	RhoGAP domain containing protein
Locus_3062_Transcript_1/3_Conf_0.667	1767	20	6.71E-101	NP_491793.1	57	372.859	511	296	hypothetical protein T08B2.5

Locus_3062_Transcript_2/3_Conf_0.667	1824	20	1.67E-102	NP_491793.1	56	378.252	550	313	hypothetical protein T08B2.5
Locus_3062_Transcript_3/3_Conf_0.667	1761	20	5.12E-101	NP_491793.1	56	373.244	541	308	hypothetical protein T08B2.5
Locus_3063_Transcript_1/4_Conf_0.333	268	0							
Locus_3063_Transcript_2/4_Conf_0.667	2019	20	7.50E-121	NP_498834.1	63	424.476	498	315	hypothetical protein ZC262.3
Locus_3063_Transcript_3/4_Conf_0.556	2022	20	3.78E-127	NP_498834.1	63	460.299	562	357	hypothetical protein ZC262.3
Locus_3063_Transcript_4/4_Conf_0.667	2026	20	3.79E-127	NP_498834.1	63	460.299	562	357	hypothetical protein ZC262.3
Locus_3064_Transcript_1/1_Conf_1.000	348	0							
Locus_3065_Transcript_1/1_Conf_1.000	316	0							
Locus_3066_Transcript_1/1_Conf_1.000	837	20	4.67E-107	NP_505613.1	86	391.734	277	239	hypothetical protein C51E3.6
Locus_3067_Transcript_1/2_Conf_1.000	1354	2	2.76E-08	XP_001901141.1	54	64.6994	96	52	hypothetical protein Bm1_48395
Locus_3067_Transcript_2/2_Conf_1.000	1311	2	2.64E-08	XP_001901141.1	54	64.6994	96	52	hypothetical protein Bm1_48395
Locus_3068_Transcript_1/1_Conf_1.000	1076	7	2.10E-26	XP_002635262.1	50	124.405	281	143	Hypothetical protein CBG11506
Locus_3069_Transcript_1/1_Conf_1.000	764	20	1.82E-96	XP_002641488.1	86	356.295	236	205	Hypothetical protein CBG09779
Locus_307_Transcript_1/1_Conf_1.000	2193	20	0	XP_002642214.1	80	922.539	716	576	C. briggsae CBR-RRT-1 protein

Locus_3070_Transcript_1/1_Conf_1.000	2533	20	1.13E-139	EFO25200.1	65	502.286	539	351	AGC/PDK1 protein kinase
Locus_3071_Transcript_1/1_Conf_1.000	1589	20	4.31E-120	XP_002640623.1	67	436.417	463	312	Hypothetical protein CBG08741
Locus_3072_Transcript_1/1_Conf_1.000	706	5	3.65E-21	NP_506082.2	74	105.916	81	60	hypothetical protein F55C5.7
Locus_3073_Transcript_1/1_Conf_1.000	1321	20	0	NP_491515.2	97	671.003	348	338	Vacuolar H ATPase family member (vha-16)
Locus_3074_Transcript_1/1_Conf_1.000	655	2	7.48E-15	NP_001041133.1	52	84.7297	162	85	hypothetical protein F58E10.1
Locus_3075_Transcript_1/1_Conf_1.000	694	20	9.51E-83	XP_002634020.1	80	310.457	230	186	C. briggsae CBR-PMK-3 protein
Locus_3076_Transcript_1/1_Conf_1.000	985	20	1.25E-83	CAA10033.1	71	314.309	301	215	DYS-1 protein
Locus_3077_Transcript_1/1_Conf_1.000	808	20	2.91E-34	XP_001902547.1	60	149.828	215	129	hypothetical protein Bm1_55450

Locus_3078_Transcript_1/2_Conf_1.000	2180	20	0	XP_002633115.1	86	785.793	534	461	C. briggsae CBR-KCC-1 protein
Locus_3078_Transcript_2/2_Conf_1.000	2179	20	0	XP_002633115.1	86	785.793	534	461	C. briggsae CBR-KCC-1 protein
Locus_3079_Transcript_1/1_Conf_1.000	767	20	1.98E-66	EFO24807.1	85	256.529	162	138	adaptin ear-binding coat-associated protein 1
Locus_308_Transcript_1/1_Conf_1.000	352	0							
Locus_3080_Transcript_1/4_Conf_0.500	581	0							
Locus_3080_Transcript_2/4_Conf_0.625	680	1	2.20E-04	XP_002645979.1	47	50.0618	127	60	C. briggsae CBR-NHR-48 protein
Locus_3080_Transcript_3/4_Conf_0.250	703	0							
Locus_3080_Transcript_4/4_Conf_0.625	680	4	2.60E-05	XP_002645979.1	47	53.1434	132	63	C. briggsae CBR-NHR-48 protein
Locus_3081_Transcript_1/3_Conf_0.571	769	17	5.99E-71	CAA85341.2	78	271.552	198	155	C. elegans protein T09A5.12, confirmed by transcript evidence
Locus_3081_Transcript_2/3_Conf_0.714	171	3	3.38E-10	CAA85341.2	89	68.1662	39	35	C. elegans protein T09A5.12, confirmed by transcript evidence
Locus_3081_Transcript_3/3_Conf_0.571	679	17	2.31E-70	CAA85341.2	78	269.24	196	153	C. elegans protein T09A5.12, confirmed by transcript evidence
Locus_3082_Transcript_1/1_Conf_1.000	307	0							

Locus_3083_Transcript_1/1_Conf_1.000	2015	20	6.42E-10	NP_491738.2	38	70.8626	307	118	RiNg Finger protein family member (rnf-1)
Locus_3084_Transcript_1/2_Conf_1.000	807	20	1.76E-39	XP_001893275.1	77	167.162	158	122	LMBR1-like conserved region family protein
Locus_3084_Transcript_2/2_Conf_1.000	1569	20	5.81E-69	XP_308875.3	55	266.544	483	269	AGAP006880-PA
Locus_3085_Transcript_1/1_Conf_1.000	1036	20	8.29E-57	NP_490957.1	58	225.328	302	176	hypothetical protein Y39G10AR.9
Locus_3086_Transcript_1/1_Conf_1.000	243	8	3.73E-09	EFO21370.1	71	64.6994	80	57	hypothetical protein LOAG_07121
Locus_3087_Transcript_1/1_Conf_1.000	1314	2	6.48E-31	XP_001902033.1	55	139.813	225	125	ring finger protein 1
Locus_3088_Transcript_1/1_Conf_1.000	1753	20	1.82E-66	EFO28449.1	56	258.455	428	240	hypothetical protein LOAG_00045
Locus_3089_Transcript_1/1_Conf_1.000	451	7	5.96E-31	NP_001122868.1	69	137.117	146	101	GLIoTactin (Drosophila neuroligin-like) homolog family member (nrx-1)
Locus_309_Transcript_1/6_Conf_0.389	1013	20	3.59E-158	XP_002638989.1	92	561.992	330	304	C. briggsae CBR-RPL-4 protein
Locus_309_Transcript_2/6_Conf_0.389	1055	20	5.31E-160	XP_002638989.1	91	568.155	336	308	C. briggsae CBR-RPL-4 protein

Locus_309_Transcript_3/6_Conf_0.278	489	20	1.05E-51	CAR63711.1	98	206.068	107	105	putative Ribosomal Protein
Locus_309_Transcript_4/6_Conf_0.278	447	20	5.21E-51	CAR63711.1	98	203.756	106	104	putative Ribosomal Protein
Locus_309_Transcript_5/6_Conf_0.389	1144	20	6.65E-159	XP_002638989.1	92	564.688	331	305	C. briggsae CBR-RPL-4 protein
Locus_309_Transcript_6/6_Conf_0.389	1144	20	6.65E-159	XP_002638989.1	92	564.688	331	305	C. briggsae CBR-RPL-4 protein
Locus_3090_Transcript_1/1_Conf_1.000	2046	20	0	NP_503733.1	87	1034.25	686	598	NADH Ubiquinone Oxidoreductase family member (nuo-5)
Locus_3091_Transcript_1/1_Conf_1.000	351	0							
Locus_3092_Transcript_1/1_Conf_1.000	953	15	3.81E-50	NP_001040777.1	55	202.986	307	171	hypothetical protein F41C3.8
Locus_3093_Transcript_1/2_Conf_1.000	522	0							
Locus_3093_Transcript_2/2_Conf_1.000	522	0							
Locus_3094_Transcript_1/1_Conf_1.000	1275	2	9.96E-05	XP_002634488.1	59	52.7582	96	57	C. briggsae CBR-VAB-2 protein
Locus_3095_Transcript_1/2_Conf_1.000	1866	20	2.78E-161	NP_001129859.1	72	573.548	513	374	Nuclear Hormone Receptor family member (nhr-34)

Locus_3095_Transcript_2/2_Conf_1.000	1849	20	1.84E-165	NP_001129859.1	73	587.415	520	381	Nuclear Hormone Receptor family member (nhr-34)
Locus_3096_Transcript_1/1_Conf_1.000	806	20	5.50E-110	XP_002642113.1	89	401.364	240	215	C. briggsae CBR-RPS-1 protein
Locus_3097_Transcript_1/1_Conf_1.000	521	20	1.01E-34	XP_002630640.1	87	149.828	112	98	C. briggsae CBR-RPL-22 protein
Locus_3098_Transcript_1/1_Conf_1.000	1243	20	1.68E-174	NP_509658.1	89	616.69	414	369	Multidrug Resistance Protein family member (mrp-4)
Locus_3099_Transcript_1/1_Conf_1.000	965	6	2.15E-24	CAR97825.1	68	117.472	216	148	C. elegans protein F32F2.1c, partially confirmed by transcript evidence
Locus_31_Transcript_1/2_Conf_1.000	493	20	7.29E-21	EFO21324.1	64	103.605	125	81	hypothetical protein LOAG_07166
Locus_31_Transcript_2/2_Conf_1.000	493	20	7.29E-21	EFO21324.1	64	103.605	125	81	hypothetical protein LOAG_07166

Locus_310_Transcript_1/1_Conf_1.000	1197	20	3.19E-66	XP_002634531.1	63	256.914	328	207	C. briggsae CBR-TAF-2 protein
Locus_3100_Transcript_1/1_Conf_1.000	375	2	3.54E-15	XP_002639243.1	72	84.7297	59	43	Hypothetical protein CBG03801
Locus_3101_Transcript_1/1_Conf_1.000	1595	20	6.44E-132	NP_500311.1	82	475.707	352	290	hypothetical protein W08E12.7
Locus_3102_Transcript_1/1_Conf_1.000	951	20	5.66E-102	NP_500214.1	89	375.17	276	248	hypothetical protein Y69A2AR.18
Locus_3103_Transcript_1/1_Conf_1.000	370	0							
Locus_3104_Transcript_1/1_Conf_1.000	1087	20	1.54E-125	XP_001899737.1	91	453.751	335	305	SMC proteins Flexible Hinge Domain containing protein
Locus_3105_Transcript_1/4_Conf_0.700	2125	20	0	XP_001898310.1	91	1158.28	709	651	DNA-directed RNA polymerase II largest subunit
Locus_3105_Transcript_2/4_Conf_0.700	2125	20	0	XP_001898310.1	91	1158.28	709	651	DNA-directed RNA polymerase II largest subunit

Locus_3105_Transcript_3/4_Conf_0.700	2125	20	0	XP_001898310.1	91	1158.28	709	651	DNA-directed RNA polymerase II largest subunit
Locus_3105_Transcript_4/4_Conf_0.700	2125	20	0	XP_001898310.1	91	1158.28	709	651	DNA-directed RNA polymerase II largest subunit
Locus_3106_Transcript_1/1_Conf_1.000	490	0							
Locus_3107_Transcript_1/1_Conf_1.000	368	20	1.31E-30	EFO22541.1	75	135.961	93	70	CHromoDomain protein family member
Locus_3108_Transcript_1/4_Conf_0.667	1940	20	0	EFO25190.1	79	826.239	647	516	hypothetical protein LOAG_03297
Locus_3108_Transcript_2/4_Conf_0.667	1940	20	0	EFO25190.1	79	826.239	647	516	hypothetical protein LOAG_03297
Locus_3108_Transcript_3/4_Conf_0.667	1969	20	0	EFO25190.1	80	842.417	657	526	hypothetical protein LOAG_03297
Locus_3108_Transcript_4/4_Conf_0.667	1940	20	0	EFO25190.1	79	826.239	647	516	hypothetical protein LOAG_03297
Locus_3109_Transcript_1/1_Conf_1.000	2903	6	1.20E-07	EFO25743.1	38	63.929	263	102	hypothetical protein LOAG_02738

Locus_311_Transcript_1/1_Conf_1.000	1554	20	1.46E-173	XP_002644215.1	83	613.994	478	400	C. briggsae CBR-ACL-5 protein
Locus_3110_Transcript_1/1_Conf_1.000	178	0							
Locus_3111_Transcript_1/2_Conf_1.000	807	20	2.27E-79	NP_001023903.1	80	299.671	202	163	hypothetical protein F40A3.3
Locus_3111_Transcript_2/2_Conf_1.000	810	20	8.59E-79	NP_001023903.1	85	297.745	188	160	hypothetical protein F40A3.3
Locus_3112_Transcript_1/2_Conf_1.000	2176	20	2.47E-164	NP_505174.3	82	583.948	433	356	hypothetical protein F52E1.13
Locus_3112_Transcript_2/2_Conf_1.000	2176	20	2.47E-164	NP_505174.3	82	583.948	433	356	hypothetical protein F52E1.13
Locus_3113_Transcript_1/1_Conf_1.000	278	0							
Locus_3114_Transcript_1/1_Conf_1.000	1495	20	1.51E-135	NP_504452.1	71	487.649	436	313	DNaJ domain (prokaryotic heat shock protein) family member (dnj-19)
Locus_3115_Transcript_1/2_Conf_1.000	1182	20	3.94E-77	XP_002641753.1	66	293.123	314	209	Hypothetical protein CBG10092
Locus_3115_Transcript_2/2_Conf_1.000	1181	20	8.17E-75	XP_002641753.1	84	285.419	186	157	Hypothetical protein CBG10092
Locus_3116_Transcript_1/1_Conf_1.000	1008	20	2.26E-128	XP_002642775.1	88	462.996	307	271	C. briggsae CBR-NEX-1 protein
Locus_3117_Transcript_1/2_Conf_1.000	1160	20	6.52E-69	NP_001021501.1	60	265.774	377	227	UNCoordinated family member (unc-73)
Locus_3117_Transcript_2/2_Conf_1.000	974	20	4.37E-57	ACM46029.1	60	226.098	316	192	Uncoordinated protein 73, isoform h, confirmed by transcript evidence

Locus_3118_Transcript_1/2_Conf_1.000	930	20	2.32E-52	EFO20982.1	73	210.305	212	156	ThiF family protein
Locus_3118_Transcript_2/2_Conf_1.000	930	20	3.03E-52	EFO20982.1	73	209.92	212	156	ThiF family protein
Locus_3119_Transcript_1/1_Conf_1.000	609	20	2.53E-56	XP_002641486.1	85	222.246	135	116	Hypothetical protein CBG09777
Locus_312_Transcript_1/1_Conf_1.000	1360	20	9.17E-36	XP_001895788.1	76	155.992	122	93	RNase H family protein
Locus_3120_Transcript_1/1_Conf_1.000	334	20	2.76E-12	EFO20638.1	77	75.0998	59	46	oxidoreductase
Locus_3121_Transcript_1/5_Conf_0.545	811	20	2.89E-42	CBA11992.1	58	176.407	267	157	endonuclease-reverse transcriptase HmRTE-e01
Locus_3121_Transcript_2/5_Conf_0.455	930	20	1.83E-57	CBA11992.1	62	227.254	306	190	endonuclease-reverse transcriptase HmRTE-e01
Locus_3121_Transcript_3/5_Conf_0.545	1113	20	6.16E-77	CBA11992.1	63	292.352	368	233	endonuclease-reverse transcriptase HmRTE-e01
Locus_3121_Transcript_4/5_Conf_0.273	788	20	2.11E-42	CBA11992.1	59	176.792	265	157	endonuclease-reverse transcriptase HmRTE-e01
Locus_3121_Transcript_5/5_Conf_0.545	811	20	2.89E-42	CBA11992.1	58	176.407	267	157	endonuclease-reverse transcriptase HmRTE-e01
Locus_3122_Transcript_1/1_Conf_1.000	852	20	1.67E-83	EFO24144.1	85	313.538	191	164	eukaryotic translation initiation factor 4E type 3
Locus_3123_Transcript_1/2_Conf_1.000	1232	20	1.06E-88	AAK57805.1	100	331.643	170	170	putative retinol-binding protein

Locus_3123_Transcript_2/2_Conf_1.000	1232	20	1.06E-88	AAK57805.1	100	331.643	170	170	putative retinol-binding protein
Locus_3124_Transcript_1/1_Conf_1.000	313	0							
Locus_3125_Transcript_1/2_Conf_1.000	376	20	9.92E-26	XP_002640523.1	82	119.783	81	67	Hypothetical protein CBG18685
Locus_3125_Transcript_2/2_Conf_1.000	280	20	1.72E-22	NP_493023.1	82	108.997	73	60	hypothetical protein R09B3.3
Locus_3126_Transcript_1/1_Conf_1.000	704	20	4.63E-24	XP_001894364.1	55	115.546	173	96	YEATS family protein
Locus_3127_Transcript_1/3_Conf_0.400	641	8	6.75E-50	NP_495747.1	75	201.06	192	145	hypothetical protein K01C8.6
Locus_3127_Transcript_2/3_Conf_0.400	294	1	5.66E-05	XP_001902818.1	75	50.8322	40	30	50S ribosomal protein L10
Locus_3127_Transcript_3/3_Conf_0.400	635	8	5.04E-50	NP_495747.1	74	201.445	204	151	hypothetical protein K01C8.6
Locus_3128_Transcript_1/1_Conf_1.000	577	20	5.38E-55	AAK31527.3	74	217.624	195	145	Neuronal symmetry protein 1, partially confirmed by transcript evidence
Locus_3129_Transcript_1/1_Conf_1.000	880	11	9.16E-24	NP_001022602.1	79	115.161	83	66	MTM (myotubularin) family member (mtm-6)
Locus_313_Transcript_1/2_Conf_1.000	362	6	1.56E-23	XP_002634040.1	69	112.464	120	83	C. briggsae CBR-VIT-6 protein
Locus_313_Transcript_2/2_Conf_1.000	249	6	5.53E-13	XP_002634040.1	71	77.411	82	59	C. briggsae CBR-VIT-6 protein

Locus_3130_Transcript_1/6_Conf_0.667	2085	20	1.60E-128	XP_002641367.1	78	464.922	359	282	C. briggsae CBR-GBF-1 protein
Locus_3130_Transcript_2/6_Conf_0.667	2085	20	1.60E-128	XP_002641367.1	78	464.922	359	282	C. briggsae CBR-GBF-1 protein
Locus_3130_Transcript_3/6_Conf_0.667	2085	20	1.60E-128	XP_002641367.1	78	464.922	359	282	C. briggsae CBR-GBF-1 protein
Locus_3130_Transcript_4/6_Conf_0.667	2092	20	6.50E-130	XP_002641367.1	78	469.544	362	284	C. briggsae CBR-GBF-1 protein

Locus_3130_Transcript_5/6_Conf_0.667	2097	20	1.61E-128	XP_002641367.1	78	464.922	359	282	C. briggsae CBR-GBF-1 protein
Locus_3130_Transcript_6/6_Conf_0.667	2085	20	1.60E-128	XP_002641367.1	78	464.922	359	282	C. briggsae CBR-GBF-1 protein
Locus_3131_Transcript_1/1_Conf_1.000	1152	20	5.47E-68	XP_002639261.1	64	262.692	388	249	Hypothetical protein CBG03822
Locus_3132_Transcript_1/1_Conf_1.000	148	2	1.06E-18	AAF36134.1	100	87.0409	37	37	AF151048_1HSPC214
Locus_3133_Transcript_1/1_Conf_1.000	141	0							
Locus_3134_Transcript_1/1_Conf_1.000	211	0							
Locus_3135_Transcript_1/1_Conf_1.000	1416	20	3.54E-46	XP_002631000.1	66	190.66	321	213	Hypothetical protein CBG02746

Locus_3136_Transcript_1/1_Conf_1.000	649	20	1.42E-34	NP_491122.2	62	150.214	152	95	hypothetical protein Y54E10A.17
Locus_3137_Transcript_1/1_Conf_1.000	132	0							
Locus_3138_Transcript_1/1_Conf_1.000	648	3	9.85E-20	XP_002632658.1	61	100.908	111	68	Hypothetical protein CBG21582
Locus_3139_Transcript_1/1_Conf_1.000	423	20	1.10E-08	XP_002573439.1	53	63.1586	117	63	syntaxin
Locus_314_Transcript_1/3_Conf_0.250	2506	20	4.66E-162	NP_001021644.1	75	576.63	480	360	hypothetical protein T28F2.4
Locus_314_Transcript_2/3_Conf_0.625	1066	20	0	NP_508841.1	100	675.626	335	335	ACTin family member (act-4)

Locus_314_Transcript_3/3_Conf_0.625	1066	20	0	NP_505817.1	99	671.774	335	333	ACTin family member (act-3)
Locus_3140_Transcript_1/3_Conf_0.500	409	0							
Locus_3140_Transcript_2/3_Conf_0.667	448	0							
Locus_3140_Transcript_3/3_Conf_0.667	454	0							
Locus_3141_Transcript_1/3_Conf_0.714	2579	20	1.28E-122	NP_001021969.1	71	445.662	386	276	Cell Division Cycle related family member (cdc-14)
Locus_3141_Transcript_2/3_Conf_0.714	2575	20	1.28E-122	NP_001021969.1	71	445.662	386	276	Cell Division Cycle related family member (cdc-14)
Locus_3141_Transcript_3/3_Conf_0.714	2571	20	1.28E-122	NP_001021969.1	71	445.662	386	276	Cell Division Cycle related family member (cdc-14)

Locus_3142_Transcript_1/1_Conf_1.000	1419	20	0	NP_498047.1	97	819.305	424	412	RNA Polymerase II (B) subunit family member (rpb-2)
Locus_3143_Transcript_1/1_Conf_1.000	414	20	2.56E-18	NP_498407.1	62	95.1301	135	84	hypothetical protein C05D11.8
Locus_3144_Transcript_1/4_Conf_0.625	1127	20	1.11E-73	XP_001899238.1	57	281.567	399	230	Low-density lipoprotein receptor repeat class B containing protein
Locus_3144_Transcript_2/4_Conf_0.250	481	2	5.71E-18	XP_001899238.1	58	93.9745	148	86	Low-density lipoprotein receptor repeat class B containing protein
Locus_3144_Transcript_3/4_Conf_0.625	1007	20	1.14E-55	XP_001899238.1	51	221.476	399	207	Low-density lipoprotein receptor repeat class B containing protein
Locus_3144_Transcript_4/4_Conf_0.625	1118	20	2.20E-74	XP_001899238.1	57	283.878	399	230	Low-density lipoprotein receptor repeat class B containing protein
Locus_3145_Transcript_1/3_Conf_0.571	1281	0							
Locus_3145_Transcript_2/3_Conf_0.571	1340	0							
Locus_3145_Transcript_3/3_Conf_0.714	1275	0							
Locus_3146_Transcript_1/1_Conf_1.000	322	20	9.26E-40	ADD24466.1	86	166.392	106	92	Ubiquitin

Locus_3147_Transcript_1/1_Conf_1.000	897	20	1.67E-28	NP_505565.2	79	130.954	110	87	hypothetical protein T07C12.11
Locus_3148_Transcript_1/1_Conf_1.000	302	20	3.38E-26	XP_002637423.1	78	121.324	87	68	C. briggsae CBR-TTR-47 protein
Locus_3149_Transcript_1/1_Conf_1.000	739	8	1.49E-07	XP_002644389.1	84	60.8474	38	32	C. briggsae CBR-UVT-5 protein
Locus_315_Transcript_1/1_Conf_1.000	1022	20	3.75E-62	NP_504826.2	69	243.047	244	170	hypothetical protein F09G2.2
Locus_3150_Transcript_1/1_Conf_1.000	1721	20	0	NP_498984.1	82	781.171	569	468	Eukaryotic Initiation Factor family member (eif-3.D)
Locus_3151_Transcript_1/1_Conf_1.000	139	0							
Locus_3152_Transcript_1/1_Conf_1.000	557	0							
Locus_3153_Transcript_1/1_Conf_1.000	741	20	2.35E-77	NP_001022062.1	75	292.738	248	188	Acyl CoA DeHydrogenase family member (acdh-12)
Locus_3154_Transcript_1/1_Conf_1.000	740	20	2.63E-12	ACI49237.1	50	76.6406	118	59	hypothetical protein Csp3_JD06.003
Locus_3155_Transcript_1/1_Conf_1.000	923	20	2.06E-53	NP_500551.2	61	213.772	308	189	hypothetical protein F55F10.1
Locus_3156_Transcript_1/1_Conf_1.000	1118	20	2.77E-93	NP_501548.2	65	346.665	381	251	hypothetical protein C27B7.7
Locus_3157_Transcript_1/1_Conf_1.000	382	20	9.86E-18	XP_798273.2	59	93.2041	122	73	PREDICTED: similar to ABC transporter ABCA2, partial
Locus_3158_Transcript_1/1_Conf_1.000	868	10	1.69E-38	XP_002644340.1	56	164.081	313	177	C. briggsae CBR-RGL-1 protein
Locus_3159_Transcript_1/2_Conf_1.000	1805	20	6.77E-165	AAA97973.2	75	585.489	560	420	Hypothetical protein F21C10.7
Locus_3159_Transcript_2/2_Conf_1.000	1333	20	3.22E-94	AAA97973.2	74	350.132	343	254	Hypothetical protein F21C10.7

Locus_316_Transcript_1/1_Conf_1.000	681	5	7.62E-13	XP_002639910.1	44	78.1814	232	103	C. briggsae CBR-RBG-2 protein
Locus_3160_Transcript_1/1_Conf_1.000	2945	20	0	XP_002634092.1	60	648.662	860	522	Hypothetical protein CBG01639
Locus_3161_Transcript_1/2_Conf_1.000	299	0							
Locus_3161_Transcript_2/2_Conf_1.000	2168	20	0	XP_001899078.1	79	760.37	584	463	Ubiquitin carboxyl-terminal hydrolase family protein
Locus_3162_Transcript_1/1_Conf_1.000	430	0							
Locus_3163_Transcript_1/1_Conf_1.000	599	20	4.20E-61	XP_002646914.1	85	238.039	160	137	Hypothetical protein CBG19616
Locus_3164_Transcript_1/1_Conf_1.000	1442	20	0	XP_002645390.1	85	692.575	480	410	C. briggsae CBR-SEC-15 protein
Locus_3165_Transcript_1/1_Conf_1.000	322	2	5.12E-14	ABH10659.1	86	80.8777	50	43	FMRFamide-related peptide FLP-21 precursor
Locus_3166_Transcript_1/1_Conf_1.000	1627	4	1.17E-11	XP_422162.2	39	76.2554	541	216	PREDICTED: similar to telomere-associated protein RIF1
Locus_3167_Transcript_1/1_Conf_1.000	560	0							
Locus_3168_Transcript_1/1_Conf_1.000	449	9	2.21E-17	XP_002631214.1	89	92.0485	59	53	C. briggsae CBR-MPZ-1 protein

Locus_3169_Transcript_1/1_Conf_1.000	776	20	2.98E-118	EAW63270.1	100	428.713	212	212	indoleamine-pyrrole 2,3 dioxygenase, isoform CRA_a
Locus_317_Transcript_1/1_Conf_1.000	1443	20	0	XP_002630542.1	84	643.269	449	379	Hypothetical protein CBG12983
Locus_3170_Transcript_1/1_Conf_1.000	755	0							
Locus_3171_Transcript_1/1_Conf_1.000	472	0							
Locus_3172_Transcript_1/1_Conf_1.000	720	20	2.34E-111	XP_002646301.1	95	405.601	229	219	C. briggsae CBR-UNC-11 protein
Locus_3173_Transcript_1/2_Conf_1.000	2483	20	2.41E-86	XP_001664250.1	54	325.094	526	285	hypothetical protein AaeL_AAEL014030
Locus_3173_Transcript_2/2_Conf_1.000	2421	20	2.36E-86	XP_001664250.1	54	325.094	526	285	hypothetical protein AaeL_AAEL014030
Locus_3174_Transcript_1/2_Conf_1.000	2190	20	0	NP_001023556.1	91	1162.13	732	673	Membrane Calcium ATPase family member (mca-3)

Locus_3174_Transcript_2/2_Conf_1.000	2142	20	0	NP_001023556.1	93	1170.22	717	673	Membrane Calcium ATPase family member (mca-3)
Locus_3175_Transcript_1/1_Conf_1.000	395	0							
Locus_3176_Transcript_1/1_Conf_1.000	281	0							
Locus_3177_Transcript_1/1_Conf_1.000	1163	20	1.47E-44	EFO27677.1	86	184.882	138	120	hypothetical protein LOAG_00808
Locus_3178_Transcript_1/4_Conf_0.333	389	20	1.85E-16	XP_002639457.1	73	88.9669	71	52	C. briggsae CBR-HRPF-1 protein
Locus_3178_Transcript_2/4_Conf_0.667	1032	20	3.05E-35	XP_002639457.1	42	153.68	388	166	C. briggsae CBR-HRPF-1 protein
Locus_3178_Transcript_3/4_Conf_0.667	1186	20	6.60E-32	NP_740877.1	47	142.895	379	180	HnRNP F homolog family member (hrpf-1)
Locus_3178_Transcript_4/4_Conf_0.667	1212	20	6.84E-32	NP_740877.1	47	142.895	379	180	HnRNP F homolog family member (hrpf-1)
Locus_3179_Transcript_1/1_Conf_1.000	573	0							
Locus_318_Transcript_1/3_Conf_0.700	2396	8	1.39E-22	EFO22283.1	68	113.235	119	81	WNK protein kinase
Locus_318_Transcript_2/3_Conf_0.800	4174	20	0	XP_001896032.1	77	721.465	553	431	Protein kinase domain containing protein

Locus_318_Transcript_3/3_Conf_0.800	4183	20	0	XP_001896032.1	77	721.465	553	431	Protein kinase domain containing protein
Locus_3180_Transcript_1/1_Conf_1.000	1318	20	3.09E-65	XP_001902430.1	60	253.832	374	225	WD repeat domain, X-linked 1
Locus_3181_Transcript_1/1_Conf_1.000	232	0							
Locus_3182_Transcript_1/1_Conf_1.000	1239	20	4.30E-138	EFO26116.1	74	495.738	409	303	BRCA1-associated protein 2 containing protein
Locus_3183_Transcript_1/1_Conf_1.000	676	20	1.25E-76	AAK31453.4	77	290.041	223	173	Hypothetical protein C25H3.8
Locus_3184_Transcript_1/1_Conf_1.000	371	14	1.31E-25	XP_002643051.1	69	119.398	111	77	C. briggsae CBR-DPF-6 protein
Locus_3185_Transcript_1/1_Conf_1.000	186	20	1.83E-19	XP_002646487.1	85	98.9821	61	52	Hypothetical protein CBG19469
Locus_3186_Transcript_1/1_Conf_1.000	1263	20	4.95E-65	EFO16437.1	54	253.062	389	211	WD-repeat protein 22
Locus_3187_Transcript_1/1_Conf_1.000	885	20	5.37E-64	NP_501500.1	75	248.825	224	168	hypothetical protein F21D5.1
Locus_3188_Transcript_1/1_Conf_1.000	1388	20	5.30E-71	XP_001895415.1	56	273.092	424	240	TTC5 protein

Locus_3189_Transcript_1/1_Conf_1.000	995	20	1.80E-130	XP_002639121.1	91	469.929	271	248	Hypothetical protein CBG14940
Locus_319_Transcript_1/1_Conf_1.000	332	20	7.05E-16	XP_001896614.1	78	87.0409	65	51	hypothetical protein Bm1_25775
Locus_3190_Transcript_1/1_Conf_1.000	1395	4	1.37E-18	NP_001040729.1	68	98.9821	85	58	hypothetical protein C05C10.5
Locus_3191_Transcript_1/2_Conf_1.000	407	20	3.72E-49	XP_002641975.1	88	197.593	125	111	C. briggsae CBR-RPL-21 protein
Locus_3191_Transcript_2/2_Conf_1.000	407	20	3.72E-49	XP_002641975.1	88	197.593	125	111	C. briggsae CBR-RPL-21 protein
Locus_3192_Transcript_1/1_Conf_1.000	200	0							
Locus_3193_Transcript_1/1_Conf_1.000	304	0							
Locus_3194_Transcript_1/2_Conf_1.000	1016	6	4.24E-66	XP_002634901.1	64	256.144	346	223	Hypothetical protein CBG22497
Locus_3194_Transcript_2/2_Conf_1.000	1156	6	2.81E-80	XP_002634901.1	65	303.523	391	255	Hypothetical protein CBG22497
Locus_3195_Transcript_1/1_Conf_1.000	2313	20	0	NP_490830.2	77	759.985	598	462	hypothetical protein Y48G8AL.5
Locus_3196_Transcript_1/3_Conf_0.444	244	0							
Locus_3196_Transcript_2/3_Conf_0.778	960	20	1.75E-34	NP_495483.1	82	150.984	97	80	hypothetical protein C27H5.3
Locus_3196_Transcript_3/3_Conf_0.778	966	20	1.77E-34	NP_495483.1	82	150.984	97	80	hypothetical protein C27H5.3

Locus_3197_Transcript_1/3_Conf_0.714	687	6	2.66E-37	XP_002630066.1	89	159.458	95	85	Hypothetical protein CBG13442
Locus_3197_Transcript_2/3_Conf_0.714	687	6	2.66E-37	XP_002630066.1	89	159.458	95	85	Hypothetical protein CBG13442
Locus_3197_Transcript_3/3_Conf_0.714	687	6	2.66E-37	XP_002630066.1	89	159.458	95	85	Hypothetical protein CBG13442
Locus_3198_Transcript_1/1_Conf_1.000	774	20	1.06E-06	XP_002436012.1	42	58.151	141	60	hemolectin, putative
Locus_3199_Transcript_1/1_Conf_1.000	422	20	3.78E-33	XP_002633344.1	67	144.436	144	97	C. briggsae CBR-MAGI-1 protein
Locus_32_Transcript_1/1_Conf_1.000	1084	20	1.32E-161	XP_002630674.1	94	573.548	305	289	Hypothetical protein CBG02349
Locus_320_Transcript_1/1_Conf_1.000	931	20	2.62E-88	CAR63544.1	97	329.717	200	194	putative Ribosomal Protein

Locus_3200_Transcript_1/1_Conf_1.000	1313	20	1.22E-138	NP_001024798.1	86	497.664	330	286	Suppressor of LIneage defect family member (sli-1)
Locus_3201_Transcript_1/1_Conf_1.000	990	20	2.65E-49	NP_498690.2	64	200.29	295	190	hypothetical protein ZK686.2
Locus_3202_Transcript_1/1_Conf_1.000	1602	20	1.16E-72	EFO21763.1	60	278.87	370	223	WD domain-containing protein
Locus_3203_Transcript_1/1_Conf_1.000	482	20	2.73E-28	NP_001076680.1	71	128.257	123	88	hypothetical protein F13H10.3
Locus_3204_Transcript_1/1_Conf_1.000	216	0							
Locus_3205_Transcript_1/1_Conf_1.000	348	0							
Locus_3206_Transcript_1/1_Conf_1.000	210	5	1.20E-07	NP_497707.1	70	59.6918	51	36	hypothetical protein K01A11.2
Locus_3207_Transcript_1/2_Conf_1.000	813	1	1.84E-04	XP_001894039.1	64	50.8322	56	36	Rhodanese-like domain containing protein
Locus_3207_Transcript_2/2_Conf_1.000	783	1	3.48E-05	XP_001894039.1	49	53.1434	116	57	Rhodanese-like domain containing protein
Locus_3208_Transcript_1/1_Conf_1.000	1040	20	7.99E-52	NP_495166.2	56	208.764	338	190	hypothetical protein H41C03.3
Locus_3209_Transcript_1/6_Conf_0.250	374	20	9.62E-29	NP_492616.1	66	129.798	111	74	Nematode AStacin protease family member (nas-5)
Locus_3209_Transcript_2/6_Conf_0.438	521	20	1.36E-39	NP_492616.1	66	166.007	143	95	Nematode AStacin protease family member (nas-5)
Locus_3209_Transcript_3/6_Conf_0.375	392	20	2.47E-29	NP_492616.1	66	131.724	111	74	Nematode AStacin protease family member (nas-5)
Locus_3209_Transcript_4/6_Conf_0.375	426	20	2.51E-29	NP_492616.1	66	131.724	111	74	Nematode AStacin protease family member (nas-5)
Locus_3209_Transcript_5/6_Conf_0.312	258	20	6.27E-20	NP_492616.1	66	100.523	86	57	Nematode AStacin protease family member (nas-5)

Locus_3209_Transcript_6/6_Conf_0.375	258	20	6.27E-20	NP_492616.1	66	100.523	86	57	Nematode AStacin protease family member (nas-5)
Locus_321_Transcript_1/1_Conf_1.000	969	20	3.64E-96	NP_505979.1	75	355.91	319	241	hypothetical protein D2023.5
Locus_3210_Transcript_1/2_Conf_1.000	1343	20	1.75E-39	NP_497592.1	52	168.318	317	167	hypothetical protein Y71H2B.2
Locus_3210_Transcript_2/2_Conf_1.000	1343	20	1.03E-39	NP_497592.1	52	169.088	317	168	hypothetical protein Y71H2B.2
Locus_3211_Transcript_1/1_Conf_1.000	1095	20	4.65E-37	NP_492456.2	62	159.844	235	146	hypothetical protein F25H5.5
Locus_3212_Transcript_1/1_Conf_1.000	1298	0							
Locus_3213_Transcript_1/1_Conf_1.000	1318	20	9.09E-142	NP_001041137.1	73	508.064	427	315	Alpha MANnosidase family member (aman-2)
Locus_3214_Transcript_1/1_Conf_1.000	1520	20	0	XP_002640929.1	91	743.806	464	426	C. briggsae CBR-TUFM-1 protein
Locus_3215_Transcript_1/1_Conf_1.000	625	0							
Locus_3216_Transcript_1/1_Conf_1.000	794	20	5.07E-60	EFO24908.1	68	235.343	224	154	oxysterol binding protein
Locus_3217_Transcript_1/2_Conf_1.000	1570	20	2.31E-150	XP_002636889.1	68	536.954	528	360	C. briggsae CBR-HEX-2 protein
Locus_3217_Transcript_2/2_Conf_1.000	580	20	1.89E-31	XP_002636889.1	56	139.428	199	113	C. briggsae CBR-HEX-2 protein
Locus_3218_Transcript_1/1_Conf_1.000	410	0							
Locus_3219_Transcript_1/1_Conf_1.000	1319	20	2.66E-117	CBW48561.1	73	426.787	373	273	Hypothetical protein Y111B2A.12a
Locus_322_Transcript_1/1_Conf_1.000	592	20	1.27E-54	XP_002646548.1	84	216.468	145	122	C. briggsae CBR-CPN-4 protein
Locus_3220_Transcript_1/2_Conf_1.000	647	20	4.64E-46	NP_491198.1	83	188.348	159	133	FerriTiN family member (ftn-2)

Locus_3220_Transcript_2/2_Conf_1.000	632	20	6.08E-48	NP_491198.1	86	194.512	154	133	FerriTiN family member (ftn-2)
Locus_3221_Transcript_1/1_Conf_1.000	610	20	2.60E-69	EFO15646.1	79	265.388	203	162	hypothetical protein LOAG_12863
Locus_3222_Transcript_1/1_Conf_1.000	1009	20	8.91E-117	XP_002639985.1	96	424.476	226	219	C. briggsae CBR-PAS-3 protein
Locus_3223_Transcript_1/1_Conf_1.000	757	20	1.56E-108	XP_002643138.1	86	396.356	251	218	Hypothetical protein CBG15316
Locus_3224_Transcript_1/1_Conf_1.000	146	0							
Locus_3225_Transcript_1/1_Conf_1.000	1077	20	4.97E-177	NP_001022641.1	91	624.78	358	329	LEThal family member (let-805)
Locus_3226_Transcript_1/1_Conf_1.000	338	20	2.55E-42	NP_495808.2	86	174.866	112	97	STCH (truncated HSP) family member (stc-1)
Locus_3227_Transcript_1/1_Conf_1.000	382	0							
Locus_3228_Transcript_1/8_Conf_0.667	2038	0							
Locus_3228_Transcript_2/8_Conf_0.667	2038	0							
Locus_3228_Transcript_3/8_Conf_0.381	1404	0							
Locus_3228_Transcript_4/8_Conf_0.667	2038	0							

Locus_3228_Transcript_5/8_Conf_0.667	2038	0							
Locus_3228_Transcript_6/8_Conf_0.667	2038	0							
Locus_3228_Transcript_7/8_Conf_0.667	2038	0							
Locus_3228_Transcript_8/8_Conf_0.667	2038	0							
Locus_3229_Transcript_1/1_Conf_1.000	1590	1	1.06E-17		53	96.2857	150	80	hypothetical 18K protein
Locus_323_Transcript_1/1_Conf_1.000	1073	20	3.33E-24	NP_501527.1	71	117.087	99	71	COLlagen family member (col-3)
Locus_3230_Transcript_1/1_Conf_1.000	138	14	2.75E-12	XP_002631560.1	86	75.0998	46	40	Hypothetical protein CBG20736
Locus_3231_Transcript_1/1_Conf_1.000	128	0							
Locus_3232_Transcript_1/1_Conf_1.000	261	0							
Locus_3233_Transcript_1/2_Conf_1.000	1534	20	0	XP_002644811.1	93	702.205	437	407	C. briggsae CBR-HSP-3 protein

Locus_3233_Transcript_2/2_Conf_1.000	1534	20	0	XP_002644811.1	93	702.205	437	407	C. briggsae CBR-HSP-3 protein
Locus_3234_Transcript_1/1_Conf_1.000	385	0							
Locus_3235_Transcript_1/1_Conf_1.000	419	20	2.14E-52	EAX01930.1	100	208.379	113	113	cytochrome c oxidase subunit Vb
Locus_3236_Transcript_1/1_Conf_1.000	207	0							
Locus_3237_Transcript_1/1_Conf_1.000	1109	20	1.07E-97	XP_002643973.1	71	361.303	345	245	C. briggsae CBR-PRX-12 protein
Locus_3238_Transcript_1/1_Conf_1.000	892	20	4.92E-65	NP_001122749.1	64	252.292	296	190	hypothetical protein ZK643.3
Locus_3239_Transcript_1/1_Conf_1.000	719	20	6.66E-34	XP_001893083.1	57	148.288	180	103	PHD-finger family protein
Locus_324_Transcript_1/2_Conf_1.000	719	20	1.06E-47	XP_002634550.1	99	194.126	116	115	C. briggsae CBR-RPS-14 protein

Locus_324_Transcript_2/2_Conf_1.000	719	20	6.86E-47	XP_002634550.1	99	191.43	116	115	C. briggsae CBR-RPS-14 protein
Locus_3240_Transcript_1/1_Conf_1.000	2314	20	7.11E-117	XP_002630611.1	67	426.402	488	328	Hypothetical protein CBG02274
Locus_3241_Transcript_1/1_Conf_1.000	918	20	3.95E-89	XP_002643058.1	69	332.413	323	225	C. briggsae CBR-DCR-1 protein
Locus_3242_Transcript_1/2_Conf_1.000	473	4	6.62E-14	NP_501671.1	72	80.4925	81	59	hypothetical protein F38E11.5
Locus_3242_Transcript_2/2_Conf_1.000	482	4	6.53E-14	NP_501671.1	72	80.4925	81	59	hypothetical protein F38E11.5
Locus_3243_Transcript_1/1_Conf_1.000	1318	20	2.56E-27	XP_002644673.1	54	127.872	238	129	C. briggsae CBR-AGS-3 protein
Locus_3244_Transcript_1/1_Conf_1.000	1634	20	1.41E-73	NP_491642.2	53	281.952	549	296	hypothetical protein F46F11.9
Locus_3245_Transcript_1/1_Conf_1.000	792	20	4.11E-94	XP_002636822.1	99	348.591	179	178	C. briggsae CBR-RPT-2 protein

Locus_3246_Transcript_1/1_Conf_1.000	684	20	1.78E-110	AAC47514.1	97	402.519	215	209	RRM-type RNA binding protein
Locus_3247_Transcript_1/2_Conf_1.000	1434	20	4.06E-88	XP_002639179.1	82	317.005	198	164	Hypothetical protein CBG03720
Locus_3247_Transcript_2/2_Conf_1.000	1423	20	1.74E-93	XP_002639179.1	81	347.821	229	186	Hypothetical protein CBG03720
Locus_3248_Transcript_1/1_Conf_1.000	243	0							
Locus_3249_Transcript_1/1_Conf_1.000	968	20	2.26E-106	XP_001894227.1	82	389.808	271	223	prolyl oligopeptidase family protein
Locus_325_Transcript_1/1_Conf_1.000	304	0							
Locus_3250_Transcript_1/1_Conf_1.000	295	20	6.44E-17	XP_002636703.1	67	90.5077	96	65	Hypothetical protein CBG23421
Locus_3251_Transcript_1/2_Conf_1.000	447	20	4.12E-56	NP_492193.2	83	220.705	151	126	JunctoPHilin family member (jph-1)
Locus_3251_Transcript_2/2_Conf_1.000	456	20	1.03E-59	NP_492193.2	85	232.646	151	129	JunctoPHilin family member (jph-1)
Locus_3252_Transcript_1/2_Conf_1.000	1386	20	9.42E-161	NP_001022992.1	81	571.237	387	315	CYtoKinesis defect family member (cyk-3)
Locus_3252_Transcript_2/2_Conf_1.000	1272	20	8.30E-161	NP_001022992.1	81	571.237	387	315	CYtoKinesis defect family member (cyk-3)
Locus_3253_Transcript_1/1_Conf_1.000	524	20	4.03E-55	XP_002630351.1	89	217.624	123	110	C. briggsae CBR-TTR-41 protein
Locus_3254_Transcript_1/1_Conf_1.000	357	0							
Locus_3255_Transcript_1/1_Conf_1.000	479	20	3.00E-67	NP_502365.1	95	257.684	134	128	Ribosomal Protein, Small subunit family member (rps-23)
Locus_3256_Transcript_1/1_Conf_1.000	865	20	2.46E-114		86	416.001	288	248	protein C43E11.4

Locus_3257_Transcript_1/3_Conf_0.714	1230	20	6.21E-97	XP_001901521.1	68	358.992	349	240	Protein kinase domain containing protein
Locus_3257_Transcript_2/3_Conf_0.286	318	0							
Locus_3257_Transcript_3/3_Conf_0.714	1230	20	6.21E-97	XP_001901521.1	68	358.992	349	240	Protein kinase domain containing protein
Locus_3258_Transcript_1/1_Conf_1.000	499	20	3.91E-67	XP_002637724.1	97	257.299	140	136	C. briggsae CBR-RPS-16 protein
Locus_3259_Transcript_1/2_Conf_1.000	624	20	1.91E-46	NP_001022619.1	68	189.504	209	143	NorDiHydroGuaiaretic acid resistant family member (ndg-4)
Locus_3259_Transcript_2/2_Conf_1.000	624	20	1.91E-46	NP_001022619.1	68	189.504	209	143	NorDiHydroGuaiaretic acid resistant family member (ndg-4)

Locus_326_Transcript_1/1_Conf_1.000	1656	20	4.45E-91	NP_872037.1	76	340.117	350	268	hypothetical protein F55C12.1
Locus_3260_Transcript_1/1_Conf_1.000	248	0							
Locus_3261_Transcript_1/1_Conf_1.000	2313	7	4.59E-15	EFO26059.1	41	88.1965	666	278	hypothetical protein LOAG_02422
Locus_3262_Transcript_1/1_Conf_1.000	189	8	3.34E-13	NP_510810.3	75	78.1814	61	46	PaTched Related family member (ptr-5)
Locus_3263_Transcript_1/1_Conf_1.000	677	20	1.82E-51	NP_492981.1	59	206.453	204	121	hypothetical protein T22H2.6
Locus_3264_Transcript_1/1_Conf_1.000	248	0							
Locus_3265_Transcript_1/1_Conf_1.000	710	20	2.10E-125	XP_001915548.1	100	452.21	217	217	PREDICTED: similar to QM protein
Locus_3266_Transcript_1/1_Conf_1.000	2137	20	0	XP_002639653.1	82	1087.4	725	600	C. briggsae CBR-SUP-17 protein
Locus_3267_Transcript_1/1_Conf_1.000	842	20	1.48E-68	XP_002641467.1	83	263.848	206	173	Hypothetical protein CBG09751
Locus_3268_Transcript_1/1_Conf_1.000	276	0							
Locus_3269_Transcript_1/1_Conf_1.000	2326	20	0	XP_001891733.1	70	774.622	763	537	Laminin related. see also lmb- protein 1
Locus_327_Transcript_1/2_Conf_1.000	673	20	3.42E-18	NP_502288.1	48	95.9005	230	111	hypothetical protein K08E4.6

Locus_327_Transcript_2/2_Conf_1.000	673	20	3.42E-18	NP_502288.1	48	95.9005	230	111	hypothetical protein K08E4.6
Locus_3270_Transcript_1/1_Conf_1.000	1143	20	6.10E-112	XP_966556.1	76	408.683	312	240	PREDICTED: similar to WD40 protein
Locus_3271_Transcript_1/1_Conf_1.000	1072	20	8.79E-134	XP_002630463.1	85	481.1	304	260	C. briggsae CBR-ART-1 protein
Locus_3272_Transcript_1/1_Conf_1.000	1448	20	1.65E-123	XP_002631349.1	72	447.588	454	329	Hypothetical protein CBG03180
Locus_3273_Transcript_1/1_Conf_1.000	468	3	7.61E-10	NP_740837.1	88	67.0106	76	67	NeurABin family member (nab-1)
Locus_3274_Transcript_1/1_Conf_1.000	1154	20	4.79E-64	NP_491872.1	61	249.595	285	175	hypothetical protein C55B7.3
Locus_3275_Transcript_1/1_Conf_1.000	804	20	2.37E-20	XP_001629765.1	58	103.605	178	104	predicted protein
Locus_3276_Transcript_1/1_Conf_1.000	558	2	2.99E-04	EFO26732.1	71	48.9062	52	37	hypothetical protein LOAG_01748
Locus_3277_Transcript_1/1_Conf_1.000	1156	20	1.73E-146	NP_001021908.1	81	523.472	389	316	CAN cell Migration defective family member (cam-1)
Locus_3278_Transcript_1/1_Conf_1.000	226	9	2.73E-07	NP_001040795.1	60	58.5362	75	45	Nuclear Pore complex Protein family member (npp-21)
Locus_3279_Transcript_1/1_Conf_1.000	447	0							
Locus_328_Transcript_1/1_Conf_1.000	589	11	6.71E-16	NP_492102.1	68	87.8113	99	68	hypothetical protein T28F4.5
Locus_3280_Transcript_1/2_Conf_1.000	1042	20	7.36E-122	XP_002636969.1	90	441.425	252	227	Hypothetical protein CBG09450
Locus_3280_Transcript_2/2_Conf_1.000	1042	20	5.64E-122	XP_002636969.1	90	441.81	252	227	Hypothetical protein CBG09450
Locus_3281_Transcript_1/2_Conf_1.000	677	20	1.06E-59	NP_001023605.1	84	233.802	197	166	hypothetical protein ZC477.3
Locus_3281_Transcript_2/2_Conf_1.000	677	20	1.06E-59	NP_001023605.1	84	233.802	197	166	hypothetical protein ZC477.3
Locus_3282_Transcript_1/2_Conf_0.667	336								

Locus_3282_Transcript_2/2_Conf_0.667	336								
Locus_3283_Transcript_1/1_Conf_1.000	679	20	2.17E-44	XP_001898089.1	74	182.956	203	151	uridine monophosphate kinase
Locus_3284_Transcript_1/1_Conf_1.000	1217	20	3.33E-111	NP_492207.1	90	406.371	283	257	CYtochrome C family member (cyc-1)
Locus_3285_Transcript_1/1_Conf_1.000	1106	20	6.82E-145	XP_002643138.1	89	518.079	319	285	Hypothetical protein CBG15316
Locus_3286_Transcript_1/1_Conf_1.000	406	20	7.30E-21	XP_001895616.1	64	103.605	137	89	CG8232-PA
Locus_3287_Transcript_1/1_Conf_1.000	185	0							
Locus_3288_Transcript_1/1_Conf_1.000	414	20	3.69E-33	NP_498778.1	82	144.436	104	86	hypothetical protein D2007.4
Locus_3289_Transcript_1/1_Conf_1.000	299	0							
Locus_329_Transcript_1/1_Conf_1.000	1222	20	7.04E-85	XP_002640778.1	67	318.931	324	218	C. briggsae CBR-FRL-1 protein
Locus_3290_Transcript_1/2_Conf_1.000	207	0							
Locus_3290_Transcript_2/2_Conf_1.000	1877	20	0	NP_499087.2	93	719.539	455	424	BT (Bacillus thuringiensis) toxin REsistant family member (bre-3)
Locus_3291_Transcript_1/2_Conf_1.000	3308	20	0	NP_001033397.1	78	1413.67	1060	833	Sensory AXon guidance family member (sax-7)

Locus_3291_Transcript_2/2_Conf_1.000	3674	20	0	NP_001033395.1	78	1638.62	1240	971	Sensory AXon guidance family member (sax-7)
Locus_3292_Transcript_1/1_Conf_1.000	167	0							
Locus_3293_Transcript_1/1_Conf_1.000	379	20	1.93E-21	XP_002647137.1	64	105.531	119	77	Hypothetical protein CBG16435
Locus_3294_Transcript_1/1_Conf_1.000	2195	20	0	ACI49172.1	65	642.114	745	491	hypothetical protein Csp3_JD01.004
Locus_3295_Transcript_1/1_Conf_1.000	692	20	2.18E-63	XP_002640222.1	81	246.128	172	141	Hypothetical protein CBG12733
Locus_3296_Transcript_1/1_Conf_1.000	690	20	5.00E-76	XP_002639744.1	77	288.115	230	179	C. briggsae CBR-LAM-3 protein
Locus_3297_Transcript_1/1_Conf_1.000	622	8	6.63E-76	XP_002632697.1	83	287.345	206	172	Hypothetical protein CBG21629
Locus_3298_Transcript_1/1_Conf_1.000	499	20	6.48E-54	NP_499892.1	72	213.386	158	114	hypothetical protein T21D12.12
Locus_3299_Transcript_1/1_Conf_1.000	2439	20	0	XP_002648413.1	71	788.489	774	551	Hypothetical protein CBG24676
Locus_33_Transcript_1/2_Conf_1.000	1770	20	0	NP_502793.1	98	906.36	474	466	hypothetical protein Y57G11C.15
Locus_33_Transcript_2/2_Conf_1.000	1159	20	2.28E-114	XP_001899170.1	98	416.772	216	212	probable transport protein Sec61 alpha subunit

Locus_330_Transcript_1/1_Conf_1.000	456	20	1.61E-28	XP_002633496.1	76	129.028	93	71	Hypothetical protein CBG06268
Locus_3300_Transcript_1/1_Conf_1.000	1728	20	0	NP_497809.1	85	880.167	578	497	Heavy chain, Unconventional Myosin family member (hum-5)
Locus_3301_Transcript_1/1_Conf_1.000	1654	20	4.87E-122	XP_001897908.1	72	442.965	385	280	Innexin family protein
Locus_3302_Transcript_1/1_Conf_1.000	616	20	1.37E-65	NP_499797.1	78	253.062	191	149	Polarity and Osmotic sensitivity Defect family member (pod-1)
Locus_3303_Transcript_1/1_Conf_1.000	321	0							
Locus_3304_Transcript_1/1_Conf_1.000	625	20	2.23E-79	EFO19891.1	86	298.901	197	170	HCFC1 protein
Locus_3305_Transcript_1/1_Conf_1.000	1407	20	0	XP_002633963.1	89	647.121	457	411	C. briggsae CBR-AAT-1 protein
Locus_3306_Transcript_1/1_Conf_1.000	2161	20	0	NP_492638.1	84	943.725	628	529	Eukaryotic Initiation Factor family member (eif-3.C)
Locus_3307_Transcript_1/1_Conf_1.000	2718	20	2.84E-27	XP_002639769.1	46	129.028	274	128	C. briggsae CBR-DUO-3 protein
Locus_3308_Transcript_1/1_Conf_1.000	2562	20	0	EFO27141.1	83	690.263	510	425	importin alpha-3 subunit
Locus_3309_Transcript_1/1_Conf_1.000	756	0							
Locus_331_Transcript_1/1_Conf_1.000	1021	20	3.38E-79	NP_494564.2	68	299.671	328	224	CYclin H family member (cyh-1)

Locus_3310_Transcript_1/3_Conf_0.667	2701	20	8.09E-67	EFO22156.1	64	260.381	295	190	hypothetical protein LOAG_06328
Locus_3310_Transcript_2/3_Conf_0.667	2713	20	8.13E-67	EFO22156.1	64	260.381	295	190	hypothetical protein LOAG_06328
Locus_3310_Transcript_3/3_Conf_0.667	2713	20	8.13E-67	EFO22156.1	64	260.381	295	190	hypothetical protein LOAG_06328
Locus_3311_Transcript_1/1_Conf_1.000	1410	20	3.78E-141	XP_002633656.1	76	506.138	472	359	C. briggsae CBR-GEX-3 protein
Locus_3312_Transcript_1/1_Conf_1.000	1202	20	2.65E-137	XP_002634116.1	81	493.041	383	314	C. briggsae CBR-SRS-1 protein
Locus_3313_Transcript_1/1_Conf_1.000	467	0							
Locus_3314_Transcript_1/1_Conf_1.000	2237	20	2.00E-99	NP_001122626.1	62	362.073	487	304	DAB (Drosophila disabled) homolog family member (dab-1)
Locus_3315_Transcript_1/1_Conf_1.000	485	0							
Locus_3316_Transcript_1/1_Conf_1.000	2044	20	0	AAA93233.1	95	810.831	516	491	CCT-2
Locus_3317_Transcript_1/1_Conf_1.000	591	20	6.26E-78	NP_502542.1	100	293.893	150	150	Ribosomal Protein, Large subunit family member (rpl-12)

Locus_3319_Transcript_1/1_Conf_1.000	1057	20	2.59E-122	NP_496336.1	87	442.965	271	238	CAP-z protein family member (cap-2)
Locus_332_Transcript_1/1_Conf_1.000	3010	20	0	NP_508811.1	70	1024.23	957	675	Alpha MANnosidase family member (aman-1)
Locus_3320_Transcript_1/1_Conf_1.000	1047	20	2.56E-114	XP_002639636.1	94	416.387	238	224	C. briggsae CBR-PAS-4 protein
Locus_3321_Transcript_1/1_Conf_1.000	796	20	4.38E-128	NP_505722.1	92	461.455	264	244	SCP(Small C-terminal domain Phosphatase)-Like phosphatase family member (scpl-4)
Locus_3322_Transcript_1/1_Conf_1.000	262	0							
Locus_3323_Transcript_1/1_Conf_1.000	147	0							
Locus_3324_Transcript_1/2_Conf_1.000	540	20	6.90E-40	CBA11992.1	65	167.162	179	118	endonuclease-reverse transcriptase HmRTE-e01

Locus_3324_Transcript_2/2_Conf_1.000	265	20	2.62E-10	CBA11992.1	60	68.5514	87	53	endonuclease-reverse transcriptase HmRTE-e01
Locus_3325_Transcript_1/1_Conf_1.000	897	3	1.38E-06	XP_729910.1	47	58.151	213	101	hypothetical protein
Locus_3326_Transcript_1/1_Conf_1.000	382	0							
Locus_3327_Transcript_1/1_Conf_1.000	532	4	8.48E-11	XP_002647160.1	61	70.4774	83	51	C. briggsae CBR-FLP-9 protein
Locus_3328_Transcript_1/1_Conf_1.000	305	20	1.42E-16	XP_001604031.1	85	89.3521	62	53	PREDICTED: similar to conserved hypothetical protein
Locus_3329_Transcript_1/1_Conf_1.000	483	20	2.70E-47	NP_491792.1	95	191.43	100	95	phenylalanyl (F) tRNA Synthetase family member (frs-1)
Locus_333_Transcript_1/5_Conf_0.167	203	0							
Locus_333_Transcript_2/5_Conf_0.667	745	2	2.77E-09	XP_002644899.1	55	66.6254	142	79	C. briggsae CBR-CEH-60 protein
Locus_333_Transcript_3/5_Conf_0.167	339	0							
Locus_333_Transcript_4/5_Conf_0.667	1071	20	1.54E-29	XP_002644899.1	56	134.806	233	132	C. briggsae CBR-CEH-60 protein

Locus_333_Transcript_5/5_Conf_0.667	997	20	1.38E-29	XP_002644899.1	56	134.806	233	132	C. briggsae CBR-CEH-60 protein
Locus_3330_Transcript_1/1_Conf_1.000	179	0							
Locus_3331_Transcript_1/1_Conf_1.000	438	0							
Locus_3332_Transcript_1/2_Conf_1.000	360	0							
Locus_3332_Transcript_2/2_Conf_1.000	354	0							
Locus_3333_Transcript_1/1_Conf_1.000	1778	20	5.32E-122	NP_501354.1	77	442.965	336	259	hypothetical protein Y42H9AR.1
Locus_3334_Transcript_1/1_Conf_1.000	874	20	1.06E-80	XP_002644659.1	70	304.294	271	192	Hypothetical protein CBG14639
Locus_3335_Transcript_1/2_Conf_1.000	480	2	2.49E-05	EFO22995.1	62	51.9878	48	30	hypothetical protein LOAG_05488
Locus_3335_Transcript_2/2_Conf_1.000	482	0							
Locus_3336_Transcript_1/1_Conf_1.000	359	0							
Locus_3337_Transcript_1/1_Conf_1.000	610	20	3.40E-55	ABW90417.1	81	154.451	101	82	putative ribosomal protein S11
Locus_3338_Transcript_1/1_Conf_1.000	641	4	1.05E-10	NP_499780.1	53	70.8626	99	53	Temporarily Assigned Gene name family member (tag-164)
Locus_3339_Transcript_1/1_Conf_1.000	559	0							
Locus_334_Transcript_1/1_Conf_1.000	1118	20	1.55E-19	XP_002647027.1	56	101.679	187	106	Hypothetical protein CBG03541
Locus_3340_Transcript_1/1_Conf_1.000	893	20	6.31E-129	XP_002633912.1	92	464.537	265	246	C. briggsae CBR-IVD-1 protein
Locus_3341_Transcript_1/1_Conf_1.000	746	20	1.95E-71	EFO27286.1	77	273.092	248	191	peptidase M16 inactive domain-containing protein

Locus_3342_Transcript_1/1_Conf_1.000	328	0							
Locus_3343_Transcript_1/2_Conf_1.000	2310	0							
Locus_3343_Transcript_2/2_Conf_1.000	2211	0							
Locus_3344_Transcript_1/1_Conf_1.000	1743	20	0	XP_001898481.1	82	760.755	566	469	Membrane-associated protein gex-3
Locus_3345_Transcript_1/1_Conf_1.000	627	20	1.43E-57	CAA90256.2	75	226.483	185	139	C. elegans protein F54C9.11, confirmed by transcript evidence
Locus_3346_Transcript_1/1_Conf_1.000	1511	20	2.23E-110	NP_498475.1	70	404.06	399	281	hypothetical protein F37A4.1
Locus_3347_Transcript_1/1_Conf_1.000	356	20	3.37E-50	CAR63538.1	84	201.06	118	100	putative MFP2
Locus_3348_Transcript_1/1_Conf_1.000	1532	20	0	Q60V73.3	89	762.296	463	415	Serine hydroxymethyltransferase
Locus_3349_Transcript_1/1_Conf_1.000	782	20	5.95E-90	XP_002634069.1	79	334.724	247	196	Hypothetical protein CBG01611

Locus_335_Transcript_1/1_Conf_1.000	1260	20	1.70E-49	NP_498943.2	44	201.445	491	220	Zinc Finger Protein family member (zfp-1)
Locus_3350_Transcript_1/1_Conf_1.000	736	3	2.60E-20	XP_002630955.1	59	103.219	183	109	C. briggsae CBR-WRN-1 protein
Locus_3351_Transcript_1/1_Conf_1.000	678	20	1.99E-05	XP_002192259.1	42	53.5286	271	114	PREDICTED: similar to myosin heavy chain 6
Locus_3352_Transcript_1/1_Conf_1.000	1147	20	8.17E-40	NP_498484.1	58	169.088	227	132	LIM domain family member (lim-8)
Locus_3353_Transcript_1/1_Conf_1.000	269	20	9.24E-24	XP_001898868.1	84	113.235	75	63	fructose-1,6-bisphosphatase
Locus_3354_Transcript_1/1_Conf_1.000	2074	20	3.08E-15	NP_501981.2	45	88.5817	410	185	hypothetical protein R102.5
Locus_3355_Transcript_1/1_Conf_1.000	968	20	5.44E-68	NP_504411.1	76	262.307	224	172	hypothetical protein B0238.10
Locus_3356_Transcript_1/1_Conf_1.000	598	0							
Locus_3357_Transcript_1/1_Conf_1.000	582	4	4.14E-34	XP_001892872.1	54	148.288	192	104	hypothetical protein Bm1_07015
Locus_3358_Transcript_1/1_Conf_1.000	282	20	1.11E-32	XP_002637177.1	80	142.895	94	76	Hypothetical protein CBG09695

Locus_3359_Transcript_1/1_Conf_1.000	528	20	4.53E-33	NP_501757.1	72	144.436	151	110	yeast MTR (mRNA TRansport) homolog family member (mtr-4)
Locus_336_Transcript_1/1_Conf_1.000	762	20	2.75E-44	NP_498872.1	74	182.956	157	117	hypothetical protein F42H10.6
Locus_3360_Transcript_1/1_Conf_1.000	1636	20	7.86E-141	XP_001899636.1	77	505.368	394	304	Chain A, Two Seven-Bladed Beta-Propeller Domains Revealed By The Structure Of A C. Elegans Homologue Of Yeast Actin Interacting Protein 1, putative
Locus_3361_Transcript_1/1_Conf_1.000	338	1	3.85E-06	XP_001901288.1	64	54.6842	101	65	hypothetical protein Bm1_49115
Locus_3362_Transcript_1/1_Conf_1.000	768	20	5.25E-59	NP_001129848.1	73	231.876	245	179	hypothetical protein C27H2.2
Locus_3363_Transcript_1/1_Conf_1.000	1400	0							
Locus_3364_Transcript_1/1_Conf_1.000	1812	20	1.07E-93	AAL92523.1	51	348.977	680	352	MAT-1
Locus_3365_Transcript_1/1_Conf_1.000	567	20	1.23E-32	XP_001901116.1	65	143.28	154	101	BSD domain containing protein
Locus_3366_Transcript_1/1_Conf_1.000	1530	20	1.63E-92	NP_504629.1	61	344.739	446	276	hypothetical protein T05H4.10
Locus_3367_Transcript_1/1_Conf_1.000	559	0							
Locus_3368_Transcript_1/3_Conf_0.714	1993	20	5.36E-09	XP_002547406.1	46	67.781	235	110	conserved hypothetical protein

Locus_3368_Transcript_2/3_Conf_0.714	1984	20	5.33E-09	XP_002547406.1	46	67.781	235	109	conserved hypothetical protein
Locus_3368_Transcript_3/3_Conf_0.714	1978	20	5.31E-09	XP_002547406.1	46	67.781	235	110	conserved hypothetical protein
Locus_3369_Transcript_1/1_Conf_1.000	1036	20	1.22E-108	NP_495629.2	79	397.512	278	222	hypothetical protein B0228.7
Locus_337_Transcript_1/1_Conf_1.000	178	20	7.71E-23	EFO13894.1	100	110.153	54	54	hypothetical protein LOAG_14633
Locus_3370_Transcript_1/1_Conf_1.000	1360	20	1.05E-156	XP_002642568.1	85	557.755	368	314	C. briggsae CBR-RNR-2 protein

Locus_3371_Transcript_1/1_Conf_1.000	859	20	6.17E-118	XP_002637181.1	95	427.943	231	220	C. briggsae CBR-PAS-2 protein
Locus_3372_Transcript_1/1_Conf_1.000	402	20	3.28E-37	EFO22188.1	73	157.918	135	99	hypothetical protein LOAG_06298
Locus_3373_Transcript_1/2_Conf_1.000	2190	20	0	ACI49130.1	92	1107.05	673	621	hypothetical protein Cbre_JD16.002
Locus_3373_Transcript_2/2_Conf_1.000	2190	20	0	ACI49130.1	92	1107.05	673	621	hypothetical protein Cbre_JD16.002
Locus_3374_Transcript_1/1_Conf_1.000	2489	20	1.53E-173	NP_497969.1	65	614.764	851	558	abnormal EMBroygenesis family member (emb-5)
Locus_3375_Transcript_1/1_Conf_1.000	990	20	8.24E-51	NP_497852.1	56	205.297	304	173	hypothetical protein T08A11.1
Locus_3376_Transcript_1/1_Conf_1.000	1000	20	6.35E-68	NP_496458.2	59	177.563	255	152	hypothetical protein B0334.5
Locus_3377_Transcript_1/1_Conf_1.000	843	20	2.63E-65	NP_492711.1	63	253.062	321	203	glutamyl(E)/glutaminyl(Q) tRNA Synthetase family member (ers-2)
Locus_3378_Transcript_1/1_Conf_1.000	322	2	3.00E-14	NP_493710.2	64	81.6481	104	67	SarcoGlyCan Beta homolog family member (sgcb-1)
Locus_3379_Transcript_1/1_Conf_1.000	252	20	6.50E-33	P15941.3	100	143.665	64	64	Mucin-1

Locus_338_Transcript_1/1_Conf_1.000	995	5	2.77E-30	NP_499883.1	52	137.117	267	139	Conserved Oligomeric Golgi (COG) Component family member (cogc-8)
Locus_3380_Transcript_1/1_Conf_1.000	530	20	7.94E-54	XP_002633876.1	74	213.386	177	131	C. briggsae CBR-UNC-5 protein
Locus_3381_Transcript_1/1_Conf_1.000	904	20	3.62E-63	XP_001896403.1	83	246.128	173	145	Hypothetical UPF0101 protein E02H1.6 in chromosome II
Locus_3382_Transcript_1/1_Conf_1.000	1143	20	4.65E-11	NP_956425.1	51	73.559	145	74	serine/threonine-protein phosphatase 2A regulatory subunit B'' subunit gamma
Locus_3383_Transcript_1/1_Conf_1.000	1037	20	2.11E-52	XP_001900891.1	59	210.69	351	210	Prion-like-
Locus_3384_Transcript_1/2_Conf_1.000	1406	20	3.68E-96	XP_002634609.1	67	356.681	399	270	C. briggsae CBR-CSN-4 protein
Locus_3384_Transcript_2/2_Conf_1.000	1388	20	3.64E-96	XP_002634609.1	67	356.681	399	270	C. briggsae CBR-CSN-4 protein
Locus_3385_Transcript_1/1_Conf_1.000	744	5	1.46E-18	NP_001041142.1	69	97.4413	115	80	hypothetical protein H24G06.1
Locus_3386_Transcript_1/1_Conf_1.000	1089	20	3.40E-48	XP_002643585.1	62	196.823	323	203	Hypothetical protein CBG16307
Locus_3387_Transcript_1/1_Conf_1.000	1302	20	4.73E-34	NP_001021463.1	44	150.214	449	202	SUppressor of activated let-60 Ras family member (sur-2)
Locus_3388_Transcript_1/1_Conf_1.000	629	2	6.95E-04	ACI49256.1	53	48.1358	88	47	hypothetical protein Csp3_JD07.006
Locus_3389_Transcript_1/1_Conf_1.000	421	2	4.80E-12	XP_002630704.1	62	74.3294	124	77	C. briggsae CBR-PINK-1 protein
Locus_339_Transcript_1/1_Conf_1.000	330	0							
Locus_3390_Transcript_1/1_Conf_1.000	370	5	2.24E-09	XP_001895978.1	57	65.4698	90	52	hypothetical protein
Locus_3391_Transcript_1/1_Conf_1.000	1372	20	3.27E-73	NP_741589.2	66	280.411	380	253	hypothetical protein F44A2.5
Locus_3392_Transcript_1/1_Conf_1.000	998	20	1.52E-44	XP_001893642.1	55	184.496	346	193	hypothetical protein

Locus_3393_Transcript_1/2_Conf_1.000	2190	20	0	NP_496958.2	83	1092.03	738	619	XRN (mouse/S. cerevisiae) ribonuclease related family member (xrn-2)
Locus_3393_Transcript_2/2_Conf_1.000	2205	20	0	NP_496958.2	82	1087.02	748	619	XRN (mouse/S. cerevisiae) ribonuclease related family member (xrn-2)
Locus_3394_Transcript_1/1_Conf_1.000	299	3	5.26E-11	NP_497918.1	57	70.8626	100	57	UDP-GlucuronosylTransferase family member (ugt-62)
Locus_3395_Transcript_1/1_Conf_1.000	697	20	4.55E-08	XP_001024133.1	50	62.3882	230	116	Viral A-type inclusion protein repeat containing protein
Locus_3396_Transcript_1/1_Conf_1.000	1296	20	1.41E-163	NP_492613.1	79	580.482	421	334	Nuclear Hormone Receptor family member (nhr-49)
Locus_3397_Transcript_1/1_Conf_1.000	410	0							
Locus_3398_Transcript_1/2_Conf_1.000	218	0							
Locus_3398_Transcript_2/2_Conf_1.000	224	0							
Locus_3399_Transcript_1/2_Conf_1.000	190	6	1.23E-07	Q94637.1	74	59.6918	50	37	Vitellogenin-6
Locus_3399_Transcript_2/2_Conf_1.000	213	13	5.01E-14	Q94637.1	75	80.8777	70	53	Vitellogenin-6
Locus_34_Transcript_1/1_Conf_1.000	1876	8	1.02E-70	NP_502674.1	70	272.707	256	180	abnormal cell LINeage family member (lin-66)
Locus_340_Transcript_1/1_Conf_1.000	1891	20	6.06E-63	EFA02576.1	55	246.899	362	200	hypothetical protein TcasGA2_TC008294
Locus_3400_Transcript_1/1_Conf_1.000	1047	20	2.18E-97	XP_002638764.1	73	360.147	351	257	C. briggsae CBR-PTR-11 protein

Locus_3401_Transcript_1/1_Conf_1.000	809	20	8.92E-84	XP_002632974.1	80	314.309	236	191	Hypothetical protein CBG21734
Locus_3402_Transcript_1/1_Conf_1.000	618	1	8.36E-06	XP_001481202.1	66	35.8094	36	24	PREDICTED: hypothetical protein
Locus_3403_Transcript_1/1_Conf_1.000	3592	20	0	AAV41897.1	71	1094.34	1135	814	SAX-2
Locus_3404_Transcript_1/1_Conf_1.000	1311	0							
Locus_3405_Transcript_1/1_Conf_1.000	791	20	4.01E-33	CAB03248.2	63	145.976	244	154	C. elegans protein R10D12.13a, confirmed by transcript evidence
Locus_3406_Transcript_1/1_Conf_1.000	329	0							
Locus_3407_Transcript_1/1_Conf_1.000	1757	20	6.27E-75	EFO20911.1	56	286.574	467	265	hypothetical protein LOAG_07578
Locus_3408_Transcript_1/1_Conf_1.000	712	20	8.19E-61	CAB97366.2	75	237.654	172	130	putative cathepsin B.3
Locus_3409_Transcript_1/1_Conf_1.000	377	20	1.07E-11	XP_002631622.1	70	73.1738	65	46	Hypothetical protein CBG20808
Locus_341_Transcript_1/1_Conf_1.000	267	20	2.60E-26	NP_499301.2	74	121.709	89	66	hypothetical protein M03C11.8
Locus_3410_Transcript_1/1_Conf_1.000	513	20	1.39E-49	NP_497186.3	81	199.134	166	136	hypothetical protein Y50D7A.8
Locus_3411_Transcript_1/1_Conf_1.000	193	0							
Locus_3412_Transcript_1/1_Conf_1.000	376	0							
Locus_3413_Transcript_1/1_Conf_1.000	2015	20	0	XP_001898016.1	74	728.398	619	462	Valyl-tRNA synthetase
Locus_3414_Transcript_1/1_Conf_1.000	415	20	1.22E-60	NP_491357.1	88	235.728	137	121	hypothetical protein ZK973.3
Locus_3415_Transcript_1/1_Conf_1.000	1686	20	0	XP_002640648.1	80	710.679	557	447	C. briggsae CBR-SMP-1 protein
Locus_3416_Transcript_1/1_Conf_1.000	1473	2	8.41E-14	NP_505580.2	49	83.1889	231	114	hypothetical protein F57A8.1
Locus_3417_Transcript_1/1_Conf_1.000	800	20	1.49E-75	NP_509566.1	74	286.96	217	162	GLYcosylation related family member (gly-13)
Locus_3418_Transcript_1/1_Conf_1.000	642	20	8.52E-93	NP_499359.1	92	343.584	200	185	hypothetical protein Y39A1A.22

Locus_3419_Transcript_1/1_Conf_1.000	784	20	8.62E-105	NP_001022621.1	94	384.03	243	229	proteasome Regulatory Particle, Non-ATPase-like family member (rpn-6)
Locus_342_Transcript_1/1_Conf_1.000	2481	20	0	XP_002647701.1	67	761.911	843	565	Hypothetical protein CBG17890
Locus_3420_Transcript_1/1_Conf_1.000	555	20	3.91E-20	XP_001897339.1	63	101.679	113	72	Negative elongation factor A homolog
Locus_3421_Transcript_1/1_Conf_1.000	2260	20	0	NP_506069.1	74	699.508	592	443	hypothetical protein T04H1.2
Locus_3422_Transcript_1/1_Conf_1.000	344	20	5.67E-29	A8XQD5.2	89	130.568	77	69	Serine/threonine-protein kinase dkf-2
Locus_3423_Transcript_1/1_Conf_1.000	722	9	6.10E-27	XP_002641370.1	88	125.176	75	66	Hypothetical protein CBG13227
Locus_3424_Transcript_1/2_Conf_1.000	767	20	4.86E-73	NP_001040919.1	76	278.485	204	157	hypothetical protein C34D4.4
Locus_3424_Transcript_2/2_Conf_1.000	761	20	1.48E-74	NP_001040919.1	77	283.493	202	157	hypothetical protein C34D4.4
Locus_3425_Transcript_1/1_Conf_1.000	3824	20	0	NP_001023059.1	57	741.88	1221	701	hypothetical protein C42C1.4
Locus_3426_Transcript_1/1_Conf_1.000	986	20	6.99E-119	NP_001022986.1	83	431.409	281	236	Tubulin Tyrosine Ligase Like family member (ttll-4)
Locus_3427_Transcript_1/1_Conf_1.000	499	0							
Locus_3428_Transcript_1/1_Conf_1.000	1343	20	1.83E-129	NP_491977.1	85	467.233	289	248	hypothetical protein T10B11.2
Locus_3429_Transcript_1/1_Conf_1.000	283	20	8.83E-14	Q16937.1	62	80.1073	72	45	Ancylostoma secreted protein
Locus_343_Transcript_1/2_Conf_1.000	1889	20	3.49E-119	NP_741086.1	60	433.721	546	332	hypothetical protein F42G9.1
Locus_343_Transcript_2/2_Conf_1.000	1862	20	3.10E-120	NP_741086.1	60	437.187	541	330	hypothetical protein F42G9.1

Locus_3430_Transcript_1/1_Conf_1.000	3165	20	5.51E-155	XP_002642899.1	57	553.518	814	470	Hypothetical protein CBG15173
Locus_3431_Transcript_1/1_Conf_1.000	767	20	1.29E-49	NP_872030.2	77	200.675	161	125	hypothetical protein T02H6.1
Locus_3432_Transcript_1/1_Conf_1.000	378	20	2.77E-36	XP_002639351.1	76	154.836	113	87	C. briggsae CBR-PCBD-1 protein
Locus_3433_Transcript_1/1_Conf_1.000	977	20	8.36E-24	XP_002922036.1	46	115.546	250	117	PREDICTED: serologically defined colon cancer antigen 1-like
Locus_3434_Transcript_1/1_Conf_1.000	350	0							
Locus_3435_Transcript_1/1_Conf_1.000	1042	20	3.57E-84	NP_740931.2	79	316.235	266	211	hypothetical protein Y105E8A.3
Locus_3436_Transcript_1/1_Conf_1.000	470	20	3.72E-65	NP_001022234.1	90	250.751	155	141	hypothetical protein K05F1.6
Locus_3437_Transcript_1/2_Conf_1.000	1155	19	1.20E-06	XP_001583187.1	41	58.9214	221	91	hypothetical protein
Locus_3437_Transcript_2/2_Conf_1.000	2134	20	1.06E-10	XP_001651055.1	37	73.559	561	211	hypothetical protein AaeL_AAEL005529
Locus_3438_Transcript_1/1_Conf_1.000	695	20	1.86E-70	EFO21591.1	76	269.626	224	172	hypothetical protein LOAG_06900
Locus_3439_Transcript_1/3_Conf_0.714	1879	20	0	NP_497939.2	77	774.622	626	485	Suppressor/Enhancer of Lin-12 family member (sel-2)
Locus_3439_Transcript_2/3_Conf_0.714	1879	20	0	NP_497939.2	77	774.622	626	485	Suppressor/Enhancer of Lin-12 family member (sel-2)
Locus_3439_Transcript_3/3_Conf_0.714	1879	20	0	NP_497939.2	77	774.622	626	485	Suppressor/Enhancer of Lin-12 family member (sel-2)
Locus_344_Transcript_1/2_Conf_1.000	2192	20	9.52E-140	NP_504721.1	70	502.286	504	354	Germinal Center Kinase family member (gck-2)
Locus_344_Transcript_2/2_Conf_1.000	2192	20	9.52E-140	NP_504721.1	70	502.286	504	354	Germinal Center Kinase family member (gck-2)

Locus_3440_Transcript_1/4_Conf_0.667	1566	20	2.77E-79	CAA93884.2	53	300.827	537	287	C. elegans protein ZK1067.2, partially confirmed by transcript evidence
Locus_3440_Transcript_2/4_Conf_0.333	393	20	6.06E-31	XP_797977.1	70	137.117	131	92	PREDICTED: similar to KIAA1404 protein
Locus_3440_Transcript_3/4_Conf_0.667	1845	20	1.29E-102	CAA93884.2	54	378.637	635	349	C. elegans protein ZK1067.2, partially confirmed by transcript evidence
Locus_3440_Transcript_4/4_Conf_0.667	1566	20	4.73E-79	CAA93884.2	53	300.056	537	288	C. elegans protein ZK1067.2, partially confirmed by transcript evidence
Locus_3441_Transcript_1/5_Conf_0.600	1021	0							
Locus_3441_Transcript_2/5_Conf_0.300	455	0							
Locus_3441_Transcript_3/5_Conf_0.600	1008	0							
Locus_3441_Transcript_4/5_Conf_0.400	557	0							
Locus_3441_Transcript_5/5_Conf_0.600	1008	0							
Locus_3442_Transcript_1/2_Conf_1.000	3228	20	0	NP_001122796.1	69	942.184	1038	721	Kinesin-Like Protein family member (klp-12)
Locus_3442_Transcript_2/2_Conf_1.000	3192	20	0	NP_001122796.1	70	944.495	1030	721	Kinesin-Like Protein family member (klp-12)
Locus_3443_Transcript_1/3_Conf_0.600	423	1	6.26E-04	XP_002648823.1	51	47.3654	62	32	Hypothetical protein CBG16936
Locus_3443_Transcript_2/3_Conf_0.600	457	1	2.12E-04	XP_002648823.1	56	48.9062	57	32	Hypothetical protein CBG16936
Locus_3443_Transcript_3/3_Conf_0.600	455	1	6.19E-04	XP_002648823.1	51	47.3654	62	32	Hypothetical protein CBG16936
Locus_3444_Transcript_1/1_Conf_1.000	145	5	3.85E-09	NP_001122913.1	75	64.6994	48	36	hypothetical protein F13H6.1
Locus_3445_Transcript_1/1_Conf_1.000	1060	20	2.69E-119	XP_002634504.1	75	432.95	344	260	Hypothetical protein CBG08294
Locus_3446_Transcript_1/1_Conf_1.000	1530	20	4.09E-152	NP_506677.3	66	542.732	505	338	hypothetical protein H12D21.10

Locus_3447_Transcript_1/2_Conf_1.000	784	20	3.32E-56	NP_491033.1	82	222.631	173	143	YOP (yeast membrane trafficking protein) homolog family member (yop-1)
Locus_3447_Transcript_2/2_Conf_1.000	784	20	3.32E-56	NP_491033.1	82	222.631	173	143	YOP (yeast membrane trafficking protein) homolog family member (yop-1)
Locus_3448_Transcript_1/1_Conf_1.000	835	20	5.01E-69	NP_505267.1	69	265.388	279	193	Regulator of Presynaptic Morphology family member (rpm-1)
Locus_3449_Transcript_1/1_Conf_1.000	206	2	2.98E-06	CAA85409.2	66	55.0694	45	30	C. elegans protein D2089.2, partially confirmed by transcript evidence
Locus_345_Transcript_1/1_Conf_1.000	1148	20	5.65E-41	XP_002632956.1	70	172.94	141	99	C. briggsae CBR-OMA-2 protein
Locus_3450_Transcript_1/5_Conf_0.333	367	0							
Locus_3450_Transcript_2/5_Conf_0.333	244	0							
Locus_3450_Transcript_3/5_Conf_0.444	261	0							
Locus_3450_Transcript_4/5_Conf_0.333	389	0							
Locus_3450_Transcript_5/5_Conf_0.444	265	0							
Locus_3451_Transcript_1/1_Conf_1.000	474	20	7.53E-18	ACF74367.1	51	93.5893	154	80	Hypothetical protein R13F6.4d
Locus_3452_Transcript_1/1_Conf_1.000	1211	20	3.18E-130	NP_501071.1	77	469.544	393	306	hypothetical protein T22D1.12
Locus_3453_Transcript_1/1_Conf_1.000	607	20	2.09E-79	NP_501866.1	81	298.901	202	165	hypothetical protein C24F3.4
Locus_3454_Transcript_1/1_Conf_1.000	260	0							
Locus_3455_Transcript_1/1_Conf_1.000	492	2	3.29E-05	NP_497809.1	75	51.6026	37	28	Heavy chain, Unconventional Myosin family member (hum-5)
Locus_3456_Transcript_1/2_Conf_1.000	685	20	4.32E-48	CAR63522.1	82	195.282	150	123	putative heat shock protein
Locus_3456_Transcript_2/2_Conf_1.000	663	20	4.00E-48	CAR63522.1	82	195.282	150	123	putative heat shock protein

Locus_3457_Transcript_1/1_Conf_1.000	1051	20	2.68E-95	XP_002645228.1	75	353.214	293	221	C. briggsae CBR-NHR-17 protein
Locus_3458_Transcript_1/1_Conf_1.000	1116	0							
Locus_3459_Transcript_1/1_Conf_1.000	215	5	2.94E-14	NP_508212.3	71	81.6481	57	41	hypothetical protein C05D9.3
Locus_346_Transcript_1/1_Conf_1.000	880	2	7.25E-21	EFO27722.1	42	105.531	304	129	zinc finger protein
Locus_3460_Transcript_1/1_Conf_1.000	396	20	5.26E-43	AAP36438.1	100	177.178	86	86	Homo sapiens cystatin B (stefin B)
Locus_3461_Transcript_1/1_Conf_1.000	1399	20	0	XP_002644944.1	87	647.506	434	378	C. briggsae CBR-DHS-28 protein
Locus_3462_Transcript_1/1_Conf_1.000	1501	20	8.95E-120	NP_491339.2	68	435.261	502	346	hypothetical protein C43E11.11
Locus_3463_Transcript_1/2_Conf_1.000	445	20	2.21E-33	XP_002641305.1	76	145.206	107	82	C. briggsae CBR-TTR-15 protein
Locus_3463_Transcript_2/2_Conf_1.000	269	0							
Locus_3464_Transcript_1/1_Conf_1.000	993	20	7.11E-119	NP_001021041.1	84	431.409	320	271	NeurABin family member (nab-1)
Locus_3465_Transcript_1/3_Conf_0.312	650	0							
Locus_3465_Transcript_2/3_Conf_0.812	716	0							
Locus_3465_Transcript_3/3_Conf_0.781	870	0							
Locus_3466_Transcript_1/1_Conf_1.000	2583	20	0	XP_002635777.1	65	806.979	812	533	Hypothetical protein CBG10433
Locus_3467_Transcript_1/1_Conf_1.000	163	0							

Locus_3468_Transcript_1/1_Conf_1.000	500	20	2.52E-82	AAR07614.1	94	307.76	166	157	UNC-18
Locus_3469_Transcript_1/1_Conf_1.000	369	0							
Locus_347_Transcript_1/1_Conf_1.000	384	0							
Locus_3470_Transcript_1/1_Conf_1.000	1024	20	4.57E-92	NP_001122615.1	76	342.428	312	238	PhytoChelatin Synthase family member (pcs-1)
Locus_3471_Transcript_1/1_Conf_1.000	571	20	8.57E-66	NP_508993.2	85	253.447	190	162	fatty Acid CoA Synthetase family member (acs-17)
Locus_3472_Transcript_1/3_Conf_0.667	885	20	4.25E-69	XP_002629686.1	56	265.774	296	167	Hypothetical protein CBG00906
Locus_3472_Transcript_2/3_Conf_0.667	885	20	3.98E-67	XP_002629686.1	55	259.225	296	165	Hypothetical protein CBG00906
Locus_3472_Transcript_3/3_Conf_0.667	885	20	3.60E-68	XP_002629686.1	56	262.692	296	166	Hypothetical protein CBG00906
Locus_3473_Transcript_1/1_Conf_1.000	152	0							
Locus_3474_Transcript_1/1_Conf_1.000	468	20	6.81E-51	NP_001022362.1	77	203.371	154	120	hypothetical protein T24F1.3
Locus_3475_Transcript_1/1_Conf_1.000	351	20	2.97E-30	NP_001021765.1	71	134.806	119	85	hypothetical protein Y47G6A.22
Locus_3476_Transcript_1/1_Conf_1.000	203	0							

Locus_3477_Transcript_1/1_Conf_1.000	1267	20	1.48E-109	NP_492206.1	70	400.979	365	257	hypothetical protein C54G4.7
Locus_3478_Transcript_1/1_Conf_1.000	401	0							
Locus_3479_Transcript_1/1_Conf_1.000	524	0							
Locus_348_Transcript_1/2_Conf_1.000	1301	20	2.59E-24	NP_497276.2	84	117.857	77	65	RNP (RRM RNA binding domain) containing family member (rnp-5)
Locus_348_Transcript_2/2_Conf_1.000	884	20	1.42E-24	NP_497276.2	84	117.857	77	65	RNP (RRM RNA binding domain) containing family member (rnp-5)
Locus_3480_Transcript_1/2_Conf_1.000	532	0							
Locus_3480_Transcript_2/2_Conf_1.000	552	0							
Locus_3481_Transcript_1/1_Conf_1.000	273	20	6.13E-36	XP_001115060.2	100	153.68	90	90	PREDICTED: heat shock 70 kDa protein 1A/1B, partial
Locus_3482_Transcript_1/1_Conf_1.000	553	1	4.55E-05	XP_001893891.1	48	51.6026	110	53	hypothetical protein Bm1_12105
Locus_3483_Transcript_1/5_Conf_0.762	1118	3	1.29E-31	NP_493601.2	49	138.272	365	179	FERM domain (protein4.1-ezrin-radixin-moesin) family member (frm-1)
Locus_3483_Transcript_2/5_Conf_0.095	239	0							
Locus_3483_Transcript_3/5_Conf_0.095	211	3	8.05E-04	NP_493601.2	55	46.9802	61	34	FERM domain (protein4.1-ezrin-radixin-moesin) family member (frm-1)
Locus_3483_Transcript_4/5_Conf_0.286	548	3	1.45E-11	NP_493601.2	49	72.0182	151	75	FERM domain (protein4.1-ezrin-radixin-moesin) family member (frm-1)
Locus_3483_Transcript_5/5_Conf_0.667	1112	3	9.15E-33	NP_493601.2	49	142.124	364	180	FERM domain (protein4.1-ezrin-radixin-moesin) family member (frm-1)
Locus_3484_Transcript_1/1_Conf_1.000	1132	20	9.93E-131	NP_494926.1	88	471.085	297	264	hypothetical protein F33G12.2

Locus_3485_Transcript_1/1_Conf_1.000	1027	20	1.67E-126	NP_505798.2	85	456.833	342	292	Temporarily Assigned Gene name family member (tag-318)
Locus_3486_Transcript_1/1_Conf_1.000	528	5	9.72E-44	NP_494812.2	70	179.874	160	113	hypothetical protein F35D11.3
Locus_3487_Transcript_1/1_Conf_1.000	286	0							
Locus_3488_Transcript_1/1_Conf_1.000	2326	11	0	ACI49173.1	80	1033.86	770	619	hypothetical protein Csp3_JD02.001
Locus_3489_Transcript_1/1_Conf_1.000	1051	0							
Locus_349_Transcript_1/1_Conf_1.000	431	20	6.98E-56	EFO21508.1	100	219.935	111	111	ubiquitin C II
Locus_3490_Transcript_1/1_Conf_1.000	344	20	2.30E-38	XP_002641745.1	93	161.77	89	83	C. briggsae CBR-BAF-1 protein
Locus_3491_Transcript_1/2_Conf_1.000	2553								
Locus_3491_Transcript_2/2_Conf_1.000	2463								
Locus_3492_Transcript_1/1_Conf_1.000	1582	0							
Locus_3493_Transcript_1/1_Conf_1.000	429	20	8.29E-41	NP_500824.1	77	169.859	144	111	FEMinization of XX and XO animals family member (fem-1)
Locus_3494_Transcript_1/1_Conf_1.000	575	20	6.52E-29	EFO20453.1	89	130.954	67	60	hypothetical protein LOAG_08036
Locus_3495_Transcript_1/1_Conf_1.000	1150	20	3.82E-146	XP_002630335.1	86	522.316	337	290	Hypothetical protein CBG04264
Locus_3496_Transcript_1/1_Conf_1.000	1943	20	0	NP_500306.1	85	738.413	505	434	hypothetical protein T26C12.1

Locus_3497_Transcript_1/1_Conf_1.000	198	9	9.64E-05	NP_001124681.1	69	50.0618	43	30	tissue factor pathway inhibitor
Locus_3498_Transcript_1/1_Conf_1.000	2172	20	5.92E-134	NP_001024066.1	70	483.026	491	345	hypothetical protein R02F11.3
Locus_3499_Transcript_1/1_Conf_1.000	972	20	1.58E-115	XP_002639232.1	93	420.239	263	247	Hypothetical protein CBG03788
Locus_35_Transcript_1/1_Conf_1.000	608	0							
Locus_350_Transcript_1/4_Conf_0.727	7517	20	0	NP_501120.1	66	1180.62	1328	882	hypothetical protein C34D4.14
Locus_350_Transcript_2/4_Conf_0.727	7514	20	0	NP_501120.1	66	1177.54	1321	875	hypothetical protein C34D4.14
Locus_350_Transcript_3/4_Conf_0.727	7568	20	0	NP_501120.1	66	1177.54	1321	875	hypothetical protein C34D4.14
Locus_350_Transcript_4/4_Conf_0.727	7523	20	0	NP_501120.1	66	1177.54	1321	875	hypothetical protein C34D4.14
Locus_3500_Transcript_1/2_Conf_1.000	1933	20	2.61E-170	EFO25931.1	72	603.594	479	348	hypothetical protein LOAG_02553
Locus_3500_Transcript_2/2_Conf_1.000	1933	20	2.61E-170	EFO25931.1	72	603.594	479	348	hypothetical protein LOAG_02553
Locus_3501_Transcript_1/1_Conf_1.000	867	20	1.03E-27	NP_505643.1	54	128.257	217	119	LYSozyme family member (lys-2)
Locus_3502_Transcript_1/2_Conf_1.000	647	0							
Locus_3502_Transcript_2/2_Conf_1.000	647	0							
Locus_3503_Transcript_1/1_Conf_1.000	375	20	2.20E-49	NP_001021602.1	91	198.364	114	104	RSK-pNinety (RSK-p90 kinase) homolog family member (rskn-1)

Locus_3504_Transcript_1/1_Conf_1.000	1014	20	4.35E-95	XP_001898811.1	92	352.443	194	180	GTP-binding protein SAR1
Locus_3505_Transcript_1/1_Conf_1.000	430	0							
Locus_3506_Transcript_1/3_Conf_0.571	550	0							
Locus_3506_Transcript_2/3_Conf_0.714	652	0							
Locus_3506_Transcript_3/3_Conf_0.714	652	0							
Locus_3507_Transcript_1/1_Conf_1.000	767	20	4.13E-56	NP_497852.1	70	222.246	207	145	hypothetical protein T08A11.1
Locus_3508_Transcript_1/2_Conf_1.000	2381	20	2.20E-28	NP_001041193.1	44	132.494	407	183	hypothetical protein Y45G5AM.9
Locus_3508_Transcript_2/2_Conf_1.000	2285	20	2.16E-33	NP_001041193.1	48	149.058	375	183	hypothetical protein Y45G5AM.9
Locus_3509_Transcript_1/1_Conf_1.000	380	6	4.45E-18	NP_498205.1	58	94.3597	126	74	hypothetical protein C05D2.10

Locus_351_Transcript_1/1_Conf_1.000	1255	20	4.07E-152	CAZ44323.1	98	542.347	297	293	ADP/ATP translocase
Locus_3510_Transcript_1/1_Conf_1.000	440	0							
Locus_3511_Transcript_1/1_Conf_1.000	427	20	2.78E-28	EFO25877.1	68	128.257	144	98	hypothetical protein LOAG_02605
Locus_3512_Transcript_1/1_Conf_1.000	467	3	2.38E-11	NP_001122666.1	55	72.0182	108	60	hypothetical protein Y62F5A.12
Locus_3513_Transcript_1/1_Conf_1.000	1171	20	3.78E-48	ACV72655.1	64	196.823	219	141	ZAG-1
Locus_3514_Transcript_1/1_Conf_1.000	1144	20	6.88E-39	CAR63700.1	72	166.007	146	106	hypothetical protein
Locus_3515_Transcript_1/1_Conf_1.000	667	0							
Locus_3516_Transcript_1/2_Conf_1.000	657	20	2.17E-70	P51535.1	91	269.24	153	140	Myoglobin
Locus_3516_Transcript_2/2_Conf_1.000	588	20	3.07E-69	P51535.1	90	265.003	153	139	Myoglobin
Locus_3517_Transcript_1/1_Conf_1.000	277	0							
Locus_3518_Transcript_1/4_Conf_0.333	878	20	1.75E-67	XP_001891995.1	65	260.381	288	188	Not1 N-terminal domain, CCR4-Not complex component family protein

Locus_3518_Transcript_2/4_Conf_0.556	1743	20	1.11E-132	NP_001076652.1	59	478.404	643	384	NOT-Like (yeast CCR4/NOT complex component) family member (ntl-3)
Locus_3518_Transcript_3/4_Conf_0.667	1854	20	6.41E-134	NP_001076652.1	62	482.641	636	395	NOT-Like (yeast CCR4/NOT complex component) family member (ntl-3)
Locus_3518_Transcript_4/4_Conf_0.556	1752	20	1.12E-132	NP_001076652.1	61	478.404	643	393	NOT-Like (yeast CCR4/NOT complex component) family member (ntl-3)
Locus_3519_Transcript_1/1_Conf_1.000	307	2	1.08E-16	NP_001023480.2	63	89.7373	82	52	hypothetical protein Y4C6B.7
Locus_352_Transcript_1/1_Conf_1.000	664	2	2.07E-12	XP_002634845.1	45	76.6406	149	68	Hypothetical protein CBG13961
Locus_3520_Transcript_1/1_Conf_1.000	1084	20	2.44E-14	XP_462314.1	47	84.3445	109	52	DEHA2G17820p
Locus_3521_Transcript_1/3_Conf_0.667	1278	20	1.37E-62	XP_001895616.1	53	244.973	434	234	CG8232-PA
Locus_3521_Transcript_2/3_Conf_0.667	1278	20	1.37E-62	XP_001895616.1	53	244.973	434	234	CG8232-PA
Locus_3521_Transcript_3/3_Conf_0.667	1278	20	1.37E-62	XP_001895616.1	53	244.973	434	234	CG8232-PA
Locus_3522_Transcript_1/3_Conf_0.400	263	0							
Locus_3522_Transcript_2/3_Conf_0.600	513	0							
Locus_3522_Transcript_3/3_Conf_0.600	517	0							
Locus_3523_Transcript_1/1_Conf_1.000	841	0							
Locus_3524_Transcript_1/1_Conf_1.000	205	0							
Locus_3525_Transcript_1/1_Conf_1.000	738	0							
Locus_3526_Transcript_1/1_Conf_1.000	629	20	5.65E-30	XP_001901339.1	72	134.806	161	117	KIAA1259 protein
Locus_3527_Transcript_1/1_Conf_1.000	286	0							
Locus_3528_Transcript_1/1_Conf_1.000	1387	0							

Locus_3529_Transcript_1/1_Conf_1.000	427	20	2.89E-09	XP_001897817.1	67	65.0846	88	59	immunodominant antigen homologue
Locus_353_Transcript_1/1_Conf_1.000	2614	20	0	ACE63490.1	83	1102.43	767	639	GABAB1 receptor subunit
Locus_3530_Transcript_1/2_Conf_1.000	2551	0							
Locus_3530_Transcript_2/2_Conf_1.000	2159	0							
Locus_3531_Transcript_1/1_Conf_1.000	1527	20	7.49E-130	NP_741208.1	81	468.774	377	309	FLi1-Associated Protein homolog family member (flap-1)
Locus_3532_Transcript_1/1_Conf_1.000	2419	20	3.52E-82	XP_001894363.1	57	311.227	538	309	Helicase conserved C-terminal domain containing protein
Locus_3533_Transcript_1/6_Conf_0.615	2189	20	0	NP_505177.1	71	701.434	685	491	hypothetical protein T23B12.6
Locus_3533_Transcript_2/6_Conf_0.615	2284	20	0	NP_505177.1	71	701.434	685	491	hypothetical protein T23B12.6
Locus_3533_Transcript_3/6_Conf_0.615	2288	20	0	NP_505177.1	72	707.597	685	494	hypothetical protein T23B12.6
Locus_3533_Transcript_4/6_Conf_0.615	2288	20	0	NP_505177.1	71	701.049	685	491	hypothetical protein T23B12.6
Locus_3533_Transcript_5/6_Conf_0.615	2288	20	0	NP_505177.1	71	701.434	685	491	hypothetical protein T23B12.6
Locus_3533_Transcript_6/6_Conf_0.615	2288	20	0	NP_505177.1	71	701.434	685	491	hypothetical protein T23B12.6
Locus_3534_Transcript_1/2_Conf_1.000	628	0							
Locus_3534_Transcript_2/2_Conf_1.000	639	0							
Locus_3535_Transcript_1/2_Conf_1.000	701	20	2.46E-94	NP_502203.1	84	348.977	212	179	hypothetical protein ZK809.3
Locus_3535_Transcript_2/2_Conf_1.000	701	20	6.48E-95	NP_502203.1	84	350.903	212	180	hypothetical protein ZK809.3
Locus_3536_Transcript_1/2_Conf_1.000	965	20	1.67E-85	EFO22493.1	91	320.472	184	169	U2af splicing factor protein 1

Locus_3536_Transcript_2/2_Conf_1.000	3157	20	1.17E-88	EFO22493.1	94	333.183	185	174	U2af splicing factor protein 1
Locus_3537_Transcript_1/1_Conf_1.000	514	20	1.02E-68	XP_001894537.1	83	262.692	170	142	Protein kinase domain containing protein
Locus_3538_Transcript_1/4_Conf_0.700	2499	20	2.88E-87	XP_002642053.1	49	328.176	678	338	Hypothetical protein CBG17991
Locus_3538_Transcript_2/4_Conf_0.700	2499	20	4.91E-87	NP_497980.1	56	327.405	505	284	hypothetical protein B0393.3
Locus_3538_Transcript_3/4_Conf_0.700	2499	20	2.88E-87	XP_002642053.1	49	328.176	678	338	Hypothetical protein CBG17991
Locus_3538_Transcript_4/4_Conf_0.700	2499	20	2.88E-87	XP_002642053.1	49	328.176	678	338	Hypothetical protein CBG17991
Locus_3539_Transcript_1/1_Conf_1.000	250	2	9.43E-13	XP_001893179.1	57	76.6406	90	52	Mediator protein 4
Locus_354_Transcript_1/1_Conf_1.000	1084	14	1.51E-48	XP_002638589.1	67	197.978	187	126	Hypothetical protein CBG05638
Locus_3540_Transcript_1/1_Conf_1.000	183	0							
Locus_3541_Transcript_1/1_Conf_1.000	820	2	1.52E-38	EFO21691.1	69	164.081	162	112	hypothetical protein LOAG_06796
Locus_3542_Transcript_1/1_Conf_1.000	782	20	1.64E-55	NP_494997.1	64	220.32	250	162	VH1 dual-specificity phosphatase family member (vhp-1)

Locus_3543_Transcript_1/1_Conf_1.000	675	20	3.33E-29	XP_001898670.1	83	132.494	90	75	ATPase, AAA family protein
Locus_3544_Transcript_1/2_Conf_0.833	434	0							
Locus_3544_Transcript_2/2_Conf_0.833	533	0							
Locus_3545_Transcript_1/1_Conf_1.000	377	0							
Locus_3546_Transcript_1/1_Conf_1.000	892	2	6.11E-07	XP_002632959.1	58	59.3066	74	43	C. briggsae CBR-RAD-26 protein
Locus_3547_Transcript_1/1_Conf_1.000	417	0							
Locus_3548_Transcript_1/3_Conf_0.667	1319	20	3.01E-153	XP_001900091.1	90	546.199	381	345	U5 small nuclear ribonucleoprotein 200 kDa helicase
Locus_3548_Transcript_2/3_Conf_0.667	1086	20	3.50E-53	XP_001900091.1	85	213.386	165	141	U5 small nuclear ribonucleoprotein 200 kDa helicase
Locus_3548_Transcript_3/3_Conf_0.667	1319	20	3.01E-153	XP_001900091.1	90	546.199	381	345	U5 small nuclear ribonucleoprotein 200 kDa helicase

Locus_3549_Transcript_1/1_Conf_1.000	597	13	7.43E-50	CAE54905.2	66	200.675	212	141	C. elegans protein T12G3.2c, confirmed by transcript evidence
Locus_355_Transcript_1/1_Conf_1.000	1504	20	2.75E-169	XP_002641541.1	79	599.742	460	367	Hypothetical protein CBG09840
Locus_3550_Transcript_1/1_Conf_1.000	1637	20	5.05E-172	XP_002633647.1	74	608.986	539	400	Hypothetical protein CBG03319
Locus_3551_Transcript_1/1_Conf_1.000	445	6	2.62E-26	XP_002637252.1	81	121.709	92	75	C. briggsae CBR-ATP-4 protein
Locus_3552_Transcript_1/1_Conf_1.000	1787	20	0	XP_001898861.1	83	673.315	496	414	Amino acid permease family protein
Locus_3553_Transcript_1/1_Conf_1.000	811	20	1.51E-91	XP_002647020.1	77	340.117	251	194	Hypothetical protein CBG24043
Locus_3554_Transcript_1/1_Conf_1.000	509	20	5.40E-14	XP_001298658.1	54	80.8777	102	56	ankyrin repeat protein
Locus_3555_Transcript_1/1_Conf_1.000	688	20	4.51E-53	EFO27367.1	74	211.846	171	127	hypothetical protein LOAG_01110
Locus_3556_Transcript_1/1_Conf_1.000	4967	20	0	NP_001076722.2	55	990.719	1537	848	hypothetical protein Y37A1B.17
Locus_3557_Transcript_1/1_Conf_1.000	857	9	1.11E-34	NP_498408.1	62	151.369	210	131	hypothetical protein C05D11.9
Locus_3558_Transcript_1/1_Conf_1.000	754	20	7.03E-61	XP_002629766.1	74	238.039	203	151	Hypothetical protein CBG01004
Locus_3559_Transcript_1/1_Conf_1.000	136	0							
Locus_356_Transcript_1/1_Conf_1.000	1003	20	2.81E-38	EFO23006.1	59	163.696	286	171	mast family protein

Locus_3560_Transcript_1/1_Conf_1.000	2595	20	1.05E-156	XP_002641665.1	61	558.91	749	462	Hypothetical protein CBG09993
Locus_3561_Transcript_1/1_Conf_1.000	291	0							
Locus_3562_Transcript_1/1_Conf_1.000	568								
Locus_3563_Transcript_1/1_Conf_1.000	554	20	7.47E-24	CAZ65519.1	60	114.005	155	94	C. elegans protein R10D12.14d, confirmed by transcript evidence
Locus_3564_Transcript_1/1_Conf_1.000	245	20	4.70E-20	XP_001894289.1	79	100.908	81	64	hypothetical protein
Locus_3565_Transcript_1/1_Conf_1.000	1281	20	3.66E-140	XP_001896024.1	76	502.671	403	309	DNA ligase III
Locus_3566_Transcript_1/4_Conf_0.700	2047	20	3.98E-116	EFO18984.1	62	423.705	517	322	hypothetical protein LOAG_09511
Locus_3566_Transcript_2/4_Conf_0.700	2046	20	3.05E-116	EFO18984.1	62	424.091	517	322	hypothetical protein LOAG_09511
Locus_3566_Transcript_3/4_Conf_0.700	2046	20	3.98E-116	EFO18984.1	62	423.705	517	322	hypothetical protein LOAG_09511
Locus_3566_Transcript_4/4_Conf_0.700	2046	20	3.98E-116	EFO18984.1	62	423.705	517	322	hypothetical protein LOAG_09511
Locus_3567_Transcript_1/1_Conf_1.000	606	0							
Locus_3568_Transcript_1/1_Conf_1.000	493	20	5.14E-75	EFO24176.1	90	283.493	164	148	hypothetical protein LOAG_04307

Locus_3569_Transcript_1/3_Conf_0.714	729	20	1.12E-100	XP_001897925.1	85	370.163	214	184	zinc finger protein
Locus_3569_Transcript_2/3_Conf_0.714	735	20	1.14E-100	XP_001897925.1	85	370.163	214	184	zinc finger protein
Locus_3569_Transcript_3/3_Conf_0.714	735	20	1.14E-100	XP_001897925.1	85	370.163	214	184	zinc finger protein
Locus_357_Transcript_1/1_Conf_1.000	1332	20	1.35E-100	NP_499183.1	79	371.318	279	222	hypothetical protein ZK632.12
Locus_3570_Transcript_1/2_Conf_1.000	1536	20	3.33E-77	NP_492527.1	54	293.893	491	266	Kinesin-Like Protein family member (klp-16)
Locus_3570_Transcript_2/2_Conf_1.000	1333	20	4.83E-74	NP_492527.1	55	283.108	431	240	Kinesin-Like Protein family member (klp-16)
Locus_3571_Transcript_1/1_Conf_1.000	964	20	1.22E-136	XP_002643251.1	86	490.345	318	274	C. briggsae CBR-ILE-2 protein
Locus_3572_Transcript_1/2_Conf_1.000	1032	20	2.88E-118	CBK19479.1	77	429.483	346	269	C. elegans protein W08D2.5b, confirmed by transcript evidence
Locus_3572_Transcript_2/2_Conf_1.000	1036	20	2.22E-118	CBK19479.1	78	429.869	343	268	C. elegans protein W08D2.5b, confirmed by transcript evidence
Locus_3573_Transcript_1/1_Conf_1.000	1292	20	0	NP_509083.1	86	669.078	413	356	hypothetical protein K10C2.4
Locus_3574_Transcript_1/1_Conf_1.000	527	0							

Locus_3575_Transcript_1/3_Conf_0.667	1060	20	4.68E-55	XP_002647238.1	82	219.55	172	142	Hypothetical protein CBG24582
Locus_3575_Transcript_2/3_Conf_0.667	1088	20	1.16E-56	XP_002647238.1	63	224.942	283	180	Hypothetical protein CBG24582
Locus_3575_Transcript_3/3_Conf_0.667	1060	20	4.68E-55	XP_002647238.1	82	219.55	172	142	Hypothetical protein CBG24582
Locus_3576_Transcript_1/1_Conf_1.000	1441	20	1.46E-71	ABD37724.1	66	275.018	340	227	catsup protein
Locus_3577_Transcript_1/2_Conf_1.000	812	20	1.95E-22	XP_002641634.1	74	110.538	117	87	Hypothetical protein CBG09956
Locus_3577_Transcript_2/2_Conf_1.000	582	20	1.58E-25	NP_001122751.1	61	119.783	183	113	hypothetical protein ZK757.4
Locus_3578_Transcript_1/1_Conf_1.000	840	20	3.79E-48	NP_492782.2	65	196.052	180	118	hypothetical protein B0511.13
Locus_3579_Transcript_1/1_Conf_1.000	506	20	1.57E-42	NP_500377.1	70	175.637	164	115	hypothetical protein Y37E11B.3
Locus_358_Transcript_1/1_Conf_1.000	149	0							
Locus_3580_Transcript_1/1_Conf_1.000	774	20	4.65E-79	XP_002636980.1	74	298.516	264	197	Hypothetical protein CBG09463
Locus_3581_Transcript_1/1_Conf_1.000	338	1	6.15E-04	XP_001901253.1	69	47.3654	46	32	Helicase conserved C-terminal domain containing protein
Locus_3582_Transcript_1/2_Conf_1.000	533	20	7.13E-34	EFO22891.1	93	147.132	88	82	small nuclear ribonucleoprotein sm d1
Locus_3582_Transcript_2/2_Conf_1.000	518	20	2.43E-33	EFO22891.1	93	145.206	87	81	small nuclear ribonucleoprotein sm d1
Locus_3583_Transcript_1/1_Conf_1.000	516	0							
Locus_3584_Transcript_1/2_Conf_1.000	796	20	1.35E-52	NP_497836.2	68	210.69	212	145	hypothetical protein C16C10.1

Locus_3584_Transcript_2/2_Conf_1.000	1136	20	7.69E-107	NP_497836.2	74	391.734	315	236	hypothetical protein C16C10.1
Locus_3585_Transcript_1/1_Conf_1.000	733	20	2.03E-33	AAB42328.2	57	146.747	255	146	Hypothetical protein C32E8.11
Locus_3586_Transcript_1/1_Conf_1.000	625	20	1.13E-22	XP_001902835.1	58	110.538	162	95	G-patch domain containing protein
Locus_3587_Transcript_1/2_Conf_1.000	1565	4	2.31E-09	XP_001894598.1	60	68.5514	96	58	BTB/POZ domain containing protein
Locus_3587_Transcript_2/2_Conf_1.000	1772	2	4.79E-06	XP_001894599.1	57	57.7658	82	47	Zinc finger, C2H2 type family protein
Locus_3588_Transcript_1/1_Conf_1.000	1083	2	9.16E-54	NP_496193.1	63	215.312	369	234	hypothetical protein F33H1.3
Locus_3589_Transcript_1/1_Conf_1.000	1103	20	2.32E-44	CAA98127.3	54	184.111	335	181	C. elegans protein F53B2.5, partially confirmed by transcript evidence
Locus_359_Transcript_1/1_Conf_1.000	654	20	5.05E-104	NP_505411.1	90	380.948	209	189	ACyLtransferase-like family member (acl-14)
Locus_3590_Transcript_1/1_Conf_1.000	258	20	1.07E-27	NP_498579.2	93	126.331	72	67	Ribosomal Protein, Small subunit family member (rps-21)
Locus_3591_Transcript_1/2_Conf_1.000	1448	20	0	NP_493745.1	90	785.408	460	416	hypothetical protein W07E6.2

Locus_3591_Transcript_2/2_Conf_1.000	661	20	2.37E-93	XP_002632198.1	91	345.51	197	180	Hypothetical protein CBG07064
Locus_3592_Transcript_1/1_Conf_1.000	277	20	2.10E-28	CBA11608.1	81	128.642	88	72	C. elegans protein F45H7.2d, partially confirmed by transcript evidence
Locus_3593_Transcript_1/1_Conf_1.000	570	20	7.54E-46	EFO23137.1	75	187.193	165	125	xeroderma Pigmentosum Group E Complementing protein
Locus_3594_Transcript_1/1_Conf_1.000	755	20	1.99E-47	XP_002629739.1	60	193.356	254	153	C. briggsae CBR-UFD-3 protein
Locus_3595_Transcript_1/1_Conf_1.000	196	0							
Locus_3596_Transcript_1/2_Conf_1.000	1714	6	7.08E-31	XP_002640485.1	47	140.198	386	184	Hypothetical protein CBG13621
Locus_3596_Transcript_2/2_Conf_1.000	2113	8	4.83E-48	XP_002640485.1	47	197.593	550	262	Hypothetical protein CBG13621
Locus_3597_Transcript_1/1_Conf_1.000	386	20	1.84E-32	NP_001021779.1	77	142.124	125	97	hypothetical protein Y48G8AL.15
Locus_3598_Transcript_1/1_Conf_1.000	1011	20	1.05E-40	XP_002635613.1	56	171.785	287	162	Hypothetical protein CBG21806
Locus_3599_Transcript_1/2_Conf_1.000	514	0							
Locus_3599_Transcript_2/2_Conf_1.000	719	20	1.35E-10	EFO18927.1	78	70.8626	64	50	DNA polymerase epsilon p17 subunit
Locus_36_Transcript_1/1_Conf_1.000	799	20	1.96E-51	XP_002632297.1	66	206.838	264	175	C. briggsae CBR-NOL-6 protein
Locus_360_Transcript_1/1_Conf_1.000	1491	20	1.10E-53	NP_495955.1	73	215.698	216	159	hypothetical protein T23G7.3

Locus_3600_Transcript_1/1_Conf_1.000	979	20	6.22E-27	NP_496969.2	53	125.946	205	110	JuMonJi (transcription factor) Domain protein family member (jmjd-2)
Locus_3601_Transcript_1/1_Conf_1.000	492	3	7.80E-23	NP_504457.2	63	110.153	134	85	hypothetical protein C24G6.3
Locus_3602_Transcript_1/1_Conf_1.000	440	0							
Locus_3603_Transcript_1/1_Conf_1.000	1466	20	8.87E-149	XP_002645112.1	89	531.561	320	286	C. briggsae CBR-SEK-1 protein
Locus_3604_Transcript_1/1_Conf_1.000	597	20	2.03E-31	XP_002639296.1	66	139.428	179	119	Hypothetical protein CBG03866
Locus_3605_Transcript_1/2_Conf_1.000	2438	3	3.96E-33	NP_871911.1	53	148.288	328	174	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-35)
Locus_3605_Transcript_2/2_Conf_1.000	952	3	1.11E-33	NP_871911.1	53	148.288	328	174	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-35)
Locus_3606_Transcript_1/4_Conf_0.222	645	19	1.11E-23	EFO22278.1	65	114.005	198	129	hypothetical protein LOAG_06208
Locus_3606_Transcript_2/4_Conf_0.667	1797	20	1.74E-112	NP_492041.1	64	411.379	494	319	Temporarily Assigned Gene name family member (tag-298)
Locus_3606_Transcript_3/4_Conf_0.667	1797	20	1.74E-112	NP_492041.1	64	411.379	494	319	Temporarily Assigned Gene name family member (tag-298)
Locus_3606_Transcript_4/4_Conf_0.667	1797	20	1.74E-112	NP_492041.1	64	411.379	494	319	Temporarily Assigned Gene name family member (tag-298)
Locus_3607_Transcript_1/2_Conf_1.000	2031	20	3.62E-178	NP_490688.1	73	629.787	551	403	hypothetical protein F56C11.6
Locus_3607_Transcript_2/2_Conf_1.000	1596	20	1.31E-148	NP_490688.1	76	526.554	437	334	hypothetical protein F56C11.6
Locus_3608_Transcript_1/1_Conf_1.000	1701	20	2.16E-64	XP_969757.1	56	251.521	387	219	PREDICTED: similar to amsh
Locus_3609_Transcript_1/1_Conf_1.000	441	20	4.04E-35	NP_498990.1	75	150.984	134	101	hypothetical protein F59B2.3

Locus_361_Transcript_1/1_Conf_1.000	1326	20	3.49E-141	CAR97838.1	71	506.138	440	316	C. elegans protein F54F11.2b, partially confirmed by transcript evidence
Locus_3610_Transcript_1/1_Conf_1.000	1133	20	0	AAA50224.1	97	677.937	378	368	RNA polymerase II, second largest subunit
Locus_3611_Transcript_1/1_Conf_1.000	1452	20	0	XP_002636649.1	93	823.157	484	454	Hypothetical protein CBG23360
Locus_3612_Transcript_1/1_Conf_1.000	2002	20	0	XP_002638871.1	74	670.618	594	442	C. briggsae CBR-NPP-13 protein
Locus_3613_Transcript_1/1_Conf_1.000	765	1	7.39E-05	EFO27965.1	47	51.9878	123	58	hypothetical protein LOAG_00531

Locus_3614_Transcript_1/1_Conf_1.000	998	20	7.67E-105	NP_001020979.1	70	384.8	340	239	mRNA Capping Enzyme Like family member (cel-1)
Locus_3615_Transcript_1/1_Conf_1.000	1036	20	5.36E-64	XP_001892710.1	79	249.21	215	170	cleavage stimulation factor
Locus_3616_Transcript_1/1_Conf_1.000	570	2	5.27E-15	NP_491922.1	88	84.7297	77	68	hypothetical protein T23B3.2
Locus_3617_Transcript_1/1_Conf_1.000	1313	1	1.60E-13	NP_505141.1	68	82.0333	72	49	hypothetical protein W02D7.3
Locus_3618_Transcript_1/1_Conf_1.000	1489	20	4.06E-48	NP_490811.3	53	197.208	391	209	hypothetical protein Y34D9A.7
Locus_3619_Transcript_1/1_Conf_1.000	1106	20	2.83E-66	AAC31568.1	76	256.914	226	173	putative zinc metallopeptidase
Locus_362_Transcript_1/2_Conf_1.000	1473	20	1.12E-50	XP_002646695.1	56	205.682	277	156	Hypothetical protein CBG13072
Locus_362_Transcript_2/2_Conf_1.000	1425	20	6.09E-46	XP_002646695.1	55	189.889	267	147	Hypothetical protein CBG13072
Locus_3620_Transcript_1/1_Conf_1.000	1721	20	3.26E-44	NP_499537.2	56	184.496	315	179	hypothetical protein Y56A3A.2
Locus_3621_Transcript_1/1_Conf_1.000	371	3	1.90E-08	NP_001021144.1	52	62.3882	97	51	hypothetical protein C05D10.1
Locus_3622_Transcript_1/1_Conf_1.000	1328	20	3.26E-30	EFO28160.1	51	137.502	249	127	abnormal cell lineage protein 37
Locus_3623_Transcript_1/1_Conf_1.000	484	0							

Locus_3624_Transcript_1/1_Conf_1.000	680	20	1.13E-101	1TW9	98	373.244	187	185	Glutathione Transferase-2
Locus_3625_Transcript_1/1_Conf_1.000	336	0							
Locus_3626_Transcript_1/5_Conf_0.450	382	20	2.77E-20	NP_492616.1	56	101.679	133	75	Nematode AStacin protease family member (nas-5)
Locus_3626_Transcript_2/5_Conf_0.500	382	20	3.28E-21	NP_492616.1	58	104.76	133	78	Nematode AStacin protease family member (nas-5)
Locus_3626_Transcript_3/5_Conf_0.500	382	20	5.59E-21	NP_492616.1	57	103.99	133	77	Nematode AStacin protease family member (nas-5)
Locus_3626_Transcript_4/5_Conf_0.350	329	20	1.58E-15	NP_492616.1	55	85.8853	115	64	Nematode AStacin protease family member (nas-5)
Locus_3626_Transcript_5/5_Conf_0.600	382	20	4.28E-21	NP_492616.1	57	104.375	133	77	Nematode AStacin protease family member (nas-5)
Locus_3627_Transcript_1/1_Conf_1.000	445	2	4.18E-16	NP_503135.1	56	87.8113	162	91	hypothetical protein F56E10.1
Locus_3628_Transcript_1/1_Conf_1.000	854	13	1.03E-40	NP_506519.1	60	171.4	263	159	hypothetical protein T16A9.5
Locus_3629_Transcript_1/1_Conf_1.000	1950	3	1.54E-77	XP_002647904.1	65	295.434	297	194	Hypothetical protein CBG23772
Locus_363_Transcript_1/7_Conf_0.333	1494	20	1.28E-50	NP_001041009.1	91	201.445	111	102	GLutamiNe synthetase (glutamate-ammonia ligase) family member (gln-3)
Locus_363_Transcript_2/7_Conf_0.500	2077	20	1.48E-33	EFO21829.1	39	149.443	487	194	hypothetical protein LOAG_06652

Locus_363_Transcript_3/7_Conf_0.444	2041	20	1.35E-23	XP_002641290.1	39	116.316	427	168	Hypothetical protein CBG05204
Locus_363_Transcript_4/7_Conf_0.556	2140	20	5.82E-33	EFO21829.1	39	147.517	483	191	hypothetical protein LOAG_06652
Locus_363_Transcript_5/7_Conf_0.556	2092	20	1.49E-33	EFO21829.1	39	149.443	487	194	hypothetical protein LOAG_06652
Locus_363_Transcript_6/7_Conf_0.389	2273	20	0	NP_001041010.1	90	685.641	378	342	GLutamiNe synthetase (glutamate-ammonia ligase) family member (gln-3)
Locus_363_Transcript_7/7_Conf_0.556	2146	20	1.54E-33	EFO21829.1	39	149.443	487	194	hypothetical protein LOAG_06652
Locus_3630_Transcript_1/4_Conf_0.500	753	6	2.13E-33		59	146.747	235	139	hypothetical protein B0511.12 - Caenorhabditis elegans
Locus_3630_Transcript_2/4_Conf_0.625	708	6	1.88E-33		59	146.747	235	139	hypothetical protein B0511.12 - Caenorhabditis elegans
Locus_3630_Transcript_3/4_Conf_0.500	759	6	2.17E-33		59	146.747	235	139	hypothetical protein B0511.12
Locus_3630_Transcript_4/4_Conf_0.625	759	6	2.17E-33		59	146.747	235	139	hypothetical protein B0511.12
Locus_3631_Transcript_1/1_Conf_1.000	904	20	6.34E-84	XP_002640662.1	67	315.079	327	220	Hypothetical protein CBG19722

Locus_3632_Transcript_1/1_Conf_1.000	1345	20	1.01E-111	NP_001024778.2	66	408.297	438	293	neuRonal IGCAM family member (rig-1)
Locus_3633_Transcript_1/1_Conf_1.000	1323	20	0	NP_001076658.1	94	790.03	425	401	abnormal CHEmotaxis family member (tax-6)
Locus_3634_Transcript_1/1_Conf_1.000	286	0							
Locus_3635_Transcript_1/2_Conf_1.000	1186	20	8.45E-104	NP_491614.1	77	381.719	343	267	hypothetical protein F59A3.4
Locus_3635_Transcript_2/2_Conf_1.000	1129	20	1.35E-103	NP_491614.1	82	380.948	322	266	hypothetical protein F59A3.4
Locus_3636_Transcript_1/1_Conf_1.000	462	20	1.13E-53	XP_002644337.1	84	212.616	144	122	C. briggsae CBR-KLP-4 protein
Locus_3637_Transcript_1/4_Conf_0.667	1004	20	1.75E-48	XP_002200515.1	76	197.593	166	127	PREDICTED: similar to splicing factor, arginine/serine-rich 5
Locus_3637_Transcript_2/4_Conf_0.667	1094	20	1.13E-51	ACI33535.1	73	208.379	186	137	Splicing factor, arginine/serine-rich 5
Locus_3637_Transcript_3/4_Conf_0.444	1176	20	4.85E-19	EFO18201.1	90	100.138	61	55	Sfrs5 protein
Locus_3637_Transcript_4/4_Conf_0.667	1049	20	2.21E-49	XP_002200515.1	75	200.675	172	130	PREDICTED: similar to splicing factor, arginine/serine-rich 5
Locus_3638_Transcript_1/1_Conf_1.000	1453	20	2.05E-89	NP_498516.2	64	334.339	425	274	LEThal family member (let-711)
Locus_3639_Transcript_1/2_Conf_1.000	328	14	4.60E-07	AAN11402.1	58	57.7658	65	38	secreted-protein 1 precursor
Locus_3639_Transcript_2/2_Conf_1.000	773	20	4.85E-20	AAO63577.1	48	102.449	207	100	secreted protein 5 precursor
Locus_364_Transcript_1/1_Conf_1.000	975	20	9.69E-89	NP_501684.1	85	331.257	226	193	hypothetical protein C33A12.7
Locus_3640_Transcript_1/1_Conf_1.000	474	20	7.00E-40	XP_002631404.1	93	166.777	109	102	C. briggsae CBR-RPL-32 protein

Locus_3641_Transcript_1/1_Conf_1.000	539	20	6.92E-77	NP_001022571.1	87	290.041	180	157	NeuroFibroMatosis homolog family member (nfm-1)
Locus_3642_Transcript_1/1_Conf_1.000	2000	20	3.00E-68	NP_001022181.1	65	264.618	346	228	UBX-containing protein in Nematode family member (ubxn-3)
Locus_3643_Transcript_1/1_Conf_1.000	802	20	2.85E-58	XP_002642531.1	81	229.565	144	117	C. briggsae CBR-RNF-121 protein
Locus_3644_Transcript_1/5_Conf_0.385	562	0							
Locus_3644_Transcript_2/5_Conf_0.692	2252	1	7.85E-04	XP_001612950.1	39	50.8322	229	91	hypothetical protein
Locus_3644_Transcript_3/5_Conf_0.538	2242	1	7.81E-04	XP_001612950.1	39	50.8322	229	91	hypothetical protein
Locus_3644_Transcript_4/5_Conf_0.692	2182	0							
Locus_3644_Transcript_5/5_Conf_0.692	2302	1	8.07E-04	XP_001612950.1	39	50.8322	229	91	hypothetical protein
Locus_3645_Transcript_1/1_Conf_1.000	1287	20	1.72E-121	XP_002634705.1	72	440.654	385	280	Hypothetical protein CBG19691
Locus_3646_Transcript_1/1_Conf_1.000	3759	20	0	XP_001895215.1	85	1762.27	1171	1002	Disco-interacting protein 2 homolog
Locus_3647_Transcript_1/2_Conf_1.000	1389	20	1.88E-52	NP_500023.1	69	211.46	197	136	hypothetical protein Y55F3AM.9
Locus_3647_Transcript_2/2_Conf_1.000	1340	20	1.29E-50	NP_500023.1	69	205.297	185	129	hypothetical protein Y55F3AM.9
Locus_3648_Transcript_1/2_Conf_1.000	538	20	1.60E-57	CAR63695.1	94	225.713	117	111	putative GRP1 protein
Locus_3648_Transcript_2/2_Conf_1.000	209	0							
Locus_3649_Transcript_1/2_Conf_1.000	533	0							
Locus_3649_Transcript_2/2_Conf_1.000	492	0							
Locus_365_Transcript_1/3_Conf_0.375	784	20	3.53E-74	ABV44405.1	100	282.337	203	203	tropomyosin
Locus_365_Transcript_2/3_Conf_0.500	1036	20	1.76E-107	ABV44405.1	95	393.66	283	270	tropomyosin
Locus_365_Transcript_3/3_Conf_0.750	1468	20	4.30E-119	ABV44405.1	100	432.95	284	284	tropomyosin

Locus_3650_Transcript_1/1_Conf_1.000	944	20	2.45E-116	XP_001893694.1	92	348.591	209	193	DNA replication licensing factor MCM3
Locus_3651_Transcript_1/1_Conf_1.000	403	0							
Locus_3652_Transcript_1/1_Conf_1.000	630	20	4.67E-40	CBK55599.1	80	168.318	118	95	C. elegans protein R10E4.5b, confirmed by transcript evidence
Locus_3653_Transcript_1/1_Conf_1.000	361	20	4.72E-12	NP_498790.1	75	74.3294	72	54	SyNaptoBrevin related family member (snb-5)
Locus_3654_Transcript_1/1_Conf_1.000	994	0							
Locus_3655_Transcript_1/1_Conf_1.000	1229	0							
Locus_3656_Transcript_1/1_Conf_1.000	1021	20	1.71E-123	NP_497842.1	89	446.817	289	258	hypothetical protein R74.6
Locus_3657_Transcript_1/2_Conf_1.000	2327	20	5.44E-24	XP_002646538.1	56	117.857	167	95	Hypothetical protein CBG20393
Locus_3657_Transcript_2/2_Conf_1.000	2327	20	5.44E-24	XP_002646538.1	56	117.857	167	95	Hypothetical protein CBG20393

Locus_3658_Transcript_1/1_Conf_1.000	934	20	7.85E-125	XP_002641827.1	86	451.055	309	267	C. briggsae CBR-CEH-20 protein
Locus_3659_Transcript_1/2_Conf_1.000	2536	20	3.86E-172	XP_002634030.1	64	610.142	774	499	C. briggsae CBR-HGRS-1 protein
Locus_3659_Transcript_2/2_Conf_1.000	2462	20	2.50E-168	XP_002634030.1	70	597.43	646	455	C. briggsae CBR-HGRS-1 protein
Locus_366_Transcript_1/2_Conf_1.000	2344	20	0	XP_002630695.1	80	1013.83	788	636	C. briggsae CBR-SEC-6 protein
Locus_366_Transcript_2/2_Conf_1.000	2344	20	0	XP_002630695.1	80	1013.83	788	636	C. briggsae CBR-SEC-6 protein
Locus_3660_Transcript_1/1_Conf_1.000	1498	20	3.55E-76	NP_505468.1	65	290.426	379	249	EH (Eps-15-homology) domain Binding Protein family member (ehbp-1)
Locus_3661_Transcript_1/1_Conf_1.000	1310	20	2.73E-106	XP_002641844.1	72	390.193	384	278	Hypothetical protein CBG16518
Locus_3662_Transcript_1/1_Conf_1.000	781	20	1.22E-42	XP_002641444.1	60	177.563	217	132	C. briggsae CBR-NPP-16 protein

Locus_3663_Transcript_1/1_Conf_1.000	950	20	6.20E-117	XP_002638962.1	79	424.861	296	234	Hypothetical protein CBG22199
Locus_3664_Transcript_1/1_Conf_1.000	518	2	5.10E-09	XP_002640455.1	54	60.077	72	39	Hypothetical protein CBG08512
Locus_3665_Transcript_1/2_Conf_1.000	404	0							
Locus_3665_Transcript_2/2_Conf_1.000	556	0							
Locus_3666_Transcript_1/1_Conf_1.000	294	0							
Locus_3667_Transcript_1/1_Conf_1.000	820	20	1.23E-80	NP_495409.3	92	303.908	175	162	hypothetical protein C44B7.10
Locus_3668_Transcript_1/3_Conf_0.333	250	0							
Locus_3668_Transcript_2/3_Conf_0.667	1324	9	3.96E-36	NP_001022854.1	70	157.147	202	142	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-83)
Locus_3668_Transcript_3/3_Conf_0.667	1289	9	1.18E-37	NP_001022853.1	65	162.155	283	184	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-83)
Locus_3669_Transcript_1/2_Conf_1.000	1014	2	3.09E-08	XP_001894767.1	50	63.929	96	48	hypothetical protein
Locus_3669_Transcript_2/2_Conf_1.000	389	2	4.12E-08	XP_001894767.1	74	61.2326	39	29	hypothetical protein
Locus_367_Transcript_1/1_Conf_1.000	855	20	4.51E-20	XP_002637324.1	73	102.834	97	71	C. briggsae CBR-SPN-4 protein
Locus_3670_Transcript_1/2_Conf_1.000	1675	20	4.64E-112	NP_500088.1	89	409.838	278	249	hypothetical protein Y77E11A.1
Locus_3670_Transcript_2/2_Conf_1.000	1592	20	4.33E-112	NP_500088.1	89	409.838	278	249	hypothetical protein Y77E11A.1

Locus_3671_Transcript_1/1_Conf_1.000	934	20	1.22E-109	XP_002632654.1	84	400.593	259	218	Hypothetical protein CBG21577
Locus_3672_Transcript_1/1_Conf_1.000	420	20	4.04E-27	EFO16801.1	82	124.405	85	70	RNA-binding protein
Locus_3673_Transcript_1/1_Conf_1.000	518	0							
Locus_3674_Transcript_1/1_Conf_1.000	228	20	9.60E-37	XP_002925885.1	100	156.377	75	75	PREDICTED: alpha-actinin-4-like isoform 3
Locus_3675_Transcript_1/1_Conf_1.000	155	0							
Locus_3676_Transcript_1/3_Conf_0.667	624	20	4.55E-40	ADJ94115.1	62	168.318	214	134	aspartic protease
Locus_3676_Transcript_2/3_Conf_0.667	615	20	6.86E-41	ADJ94115.1	63	171.014	214	135	aspartic protease

Locus_3676_Transcript_3/3_Conf_0.667	615	20	9.91E-40	ADJ94115.1	62	167.162	214	133	aspartic protease
Locus_3677_Transcript_1/1_Conf_1.000	594	20	2.13E-57	NP_001021702.1	74	225.713	201	150	EXOCyst component family member (exoc-8)
Locus_3678_Transcript_1/3_Conf_0.818	2009	4	2.42E-17	NP_498116.2	54	95.5153	185	100	hypothetical protein C34E10.8
Locus_3678_Transcript_2/3_Conf_0.818	2009	4	2.42E-17	NP_498116.2	54	95.5153	185	100	hypothetical protein C34E10.8
Locus_3678_Transcript_3/3_Conf_0.818	2009	4	2.42E-17	NP_498116.2	54	95.5153	185	100	hypothetical protein C34E10.8
Locus_3679_Transcript_1/1_Conf_1.000	594	20	1.90E-98	XP_002637043.1	90	362.073	196	177	C. briggsae CBR-EGL-3 protein
Locus_368_Transcript_1/2_Conf_1.000	642	5	1.55E-14	NP_492047.1	60	60.077	66	40	Chondroitin ProteoGlycan family member (cpg-3)
Locus_368_Transcript_2/2_Conf_1.000	635	6	2.28E-18	NP_492047.1	56	96.2857	102	58	Chondroitin ProteoGlycan family member (cpg-3)
Locus_3680_Transcript_1/1_Conf_1.000	1934	20	0	XP_001891856.1	89	1097.42	662	593	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase
Locus_3681_Transcript_1/1_Conf_1.000	2071	20	9.18E-161	EFO26155.1	75	572.007	469	352	pellino family protein
Locus_3682_Transcript_1/1_Conf_1.000	2254	20	0	XP_002645843.1	69	846.269	756	523	C. briggsae CBR-TAG-53 protein
Locus_3683_Transcript_1/1_Conf_1.000	542	20	2.70E-52	XP_002639062.1	84	208.379	133	113	Hypothetical protein CBG14873
Locus_3684_Transcript_1/1_Conf_1.000	1008	20	4.19E-74	XP_001898464.1	71	282.722	249	177	Innexin inx-3
Locus_3685_Transcript_1/1_Conf_1.000	291	0							
Locus_3686_Transcript_1/1_Conf_1.000	465	2	5.13E-06	CAB02779.3	48	54.299	162	78	C. elegans protein C25D7.10, confirmed by transcript evidence
Locus_3687_Transcript_1/2_Conf_1.000	901	20	1.42E-51	ABD39381.1	86	207.608	144	124	putative galectin protein 10

Locus_3687_Transcript_2/2_Conf_1.000	504	20	8.59E-57	ABD39381.1	84	223.016	154	130	putative galectin protein 10
Locus_3688_Transcript_1/1_Conf_1.000	2120	20	0	XP_002647979.1	86	863.603	622	541	Hypothetical protein CBG23896
Locus_3689_Transcript_1/1_Conf_1.000	848	20	1.42E-143	EFO24473.1	93	513.072	282	264	hypothetical protein LOAG_04011
Locus_369_Transcript_1/2_Conf_1.000	1382	20	5.51E-28	EFO20907.1	60	130.183	156	95	MH2 domain-containing protein
Locus_369_Transcript_2/2_Conf_1.000	1382	20	5.51E-28	EFO20907.1	60	130.183	156	95	MH2 domain-containing protein
Locus_3690_Transcript_1/1_Conf_1.000	513	0							

Locus_3691_Transcript_1/1_Conf_1.000	1319	20	1.89E-38	NP_498856.1	60	164.851	266	161	UBX-containing protein in Nematode family member (ubxn-4)
Locus_3692_Transcript_1/2_Conf_1.000	405	0							
Locus_3692_Transcript_2/2_Conf_1.000	403	0							
Locus_3693_Transcript_1/1_Conf_1.000	360	0							
Locus_3694_Transcript_1/2_Conf_1.000	771	2	8.03E-07	NP_509351.1	54	58.5362	122	66	hypothetical protein C34D10.1
Locus_3694_Transcript_2/2_Conf_1.000	364	0							
Locus_3695_Transcript_1/1_Conf_1.000	467	20	9.35E-08	XP_001910957.1	76	60.077	38	29	hypothetical protein
Locus_3696_Transcript_1/2_Conf_1.000	672	0							
Locus_3696_Transcript_2/2_Conf_1.000	670	0							
Locus_3697_Transcript_1/1_Conf_1.000	920	20	6.09E-70	EFO24920.1	83	261.151	165	137	hypothetical protein LOAG_03565
Locus_3698_Transcript_1/1_Conf_1.000	614	20	1.88E-83	NP_498948.1	83	312.383	207	173	Paralysed Arrest at Two-fold family member (pat-2)
Locus_3699_Transcript_1/2_Conf_1.000	1219	20	1.91E-90	NP_490836.1	81	337.421	250	203	hypothetical protein Y48G8AL.13
Locus_3699_Transcript_2/2_Conf_1.000	1148	20	1.73E-90	NP_490836.1	81	337.421	250	203	hypothetical protein Y48G8AL.13
Locus_37_Transcript_1/1_Conf_1.000	684	20	6.37E-92	NP_501167.1	91	340.887	199	183	Ribosomal Protein, Small subunit family member (rps-8)

Locus_370_Transcript_1/1_Conf_1.000	438	20	1.14E-50	XP_001892564.1	79	202.601	147	117	GTP-ase activating protein for Arf containing protein
Locus_3700_Transcript_1/1_Conf_1.000	4041	20	0	NP_502082.1	86	1636.7	1171	1015	Phasmid Socket Absent family member (psa-4)
Locus_3701_Transcript_1/1_Conf_1.000	330	0							
Locus_3702_Transcript_1/1_Conf_1.000	1934								
Locus_3703_Transcript_1/1_Conf_1.000	141	0							
Locus_3704_Transcript_1/2_Conf_1.000	1232	20	2.21E-86	XP_002641003.1	78	323.939	266	209	C. briggsae CBR-TAT-1 protein
Locus_3704_Transcript_2/2_Conf_1.000	1223	20	2.26E-83	XP_002641003.1	77	313.923	266	206	C. briggsae CBR-TAT-1 protein
Locus_3705_Transcript_1/1_Conf_1.000	463	20	3.81E-09	EFA76032.1	49	64.6994	135	67	pleckstrin domain-containing protein
Locus_3706_Transcript_1/1_Conf_1.000	648	14	3.48E-41	XP_002641580.1	78	172.17	121	95	Hypothetical protein CBG09882
Locus_3707_Transcript_1/1_Conf_1.000	296	2	2.90E-09	XP_002633740.1	67	65.0846	56	38	Hypothetical protein CBG03425
Locus_3708_Transcript_1/1_Conf_1.000	2473	20	0	XP_002643033.1	92	1326.23	771	711	C. briggsae CBR-ACO-2 protein
Locus_3709_Transcript_1/1_Conf_1.000	1558	2	2.62E-13	XP_002637225.1	52	81.6481	330	174	Hypothetical protein CBG18891

Locus_371_Transcript_1/1_Conf_1.000	199	0							
Locus_3710_Transcript_1/1_Conf_1.000	779	20	3.25E-72	EFO23722.1	71	275.789	262	188	hypothetical protein LOAG_04763
Locus_3711_Transcript_1/1_Conf_1.000	496	0							
Locus_3712_Transcript_1/1_Conf_1.000	621	20	1.79E-105	BAB63947.1	95	385.571	195	186	Ser/Thr protein phosphatase
Locus_3713_Transcript_1/1_Conf_1.000	2188	20	1.15E-169	NP_495701.2	72	601.668	525	383	IRE1 kinase related family member (ire-1)
Locus_3714_Transcript_1/1_Conf_1.000	539	20	1.84E-45	NP_500566.1	72	185.652	179	130	WAPL (Drosophila Wings APart-Like cohesin interactor) family member (wapl-1)
Locus_3715_Transcript_1/1_Conf_1.000	891	20	7.84E-71	NP_498323.2	85	271.552	188	160	hypothetical protein C05D10.4
Locus_3716_Transcript_1/1_Conf_1.000	758	20	1.37E-96	NP_508182.1	87	356.681	217	190	SphingoMyelin Synthase family member (sms-2)
Locus_3717_Transcript_1/1_Conf_1.000	819	20	1.79E-39	XP_001897933.1	75	167.162	163	123	RE01069p

Locus_3718_Transcript_1/1_Conf_1.000	1661	20	6.29E-61	NP_504654.1	76	239.965	217	165	UBiquitin C-terminal Hydrolase (family 1) family member (ubh-1)
Locus_3719_Transcript_1/1_Conf_1.000	382	0							
Locus_372_Transcript_1/1_Conf_1.000	2982	20	0	NP_492113.2	77	1213.36	1011	781	CHitin Synthase family member (chs-1)
Locus_3720_Transcript_1/2_Conf_1.000	1261	20	3.38E-98	XP_002629732.1	66	363.229	379	252	Hypothetical protein CBG00964
Locus_3720_Transcript_2/2_Conf_1.000	1262	20	3.38E-98	XP_002629732.1	66	363.229	379	252	Hypothetical protein CBG00964
Locus_3721_Transcript_1/1_Conf_1.000	924	20	1.13E-67	NP_495001.1	73	261.151	241	178	hypothetical protein F09E5.8
Locus_3722_Transcript_1/1_Conf_1.000	836	20	2.00E-09	EFO23681.1	75	67.3958	49	37	hypothetical protein LOAG_04805
Locus_3723_Transcript_1/1_Conf_1.000	477	20	3.57E-44	NP_501221.1	77	181.03	140	108	CytiDine Deaminase family member (cdd-2)
Locus_3724_Transcript_1/2_Conf_1.000	3259	4	4.79E-61	NP_492524.2	58	241.506	348	204	hypothetical protein F30A10.10
Locus_3724_Transcript_2/2_Conf_1.000	3226	4	4.73E-61	NP_492524.2	58	241.506	348	204	hypothetical protein F30A10.10

Locus_3725_Transcript_1/1_Conf_1.000	633	20	1.44E-105	NP_001022641.1	94	385.956	211	200	LEThal family member (let-805)
Locus_3726_Transcript_1/1_Conf_1.000	310	0							
Locus_3727_Transcript_1/1_Conf_1.000	329	2	2.35E-19	NP_498941.1	72	98.5969	76	55	hypothetical protein K02D10.4
Locus_3728_Transcript_1/2_Conf_1.000	1290	20	4.63E-58	XP_002633353.1	66	229.95	250	167	Hypothetical protein CBG06097
Locus_3728_Transcript_2/2_Conf_1.000	678	2	4.90E-04	XP_002633353.1	62	48.9062	51	32	Hypothetical protein CBG06097
Locus_3729_Transcript_1/1_Conf_1.000	513	20	4.27E-83	NP_505708.2	92	310.457	170	158	hypothetical protein F32G8.4
Locus_373_Transcript_1/1_Conf_1.000	2864	20	0	Q27665.1	94	1414.82	792	747	6-phosphofructokinase
Locus_3730_Transcript_1/2_Conf_0.667	282	20	2.32E-14	EFN87118.1	71	82.0333	59	42	Four-domain proteases inhibitor
Locus_3730_Transcript_2/2_Conf_0.667	282	20	2.32E-14	EFN87118.1	71	82.0333	59	42	Four-domain proteases inhibitor
Locus_3731_Transcript_1/1_Conf_1.000	443	0							
Locus_3732_Transcript_1/1_Conf_1.000	232	0							
Locus_3733_Transcript_1/4_Conf_0.200	621	20	4.78E-50	NP_740900.1	71	201.445	211	150	hypothetical protein T08G11.1
Locus_3733_Transcript_2/4_Conf_0.200	663	20	8.62E-51	NP_740900.1	71	204.142	212	151	hypothetical protein T08G11.1
Locus_3733_Transcript_3/4_Conf_0.400	936	20	2.33E-76	XP_002639673.1	69	290.041	313	216	Hypothetical protein CBG12391
Locus_3733_Transcript_4/4_Conf_0.400	936	20	1.16E-75	XP_002639673.1	69	287.73	313	216	Hypothetical protein CBG12391
Locus_3734_Transcript_1/2_Conf_1.000	2440	20	3.36E-141	XP_002639317.1	59	507.294	764	454	C. briggsae CBR-ABT-2 protein
Locus_3734_Transcript_2/2_Conf_1.000	2392	20	6.23E-140	XP_002639317.1	58	503.056	762	449	C. briggsae CBR-ABT-2 protein

Locus_3735_Transcript_1/2_Conf_1.000	908	20	4.72E-87	XP_002630833.1	74	325.479	304	227	C. briggsae CBR-VRK-1 protein
Locus_3735_Transcript_2/2_Conf_1.000	984	20	3.50E-94	NP_495185.1	72	349.362	329	239	Vaccinia Related Kinase family member (vrk-1)
Locus_3736_Transcript_1/2_Conf_1.000	1290	20	1.26E-111	NP_498949.2	72	305.834	283	206	hypothetical protein F54F2.9
Locus_3736_Transcript_2/2_Conf_1.000	1273	20	5.63E-117	NP_498949.2	71	425.631	407	289	hypothetical protein F54F2.9
Locus_3737_Transcript_1/1_Conf_1.000	1512	1	1.59E-07	XP_002641068.1	38	62.3882	289	110	Hypothetical protein CBG22485
Locus_3738_Transcript_1/1_Conf_1.000	305	17	1.09E-08	NP_491980.1	63	63.1586	79	50	hypothetical protein T10B11.6
Locus_3739_Transcript_1/1_Conf_1.000	405	20	3.05E-35	EFN69632.1	70	151.369	135	95	Poly [ADP-ribose] polymerase
Locus_374_Transcript_1/2_Conf_1.000	496	0							
Locus_374_Transcript_2/2_Conf_1.000	417	0							
Locus_3740_Transcript_1/1_Conf_1.000	874	20	6.40E-102	NP_497716.1	86	374.785	267	231	hypothetical protein C34C12.5
Locus_3741_Transcript_1/2_Conf_1.000	171	20	5.13E-13	XP_001897838.1	81	70.8626	44	36	GH25683p
Locus_3741_Transcript_2/2_Conf_1.000	687	20	2.01E-77	XP_002631727.1	85	292.738	229	196	Hypothetical protein CBG20929
Locus_3742_Transcript_1/1_Conf_1.000	479	20	1.49E-58	XP_002642088.1	87	228.794	140	122	C. briggsae CBR-SEL-2 protein
Locus_3743_Transcript_1/1_Conf_1.000	647	1	3.47E-09	CAH88354.1	86	65.855	38	33	hypothetical protein PC101070.00.0
Locus_3744_Transcript_1/1_Conf_1.000	1542	6	1.67E-28	XP_002642047.1	50	132.109	378	189	C. briggsae CBR-MEL-28 protein
Locus_3745_Transcript_1/1_Conf_1.000	296	20	4.93E-17	NP_496557.1	69	90.8929	100	69	hypothetical protein Y17G7B.4
Locus_3746_Transcript_1/1_Conf_1.000	2079	0							

Locus_3747_Transcript_1/1_Conf_1.000	623	20	2.54E-43	XP_002646224.1	83	179.104	125	104	Hypothetical protein CBG11916
Locus_3748_Transcript_1/1_Conf_1.000	824	0							
Locus_3749_Transcript_1/1_Conf_1.000	1869	20	7.26E-85	EFO18886.1	54	319.701	509	277	GPI transamidase component PIG-T
Locus_375_Transcript_1/1_Conf_1.000	228	0							
Locus_3750_Transcript_1/1_Conf_1.000	275	0							
Locus_3751_Transcript_1/1_Conf_1.000	139	2	9.48E-05	CAD20812.1	63	50.0618	44	28	SXC2 protein
Locus_3752_Transcript_1/1_Conf_1.000	224	20	3.45E-18	EFO17497.1	72	94.7449	73	53	timeless protein
Locus_3753_Transcript_1/1_Conf_1.000	189	0							
Locus_3754_Transcript_1/1_Conf_1.000	851	20	3.26E-63	NP_503010.2	72	246.128	211	154	hypothetical protein Y116A8C.9

Locus_3755_Transcript_1/2_Conf_1.000	1483	20	5.27E-48	XP_002639198.1	85	196.823	145	124	C. briggsae CBR-PABP-2 protein
Locus_3755_Transcript_2/2_Conf_1.000	1148	20	3.66E-48	XP_002639198.1	85	196.823	145	124	C. briggsae CBR-PABP-2 protein
Locus_3756_Transcript_1/1_Conf_1.000	1232	20	1.62E-12	XP_001686160.1	49	78.5666	207	102	hypothetical protein

Locus_3757_Transcript_1/2_Conf_1.000	1576	20	4.44E-93	XP_001901466.1	61	346.665	452	276	Paired amphipathic helix repeat family protein
Locus_3757_Transcript_2/2_Conf_1.000	762	20	1.92E-13	XP_001901466.1	61	80.4925	107	66	Paired amphipathic helix repeat family protein
Locus_3758_Transcript_1/1_Conf_1.000	581	1	5.74E-04	XP_002640488.1	41	48.1358	219	91	Hypothetical protein CBG13624
Locus_3759_Transcript_1/1_Conf_1.000	1090	20	6.19E-58	NP_001122646.1	66	229.18	269	178	hypothetical protein T28D9.3
Locus_376_Transcript_1/1_Conf_1.000	759	20	1.22E-60	EFO23916.1	66	237.269	260	174	transcription accessory protein
Locus_3760_Transcript_1/1_Conf_1.000	446	9	2.44E-14	AAA63241.1	84	65.855	38	32	unknown
Locus_3761_Transcript_1/1_Conf_1.000	2360	20	0	XP_002641127.1	92	1183.32	690	635	Hypothetical protein CBG08977
Locus_3762_Transcript_1/1_Conf_1.000	525	20	1.09E-23	NP_496958.2	57	113.235	145	83	XRN (mouse/S. cerevisiae) ribonuclease related family member (xrn-2)

Locus_3763_Transcript_1/1_Conf_1.000	409	20	9.81E-26	XP_002640785.1	73	119.783	96	71	Hypothetical protein CBG15660
Locus_3764_Transcript_1/1_Conf_1.000	386	0							
Locus_3765_Transcript_1/1_Conf_1.000	550	8	5.63E-16	NP_492071.1	67	87.8113	105	71	hypothetical protein F52A8.1
Locus_3766_Transcript_1/1_Conf_1.000	959	19	7.56E-30	NP_001022050.1	55	135.576	247	138	hypothetical protein D1069.3
Locus_3767_Transcript_1/1_Conf_1.000	466	4	3.66E-20	XP_002631353.1	74	101.293	89	66	Hypothetical protein CBG03186
Locus_3768_Transcript_1/1_Conf_1.000	671	4	8.90E-19	XP_002632648.1	72	97.8265	106	77	Hypothetical protein CBG21570
Locus_3769_Transcript_1/1_Conf_1.000	362	0							
Locus_377_Transcript_1/1_Conf_1.000	1711	20	0	NP_001023223.1	94	1009.59	558	529	EGg Laying defective family member (egl-4)
Locus_3770_Transcript_1/1_Conf_1.000	809	20	9.62E-54	NP_505810.2	61	214.542	266	164	P21-Activated Kinase family member (pak-2)
Locus_3771_Transcript_1/1_Conf_1.000	1726	20	8.49E-101	XP_001892143.1	74	372.474	292	218	Protein kinase domain containing protein
Locus_3772_Transcript_1/1_Conf_1.000	198	1	8.16E-04	NP_492172.1	60	46.9802	63	38	Aspergillus NUclear Division related family member (nud-2)

Locus_3773_Transcript_1/1_Conf_1.000	1317	20	6.17E-98	XP_002642672.1	72	362.459	312	226	C. briggsae CBR-TAG-307 protein
Locus_3774_Transcript_1/1_Conf_1.000	649	0							
Locus_3775_Transcript_1/1_Conf_1.000	850	20	2.02E-97	XP_002643159.1	74	359.762	298	222	C. briggsae CBR-VPS-33.1 protein
Locus_3776_Transcript_1/1_Conf_1.000	1121	1	2.41E-04	EFO17338.1	42	51.2174	291	125	hypothetical protein LOAG_11160
Locus_3777_Transcript_1/5_Conf_0.688	3033	20	0	EFO25880.1	86	1261.51	886	765	26S proteasome regulatory complex subunit p97
Locus_3777_Transcript_2/5_Conf_0.688	3033	20	0	EFO25880.1	86	1259.97	886	765	26S proteasome regulatory complex subunit p97
Locus_3777_Transcript_3/5_Conf_0.688	3033	20	0	EFO25880.1	86	1261.51	886	765	26S proteasome regulatory complex subunit p97
Locus_3777_Transcript_4/5_Conf_0.688	3033	20	0	EFO25880.1	86	1261.51	886	765	26S proteasome regulatory complex subunit p97
Locus_3777_Transcript_5/5_Conf_0.688	3033	20	0	EFO25880.1	86	1261.51	886	765	26S proteasome regulatory complex subunit p97
Locus_3778_Transcript_1/1_Conf_1.000	825	20	1.57E-83	EFO27043.1	89	313.538	189	169	small GTP binding protein
Locus_3779_Transcript_1/3_Conf_0.600	196	1	4.34E-05	NP_494766.1	59	51.2174	72	43	hypothetical protein H20J04.3
Locus_3779_Transcript_2/3_Conf_0.600	151	0							
Locus_3779_Transcript_3/3_Conf_0.600	202	1	1.64E-04	NP_494766.1	59	49.2914	74	44	hypothetical protein H20J04.3
Locus_378_Transcript_1/1_Conf_1.000	689	7	4.55E-21	ABC86839.1	80	105.531	109	88	depsiphilin

Locus_3780_Transcript_1/1_Conf_1.000	182	0							
Locus_3781_Transcript_1/1_Conf_1.000	371	0							
Locus_3782_Transcript_1/1_Conf_1.000	1181	20	1.25E-99	EFO19146.1	71	367.851	391	281	hypothetical protein LOAG_09348
Locus_3783_Transcript_1/1_Conf_1.000	428	20	1.13E-29	NP_001022585.1	75	132.88	132	100	hypothetical protein F43C1.6
Locus_3784_Transcript_1/1_Conf_1.000	628	20	8.06E-69	NP_504045.1	75	263.848	206	156	hypothetical protein R08E5.3
Locus_3785_Transcript_1/1_Conf_1.000	725	20	1.85E-39	XP_002638213.1	84	166.777	226	192	Hypothetical protein CBG22646
Locus_3786_Transcript_1/1_Conf_1.000	236	3	5.45E-08	NP_001022999.1	61	60.8474	78	48	hypothetical protein ZK418.2
Locus_3787_Transcript_1/1_Conf_1.000	151	20	1.50E-21	XP_002822871.1	100	105.916	50	50	PREDICTED: myeloid leukemia factor 2-like
Locus_3788_Transcript_1/1_Conf_1.000	373	20	1.39E-35	XP_002632353.1	75	152.525	122	92	Hypothetical protein CBG00367
Locus_3789_Transcript_1/2_Conf_1.000	536	20	2.13E-46	AAZ82856.1	83	188.734	112	93	Hypothetical protein C24B5.4
Locus_3789_Transcript_2/2_Conf_1.000	524	20	5.46E-44	AAZ82856.1	82	180.644	108	89	Hypothetical protein C24B5.4
Locus_379_Transcript_1/1_Conf_1.000	822	1	1.44E-04	XP_002632710.1	45	51.2174	183	84	Hypothetical protein CBG18736
Locus_3790_Transcript_1/1_Conf_1.000	210	17	1.67E-09	NP_498750.2	62	65.855	69	43	hypothetical protein F44B9.8
Locus_3791_Transcript_1/1_Conf_1.000	150	0							
Locus_3792_Transcript_1/2_Conf_1.000	286	20	2.64E-18	ABZ81538.1	81	95.1301	70	57	K01G5.8a
Locus_3792_Transcript_2/2_Conf_1.000	296	20	2.62E-18	ABZ81538.1	81	95.1301	70	57	K01G5.8a
Locus_3793_Transcript_1/1_Conf_1.000	1049	20	8.84E-99	XP_002631700.1	71	364.77	349	250	Hypothetical protein CBG20899

Locus_3794_Transcript_1/1_Conf_1.000	517	20	9.46E-70	XP_001147989.1	100	266.159	164	164	PREDICTED: similar to RPS27A protein
Locus_3795_Transcript_1/2_Conf_1.000	1111	0							
Locus_3795_Transcript_2/2_Conf_1.000	1111	0							
Locus_3796_Transcript_1/1_Conf_1.000	950	20	3.41E-107	NP_490886.2	80	392.504	305	244	hypothetical protein Y71G12B.11
Locus_3797_Transcript_1/1_Conf_1.000	223	20	4.68E-07	EFN83858.1	75	57.7658	52	39	Histone-lysine N-methyltransferase SETMAR
Locus_3798_Transcript_1/2_Conf_1.000	1142	5	2.14E-24	NP_499994.3	52	117.857	231	121	hypothetical protein Y55F3BL.1
Locus_3798_Transcript_2/2_Conf_1.000	1142	5	2.80E-24	NP_499994.3	52	117.472	231	121	hypothetical protein Y55F3BL.1
Locus_3799_Transcript_1/1_Conf_1.000	372	11	4.78E-28	XP_002637831.1	68	127.487	124	85	C. briggsae CBR-NXF-2 protein
Locus_38_Transcript_1/1_Conf_1.000	3553	20	0	NP_509919.2	67	1177.93	1184	794	hypothetical protein T25C12.3
Locus_380_Transcript_1/1_Conf_1.000	912	12	1.04E-33	NP_001021203.1	55	148.288	259	143	CEll Death abnormality family member (ced-4)
Locus_3800_Transcript_1/1_Conf_1.000	684	0							

Locus_3801_Transcript_1/1_Conf_1.000	1305	10	5.47E-06	NP_001093288.1	72	56.9954	50	36	hypothetical protein LOC100101190
Locus_3802_Transcript_1/4_Conf_0.375	403	0							
Locus_3802_Transcript_2/4_Conf_0.625	696	20	2.25E-31	XP_002640376.1	62	139.813	154	97	Hypothetical protein CBG20283
Locus_3802_Transcript_3/4_Conf_0.625	787	20	2.85E-31	XP_002640376.1	62	139.813	154	97	Hypothetical protein CBG20283
Locus_3802_Transcript_4/4_Conf_0.625	787	20	2.85E-31	XP_002640376.1	62	139.813	154	97	Hypothetical protein CBG20283
Locus_3803_Transcript_1/1_Conf_1.000	157	0							
Locus_3804_Transcript_1/1_Conf_1.000	1135	20	3.55E-128	XP_002641391.1	80	462.611	336	270	C. briggsae CBR-GLY-8 protein
Locus_3805_Transcript_1/1_Conf_1.000	852	20	1.29E-51	NP_502302.2	63	207.608	247	157	hypothetical protein M18.8
Locus_3806_Transcript_1/1_Conf_1.000	501	20	5.81E-58	NP_497618.1	94	226.868	113	107	hypothetical protein Y71H2AM.5
Locus_3807_Transcript_1/1_Conf_1.000	563	20	1.75E-68	NP_497809.1	81	262.307	187	153	Heavy chain, Unconventional Myosin family member (hum-5)
Locus_3808_Transcript_1/1_Conf_1.000	992	20	1.36E-37	EFO25376.1	58	161.384	262	152	hypothetical protein LOAG_03111
Locus_3809_Transcript_1/1_Conf_1.000	685	20	6.14E-103	XP_002630706.1	98	377.481	228	225	C. briggsae CBR-MOG-5 protein
Locus_381_Transcript_1/3_Conf_0.333	1111	20	7.69E-104	NP_001021158.1	76	381.719	315	241	UDP-GlucuronosylTransferase family member (ugt-60)
Locus_381_Transcript_2/3_Conf_0.667	2798	20	0	NP_001022808.1	82	676.781	470	390	Loss of InTestine family member (lit-1)

Locus_381_Transcript_3/3_Conf_0.667	2798	20	0	NP_001022808.1	82	676.781	470	390	Loss of InTestine family member (lit-1)
Locus_3810_Transcript_1/1_Conf_1.000	436	0							
Locus_3811_Transcript_1/1_Conf_1.000	487	1	1.26E-12	EFO21463.1	65	76.2554	102	67	hypothetical protein LOAG_07027
Locus_3812_Transcript_1/1_Conf_1.000	2220	20	1.07E-146	NP_499628.1	63	525.398	756	480	hypothetical protein Y49E10.23
Locus_3813_Transcript_1/1_Conf_1.000	892	18	1.49E-45	XP_001895351.1	58	187.578	236	138	hypothetical protein
Locus_3814_Transcript_1/1_Conf_1.000	485	20	5.46E-32	XP_002634232.1	93	140.584	79	74	C. briggsae CBR-TTR-51 protein
Locus_3815_Transcript_1/1_Conf_1.000	233	8	1.44E-08	ACM46025.1	60	62.7734	84	51	Let-23 fertility effector/regulator protein 2, isoform d
Locus_3816_Transcript_1/2_Conf_1.000	4970	20	0	NP_501755.2	74	1433.31	1247	934	hypothetical protein W08D2.5
Locus_3816_Transcript_2/2_Conf_1.000	4948	20	0	XP_002633783.1	78	839.721	707	556	Hypothetical protein CBG03474
Locus_3817_Transcript_1/1_Conf_1.000	618	5	7.67E-48	XP_002646179.1	71	194.126	180	128	Hypothetical protein CBG23745
Locus_3818_Transcript_1/1_Conf_1.000	866	20	1.06E-16	NP_504999.1	73	91.6633	115	84	Clathrin LIght Chain family member (clic-1)
Locus_3819_Transcript_1/1_Conf_1.000	485	0							
Locus_382_Transcript_1/2_Conf_1.000	3771	20	0	XP_001901573.1	80	1368.6	1024	822	ube1-prov protein
Locus_382_Transcript_2/2_Conf_1.000	3772	20	0	XP_001901573.1	80	1368.6	1024	822	ube1-prov protein

Locus_3820_Transcript_1/1_Conf_1.000	387	20	3.36E-18	ADI54942.1	95	94.7449	49	47	heat shock protein 70
Locus_3821_Transcript_1/1_Conf_1.000	1301	20	1.14E-96	NP_509639.1	72	358.221	312	225	hypothetical protein T09B9.2
Locus_3822_Transcript_1/1_Conf_1.000	216	20	1.55E-15	NP_001021859.1	68	85.8853	70	48	Variable ABnormal morphology family member (vab-10)
Locus_3823_Transcript_1/1_Conf_1.000	957	20	7.29E-41	NP_498575.1	59	172.17	266	157	Etoposide-Induced Protein homolog family member (eip-24)
Locus_3824_Transcript_1/1_Conf_1.000	522	0							
Locus_3825_Transcript_1/1_Conf_1.000	1801	20	0	NP_001023008.1	80	688.723	524	423	CULlin family member (cul-2)
Locus_3826_Transcript_1/1_Conf_1.000	811	20	1.36E-116	NP_491953.1	86	423.32	269	233	Temporarily Assigned Gene name family member (tag-203)
Locus_3827_Transcript_1/3_Conf_0.400	459	4	2.40E-16	NP_502207.1	62	88.5817	99	62	hypothetical protein ZK792.1
Locus_3827_Transcript_2/3_Conf_0.600	481	4	2.40E-16	NP_502207.1	62	88.5817	99	62	hypothetical protein ZK792.1

Locus_3827_Transcript_3/3_Conf_0.600	514	4	2.64E-16	NP_502207.1	62	88.5817	99	62	hypothetical protein ZK792.1
Locus_3828_Transcript_1/2_Conf_1.000	185	0							
Locus_3828_Transcript_2/2_Conf_1.000	210	0							
Locus_3829_Transcript_1/1_Conf_1.000	615	2	5.49E-06	NP_001022819.1	60	55.0694	116	70	hypothetical protein Y111B2A.27
Locus_383_Transcript_1/1_Conf_1.000	2619	20	2.40E-108	XP_002636616.1	74	398.282	380	283	C. briggsae CBR-PMS-2 protein
Locus_3830_Transcript_1/2_Conf_1.000	511	20	7.91E-66	NP_496868.1	88	253.062	169	149	hypothetical protein C31C9.2
Locus_3830_Transcript_2/2_Conf_1.000	807	20	3.04E-108	NP_496868.1	85	395.586	268	230	hypothetical protein C31C9.2
Locus_3831_Transcript_1/1_Conf_1.000	1015	20	3.07E-32	EFO27739.1	67	143.665	152	102	hypothetical protein LOAG_00741
Locus_3832_Transcript_1/1_Conf_1.000	232	0							
Locus_3833_Transcript_1/1_Conf_1.000	709	20	4.45E-59	XP_002629937.1	73	231.876	230	170	Hypothetical protein CBG03655
Locus_3834_Transcript_1/1_Conf_1.000	129	0							
Locus_3835_Transcript_1/1_Conf_1.000	2941	20	1.69E-158	NP_491206.1	59	565.074	708	423	abnormal cell LINeage family member (lin-59)

Locus_3836_Transcript_1/1_Conf_1.000	393	0							
Locus_3837_Transcript_1/1_Conf_1.000	544	20	3.23E-77	XP_002642413.1	89	291.197	179	160	Hypothetical protein CBG06810
Locus_3838_Transcript_1/2_Conf_1.000	1367	20	0	XP_002641235.1	92	730.709	417	386	C. briggsae CBR-RPT-3 protein
Locus_3838_Transcript_2/2_Conf_1.000	1367	20	0	XP_002641235.1	92	730.709	417	386	C. briggsae CBR-RPT-3 protein
Locus_3839_Transcript_1/1_Conf_1.000	951	20	8.21E-53	ACD61688.1	88	211.846	129	114	light chain 3
Locus_384_Transcript_1/9_Conf_0.472	784	19	2.49E-11	XP_710281.1	58	73.559	84	49	hypothetical protein CaO19.6835
Locus_384_Transcript_2/9_Conf_0.472	784	20	2.49E-11	XP_710281.1	58	73.559	84	49	hypothetical protein CaO19.6835
Locus_384_Transcript_3/9_Conf_0.250	1406	20	1.80E-34	P27613.1	85	151.754	100	85	Globin-like host-protective antigen
Locus_384_Transcript_4/9_Conf_0.417	1302	20	6.37E-39	NP_497227.1	86	166.392	131	113	Temporarily Assigned Gene name family member (tag-266)

Locus_384_Transcript_5/9_Conf_0.333	720	20	6.91E-55	P27613.1	85	218.009	145	124	Globin-like host-protective antigen
Locus_384_Transcript_6/9_Conf_0.222	472	20	1.86E-16	AAD51334.1	80	88.9669	55	44	Kunitz type serine protease inhibitor
Locus_384_Transcript_7/9_Conf_0.250	2495	20	5.84E-165	NP_491316.1	71	586.26	585	417	EGG sterile (unfertilizable) family member (egg-5)
Locus_384_Transcript_8/9_Conf_0.306	720	20	3.10E-55	P27613.1	86	219.164	145	125	Globin-like host-protective antigen
Locus_384_Transcript_9/9_Conf_0.472	784	20	2.49E-11	XP_710281.1	58	73.559	84	49	hypothetical protein CaO19.6835
Locus_3840_Transcript_1/1_Conf_1.000	1510	20	1.64E-121	NP_491807.1	66	441.039	498	329	hypothetical protein C48E7.2
Locus_3841_Transcript_1/1_Conf_1.000	765	4	2.36E-35	NP_510155.3	55	153.295	255	142	PIP Kinase family member (ppk-3)
Locus_3842_Transcript_1/1_Conf_1.000	2170	20	1.22E-155	NP_498784.1	85	555.058	389	331	BTB and MATH domain containing family member (bath-42)
Locus_3843_Transcript_1/1_Conf_1.000	365	0							
Locus_3844_Transcript_1/1_Conf_1.000	399	20	1.26E-20	EFO18738.1	74	102.834	98	73	hypothetical protein LOAG_09757
Locus_3845_Transcript_1/1_Conf_1.000	253	20	6.98E-19	XP_002813545.1	71	97.0561	84	60	PREDICTED: histone-lysine N-methyltransferase SETMAR-like
Locus_3846_Transcript_1/1_Conf_1.000	2080	20	0	NP_001024735.1	77	664.07	505	392	hypothetical protein H13N06.4
Locus_3847_Transcript_1/1_Conf_1.000	1331	13	1.76E-100	NP_495958.1	68	370.933	384	262	yeast SEC homolog family member (sec-5)

Locus_3848_Transcript_1/1_Conf_1.000	3098	20	0	NP_496844.3	61	729.169	1003	619	hypothetical protein Y48E1B.14
Locus_3849_Transcript_1/1_Conf_1.000	235	0							
Locus_385_Transcript_1/1_Conf_1.000	1564	20	3.44E-130	NP_506581.1	66	469.929	518	345	hypothetical protein F23B12.7
Locus_3850_Transcript_1/1_Conf_1.000	533	0							
Locus_3851_Transcript_1/2_Conf_1.000	719	20	2.12E-64	XP_001901265.1	92	249.595	140	129	KH domain containing protein
Locus_3851_Transcript_2/2_Conf_1.000	1281	20	8.04E-79	XP_001901265.1	92	298.901	171	158	KH domain containing protein
Locus_3852_Transcript_1/1_Conf_1.000	978	20	9.04E-119	NP_504231.1	83	431.024	300	250	hypothetical protein T08H10.1
Locus_3853_Transcript_1/1_Conf_1.000	360	7	4.88E-09	NP_498217.2	51	64.3142	141	73	abnormal embryonic PARtitioning of cytoplasm family member (par-3)
Locus_3854_Transcript_1/1_Conf_1.000	168	0							
Locus_3855_Transcript_1/1_Conf_1.000	737	20	3.98E-45	EFO22481.1	66	185.652	211	141	alix-SF

Locus_3856_Transcript_1/2_Conf_1.000	1480	20	0	EFO27216.1	79	647.121	461	367	NPL4 family protein
Locus_3856_Transcript_2/2_Conf_1.000	1788	20	0	XP_002632107.1	75	674.47	524	394	Hypothetical protein CBG06960
Locus_3857_Transcript_1/1_Conf_1.000	1680	20	6.72E-119	NP_508768.1	64	432.565	534	346	AuTophaGy (yeast Atg homolog) family member (atg-16.1)
Locus_3858_Transcript_1/5_Conf_0.500	968	20	1.46E-12	XP_002056110.1	44	78.1814	254	113	GJ10405
Locus_3858_Transcript_2/5_Conf_0.500	950	20	1.09E-12	BAH03485.1	43	78.5666	264	115	tick serine proteinase
Locus_3858_Transcript_3/5_Conf_0.500	842	20	1.77E-13	XP_002056110.1	44	80.8777	254	114	GJ10405
Locus_3858_Transcript_4/5_Conf_0.167	501	20	5.51E-08	XP_002002129.1	59	60.8474	57	34	GI17212
Locus_3858_Transcript_5/5_Conf_0.500	842	20	8.81E-13	BAH03485.1	43	78.5666	257	113	tick serine proteinase
Locus_3859_Transcript_1/1_Conf_1.000	508	20	2.51E-11	XP_002129449.1	48	72.0182	168	81	PREDICTED: hypothetical protein

Locus_386_Transcript_1/1_Conf_1.000	1272	20	1.10E-120	NP_491556.1	72	437.958	425	310	human CLN (neuronal ceroid lipofuscinosis) related family member (cln-3.2)
Locus_3860_Transcript_1/1_Conf_1.000	1652	20	5.15E-148	NP_509268.1	70	529.25	517	364	hypothetical protein F48E3.3
Locus_3861_Transcript_1/1_Conf_1.000	1974	20	1.14E-136	EFO19280.1	84	491.886	324	273	BTB/POZ domain-containing protein
Locus_3862_Transcript_1/1_Conf_1.000	249	0							
Locus_3863_Transcript_1/1_Conf_1.000	857	0							
Locus_3864_Transcript_1/1_Conf_1.000	145	5	1.08E-11	XP_002646369.1	82	73.1738	45	37	Hypothetical protein CBG12087
Locus_3865_Transcript_1/1_Conf_1.000	304	20	8.59E-22	EFO22068.1	69	106.686	95	66	hypothetical protein LOAG_06418
Locus_3866_Transcript_1/1_Conf_1.000	749	20	2.50E-50	NP_492760.1	70	202.986	187	132	hypothetical protein F25H2.4
Locus_3867_Transcript_1/1_Conf_1.000	820	20	4.40E-46	XP_002639398.1	69	189.119	220	153	C. briggsae CBR-UBXN-1 protein
Locus_3868_Transcript_1/1_Conf_1.000	581	20	2.46E-55	NP_499165.1	89	218.779	160	143	Vacuolar H ATPase family member (vha-1)
Locus_3869_Transcript_1/1_Conf_1.000	476	0							

Locus_387_Transcript_1/4_Conf_0.300	211	20	5.19E-19	XP_001846568.1	91	97.4413	56	51	conserved hypothetical protein
Locus_387_Transcript_2/4_Conf_0.300	253	20	4.83E-20	XP_001846568.1	91	100.908	58	53	conserved hypothetical protein
Locus_387_Transcript_3/4_Conf_0.400	629	20	4.85E-90	XP_001894478.1	92	334.339	191	176	40S ribosomal protein S9
Locus_387_Transcript_4/4_Conf_0.400	629	20	4.85E-90	XP_001894478.1	92	334.339	191	176	40S ribosomal protein S9
Locus_3870_Transcript_1/1_Conf_1.000	237	0							
Locus_3871_Transcript_1/1_Conf_1.000	368	20	4.20E-37	NP_496453.1	90	157.532	119	108	TransThyretin-Related family domain family member (ttr-18)
Locus_3872_Transcript_1/1_Conf_1.000	913	7	9.47E-27	XP_001896459.1	64	125.176	117	76	hypothetical protein Bm1_24995
Locus_3873_Transcript_1/1_Conf_1.000	1115	4	1.64E-29	XP_002638906.1	47	134.806	277	132	Hypothetical protein CBG22132
Locus_3874_Transcript_1/7_Conf_0.312	1177	6	1.46E-07	XP_002633011.1	46	62.003	151	70	C. briggsae CBR-TAG-60 protein
Locus_3874_Transcript_2/7_Conf_0.125	877	6	2.94E-06	NP_001040910.1	65	56.9954	67	44	Temporarily Assigned Gene name family member (tag-60)
Locus_3874_Transcript_3/7_Conf_0.562	1597	20	1.86E-46	XP_002633011.1	52	191.815	335	177	C. briggsae CBR-TAG-60 protein
Locus_3874_Transcript_4/7_Conf_0.438	1297	20	8.25E-47	NP_001040908.1	54	192.586	283	155	Temporarily Assigned Gene name family member (tag-60)
Locus_3874_Transcript_5/7_Conf_0.438	670	20	1.19E-39	NP_001040909.1	67	167.162	166	112	Temporarily Assigned Gene name family member (tag-60)
Locus_3874_Transcript_6/7_Conf_0.562	1657	20	1.89E-49	NP_741479.1	54	201.83	359	195	Temporarily Assigned Gene name family member (tag-60)
Locus_3874_Transcript_7/7_Conf_0.562	1657	20	1.89E-49	NP_741479.1	54	201.83	359	195	Temporarily Assigned Gene name family member (tag-60)
Locus_3875_Transcript_1/1_Conf_1.000	572	14	2.44E-20	NP_499428.1	64	102.449	110	71	hypothetical protein W09D6.5
Locus_3876_Transcript_1/1_Conf_1.000	1682	9	2.55E-09	XP_002639259.1	46	68.5514	377	175	C. briggsae CBR-SYS-1 protein
Locus_3877_Transcript_1/1_Conf_1.000	572	1	2.45E-04	XP_001638787.1	40	49.2914	114	46	predicted protein
Locus_3878_Transcript_1/2_Conf_1.000	399	20	2.22E-17	XP_002631292.1	64	92.0485	84	54	Hypothetical protein CBG03105
Locus_3878_Transcript_2/2_Conf_1.000	399	20	2.90E-17	XP_002631292.1	64	91.6633	84	54	Hypothetical protein CBG03105

Locus_3879_Transcript_1/1_Conf_1.000	1329	20	4.65E-85	XP_001898423.1	58	319.701	452	263	Mediator complex subunit rgr-1
Locus_388_Transcript_1/3_Conf_0.714	1388	20	1.20E-139	XP_002642167.1	81	501.13	388	318	C. briggsae CBR-RPN-3 protein
Locus_388_Transcript_2/3_Conf_0.714	1352	20	5.17E-140	XP_002642167.1	82	502.286	390	320	C. briggsae CBR-RPN-3 protein
Locus_388_Transcript_3/3_Conf_0.714	1352	20	5.17E-140	XP_002642167.1	82	502.286	390	320	C. briggsae CBR-RPN-3 protein
Locus_3880_Transcript_1/1_Conf_1.000	1120	20	4.96E-50	EFO25088.1	63	202.986	209	133	hypothetical protein LOAG_03398
Locus_3881_Transcript_1/1_Conf_1.000	1335	6	2.87E-42	XP_002631687.1	49	177.563	453	226	Hypothetical protein CBG20880
Locus_3882_Transcript_1/1_Conf_1.000	2363	20	3.80E-174	EFO25239.1	68	616.69	623	426	nonsense mRNA reducing factor 1 NORF1

Locus_3883_Transcript_1/1_Conf_1.000	285	0							
Locus_3884_Transcript_1/1_Conf_1.000	263	0							
Locus_3885_Transcript_1/1_Conf_1.000	662	20	7.67E-68	XP_002642264.1	96	260.766	141	136	Hypothetical protein CBG18252
Locus_3886_Transcript_1/1_Conf_1.000	758	20	4.88E-86	EFO19031.1	82	321.627	232	191	hypothetical protein LOAG_09464
Locus_3887_Transcript_1/1_Conf_1.000	280	0							
Locus_3888_Transcript_1/1_Conf_1.000	1180	0							
Locus_3889_Transcript_1/1_Conf_1.000	1252	20	6.62E-78	EFO20995.1	67	295.819	279	187	TK/EPH protein kinase
Locus_389_Transcript_1/3_Conf_0.692	1721	20	2.74E-29	EFO24026.1	37	130.954	388	146	hypothetical protein LOAG_04466
Locus_389_Transcript_2/3_Conf_0.385	1000	20	1.17E-44	XP_002640431.1	61	184.882	201	123	Hypothetical protein CBG08482
Locus_389_Transcript_3/3_Conf_0.846	2169	20	7.14E-55	XP_001895704.1	43	220.32	484	210	Chitin binding Peritrophin-A domain containing protein
Locus_3890_Transcript_1/1_Conf_1.000	1452	20	1.75E-173	NP_509673.1	85	613.609	408	348	PhosphatidylSerine SYnthase family member (pssy-1)
Locus_3891_Transcript_1/1_Conf_1.000	1728	20	8.70E-138	NP_504197.1	70	495.352	456	323	FIdGetin-Like (mammalian developmental AAA ATPase) related family member (figl-1)
Locus_3892_Transcript_1/1_Conf_1.000	1384	20	1.54E-179	NP_500620.1	87	633.639	425	371	hypothetical protein K08F11.5

Locus_3893_Transcript_1/1_Conf_1.000	651	20	7.60E-36	NP_001021667.1	53	154.451	239	127	Nuclear Hormone Receptor family member (nhr-85)
Locus_3894_Transcript_1/1_Conf_1.000	632	0							
Locus_3895_Transcript_1/1_Conf_1.000	508	20	4.38E-48	NP_001040909.1	78	194.126	141	110	Temporarily Assigned Gene name family member (tag-60)
Locus_3896_Transcript_1/1_Conf_1.000	465	20	5.05E-62	EFO24292.1	92	240.35	138	128	hypothetical protein LOAG_04189
Locus_3897_Transcript_1/1_Conf_1.000	223	20	5.13E-30	XP_002633699.1	93	134.035	73	68	Hypothetical protein CBG03382
Locus_3898_Transcript_1/1_Conf_1.000	454	0							
Locus_3899_Transcript_1/2_Conf_1.000	355	5	1.38E-07	XP_002642452.1	68	52.7582	64	44	Hypothetical protein CBG06862
Locus_3899_Transcript_2/2_Conf_1.000	850	5	3.63E-30	XP_002642452.1	60	136.346	183	110	Hypothetical protein CBG06862
Locus_39_Transcript_1/1_Conf_1.000	223	0							
Locus_390_Transcript_1/1_Conf_1.000	948	2	1.46E-33	NP_495177.2	54	147.902	278	152	hypothetical protein F59G1.4
Locus_3900_Transcript_1/1_Conf_1.000	666	0							
Locus_3901_Transcript_1/1_Conf_1.000	1019	0							

Locus_3902_Transcript_1/1_Conf_1.000	1766	20	0	AAS01769.1	96	1080.86	559	540	monoclonal IgM antibody heavy chain
Locus_3903_Transcript_1/1_Conf_1.000	576	20	1.11E-84	NP_509361.1	90	316.235	191	173	hypothetical protein K07E3.4
Locus_3904_Transcript_1/1_Conf_1.000	1026	3	2.39E-40	NP_498499.1	55	170.629	326	181	hypothetical protein K04C2.2
Locus_3905_Transcript_1/1_Conf_1.000	1078	20	6.11E-151	NP_497853.1	83	538.11	368	306	hypothetical protein T08A11.2
Locus_3906_Transcript_1/1_Conf_1.000	520	0							
Locus_3907_Transcript_1/1_Conf_1.000	773	0							
Locus_3908_Transcript_1/2_Conf_1.000	926	20	3.34E-19	XP_001896227.1	54	100.138	164	89	cDNA sequence BC017158
Locus_3908_Transcript_2/2_Conf_1.000	842	20	4.96E-40	XP_001896227.1	60	169.088	245	147	cDNA sequence BC017158
Locus_3909_Transcript_1/1_Conf_1.000	1223	20	1.49E-151	NP_506558.2	81	540.421	391	317	hypothetical protein Y49A3A.1
Locus_391_Transcript_1/2_Conf_1.000	1162	20	1.08E-79	XP_002641923.1	79	301.597	213	169	C. briggsae CBR-RPL-6 protein

Locus_391_Transcript_2/2_Conf_1.000	432	20	1.84E-32	NP_509305.1	70	142.124	142	100	VITellogenin structural genes (yolk protein genes) family member (vit-1)
Locus_3910_Transcript_1/1_Conf_1.000	1341	20	3.03E-108	XP_001899078.1	64	396.741	450	290	Ubiquitin carboxyl-terminal hydrolase family protein
Locus_3911_Transcript_1/2_Conf_1.000	2249	20	0	XP_001896636.1	83	850.892	655	548	metallopeptidase family M24 containing protein
Locus_3911_Transcript_2/2_Conf_1.000	2243	20	0	XP_001896636.1	83	848.581	655	549	metallopeptidase family M24 containing protein
Locus_3912_Transcript_1/5_Conf_0.615	2743	20	4.25E-47	EFO26053.1	47	194.897	366	174	hypothetical protein LOAG_02428
Locus_3912_Transcript_2/5_Conf_0.692	2743	20	4.25E-47	EFO26053.1	47	194.897	366	174	hypothetical protein LOAG_02428
Locus_3912_Transcript_3/5_Conf_0.692	2743	20	2.49E-47	EFO26053.1	47	195.667	366	174	hypothetical protein LOAG_02428
Locus_3912_Transcript_4/5_Conf_0.154	1993	20	2.91E-39	XP_001956619.1	35	168.318	672	239	GF25304
Locus_3912_Transcript_5/5_Conf_0.692	2743	20	4.25E-47	EFO26053.1	47	194.897	366	174	hypothetical protein LOAG_02428
Locus_3913_Transcript_1/2_Conf_1.000	2533	20	1.83E-89	EFO23006.1	56	335.495	571	321	mast family protein

Locus_3913_Transcript_2/2_Conf_1.000	2494	20	3.28E-91	EFO23006.1	57	341.273	558	321	mast family protein
Locus_3914_Transcript_1/1_Conf_1.000	441	9	3.94E-06	EFO15999.1	61	54.6842	85	52	hypothetical protein LOAG_12508
Locus_3915_Transcript_1/1_Conf_1.000	191	20	5.14E-22	XP_002639175.1	90	107.457	63	57	C. briggsae CBR-ILE-1 protein
Locus_3916_Transcript_1/1_Conf_1.000	356	0							
Locus_3917_Transcript_1/1_Conf_1.000	708	20	1.35E-31	NP_503358.1	57	140.584	218	126	hypothetical protein Y50D4C.3
Locus_3918_Transcript_1/1_Conf_1.000	2282	20	6.36E-94	NP_741149.1	54	350.132	778	422	splicing factor (Suppressor of White aPricot) related family member (swp-1)
Locus_3919_Transcript_1/1_Conf_1.000	571	20	1.63E-32	EFO26326.1	71	142.895	121	87	CAMK/TSSK protein kinase
Locus_392_Transcript_1/1_Conf_1.000	2010	20	7.96E-178	NP_498394.1	64	628.632	580	376	Temporarily Assigned Gene name family member (tag-182)
Locus_3920_Transcript_1/1_Conf_1.000	237	0							
Locus_3921_Transcript_1/1_Conf_1.000	462	0							
Locus_3922_Transcript_1/1_Conf_1.000	260	0							
Locus_3923_Transcript_1/1_Conf_1.000	261	0							

Locus_3924_Transcript_1/1_Conf_1.000	1709	20	0	NP_001022602.1	86	852.432	543	469	MTM (myotubularin) family member (mtm-6)
Locus_3925_Transcript_1/1_Conf_1.000	357	0							
Locus_3926_Transcript_1/1_Conf_1.000	422	3	3.68E-04	XP_002647667.1	44	48.1358	99	44	Hypothetical protein CBG06778
Locus_3927_Transcript_1/1_Conf_1.000	1178	20	1.58E-94	XP_002643814.1	76	350.903	327	251	C. briggsae CBR-VANG-1 protein
Locus_3928_Transcript_1/2_Conf_1.000	783	0							
Locus_3928_Transcript_2/2_Conf_1.000	771	2	2.86E-04	XP_002633747.1	64	50.0618	67	43	Hypothetical protein CBG03433
Locus_3929_Transcript_1/2_Conf_1.000	346	20	1.44E-24	CAD28559.2	64	115.931	116	75	metalloprotease I
Locus_3929_Transcript_2/2_Conf_1.000	346	20	1.44E-24	CAD28559.2	64	115.931	116	75	metalloprotease I
Locus_393_Transcript_1/1_Conf_1.000	846	20	1.48E-100	XP_001898370.1	90	370.163	208	189	Glycoprotein 25L2 precursor
Locus_3930_Transcript_1/1_Conf_1.000	480	20	1.82E-48	AAL56427.1	89	195.282	116	104	AF370722_1intracellular globin
Locus_3931_Transcript_1/1_Conf_1.000	401	20	3.07E-43	XP_002078029.1	72	177.948	122	89	GD23232
Locus_3932_Transcript_1/1_Conf_1.000	1117	20	1.11E-09	XP_002003390.1	36	68.9366	278	101	GI17886
Locus_3933_Transcript_1/1_Conf_1.000	410	0							
Locus_3934_Transcript_1/1_Conf_1.000	248	20	1.07E-40	3O47	100	169.474	82	82	CrystalStructure Of Arfgap1-Arf1 Fusion Protein
Locus_3935_Transcript_1/1_Conf_1.000	874	20	1.07E-56	XP_002640603.1	79	224.557	232	185	Hypothetical protein CBG08714
Locus_3936_Transcript_1/1_Conf_1.000	344	20	4.62E-47	NP_496210.2	86	190.66	113	98	hypothetical protein F54B3.3

Locus_3937_Transcript_1/1_Conf_1.000	626	20	6.18E-21	XP_002630862.1	65	104.76	143	93	C. briggsae CBR-RRT-2 protein
Locus_3938_Transcript_1/1_Conf_1.000	1246	20	0	NP_492072.1	96	671.003	342	329	G Protein, Beta subunit family member (gpb-2)
Locus_3939_Transcript_1/1_Conf_1.000	945	0							
Locus_394_Transcript_1/2_Conf_0.500	2228	20	4.37E-23	XP_001895972.1	41	114.775	470	194	hypothetical protein Bm1_22580
Locus_394_Transcript_2/2_Conf_0.500	972	2	5.60E-04	XP_001809190.1	41	49.6766	94	39	PREDICTED: similar to CG14607 CG14607-PA
Locus_3940_Transcript_1/1_Conf_1.000	830	6	3.70E-32	NP_001122665.1	53	142.895	261	139	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-87)
Locus_3941_Transcript_1/1_Conf_1.000	1480	20	9.33E-138	NP_493369.1	81	494.967	343	280	hypothetical protein Y48G10A.3
Locus_3942_Transcript_1/1_Conf_1.000	370	0							
Locus_3943_Transcript_1/1_Conf_1.000	468	12	1.63E-36	CAC10528.1	69	155.606	167	116	putative inositol 1,4,5-trisphosphate receptor
Locus_3944_Transcript_1/1_Conf_1.000	564	0							
Locus_3945_Transcript_1/1_Conf_1.000	377	2	1.30E-09	XP_002634371.1	51	66.2402	145	74	C. briggsae CBR-RIG-4 protein
Locus_3946_Transcript_1/1_Conf_1.000	941	20	4.97E-127	XP_002642617.1	95	458.373	267	254	C. briggsae CBR-FUM-1 protein
Locus_3947_Transcript_1/1_Conf_1.000	205	0							
Locus_3948_Transcript_1/1_Conf_1.000	2139	20	0	NP_493746.1	72	747.658	690	499	yeast PRP (splicing factor) related family member (prp-21)
Locus_3949_Transcript_1/1_Conf_1.000	1235	20	1.08E-32	NP_508206.2	59	145.591	245	145	hypothetical protein K03E6.7

Locus_395_Transcript_1/1_Conf_1.000	1266	20	0	NP_001022114.1	95	713.375	401	383	proteasome Regulatory Particle, ATPase-like family member (rpt-4)
Locus_3950_Transcript_1/1_Conf_1.000	1631	20	9.02E-113	NP_506043.1	68	412.149	445	303	hypothetical protein C27A7.6
Locus_3951_Transcript_1/1_Conf_1.000	232	2	1.03E-06	XP_002643343.1	67	56.6102	65	44	Hypothetical protein CBG15940
Locus_3952_Transcript_1/1_Conf_1.000	904	4	3.76E-44	NP_498871.2	90	182.956	99	90	hypothetical protein F42H10.5
Locus_3953_Transcript_1/1_Conf_1.000	1656	20	5.31E-60	AAK54127.1	56	236.884	387	218	AF367206_1nuclear receptor nhr-7A
Locus_3954_Transcript_1/1_Conf_1.000	253	0							
Locus_3955_Transcript_1/1_Conf_1.000	311	20	3.93E-51	3ML6	100	204.142	103	103	A Complex Between Dishevlled2 And Clathrin Adaptor Ap-2
Locus_3956_Transcript_1/4_Conf_0.625	1035	20	1.29E-33	XP_002641525.1	52	148.288	283	149	Hypothetical protein CBG09821
Locus_3956_Transcript_2/4_Conf_0.625	1071	20	1.35E-33	XP_002641525.1	52	148.288	283	149	Hypothetical protein CBG09821
Locus_3956_Transcript_3/4_Conf_0.625	1079	20	7.99E-34	XP_002641525.1	52	149.058	283	148	Hypothetical protein CBG09821

Locus_3956_Transcript_4/4_Conf_0.625	1079	20	1.36E-33	XP_002641525.1	52	148.288	283	149	Hypothetical protein CBG09821
Locus_3957_Transcript_1/1_Conf_1.000	1488	20	8.79E-27	XP_001898006.1	46	126.331	458	213	BAT2 N-terminus family protein
Locus_3958_Transcript_1/1_Conf_1.000	194	2	1.49E-21	XP_002632383.1	87	105.916	64	56	Hypothetical protein CBG00404
Locus_3959_Transcript_1/1_Conf_1.000	311	20	9.15E-08	XP_002427781.1	53	60.077	92	49	protein phosphatase 2A, 59 kDa regulatory subunit B, putative
Locus_396_Transcript_1/1_Conf_1.000	326	20	1.58E-23	XP_001900150.1	91	112.464	62	57	hypothetical protein
Locus_3960_Transcript_1/1_Conf_1.000	804	20	1.29E-58	Q8R3I3.2	65	230.72	268	176	Conserved oligomeric Golgi complex subunit 6
Locus_3961_Transcript_1/1_Conf_1.000	888	20	3.31E-146	NP_508537.1	95	521.931	295	282	SPeCtrin family member (spc-1)
Locus_3962_Transcript_1/3_Conf_0.500	785	20	2.86E-108	NP_508609.1	85	395.586	259	221	Unidentified Vitellogenin-linked Transcript family member (uvt-5)
Locus_3962_Transcript_2/3_Conf_0.333	945	20	1.33E-103	NP_741749.1	87	380.563	242	212	Unidentified Vitellogenin-linked Transcript family member (uvt-5)
Locus_3962_Transcript_3/3_Conf_0.667	824	20	5.88E-107	NP_741749.1	82	391.349	279	229	Unidentified Vitellogenin-linked Transcript family member (uvt-5)

Locus_3963_Transcript_1/1_Conf_1.000	873	20	1.32E-22	XP_002641882.1	59	111.309	181	107	C. briggsae CBR-BATH-41 protein
Locus_3964_Transcript_1/1_Conf_1.000	645	20	1.70E-48	CBW48579.1	90	196.438	104	94	Hypothetical protein Y39B6A.2b
Locus_3965_Transcript_1/1_Conf_1.000	1626	20	0	NP_499264.1	92	829.321	464	428	CiTrate Synthase family member (cts-1)
Locus_3966_Transcript_1/1_Conf_1.000	522	2	3.95E-10	AAK31527.3	85	68.1662	40	34	Neuronal symmetry protein 1, partially confirmed by transcript evidence
Locus_3967_Transcript_1/1_Conf_1.000	830	0							
Locus_3968_Transcript_1/2_Conf_1.000	1431	8	1.16E-36	XP_001898914.1	46	159.073	411	193	AN1-like Zinc finger family protein
Locus_3968_Transcript_2/2_Conf_1.000	1431	8	1.16E-36	XP_001898914.1	46	159.073	411	193	AN1-like Zinc finger family protein

Locus_3969_Transcript_1/1_Conf_1.000	944	20	1.46E-110	NP_502753.2	91	403.675	226	206	hypothetical protein LLC1.3
Locus_397_Transcript_1/2_Conf_1.000	788	20	2.33E-41	XP_001894964.1	91	173.326	98	90	ADP-ribose pyrophosphatase, mitochondrial precursor
Locus_397_Transcript_2/2_Conf_1.000	681	20	4.58E-42	XP_001894964.1	91	175.252	99	91	ADP-ribose pyrophosphatase, mitochondrial precursor
Locus_3970_Transcript_1/1_Conf_1.000	504	20	1.28E-52	ACC54555.1	94	209.149	115	109	macrophage migration inhibitory factor
Locus_3971_Transcript_1/1_Conf_1.000	598	20	2.09E-52	EFO26229.1	70	209.149	199	141	hypothetical protein LOAG_02255

Locus_3972_Transcript_1/4_Conf_0.750	1665	20	0	XP_002630445.1	89	723.776	450	401	Hypothetical protein CBG11178
Locus_3972_Transcript_2/4_Conf_0.750	1665	20	0	XP_002630445.1	89	723.776	450	401	Hypothetical protein CBG11178
Locus_3972_Transcript_3/4_Conf_0.750	1665	20	0	XP_002630445.1	89	722.235	450	401	Hypothetical protein CBG11178
Locus_3972_Transcript_4/4_Conf_0.750	1665	20	0	XP_002630445.1	89	723.776	450	401	Hypothetical protein CBG11178
Locus_3973_Transcript_1/1_Conf_1.000	933	0							
Locus_3974_Transcript_1/1_Conf_1.000	655	20	1.35E-56	EFO13664.1	75	223.402	174	132	hypothetical protein LOAG_14864
Locus_3975_Transcript_1/2_Conf_1.000	608	20	4.23E-72	NP_495885.1	84	274.633	183	155	hypothetical protein T14D7.1
Locus_3975_Transcript_2/2_Conf_1.000	608	20	4.23E-72	NP_495885.1	84	274.633	183	155	hypothetical protein T14D7.1
Locus_3976_Transcript_1/1_Conf_1.000	1145	20	1.62E-72	NP_500105.1	72	277.715	274	199	CEll Death abnormality family member (ced-2)
Locus_3977_Transcript_1/1_Conf_1.000	265	20	8.66E-30	EFO24817.1	92	133.265	68	63	immunoglobulin I-set domain-containing protein
Locus_3978_Transcript_1/1_Conf_1.000	283	20	9.12E-19	XP_002644799.1	75	96.6709	82	62	C. briggsae CBR-IPP-5 protein
Locus_3979_Transcript_1/1_Conf_1.000	2255	8	0	NP_493757.2	70	731.095	696	488	hypothetical protein C09E8.1

Locus_398_Transcript_1/1_Conf_1.000	166	0							
Locus_3980_Transcript_1/1_Conf_1.000	1662	20	1.01E-58	NP_492305.2	61	232.646	314	194	hypothetical protein K02B12.3
Locus_3981_Transcript_1/1_Conf_1.000	1118	18	6.94E-28	NP_491971.1	66	129.413	142	94	hypothetical protein C48B6.3
Locus_3982_Transcript_1/1_Conf_1.000	217	0							
Locus_3983_Transcript_1/1_Conf_1.000	255	0							
Locus_3984_Transcript_1/1_Conf_1.000	319	0							
Locus_3985_Transcript_1/1_Conf_1.000	898	20	3.06E-131	XP_002643629.1	97	472.241	233	227	C. briggsae CBR-LET-2 protein
Locus_3986_Transcript_1/1_Conf_1.000	271	0							
Locus_3987_Transcript_1/2_Conf_1.000	1263	20	3.55E-180	NP_001076670.1	92	635.565	359	333	BT (Bacillus thuringiensis) toxin REsistant family member (bre-1)
Locus_3987_Transcript_2/2_Conf_1.000	1263	20	3.55E-180	NP_001076670.1	92	635.565	359	333	BT (Bacillus thuringiensis) toxin REsistant family member (bre-1)
Locus_3988_Transcript_1/2_Conf_1.000	394	0							
Locus_3988_Transcript_2/2_Conf_1.000	346	0							
Locus_3989_Transcript_1/1_Conf_1.000	448	20	2.43E-40	XP_002646256.1	82	168.318	102	84	Hypothetical protein CBG11960
Locus_399_Transcript_1/1_Conf_1.000	668	6	2.09E-20	NP_500576.1	59	103.219	151	90	hypothetical protein M01H9.3
Locus_3990_Transcript_1/1_Conf_1.000	676	20	1.52E-98	XP_002645216.1	91	362.844	225	206	Hypothetical protein CBG00074
Locus_3991_Transcript_1/1_Conf_1.000	165	0							

Locus_3992_Transcript_1/1_Conf_1.000	477	20	2.39E-48	NP_498221.1	84	194.897	132	111	Ribosomal Protein, Small subunit family member (rps-12)
Locus_3993_Transcript_1/1_Conf_1.000	1016	20	5.00E-75	XP_002632998.1	80	285.804	214	173	C. briggsae CBR-LPL-1 protein
Locus_3994_Transcript_1/1_Conf_1.000	469	20	1.33E-46	XP_002642740.1	77	189.119	143	111	Hypothetical protein CBG21119
Locus_3995_Transcript_1/1_Conf_1.000	472	20	2.11E-52	XP_002639634.1	83	208.379	143	120	C. briggsae CBR-CLE-1 protein
Locus_3996_Transcript_1/2_Conf_1.000	1400	0							
Locus_3996_Transcript_2/2_Conf_1.000	1359	0							
Locus_3997_Transcript_1/1_Conf_1.000	783	2	2.26E-04	NP_491417.1	47	50.447	106	50	hypothetical protein B0041.8
Locus_3998_Transcript_1/4_Conf_0.667	1964	20	0	EFO24333.1	85	866.685	553	475	ring canal kelch protein
Locus_3998_Transcript_2/4_Conf_0.667	1964	20	0	EFO24333.1	85	866.685	553	475	ring canal kelch protein
Locus_3998_Transcript_3/4_Conf_0.667	1369	20	0	EFO24333.1	87	724.161	456	399	ring canal kelch protein
Locus_3998_Transcript_4/4_Conf_0.667	1964	20	0	EFO24333.1	85	866.685	553	475	ring canal kelch protein
Locus_3999_Transcript_1/2_Conf_1.000	977	8	3.85E-53	NP_740845.1	60	213.001	277	167	Nuclear Pore complex Protein family member (npp-6)
Locus_3999_Transcript_2/2_Conf_1.000	4120	20	1.11E-118	XP_002646176.1	47	433.335	1131	539	C. briggsae CBR-NPP-6 protein

Locus_4_Transcript_1/1_Conf_1.000	5417	20	0	P07928.1	98	1014.99	522	515	A' protein
Locus_40_Transcript_1/2_Conf_1.000	3846	20	0	NP_001024431.1	69	938.717	982	682	Drosophila Discs Large homolog family member (dlg-1)

Locus_40_Transcript_2/2_Conf_1.000	3834	20	0	NP_001024431.1	69	944.495	978	682	Drosophila Discs Large homolog family member (dlg-1)
Locus_400_Transcript_1/1_Conf_1.000	489	20	2.34E-43	XP_001892438.1	77	178.333	138	107	60S ribosomal protein L23a
Locus_4000_Transcript_1/1_Conf_1.000	340	20	7.15E-45	AAK29933.3	89	183.341	113	101	Rab connectin related protein 2, partially confirmed by transcript evidence
Locus_4001_Transcript_1/1_Conf_1.000	2500	20	0	XP_001899119.1	83	884.789	622	517	L-plastin
Locus_4002_Transcript_1/1_Conf_1.000	317	2	3.95E-14	XP_002638797.1	73	81.2629	71	52	Hypothetical protein CBG05152
Locus_4003_Transcript_1/2_Conf_1.000	367	20	4.50E-31	NP_494441.1	90	137.502	82	74	hypothetical protein Y25C1A.5

Locus_4003_Transcript_2/2_Conf_1.000	1036	20	8.66E-139	NP_494441.1	92	497.664	293	270	hypothetical protein Y25C1A.5
Locus_4004_Transcript_1/1_Conf_1.000	940	0							
Locus_4005_Transcript_1/1_Conf_1.000	848	20	1.42E-26	EFO24363.1	50	124.405	306	155	cytoplasmic intermediate filament protein
Locus_4006_Transcript_1/1_Conf_1.000	319	0							
Locus_4007_Transcript_1/1_Conf_1.000	1849	20	9.84E-135	NP_503724.1	66	485.337	585	389	hypothetical protein W02H5.8
Locus_4008_Transcript_1/1_Conf_1.000	220	20	3.03E-22	XP_002648832.1	82	108.227	73	60	Hypothetical protein CBG16947
Locus_4009_Transcript_1/1_Conf_1.000	508	20	1.85E-22	XP_001902835.1	68	108.997	103	71	G-patch domain containing protein
Locus_401_Transcript_1/1_Conf_1.000	922	3	6.28E-10	EFO19159.1	48	69.3218	195	95	hypothetical protein LOAG_09335
Locus_4010_Transcript_1/1_Conf_1.000	1058	20	5.43E-104	NP_036555.1	100	382.104	203	203	60S ribosomal protein L13a
Locus_4011_Transcript_1/1_Conf_1.000	1576	20	2.96E-113	NP_499390.3	78	413.69	323	254	HEXosaminidase family member (hex-3)
Locus_4012_Transcript_1/1_Conf_1.000	697	5	2.32E-28	XP_002640722.1	56	129.798	196	110	Hypothetical protein CBG19790
Locus_4013_Transcript_1/1_Conf_1.000	771	20	4.20E-56	EFO17087.1	76	222.246	173	132	acetyltransferase
Locus_4014_Transcript_1/2_Conf_1.000	455	0							
Locus_4014_Transcript_2/2_Conf_1.000	424	0							
Locus_4015_Transcript_1/1_Conf_1.000	615	20	1.91E-75	NP_506259.2	84	285.804	200	168	hypothetical protein W07G4.3
Locus_4016_Transcript_1/1_Conf_1.000	517	0							

Locus_4017_Transcript_1/1_Conf_1.000	1575	20	4.99E-153	XP_002639098.1	75	545.814	518	391	C. briggsae CBR-UNC-40 protein
Locus_4018_Transcript_1/1_Conf_1.000	473	20	1.16E-50	NP_491576.2	90	202.601	120	109	PIP Kinase family member (ppk-1)
Locus_4019_Transcript_1/4_Conf_0.429	556	20	1.63E-34	XP_002641709.1	75	149.443	132	100	C. briggsae CBR-CED-7 protein
Locus_4019_Transcript_2/4_Conf_0.286	1141	20	7.75E-75	NP_001021225.1	60	285.419	410	247	CEll Death abnormality family member (ced-7)
Locus_4019_Transcript_3/4_Conf_0.286	343	6	2.40E-11	XP_002641709.1	77	72.0182	72	56	C. briggsae CBR-CED-7 protein
Locus_4019_Transcript_4/4_Conf_0.571	2819	20	0	NP_499115.2	59	669.848	1019	609	CEll Death abnormality family member (ced-7)
Locus_402_Transcript_1/1_Conf_1.000	1135	20	1.13E-150	NP_495785.1	84	537.339	366	308	phenylalanyl (F) tRNA Synthetase family member (frs-2)
Locus_4020_Transcript_1/1_Conf_1.000	908	11	4.83E-07	NP_498234.1	43	59.6918	221	97	hypothetical protein B0336.3
Locus_4021_Transcript_1/1_Conf_1.000	877	3	2.75E-04	ABX00635.1	45	50.447	101	46	collagen-like surface protein Scl1.52
Locus_4022_Transcript_1/1_Conf_1.000	195	0							
Locus_4023_Transcript_1/1_Conf_1.000	701	20	2.13E-21	XP_001902714.1	87	106.686	73	64	GGL domain containing protein

Locus_4024_Transcript_1/1_Conf_1.000	616	20	3.15E-78	NP_493545.1	84	295.049	193	163	hypothetical protein Y105E8B.5
Locus_4025_Transcript_1/1_Conf_1.000	1260	20	0	XP_002638763.1	89	675.626	420	375	C. briggsae CBR-BLI-3 protein
Locus_4026_Transcript_1/1_Conf_1.000	131	0							
Locus_4027_Transcript_1/1_Conf_1.000	212	20	6.33E-25	NP_501339.2	91	117.087	71	65	neuRonal IGCAM family member (rig-4)
Locus_4028_Transcript_1/5_Conf_0.308	325	11	6.63E-30	NP_495743.1	93	133.65	77	72	Tyrosine DeCarboxylase family member (tdc-1)
Locus_4028_Transcript_2/5_Conf_0.385	1730	20	0	XP_002630249.1	89	888.641	524	468	C. briggsae CBR-TDC-1 protein

Locus_4028_Transcript_3/5_Conf_0.538	1939	20	0	XP_002630249.1	87	1010.75	621	545	C. briggsae CBR-TDC-1 protein
Locus_4028_Transcript_4/5_Conf_0.538	1939	20	0	XP_002630249.1	87	1011.91	621	545	C. briggsae CBR-TDC-1 protein
Locus_4028_Transcript_5/5_Conf_0.538	1939	20	0	XP_002630249.1	87	1010.75	621	545	C. briggsae CBR-TDC-1 protein
Locus_4029_Transcript_1/1_Conf_1.000	1103	20	4.17E-94	XP_002641869.1	61	349.362	398	243	C. briggsae CBR-TEN-1 protein
Locus_403_Transcript_1/1_Conf_1.000	1603	20	7.17E-131	XP_001897997.1	62	472.241	517	324	anion exchange protein
Locus_4030_Transcript_1/1_Conf_1.000	284	0							
Locus_4031_Transcript_1/3_Conf_0.714	2059	20	4.41E-131	NP_492125.1	63	473.396	555	353	WD Repeat protein family member (wdr-23)
Locus_4031_Transcript_2/3_Conf_0.714	2089	20	2.64E-131	NP_492124.1	64	474.167	544	351	WD Repeat protein family member (wdr-23)
Locus_4031_Transcript_3/3_Conf_0.714	2089	20	2.64E-131	NP_492124.1	64	474.167	544	351	WD Repeat protein family member (wdr-23)
Locus_4032_Transcript_1/1_Conf_1.000	1644	20	2.04E-104	NP_741233.2	63	384.415	494	315	associated with RAN (nuclear import/export) function family member (ran-2)
Locus_4033_Transcript_1/1_Conf_1.000	1013	6	1.05E-40	XP_001893296.1	74	171.785	135	100	hypothetical protein Bm1_09125

Locus_4034_Transcript_1/1_Conf_1.000	677	20	1.25E-60	NP_505413.1	83	236.884	166	138	hypothetical protein K07B1.4
Locus_4035_Transcript_1/1_Conf_1.000	666	20	3.44E-39	AAN05752.1	70	165.622	158	112	heat shock protein 20
Locus_4036_Transcript_1/1_Conf_1.000	283	0							
Locus_4037_Transcript_1/2_Conf_1.000	482	6	9.44E-13	NP_498822.2	95	76.6406	43	41	abnormal cell MIGration family member (mig-10)
Locus_4037_Transcript_2/2_Conf_1.000	469	6	5.09E-14	NP_498822.2	62	80.8777	170	107	abnormal cell MIGration family member (mig-10)
Locus_4038_Transcript_1/3_Conf_0.600	308	20	8.27E-25	XP_002630890.1	76	116.701	101	77	Hypothetical protein CBG02611
Locus_4038_Transcript_2/3_Conf_0.600	535	20	4.58E-49	XP_002630890.1	77	197.593	170	131	Hypothetical protein CBG02611
Locus_4038_Transcript_3/3_Conf_0.600	535	20	4.58E-49	XP_002630890.1	77	197.593	170	131	Hypothetical protein CBG02611
Locus_4039_Transcript_1/1_Conf_1.000	416	0							
Locus_404_Transcript_1/6_Conf_0.250	361	20	8.24E-41	XP_002630755.1	78	169.859	121	95	C. briggsae CBR-LYS-8 protein
Locus_404_Transcript_2/6_Conf_0.250	403	20	1.52E-42	XP_002630755.1	78	175.637	125	98	C. briggsae CBR-LYS-8 protein
Locus_404_Transcript_3/6_Conf_0.167	262	6	6.92E-11	XP_002630755.1	68	70.4774	66	45	C. briggsae CBR-LYS-8 protein
Locus_404_Transcript_4/6_Conf_0.167	262	6	6.92E-11	XP_002630755.1	68	70.4774	66	45	C. briggsae CBR-LYS-8 protein
Locus_404_Transcript_5/6_Conf_0.250	560	20	7.76E-53	XP_002630755.1	73	210.305	168	123	C. briggsae CBR-LYS-8 protein
Locus_404_Transcript_6/6_Conf_0.250	560	20	7.76E-53	XP_002630755.1	73	210.305	168	123	C. briggsae CBR-LYS-8 protein
Locus_4040_Transcript_1/1_Conf_1.000	415	0							

Locus_4041_Transcript_1/1_Conf_1.000	1045	20	1.39E-27	EFO18829.1	77	128.257	90	70	presenilin spe-4
Locus_4042_Transcript_1/1_Conf_1.000	638	5	1.40E-15	XP_002629878.1	59	87.0409	136	81	Hypothetical protein CBG21915
Locus_4043_Transcript_1/1_Conf_1.000	728	20	2.35E-42	EFO19902.1	66	176.407	215	142	hypothetical protein LOAG_08593
Locus_4044_Transcript_1/1_Conf_1.000	769	0							
Locus_4045_Transcript_1/2_Conf_1.000	2400	20	0	NP_498740.2	92	1034.25	588	542	CaLPain family member (clp-1)
Locus_4045_Transcript_2/2_Conf_1.000	2394	20	0	NP_741237.1	92	1038.1	585	540	CaLPain family member (clp-1)
Locus_4046_Transcript_1/1_Conf_1.000	1258	20	4.01E-75	EFO19846.1	63	286.574	339	215	cleavage and polyadenylation specificity factor subunit 2
Locus_4047_Transcript_1/1_Conf_1.000	2303	20	0	XP_002635521.1	93	1051.2	652	609	C. briggsae CBR-HSP-6 protein
Locus_4048_Transcript_1/1_Conf_1.000	130	3	1.48E-05	NP_495669.1	71	52.7582	42	30	hypothetical protein ZK669.3
Locus_4049_Transcript_1/1_Conf_1.000	811	20	1.70E-151	XP_002637345.1	99	539.265	270	268	C. briggsae CBR-UNC-68 protein

Locus_405_Transcript_1/1_Conf_1.000	765	20	5.95E-63	NP_491529.2	98	244.973	124	122	hypothetical protein Y110A7A.6
Locus_4050_Transcript_1/1_Conf_1.000	717	20	4.89E-69	NP_498404.1	72	265.003	234	170	hypothetical protein C05D11.5
Locus_4051_Transcript_1/1_Conf_1.000	395	0							
Locus_4052_Transcript_1/1_Conf_1.000	223	2	9.42E-08	XP_002640196.1	70	60.077	70	49	C. briggsae CBR-CKR-1 protein
Locus_4053_Transcript_1/2_Conf_1.000	537	0							
Locus_4053_Transcript_2/2_Conf_1.000	575	0							
Locus_4054_Transcript_1/2_Conf_1.000	1996	20	0	NP_496987.1	78	773.081	659	517	IMportin Beta family member (imb-2)
Locus_4054_Transcript_2/2_Conf_1.000	1996	20	0	NP_496987.1	78	773.081	659	517	IMportin Beta family member (imb-2)
Locus_4055_Transcript_1/1_Conf_1.000	1064	20	4.91E-137	NP_509604.1	78	491.886	353	277	abnormal NUClease family member (nuc-1)
Locus_4056_Transcript_1/1_Conf_1.000	493	3	3.29E-05	XP_967620.1	44	51.6026	127	57	PREDICTED: similar to anopheles stephensi ubiquitin, putative

Locus_4057_Transcript_1/1_Conf_1.000	778	5	5.28E-14	XP_002638692.1	59	82.4185	159	95	C. briggsae CBR-DCP-66 protein
Locus_4058_Transcript_1/2_Conf_1.000	518	3	3.40E-27	NP_501320.2	69	124.79	126	88	eXPOrtin (nuclear export receptor) family member (xpo-3)
Locus_4058_Transcript_2/2_Conf_1.000	518	3	2.61E-27	NP_501320.2	70	125.176	126	89	eXPOrtin (nuclear export receptor) family member (xpo-3)
Locus_4059_Transcript_1/4_Conf_0.375	678	20	2.76E-23	EFO25573.1	53	112.849	198	106	RING finger protein 20
Locus_4059_Transcript_2/4_Conf_0.375	1225	20	7.15E-45	EFO25573.1	77	186.037	140	109	RING finger protein 20
Locus_4059_Transcript_3/4_Conf_0.375	678	20	2.76E-23	EFO25573.1	53	112.849	198	106	RING finger protein 20
Locus_4059_Transcript_4/4_Conf_0.375	1224	20	7.15E-45	EFO25573.1	77	186.037	140	109	RING finger protein 20
Locus_406_Transcript_1/4_Conf_0.182	208	0							
Locus_406_Transcript_2/4_Conf_0.364	2434	20	0	NP_503306.1	88	898.656	568	501	GEX Interacting protein family member (gei-7)
Locus_406_Transcript_3/4_Conf_0.182	3197	20	0	NP_503306.1	91	1646.33	969	887	GEX Interacting protein family member (gei-7)
Locus_406_Transcript_4/4_Conf_0.455	785	20	8.78E-41	NP_492609.1	70	171.4	168	118	hypothetical protein K10C3.2
Locus_4060_Transcript_1/1_Conf_1.000	175	0							
Locus_4061_Transcript_1/1_Conf_1.000	221	0							
Locus_4062_Transcript_1/4_Conf_0.625	818	20	9.71E-54	XP_002632395.1	73	214.542	173	128	C. briggsae CBR-ITSN-1 protein
Locus_4062_Transcript_2/4_Conf_0.625	818	20	9.71E-54	XP_002632395.1	73	214.542	173	128	C. briggsae CBR-ITSN-1 protein

Locus_4062_Transcript_3/4_Conf_0.250	305	20	3.99E-19	NP_503037.2	76	97.8265	68	52	ITSN (intersectin) family member (itsn-1)
Locus_4062_Transcript_4/4_Conf_0.625	818	20	9.71E-54	XP_002632395.1	73	214.542	173	128	C. briggsae CBR-ITSN-1 protein
Locus_4063_Transcript_1/1_Conf_1.000	889	20	1.16E-82	NP_505265.1	77	310.842	245	190	Temporarily Assigned Gene name family member (tag-117)
Locus_4064_Transcript_1/1_Conf_1.000	560	20	3.86E-44	2CO0	83	181.415	125	104	Wdr5 And Unmodified Histone H3 Complex At 2.25 Angstrom
Locus_4065_Transcript_1/1_Conf_1.000	763	20	3.12E-72	NP_492523.1	89	275.789	158	142	hypothetical protein F30A10.9
Locus_4066_Transcript_1/3_Conf_0.714	1941	20	5.26E-150	NP_501023.3	79	344.739	236	187	hypothetical protein C01B10.9
Locus_4066_Transcript_2/3_Conf_0.714	1952	20	2.38E-150	NP_501023.3	78	444.121	324	255	hypothetical protein C01B10.9
Locus_4066_Transcript_3/3_Conf_0.714	1945	20	1.83E-155	NP_501023.3	73	554.288	475	350	hypothetical protein C01B10.9

Locus_4067_Transcript_1/2_Conf_1.000	760	20	4.53E-23	EFO22249.1	62	112.464	133	83	hypothetical protein LOAG_06236
Locus_4067_Transcript_2/2_Conf_1.000	893	20	6.09E-23	EFO22249.1	62	112.464	133	83	hypothetical protein LOAG_06236
Locus_4068_Transcript_1/1_Conf_1.000	574	0							
Locus_4069_Transcript_1/2_Conf_1.000	1773	20	5.08E-40	CAX65053.1	64	170.629	201	130	C. elegans protein D1046.1b, confirmed by transcript evidence
Locus_4069_Transcript_2/2_Conf_1.000	1764	20	5.05E-40	CAX65053.1	64	170.629	201	130	C. elegans protein D1046.1b, confirmed by transcript evidence
Locus_407_Transcript_1/2_Conf_1.000	263	20	3.54E-15	Q94637.1	67	84.7297	85	57	Vitellogenin-6
Locus_407_Transcript_2/2_Conf_1.000	147	0							
Locus_4070_Transcript_1/2_Conf_1.000	1094	20	4.51E-08	NP_001021459.2	35	63.5438	251	89	hypothetical protein F36H2.3
Locus_4070_Transcript_2/2_Conf_1.000	908	14	2.03E-05	EAW56013.1	52	54.299	59	31	complement component 6, isoform CRA_b

Locus_4071_Transcript_1/1_Conf_1.000	1167	20	3.97E-90	XP_002643186.1	64	336.265	392	253	C. briggsae CBR-ADR-2 protein
Locus_4072_Transcript_1/1_Conf_1.000	397	20	1.10E-40	XP_001895225.1	85	169.474	106	91	40S ribosomal protein S19S
Locus_4073_Transcript_1/3_Conf_0.667	754	20	1.41E-85	XP_002637829.1	90	320.087	198	179	C. briggsae CBR-PAS-1 protein
Locus_4073_Transcript_2/3_Conf_0.667	746	20	1.39E-85	XP_002637829.1	90	320.087	198	179	C. briggsae CBR-PAS-1 protein
Locus_4073_Transcript_3/3_Conf_0.667	746	20	1.39E-85	XP_002637829.1	90	320.087	198	179	C. briggsae CBR-PAS-1 protein
Locus_4074_Transcript_1/1_Conf_1.000	820	20	7.22E-65	XP_001893127.1	84	251.521	205	173	B-box type zinc-finger protein ncl-1
Locus_4075_Transcript_1/2_Conf_1.000	835	0							
Locus_4075_Transcript_2/2_Conf_1.000	527	0							

Locus_4076_Transcript_1/1_Conf_1.000	405	8	2.43E-16	XP_001900963.1	55	88.5817	122	68	Zinc finger, C2H2 type family protein
Locus_4077_Transcript_1/2_Conf_1.000	397	0							
Locus_4077_Transcript_2/2_Conf_1.000	397	0							
Locus_4078_Transcript_1/1_Conf_1.000	1198	20	0	XP_002634527.1	89	660.603	373	332	C. briggsae CBR-MAP-1 protein
Locus_4079_Transcript_1/1_Conf_1.000	597	0							
Locus_408_Transcript_1/7_Conf_0.159	160	9	3.92E-06	XP_002636068.1	77	54.6842	36	28	Hypothetical protein CBG01308
Locus_408_Transcript_2/7_Conf_0.068	305	0							
Locus_408_Transcript_3/7_Conf_0.136	153	7	1.15E-05	XP_002636068.1	79	53.1434	34	27	Hypothetical protein CBG01308
Locus_408_Transcript_4/7_Conf_0.250	275	20	1.47E-13	NP_505384.2	73	79.337	71	52	ASpartyl Protease family member (asp-2)
Locus_408_Transcript_5/7_Conf_0.068	357	1	7.32E-05	EFO20860.1	56	50.447	71	40	hypothetical protein LOAG_07630
Locus_408_Transcript_6/7_Conf_0.273	275	20	1.47E-13	NP_505384.2	73	79.337	71	52	ASpartyl Protease family member (asp-2)
Locus_408_Transcript_7/7_Conf_0.568	480	0							
Locus_4080_Transcript_1/2_Conf_1.000	1070	20	1.76E-142	NP_496276.1	85	509.99	327	281	hypothetical protein C06A1.3
Locus_4080_Transcript_2/2_Conf_1.000	1070	20	1.76E-142	NP_496276.1	85	509.99	327	281	hypothetical protein C06A1.3

Locus_4081_Transcript_1/1_Conf_1.000	1728	20	2.70E-147	XP_002640056.1	73	526.939	575	420	Hypothetical protein CBG12532
Locus_4082_Transcript_1/1_Conf_1.000	351	20	7.51E-58	NP_006389.2	100	226.483	116	116	ubiquitin D
Locus_4083_Transcript_1/1_Conf_1.000	476	20	6.13E-36	XP_002637110.1	81	153.68	113	92	Hypothetical protein CBG09610
Locus_4084_Transcript_1/1_Conf_1.000	1266	20	1.56E-143	XP_002634371.1	74	513.842	445	333	C. briggsae CBR-RIG-4 protein
Locus_4085_Transcript_1/3_Conf_0.714	3333	20	0	NP_001021346.1	78	924.465	781	614	EGg Laying defective family member (egl-8)
Locus_4085_Transcript_2/3_Conf_0.714	3333	20	0	NP_001021346.1	78	924.465	781	614	EGg Laying defective family member (egl-8)

Locus_4085_Transcript_3/3_Conf_0.714	3333	20	0	NP_001021346.1	78	924.465	781	614	EGg Laying defective family member (egl-8)
Locus_4086_Transcript_1/1_Conf_1.000	637	20	1.02E-82	EFO20190.1	85	310.071	195	166	hypothetical protein LOAG_08298
Locus_4087_Transcript_1/1_Conf_1.000	497	5	3.03E-43	XP_002646111.1	78	177.948	165	129	C. briggsae CBR-PAD-1 protein
Locus_4088_Transcript_1/1_Conf_1.000	954	20	7.33E-118	NP_510032.1	93	427.943	252	235	hypothetical protein M153.1
Locus_4089_Transcript_1/1_Conf_1.000	1021	20	2.31E-128	A8WPF0.2	88	462.996	265	234	Succinate dehydrogenase ubiquinone iron-sulfur subunit, mitochondria
Locus_409_Transcript_1/1_Conf_1.000	1054	20	8.45E-57	XP_002634781.1	91	225.328	135	124	C. briggsae CBR-MDF-2 protein
Locus_4090_Transcript_1/1_Conf_1.000	1066	20	1.89E-112	XP_002630122.1	72	410.223	355	257	Hypothetical protein CBG00524
Locus_4091_Transcript_1/2_Conf_1.000	288	0							
Locus_4091_Transcript_2/2_Conf_1.000	288	0							
Locus_4092_Transcript_1/1_Conf_1.000	599	4	3.38E-10	EFO21414.1	88	68.9366	45	40	hypothetical protein LOAG_07072
Locus_4093_Transcript_1/1_Conf_1.000	135	0							
Locus_4094_Transcript_1/5_Conf_0.600	439	16	2.64E-23	XP_002646276.1	77	111.694	83	64	C. briggsae CBR-ABF-2 protein
Locus_4094_Transcript_2/5_Conf_0.600	597	8	6.52E-19	XP_002646276.1	87	69.707	39	34	C. briggsae CBR-ABF-2 protein
Locus_4094_Transcript_3/5_Conf_0.600	406	16	2.68E-23	XP_002646276.1	77	111.694	83	64	C. briggsae CBR-ABF-2 protein
Locus_4094_Transcript_4/5_Conf_0.667	475	16	2.67E-23	XP_002646276.1	77	111.694	83	64	C. briggsae CBR-ABF-2 protein
Locus_4094_Transcript_5/5_Conf_0.667	539	16	3.37E-23	XP_002646276.1	77	111.694	83	64	C. briggsae CBR-ABF-2 protein

Locus_4095_Transcript_1/1_Conf_1.000	780	20	1.80E-62	NP_001023515.1	66	243.432	250	166	hypothetical protein Y55F3BR.8
Locus_4096_Transcript_1/1_Conf_1.000	1002	20	6.54E-112	XP_002639607.1	80	408.297	317	254	C. briggsae CBR-PQN-44 protein
Locus_4097_Transcript_1/1_Conf_1.000	1555	6	1.52E-53	XP_002636852.1	49	215.312	550	273	Hypothetical protein CBG09307
Locus_4098_Transcript_1/1_Conf_1.000	1184	20	5.34E-175	NP_496968.1	90	618.231	373	338	hypothetical protein Y48B6A.12
Locus_4099_Transcript_1/1_Conf_1.000	1322	20	0	XP_002636685.1	95	647.121	346	329	C. briggsae CBR-ELPC-3 protein
Locus_41_Transcript_1/2_Conf_1.000	1485	20	0	XP_002632913.1	89	800.816	494	443	Hypothetical protein CBG21666
Locus_41_Transcript_2/2_Conf_1.000	1489	20	0	XP_002632913.1	89	802.357	495	444	Hypothetical protein CBG21666
Locus_410_Transcript_1/1_Conf_1.000	2412	7	4.08E-22	NP_498236.1	47	111.694	284	136	Worm aRMadillo family member (wrm-1)
Locus_4100_Transcript_1/1_Conf_1.000	258	0							

Locus_4101_Transcript_1/1_Conf_1.000	1059	20	6.95E-75	NP_510256.1	73	285.419	249	184	Cyclin-Dependent Kinase family member (cdk-4)
Locus_4102_Transcript_1/1_Conf_1.000	237	0							
Locus_4103_Transcript_1/2_Conf_1.000	424	1	1.14E-05	NP_501319.2	49	53.1434	139	69	hypothetical protein C49H3.4
Locus_4103_Transcript_2/2_Conf_1.000	840	12	2.16E-27	NP_501319.2	52	127.102	232	122	hypothetical protein C49H3.4
Locus_4104_Transcript_1/1_Conf_1.000	326	0							
Locus_4105_Transcript_1/1_Conf_1.000	898	20	1.20E-127	XP_002644931.1	88	460.299	280	249	Hypothetical protein CBG10876
Locus_4106_Transcript_1/1_Conf_1.000	853	20	7.63E-28	XP_001897730.1	56	128.642	238	135	KH domain containing protein
Locus_4107_Transcript_1/2_Conf_1.000	1112	9	3.62E-53	EFO20752.1	55	213.386	343	191	AMOP domain-containing protein
Locus_4107_Transcript_2/2_Conf_1.000	1120	9	4.33E-54	EFO20752.1	56	216.468	346	194	AMOP domain-containing protein
Locus_4108_Transcript_1/3_Conf_0.600	991	20	2.30E-77	NP_491666.2	75	293.508	247	187	hypothetical protein T19B4.1
Locus_4108_Transcript_2/3_Conf_0.400	855	20	2.60E-76		75	289.656	245	185	hypothetical protein C04F1.2
Locus_4108_Transcript_3/3_Conf_0.600	1391	20	3.77E-77	NP_491666.2	75	293.508	247	187	hypothetical protein T19B4.1
Locus_4109_Transcript_1/2_Conf_1.000	1468	3	2.67E-44	NP_490916.4	50	184.496	478	242	GTPase Activating Protein family member (gap-3)

Locus_4109_Transcript_2/2_Conf_1.000	1359	3	1.58E-11	XP_002638860.1	51	75.485	258	132	Hypothetical protein CBG22075
Locus_411_Transcript_1/1_Conf_1.000	950	20	1.12E-41	XP_002641584.1	84	174.866	111	94	C. briggsae CBR-BATH-43 protein
Locus_4110_Transcript_1/1_Conf_1.000	948	20	1.15E-46	EFO16839.1	62	191.43	224	139	hypothetical protein LOAG_11664
Locus_4111_Transcript_1/1_Conf_1.000	651	20	1.14E-23	NP_001021488.1	59	114.005	141	84	hypothetical protein F53F10.8
Locus_4112_Transcript_1/2_Conf_1.000	1293	20	4.64E-66	EFO21711.1	65	256.529	305	200	hypothetical protein LOAG_06778
Locus_4112_Transcript_2/2_Conf_1.000	1194	20	7.07E-66	EFO21711.1	71	255.758	238	171	hypothetical protein LOAG_06778
Locus_4113_Transcript_1/3_Conf_0.714	963	20	1.06E-180	XP_002632913.1	97	636.721	319	310	Hypothetical protein CBG21666
Locus_4113_Transcript_2/3_Conf_0.714	963	20	1.06E-180	XP_002632913.1	97	636.721	319	310	Hypothetical protein CBG21666

Locus_4113_Transcript_3/3_Conf_0.714	963	20	1.06E-180	XP_002632913.1	97	636.721	319	310	Hypothetical protein CBG21666
Locus_4114_Transcript_1/1_Conf_1.000	1619	2	1.62E-05	NP_505489.1	41	55.8398	474	195	HoloCentric chromosome binding Protein family member (hcp-2)
Locus_4115_Transcript_1/1_Conf_1.000	1003	20	6.47E-35	CAR63562.1	79	152.525	147	117	putative COLlagen
Locus_4116_Transcript_1/1_Conf_1.000	595	2	4.78E-25	NP_492324.2	57	118.242	169	98	hypothetical protein R05D11.9
Locus_4117_Transcript_1/1_Conf_1.000	657	0							
Locus_4118_Transcript_1/1_Conf_1.000	491	20	1.71E-30	XP_001926354.1	86	133.65	147	127	PREDICTED: similar to 60S acidic ribosomal protein P1
Locus_4119_Transcript_1/5_Conf_0.300	352	0							
Locus_4119_Transcript_2/5_Conf_0.200	143	0							
Locus_4119_Transcript_3/5_Conf_0.500	841	0							
Locus_4119_Transcript_4/5_Conf_0.600	1145	0							
Locus_4119_Transcript_5/5_Conf_0.600	651	0							
Locus_412_Transcript_1/6_Conf_0.625	1244	20	2.92E-102	AAT28331.1	96	376.711	196	190	peroxiredoxin

Locus_412_Transcript_2/6_Conf_0.625	1244	20	1.31E-102	AAT28331.1	96	377.867	196	190	peroxiredoxin
Locus_412_Transcript_3/6_Conf_0.375	1077	20	4.92E-92	AAT28331.1	97	342.428	174	169	peroxiredoxin
Locus_412_Transcript_4/6_Conf_0.375	1077	20	4.92E-92	AAT28331.1	97	342.428	174	169	peroxiredoxin
Locus_412_Transcript_5/6_Conf_0.375	759	20	5.78E-103	AAT28331.1	96	377.867	196	190	peroxiredoxin

Locus_412_Transcript_6/6_Conf_0.375	759	20	1.29E-102	AAT28331.1	96	376.711	196	190	peroxiredoxin
Locus_4120_Transcript_1/1_Conf_1.000	803	5	3.65E-05	XP_001187240.1	40	53.1434	254	102	PREDICTED: hypothetical protein
Locus_4121_Transcript_1/1_Conf_1.000	3274	20	0	XP_002639688.1	85	1613.97	1090	932	C. briggsae CBR-FASN-1 protein
Locus_4122_Transcript_1/1_Conf_1.000	849	8	6.74E-85	CBL43423.1	70	318.161	278	197	C. elegans protein C53A5.13b, partially confirmed by transcript evidence
Locus_4123_Transcript_1/1_Conf_1.000	640	20	2.75E-43	CAE12199.1	63	179.104	213	136	aspartyl protease precursor
Locus_4124_Transcript_1/4_Conf_0.667	1289	20	3.62E-87	NP_501092.1	66	326.635	339	224	Conserved Oligomeric Golgi (COG) Component family member (cogc-2)

Locus_4124_Transcript_2/4_Conf_0.444	618	14	1.84E-25	NP_501092.1	68	119.783	135	93	Conserved Oligomeric Golgi (COG) Component family member (cogc-2)
Locus_4124_Transcript_3/4_Conf_0.667	1289	20	9.54E-88	NP_501092.1	66	328.561	339	224	Conserved Oligomeric Golgi (COG) Component family member (cogc-2)
Locus_4124_Transcript_4/4_Conf_0.667	1289	20	2.12E-87	NP_501092.1	66	327.405	339	224	Conserved Oligomeric Golgi (COG) Component family member (cogc-2)
Locus_4125_Transcript_1/1_Conf_1.000	217	17	2.83E-17		78	91.6633	61	48	hypothetical protein T07C4.5
Locus_4126_Transcript_1/2_Conf_1.000	638	20	6.00E-67	NP_496787.1	89	257.684	159	142	hypothetical protein F29C12.4
Locus_4126_Transcript_2/2_Conf_1.000	638	20	6.00E-67	NP_496787.1	89	257.684	159	142	hypothetical protein F29C12.4

Locus_4127_Transcript_1/1_Conf_1.000	194	20	3.11E-19	NP_001020988.1	85	98.2117	63	54	UNCoordinated family member (unc-89)
Locus_4128_Transcript_1/1_Conf_1.000	596	0							
Locus_4129_Transcript_1/1_Conf_1.000	515	0							
Locus_413_Transcript_1/4_Conf_0.250	113	0							
Locus_413_Transcript_2/4_Conf_0.375	1516	20	4.23E-101	XP_001900801.1	83	373.244	242	202	RNA recognition motif.
Locus_413_Transcript_3/4_Conf_0.250	267	0							
Locus_413_Transcript_4/4_Conf_0.375	1488	20	1.78E-128	NP_495121.1	85	464.151	314	267	hypothetical protein C18A3.5
Locus_4130_Transcript_1/1_Conf_1.000	925	20	6.58E-100	XP_002636807.1	81	368.237	265	215	Hypothetical protein CBG09249

Locus_4131_Transcript_1/1_Conf_1.000	649	20	2.31E-77	CAR63584.1	98	292.352	148	146	putative Rna polymerase ii (b) subunit protein 8
Locus_4132_Transcript_1/1_Conf_1.000	1349	20	1.79E-100	NP_491233.1	100	370.933	186	186	UNCoordinated family member (unc-108)
Locus_4133_Transcript_1/1_Conf_1.000	2373	9	4.58E-135	XP_002639325.1	58	486.878	652	383	Hypothetical protein CBG03903
Locus_4134_Transcript_1/5_Conf_0.636	1878	2	2.74E-15	EFO25303.1	41	88.5817	595	248	hypothetical protein LOAG_03184
Locus_4134_Transcript_2/5_Conf_0.636	1866	2	1.26E-12	XP_001894872.1	37	79.7221	601	223	hypothetical protein Bm1_17075
Locus_4134_Transcript_3/5_Conf_0.636	1878	2	2.74E-15	EFO25303.1	41	88.5817	595	247	hypothetical protein LOAG_03184
Locus_4134_Transcript_4/5_Conf_0.545	2051	2	4.39E-14	EFO25303.1	41	84.7297	527	220	hypothetical protein LOAG_03184
Locus_4134_Transcript_5/5_Conf_0.636	1878	2	2.74E-15	EFO25303.1	41	88.5817	595	248	hypothetical protein LOAG_03184
Locus_4135_Transcript_1/1_Conf_1.000	398	0							
Locus_4136_Transcript_1/1_Conf_1.000	532	1	1.19E-04	NP_492133.1	73	50.0618	38	28	hypothetical protein F26A3.4
Locus_4137_Transcript_1/1_Conf_1.000	577	20	8.90E-50	EFO28396.1	74	200.29	172	128	hypothetical protein LOAG_00085
Locus_4138_Transcript_1/2_Conf_1.000	1010	20	2.39E-45	XP_001866937.1	52	187.193	276	144	scavenger receptor cysteine-rich protein
Locus_4138_Transcript_2/2_Conf_1.000	1010	20	1.40E-45	XP_001866937.1	52	187.963	276	144	scavenger receptor cysteine-rich protein

Locus_4139_Transcript_1/1_Conf_1.000	467	20	9.52E-61	NP_001024141.1	96	236.113	152	146	Germinal Center Kinase family member (gck-1)
Locus_414_Transcript_1/1_Conf_1.000	355	20	1.43E-16	XP_002643168.1	76	89.3521	65	50	Hypothetical protein CBG15349
Locus_4140_Transcript_1/1_Conf_1.000	1277	0							
Locus_4141_Transcript_1/1_Conf_1.000	469	0							
Locus_4142_Transcript_1/2_Conf_1.000	652	4	5.66E-15	XP_001902476.1	57	85.1149	113	65	hypothetical protein Bm1_55090
Locus_4142_Transcript_2/2_Conf_1.000	580	2	1.78E-05	XP_001902476.1	51	53.1434	90	46	hypothetical protein Bm1_55090
Locus_4143_Transcript_1/1_Conf_1.000	1766	20	1.48E-124	NP_510751.3	64	451.44	552	354	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-34)
Locus_4144_Transcript_1/1_Conf_1.000	292	20	3.31E-21	AAO63577.1	65	104.76	82	54	secreted protein 5 precursor
Locus_4145_Transcript_1/1_Conf_1.000	622	2	4.69E-05	NP_001021867.1	56	51.9878	71	40	hypothetical protein ZK337.1
Locus_4146_Transcript_1/1_Conf_1.000	1884	20	0	XP_002646666.1	81	821.231	612	501	Hypothetical protein CBG11104
Locus_4147_Transcript_1/1_Conf_1.000	1145	17	1.89E-04	XP_002160262.1	53	51.6026	65	35	PREDICTED: similar to predicted protein
Locus_4148_Transcript_1/1_Conf_1.000	1546	20	1.25E-15	XP_002642641.1	42	89.3521	211	90	C. briggsae CBR-LIN-13 protein
Locus_4149_Transcript_1/1_Conf_1.000	728	20	2.76E-59	XP_002632384.1	78	232.646	193	152	Hypothetical protein CBG00405
Locus_415_Transcript_1/1_Conf_1.000	637	0							

Locus_4150_Transcript_1/1_Conf_1.000	350	0							
Locus_4151_Transcript_1/1_Conf_1.000	878	20	3.40E-79	XP_002640842.1	65	299.286	310	204	C. briggsae CBR-NHR-80 protein
Locus_4152_Transcript_1/1_Conf_1.000	979	20	7.67E-110	NP_001023646.1	88	401.364	243	214	AKT kinase family member (akt-1)
Locus_4153_Transcript_1/5_Conf_0.308	1356	20	4.25E-150	XP_001900871.1	75	535.798	454	342	CHD4 protein
Locus_4153_Transcript_2/5_Conf_0.692	4354	20	0	XP_001900871.1	82	1981.84	1465	1204	CHD4 protein

Locus_4153_Transcript_3/5_Conf_0.692	4354	20	0	XP_001900871.1	82	1981.84	1465	1204	CHD4 protein
Locus_4153_Transcript_4/5_Conf_0.692	4354	20	0	XP_001900871.1	82	1981.84	1465	1204	CHD4 protein
Locus_4153_Transcript_5/5_Conf_0.692	4354	20	0	XP_001900871.1	82	1981.84	1465	1204	CHD4 protein
Locus_4154_Transcript_1/1_Conf_1.000	3475	20	0	NP_001023165.1	88	795.423	495	440	TBC (Tre-2/Bub2/Cdc16) domain family member (tbc-3)
Locus_4155_Transcript_1/1_Conf_1.000	298	0							
Locus_4156_Transcript_1/1_Conf_1.000	822	20	1.02E-34	NP_491439.1	62	151.369	191	119	hypothetical protein C10H11.8
Locus_4157_Transcript_1/1_Conf_1.000	234	0							
Locus_4158_Transcript_1/1_Conf_1.000	691	0							

Locus_4159_Transcript_1/1_Conf_1.000	701	20	4.23E-70	NP_001041277.1	79	268.47	233	185	hypothetical protein PDB1.1
Locus_416_Transcript_1/1_Conf_1.000	425	0							
Locus_4160_Transcript_1/1_Conf_1.000	359	20	2.25E-38	XP_002636996.1	83	161.77	111	93	C. briggsae CBR-SHW-3 protein
Locus_4161_Transcript_1/1_Conf_1.000	655	20	6.69E-56	P51535.1	84	221.09	152	128	Myoglobin
Locus_4162_Transcript_1/1_Conf_1.000	593	20	7.64E-84	EFO25040.1	92	313.538	181	168	microsomal signal peptidase 21 kDa subunit
Locus_4163_Transcript_1/1_Conf_1.000	646	2	5.19E-05	NP_796363.2	47	51.9878	203	96	melanoma inhibitory activity protein 3 precursor
Locus_4164_Transcript_1/1_Conf_1.000	1507	0							
Locus_4165_Transcript_1/1_Conf_1.000	411	0							
Locus_4166_Transcript_1/1_Conf_1.000	2739	20	0	A8XYX2.2	64	827.009	891	574	Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 1A
Locus_4167_Transcript_1/1_Conf_1.000	589	2	3.45E-12	NP_496178.1	46	75.485	221	103	PUF (Pumilio/FBF) domain-containing family member (puf-12)
Locus_4168_Transcript_1/2_Conf_1.000	2389	20	1.70E-129	XP_002637508.1	58	468.389	781	456	C. briggsae CBR-TAG-232 protein
Locus_4168_Transcript_2/2_Conf_1.000	2377	20	2.60E-130	XP_002637508.1	58	471.085	777	454	C. briggsae CBR-TAG-232 protein
Locus_4169_Transcript_1/2_Conf_1.000	793	20	6.44E-39	NP_501576.2	76	165.236	149	114	Mitochondrial Processing Peptidase Beta family member (mppb-1)
Locus_4169_Transcript_2/2_Conf_1.000	774	20	6.14E-39	NP_501576.2	76	165.236	149	114	Mitochondrial Processing Peptidase Beta family member (mppb-1)
Locus_417_Transcript_1/1_Conf_1.000	1205	20	2.20E-99	XP_001902724.1	76	367.081	305	234	TPR Domain containing protein

Locus_4170_Transcript_1/1_Conf_1.000	832	20	7.15E-84	XP_002401479.1	74	314.694	241	179	U3 snoRNP-associated protein, putative
Locus_4171_Transcript_1/1_Conf_1.000	621	20	4.32E-59	XP_002630862.1	73	231.491	213	157	C. briggsae CBR-RRT-2 protein
Locus_4172_Transcript_1/1_Conf_1.000	322	20	7.91E-07	NP_506068.1	54	56.9954	82	45	TransThyretin-Related family domain family member (ttr-22)
Locus_4173_Transcript_1/1_Conf_1.000	620	14	1.62E-13	ACD85816.1	100	80.1073	38	38	forkhead transcription factor DAF-16
Locus_4174_Transcript_1/2_Conf_1.000	1414	20	0	XP_002642507.1	94	726.087	403	381	C. briggsae CBR-PDHK-2 protein

Locus_4174_Transcript_2/2_Conf_1.000	1399	20	0	XP_002642507.1	95	729.939	398	380	C. briggsae CBR-PDHK-2 protein
Locus_4175_Transcript_1/1_Conf_1.000	230	0							
Locus_4176_Transcript_1/1_Conf_1.000	1270	20	2.84E-52	XP_002641255.1	76	210.69	178	136	Hypothetical protein CBG05166
Locus_4177_Transcript_1/1_Conf_1.000	293	20	3.79E-17	EFO22910.1	63	91.2781	97	62	hypothetical protein LOAG_05577
Locus_4178_Transcript_1/2_Conf_1.000	2636	20	5.54E-121	NP_510291.1	63	440.269	472	301	ADAM (disintegrin plus metalloprotease) family member (adm-2)
Locus_4178_Transcript_2/2_Conf_1.000	2636	20	9.45E-121	NP_510291.1	63	439.499	472	301	ADAM (disintegrin plus metalloprotease) family member (adm-2)
Locus_4179_Transcript_1/1_Conf_1.000	405	20	3.39E-26	XP_001892616.1	72	121.324	129	93	60S ribosomal protein L28

Locus_418_Transcript_1/2_Conf_1.000	2055	20	0	XP_002644811.1	95	858.981	496	472	C. briggsae CBR-HSP-3 protein
Locus_418_Transcript_2/2_Conf_1.000	2186	20	0	XP_002644811.1	93	1107.82	655	612	C. briggsae CBR-HSP-3 protein
Locus_4180_Transcript_1/1_Conf_1.000	304	0							
Locus_4181_Transcript_1/1_Conf_1.000	321	0							

Locus_4182_Transcript_1/1_Conf_1.000	1275	20	1.82E-115	NP_499740.1	77	420.624	353	274	Nuclear Pore complex Protein family member (npp-18)
Locus_4183_Transcript_1/1_Conf_1.000	2086	7	1.44E-20	XP_002630547.1	51	106.301	285	147	C. briggsae CBR-NFI-1 protein
Locus_4184_Transcript_1/1_Conf_1.000	1580	20	4.46E-93	XP_002631791.1	68	346.665	384	264	Hypothetical protein CBG21009
Locus_4185_Transcript_1/1_Conf_1.000	188	2	7.99E-07	CBK19481.1	58	56.9954	77	45	C. elegans protein Y105C5A.15a, partially confirmed by transcript evidence
Locus_4186_Transcript_1/1_Conf_1.000	1086	20	1.86E-38	EFO23447.1	53	164.466	312	167	hypothetical protein LOAG_05038
Locus_4187_Transcript_1/1_Conf_1.000	821	20	2.10E-72	NP_498410.1	81	276.559	207	168	Temporarily Assigned Gene name family member (tag-170)
Locus_4188_Transcript_1/1_Conf_1.000	774	20	2.79E-108	NP_500304.3	85	395.586	257	221	hypothetical protein Y67D8A.1
Locus_4189_Transcript_1/1_Conf_1.000	1415	20	1.95E-129	XP_002639126.1	84	467.233	382	322	C. briggsae CBR-CRN-1 protein
Locus_419_Transcript_1/2_Conf_1.000	1432	20	3.34E-60	CAR63574.1	75	237.269	233	176	putative X-box Binding Protein
Locus_419_Transcript_2/2_Conf_1.000	1409	20	3.77E-52	CAR63574.1	81	168.703	137	112	putative X-box Binding Protein
Locus_4190_Transcript_1/1_Conf_1.000	509	20	6.79E-33	XP_445145.1	71	143.665	136	97	hypothetical protein
Locus_4191_Transcript_1/4_Conf_0.200	337	0							
Locus_4191_Transcript_2/4_Conf_0.500	811	0							
Locus_4191_Transcript_3/4_Conf_0.200	313	0							

Locus_4191_Transcript_4/4_Conf_0.600	1252	0							
Locus_4192_Transcript_1/1_Conf_1.000	606	5	5.34E-75	XP_002644396.1	89	284.263	188	168	Hypothetical protein CBG14241
Locus_4193_Transcript_1/1_Conf_1.000	1657	20	0	ACT34056.1	94	991.875	533	506	glutamate dehydrogenase
Locus_4194_Transcript_1/1_Conf_1.000	1111	20	3.91E-132	XP_002639434.1	81	475.707	369	299	Hypothetical protein CBG04027
Locus_4195_Transcript_1/1_Conf_1.000	289	11	2.55E-21	NP_001023856.1	72	105.145	97	70	hypothetical protein F26F12.3
Locus_4196_Transcript_1/1_Conf_1.000	1569	20	1.25E-87	XP_002639910.1	57	328.561	521	300	C. briggsae CBR-RBG-2 protein
Locus_4197_Transcript_1/1_Conf_1.000	669	0							
Locus_4198_Transcript_1/2_Conf_1.000	1115	20	2.36E-52	NP_871822.1	69	210.69	222	154	hypothetical protein T08B2.5
Locus_4198_Transcript_2/2_Conf_1.000	1121	20	2.38E-52	NP_871822.1	69	210.69	222	154	hypothetical protein T08B2.5
Locus_4199_Transcript_1/2_Conf_1.000	1776	20	6.29E-115	NP_001022054.1	66	419.468	468	311	hypothetical protein D2085.5
Locus_4199_Transcript_2/2_Conf_1.000	1782	20	6.32E-115	NP_001022054.1	66	419.468	468	311	hypothetical protein D2085.5
Locus_42_Transcript_1/1_Conf_1.000	496	4	1.37E-11	NP_496194.2	50	72.7886	127	64	hypothetical protein F33H1.4
Locus_420_Transcript_1/1_Conf_1.000	1369	20	4.28E-49	AAD31839.1	47	200.29	446	213	AF132291_1ancylostoma-secreted protein 1 precursor
Locus_4200_Transcript_1/1_Conf_1.000	488	5	3.79E-09	XP_002632516.1	56	64.6994	105	59	Hypothetical protein CBG13762
Locus_4201_Transcript_1/1_Conf_1.000	208	0							
Locus_4202_Transcript_1/1_Conf_1.000	568	20	1.95E-54	NP_496208.2	80	215.698	147	119	hypothetical protein T01E8.6

Locus_4203_Transcript_1/1_Conf_1.000	1195	20	1.28E-99	XP_002634113.1	70	367.851	331	235	Hypothetical protein CBG01666
Locus_4204_Transcript_1/1_Conf_1.000	354	0							
Locus_4205_Transcript_1/3_Conf_0.286	1039	20	1.74E-131	NP_001021395.1	81	473.396	350	284	Receptor Mediated Endocytosis family member (rme-8)
Locus_4205_Transcript_2/3_Conf_0.714	1752	20	0	NP_001021395.1	80	781.171	587	473	Receptor Mediated Endocytosis family member (rme-8)
Locus_4205_Transcript_3/3_Conf_0.714	1752	20	0	NP_001021395.1	80	781.171	587	473	Receptor Mediated Endocytosis family member (rme-8)
Locus_4206_Transcript_1/6_Conf_0.333	1170	20	8.21E-19	AAO63577.1	40	99.3673	359	146	secreted protein 5 precursor
Locus_4206_Transcript_2/6_Conf_0.333	1170	20	8.21E-19	AAO63577.1	40	99.3673	356	145	secreted protein 5 precursor
Locus_4206_Transcript_3/6_Conf_0.333	1421	13	8.55E-08	AAO63577.1	45	63.1586	180	82	secreted protein 5 precursor
Locus_4206_Transcript_4/6_Conf_0.167	827	10	3.69E-16	AAO63577.1	41	89.7373	268	111	secreted protein 5 precursor
Locus_4206_Transcript_5/6_Conf_0.167	827	10	2.82E-16	AAO63577.1	41	90.1225	265	109	secreted protein 5 precursor
Locus_4206_Transcript_6/6_Conf_0.333	1421	13	8.55E-08	AAO63577.1	45	63.1586	180	82	secreted protein 5 precursor
Locus_4207_Transcript_1/1_Conf_1.000	603	0							
Locus_4208_Transcript_1/4_Conf_0.429	463	0							
Locus_4208_Transcript_2/4_Conf_0.286	132	0							
Locus_4208_Transcript_3/4_Conf_0.286	144	0							
Locus_4208_Transcript_4/4_Conf_0.429	469	0							
Locus_4209_Transcript_1/1_Conf_1.000	1660	20	0	NP_498245.2	82	672.929	508	418	related to Islet cell Diabetes Autoantigen family member (ida-1)
Locus_421_Transcript_1/2_Conf_1.000	566	20	2.34E-52	NP_499203.1	79	208.764	145	115	TransThyretin-Related family domain family member (ttr-2)
Locus_421_Transcript_2/2_Conf_1.000	566	20	2.34E-52	NP_499203.1	79	208.764	145	115	TransThyretin-Related family domain family member (ttr-2)
Locus_4210_Transcript_1/1_Conf_1.000	297	1	2.80E-04	CAN78088.1	68	48.521	44	30	hypothetical protein

Locus_4211_Transcript_1/1_Conf_1.000	485	20	1.80E-59	EFO20716.1	82	231.876	156	129	cytoplasmic polyadenylation element binding protein 3
Locus_4212_Transcript_1/1_Conf_1.000	443	20	1.53E-50	XP_002634002.1	89	202.216	146	131	Hypothetical protein CBG20109
Locus_4213_Transcript_1/1_Conf_1.000	624	20	9.53E-22	XP_425111.1	56	107.457	155	87	PREDICTED: similar to FLJ11171 protein
Locus_4214_Transcript_1/1_Conf_1.000	355	20	1.20E-31	XP_002747045.1	94	139.428	75	71	PREDICTED: 60S ribosomal protein L39-like
Locus_4215_Transcript_1/1_Conf_1.000	487	0							
Locus_4216_Transcript_1/1_Conf_1.000	1261	20	4.18E-64	NP_504838.1	59	249.98	372	222	hypothetical protein C05C8.5
Locus_4217_Transcript_1/1_Conf_1.000	692	0							
Locus_4218_Transcript_1/2_Conf_1.000	1597	20	4.99E-100	XP_002631038.1	64	369.777	367	236	C. briggsae CBR-ZYX-1 protein
Locus_4218_Transcript_2/2_Conf_1.000	1228	20	5.26E-80	NP_496776.1	82	302.753	193	160	ZYXin family member (zyx-1)
Locus_4219_Transcript_1/1_Conf_1.000	445	2	5.29E-11	XP_002632166.1	71	70.8626	67	48	Hypothetical protein CBG07025

Locus_422_Transcript_1/1_Conf_1.000	797	20	9.28E-70	NP_491066.1	95	267.7	142	135	ARp2/3 compleX component family member (arx-1)
Locus_4220_Transcript_1/1_Conf_1.000	536	2	3.67E-06	EFO23913.1	56	55.0694	60	34	hypothetical protein LOAG_04573
Locus_4221_Transcript_1/1_Conf_1.000	257	7	2.31E-14	XP_001893855.1	70	82.0333	85	60	Viral A-type inclusion protein repeat containing protein
Locus_4222_Transcript_1/1_Conf_1.000	1702	20	1.24E-144	NP_500183.2	70	518.079	493	346	hypothetical protein M70.4
Locus_4223_Transcript_1/1_Conf_1.000	1305	20	2.15E-119	NP_492553.1	70	433.721	440	312	hypothetical protein T05F1.1
Locus_4224_Transcript_1/1_Conf_1.000	187	0							
Locus_4225_Transcript_1/1_Conf_1.000	1420	20	5.45E-63	XP_001899135.1	71	246.514	220	158	chromosome 6 open reading frame 106, isoform a
Locus_4226_Transcript_1/1_Conf_1.000	533	20	1.09E-66	XP_002639843.1	84	256.144	176	149	C. briggsae CBR-DHC-1 protein
Locus_4227_Transcript_1/2_Conf_1.000	963	20	3.52E-51	NP_506110.1	61	206.453	261	160	CaDmium Responsive family member (cdr-4)
Locus_4227_Transcript_2/2_Conf_1.000	963	20	1.13E-49	NP_506110.1	60	201.445	261	158	CaDmium Responsive family member (cdr-4)

Locus_4228_Transcript_1/1_Conf_1.000	1106	20	0	NP_001021838.1	91	650.203	368	338	Glucose-6-Phosphate Isomerase family member (gpi-1)
Locus_4229_Transcript_1/1_Conf_1.000	1255	0							
Locus_423_Transcript_1/1_Conf_1.000	418	0							
Locus_4230_Transcript_1/1_Conf_1.000	130	0							
Locus_4231_Transcript_1/1_Conf_1.000	304	20	7.29E-13	XP_002575537.1	71	77.0258	78	56	hypothetical protein
Locus_4232_Transcript_1/3_Conf_0.571	1012	11	6.12E-49	NP_499235.1	57	199.134	348	199	hypothetical protein T16G12.6
Locus_4232_Transcript_2/3_Conf_0.286	1852	20	1.02E-123	XP_002641591.1	63	448.743	601	380	Hypothetical protein CBG09895
Locus_4232_Transcript_3/3_Conf_0.571	1012	12	4.69E-49	NP_499235.1	57	199.519	348	200	hypothetical protein T16G12.6
Locus_4233_Transcript_1/1_Conf_1.000	1028	20	3.64E-81	CBX25214.1	72	306.22	332	242	Hypothetical protein ZK593.5c
Locus_4234_Transcript_1/1_Conf_1.000	706	9	3.95E-92	XP_002644423.1	84	341.658	201	170	C. briggsae CBR-TAG-18 protein
Locus_4235_Transcript_1/1_Conf_1.000	1614	20	9.71E-160	XP_002638502.1	70	568.155	512	361	C. briggsae CBR-FRE-1 protein
Locus_4236_Transcript_1/1_Conf_1.000	2423	20	0	NP_001122827.1	68	723.776	809	558	Suppressor with Morphological effect on Genitalia family member (smg-3)

Locus_4237_Transcript_1/1_Conf_1.000	1360	20	2.66E-160	NP_498119.1	86	569.696	390	336	Gro-1 OPeron gene family member (gop-3)
Locus_4238_Transcript_1/1_Conf_1.000	902	0							
Locus_4239_Transcript_1/1_Conf_1.000	894	20	1.59E-63	XP_395319.2	74	247.284	219	164	PREDICTED: similar to Peroxiredoxin-6 (Antioxidant protein 2) (1-Cys peroxiredoxin) (1-Cys PRX) (Acidic calcium-independent phospholipase A2) (aiPLA2) (Non-selenium glutathione peroxidase) (NSGPx)
Locus_424_Transcript_1/4_Conf_0.500	407	0							
Locus_424_Transcript_2/4_Conf_0.625	350	0							
Locus_424_Transcript_3/4_Conf_0.375	816	20	4.41E-14	XP_785187.1	55	82.8037	127	70	PREDICTED: similar to polymerase (DNA directed), epsilon 3 (p17 subunit)
Locus_424_Transcript_4/4_Conf_0.625	425	0							
Locus_4240_Transcript_1/1_Conf_1.000	291	20	1.25E-36	NP_495614.3	89	155.992	96	86	Na/H eXchanger family member (nhx-2)
Locus_4241_Transcript_1/1_Conf_1.000	542	20	8.68E-51	AAF71303.1	70	203.371	182	129	AF229855_1dual oxidase
Locus_4242_Transcript_1/1_Conf_1.000	176	0							
Locus_4243_Transcript_1/1_Conf_1.000	606	20	1.06E-14	NP_505017.1	42	83.9593	228	96	PaPiliN (Drosophila ECM protein) homolog family member (ppn-1)
Locus_4244_Transcript_1/1_Conf_1.000	1191	20	2.95E-72	NP_510428.1	67	276.944	316	212	TAK1 kinase/MOM-4 binding Protein family member (tap-1)
Locus_4245_Transcript_1/1_Conf_1.000	713	0							

Locus_4246_Transcript_1/1_Conf_1.000	625	20	1.86E-25	NP_001040951.1	100	119.783	56	56	MiniBrain Kinase (Drosophila) homolog family member (mbk-2)
Locus_4247_Transcript_1/1_Conf_1.000	216	20	1.55E-31	XP_002631133.1	100	139.043	71	71	C. briggsae CBR-CLH-2 protein
Locus_4248_Transcript_1/1_Conf_1.000	1398	20	3.58E-59		58	233.802	407	239	hypothetical protein C56G2.7
Locus_4249_Transcript_1/1_Conf_1.000	726	20	8.53E-85	XP_002632404.1	81	317.39	241	196	Hypothetical protein CBG00428
Locus_425_Transcript_1/1_Conf_1.000	2507	20	0	XP_002633774.1	81	874.774	648	528	Hypothetical protein CBG03464
Locus_4250_Transcript_1/1_Conf_1.000	470	2	6.03E-07	NP_499181.1	76	57.3806	52	40	hypothetical protein ZK632.10
Locus_4251_Transcript_1/1_Conf_1.000	405	0							
Locus_4252_Transcript_1/1_Conf_1.000	1069	20	5.11E-33	NP_495126.1	56	146.362	237	133	hypothetical protein C18A3.2
Locus_4253_Transcript_1/1_Conf_1.000	919	20	1.23E-90	NP_505623.1	92	337.421	195	180	hypothetical protein ZK856.8
Locus_4254_Transcript_1/1_Conf_1.000	191	20	1.11E-08	XP_792833.1	71	63.1586	53	38	PREDICTED: hypothetical protein

Locus_4255_Transcript_1/1_Conf_1.000	355	20	6.83E-27	NP_508504.2	76	123.635	117	89	Non-muscle MYosin family member (nmy-1)
Locus_4256_Transcript_1/3_Conf_0.333	337	0							
Locus_4256_Transcript_2/3_Conf_0.667	807	0							
Locus_4256_Transcript_3/3_Conf_0.667	807	0							
Locus_4257_Transcript_1/1_Conf_1.000	504	4	3.19E-27	NP_495156.1	74	124.79	100	74	TBC (Tre-2/Bub2/Cdc16) domain family member (tbc-2)
Locus_4258_Transcript_1/1_Conf_1.000	143	0							
Locus_4259_Transcript_1/1_Conf_1.000	278	20	2.84E-33	AAH36203.2	100	144.821	91	91	TMBIM6 protein
Locus_426_Transcript_1/1_Conf_1.000	3238	20	0	NP_001021793.1	68	676.011	664	455	Vasa- and Belle-like Helicase family member (vbh-1)
Locus_4260_Transcript_1/1_Conf_1.000	589	0							
Locus_4261_Transcript_1/1_Conf_1.000	1242	20	8.87E-67	NP_492185.2	66	258.84	333	222	SMG-associated and Lethal family member (smgl-1)

Locus_4262_Transcript_1/2_Conf_1.000	1280	20	1.18E-130	AAV38311.1	100	471.085	229	229	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)
Locus_4262_Transcript_2/2_Conf_1.000	814	20	4.65E-40	XP_001166356.1	100	169.088	74	74	PREDICTED: CD74 antigen isoform 17
Locus_4263_Transcript_1/1_Conf_1.000	1159	20	1.13E-12	XP_001898172.1	62	78.9518	112	70	hypothetical protein Bm1_33625

Locus_4264_Transcript_1/1_Conf_1.000	430	20	1.12E-29	EAW99547.1	100	132.88	66	66	thymosin, beta 10, isoform CRA_a
Locus_4265_Transcript_1/1_Conf_1.000	939	0							
Locus_4266_Transcript_1/1_Conf_1.000	897	20	1.68E-12	XP_002636474.1	56	77.7962	143	81	C. briggsae CBR-IMA-1 protein
Locus_4267_Transcript_1/3_Conf_0.714	980	20	1.72E-77	XP_002432576.1	79	293.893	240	190	COP9 signalosome complex subunit, putative
Locus_4267_Transcript_2/3_Conf_0.714	980	20	1.32E-77	XP_002432576.1	79	294.278	240	190	COP9 signalosome complex subunit, putative
Locus_4267_Transcript_3/3_Conf_0.714	980	20	1.32E-77	XP_002432576.1	79	294.278	240	190	COP9 signalosome complex subunit, putative
Locus_4268_Transcript_1/1_Conf_1.000	518	20	4.55E-64	EFO16320.1	81	247.284	172	140	hypothetical protein LOAG_12187
Locus_4269_Transcript_1/2_Conf_1.000	445	20	6.65E-30	XP_001892499.1	85	133.65	131	112	hypothetical protein

Locus_4269_Transcript_2/2_Conf_1.000	445	20	6.65E-30	XP_001892499.1	85	133.65	131	112	hypothetical protein
Locus_427_Transcript_1/6_Conf_0.154	167	0							
Locus_427_Transcript_2/6_Conf_0.308	1641	14	7.42E-14	EFO27228.1	43	83.5741	264	114	hypothetical protein LOAG_01257
Locus_427_Transcript_3/6_Conf_0.538	1864	20	1.75E-22	XP_002632234.1	76	112.464	142	109	C. briggsae CBR-VIG-1 protein
Locus_427_Transcript_4/6_Conf_0.538	1840	5	9.78E-18	XP_002632234.1	75	96.6709	134	101	C. briggsae CBR-VIG-1 protein
Locus_427_Transcript_5/6_Conf_0.154	970	14	1.32E-13	EFO27228.1	43	81.6481	240	105	hypothetical protein LOAG_01257
Locus_427_Transcript_6/6_Conf_0.538	1855	20	1.74E-22	XP_002632234.1	76	112.464	142	109	C. briggsae CBR-VIG-1 protein
Locus_4270_Transcript_1/1_Conf_1.000	370	15	1.11E-16	XP_002631239.1	86	89.7373	53	46	C. briggsae CBR-LACT-3 protein
Locus_4271_Transcript_1/2_Conf_1.000	1940	19	8.22E-23	NP_871687.1	46	113.62	577	269	hypothetical protein R148.3
Locus_4271_Transcript_2/2_Conf_1.000	1928	19	1.39E-22	NP_871687.1	44	112.849	575	258	hypothetical protein R148.3

Locus_4272_Transcript_1/2_Conf_1.000	1247	20	8.51E-110	CAR63699.1	82	401.749	292	241	hypothetical protein
Locus_4272_Transcript_2/2_Conf_1.000	1229	20	8.89E-112	CAR63699.1	84	408.297	286	241	hypothetical protein
Locus_4273_Transcript_1/2_Conf_1.000	1198	20	3.58E-126	CAR63589.1	97	456.062	236	231	hypothetical protein
Locus_4273_Transcript_2/2_Conf_1.000	273	0							

Locus_4274_Transcript_1/1_Conf_1.000	1122	20	1.67E-21	XP_788324.1	45	108.227	340	156	PREDICTED: hypothetical protein
Locus_4275_Transcript_1/1_Conf_1.000	1864	20	1.13E-37	XP_001892946.1	46	162.925	504	232	Leucine Rich Repeat family protein
Locus_4276_Transcript_1/1_Conf_1.000	476	20	2.18E-25	NP_504518.3	80	118.627	98	79	Nuclear Hormone Receptor family member (nhr-142)
Locus_4277_Transcript_1/4_Conf_0.375	846	20	1.11E-63	NP_493601.2	64	247.669	275	177	FERM domain (protein4.1-ezrin-radixin-moesin) family member (frm-1)
Locus_4277_Transcript_2/4_Conf_0.500	902	20	1.37E-62	XP_002640640.1	75	244.202	211	159	C. briggsae CBR-FRM-1 protein
Locus_4277_Transcript_3/4_Conf_0.500	410	1	2.05E-15	NP_493601.2	75	85.5001	70	53	FERM domain (protein4.1-ezrin-radixin-moesin) family member (frm-1)

Locus_4277_Transcript_4/4_Conf_0.500	825	20	1.17E-62	XP_002640640.1	75	244.202	211	159	C. briggsae CBR-FRM-1 protein
Locus_4278_Transcript_1/1_Conf_1.000	198	5	8.70E-14	NP_504318.2	68	80.1073	58	40	hypothetical protein H23N18.5
Locus_4279_Transcript_1/1_Conf_1.000	397	20	2.13E-60	NP_504700.2	94	234.958	132	125	hypothetical protein W02F12.5
Locus_428_Transcript_1/1_Conf_1.000	980	20	2.30E-114	ACZ13335.1	89	416.387	281	252	60S ribosomal protein L5
Locus_4280_Transcript_1/1_Conf_1.000	191	2	7.45E-05	NP_491893.1	62	50.447	62	39	BAG1 (human) homolog family member (bag-1)
Locus_4281_Transcript_1/1_Conf_1.000	515	20	4.64E-29	NP_503100.1	63	130.954	155	99	hypothetical protein C30H6.7
Locus_4282_Transcript_1/2_Conf_1.000	690	0							
Locus_4282_Transcript_2/2_Conf_1.000	690	0							
Locus_4283_Transcript_1/1_Conf_1.000	264	0							
Locus_4284_Transcript_1/1_Conf_1.000	294	0							

Locus_4285_Transcript_1/1_Conf_1.000	357	20	2.92E-62	NP_490960.1	97	241.121	119	116	hypothetical protein Y39G10AR.8
Locus_4286_Transcript_1/1_Conf_1.000	471	20	3.86E-38	XP_002641188.1	75	160.999	146	110	Hypothetical protein CBG09049
Locus_4287_Transcript_1/1_Conf_1.000	561	0							
Locus_4288_Transcript_1/1_Conf_1.000	253	20	1.31E-33	NP_507688.2	90	145.976	84	76	CYtochrome P450 family member (cyp-42A1)
Locus_4289_Transcript_1/5_Conf_0.300	510	20	1.84E-30	NP_499604.1	68	135.576	142	97	hypothetical protein Y75B8A.31
Locus_4289_Transcript_2/5_Conf_0.600	1031	20	1.83E-48	NP_499604.1	58	197.593	298	174	hypothetical protein Y75B8A.31
Locus_4289_Transcript_3/5_Conf_0.400	600	6	3.31E-13	NP_499604.1	54	78.9518	142	77	hypothetical protein Y75B8A.31
Locus_4289_Transcript_4/5_Conf_0.600	1076	20	1.76E-49	NP_499604.1	58	201.06	298	175	hypothetical protein Y75B8A.31
Locus_4289_Transcript_5/5_Conf_0.600	1076	20	1.76E-49	NP_499604.1	58	201.06	298	175	hypothetical protein Y75B8A.31
Locus_429_Transcript_1/1_Conf_1.000	1378	20	5.63E-174	XP_002645934.1	78	615.15	460	363	Hypothetical protein CBG07699
Locus_4290_Transcript_1/2_Conf_1.000	1241	20	1.45E-77	NP_001040885.1	61	294.664	414	255	Suppressor with Morphological effect on Genitalia family member (smg-6)
Locus_4290_Transcript_2/2_Conf_1.000	775	20	7.75E-42	NP_001040885.1	61	174.866	251	155	Suppressor with Morphological effect on Genitalia family member (smg-6)
Locus_4291_Transcript_1/1_Conf_1.000	1511	0							
Locus_4292_Transcript_1/7_Conf_0.667	2675	20	0	NP_001122864.1	81	908.286	680	554	hypothetical protein C27A7.5
Locus_4292_Transcript_2/7_Conf_0.667	2675	20	0	NP_001122864.1	81	908.286	680	554	hypothetical protein C27A7.5

Locus_4292_Transcript_3/7_Conf_0.667	2675	20	0	NP_001122864.1	81	908.286	680	554	hypothetical protein C27A7.5
Locus_4292_Transcript_4/7_Conf_0.667	2675	20	0	NP_001122864.1	81	908.672	680	555	hypothetical protein C27A7.5
Locus_4292_Transcript_5/7_Conf_0.667	2675	20	0	NP_001122864.1	81	908.286	680	554	hypothetical protein C27A7.5
Locus_4292_Transcript_6/7_Conf_0.667	2610	20	0	NP_001122863.1	82	889.797	654	538	hypothetical protein C27A7.5
Locus_4292_Transcript_7/7_Conf_0.667	2675	20	0	NP_001122864.1	81	908.286	680	554	hypothetical protein C27A7.5
Locus_4293_Transcript_1/1_Conf_1.000	1647	20	0	NP_498263.2	93	719.924	430	404	ALdehyde deHydrogenase family member (alh-9)
Locus_4294_Transcript_1/1_Conf_1.000	398	20	1.25E-44	XP_002643084.1	78	182.57	127	100	C. briggsae CBR-TAG-174 protein
Locus_4295_Transcript_1/1_Conf_1.000	956	9	1.99E-06	AAO63577.1	42	57.7658	195	82	secreted protein 5 precursor
Locus_4296_Transcript_1/1_Conf_1.000	1356	20	3.08E-108	XP_002637346.1	83	396.741	274	229	Hypothetical protein CBG19044
Locus_4297_Transcript_1/1_Conf_1.000	1370	6	7.83E-43	NP_502427.1	60	179.489	271	164	hypothetical protein C27D8.2
Locus_4298_Transcript_1/1_Conf_1.000	477	0							
Locus_4299_Transcript_1/1_Conf_1.000	720	1	1.12E-04	XP_002648956.1	56	51.2174	67	38	Hypothetical protein CBG21271
Locus_43_Transcript_1/1_Conf_1.000	1853	20	2.61E-119	NP_493252.3	55	434.106	685	381	PAtterning Defective family member (pad-1)
Locus_430_Transcript_1/2_Conf_1.000	381	0							
Locus_430_Transcript_2/2_Conf_1.000	348	0							

Locus_4300_Transcript_1/1_Conf_1.000	305	20	7.51E-26	XP_001524092.1	74	120.168	100	74	alanyl-tRNA synthetase
Locus_4301_Transcript_1/1_Conf_1.000	136	0							
Locus_4302_Transcript_1/1_Conf_1.000	2312	20	5.52E-61	NP_491143.2	51	240.736	479	248	hypothetical protein Y44E3A.4
Locus_4303_Transcript_1/2_Conf_1.000	1213	9	1.02E-19	XP_001895343.1	50	102.449	253	127	hypothetical protein Bm1_19440
Locus_4303_Transcript_2/2_Conf_1.000	1213	9	1.02E-19	XP_001895343.1	50	102.449	253	127	hypothetical protein Bm1_19440
Locus_4304_Transcript_1/1_Conf_1.000	1749	20	0	NP_001021458.1	93	930.628	539	503	Transbilayer Amphipath Transporters (subfamily IV P-type ATPase) family member (tat-5)
Locus_4305_Transcript_1/3_Conf_0.714	1881	20	0	XP_002638911.1	72	645.966	561	409	C. briggsae CBR-MAB-20 protein
Locus_4305_Transcript_2/3_Conf_0.714	1881	20	0	XP_002638911.1	72	644.04	561	408	C. briggsae CBR-MAB-20 protein
Locus_4305_Transcript_3/3_Conf_0.714	1881	20	0	XP_002638911.1	72	644.425	561	408	C. briggsae CBR-MAB-20 protein
Locus_4306_Transcript_1/1_Conf_1.000	332	0							
Locus_4307_Transcript_1/1_Conf_1.000	1227	20	5.33E-149	NP_001041048.1	81	531.946	372	305	EPS (human endocytosis) related family member (eps-8)
Locus_4308_Transcript_1/1_Conf_1.000	1206	20	4.25E-34	XP_002643647.1	63	150.214	182	115	Hypothetical protein CBG16396
Locus_4309_Transcript_1/1_Conf_1.000	349	20	5.06E-54	AAC08964.1	91	213.772	116	106	breakpoint cluster region protein 1
Locus_431_Transcript_1/1_Conf_1.000	1309	20	9.52E-176	XP_002635624.1	92	620.928	363	334	Hypothetical protein CBG21817
Locus_4310_Transcript_1/1_Conf_1.000	599	7	5.39E-08	XP_001902780.1	70	61.6178	82	58	Hypothetical RING finger protein C16C10.7 in chromosome III, putative

Locus_4311_Transcript_1/1_Conf_1.000	797	20	5.11E-60	XP_002637270.1	75	235.343	218	165	C. briggsae CBR-UBH-3 protein
Locus_4312_Transcript_1/1_Conf_1.000	452	20	7.86E-23	AAO63577.1	62	73.9442	69	43	secreted protein 5 precursor
Locus_4313_Transcript_1/1_Conf_1.000	610	2	2.03E-05	XP_002644841.1	52	53.1434	123	65	C. briggsae CBR-HSP-43 protein
Locus_4314_Transcript_1/1_Conf_1.000	339	2	1.89E-37	EAW57511.1	100	158.688	74	74	selenoprotein W, 1
Locus_4315_Transcript_1/1_Conf_1.000	154	0							
Locus_4316_Transcript_1/1_Conf_1.000	202	20	2.35E-19	XP_002798881.1	100	98.5969	49	49	PREDICTED: hypothetical protein LOC100426778
Locus_4317_Transcript_1/1_Conf_1.000	578	20	4.59E-30	XP_002641501.1	77	134.806	105	81	Hypothetical protein CBG09795
Locus_4318_Transcript_1/1_Conf_1.000	944	9	1.66E-21	EFO25158.1	49	107.842	321	159	hypothetical protein LOAG_03331
Locus_4319_Transcript_1/1_Conf_1.000	255	0							
Locus_432_Transcript_1/1_Conf_1.000	1133	20	3.27E-49	XP_002641402.1	62	200.29	235	147	Hypothetical protein CBG13264
Locus_4320_Transcript_1/1_Conf_1.000	821	20	6.10E-72	AAF66614.1	71	275.018	260	187	AF142441_1H+/oligopeptide symporter OPT-3
Locus_4321_Transcript_1/1_Conf_1.000	625	0							
Locus_4322_Transcript_1/1_Conf_1.000	800	20	2.31E-60	NP_491318.2	83	236.498	158	132	hypothetical protein R12E2.12
Locus_4323_Transcript_1/1_Conf_1.000	141	0							

Locus_4324_Transcript_1/1_Conf_1.000	137	20	5.56E-13	CAB40412.1	95	77.411	43	41	hexokinase
Locus_4325_Transcript_1/1_Conf_1.000	1142	20	8.17E-08	XP_002740738.1	44	62.7734	157	70	PREDICTED: mannose receptor C type 1-like
Locus_4326_Transcript_1/4_Conf_0.500	946	20	5.64E-78	XP_002631434.1	65	295.434	313	206	Hypothetical protein CBG03294
Locus_4326_Transcript_2/4_Conf_0.600	1715	20	1.74E-146	XP_002631434.1	68	524.242	504	346	Hypothetical protein CBG03294
Locus_4326_Transcript_3/4_Conf_0.200	812	20	2.25E-95	XP_002631434.1	78	352.829	250	196	Hypothetical protein CBG03294

Locus_4326_Transcript_4/4_Conf_0.500	946	20	3.31E-78	XP_002631434.1	66	296.204	313	207	Hypothetical protein CBG03294
Locus_4327_Transcript_1/2_Conf_1.000	602	20	8.08E-44	EFO22586.1	75	180.644	145	110	hypothetical protein LOAG_05898
Locus_4327_Transcript_2/2_Conf_1.000	773	20	1.40E-43	EFO22586.1	75	180.644	145	110	hypothetical protein LOAG_05898
Locus_4328_Transcript_1/1_Conf_1.000	1215	2	7.15E-05	EFO24344.1	55	53.1434	114	63	hypothetical protein LOAG_04140
Locus_4329_Transcript_1/1_Conf_1.000	149	0							
Locus_433_Transcript_1/2_Conf_1.000	1524	20	1.81E-176	ADL62852.1	91	623.624	366	335	thioredoxin reductase 1

Locus_433_Transcript_2/2_Conf_1.000	1523	20	1.81E-176	ADL62852.1	91	623.624	366	335	thioredoxin reductase 1
Locus_4330_Transcript_1/1_Conf_1.000	435	0							
Locus_4331_Transcript_1/1_Conf_1.000	890	20	6.61E-62	NP_491985.4	59	241.891	318	189	hypothetical protein C30F12.1
Locus_4332_Transcript_1/2_Conf_1.000	1608	4	3.83E-15	NP_497968.2	50	87.8113	173	87	hypothetical protein T04A8.15
Locus_4332_Transcript_2/2_Conf_1.000	651	0							
Locus_4333_Transcript_1/4_Conf_0.375	302	20	1.80E-19	NP_001040940.1	77	98.9821	71	55	PhosphatidylSerine Receptor family member (psr-1)
Locus_4333_Transcript_2/4_Conf_0.375	344	20	3.69E-20	NP_001040940.1	76	101.293	76	58	PhosphatidylSerine Receptor family member (psr-1)

Locus_4333_Transcript_3/4_Conf_0.375	1344	20	2.02E-136	NP_001040940.1	82	490.345	311	258	PhosphatidylSerine Receptor family member (psr-1)
Locus_4333_Transcript_4/4_Conf_0.375	1344	20	7.68E-136	NP_001040940.1	82	488.419	310	257	PhosphatidylSerine Receptor family member (psr-1)
Locus_4334_Transcript_1/1_Conf_1.000	309	4	3.36E-10	NP_001021494.1	61	68.1662	88	54	hypothetical protein F55A12.2
Locus_4335_Transcript_1/1_Conf_1.000	742	3	1.04E-32	XP_002631406.1	54	144.436	262	142	Hypothetical protein CBG03256
Locus_4336_Transcript_1/1_Conf_1.000	233	20	5.63E-21	NP_502295.1	87	103.99	70	61	yeast MON (monensin-resistant) homolog family member (mon-2)

Locus_4337_Transcript_1/1_Conf_1.000	254	5	8.83E-14	CAA10033.1	75	80.1073	77	58	DYS-1 protein
Locus_4338_Transcript_1/1_Conf_1.000	1015	20	1.28E-62	NP_492137.1	66	244.588	326	217	hypothetical protein T24B1.1
Locus_4339_Transcript_1/1_Conf_1.000	789	20	5.18E-73	XP_002632288.1	72	278.485	259	189	C. briggsae CBR-COGC-4 protein
Locus_434_Transcript_1/1_Conf_1.000	814	20	9.02E-52	XP_002643395.1	61	207.994	233	144	Hypothetical protein CBG16009
Locus_4340_Transcript_1/2_Conf_1.000	1669	20	5.36E-177	XP_002641207.1	78	625.55	471	369	Hypothetical protein CBG09068
Locus_4340_Transcript_2/2_Conf_1.000	1289	20	1.24E-103	XP_002641207.1	75	381.333	301	228	Hypothetical protein CBG09068
Locus_4341_Transcript_1/1_Conf_1.000	436	4	1.45E-45	NP_001023919.2	83	185.652	149	124	hypothetical protein F43D2.6
Locus_4342_Transcript_1/1_Conf_1.000	1274	20	2.20E-137	EFO18770.1	84	493.426	310	262	hypothetical protein LOAG_09726
Locus_4343_Transcript_1/1_Conf_1.000	505	20	1.21E-26	XP_002630816.1	71	122.865	135	96	Hypothetical protein CBG02517
Locus_4344_Transcript_1/1_Conf_1.000	579	0							
Locus_4345_Transcript_1/1_Conf_1.000	1042	9	3.08E-19	XP_002640504.1	42	100.523	407	173	Hypothetical protein CBG13643
Locus_4346_Transcript_1/1_Conf_1.000	1250	20	0	XP_002645884.1	87	679.863	416	362	Hypothetical protein CBG07632
Locus_4347_Transcript_1/1_Conf_1.000	174	2	1.01E-14	XP_002634119.1	77	83.1889	63	49	Hypothetical protein CBG01673
Locus_4348_Transcript_1/1_Conf_1.000	455	20	2.41E-32	XP_001895412.1	77	141.739	118	92	TB2/DP1, HVA22 family protein

Locus_4349_Transcript_1/1_Conf_1.000	312	1	4.85E-04	NP_498634.1	56	47.7506	62	35	hypothetical protein T20B12.3
Locus_435_Transcript_1/1_Conf_1.000	1063	20	9.90E-21	NP_001122564.1	75	105.531	84	63	hypothetical protein ZC434.7
Locus_4350_Transcript_1/1_Conf_1.000	192	20	5.13E-14	NP_001123038.1	84	80.8777	52	44	hypothetical protein Y39B6A.3
Locus_4351_Transcript_1/1_Conf_1.000	553	2	3.98E-09	XP_001896166.1	77	65.0846	48	37	hypothetical protein Bm1_23545
Locus_4352_Transcript_1/1_Conf_1.000	1483	14	5.67E-26	EFO25413.1	52	123.635	322	170	hypothetical protein LOAG_03070
Locus_4353_Transcript_1/1_Conf_1.000	1318	20	4.51E-24	XP_002637076.1	48	117.087	286	138	Hypothetical protein CBG09575
Locus_4354_Transcript_1/1_Conf_1.000	294	0							
Locus_4355_Transcript_1/1_Conf_1.000	151	4	2.74E-07	NP_491850.2	74	58.5362	50	37	Nuclear Cap-Binding Protein family member (ncbp-1)
Locus_4356_Transcript_1/3_Conf_0.714	1959	20	3.47E-170	EFO22264.1	80	603.208	432	348	CMGC/CDK/CDK8 protein kinase
Locus_4356_Transcript_2/3_Conf_0.714	1950	20	3.45E-170	EFO22264.1	80	603.208	432	348	CMGC/CDK/CDK8 protein kinase
Locus_4356_Transcript_3/3_Conf_0.714	1950	20	3.45E-170	EFO22264.1	80	603.208	432	348	CMGC/CDK/CDK8 protein kinase

Locus_4357_Transcript_1/1_Conf_1.000	131	0							
Locus_4358_Transcript_1/1_Conf_1.000	4197	20	0	A8PJX4.2	69	1171.76	1255	876	Protein KIAA0664 homolog
Locus_4359_Transcript_1/2_Conf_1.000	314	1	6.34E-04		57	47.3654	54	31	hypothetical protein F55C12.3
Locus_4359_Transcript_2/2_Conf_1.000	314	0							
Locus_436_Transcript_1/1_Conf_1.000	2656	20	0	NP_499039.1	90	1336.63	788	713	RiboNucleotide Reductase family member (rnr-1)
Locus_4360_Transcript_1/1_Conf_1.000	691	0							
Locus_4361_Transcript_1/1_Conf_1.000	479	20	3.02E-43	XP_002646753.1	73	177.948	152	111	Hypothetical protein CBG13150
Locus_4362_Transcript_1/1_Conf_1.000	1411	20	1.49E-12	XP_002645688.1	65	78.9518	76	50	C. briggsae CBR-ELT-3 protein
Locus_4363_Transcript_1/1_Conf_1.000	1977	20	2.21E-156	XP_001892663.1	68	557.37	607	413	Elongation factor Tu C-terminal domain containing protein
Locus_4364_Transcript_1/1_Conf_1.000	583	20	3.51E-33	CBW48565.1	60	145.206	190	115	Hypothetical protein Y111B2A.22d
Locus_4365_Transcript_1/1_Conf_1.000	932	20	1.65E-82	XP_002640293.1	75	310.457	260	196	Hypothetical protein CBG12819
Locus_4366_Transcript_1/1_Conf_1.000	803	20	3.05E-44	XP_001893343.1	58	182.956	230	135	threonyl-tRNA synthetase, cytoplasmic
Locus_4367_Transcript_1/1_Conf_1.000	2216	20	0	EFO24137.1	82	644.81	464	384	structure-specific recognition protein 1
Locus_4368_Transcript_1/1_Conf_1.000	279	20	8.83E-19	NP_001123180.1	76	96.6709	71	54	hypothetical protein T08A9.11

Locus_4369_Transcript_1/1_Conf_1.000	429	20	3.26E-37	XP_001896422.1	81	157.918	111	91	28S ribosomal protein S21, mitochondrial
Locus_437_Transcript_1/1_Conf_1.000	1553	20	0	NP_498915.1	92	721.079	425	391	hypothetical protein B0303.3
Locus_4370_Transcript_1/1_Conf_1.000	140	0							
Locus_4371_Transcript_1/1_Conf_1.000	2195	20	1.46E-172	NP_495257.3	71	611.298	573	412	Biotin Protein Ligase family member (bpl-1)
Locus_4372_Transcript_1/1_Conf_1.000	254	0							
Locus_4373_Transcript_1/5_Conf_0.300	732	20	3.86E-125	AAL06641.1	97	451.44	244	238	serine-threonine protein kinase
Locus_4373_Transcript_2/5_Conf_0.200	456	20	1.22E-68	AAL06641.1	98	262.307	134	132	serine-threonine protein kinase
Locus_4373_Transcript_3/5_Conf_0.200	720	8	5.52E-28	AAL06641.1	100	128.642	65	65	serine-threonine protein kinase
Locus_4373_Transcript_4/5_Conf_0.300	1432	20	1.09E-135	AAL06641.1	90	488.034	312	282	serine-threonine protein kinase
Locus_4373_Transcript_5/5_Conf_0.600	2292	20	0	AAL06641.1	93	1006.13	599	559	serine-threonine protein kinase
Locus_4374_Transcript_1/1_Conf_1.000	1524	20	5.63E-69	XP_002630560.1	59	266.544	506	302	C. briggsae CBR-NPP-21 protein

Locus_4375_Transcript_1/1_Conf_1.000	377	20	3.28E-45	NP_495680.1	77	184.496	122	95	Nose Resistant to Fluoxetine family member (nrf-6)
Locus_4376_Transcript_1/1_Conf_1.000	508	20	1.16E-32	XP_001900891.1	65	142.895	169	110	Prion-like-
Locus_4377_Transcript_1/1_Conf_1.000	1218	20	1.76E-128	NP_501067.1	83	463.766	347	289	RUVB (recombination protein) homolog family member (ruvb-2)
Locus_4378_Transcript_1/1_Conf_1.000	347	0							
Locus_4379_Transcript_1/1_Conf_1.000	129	0							
Locus_438_Transcript_1/2_Conf_1.000	1127	20	6.16E-133	XP_002638927.1	79	478.404	370	293	Hypothetical protein CBG22153
Locus_438_Transcript_2/2_Conf_1.000	1103	20	8.90E-129	XP_002638927.1	80	464.537	362	293	Hypothetical protein CBG22153

Locus_4380_Transcript_1/1_Conf_1.000	1366	20	0	XP_002641617.1	93	666.766	398	372	C. briggsae CBR-MOG-1 protein
Locus_4381_Transcript_1/2_Conf_1.000	886	7	2.15E-04	XP_001179012.1	49	50.8322	121	60	PREDICTED: similar to ankyrin 2,3/unc44
Locus_4381_Transcript_2/2_Conf_1.000	886	7	2.15E-04	XP_001179012.1	49	50.8322	121	60	PREDICTED: similar to ankyrin 2,3/unc44
Locus_4382_Transcript_1/1_Conf_1.000	2041	20	3.60E-109	NP_497766.3	55	400.593	715	395	MTM (myotubularin) family member (mtm-3)
Locus_4383_Transcript_1/1_Conf_1.000	653	0							
Locus_4384_Transcript_1/2_Conf_1.000	507	0							
Locus_4384_Transcript_2/2_Conf_1.000	504	0							
Locus_4385_Transcript_1/1_Conf_1.000	153	0							
Locus_4386_Transcript_1/1_Conf_1.000	813	7	4.82E-29	XP_002646135.1	60	132.494	190	114	Hypothetical protein CBG08014
Locus_4387_Transcript_1/1_Conf_1.000	462	20	9.22E-72	NP_498231.1	98	272.707	140	138	Ribosomal Protein, Large subunit family member (rpl-23)
Locus_4388_Transcript_1/1_Conf_1.000	285	20	5.67E-37	EFO25086.1	88	157.147	95	84	DNA topoisomerase III
Locus_4389_Transcript_1/1_Conf_1.000	542	5	3.80E-22	NP_496303.1	63	108.227	133	85	hypothetical protein D2089.3
Locus_439_Transcript_1/1_Conf_1.000	812	4	3.64E-53	NP_504396.1	55	212.616	268	150	hypothetical protein Y49G5B.1

Locus_4390_Transcript_1/1_Conf_1.000	343	20	1.49E-29	XP_002633281.1	88	132.494	85	75	Hypothetical protein CBG06010
Locus_4391_Transcript_1/1_Conf_1.000	186	3	2.25E-09	EFO23813.1	78	65.4698	47	37	cuticlin 1
Locus_4392_Transcript_1/1_Conf_1.000	750	20	3.87E-67	XP_002637159.1	72	258.84	226	163	C. briggsae CBR-AQP-6 protein
Locus_4393_Transcript_1/1_Conf_1.000	1565	20	0	NP_495986.3	86	706.442	465	402	EATing: abnormal pharyngeal pumping family member (eat-3)
Locus_4394_Transcript_1/1_Conf_1.000	380	0							
Locus_4395_Transcript_1/1_Conf_1.000	1140	20	2.68E-51	EFO18896.1	62	207.223	267	167	hypothetical protein LOAG_09599
Locus_4396_Transcript_1/1_Conf_1.000	576	2	2.06E-22	NP_494855.1	77	109.383	94	73	Toxin-regulated Target of p38MAPK family member (ttm-2)
Locus_4397_Transcript_1/1_Conf_1.000	1167	20	4.33E-137	XP_002631107.1	90	492.271	274	249	Hypothetical protein CBG02882
Locus_4398_Transcript_1/1_Conf_1.000	134	0							
Locus_4399_Transcript_1/1_Conf_1.000	274	20	7.04E-16	EFO15742.1	74	87.0409	75	56	hypothetical protein LOAG_12768
Locus_44_Transcript_1/1_Conf_1.000	1749	20	7.66E-174	NP_505626.1	70	615.15	591	417	Temporarily Assigned Gene name family member (tag-315)
Locus_440_Transcript_1/3_Conf_0.818	456	0							
Locus_440_Transcript_2/3_Conf_0.727	449	0							
Locus_440_Transcript_3/3_Conf_0.818	449	0							
Locus_4400_Transcript_1/1_Conf_1.000	323	4	1.06E-19	XP_002632143.1	67	99.7525	108	73	Hypothetical protein CBG07002
Locus_4401_Transcript_1/1_Conf_1.000	1086	20	4.89E-47	NP_491524.1	54	192.971	355	194	ELongator complex Protein Component family member (elpc-1)
Locus_4402_Transcript_1/2_Conf_0.500	1272	20	2.85E-44	XP_002593284.1	73	184.111	157	115	hypothetical protein BRAFLDRAFT_123638

Locus_4402_Transcript_2/2_Conf_0.500	1421	20	1.75E-61	XP_002637106.1	87	241.506	137	120	Hypothetical protein CBG09606
Locus_4403_Transcript_1/4_Conf_0.250	798	0							
Locus_4403_Transcript_2/4_Conf_0.250	756	0							
Locus_4403_Transcript_3/4_Conf_0.375	1318	20	8.19E-42	XP_001895085.1	71	176.022	163	117	MGC80088 protein
Locus_4403_Transcript_4/4_Conf_0.375	1318	20	2.38E-41	XP_001895085.1	71	174.481	162	116	MGC80088 protein
Locus_4404_Transcript_1/1_Conf_1.000	479	20	2.30E-67	NP_509528.1	83	258.07	159	133	hypothetical protein T25B6.2
Locus_4405_Transcript_1/2_Conf_1.000	447	8	2.06E-31	NP_741590.1	72	138.658	125	91	Heavy chain, Unconventional Myosin family member (hum-2)
Locus_4405_Transcript_2/2_Conf_1.000	345	8	1.39E-27	NP_505433.3	73	125.946	116	85	Heavy chain, Unconventional Myosin family member (hum-2)
Locus_4406_Transcript_1/1_Conf_1.000	304	11	5.39E-16	ABW05396.1	97	87.4261	45	44	paramyosin isoform 3
Locus_4407_Transcript_1/1_Conf_1.000	436	20	2.09E-52	XP_002639557.1	90	208.379	120	109	Hypothetical protein CBG04188
Locus_4408_Transcript_1/1_Conf_1.000	2007	20	1.15E-176	XP_002644619.1	75	624.78	603	456	C. briggsae CBR-LFI-1 protein
Locus_4409_Transcript_1/2_Conf_1.000	434	0							
Locus_4409_Transcript_2/2_Conf_1.000	434	0							
Locus_441_Transcript_1/3_Conf_0.714	3236	20	0	EFO26360.1	90	1665.59	1008	911	TOPoisomerase family member

Locus_441_Transcript_2/3_Conf_0.714	3236	20	0	EFO26360.1	90	1665.59	1008	911	TOPoisomerase family member
Locus_441_Transcript_3/3_Conf_0.714	3236	20	0	EFO26360.1	90	1665.59	1008	911	TOPoisomerase family member
Locus_4410_Transcript_1/1_Conf_1.000	955	20	1.43E-84	XP_002639511.1	76	189.504	190	145	Hypothetical protein CBG04116
Locus_4411_Transcript_1/1_Conf_1.000	522	20	3.32E-33	EFO27393.1	66	144.821	166	110	cisplatin
Locus_4412_Transcript_1/1_Conf_1.000	740	20	1.53E-44	NP_510225.2	68	183.726	227	156	hypothetical protein C49F8.2
Locus_4413_Transcript_1/1_Conf_1.000	166	0							
Locus_4414_Transcript_1/1_Conf_1.000	266	1	7.14E-08	XP_001899340.1	72	60.4622	50	36	c-MYC promoter-binding protein IRLB
Locus_4415_Transcript_1/1_Conf_1.000	213	0							
Locus_4416_Transcript_1/1_Conf_1.000	438	20	3.21E-45	XP_002646760.1	85	184.496	114	98	C. briggsae CBR-NAS-7 protein

Locus_4417_Transcript_1/4_Conf_0.375	814	20	1.08E-113	XP_002642846.1	92	413.69	258	238	C. briggsae CBR-PPK-2 protein
Locus_4417_Transcript_2/4_Conf_0.375	772	20	5.77E-114	XP_002642846.1	92	414.461	257	237	C. briggsae CBR-PPK-2 protein
Locus_4417_Transcript_3/4_Conf_0.375	1083	20	3.42E-117	XP_002642846.1	92	426.017	269	249	C. briggsae CBR-PPK-2 protein
Locus_4417_Transcript_4/4_Conf_0.375	1083	20	6.88E-118	XP_002642846.1	92	428.328	269	249	C. briggsae CBR-PPK-2 protein
Locus_4418_Transcript_1/1_Conf_1.000	1295	20	1.55E-45	Q16937.1	47	188.348	427	204	Ancylostoma secreted protein
Locus_4419_Transcript_1/1_Conf_1.000	336	20	5.01E-22	XP_002399229.1	70	107.457	103	73	spermatogenesis-associated protein, putative
Locus_442_Transcript_1/2_Conf_1.000	592	20	4.11E-37	XP_002641835.1	61	158.303	195	120	C. briggsae CBR-CYK-1 protein
Locus_442_Transcript_2/2_Conf_1.000	592	20	4.11E-37	XP_002641835.1	61	158.303	195	120	C. briggsae CBR-CYK-1 protein
Locus_4420_Transcript_1/1_Conf_1.000	148	0							
Locus_4421_Transcript_1/1_Conf_1.000	628	20	4.80E-13	XP_001956818.1	75	78.5666	86	65	GF24383
Locus_4422_Transcript_1/1_Conf_1.000	367	0							
Locus_4423_Transcript_1/1_Conf_1.000	626	0							
Locus_4424_Transcript_1/1_Conf_1.000	720	20	2.80E-64	NP_508919.2	67	249.21	247	166	hypothetical protein C03F11.3
Locus_4425_Transcript_1/1_Conf_1.000	667	2	3.14E-08	EFO19250.1	50	62.7734	189	96	hypothetical protein LOAG_09244
Locus_4426_Transcript_1/1_Conf_1.000	831	2	1.17E-09	AAT78565.1	92	68.1662	65	60	putative protein
Locus_4427_Transcript_1/5_Conf_0.667	2549	20	0	XP_002642903.1	73	963.755	854	628	C. briggsae CBR-ZER-1 protein
Locus_4427_Transcript_2/5_Conf_0.167	513	5	1.35E-20	XP_002642903.1	57	102.834	188	108	C. briggsae CBR-ZER-1 protein
Locus_4427_Transcript_3/5_Conf_0.667	2549	20	0	XP_002642903.1	73	963.755	854	628	C. briggsae CBR-ZER-1 protein
Locus_4427_Transcript_4/5_Conf_0.667	2549	20	0	XP_002642903.1	73	963.755	854	628	C. briggsae CBR-ZER-1 protein
Locus_4427_Transcript_5/5_Conf_0.667	2549	20	0	XP_002642903.1	73	963.755	854	628	C. briggsae CBR-ZER-1 protein
Locus_4428_Transcript_1/1_Conf_1.000	618	20	3.93E-52	XP_001902415.1	69	208.379	193	135	RNA-metabolising metallo-beta-lactamase family protein
Locus_4429_Transcript_1/1_Conf_1.000	1197	0							
Locus_443_Transcript_1/1_Conf_1.000	812	18	2.14E-37	NP_001023053.1	55	160.229	231	129	hypothetical protein C39E9.8

Locus_4430_Transcript_1/1_Conf_1.000	699	20	1.85E-49	NP_492550.3	82	199.904	186	153	hypothetical protein K07A1.10
Locus_4431_Transcript_1/1_Conf_1.000	205	0							
Locus_4432_Transcript_1/2_Conf_1.000	2034	1	8.22E-05	NP_497945.1	43	53.9138	130	56	C-type LECtin family member (clec-152)
Locus_4432_Transcript_2/2_Conf_1.000	395	0							
Locus_4433_Transcript_1/1_Conf_1.000	270	0							
Locus_4434_Transcript_1/1_Conf_1.000	384	0							
Locus_4435_Transcript_1/1_Conf_1.000	662	0							
Locus_4436_Transcript_1/2_Conf_1.000	1351	20	9.34E-57	NP_506514.1	52	225.713	480	251	hypothetical protein ZC376.6
Locus_4436_Transcript_2/2_Conf_1.000	1342	20	7.08E-57	EFO25154.1	53	226.098	461	247	hypothetical protein LOAG_03327
Locus_4437_Transcript_1/2_Conf_1.000	1059	20	9.35E-88	NP_494919.1	91	328.176	208	190	hypothetical protein T27F7.1
Locus_4437_Transcript_2/2_Conf_1.000	1049	20	9.17E-88	NP_494919.1	91	328.176	208	190	hypothetical protein T27F7.1
Locus_4438_Transcript_1/1_Conf_1.000	1213	20	5.28E-117	NP_491780.1	86	425.631	269	233	hypothetical protein T09B4.9
Locus_4439_Transcript_1/3_Conf_0.500	1149	20	3.91E-66	AAM98022.4	75	256.529	239	181	Abnormal dye filling protein 14, isoform d, partially confirmed by transcript evidence
Locus_4439_Transcript_2/3_Conf_0.500	1151	20	1.88E-52	AAM98022.4	73	211.075	203	149	Abnormal dye filling protein 14, isoform d, partially confirmed by transcript evidence

Locus_4439_Transcript_3/3_Conf_0.500	901	20	2.66E-66	AAM98022.4	75	256.529	239	181	Abnormal dye filling protein 14, isoform d, partially confirmed by transcript evidence
Locus_444_Transcript_1/1_Conf_1.000	467	2	2.08E-07	NP_001024433.1	76	58.9214	43	33	hypothetical protein C26B9.1
Locus_4440_Transcript_1/1_Conf_1.000	575	20	4.81E-40	NP_508166.1	64	167.933	193	124	ImmunoGlobulin-like Cell adhesion Molecule family member (igcm-1)
Locus_4441_Transcript_1/1_Conf_1.000	1131	10	2.19E-45	NP_508610.3	52	187.578	382	200	Regulator of G protein Signaling family member (rgs-7)
Locus_4442_Transcript_1/1_Conf_1.000	756	20	2.71E-44	XP_002640702.1	73	182.956	175	128	Hypothetical protein CBG19768
Locus_4443_Transcript_1/1_Conf_1.000	492	20	1.85E-40	XP_002631925.1	91	168.703	104	95	Hypothetical protein CBG07915
Locus_4444_Transcript_1/1_Conf_1.000	487	2	2.21E-25	NP_508128.1	64	118.627	139	90	hypothetical protein F13C5.5
Locus_4445_Transcript_1/1_Conf_1.000	1570	20	4.40E-109	NP_494782.1	63	399.823	484	306	hypothetical protein ZK430.1
Locus_4446_Transcript_1/2_Conf_1.000	630	2	2.33E-15	CAR63657.1	88	86.2705	52	46	hypothetical protein
Locus_4446_Transcript_2/2_Conf_1.000	626	2	2.27E-15	CAR63657.1	88	86.2705	52	46	hypothetical protein
Locus_4447_Transcript_1/1_Conf_1.000	387	20	5.73E-26	EFO15541.1	77	120.553	90	70	speckle-type POZ protein
Locus_4448_Transcript_1/1_Conf_1.000	1345	20	1.14E-155	XP_002641168.1	78	554.288	430	338	Hypothetical protein CBG09025
Locus_4449_Transcript_1/1_Conf_1.000	569	20	2.73E-40	XP_002641669.1	68	168.703	158	108	Hypothetical protein CBG09999
Locus_445_Transcript_1/1_Conf_1.000	656	3	3.56E-41	XP_001136340.1	97	172.17	107	104	PREDICTED: hypothetical protein
Locus_4450_Transcript_1/1_Conf_1.000	1187	20	1.40E-82	XP_002639996.1	64	311.227	374	241	Hypothetical protein CBG10826

Locus_4451_Transcript_1/4_Conf_0.444	1198	20	4.51E-20	XP_002642641.1	39	103.605	426	169	C. briggsae CBR-LIN-13 protein
Locus_4451_Transcript_2/4_Conf_0.667	2980	20	1.41E-35	XP_002642641.1	38	156.762	723	275	C. briggsae CBR-LIN-13 protein
Locus_4451_Transcript_3/4_Conf_0.667	2409	20	1.03E-33	XP_002642641.1	39	150.214	504	201	C. briggsae CBR-LIN-13 protein
Locus_4451_Transcript_4/4_Conf_0.667	2980	20	1.41E-35	XP_002642641.1	38	156.762	723	275	C. briggsae CBR-LIN-13 protein
Locus_4452_Transcript_1/1_Conf_1.000	396	0							
Locus_4453_Transcript_1/3_Conf_0.571	626	0							
Locus_4453_Transcript_2/3_Conf_0.571	715	0							
Locus_4453_Transcript_3/3_Conf_0.714	737	0							
Locus_4454_Transcript_1/2_Conf_1.000	702	20	2.90E-26	XP_002631067.1	46	122.865	272	126	C. briggsae CBR-TRR-1 protein
Locus_4454_Transcript_2/2_Conf_1.000	702	20	2.90E-26	XP_002631067.1	46	122.865	272	126	C. briggsae CBR-TRR-1 protein
Locus_4455_Transcript_1/1_Conf_1.000	716	0							
Locus_4456_Transcript_1/1_Conf_1.000	460	20	5.17E-19	XP_001898200.1	65	97.4413	99	65	hypothetical protein Bm1_33765
Locus_4457_Transcript_1/2_Conf_1.000	724	1	4.29E-04	CAR63546.1	51	49.2914	92	47	hypothetical protein
Locus_4457_Transcript_2/2_Conf_1.000	535	1	3.43E-04	CAR63546.1	51	48.521	92	47	hypothetical protein
Locus_4458_Transcript_1/1_Conf_1.000	621	3	1.36E-04	XP_002637469.1	75	50.447	45	34	Hypothetical protein CBG19185
Locus_4459_Transcript_1/2_Conf_1.000	942	20	5.72E-123	AAC78238.2	89	444.891	315	281	Guanylyl cyclase protein 28, isoform d

Locus_4459_Transcript_2/2_Conf_1.000	981	20	8.18E-136	NP_001021600.1	88	487.649	328	290	Guanylyl CYclase family member (gcy-28)
Locus_446_Transcript_1/1_Conf_1.000	1139	20	2.01E-22	EFO23042.1	63	111.309	177	113	hypothetical protein LOAG_05445
Locus_4460_Transcript_1/1_Conf_1.000	1368	20	2.69E-160	XP_001895648.1	82	569.696	424	348	Pre-mRNA cleavage complex II protein Clp1
Locus_4461_Transcript_1/1_Conf_1.000	573	20	3.58E-27	NP_500829.2	60	125.176	144	87	hypothetical protein T12E12.1
Locus_4462_Transcript_1/1_Conf_1.000	323	0							
Locus_4463_Transcript_1/7_Conf_0.667	4125	20	0	NP_500102.3	70	847.81	859	603	Nuclear Pore complex Protein family member (npp-8)
Locus_4463_Transcript_2/7_Conf_0.667	4125	20	0	NP_500102.3	70	847.81	859	603	Nuclear Pore complex Protein family member (npp-8)
Locus_4463_Transcript_3/7_Conf_0.667	4125	20	0	NP_500102.3	70	847.81	859	603	Nuclear Pore complex Protein family member (npp-8)
Locus_4463_Transcript_4/7_Conf_0.667	4125	20	0	NP_500102.3	70	847.81	859	603	Nuclear Pore complex Protein family member (npp-8)
Locus_4463_Transcript_5/7_Conf_0.667	4125	20	0	NP_500102.3	70	848.966	859	603	Nuclear Pore complex Protein family member (npp-8)

Locus_4463_Transcript_6/7_Conf_0.333	1543	20	4.56E-135	NP_500102.3	70	486.108	471	331	Nuclear Pore complex Protein family member (npp-8)
Locus_4463_Transcript_7/7_Conf_0.667	4125	20	0	NP_500102.3	70	847.81	859	603	Nuclear Pore complex Protein family member (npp-8)
Locus_4464_Transcript_1/2_Conf_1.000	539	0							
Locus_4464_Transcript_2/2_Conf_1.000	539	0							
Locus_4465_Transcript_1/1_Conf_1.000	620	20	5.49E-54	NP_494921.1	66	214.542	206	136	hypothetical protein F59A6.5
Locus_4466_Transcript_1/1_Conf_1.000	711	20	1.74E-111	EFB23493.1	94	405.986	224	211	hypothetical protein PANDA_016815
Locus_4467_Transcript_1/1_Conf_1.000	362	0							
Locus_4468_Transcript_1/1_Conf_1.000	176	0							
Locus_4469_Transcript_1/1_Conf_1.000	451	20	5.71E-66	XP_001172323.1	100	253.447	125	125	PREDICTED: similar to Proteasome (prosome, macropain) subunit, beta type, 4 isoform 1
Locus_447_Transcript_1/1_Conf_1.000	889	20	1.66E-105	AAK62032.1	77	386.726	296	229	metalloprotease 1 precursor
Locus_4470_Transcript_1/1_Conf_1.000	1700	20	1.08E-151	NP_507025.1	82	505.368	384	318	hypothetical protein T10C6.6

Locus_4471_Transcript_1/1_Conf_1.000	1431	20	9.71E-68	XP_002641056.1	85	262.307	199	170	Hypothetical protein CBG22467
Locus_4472_Transcript_1/1_Conf_1.000	380	0							
Locus_4473_Transcript_1/1_Conf_1.000	525	20	1.52E-49	CAG25499.1	75	199.134	159	120	heat shock protein 20
Locus_4474_Transcript_1/1_Conf_1.000	130	0							
Locus_4475_Transcript_1/4_Conf_0.333	250	20	3.46E-15	NP_497979.1	64	84.7297	78	50	RaB GAP related family member (rbg-3)
Locus_4475_Transcript_2/4_Conf_0.222	250	20	3.46E-15	NP_497979.1	64	84.7297	78	50	RaB GAP related family member (rbg-3)
Locus_4475_Transcript_3/4_Conf_0.556	1800	20	4.41E-140	NP_497979.1	65	503.056	552	361	RaB GAP related family member (rbg-3)
Locus_4475_Transcript_4/4_Conf_0.556	1800	20	4.41E-140	NP_497979.1	65	503.056	552	361	RaB GAP related family member (rbg-3)
Locus_4476_Transcript_1/1_Conf_1.000	1207	0							
Locus_4477_Transcript_1/1_Conf_1.000	439	3	8.00E-04	NP_510264.1	71	46.9802	38	27	Carbonic AnHydrase family member (cah-4)
Locus_4478_Transcript_1/1_Conf_1.000	1017	0							
Locus_4479_Transcript_1/1_Conf_1.000	206	3	1.58E-07	NP_001024958.1	81	59.3066	55	45	hypothetical protein Y34B4A.4
Locus_448_Transcript_1/1_Conf_1.000	695	3	9.36E-22	XP_002642236.1	52	107.842	198	104	Hypothetical protein CBG18218
Locus_4480_Transcript_1/1_Conf_1.000	705	20	3.86E-55	XP_002645121.1	86	218.779	178	154	C. briggsae CBR-TRAP-3 protein
Locus_4481_Transcript_1/2_Conf_1.000	965	2	1.40E-07	NP_496943.1	47	61.6178	160	76	hypothetical protein W01G7.4
Locus_4481_Transcript_2/2_Conf_1.000	953	2	1.37E-07	NP_496943.1	47	61.6178	160	76	hypothetical protein W01G7.4
Locus_4482_Transcript_1/1_Conf_1.000	1532	20	2.95E-09	ACI47264.1	48	68.1662	196	96	high mobility group protein A2

Locus_4483_Transcript_1/1_Conf_1.000	1306	20	1.48E-144	XP_002637506.1	78	517.309	380	300	C. briggsae CBR-INX-10 protein
Locus_4484_Transcript_1/1_Conf_1.000	372	0							
Locus_4485_Transcript_1/1_Conf_1.000	441								
Locus_4486_Transcript_1/1_Conf_1.000	1742	7	3.83E-08	XP_001508179.1	39	64.6994	268	107	PREDICTED: similar to single-strand telomeric DNA-binding protein; cPot1
Locus_4487_Transcript_1/1_Conf_1.000	464	20	3.91E-38	XP_002640722.1	76	160.999	151	115	Hypothetical protein CBG19790
Locus_4488_Transcript_1/1_Conf_1.000	872	20	2.21E-62	XP_001902350.1	64	243.432	270	174	Myosin XVIIIA
Locus_4489_Transcript_1/3_Conf_0.667	744	20	2.50E-18	XP_002198796.1	46	96.6709	238	110	PREDICTED: similar to sqstm1 protein, partial
Locus_4489_Transcript_2/3_Conf_0.667	726	20	3.30E-20	XP_002198796.1	48	102.834	232	113	PREDICTED: similar to sqstm1 protein, partial
Locus_4489_Transcript_3/3_Conf_0.667	750	20	4.63E-20	XP_002198796.1	47	102.449	240	113	PREDICTED: similar to sqstm1 protein, partial
Locus_449_Transcript_1/1_Conf_1.000	582	0							
Locus_4490_Transcript_1/2_Conf_1.000	586	20	1.94E-55	NP_504577.1	76	219.164	183	140	hypothetical protein F17A9.2
Locus_4490_Transcript_2/2_Conf_1.000	390	20	1.77E-35	NP_504577.1	78	152.14	129	101	hypothetical protein F17A9.2
Locus_4491_Transcript_1/1_Conf_1.000	236	1	8.14E-04	NP_495034.1	63	46.9802	46	29	CalEXcitin family member (cex-1)
Locus_4492_Transcript_1/1_Conf_1.000	407	0							
Locus_4493_Transcript_1/1_Conf_1.000	335	20	3.25E-29	XP_002631614.1	84	131.339	112	95	C. briggsae CBR-MAC-1 protein
Locus_4494_Transcript_1/1_Conf_1.000	509	8	2.51E-11	EFO20561.1	80	72.0182	52	42	frizzled/Smoothened family membrane region containing protein
Locus_4495_Transcript_1/1_Conf_1.000	1623	20	5.34E-174	XP_002639918.1	78	615.535	517	407	C. briggsae CBR-NMY-2 protein

Locus_4496_Transcript_1/1_Conf_1.000	1381	8	1.89E-36	ABC70182.1	45	158.303	531	243	sprint
Locus_4497_Transcript_1/1_Conf_1.000	140	0							
Locus_4498_Transcript_1/1_Conf_1.000	180	0							
Locus_4499_Transcript_1/1_Conf_1.000	542	0							
Locus_45_Transcript_1/1_Conf_1.000	458	0							
Locus_450_Transcript_1/2_Conf_1.000	726	20	2.11E-67	NP_510606.1	77	259.61	201	155	ACyLtransferase-like family member (acl-1)
Locus_450_Transcript_2/2_Conf_1.000	726	20	2.11E-67	NP_510606.1	77	259.61	201	155	ACyLtransferase-like family member (acl-1)
Locus_4500_Transcript_1/3_Conf_0.714	936	10	1.57E-64	NP_510687.2	64	250.751	262	170	ALG-1 INteracting protein family member (ain-1)
Locus_4500_Transcript_2/3_Conf_0.714	1893	11	3.00E-78	NP_510687.2	64	297.745	319	205	ALG-1 INteracting protein family member (ain-1)
Locus_4500_Transcript_3/3_Conf_0.714	948	11	8.79E-63	NP_510687.2	63	244.973	266	170	ALG-1 INteracting protein family member (ain-1)
Locus_4501_Transcript_1/1_Conf_1.000	1302	20	2.35E-142	A8XEQ8.2	81	509.99	397	323	Ubiquitin-like modifier-activating enzyme 5
Locus_4502_Transcript_1/1_Conf_1.000	468	20	7.06E-40	CAX32485.1	66	166.777	155	103	C. elegans protein T20D3.11b, partially confirmed by transcript evidence
Locus_4503_Transcript_1/1_Conf_1.000	2744	20	7.73E-174	XP_002640239.1	57	615.92	852	491	C. briggsae CBR-DPF-3 protein
Locus_4504_Transcript_1/1_Conf_1.000	2171	20	0	NP_508988.2	70	748.429	718	508	TBC (Tre-2/Bub2/Cdc16) domain family member (tbc-16)
Locus_4505_Transcript_1/1_Conf_1.000	251	1	1.46E-05	EFO14401.1	61	52.7582	68	42	hypothetical protein LOAG_14117
Locus_4506_Transcript_1/1_Conf_1.000	539	0							
Locus_4507_Transcript_1/1_Conf_1.000	220	20	3.96E-14	XP_002763591.1	100	81.2629	40	40	PREDICTED: programmed cell death protein 5-like, partial
Locus_4508_Transcript_1/1_Conf_1.000	961	12	2.61E-38	CAR97833.1	55	163.696	280	154	C. elegans protein F46G10.5b, partially confirmed by transcript evidence
Locus_4509_Transcript_1/1_Conf_1.000	335	20	5.40E-08		60	60.8474	86	52	hypothetical protein C45H4.5

Locus_451_Transcript_1/1_Conf_1.000	1747	20	1.29E-96	EFO21369.1	75	358.607	400	301	hypothetical protein LOAG_07120
Locus_4510_Transcript_1/1_Conf_1.000	796	20	1.93E-75	EFO20638.1	73	286.574	266	196	oxidoreductase
Locus_4511_Transcript_1/1_Conf_1.000	384	6	1.92E-05	EFO26532.1	73	52.373	41	30	hypothetical protein LOAG_01952
Locus_4512_Transcript_1/2_Conf_1.000	494	0							
Locus_4512_Transcript_2/2_Conf_1.000	494	0							
Locus_4513_Transcript_1/1_Conf_1.000	636	20	8.41E-53	XP_002630191.1	71	210.69	213	153	C. briggsae CBR-KAP-1 protein
Locus_4514_Transcript_1/1_Conf_1.000	241	0							
Locus_4515_Transcript_1/1_Conf_1.000	963	20	2.36E-164	NP_501507.1	95	582.408	319	306	hypothetical protein F21D5.7
Locus_4516_Transcript_1/1_Conf_1.000	574	0							
Locus_4517_Transcript_1/1_Conf_1.000	833	20	7.71E-54	ACI49101.1	58	214.927	282	166	hypothetical protein Cbre_JD13.003

Locus_4518_Transcript_1/1_Conf_1.000	1575	2	1.46E-27	NP_505209.2	41	129.028	517	215	hypothetical protein F25G6.9
Locus_4519_Transcript_1/1_Conf_1.000	1105	13	2.74E-61	NP_505472.1	57	240.35	312	180	hypothetical protein F25B3.2
Locus_452_Transcript_1/1_Conf_1.000	1284	20	1.99E-77	XP_001900502.1	89	294.278	178	160	High mobility group protein 1.2
Locus_4520_Transcript_1/1_Conf_1.000	1095	3	7.17E-38	NP_492450.2	52	162.54	261	136	hypothetical protein ZK858.5
Locus_4521_Transcript_1/1_Conf_1.000	1563	20	4.81E-132	XP_002637141.1	67	476.093	530	359	C. briggsae CBR-VPS-54 protein
Locus_4522_Transcript_1/1_Conf_1.000	171	10	1.02E-06	NP_493023.1	81	56.6102	37	30	hypothetical protein R09B3.3
Locus_4523_Transcript_1/1_Conf_1.000	242	20	9.79E-34	XP_002641514.1	89	146.362	78	70	Hypothetical protein CBG09809
Locus_4524_Transcript_1/1_Conf_1.000	1195	20	1.37E-85	NP_001122662.1	71	321.242	284	202	hypothetical protein Y51H1A.1
Locus_4525_Transcript_1/1_Conf_1.000	133	20	6.37E-17	XP_002923730.1	100	90.5077	44	44	PREDICTED: heterogeneous nuclear ribonucleoprotein U-like protein 1-like
Locus_4526_Transcript_1/1_Conf_1.000	637	0							
Locus_4527_Transcript_1/1_Conf_1.000	483	20	9.88E-58	NP_497892.1	94	226.098	119	112	PeRoxireDoXin family member (prdx-3)

Locus_4528_Transcript_1/1_Conf_1.000	674	20	2.35E-51	NP_498232.3	62	206.068	240	151	hypothetical protein B0336.11
Locus_4529_Transcript_1/1_Conf_1.000	431	20	4.01E-11	EFO22187.1	52	71.2478	121	63	hypothetical protein LOAG_06297
Locus_453_Transcript_1/1_Conf_1.000	592	20	7.67E-68	NP_501876.2	79	260.381	197	157	Enoyl-CoA Hydratase family member (ech-8)
Locus_4530_Transcript_1/1_Conf_1.000	966	20	3.07E-87	NP_493559.1	87	326.25	189	166	hypothetical protein K05C4.2
Locus_4531_Transcript_1/1_Conf_1.000	1373	20	2.68E-176	XP_002630542.1	84	622.854	434	365	Hypothetical protein CBG12983
Locus_4532_Transcript_1/2_Conf_1.000	925	20	8.97E-65	XP_002630642.1	68	251.521	250	170	Hypothetical protein CBG02311
Locus_4532_Transcript_2/2_Conf_1.000	932	20	9.08E-65	XP_002630642.1	68	251.521	250	170	Hypothetical protein CBG02311
Locus_4533_Transcript_1/1_Conf_1.000	196	0							
Locus_4534_Transcript_1/1_Conf_1.000	806	2	8.46E-10	XP_002642839.1	48	68.5514	146	71	Hypothetical protein CBG21243
Locus_4535_Transcript_1/1_Conf_1.000	164	10	5.63E-13	NP_001129757.1	77	77.411	54	42	hypothetical protein C31H5.6
Locus_4536_Transcript_1/1_Conf_1.000	1471	20	1.24E-174	XP_002633787.1	80	617.461	439	355	C. briggsae CBR-FAT-3 protein
Locus_4537_Transcript_1/1_Conf_1.000	617	0							
Locus_4538_Transcript_1/1_Conf_1.000	511	0							
Locus_4539_Transcript_1/1_Conf_1.000	1568	20	4.91E-68	XP_001901161.1	68	263.462	264	181	EF hand family protein
Locus_454_Transcript_1/1_Conf_1.000	327	0							
Locus_4540_Transcript_1/1_Conf_1.000	323	20	5.24E-43	XP_002638500.1	84	177.178	106	90	C. briggsae CBR-SSU-1 protein
Locus_4541_Transcript_1/1_Conf_1.000	1282	20	3.42E-146	XP_002639894.1	80	522.702	422	341	C. briggsae CBR-CDC-48.3 protein
Locus_4542_Transcript_1/1_Conf_1.000	581	0							
Locus_4543_Transcript_1/1_Conf_1.000	179	2	1.46E-05	NP_499455.1	74	52.7582	43	32	Tumorous Enhancer of Glp-1(gf) family member (teg-1)
Locus_4544_Transcript_1/1_Conf_1.000	2302	20	5.16E-51	NP_001122786.1	52	207.608	376	199	abnormal GONad development family member (gon-4)

Locus_4545_Transcript_1/1_Conf_1.000	275	7	3.49E-23	NP_499632.1	76	111.309	81	62	hypothetical protein Y111B2A.2
Locus_4546_Transcript_1/1_Conf_1.000	312	1	2.93E-17	NP_001023963.1	82	91.6633	64	53	hypothetical protein F53F4.16
Locus_4547_Transcript_1/2_Conf_1.000	1312	20	2.19E-79	NP_495428.1	64	300.827	386	250	PyroPhosPhorylase family member (ppp-1)
Locus_4547_Transcript_2/2_Conf_1.000	1312	20	4.88E-79	NP_495428.1	64	299.671	386	250	PyroPhosPhorylase family member (ppp-1)
Locus_4548_Transcript_1/1_Conf_1.000	142	0							
Locus_4549_Transcript_1/1_Conf_1.000	1178	20	3.11E-175	AAT06310.2	90	619.002	392	355	putative calcium-independent phospholipase A2 isoform a
Locus_455_Transcript_1/2_Conf_1.000	1431	20	6.19E-123	XP_002633002.1	68	445.662	485	331	Hypothetical protein CBG21768
Locus_455_Transcript_2/2_Conf_1.000	378	2	2.36E-11	XP_002633002.1	55	72.0182	127	71	Hypothetical protein CBG21768

Locus_4550_Transcript_1/1_Conf_1.000	210	20	4.12E-16	XP_509413.2	100	87.8113	40	40	PREDICTED: similar to phosphatidylethanolamine binding protein
Locus_4551_Transcript_1/1_Conf_1.000	188	0							
Locus_4552_Transcript_1/1_Conf_1.000	890	20	1.92E-61	XP_001894591.1	68	240.35	230	157	Twik (KCNK-like) family of potassium channels, alpha subunit 5
Locus_4553_Transcript_1/1_Conf_1.000	356	20	2.69E-15	EFO21183.1	67	85.1149	118	80	cell cycle-regulated factor p78
Locus_4554_Transcript_1/1_Conf_1.000	1702	20	5.85E-78	EFO19556.1	65	296.59	331	217	hypothetical protein LOAG_08937
Locus_4555_Transcript_1/1_Conf_1.000	458	0							

Locus_4556_Transcript_1/2_Conf_1.000	307	20	1.72E-22	XP_001901402.1	76	108.997	82	63	SacI homology domain containing protein
Locus_4556_Transcript_2/2_Conf_1.000	991	20	2.86E-128	XP_001901402.1	79	462.611	335	267	SacI homology domain containing protein
Locus_4557_Transcript_1/1_Conf_1.000	354	20	4.59E-15	NP_496453.1	60	84.3445	101	61	TransThyretin-Related family domain family member (ttr-18)
Locus_4558_Transcript_1/1_Conf_1.000	295	20	3.64E-28	AAB62695.1	90	127.872	98	89	P-type ATPase
Locus_4559_Transcript_1/1_Conf_1.000	1358	20	2.74E-48	XP_002645668.1	60	197.593	293	177	C. briggsae CBR-DYC-1 protein
Locus_456_Transcript_1/1_Conf_1.000	1545	20	5.99E-119	CBL87054.2	67	432.565	510	345	C. elegans protein F54E4.1, partially confirmed by transcript evidence
Locus_4560_Transcript_1/1_Conf_1.000	200	0							

Locus_4561_Transcript_1/1_Conf_1.000	652	0							
Locus_4562_Transcript_1/1_Conf_1.000	347	20	1.77E-14	AAD51334.1	77	82.4185	54	42	Kunitz type serine protease inhibitor
Locus_4563_Transcript_1/3_Conf_0.714	1713	4	3.77E-16	XP_002642660.1	38	91.2781	348	133	Hypothetical protein CBG12241
Locus_4563_Transcript_2/3_Conf_0.714	1731	4	8.45E-16	XP_002642660.1	41	90.1225	285	119	Hypothetical protein CBG12241
Locus_4563_Transcript_3/3_Conf_0.714	1746	4	8.55E-16	XP_002642660.1	41	90.1225	285	119	Hypothetical protein CBG12241
Locus_4564_Transcript_1/1_Conf_1.000	566	20	3.84E-71	NP_495527.2	80	271.166	178	144	hypothetical protein F45E12.5
Locus_4565_Transcript_1/1_Conf_1.000	817	20	3.11E-68	XP_001892948.1	81	262.692	186	151	Nuclear movement protein
Locus_4566_Transcript_1/1_Conf_1.000	1323	20	1.13E-91	EFO22421.1	68	341.658	342	234	hypothetical protein LOAG_06064
Locus_4567_Transcript_1/1_Conf_1.000	944	20	3.64E-69	XP_002637052.1	61	266.159	307	189	C. briggsae CBR-TAG-143 protein
Locus_4568_Transcript_1/1_Conf_1.000	809	20	3.86E-95	NP_499340.1	87	352.058	224	196	hypothetical protein Y39A1A.6
Locus_4569_Transcript_1/2_Conf_1.000	435	0							
Locus_4569_Transcript_2/2_Conf_1.000	313	0							
Locus_457_Transcript_1/1_Conf_1.000	844	20	3.50E-53	XP_002723895.1	97	154.836	76	74	PREDICTED: hypothetical protein
Locus_4570_Transcript_1/1_Conf_1.000	2146	20	0	XP_002640017.1	76	882.478	701	536	Hypothetical protein CBG12487
Locus_4571_Transcript_1/1_Conf_1.000	198	0							
Locus_4572_Transcript_1/1_Conf_1.000	293	0							
Locus_4573_Transcript_1/1_Conf_1.000	1573	20	1.15E-141	NP_495226.1	87	508.064	374	329	hypothetical protein C29H12.2

Locus_4574_Transcript_1/1_Conf_1.000	481	20	3.40E-79	AAH82286.1	96	297.36	157	152	Rps16 protein
Locus_4575_Transcript_1/1_Conf_1.000	261	0							
Locus_4576_Transcript_1/1_Conf_1.000	250	20	9.69E-34	EFO25239.1	92	146.362	82	76	nonsense mRNA reducing factor 1 NORF1
Locus_4577_Transcript_1/1_Conf_1.000	684	10	1.15E-16	NP_499594.2	55	90.8929	177	98	TIMeless (Drosophila/mammal) related family member (tim-1)
Locus_4578_Transcript_1/2_Conf_1.000	1889	20	9.79E-130	XP_002629661.1	80	468.774	356	288	C. briggsae CBR-MEL-11 protein
Locus_4578_Transcript_2/2_Conf_1.000	939	20	9.05E-20	NP_001021929.1	70	102.064	106	75	Maternal Effect Lethal family member (mel-11)
Locus_4579_Transcript_1/2_Conf_1.000	696	0							
Locus_4579_Transcript_2/2_Conf_1.000	657	0							
Locus_458_Transcript_1/1_Conf_1.000	2445	20	0	NP_505188.3	77	1075.85	818	636	PeroXidasiN (Drosophila peroxidase) homolog family member (pxn-1)
Locus_4580_Transcript_1/1_Conf_1.000	1626	20	2.41E-166	XP_002642943.1	88	590.112	378	336	Hypothetical protein CBG15221
Locus_4581_Transcript_1/2_Conf_1.000	1656	20	1.23E-48	EFO24260.1	53	199.134	324	172	hypothetical protein LOAG_04229
Locus_4581_Transcript_2/2_Conf_1.000	1662	20	1.23E-48	EFO24260.1	53	199.134	324	172	hypothetical protein LOAG_04229

Locus_4582_Transcript_1/1_Conf_1.000	1306	20	4.12E-62	XP_002643053.1	69	243.432	235	164	C. briggsae CBR-IDI-1 protein
Locus_4583_Transcript_1/1_Conf_1.000	482	20	1.27E-17	CAO00417.1	72	92.8189	80	58	two-domain activation associated secreted protein ASP4 precursor
Locus_4584_Transcript_1/1_Conf_1.000	312	0							
Locus_4585_Transcript_1/1_Conf_1.000	452	4	1.63E-12	XP_001894575.1	61	75.8702	93	57	MGC80099 protein
Locus_4586_Transcript_1/1_Conf_1.000	1067	5	3.64E-39	XP_002639270.1	53	166.777	310	166	Hypothetical protein CBG03832
Locus_4587_Transcript_1/1_Conf_1.000	587	15	1.11E-18	NP_510576.2	61	97.0561	127	78	hypothetical protein K09E9.1
Locus_4588_Transcript_1/1_Conf_1.000	1444	20	1.09E-167	NP_500801.2	83	594.349	437	363	hypothetical protein ZK616.4
Locus_4589_Transcript_1/1_Conf_1.000	857	20	8.75E-40	NP_496722.1	53	168.318	277	149	hypothetical protein Y46G5A.18
Locus_459_Transcript_1/1_Conf_1.000	698	20	2.01E-72	NP_001021128.1	82	276.174	185	153	PhosphatidylSerine Decarboxylase family member (psd-1)
Locus_4590_Transcript_1/1_Conf_1.000	145	0							
Locus_4591_Transcript_1/1_Conf_1.000	566	0							
Locus_4592_Transcript_1/3_Conf_0.667	1744	2	4.47E-57	XP_002640509.1	48	227.254	593	285	C. briggsae CBR-RGA-2 protein
Locus_4592_Transcript_2/3_Conf_0.667	1962	20	1.89E-83	XP_002640509.1	51	315.079	666	342	C. briggsae CBR-RGA-2 protein
Locus_4592_Transcript_3/3_Conf_0.667	1962	20	5.87E-85	XP_002640509.1	51	320.087	665	343	C. briggsae CBR-RGA-2 protein
Locus_4593_Transcript_1/1_Conf_1.000	308	20	9.17E-16	XP_002640530.1	77	86.6557	63	49	Hypothetical protein CBG18692
Locus_4594_Transcript_1/1_Conf_1.000	1520	20	6.84E-67	AAF04557.1	58	259.61	391	227	AF177870_1putative PP2C protein phosphatase FEM-2
Locus_4595_Transcript_1/1_Conf_1.000	1642	20	4.33E-147	NP_495411.2	66	526.168	527	350	hypothetical protein C44B7.2

Locus_4596_Transcript_1/1_Conf_1.000	2185	20	8.04E-22	EFO26676.1	50	110.538	224	113	hypothetical protein LOAG_01812
Locus_4597_Transcript_1/1_Conf_1.000	166	2	9.28E-08	XP_001900302.1	77	60.077	48	37	MSP domain protein
Locus_4598_Transcript_1/1_Conf_1.000	1087	20	6.27E-111	NP_001024378.1	75	405.216	365	275	P21-Activated Kinase family member (pak-1)
Locus_4599_Transcript_1/1_Conf_1.000	1107	20	5.51E-86	NP_001024374.1	86	322.398	207	180	Heat Shock Protein family member (hsp-25)
Locus_46_Transcript_1/4_Conf_0.625	1770	20	2.81E-123	NP_510300.1	82	447.203	312	258	hypothetical protein F55F3.3
Locus_46_Transcript_2/4_Conf_0.625	2140	20	2.72E-123	NP_510300.1	81	447.588	320	262	hypothetical protein F55F3.3

Locus_46_Transcript_3/4_Conf_0.625	1792	20	4.86E-123	NP_510300.1	83	446.432	312	259	hypothetical protein F55F3.3
Locus_46_Transcript_4/4_Conf_0.625	1792	20	1.08E-122	NP_510300.1	82	445.277	312	258	hypothetical protein F55F3.3
Locus_460_Transcript_1/1_Conf_1.000	2043	20	0	NP_491994.2	80	902.508	688	555	hypothetical protein H06O01.2
Locus_4600_Transcript_1/1_Conf_1.000	411	0							
Locus_4601_Transcript_1/1_Conf_1.000	322	0							
Locus_4602_Transcript_1/1_Conf_1.000	1510	20	2.27E-155	NP_507906.1	82	553.518	384	318	Phasmid Socket Absent family member (psa-1)

Locus_4603_Transcript_1/1_Conf_1.000	1829	20	4.60E-177	NP_509122.1	71	625.935	615	439	hypothetical protein F38B6.4
Locus_4604_Transcript_1/1_Conf_1.000	549	20	3.51E-34	NP_741467.1	63	148.288	167	106	hypothetical protein C09G4.2
Locus_4605_Transcript_1/2_Conf_1.000	1170	20	1.87E-55	XP_001900783.1	62	221.09	256	161	Protein kinase domain containing protein
Locus_4605_Transcript_2/2_Conf_1.000	1205	20	1.95E-55	XP_001900783.1	62	221.09	256	161	Protein kinase domain containing protein
Locus_4606_Transcript_1/1_Conf_1.000	369	0							
Locus_4607_Transcript_1/3_Conf_0.429	230	0							
Locus_4607_Transcript_2/3_Conf_0.429	685	20	4.82E-15	NP_741604.1	55	85.5001	105	58	hypothetical protein T11A5.6
Locus_4607_Transcript_3/3_Conf_0.571	814	20	6.76E-15	NP_741604.1	55	85.5001	105	58	hypothetical protein T11A5.6
Locus_4608_Transcript_1/3_Conf_0.571	992	20	4.08E-58	XP_002636579.1	91	229.565	128	117	Hypothetical protein CBG23273

Locus_4608_Transcript_2/3_Conf_0.429	1023	20	4.31E-58	XP_002636579.1	91	229.565	128	117	Hypothetical protein CBG23273
Locus_4608_Transcript_3/3_Conf_0.429	949	20	2.65E-59	NP_505967.1	76	233.417	171	131	hypothetical protein F55A11.1
Locus_4609_Transcript_1/1_Conf_1.000	2472	20	2.37E-134	XP_001900503.1	70	484.567	471	332	Ubiquitin interaction motif family protein
Locus_461_Transcript_1/1_Conf_1.000	987	20	4.39E-129	ABP52061.1	99	465.307	255	254	ribosomal protein s4a
Locus_4610_Transcript_1/3_Conf_0.667	1174	20	1.15E-121	XP_002641869.1	71	441.039	399	287	C. briggsae CBR-TEN-1 protein
Locus_4610_Transcript_2/3_Conf_0.333	845	20	6.21E-91	XP_002641869.1	75	338.191	269	202	C. briggsae CBR-TEN-1 protein
Locus_4610_Transcript_3/3_Conf_0.500	1083	20	6.44E-116	XP_002641869.1	71	421.779	381	273	C. briggsae CBR-TEN-1 protein
Locus_4611_Transcript_1/1_Conf_1.000	178	0							
Locus_4612_Transcript_1/1_Conf_1.000	204	20	5.59E-21	NP_503392.2	88	103.99	68	60	hypothetical protein Y50D4A.4
Locus_4613_Transcript_1/2_Conf_1.000	2675	20	0	NP_001023309.1	65	701.819	786	513	Zygotic epidermal ENclosure defective family member (zen-4)
Locus_4613_Transcript_2/2_Conf_1.000	560	2	1.34E-04	XP_002572590.1	53	50.0618	58	31	rabkinesin-6-related
Locus_4614_Transcript_1/1_Conf_1.000	609	20	6.41E-68	XP_002647499.1	92	260.766	150	139	Hypothetical protein CBG06573

Locus_4615_Transcript_1/1_Conf_1.000	1016	20	1.40E-85	ABV03828.1	95	320.857	189	180	hypothetical protein
Locus_4616_Transcript_1/1_Conf_1.000	507	20	1.79E-33	XP_002631110.1	72	145.591	118	85	Hypothetical protein CBG02885
Locus_4617_Transcript_1/1_Conf_1.000	213	4	6.11E-20	XP_002640432.1	81	100.523	74	60	C. briggsae CBR-GRH-1 protein
Locus_4618_Transcript_1/1_Conf_1.000	352	0							
Locus_4619_Transcript_1/2_Conf_1.000	400	0							
Locus_4619_Transcript_2/2_Conf_1.000	352	0							
Locus_462_Transcript_1/1_Conf_1.000	4236	20	0	NP_498926.2	82	1436.01	1096	909	hypothetical protein ZK370.4
Locus_4620_Transcript_1/1_Conf_1.000	1177	0							
Locus_4621_Transcript_1/1_Conf_1.000	645								
Locus_4622_Transcript_1/1_Conf_1.000	800	20	6.75E-44	XP_002646141.1	70	181.8	177	124	Hypothetical protein CBG08021
Locus_4623_Transcript_1/1_Conf_1.000	567	20	1.95E-54	XP_002641356.1	74	215.698	182	136	Hypothetical protein CBG13210
Locus_4624_Transcript_1/2_Conf_1.000	1342	20	1.25E-45	EFO27300.1	55	188.734	276	152	hypothetical protein LOAG_01183
Locus_4624_Transcript_2/2_Conf_1.000	697	0							
Locus_4625_Transcript_1/3_Conf_0.714	1312	20	3.42E-40	NP_493727.1	46	170.629	470	219	hypothetical protein C24H12.5
Locus_4625_Transcript_2/3_Conf_0.714	1312	20	5.27E-41	NP_493727.1	46	173.326	470	220	hypothetical protein C24H12.5
Locus_4625_Transcript_3/3_Conf_0.714	1312	20	1.53E-40	NP_493727.1	46	171.785	470	219	hypothetical protein C24H12.5
Locus_4626_Transcript_1/1_Conf_1.000	538	0							
Locus_4627_Transcript_1/1_Conf_1.000	733	4	6.58E-08	EFO24085.1	49	62.003	205	101	hypothetical protein LOAG_04401
Locus_4628_Transcript_1/1_Conf_1.000	313	0							

Locus_4629_Transcript_1/1_Conf_1.000	2356	20	0	NP_499309.1	72	647.892	580	422	CULlin family member (cul-1)
Locus_463_Transcript_1/1_Conf_1.000	730	20	2.60E-73	NP_740998.1	80	279.256	212	171	hypothetical protein C25H3.7
Locus_4630_Transcript_1/1_Conf_1.000	255	2	2.82E-28	NP_491808.1	83	128.257	79	66	hypothetical protein C48E7.1
Locus_4631_Transcript_1/1_Conf_1.000	813	20	6.21E-77	NP_001022958.1	79	291.582	213	169	hypothetical protein Y82E9BR.14
Locus_4632_Transcript_1/1_Conf_1.000	1023	10	1.90E-05	XP_002632458.1	52	54.6842	84	44	Hypothetical protein CBG13680
Locus_4633_Transcript_1/1_Conf_1.000	385	20	3.03E-51	NP_491357.1	86	204.527	127	110	hypothetical protein ZK973.3
Locus_4634_Transcript_1/2_Conf_1.000	583	20	5.80E-20	BAB68205.1	71	101.293	109	78	keratin-like protein
Locus_4634_Transcript_2/2_Conf_1.000	583	20	5.80E-20	BAB68205.1	71	101.293	109	78	keratin-like protein
Locus_4635_Transcript_1/1_Conf_1.000	469	0							
Locus_4636_Transcript_1/1_Conf_1.000	674	20	8.69E-22	NP_741210.2	66	107.842	108	72	CYtoKinesis defect family member (cyk-1)
Locus_4637_Transcript_1/1_Conf_1.000	1654	20	1.05E-100	NP_510485.2	68	372.089	400	275	TBC (Tre-2/Bub2/Cdc16) domain family member (tbc-1)
Locus_4638_Transcript_1/2_Conf_1.000	1823	20	1.37E-72	XP_002638661.1	49	278.87	629	312	C. briggsae CBR-LIN-10 protein
Locus_4638_Transcript_2/2_Conf_1.000	1147	20	3.78E-45	XP_002638661.1	51	186.808	395	202	C. briggsae CBR-LIN-10 protein
Locus_4639_Transcript_1/1_Conf_1.000	1126	5	3.75E-05	CBK19446.1	49	53.9138	101	50	C. elegans protein F25H8.5f, partially confirmed by transcript evidence
Locus_464_Transcript_1/1_Conf_1.000	2760	20	0	NP_001024053.1	95	1477.23	918	874	UNCoordinated family member (unc-70)

Locus_4640_Transcript_1/1_Conf_1.000	370	20	1.14E-29	XP_002635292.1	88	132.88	85	75	Hypothetical protein CBG11539
Locus_4641_Transcript_1/1_Conf_1.000	997	20	7.06E-159	NP_492714.1	92	564.303	315	290	hypothetical protein ZC434.8
Locus_4642_Transcript_1/1_Conf_1.000	556	20	1.17E-40	NP_506225.1	77	169.859	136	105	TransThyretin-Related family domain family member (ttr-27)
Locus_4643_Transcript_1/3_Conf_0.714	1746	0							
Locus_4643_Transcript_2/3_Conf_0.714	1835	0							
Locus_4643_Transcript_3/3_Conf_0.714	1736	0							
Locus_4644_Transcript_1/1_Conf_1.000	682	20	1.04E-78	XP_002634015.1	91	296.975	171	156	Hypothetical protein CBG01548
Locus_4645_Transcript_1/1_Conf_1.000	465	0							
Locus_4646_Transcript_1/1_Conf_1.000	209	1	2.13E-04	XP_001891653.1	63	48.9062	55	35	2700029M09Rik protein
Locus_4647_Transcript_1/1_Conf_1.000	258	0							
Locus_4648_Transcript_1/1_Conf_1.000	235	0							
Locus_4649_Transcript_1/1_Conf_1.000	180	0							
Locus_465_Transcript_1/1_Conf_1.000	2975	0							
Locus_4650_Transcript_1/1_Conf_1.000	872	20	1.67E-110	NP_498925.1	83	403.29	273	227	Huntingtin Interacting Protein Related family member (hipr-1)
Locus_4651_Transcript_1/1_Conf_1.000	516	3	3.77E-18	NP_496534.1	54	94.7449	166	91	Nuclear Pore complex Protein family member (npp-3)
Locus_4652_Transcript_1/2_Conf_1.000	1460	20	7.38E-71	XP_002633363.1	64	272.707	331	215	Hypothetical protein CBG06107
Locus_4652_Transcript_2/2_Conf_1.000	1460	20	5.65E-71	XP_002633363.1	65	273.092	331	216	Hypothetical protein CBG06107
Locus_4653_Transcript_1/1_Conf_1.000	568	3	5.93E-11	ABB53347.1	46	71.2478	175	81	secreted protein 5 precursor

Locus_4654_Transcript_1/1_Conf_1.000	1548	20	0	XP_002642624.1	86	785.408	497	432	C. briggsae CBR-ALH-12 protein
Locus_4655_Transcript_1/2_Conf_1.000	2128	4	4.57E-38	NP_001022043.1	49	164.466	525	258	hypothetical protein C56E6.3
Locus_4655_Transcript_2/2_Conf_1.000	2128	4	4.57E-38	NP_001022043.1	49	164.466	525	258	hypothetical protein C56E6.3
Locus_4656_Transcript_1/1_Conf_1.000	1243	3	3.83E-86	XP_002636840.1	68	323.168	316	218	Hypothetical protein CBG09291
Locus_4657_Transcript_1/1_Conf_1.000	555	20	9.30E-22	EFO17919.1	59	107.071	149	88	hypothetical protein LOAG_10578
Locus_4658_Transcript_1/1_Conf_1.000	363	20	7.67E-47	EAW59538.1	96	189.889	106	102	hCG2043238
Locus_4659_Transcript_1/1_Conf_1.000	1415	20	1.91E-84	EFO18353.1	64	317.775	348	225	protein-tyrosine phosphatase
Locus_466_Transcript_1/1_Conf_1.000	874	20	6.27E-57	XP_002637708.1	66	225.328	253	168	Hypothetical protein CBG11573
Locus_4660_Transcript_1/1_Conf_1.000	1297	1	5.41E-06	EFO21658.1	48	56.9954	201	97	hypothetical protein LOAG_06829
Locus_4661_Transcript_1/1_Conf_1.000	1761	20	2.29E-117	XP_002636578.1	73	427.557	409	302	C. briggsae CBR-SYN-3 protein
Locus_4662_Transcript_1/1_Conf_1.000	1650	20	1.89E-150	CAB40412.1	75	537.339	478	362	hexokinase
Locus_4663_Transcript_1/2_Conf_0.667	150	0							
Locus_4663_Transcript_2/2_Conf_0.667	150	0							

Locus_4664_Transcript_1/1_Conf_1.000	128	0							
Locus_4665_Transcript_1/2_Conf_1.000	1242	20	1.93E-146	NP_510634.1	88	523.472	325	289	hypothetical protein ZK1073.1
Locus_4665_Transcript_2/2_Conf_1.000	1233	20	1.91E-146	NP_510634.1	89	523.472	322	288	hypothetical protein ZK1073.1
Locus_4666_Transcript_1/1_Conf_1.000	1129	2	2.00E-06	XP_001902477.1	42	58.151	291	123	hypothetical protein Bm1_55095
Locus_4667_Transcript_1/1_Conf_1.000	614	0							
Locus_4668_Transcript_1/1_Conf_1.000	913	20	1.65E-63	NP_496489.1	71	247.284	232	167	proteasome Regulatory Particle, Non-ATPase-like family member (rpn-12)
Locus_4669_Transcript_1/2_Conf_1.000	685	20	3.12E-22	NP_499554.1	75	109.383	113	85	TRanslocon-Associated Protein family member (trap-4)
Locus_4669_Transcript_2/2_Conf_1.000	685	20	2.02E-21	NP_499554.1	75	106.686	113	85	TRanslocon-Associated Protein family member (trap-4)
Locus_467_Transcript_1/3_Conf_0.571	794	20	3.43E-24	NP_492722.2	57	116.316	165	95	Temporarily Assigned Gene name family member (tag-353)
Locus_467_Transcript_2/3_Conf_0.714	1290	20	8.48E-44	NP_492722.2	48	182.57	404	197	Temporarily Assigned Gene name family member (tag-353)
Locus_467_Transcript_3/3_Conf_0.714	1233	20	2.18E-41	NP_492722.2	48	174.481	393	190	Temporarily Assigned Gene name family member (tag-353)
Locus_4670_Transcript_1/1_Conf_1.000	512	0							
Locus_4671_Transcript_1/3_Conf_0.667	2699	20	0	XP_002640712.1	79	1191.79	903	721	C. briggsae CBR-AGEF-1 protein

Locus_4671_Transcript_2/3_Conf_0.667	2697	20	0	XP_002640712.1	79	1182.55	903	719	C. briggsae CBR-AGEF-1 protein
Locus_4671_Transcript_3/3_Conf_0.667	2691	20	0	XP_002640712.1	79	1187.56	901	719	C. briggsae CBR-AGEF-1 protein
Locus_4672_Transcript_1/1_Conf_1.000	461	0							
Locus_4673_Transcript_1/1_Conf_1.000	812	16	2.51E-62	NP_508891.1	65	243.047	220	144	hypothetical protein Y34B4A.9
Locus_4674_Transcript_1/1_Conf_1.000	332	20	5.21E-27	NP_501808.1	82	124.02	107	88	hypothetical protein F44D12.3
Locus_4675_Transcript_1/1_Conf_1.000	360	20	3.26E-21	XP_001895511.1	97	104.76	75	73	histone H2A
Locus_4676_Transcript_1/1_Conf_1.000	1193	0							
Locus_4677_Transcript_1/1_Conf_1.000	372	20	5.44E-40	EFO24868.1	74	167.162	119	89	hypothetical protein LOAG_03617

Locus_4678_Transcript_1/1_Conf_1.000	951	20	7.29E-118	NP_493393.1	81	427.943	298	243	hypothetical protein W09C5.7
Locus_4679_Transcript_1/1_Conf_1.000	577	20	7.23E-76	NP_001023236.1	78	286.96	191	150	hypothetical protein F56H11.1
Locus_468_Transcript_1/2_Conf_1.000	124	0							
Locus_468_Transcript_2/2_Conf_1.000	117	0							
Locus_4680_Transcript_1/1_Conf_1.000	1582	20	3.65E-103	NP_501841.1	64	380.178	465	302	hypothetical protein K08F4.1
Locus_4681_Transcript_1/1_Conf_1.000	1624	20	1.21E-125	EFO23482.1	69	454.907	479	332	DIRP family protein
Locus_4682_Transcript_1/1_Conf_1.000	739	0							
Locus_4683_Transcript_1/1_Conf_1.000	284	0							
Locus_4684_Transcript_1/1_Conf_1.000	533	20	1.62E-86	AAX29372.1	100	322.013	158	158	ribosomal protein S11
Locus_4685_Transcript_1/1_Conf_1.000	552	20	2.83E-31	AAG22849.1	94	138.658	84	79	histone H3
Locus_4686_Transcript_1/1_Conf_1.000	443	20	9.28E-48	XP_002646073.1	78	192.971	144	113	Hypothetical protein CBG07939
Locus_4687_Transcript_1/1_Conf_1.000	451	0							
Locus_4688_Transcript_1/3_Conf_0.500	764	20	9.97E-95	EFB25528.1	100	350.517	172	172	hypothetical protein PANDA_002954

Locus_4688_Transcript_2/3_Conf_0.500	764	20	9.97E-95	EFB25528.1	100	350.517	172	172	hypothetical protein PANDA_002954
Locus_4688_Transcript_3/3_Conf_0.500	743	20	7.63E-52	XP_002819177.1	100	207.994	103	103	PREDICTED: translationally-controlled tumor protein-like isoform 1
Locus_4689_Transcript_1/2_Conf_1.000	232	0							
Locus_4689_Transcript_2/2_Conf_1.000	251	0							
Locus_469_Transcript_1/3_Conf_0.429	516	0							
Locus_469_Transcript_2/3_Conf_0.429	1128	20	1.11E-73	NP_503425.2	94	281.567	164	155	UNCoordinated family member (unc-60)
Locus_469_Transcript_3/3_Conf_0.429	1325	20	3.47E-32	NP_495483.1	82	144.05	97	80	hypothetical protein C27H5.3
Locus_4690_Transcript_1/2_Conf_1.000	430	0							
Locus_4690_Transcript_2/2_Conf_1.000	428	0							
Locus_4691_Transcript_1/1_Conf_1.000	313	1	9.78E-05	EDL84402.1	82	50.0618	52	43	procollagen, type I, alpha 2
Locus_4692_Transcript_1/1_Conf_1.000	449	0							
Locus_4693_Transcript_1/1_Conf_1.000	538	0							

Locus_4694_Transcript_1/1_Conf_1.000	279	20	2.10E-28	BAI45831.1	100	128.642	92	92	lipolysis stimulated lipoprotein receptor
Locus_4695_Transcript_1/1_Conf_1.000	1095	20	1.01E-116	XP_002639317.1	75	424.476	366	275	C. briggsae CBR-ABT-2 protein
Locus_4696_Transcript_1/1_Conf_1.000	420	10	1.03E-14	EFO27265.1	76	83.1889	65	50	hypothetical protein LOAG_01219
Locus_4697_Transcript_1/1_Conf_1.000	1227	20	1.61E-20	NP_497863.2	50	105.145	191	96	hypothetical protein R10E4.11
Locus_4698_Transcript_1/1_Conf_1.000	997	0							
Locus_4699_Transcript_1/2_Conf_1.000	3473	20	0	NP_495387.2	69	1041.95	881	610	hypothetical protein T13C2.6
Locus_4699_Transcript_2/2_Conf_1.000	3410	20	0	NP_495387.2	69	1046.57	890	615	hypothetical protein T13C2.6
Locus_47_Transcript_1/1_Conf_1.000	1662	20	1.84E-52	XP_002630615.1	53	211.846	394	210	Hypothetical protein CBG02280
Locus_470_Transcript_1/1_Conf_1.000	389	20	8.02E-12	XP_002589394.1	61	73.559	92	57	hypothetical protein BRAFLDRAFT_121800
Locus_4700_Transcript_1/1_Conf_1.000	714	20	7.23E-65	NP_499489.1	70	251.136	231	163	hypothetical protein Y66D12A.13
Locus_4701_Transcript_1/4_Conf_0.700	1192	20	9.95E-28	NP_001122519.1	70	129.028	140	99	hypothetical protein T19A6.3

Locus_4701_Transcript_2/4_Conf_0.700	1192	20	5.83E-28	NP_001122519.1	70	129.798	140	99	hypothetical protein T19A6.3
Locus_4701_Transcript_3/4_Conf_0.700	1186	20	5.79E-28	NP_001122519.1	70	129.798	140	99	hypothetical protein T19A6.3
Locus_4701_Transcript_4/4_Conf_0.700	1186	20	5.79E-28	NP_001122519.1	70	129.798	140	99	hypothetical protein T19A6.3
Locus_4702_Transcript_1/2_Conf_1.000	290	5	2.15E-28	NP_502016.2	87	128.642	83	73	hypothetical protein F13E9.1
Locus_4702_Transcript_2/2_Conf_1.000	291	5	2.14E-28	NP_502016.2	87	128.642	83	73	hypothetical protein F13E9.1
Locus_4703_Transcript_1/1_Conf_1.000	1421	1	7.49E-04	XP_505344.1	40	50.0618	124	50	YALI0F12793p
Locus_4704_Transcript_1/1_Conf_1.000	229	20	1.14E-29	XP_001082945.2	100	132.88	59	59	PREDICTED: 40S ribosomal protein S29-like, partial
Locus_4705_Transcript_1/1_Conf_1.000	671	20	2.84E-41	EFO25736.1	65	172.555	199	131	hypothetical protein LOAG_02750
Locus_4706_Transcript_1/12_Conf_1.000	161	0							
Locus_4706_Transcript_10/12_Conf_0.179	1059	0							
Locus_4706_Transcript_11/12_Conf_0.179	1059	0							
Locus_4706_Transcript_12/12_Conf_0.321	1011	0							
Locus_4706_Transcript_2/12_Conf_1.000	161	0							
Locus_4706_Transcript_3/12_Conf_0.179	1059	0							
Locus_4706_Transcript_4/12_Conf_0.179	1059	0							
Locus_4706_Transcript_5/12_Conf_0.321	1011	0							
Locus_4706_Transcript_6/12_Conf_0.286	1621	0							
Locus_4706_Transcript_7/12_Conf_0.286	1621	0							
Locus_4706_Transcript_8/12_Conf_0.179	1084	0							
Locus_4706_Transcript_9/12_Conf_0.179	1084	0							
Locus_4707_Transcript_1/1_Conf_1.000	1956	20	1.21E-114	P0C657.2	71	418.698	401	288	Mediator of RNA polymerase II transcription subunit 13
Locus_4708_Transcript_1/1_Conf_1.000	1394	20	2.39E-164	XP_002642536.1	79	583.178	466	371	C. briggsae CBR-LRS-1 protein
Locus_4709_Transcript_1/1_Conf_1.000	677	20	1.34E-54	AAK29933.3	68	216.853	224	154	Rab connectin related protein 2, partially confirmed by transcript evidence

Locus_471_Transcript_1/1_Conf_1.000	1304	20	6.27E-95	NP_741757.1	84	352.443	240	203	Endophilin-Related Protein family member (erp-1)
Locus_4710_Transcript_1/1_Conf_1.000	1237	20	4.48E-95	NP_501006.1	78	352.829	298	234	DNaJ domain (prokaryotic heat shock protein) family member (dnj-11)
Locus_4711_Transcript_1/1_Conf_1.000	204	0							
Locus_4712_Transcript_1/1_Conf_1.000	502	0							
Locus_4713_Transcript_1/1_Conf_1.000	1224	20	7.38E-50	NP_492079.1	55	202.601	362	200	INneXin family member (inx-14)
Locus_4714_Transcript_1/1_Conf_1.000	858	7	2.71E-73	XP_002630128.1	78	279.641	226	177	Hypothetical protein CBG00530
Locus_4715_Transcript_1/1_Conf_1.000	1395	20	4.77E-96	XP_002639374.1	60	356.295	461	279	Hypothetical protein CBG03958
Locus_4716_Transcript_1/1_Conf_1.000	402	3	8.09E-28	XP_002643229.1	64	126.716	130	84	Hypothetical protein CBG08094
Locus_4717_Transcript_1/1_Conf_1.000	399	5	1.88E-16	AAL77521.1	86	88.9669	59	51	L80003_1guanylyl cyclase
Locus_4718_Transcript_1/1_Conf_1.000	412	0							
Locus_4719_Transcript_1/1_Conf_1.000	1150	20	3.76E-85	NP_509396.1	66	319.701	374	247	Kinase Suppressor of activated Ras family member (ksr-1)
Locus_472_Transcript_1/1_Conf_1.000	357	20	4.56E-54	XP_001231536.1	97	184.496	89	87	PREDICTED: similar to Ac1147
Locus_4720_Transcript_1/1_Conf_1.000	306	0							
Locus_4721_Transcript_1/1_Conf_1.000	186	0							
Locus_4722_Transcript_1/1_Conf_1.000	260	20	2.01E-26	XP_002629686.1	66	122.094	86	57	Hypothetical protein CBG00906

Locus_4723_Transcript_1/3_Conf_0.600	2038	20	7.76E-96	XP_002639673.1	74	356.295	325	242	Hypothetical protein CBG12391
Locus_4723_Transcript_2/3_Conf_0.400	785	20	2.59E-109	ACD85815.1	91	399.053	251	229	forkhead transcription factor DAF-16
Locus_4723_Transcript_3/3_Conf_0.600	2696	20	6.63E-170	XP_002639673.1	73	602.823	549	406	Hypothetical protein CBG12391

Locus_4724_Transcript_1/1_Conf_1.000	792	20	3.05E-89	NP_509768.1	89	332.413	221	198	SYnapse Defective family member (syd-2)
Locus_4725_Transcript_1/1_Conf_1.000	497	20	7.99E-36	NP_498091.1	68	153.295	148	102	hypothetical protein Y54H5A.1
Locus_4726_Transcript_1/1_Conf_1.000	469	19	3.90E-14	NP_001022134.1	54	81.2629	150	81	hypothetical protein F32A5.1
Locus_4727_Transcript_1/1_Conf_1.000	753	20	1.36E-80	EFO15635.1	73	303.523	257	190	histone deacetylase 7A
Locus_4728_Transcript_1/1_Conf_1.000	316	1	2.83E-12	NP_497506.3	62	75.0998	96	60	hypothetical protein Y48G9A.3
Locus_4729_Transcript_1/1_Conf_1.000	1142	20	2.85E-77	XP_002639579.1	72	293.508	287	207	C. briggsae CBR-COGC-3 protein
Locus_473_Transcript_1/1_Conf_1.000	1200	20	1.82E-45	NP_001021222.1	83	187.963	123	103	hypothetical protein C46F11.6
Locus_4730_Transcript_1/1_Conf_1.000	434	8	3.72E-25	EFO25373.1	90	117.857	71	64	laterally symmetric protein 2
Locus_4731_Transcript_1/1_Conf_1.000	792	0							
Locus_4732_Transcript_1/1_Conf_1.000	640	0							
Locus_4733_Transcript_1/1_Conf_1.000	843	20	2.38E-58	XP_002636734.1	82	229.95	187	154	Hypothetical protein CBG23457

Locus_4734_Transcript_1/1_Conf_1.000	693	0							
Locus_4735_Transcript_1/1_Conf_1.000	1299	20	6.84E-17	XP_001686160.1	45	93.2041	337	154	hypothetical protein
Locus_4736_Transcript_1/1_Conf_1.000	171	20	6.59E-14	NP_001033378.1	82	80.4925	56	46	Acyl CoA DeHydrogenase family member (acdh-11)
Locus_4737_Transcript_1/1_Conf_1.000	313	0							
Locus_4738_Transcript_1/1_Conf_1.000	226	0							
Locus_4739_Transcript_1/1_Conf_1.000	1066	4	2.62E-13	NP_001022570.1	45	80.8777	286	131	CYLinDromatosis (human disease gene) homolog family member (cyld-1)
Locus_474_Transcript_1/1_Conf_1.000	1263	20	3.54E-71	XP_002638777.1	57	273.478	384	219	C. briggsae CBR-NAS-30 protein
Locus_4740_Transcript_1/1_Conf_1.000	267	20	2.06E-15	NP_510369.2	66	85.5001	78	52	CYtochrome P450 family member (cyp-13B2)
Locus_4741_Transcript_1/1_Conf_1.000	2195	20	0	XP_002641659.1	81	660.603	475	387	C. briggsae CBR-CNX-1 protein
Locus_4742_Transcript_1/1_Conf_1.000	307	0							
Locus_4743_Transcript_1/2_Conf_0.500	620	20	6.23E-74	XP_002631314.1	92	280.796	164	151	C. briggsae CBR-LDH-1 protein
Locus_4743_Transcript_2/2_Conf_0.750	1200	20	1.27E-155	XP_002631314.1	93	553.903	333	311	C. briggsae CBR-LDH-1 protein
Locus_4744_Transcript_1/1_Conf_1.000	913	3	3.02E-57	XP_002644945.1	79	226.483	165	131	C. briggsae CBR-GEI-15 protein
Locus_4745_Transcript_1/1_Conf_1.000	736	20	1.51E-52	XP_002637823.1	75	210.305	169	128	Hypothetical protein CBG04612

Locus_4746_Transcript_1/1_Conf_1.000	353	0							
Locus_4747_Transcript_1/1_Conf_1.000	494	20	5.06E-14	EFO19472.1	76	80.8777	55	42	hypothetical protein LOAG_09023
Locus_4748_Transcript_1/1_Conf_1.000	200	20	7.86E-15	EFO25038.1	73	83.5741	57	42	ribosomal protein rps15a
Locus_4749_Transcript_1/1_Conf_1.000	1128	20	6.10E-72	NP_001122953.1	64	275.789	334	217	hypothetical protein F53H10.2
Locus_475_Transcript_1/1_Conf_1.000	1129	20	1.09E-137	XP_002642128.1	87	494.197	324	285	Hypothetical protein CBG18075
Locus_4750_Transcript_1/1_Conf_1.000	1415	3	5.70E-04	EFN86671.1	47	50.447	104	49	hypothetical protein EAI_03706
Locus_4751_Transcript_1/1_Conf_1.000	211	0							
Locus_4752_Transcript_1/1_Conf_1.000	216	20	1.50E-10	NP_501645.1	81	69.3218	43	35	hypothetical protein T20D3.8
Locus_4753_Transcript_1/1_Conf_1.000	257	20	3.56E-23	XP_002642088.1	86	111.309	67	58	C. briggsae CBR-SEL-2 protein
Locus_4754_Transcript_1/1_Conf_1.000	451	20	5.05E-30	XP_002642343.1	65	134.035	158	103	C. briggsae CBR-CNT-2 protein

Locus_4755_Transcript_1/1_Conf_1.000	334	20	9.46E-29	XP_002640337.1	80	129.798	102	82	Hypothetical protein CBG12886
Locus_4756_Transcript_1/1_Conf_1.000	659	20	5.18E-56	A8Y1R8.2	86	221.476	144	124	Nuclear cap-binding protein subunit 2
Locus_4757_Transcript_1/1_Conf_1.000	361	4	5.57E-13	NP_491231.2	59	77.411	103	61	hypothetical protein C32E8.11
Locus_4758_Transcript_1/1_Conf_1.000	2090	20	2.93E-106	XP_001897036.1	72	390.963	517	373	Laminin-like protein C54D1.5 precursor
Locus_4759_Transcript_1/1_Conf_1.000	518	3	2.21E-18	XP_001896542.1	55	95.5153	186	104	hypothetical protein Bm1_25410
Locus_476_Transcript_1/1_Conf_1.000	449	0							
Locus_4760_Transcript_1/1_Conf_1.000	687	20	6.92E-70	NP_505399.1	76	267.7	229	175	hypothetical protein ZK682.2
Locus_4761_Transcript_1/1_Conf_1.000	258	4	2.47E-08	EFO22604.1	67	62.003	76	51	RPN-3 protein
Locus_4762_Transcript_1/1_Conf_1.000	650	20	1.67E-51	NP_506166.1	75	206.453	169	128	hypothetical protein W05B10.4
Locus_4763_Transcript_1/1_Conf_1.000	407	20	1.05E-43	NP_001023224.1	96	179.489	84	81	EGg Laying defective family member (egl-4)
Locus_4764_Transcript_1/1_Conf_1.000	289	20	3.79E-33	XP_002637628.1	84	144.436	96	81	Hypothetical protein CBG19373
Locus_4765_Transcript_1/1_Conf_1.000	485	20	4.02E-51	XP_002639970.1	80	204.142	150	120	C. briggsae CBR-LFE-2 protein
Locus_4766_Transcript_1/1_Conf_1.000	963	0							
Locus_4767_Transcript_1/1_Conf_1.000	945	20	3.54E-72	XP_001901072.1	74	276.174	254	190	Negative elongation factor C/D
Locus_4768_Transcript_1/1_Conf_1.000	800	0							

Locus_4769_Transcript_1/1_Conf_1.000	316	0							
Locus_477_Transcript_1/1_Conf_1.000	610	20	1.12E-88	NP_497791.1	86	329.717	202	175	NITrilase family member (nit-1)
Locus_4770_Transcript_1/1_Conf_1.000	1491	5	1.56E-07	XP_002641851.1	56	62.3882	87	49	C. briggsae CBR-WIP-1 protein
Locus_4771_Transcript_1/1_Conf_1.000	450	3	5.07E-14	NP_001024707.1	55	80.8777	141	78	UNCoordinated family member (unc-84)
Locus_4772_Transcript_1/1_Conf_1.000	804	20	1.24E-85	XP_002632607.1	98	320.472	163	161	C. briggsae CBR-ARL-8 protein
Locus_4773_Transcript_1/1_Conf_1.000	329	20	2.05E-31	XP_001895767.1	77	138.658	109	84	ncbp1-prov protein-like
Locus_4774_Transcript_1/1_Conf_1.000	337	0							
Locus_4775_Transcript_1/2_Conf_1.000	1921	20	0	NP_491281.1	79	646.351	499	396	Alanyl tRNA Synthetase family member (ars-2)

Locus_4775_Transcript_2/2_Conf_1.000	3179	20	0	NP_491281.1	86	1490.71	968	833	Alanyl tRNA Synthetase family member (ars-2)
Locus_4776_Transcript_1/1_Conf_1.000	402	20	9.30E-08	XP_001945955.1	57	60.077	85	49	PREDICTED: similar to conserved hypothetical protein
Locus_4777_Transcript_1/1_Conf_1.000	342	5	1.96E-13	AAL35733.2	65	78.9518	82	54	AC103567_7Hypothetical protein Y51F10.6
Locus_4778_Transcript_1/1_Conf_1.000	129	0							
Locus_4779_Transcript_1/1_Conf_1.000	398	1	8.48E-09	NP_741716.2	67	63.5438	80	54	hypothetical protein F55A4.8
Locus_478_Transcript_1/1_Conf_1.000	547	20	2.54E-53	XP_002633479.1	79	211.846	173	137	Hypothetical protein CBG06250
Locus_4780_Transcript_1/1_Conf_1.000	325	20	2.97E-30	EFO19570.1	80	134.806	91	73	MH2 domain-containing protein
Locus_4781_Transcript_1/1_Conf_1.000	1553	20	3.97E-179	NP_001033376.1	84	632.484	408	343	hypothetical protein Y39E4A.3
Locus_4782_Transcript_1/1_Conf_1.000	535	0							
Locus_4783_Transcript_1/1_Conf_1.000	258	0							
Locus_4784_Transcript_1/1_Conf_1.000	484	0							
Locus_4785_Transcript_1/1_Conf_1.000	247	0							
Locus_4786_Transcript_1/1_Conf_1.000	129	0							
Locus_4787_Transcript_1/2_Conf_1.000	2230	20	2.20E-91	CAA92687.2	57	341.658	624	357	C. elegans protein T01H3.3, confirmed by transcript evidence
Locus_4787_Transcript_2/2_Conf_1.000	2230	20	6.40E-91	CAA92687.2	57	340.117	624	357	C. elegans protein T01H3.3, confirmed by transcript evidence
Locus_4788_Transcript_1/1_Conf_1.000	301	0							
Locus_4789_Transcript_1/2_Conf_1.000	1881	20	2.01E-58	NP_740838.1	49	231.876	616	303	hypothetical protein C44E4.1
Locus_4789_Transcript_2/2_Conf_1.000	2508	20	1.69E-87		50	328.946	792	403	protein C44E4.1a

Locus_479_Transcript_1/1_Conf_1.000	669	20	3.68E-73	NP_493394.1	88	278.485	177	156	hypothetical protein W09C5.8
Locus_4790_Transcript_1/1_Conf_1.000	719	20	1.81E-39	XP_001900667.1	69	166.777	162	112	Hypothetical 26.6 kDa protein T19C3.4 in chromosome III, putative
Locus_4791_Transcript_1/1_Conf_1.000	1444	20	9.67E-124	XP_002646894.1	72	448.358	482	348	Hypothetical protein CBG19592
Locus_4792_Transcript_1/2_Conf_1.000	411	0							
Locus_4792_Transcript_2/2_Conf_1.000	520	0							
Locus_4793_Transcript_1/1_Conf_1.000	1470	20	1.41E-170	EFO22286.1	85	603.979	415	353	hypothetical protein LOAG_06198
Locus_4794_Transcript_1/1_Conf_1.000	402	20	3.29E-21	CAN99691.2	65	104.76	140	91	C. elegans protein F54B3.1b, partially confirmed by transcript evidence
Locus_4795_Transcript_1/1_Conf_1.000	392	20	2.91E-38	XP_001897484.1	100	161.384	75	75	Dynein light chain 1, cytoplasmic
Locus_4796_Transcript_1/1_Conf_1.000	753	8	1.34E-19	NP_001122567.1	63	100.908	118	75	hypothetical protein ZK484.1
Locus_4797_Transcript_1/1_Conf_1.000	608	0							
Locus_4798_Transcript_1/1_Conf_1.000	334	0							
Locus_4799_Transcript_1/1_Conf_1.000	290	5	3.01E-14	XP_002639656.1	73	81.6481	65	48	Hypothetical protein CBG12372
Locus_48_Transcript_1/3_Conf_0.714	2079	20	0	NP_001022777.1	83	854.744	574	480	Prolyl tRNA Synthetase family member (prs-1)
Locus_48_Transcript_2/3_Conf_0.714	2079	20	0	NP_001022777.1	83	856.67	574	480	Prolyl tRNA Synthetase family member (prs-1)

Locus_48_Transcript_3/3_Conf_0.714	2079	20	0	NP_001022777.1	83	856.67	574	480	Prolyl tRNA Synthetase family member (prs-1)
Locus_480_Transcript_1/1_Conf_1.000	391	5	2.73E-28	XP_002629758.1	72	128.257	108	78	Hypothetical protein CBG00994
Locus_4800_Transcript_1/1_Conf_1.000	223	20	2.28E-26	XP_002825112.1	96	98.2117	51	49	PREDICTED: 40S ribosomal protein SA-like, partial
Locus_4801_Transcript_1/3_Conf_0.500	823	20	2.30E-119	NP_001122815.1	89	432.565	264	236	STAT transcription factor family member (sta-1)
Locus_4801_Transcript_2/3_Conf_0.500	823	20	2.30E-119	NP_001122815.1	89	432.565	264	236	STAT transcription factor family member (sta-1)
Locus_4801_Transcript_3/3_Conf_0.333	385	0							
Locus_4802_Transcript_1/2_Conf_1.000	639	20	5.56E-28	XP_002642547.1	81	128.257	96	78	Hypothetical protein CBG20173
Locus_4802_Transcript_2/2_Conf_1.000	636	20	5.49E-28	XP_002642547.1	81	128.257	96	78	Hypothetical protein CBG20173

Locus_4803_Transcript_1/1_Conf_1.000	791	20	1.35E-105	XP_001898121.1	86	386.726	253	220	Cab39 protein
Locus_4804_Transcript_1/1_Conf_1.000	428	20	5.41E-32	NP_507590.2	65	140.584	137	90	hypothetical protein C08E8.2
Locus_4805_Transcript_1/2_Conf_1.000	2576	20	0	NP_498362.1	90	1243.02	743	669	hypothetical protein T12A2.2
Locus_4805_Transcript_2/2_Conf_1.000	2576	20	0	NP_498362.1	90	1243.02	743	669	hypothetical protein T12A2.2
Locus_4806_Transcript_1/1_Conf_1.000	660	20	8.27E-38	NP_001022574.1	73	160.999	136	100	hypothetical protein F42A10.9

Locus_4807_Transcript_1/2_Conf_1.000	794	20	1.05E-89	NP_501105.2	94	333.954	194	183	DEnse Body family member (deb-1)
Locus_4807_Transcript_2/2_Conf_1.000	761	20	1.87E-85	NP_741437.1	95	319.701	183	175	DEnse Body family member (deb-1)
Locus_4808_Transcript_1/1_Conf_1.000	449	20	6.61E-38	XP_002640077.1	80	160.229	148	119	Hypothetical protein CBG12562
Locus_4809_Transcript_1/1_Conf_1.000	467	20	2.79E-28	XP_002646150.1	83	128.257	80	67	C. briggsae CBR-VRS-2 protein
Locus_481_Transcript_1/8_Conf_0.300	614	0							
Locus_481_Transcript_2/8_Conf_0.300	656	0							
Locus_481_Transcript_3/8_Conf_0.200	224	0							

Locus_481_Transcript_4/8_Conf_0.200	224	0							
Locus_481_Transcript_5/8_Conf_0.350	515	0							
Locus_481_Transcript_6/8_Conf_0.350	515	0							
Locus_481_Transcript_7/8_Conf_0.200	210	0							
Locus_481_Transcript_8/8_Conf_0.200	210	0							
Locus_4810_Transcript_1/1_Conf_1.000	1331	20	1.20E-141	NP_497545.1	73	507.679	434	318	hypothetical protein H14E04.2
Locus_4811_Transcript_1/1_Conf_1.000	243	0							
Locus_4812_Transcript_1/1_Conf_1.000	897	11	1.67E-28	NP_506519.1	57	130.954	266	154	hypothetical protein T16A9.5
Locus_4813_Transcript_1/1_Conf_1.000	161	0							
Locus_4814_Transcript_1/1_Conf_1.000	759	20	6.85E-96	NP_497088.3	85	354.369	228	195	hypothetical protein Y53F4B.4
Locus_4815_Transcript_1/1_Conf_1.000	923	20	4.54E-93	XP_002637195.1	75	345.51	307	231	C. briggsae CBR-LIG-1 protein
Locus_4816_Transcript_1/1_Conf_1.000	279	0							
Locus_4817_Transcript_1/2_Conf_1.000	639	0							
Locus_4817_Transcript_2/2_Conf_1.000	619	0							
Locus_4818_Transcript_1/1_Conf_1.000	1915	20	3.89E-158	CAR63668.1	96	563.148	341	328	putative eukaryotic translation initiation factor 5
Locus_4819_Transcript_1/2_Conf_1.000	1240	20	6.60E-155	NP_001040645.1	86	551.592	387	336	RSK-pNinety (RSK-p90 kinase) homolog family member (rskn-2)

Locus_4819_Transcript_2/2_Conf_1.000	1222	20	1.14E-151	NP_001040645.1	85	540.806	387	331	RSK-pNinety (RSK-p90 kinase) homolog family member (rskn-2)
Locus_482_Transcript_1/1_Conf_1.000	797	4	2.56E-19	XP_002639966.1	53	100.138	129	69	Hypothetical protein CBG10790
Locus_4820_Transcript_1/1_Conf_1.000	1240	20	7.87E-124	XP_002631383.1	82	448.358	297	245	Hypothetical protein CBG03225
Locus_4821_Transcript_1/2_Conf_1.000	1360	20	1.50E-70	NP_498908.2	72	271.552	252	183	hypothetical protein F22B7.9
Locus_4821_Transcript_2/2_Conf_1.000	1348	20	1.17E-67	NP_498908.2	71	261.922	252	181	hypothetical protein F22B7.9
Locus_4822_Transcript_1/1_Conf_1.000	608	2	2.52E-16	NP_497585.1	47	89.3521	190	91	G Protein, Alpha subunit family member (gpa-17)
Locus_4823_Transcript_1/1_Conf_1.000	927	20	7.78E-117	NP_506620.1	87	424.476	309	271	Peroxisomal Membrane Protein related family member (pmp-3)

Locus_4824_Transcript_1/1_Conf_1.000	356	20	2.35E-27	EAW76795.1	100	125.176	118	118	collagen, type I, alpha 2, isoform CRA_b
Locus_4825_Transcript_1/3_Conf_0.600	642	4	6.45E-16	XP_002642726.1	62	88.1965	136	85	Hypothetical protein CBG21101
Locus_4825_Transcript_2/3_Conf_0.400	1017	20	4.91E-38	NP_509098.2	81	162.925	119	97	TransThyretin-Related family domain family member (ttr-35)
Locus_4825_Transcript_3/3_Conf_0.600	636	4	1.19E-14	XP_002642726.1	63	83.9593	133	84	Hypothetical protein CBG21101
Locus_4826_Transcript_1/1_Conf_1.000	1479	20	4.45E-156	NP_500829.2	87	555.829	314	276	hypothetical protein T12E12.1
Locus_4827_Transcript_1/1_Conf_1.000	255	0							
Locus_4828_Transcript_1/1_Conf_1.000	369	20	6.73E-14	NP_490924.1	86	80.4925	51	44	hypothetical protein Y37E3.4
Locus_4829_Transcript_1/1_Conf_1.000	1107	20	1.87E-134	NP_741458.2	84	483.411	335	282	P38 Map Kinase family member (pmk-2)
Locus_483_Transcript_1/1_Conf_1.000	154	0							
Locus_4830_Transcript_1/1_Conf_1.000	626	7	9.35E-86	XP_002639961.1	93	320.087	172	160	Hypothetical protein CBG10781
Locus_4831_Transcript_1/1_Conf_1.000	602	20	3.64E-28	EFO17895.1	58	128.642	199	117	hypothetical protein LOAG_10603
Locus_4832_Transcript_1/2_Conf_1.000	2329	20	4.60E-148	NP_741253.1	74	530.02	546	406	Huntingtin Interacting Protein Related family member (hipr-1)

Locus_4832_Transcript_2/2_Conf_1.000	2220	20	1.95E-148	NP_741253.1	74	531.176	549	409	Huntingtin Interacting Protein Related family member (hipr-1)
Locus_4833_Transcript_1/2_Conf_1.000	771	20	9.59E-85	NP_500420.3	79	317.39	256	204	hypothetical protein M02B7.5
Locus_4833_Transcript_2/2_Conf_1.000	771	20	9.59E-85	NP_500420.3	79	317.39	256	204	hypothetical protein M02B7.5
Locus_4834_Transcript_1/1_Conf_1.000	943	20	5.76E-99	NP_505433.3	73	365.155	326	240	Heavy chain, Unconventional Myosin family member (hum-2)
Locus_4835_Transcript_1/1_Conf_1.000	758	20	5.24E-72	NP_495226.1	75	275.018	244	183	hypothetical protein C29H12.2
Locus_4836_Transcript_1/1_Conf_1.000	936	20	3.47E-88	EFO23001.1	75	329.331	276	208	DnaJ domain-containing protein
Locus_4837_Transcript_1/1_Conf_1.000	350	0							
Locus_4838_Transcript_1/1_Conf_1.000	947	20	6.22E-85	NP_001022321.1	74	318.546	276	205	hypothetical protein T05H10.7
Locus_4839_Transcript_1/1_Conf_1.000	1925	20	5.49E-112	EFO19589.1	60	409.838	610	369	hypothetical protein LOAG_08898
Locus_484_Transcript_1/2_Conf_1.000	2369	20	0	XP_002637005.1	78	944.88	790	618	Hypothetical protein CBG09497
Locus_484_Transcript_2/2_Conf_1.000	449	15	1.79E-43	XP_002637005.1	85	178.718	141	121	Hypothetical protein CBG09497
Locus_4840_Transcript_1/1_Conf_1.000	212	0							
Locus_4841_Transcript_1/1_Conf_1.000	1076	20	9.35E-168	ACI49189.1	86	593.964	360	312	hypothetical protein Csp3_JD02.017
Locus_4842_Transcript_1/2_Conf_1.000	1476	7	1.93E-34	XP_002639516.1	50	151.754	350	175	C. briggsae CBR-SOP-3 protein
Locus_4842_Transcript_2/2_Conf_1.000	1476	7	3.30E-34	XP_002639516.1	50	150.984	350	175	C. briggsae CBR-SOP-3 protein

Locus_4843_Transcript_1/2_Conf_1.000	1686	20	8.96E-180	NP_509562.1	83	634.795	497	417	hypothetical protein B0416.5
Locus_4843_Transcript_2/2_Conf_1.000	1686	20	8.96E-180	NP_509562.1	83	634.795	497	417	hypothetical protein B0416.5
Locus_4844_Transcript_1/1_Conf_1.000	447	20	4.61E-15	XP_001951470.1	70	84.3445	116	82	PREDICTED: similar to Histone H2B
Locus_4845_Transcript_1/1_Conf_1.000	841	20	8.59E-101	NP_741567.1	86	370.933	267	231	eXPOrtin (nuclear export receptor) family member (xpo-1)
Locus_4846_Transcript_1/1_Conf_1.000	650	20	2.24E-72	XP_002636805.1	74	275.789	216	161	C. briggsae CBR-TTN-1 protein
Locus_4847_Transcript_1/1_Conf_1.000	345	7	8.49E-09	NP_506102.2	66	63.5438	84	56	hypothetical protein K01D12.15
Locus_4848_Transcript_1/1_Conf_1.000	1109	20	3.15E-174	NP_490817.3	91	615.535	355	326	G protein, Subunit Alpha family member (gsa-1)
Locus_4849_Transcript_1/1_Conf_1.000	377	20	2.50E-61	NP_001022488.1	94	238.039	125	118	UNCoordinated family member (unc-52)
Locus_485_Transcript_1/1_Conf_1.000	545	20	2.58E-50	XP_002644436.1	80	201.83	146	118	C. briggsae CBR-TTR-48 protein
Locus_4850_Transcript_1/1_Conf_1.000	545	0							
Locus_4851_Transcript_1/1_Conf_1.000	1536	20	3.11E-75	NP_499691.1	84	287.345	245	208	Toxin-regulated Target of p38MAPK family member (ttm-1)
Locus_4852_Transcript_1/1_Conf_1.000	840	2	5.53E-07	EFO28396.1	51	59.3066	128	66	hypothetical protein LOAG_00085
Locus_4853_Transcript_1/1_Conf_1.000	140	0							

Locus_4854_Transcript_1/1_Conf_1.000	479	20	5.72E-26	ACG69807.1	95	120.553	62	59	putative cytochrome c
Locus_4855_Transcript_1/1_Conf_1.000	2491	20	8.17E-42	NP_001129758.1	54	177.178	298	163	hypothetical protein C41D11.3
Locus_4856_Transcript_1/2_Conf_1.000	1052	20	2.73E-31	XP_002642169.1	87	140.584	110	96	Hypothetical protein CBG18134
Locus_4856_Transcript_2/2_Conf_1.000	1052	20	2.73E-31	XP_002642169.1	87	140.584	110	96	Hypothetical protein CBG18134
Locus_4857_Transcript_1/1_Conf_1.000	1584	20	6.65E-113	NP_001122530.1	72	412.535	445	324	Enhancer of Ksr-1 Lethality family member (ekl-4)
Locus_4858_Transcript_1/1_Conf_1.000	826	0							
Locus_4859_Transcript_1/1_Conf_1.000	1228	20	2.78E-89	XP_002639463.1	83	333.569	223	186	C. briggsae CBR-OBR-4 protein
Locus_486_Transcript_1/1_Conf_1.000	486	20	3.41E-26	ACS37721.1	58	121.324	129	75	C-type lectin-1
Locus_4860_Transcript_1/1_Conf_1.000	772	20	1.31E-49	XP_001901087.1	77	200.675	155	120	Phosphatidylinositol 3- and 4-kinase family protein
Locus_4861_Transcript_1/1_Conf_1.000	474	20	3.99E-19	XP_002630586.1	68	97.8265	74	51	Hypothetical protein CBG13044
Locus_4862_Transcript_1/1_Conf_1.000	1366	20	0	EFO27753.1	85	657.136	454	388	RNA helicase
Locus_4863_Transcript_1/1_Conf_1.000	498	20	1.84E-24	XP_002641305.1	68	115.546	124	85	C. briggsae CBR-TTR-15 protein
Locus_4864_Transcript_1/1_Conf_1.000	1186	20	3.58E-70	NP_509826.1	59	270.011	399	236	DystroGlycaN family member (dgn-1)

Locus_4865_Transcript_1/1_Conf_1.000	840	20	5.73E-113	XP_002648488.1	90	411.379	247	223	C. briggsae CBR-PBS-6 protein
Locus_4866_Transcript_1/1_Conf_1.000	1705	20	0	CAR63601.1	96	710.679	407	391	putative ABC transporter family protein
Locus_4867_Transcript_1/1_Conf_1.000	373	20	2.29E-38	XP_002629818.1	90	161.77	94	85	Hypothetical protein CBG01062
Locus_4868_Transcript_1/1_Conf_1.000	139	20	1.51E-18	NP_001139295.1	97	95.9005	46	45	glutathione peroxidase 4
Locus_4869_Transcript_1/1_Conf_1.000	863	4	8.05E-25	EFO24091.1	52	118.627	247	129	hypothetical protein LOAG_04390
Locus_487_Transcript_1/1_Conf_1.000	151	0							
Locus_4870_Transcript_1/1_Conf_1.000	237	0							
Locus_4871_Transcript_1/1_Conf_1.000	575	20	3.97E-18	XP_001892000.1	75	95.1301	80	60	linker histone H1 and H5 family protein
Locus_4872_Transcript_1/1_Conf_1.000	131	20	5.42E-08	XP_002643552.1	76	60.8474	43	33	Hypothetical protein CBG16248

Locus_4873_Transcript_1/1_Conf_1.000	573	20	2.09E-35	NP_505651.2	91	152.525	91	83	ThioRedoXin
Locus_4874_Transcript_1/1_Conf_1.000	765	20	8.59E-62	XP_002641517.1	70	241.121	258	181	Hypothetical protein CBG09813
Locus_4875_Transcript_1/1_Conf_1.000	606	4	2.36E-14	EFO19606.1	53	82.8037	163	88	hypothetical protein LOAG_08888
Locus_4876_Transcript_1/2_Conf_1.000	568	20	1.77E-31	XP_002631556.1	57	139.428	207	119	Hypothetical protein CBG20732
Locus_4876_Transcript_2/2_Conf_1.000	303	20	5.04E-22	XP_002631556.1	75	107.457	100	75	Hypothetical protein CBG20732
Locus_4877_Transcript_1/1_Conf_1.000	544	20	5.25E-11	EFN60827.1	52	71.2478	184	96	Integrator complex subunit 1
Locus_4878_Transcript_1/1_Conf_1.000	503	2	2.91E-25	XP_002631529.1	75	118.242	89	67	Hypothetical protein CBG20695
Locus_4879_Transcript_1/1_Conf_1.000	522	18	2.64E-14	XP_002637399.1	59	82.0333	100	59	Hypothetical protein CBG19106
Locus_488_Transcript_1/1_Conf_1.000	2103	20	0	P29190.1	97	1232.24	617	599	Phosphoenolpyruvate carboxylase
Locus_4880_Transcript_1/1_Conf_1.000	1372	20	3.52E-51	EFO18525.1	86	207.223	116	100	translocation protein 1
Locus_4881_Transcript_1/1_Conf_1.000	284	20	2.25E-17	ADF88235.1	96	92.0485	62	60	NADH dehydrogenase subunit 2
Locus_4882_Transcript_1/1_Conf_1.000	552	20	6.88E-78	XP_002013329.1	87	293.508	179	156	GL23471

Locus_4883_Transcript_1/1_Conf_1.000	1609	20	7.92E-154	XP_002645854.1	77	548.51	453	352	Hypothetical protein CBG07591
Locus_4884_Transcript_1/1_Conf_1.000	627	20	4.00E-68	XP_002630697.1	80	261.536	201	161	Hypothetical protein CBG02379
Locus_4885_Transcript_1/2_Conf_1.000	1159	20	8.61E-29	NP_491442.1	61	132.494	136	84	VILLiN related family member (viln-1)
Locus_4885_Transcript_2/2_Conf_1.000	1472	20	4.16E-13	NP_491442.1	56	80.8777	97	55	VILLiN related family member (viln-1)
Locus_4886_Transcript_1/1_Conf_1.000	2412	0							
Locus_4887_Transcript_1/1_Conf_1.000	376	20	1.75E-22	XP_001894296.1	66	108.997	130	87	hypothetical protein
Locus_4888_Transcript_1/1_Conf_1.000	2056	20	0	ACJ65163.1	74	677.167	661	492	Dishevelled related protein 1, isoform c, confirmed by transcript evidence
Locus_4889_Transcript_1/1_Conf_1.000	253	0							
Locus_489_Transcript_1/1_Conf_1.000	997	20	2.59E-161	NP_001021269.1	95	572.392	332	318	UNCoordinated family member (unc-44)
Locus_4890_Transcript_1/1_Conf_1.000	525	1	5.65E-04	XP_002640830.1	53	47.7506	71	38	Hypothetical protein CBG15717
Locus_4891_Transcript_1/1_Conf_1.000	352	0							
Locus_4892_Transcript_1/1_Conf_1.000	768	20	1.45E-08	XP_002166584.1	45	64.3142	195	89	PREDICTED: similar to harbinger transposase derived 1
Locus_4893_Transcript_1/1_Conf_1.000	369	20	1.59E-39	XP_002634501.1	95	165.622	122	117	C. briggsae CBR-SMGL-2 protein

Locus_4894_Transcript_1/1_Conf_1.000	1067	20	7.24E-80	XP_001895783.1	80	301.982	210	170	BTB/POZ domain containing protein 9
Locus_4895_Transcript_1/1_Conf_1.000	414	20	2.46E-53	A8XP97.2	73	211.46	168	123	Voltage-dependent calcium channel unc-36
Locus_4896_Transcript_1/2_Conf_1.000	392	2	3.84E-06	XP_002643096.1	60	54.6842	70	42	Hypothetical protein CBG23020
Locus_4896_Transcript_2/2_Conf_1.000	382	2	3.89E-06	XP_002643096.1	60	54.6842	70	42	Hypothetical protein CBG23020
Locus_4897_Transcript_1/1_Conf_1.000	305	20	2.05E-15	EFN66847.1	60	85.5001	96	58	hypothetical protein EAG_08499
Locus_4898_Transcript_1/2_Conf_1.000	1506	20	0	NP_001023021.1	92	815.839	497	461	UNCoordinated family member (unc-32)
Locus_4898_Transcript_2/2_Conf_1.000	550	20	1.91E-64	NP_001023017.1	97	248.825	148	144	UNCoordinated family member (unc-32)
Locus_4899_Transcript_1/1_Conf_1.000	324	4	2.52E-21	XP_002630899.1	72	105.145	95	69	Hypothetical protein CBG02621
Locus_49_Transcript_1/10_Conf_0.069	335	0							
Locus_49_Transcript_10/10_Conf_0.172	1558	20	1.04E-86	XP_002646109.1	72	325.479	295	213	C. briggsae CBR-CAR-1 protein
Locus_49_Transcript_2/10_Conf_0.276	3217	20	0	XP_002647053.1	85	845.884	572	488	Hypothetical protein CBG03574
Locus_49_Transcript_3/10_Conf_0.172	747	0							
Locus_49_Transcript_4/10_Conf_0.138	637	20	9.40E-12	NP_505347.1	49	74.3294	97	48	hypothetical protein C25E10.10
Locus_49_Transcript_5/10_Conf_0.310	794	0							
Locus_49_Transcript_6/10_Conf_0.172	507	20	6.60E-12	NP_505347.1	49	73.9442	97	48	hypothetical protein C25E10.10

Locus_49_Transcript_7/10_Conf_0.276	3202	20	0	XP_002647053.1	86	851.277	567	488	Hypothetical protein CBG03574
Locus_49_Transcript_8/10_Conf_0.241	670	0							
Locus_49_Transcript_9/10_Conf_0.172	637	20	1.23E-11	NP_505347.1	49	73.9442	97	48	hypothetical protein C25E10.10
Locus_490_Transcript_1/1_Conf_1.000	2088	20	3.23E-121	NP_500128.2	71	440.654	392	279	hypothetical protein Y41D4A.5
Locus_4900_Transcript_1/1_Conf_1.000	884	5	2.23E-86	NP_508189.2	72	323.168	262	189	hypothetical protein C44C1.1
Locus_4901_Transcript_1/1_Conf_1.000	400	20	4.44E-42	NP_741118.1	86	174.096	102	88	hypothetical protein C35D10.17
Locus_4902_Transcript_1/1_Conf_1.000	2191	20	0	XP_002641856.1	83	773.852	539	452	Hypothetical protein CBG16531
Locus_4903_Transcript_1/1_Conf_1.000	277	0							
Locus_4904_Transcript_1/1_Conf_1.000	685	1	3.46E-05	EFA84423.1	37	52.7582	215	81	hypothetical protein PPL_02455
Locus_4905_Transcript_1/1_Conf_1.000	1252	20	5.97E-87	XP_002640292.1	74	325.865	343	255	C. briggsae CBR-RPN-10 protein
Locus_4906_Transcript_1/1_Conf_1.000	195	20	9.65E-13	XP_002639478.1	78	76.6406	65	51	C. briggsae CBR-CYP-36A1 protein
Locus_4907_Transcript_1/1_Conf_1.000	124	0							
Locus_4908_Transcript_1/1_Conf_1.000	215	2	1.19E-15	XP_002632399.1	87	86.2705	54	47	Hypothetical protein CBG00422
Locus_4909_Transcript_1/1_Conf_1.000	413	20	1.83E-56	BAG61974.1	100	221.861	133	133	unnamed protein product
Locus_491_Transcript_1/1_Conf_1.000	261	4	1.10E-24	NP_491427.1	84	116.316	86	73	hypothetical protein W09C3.4
Locus_4910_Transcript_1/1_Conf_1.000	460	0							

Locus_4911_Transcript_1/2_Conf_1.000	2430	20	5.16E-166	NP_505433.3	70	589.726	671	470	Heavy chain, Unconventional Myosin family member (hum-2)
Locus_4911_Transcript_2/2_Conf_1.000	2032	20	2.78E-170	NP_505433.3	69	603.594	702	489	Heavy chain, Unconventional Myosin family member (hum-2)
Locus_4912_Transcript_1/2_Conf_1.000	1033	20	2.02E-79	NP_499811.1	68	300.442	352	241	hypothetical protein T12D8.8
Locus_4912_Transcript_2/2_Conf_1.000	1027	20	1.81E-80	NP_499811.1	69	303.908	352	243	hypothetical protein T12D8.8
Locus_4913_Transcript_1/1_Conf_1.000	361	9	6.36E-17	NP_502038.1	56	90.5077	120	68	hypothetical protein Y69E1A.1
Locus_4914_Transcript_1/1_Conf_1.000	1553	4	1.24E-39	NP_741760.1	61	169.088	249	152	hypothetical protein ZK470.2
Locus_4915_Transcript_1/3_Conf_0.571	410	4	4.73E-12	NP_492733.2	71	74.3294	102	73	hypothetical protein Y106G6H.8
Locus_4915_Transcript_2/3_Conf_0.286	334	0							
Locus_4915_Transcript_3/3_Conf_0.571	649	20	5.77E-28	NP_492733.2	84	128.257	113	95	hypothetical protein Y106G6H.8
Locus_4916_Transcript_1/1_Conf_1.000	191	0							

Locus_4917_Transcript_1/1_Conf_1.000	136	20	9.79E-18	XP_002924612.1	100	93.2041	43	43	PREDICTED: thioredoxin-interacting protein-like
Locus_4918_Transcript_1/2_Conf_1.000	1705	20	9.45E-44	NP_001122631.1	64	182.956	206	132	ELAV-Type RNA binding protein family member (etr-1)
Locus_4918_Transcript_2/2_Conf_1.000	1155	20	5.53E-44	NP_001122631.1	64	182.956	206	132	ELAV-Type RNA binding protein family member (etr-1)
Locus_4919_Transcript_1/1_Conf_1.000	488	20	5.57E-61	XP_002640340.1	81	236.884	162	132	Hypothetical protein CBG12889
Locus_492_Transcript_1/1_Conf_1.000	614	20	4.25E-35	NP_499850.2	64	151.754	210	135	hypothetical protein Y38C1AB.4
Locus_4920_Transcript_1/1_Conf_1.000	533	0							

Locus_4921_Transcript_1/1_Conf_1.000	651	20	1.02E-56	NP_001022032.1	78	223.787	214	168	TRRAP-like (transcription/transformation domain-associated protein) family member (trr-1)
Locus_4922_Transcript_1/2_Conf_1.000	1597	0							
Locus_4922_Transcript_2/2_Conf_1.000	1684	0							
Locus_4923_Transcript_1/1_Conf_1.000	1205	20	1.29E-107	NP_501179.1	91	394.43	223	204	hypothetical protein T12B3.4
Locus_4924_Transcript_1/1_Conf_1.000	793	20	1.42E-78	XP_001892448.1	71	296.975	259	184	Hypothetical FAD-dependent oxidoreductase YEL047C
Locus_4925_Transcript_1/1_Conf_1.000	497	20	6.73E-51	XP_002646932.1	80	203.371	150	120	Hypothetical protein CBG19637
Locus_4926_Transcript_1/2_Conf_1.000	1248	20	1.18E-42	NP_501537.2	55	178.718	338	188	hypothetical protein C09G9.2
Locus_4926_Transcript_2/2_Conf_1.000	1260	20	1.18E-42	NP_501537.2	55	178.718	338	188	hypothetical protein C09G9.2
Locus_4927_Transcript_1/1_Conf_1.000	522	0							
Locus_4928_Transcript_1/1_Conf_1.000	497	20	1.77E-59	3ICH	100	231.876	111	111	CrystalStructure Of Cyclophilin B At 1.2 A Resolution
Locus_4929_Transcript_1/1_Conf_1.000	2178	20	2.09E-54	NP_001024674.1	56	218.779	422	238	hypothetical protein F46H5.2
Locus_493_Transcript_1/2_Conf_1.000	1083	20	5.42E-22	EFO25448.1	61	109.768	124	76	hypothetical protein LOAG_03031

Locus_493_Transcript_2/2_Conf_1.000	1083	20	5.42E-22	EFO25448.1	61	109.768	124	76	hypothetical protein LOAG_03031
Locus_4930_Transcript_1/1_Conf_1.000	131	0							
Locus_4931_Transcript_1/1_Conf_1.000	159	0							
Locus_4932_Transcript_1/1_Conf_1.000	356	20	1.91E-53	NP_506269.1	94	211.846	117	110	EATing: abnormal pharyngeal pumping family member (eat-6)
Locus_4933_Transcript_1/1_Conf_1.000	581	20	3.13E-26	NP_001023538.1	92	122.094	75	69	hypothetical protein Y59E9AL.7
Locus_4934_Transcript_1/1_Conf_1.000	1195	20	3.62E-70	XP_002642930.1	66	270.011	277	184	Hypothetical protein CBG15206
Locus_4935_Transcript_1/1_Conf_1.000	534	18	7.86E-25	ABU49430.1	60	117.087	186	113	PRO-2
Locus_4936_Transcript_1/1_Conf_1.000	926	20	5.37E-110	EFO21345.1	85	401.749	306	261	hypothetical protein LOAG_07143
Locus_4937_Transcript_1/1_Conf_1.000	1102	20	2.08E-77	XP_002634984.1	67	293.893	299	203	Hypothetical protein CBG13522

Locus_4938_Transcript_1/1_Conf_1.000	2317	20	8.97E-128	XP_002120082.1	60	462.611	728	439	PREDICTED: similar to predicted protein
Locus_4939_Transcript_1/1_Conf_1.000	115	0							
Locus_494_Transcript_1/1_Conf_1.000	2365	20	0	NP_001122768.1	79	833.558	671	536	Lin-48 EXpression abnormal family member (lex-1)
Locus_4940_Transcript_1/1_Conf_1.000	552	20	1.88E-59	ACD88896.1	90	232.261	122	111	conserved hypothetical protein
Locus_4941_Transcript_1/1_Conf_1.000	1324	6	3.45E-48	NP_490757.2	54	197.208	348	191	hypothetical protein F56A6.4
Locus_4942_Transcript_1/1_Conf_1.000	579	20	6.05E-54	AAN61521.1	71	214.157	184	132	301KDa_2 protein
Locus_4943_Transcript_1/1_Conf_1.000	377	20	1.02E-38	AAV38313.1	100	162.925	123	123	CD81 antigen (target of antiproliferative antibody 1)
Locus_4944_Transcript_1/1_Conf_1.000	1454	20	2.20E-75	XP_001900175.1	58	287.73	467	271	hypothetical protein Bm1_43570
Locus_4945_Transcript_1/5_Conf_0.692	1763	20	4.82E-75	XP_002637065.1	75	286.96	255	192	Hypothetical protein CBG09562
Locus_4945_Transcript_2/5_Conf_0.692	1907	20	4.16E-136	XP_001892930.1	64	489.96	547	353	KH domain containing protein
Locus_4945_Transcript_3/5_Conf_0.692	1900	20	8.34E-137	XP_001892930.1	64	492.271	548	354	KH domain containing protein

Locus_4945_Transcript_4/5_Conf_0.538	2094	20	1.31E-138	XP_001892446.1	66	498.434	508	339	KH domain containing protein
Locus_4945_Transcript_5/5_Conf_0.692	1964	20	8.64E-137	XP_001892930.1	64	492.271	548	354	KH domain containing protein
Locus_4946_Transcript_1/1_Conf_1.000	1200	6	2.46E-58	NP_506085.2	53	230.72	413	220	FERM domain (protein4.1-ezrin-radixin-moesin) family member (frm-7)
Locus_4947_Transcript_1/1_Conf_1.000	874	20	3.27E-114	XP_001897557.1	92	415.616	233	216	Tyrosine-protein kinase abl-1
Locus_4948_Transcript_1/1_Conf_1.000	312	20	5.13E-46	NP_493549.1	93	187.193	104	97	hypothetical protein Y54E5A.1
Locus_4949_Transcript_1/1_Conf_1.000	225	0							
Locus_495_Transcript_1/1_Conf_1.000	654	20	5.09E-80	ACV20978.1	91	301.212	190	174	small subunit ribosomal protein 7
Locus_4950_Transcript_1/1_Conf_1.000	461	20	1.90E-13	XP_002647593.1	57	78.9518	109	63	C. briggsae CBR-TTR-44 protein
Locus_4951_Transcript_1/2_Conf_1.000	1860	20	1.10E-117	NP_510751.3	60	428.713	588	357	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-34)
Locus_4951_Transcript_2/2_Conf_1.000	1908	20	6.68E-118	NP_510751.3	59	429.483	600	356	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-34)
Locus_4952_Transcript_1/1_Conf_1.000	1430	20	0	XP_002649082.1	89	728.398	473	422	C. briggsae CBR-HAF-4 protein
Locus_4953_Transcript_1/1_Conf_1.000	375	20	2.85E-65	NP_501921.1	99	251.136	124	123	G Protein, Alpha subunit family member (gpa-7)
Locus_4954_Transcript_1/1_Conf_1.000	203	0							
Locus_4955_Transcript_1/1_Conf_1.000	284	0							

Locus_4956_Transcript_1/1_Conf_1.000	506	20	3.27E-56	AAR07614.1	96	221.09	117	113	UNC-18
Locus_4957_Transcript_1/1_Conf_1.000	1795	0							
Locus_4958_Transcript_1/3_Conf_0.571	567	20	6.28E-45	NP_495437.2	81	184.111	128	104	hypothetical protein C52E12.4
Locus_4958_Transcript_2/3_Conf_0.714	1581	20	6.10E-167	NP_495437.2	79	592.038	473	374	hypothetical protein C52E12.4
Locus_4958_Transcript_3/3_Conf_0.714	1581	20	6.10E-167	NP_495437.2	79	592.038	473	374	hypothetical protein C52E12.4
Locus_4959_Transcript_1/1_Conf_1.000	749	20	6.51E-83	XP_002645375.1	88	311.227	198	175	Hypothetical protein CBG15443
Locus_496_Transcript_1/1_Conf_1.000	918	20	3.00E-121	XP_002642328.1	81	439.113	316	256	Hypothetical protein CBG18323
Locus_4960_Transcript_1/1_Conf_1.000	210	0							
Locus_4961_Transcript_1/1_Conf_1.000	826	20	1.96E-126	XP_002920761.1	98	456.062	246	243	PREDICTED: 60S ribosomal protein L7a-like
Locus_4962_Transcript_1/1_Conf_1.000	1521	20	7.69E-135	NP_501005.2	71	485.337	435	313	hypothetical protein F38A5.2
Locus_4963_Transcript_1/1_Conf_1.000	536	0							

Locus_4964_Transcript_1/1_Conf_1.000	732	20	2.89E-88	NP_498666.2	77	328.946	244	189	hypothetical protein R13A5.11
Locus_4965_Transcript_1/1_Conf_1.000	1863	20	1.14E-122	NP_001024265.1	84	445.277	353	300	hypothetical protein Y58G8A.4
Locus_4966_Transcript_1/1_Conf_1.000	913	20	1.77E-49	XP_002630879.1	66	200.675	213	141	C. briggsae CBR-TAT-4.2 protein
Locus_4967_Transcript_1/1_Conf_1.000	792	20	4.70E-90	NP_491477.2	78	335.109	262	205	IMportin Beta family member (imb-1)
Locus_4968_Transcript_1/2_Conf_1.000	457	0							
Locus_4968_Transcript_2/2_Conf_1.000	364	0							
Locus_4969_Transcript_1/1_Conf_1.000	637	20	6.08E-19	NP_503713.1	69	98.2117	114	79	hypothetical protein F53E10.6
Locus_497_Transcript_1/1_Conf_1.000	221	0							
Locus_4970_Transcript_1/1_Conf_1.000	372	20	4.34E-13	NP_001022032.1	52	77.7962	131	69	TRRAP-like (transcription/transformation domain-associated protein) family member (trr-1)
Locus_4971_Transcript_1/1_Conf_1.000	1054	20	1.92E-109	XP_002642775.1	79	400.208	318	254	C. briggsae CBR-NEX-1 protein
Locus_4972_Transcript_1/1_Conf_1.000	333	0							
Locus_4973_Transcript_1/1_Conf_1.000	893	20	5.37E-112	XP_002635351.1	80	408.297	289	234	Hypothetical protein CBG01522
Locus_4974_Transcript_1/3_Conf_0.714	2715	20	0	XP_002634170.1	90	1548.1	909	823	Hypothetical protein CBG01737
Locus_4974_Transcript_2/3_Conf_0.714	2715	20	0	XP_002634170.1	90	1548.1	909	823	Hypothetical protein CBG01737

Locus_4974_Transcript_3/3_Conf_0.714	2715	20	0	XP_002634170.1	90	1548.1	909	823	Hypothetical protein CBG01737
Locus_4975_Transcript_1/1_Conf_1.000	329	0							
Locus_4976_Transcript_1/1_Conf_1.000	226	0							
Locus_4977_Transcript_1/1_Conf_1.000	1247	20	3.65E-153	NP_501838.2	79	545.814	373	296	hypothetical protein C04G2.9
Locus_4978_Transcript_1/1_Conf_1.000	635	20	2.56E-86	XP_002642565.1	85	322.013	213	182	C. briggsae CBR-UNC-79.2 protein
Locus_4979_Transcript_1/1_Conf_1.000	659	20	1.17E-23	XP_001895818.1	59	114.005	158	94	BC023488 protein
Locus_498_Transcript_1/2_Conf_1.000	1157	20	4.14E-124	ACO59962.1	99	449.129	232	230	14-3-3 protein isoform 2
Locus_498_Transcript_2/2_Conf_1.000	1157	20	4.29E-113	ACO59962.1	94	412.535	232	219	14-3-3 protein isoform 2
Locus_4980_Transcript_1/1_Conf_1.000	381	20	1.67E-49	CAB40412.1	86	198.749	124	107	hexokinase
Locus_4981_Transcript_1/1_Conf_1.000	223	0							
Locus_4982_Transcript_1/2_Conf_1.000	676	0							
Locus_4982_Transcript_2/2_Conf_1.000	658	0							
Locus_4983_Transcript_1/2_Conf_1.000	765	20	4.43E-42	NP_495256.1	69	175.637	245	171	hypothetical protein F13H8.2
Locus_4983_Transcript_2/2_Conf_1.000	765	20	2.05E-47	NP_495256.1	71	193.356	245	174	hypothetical protein F13H8.2

Locus_4984_Transcript_1/1_Conf_1.000	743	20	6.52E-19	XP_001773533.1	49	98.5969	229	114	predicted protein
Locus_4985_Transcript_1/2_Conf_1.000	1487	20	4.40E-103	NP_001024648.1	66	379.793	403	266	Wrapper/Rega-1/Klingon homolog family member (wrk-1)
Locus_4985_Transcript_2/2_Conf_1.000	1463	20	2.52E-103	XP_002645506.1	66	380.563	394	262	C. briggsae CBR-WRK-1 protein
Locus_4986_Transcript_1/1_Conf_1.000	213	20	2.16E-33	AAX36984.1	100	145.206	71	71	cystatin C
Locus_4987_Transcript_1/2_Conf_1.000	2227	20	0	XP_002646666.1	78	963.37	736	576	Hypothetical protein CBG11104
Locus_4987_Transcript_2/2_Conf_1.000	2227	20	0	XP_002646666.1	78	960.674	736	575	Hypothetical protein CBG11104

Locus_4988_Transcript_1/1_Conf_1.000	715	20	1.86E-28	NP_497591.1	58	130.183	195	115	Protein Phosphatase Four Regulatory subunit family member (ppfr-4)
Locus_4989_Transcript_1/1_Conf_1.000	783	8	1.40E-30	NP_494855.1	51	137.502	242	125	Toxin-regulated Target of p38MAPK family member (ttm-2)
Locus_499_Transcript_1/1_Conf_1.000	1298	20	0	EFO19684.1	97	641.728	315	308	LEThal family member

Locus_4990_Transcript_1/1_Conf_1.000	376	20	1.57E-55	XP_001892323.1	89	218.779	125	112	Histone deacetylase family protein
Locus_4991_Transcript_1/4_Conf_0.700	943	20	2.55E-155	XP_002634908.1	92	552.362	317	293	Hypothetical protein CBG22506
Locus_4991_Transcript_2/4_Conf_0.700	943	20	2.55E-155	XP_002634908.1	92	552.362	317	293	Hypothetical protein CBG22506
Locus_4991_Transcript_3/4_Conf_0.700	943	20	2.55E-155	XP_002634908.1	92	552.362	317	293	Hypothetical protein CBG22506
Locus_4991_Transcript_4/4_Conf_0.700	943	20	2.55E-155	XP_002634908.1	92	552.362	317	293	Hypothetical protein CBG22506
Locus_4992_Transcript_1/1_Conf_1.000	1146								
Locus_4993_Transcript_1/1_Conf_1.000	193	0							
Locus_4994_Transcript_1/1_Conf_1.000	1566	6	1.75E-49	NP_491682.1	52	201.83	391	206	MTK1/MEKK4 homolog family member (mtk-1)
Locus_4995_Transcript_1/1_Conf_1.000	473	20	2.68E-23	EFO23433.1	64	111.694	164	105	hypothetical protein LOAG_05051

Locus_4996_Transcript_1/4_Conf_0.333	759	20	1.10E-85	XP_002634246.1	75	320.472	251	190	Hypothetical protein CBG01816
Locus_4996_Transcript_2/4_Conf_0.333	304	0							
Locus_4996_Transcript_3/4_Conf_0.333	304	0							
Locus_4996_Transcript_4/4_Conf_0.333	1075	20	9.20E-107	XP_002634246.1	74	391.349	331	245	Hypothetical protein CBG01816
Locus_4997_Transcript_1/1_Conf_1.000	412	0							
Locus_4998_Transcript_1/1_Conf_1.000	1151	20	2.77E-96	XP_002642492.1	81	356.681	277	225	Hypothetical protein CBG06912
Locus_4999_Transcript_1/1_Conf_1.000	550	4	1.87E-11	AAQ23189.1	83	72.7886	61	51	FMRFamide-related peptide FLP-12 precursor
Locus_5_Transcript_1/2_Conf_1.000	203	1	2.44E-08	Q94637.1	70	62.003	58	41	Vitellogenin-6
Locus_5_Transcript_2/2_Conf_1.000	228	7	1.07E-11	Q94637.1	69	73.1738	72	50	Vitellogenin-6
Locus_50_Transcript_1/1_Conf_1.000	3336	20	0	NP_498516.2	75	1287.71	1136	855	LEThal family member (let-711)
Locus_500_Transcript_1/1_Conf_1.000	567	20	6.97E-28	AAH70248.1	100	127.487	64	64	TMSB4X protein
Locus_5000_Transcript_1/1_Conf_1.000	706	20	2.55E-107	ACY40018.1	92	392.119	234	217	C. elegans FLN-1 protein, isoform g
Locus_5001_Transcript_1/1_Conf_1.000	703	2	1.26E-21	NP_507188.3	52	107.457	206	109	hypothetical protein Y32B12B.2
Locus_5002_Transcript_1/1_Conf_1.000	1120	0							
Locus_5003_Transcript_1/1_Conf_1.000	388	20	1.67E-25	CBL87054.2	71	119.013	118	84	C. elegans protein F54E4.1, partially confirmed by transcript evidence
Locus_5004_Transcript_1/2_Conf_1.000	2235	20	0	CAD44516.1	85	1039.25	754	642	VAB-10B protein

Locus_5004_Transcript_2/2_Conf_1.000	1718	20	0	NP_001040721.1	91	850.121	572	524	Variable ABnormal morphology family member (vab-10)
Locus_5005_Transcript_1/1_Conf_1.000	183	0							
Locus_5006_Transcript_1/2_Conf_1.000	461	0							
Locus_5006_Transcript_2/2_Conf_1.000	332	0							
Locus_5007_Transcript_1/1_Conf_1.000	579	6	1.97E-04	XP_605047.5	50	49.6766	104	52	PREDICTED: myosin, heavy polypeptide 15
Locus_5008_Transcript_1/1_Conf_1.000	225	0							
Locus_5009_Transcript_1/1_Conf_1.000	839	20	5.99E-54	XP_001896299.1	64	215.312	283	182	PHD-finger family protein
Locus_501_Transcript_1/2_Conf_1.000	470	20	4.15E-32	XP_002632184.1	69	140.969	136	94	C. briggsae CBR-FAR-7 protein
Locus_501_Transcript_2/2_Conf_1.000	470	20	1.09E-32	XP_002632184.1	69	142.895	136	95	C. briggsae CBR-FAR-7 protein
Locus_5010_Transcript_1/1_Conf_1.000	314	0							
Locus_5011_Transcript_1/1_Conf_1.000	182	0							
Locus_5012_Transcript_1/1_Conf_1.000	465	8	9.01E-19	NP_001122883.1	66	96.6709	109	72	Temporarily Assigned Gene name family member (tag-333)
Locus_5013_Transcript_1/1_Conf_1.000	2557	20	0	NP_502032.2	70	745.347	691	484	RB (Retinoblastoma Binding protein) Related family member (rbr-2)
Locus_5014_Transcript_1/1_Conf_1.000	251	0							
Locus_5015_Transcript_1/1_Conf_1.000	511	20	4.82E-47	XP_001900792.1	77	190.66	159	124	Transcription initiation factor IIE, beta subunit
Locus_5016_Transcript_1/2_Conf_1.000	1678	20	3.32E-09	NP_957423.1	55	68.1662	139	77	nuclear receptor coactivator 4
Locus_5016_Transcript_2/2_Conf_1.000	1678	20	3.32E-09	NP_957423.1	55	68.1662	139	77	nuclear receptor coactivator 4
Locus_5017_Transcript_1/1_Conf_1.000	338	2	6.57E-06	EFO16139.1	59	53.9138	66	39	hypothetical protein LOAG_12369
Locus_5018_Transcript_1/1_Conf_1.000	363	3	2.32E-27	XP_002634982.1	70	125.176	120	85	C. briggsae CBR-DSC-4 protein
Locus_5019_Transcript_1/1_Conf_1.000	548	20	3.00E-46	XP_002629673.1	76	188.348	143	109	Hypothetical protein CBG00891
Locus_502_Transcript_1/1_Conf_1.000	1472	20	6.52E-75	NP_741591.1	79	286.189	201	160	hypothetical protein F36D4.5
Locus_5020_Transcript_1/1_Conf_1.000	592	20	6.77E-40	CAR63685.1	81	167.548	112	91	putative Nuclear/nucleolar GTP-binding Protein
Locus_5021_Transcript_1/1_Conf_1.000	873	0							

Locus_5022_Transcript_1/1_Conf_1.000	763	20	1.18E-79	XP_002633490.1	84	300.442	205	173	Hypothetical protein CBG06262
Locus_5023_Transcript_1/1_Conf_1.000	811	0							
Locus_5024_Transcript_1/1_Conf_1.000	168	0							
Locus_5025_Transcript_1/2_Conf_1.000	392	20	1.03E-43	NP_491217.1	87	179.489	113	99	hypothetical protein C32E8.5
Locus_5025_Transcript_2/2_Conf_1.000	392	20	1.03E-43	NP_491217.1	87	179.489	113	99	hypothetical protein C32E8.5
Locus_5026_Transcript_1/1_Conf_1.000	1165	20	8.12E-27	XP_002634838.1	70	125.946	113	80	Hypothetical protein CBG13948
Locus_5027_Transcript_1/1_Conf_1.000	978	20	2.23E-117	NP_497288.1	83	426.402	307	257	hypothetical protein F23H11.3
Locus_5028_Transcript_1/1_Conf_1.000	609	4	2.23E-28	NP_492856.1	82	129.413	117	96	hypothetical protein Y52B11A.4
Locus_5029_Transcript_1/1_Conf_1.000	576	20	5.58E-44	XP_001901288.1	67	181.03	174	118	hypothetical protein Bm1_49115
Locus_503_Transcript_1/1_Conf_1.000	1366	5	5.09E-18	XP_001896971.1	48	97.0561	270	130	hypothetical protein Bm1_27600
Locus_5030_Transcript_1/1_Conf_1.000	1131	20	1.86E-36	XP_002640157.1	73	157.918	138	101	C. briggsae CBR-XPG-1 protein
Locus_5031_Transcript_1/1_Conf_1.000	1080	0							

Locus_5032_Transcript_1/1_Conf_1.000	1018	20	3.37E-71	AAC47238.1	71	273.092	326	232	non-muscle myosin heavy chain II
Locus_5033_Transcript_1/1_Conf_1.000	1472	12	1.43E-21	EFO22036.1	43	108.997	393	171	hypothetical protein LOAG_06451
Locus_5034_Transcript_1/2_Conf_1.000	1418	20	1.10E-39	EFO18357.1	47	169.088	428	204	hypothetical protein LOAG_10138
Locus_5034_Transcript_2/2_Conf_1.000	1343	20	1.35E-31	EFO18357.1	47	142.124	370	174	hypothetical protein LOAG_10138
Locus_5035_Transcript_1/1_Conf_1.000	685	13	1.19E-21	XP_002644671.1	55	107.457	196	108	Hypothetical protein CBG14652
Locus_5036_Transcript_1/1_Conf_1.000	156	0							

Locus_5037_Transcript_1/1_Conf_1.000	672	20	3.76E-33	EFO27562.1	63	145.591	163	103	hypothetical protein LOAG_00926
Locus_5038_Transcript_1/2_Conf_1.000	536	20	1.79E-69	NP_495617.1	92	265.388	174	161	hypothetical protein B0495.2
Locus_5038_Transcript_2/2_Conf_1.000	530	20	1.49E-68	NP_495617.1	92	262.307	172	159	hypothetical protein B0495.2
Locus_5039_Transcript_1/1_Conf_1.000	754	20	1.52E-47	NP_505561.1	75	193.741	145	110	TransThyretin-Related family domain family member (ttr-46)
Locus_504_Transcript_1/4_Conf_0.556	1636	20	2.15E-122	XP_002641173.1	96	444.121	261	251	Hypothetical protein CBG09034
Locus_504_Transcript_2/4_Conf_0.444	373	0							
Locus_504_Transcript_3/4_Conf_0.667	1813	20	2.45E-122	XP_002641173.1	96	444.121	261	251	Hypothetical protein CBG09034
Locus_504_Transcript_4/4_Conf_0.667	1807	20	2.44E-122	XP_002641173.1	96	444.121	261	251	Hypothetical protein CBG09034
Locus_5040_Transcript_1/1_Conf_1.000	269	3	4.44E-18	NP_500238.1	73	94.3597	82	60	hypothetical protein Y69A2AR.3
Locus_5041_Transcript_1/1_Conf_1.000	906	20	8.48E-137	NP_002267.2	100	490.73	271	271	keratin, type I cytoskeletal 19
Locus_5042_Transcript_1/1_Conf_1.000	536	0							

Locus_5043_Transcript_1/1_Conf_1.000	688	20	1.03E-97	NP_509898.1	90	360.147	227	206	ACOnitase family member (aco-1)
Locus_5044_Transcript_1/1_Conf_1.000	606	20	1.92E-40	XP_001899743.1	62	169.474	203	127	ATP-dependent DNA helicase II, 70 kDa subunit
Locus_5045_Transcript_1/1_Conf_1.000	727	20	4.62E-14	XP_001894238.1	42	82.4185	273	116	Zinc finger, C2H2 type family protein
Locus_5046_Transcript_1/1_Conf_1.000	1449	20	1.60E-134	NP_498454.2	67	484.182	439	295	hypothetical protein F20H11.1
Locus_5047_Transcript_1/1_Conf_1.000	1162	20	3.42E-118	NP_001041162.1	89	429.483	259	232	Bacterially Un-Swollen (M. nematophilum resistant) family member (bus-19)
Locus_5048_Transcript_1/1_Conf_1.000	811	20	1.17E-43	NP_491682.1	68	181.03	174	119	MTK1/MEKK4 homolog family member (mtk-1)
Locus_5049_Transcript_1/1_Conf_1.000	374	2	3.33E-05	EFO26501.1	49	51.6026	97	48	hypothetical protein LOAG_01987
Locus_505_Transcript_1/1_Conf_1.000	956	20	1.50E-70	XP_002640350.1	73	270.781	241	176	Hypothetical protein CBG20246
Locus_5050_Transcript_1/1_Conf_1.000	470	20	2.05E-47	XP_002639628.1	87	191.815	117	102	C. briggsae CBR-ASG-1 protein
Locus_5051_Transcript_1/1_Conf_1.000	164	0							
Locus_5052_Transcript_1/1_Conf_1.000	263	20	2.54E-13	XP_001891725.1	64	78.5666	87	56	hypothetical protein

Locus_5053_Transcript_1/1_Conf_1.000	717	4	1.88E-20	XP_002640718.1	50	103.605	186	94	Hypothetical protein CBG19785
Locus_5054_Transcript_1/1_Conf_1.000	734	20	7.90E-70	NP_508020.1	84	267.7	178	151	Seven B Two (mammalian 7BT prohormone convertase chaperone) homolog family member (sbt-1)
Locus_5055_Transcript_1/2_Conf_1.000	817	20	1.84E-36	EFO20733.1	58	157.147	198	116	hypothetical protein LOAG_07757
Locus_5055_Transcript_2/2_Conf_1.000	817	20	1.84E-36	EFO20733.1	58	157.147	198	116	hypothetical protein LOAG_07757
Locus_5056_Transcript_1/1_Conf_1.000	1087	20	1.33E-60	XP_001902393.1	74	238.039	192	143	hypothetical protein
Locus_5057_Transcript_1/2_Conf_1.000	726	20	2.07E-22	NP_492671.1	76	110.153	86	66	hypothetical protein Y106G6D.7
Locus_5057_Transcript_2/2_Conf_1.000	1487	20	6.93E-32	NP_492671.1	83	143.28	104	87	hypothetical protein Y106G6D.7
Locus_5058_Transcript_1/1_Conf_1.000	541	20	4.05E-32	NP_501668.1	75	141.354	107	81	Heat Shock Protein family member (hsp-12.6)
Locus_5059_Transcript_1/2_Conf_1.000	828	20	1.62E-120	CAR63570.1	91	436.417	270	248	putative epsilon subunit of coatomer protein complex isoform 2
Locus_5059_Transcript_2/2_Conf_1.000	828	20	1.62E-120	CAR63570.1	91	436.417	270	248	putative epsilon subunit of coatomer protein complex isoform 2
Locus_506_Transcript_1/1_Conf_1.000	698	20	1.69E-95	NP_501835.2	88	352.829	231	205	DIS3 (yeast disjunction abnormal) exonuclease homolog family member (dis-3)
Locus_5060_Transcript_1/1_Conf_1.000	421	20	5.62E-45	NP_495261.1	84	183.726	120	101	hypothetical protein F13H8.7
Locus_5061_Transcript_1/1_Conf_1.000	428	20	5.61E-21	XP_002630359.1	68	103.99	138	95	C. briggsae CBR-TAG-151 protein
Locus_5062_Transcript_1/2_Conf_1.000	387	0							
Locus_5062_Transcript_2/2_Conf_1.000	444	0							
Locus_5063_Transcript_1/1_Conf_1.000	512	0							
Locus_5064_Transcript_1/1_Conf_1.000	979	20	3.62E-51	XP_002639893.1	96	206.453	104	100	Hypothetical protein CBG08215
Locus_5065_Transcript_1/1_Conf_1.000	176	20	2.26E-06	XP_002640064.1	67	55.4546	56	38	Hypothetical protein CBG12546
Locus_5066_Transcript_1/1_Conf_1.000	223	0							
Locus_5067_Transcript_1/1_Conf_1.000	1247	15	8.93E-59	XP_002642646.1	72	232.261	208	150	Hypothetical protein CBG00026

Locus_5068_Transcript_1/1_Conf_1.000	1034	20	1.91E-154	NP_502054.2	87	549.666	341	297	ALdehyde deHydrogenase family member (alh-3)
Locus_5069_Transcript_1/2_Conf_1.000	784	20	7.83E-90	XP_002639463.1	83	334.339	233	194	C. briggsae CBR-OBR-4 protein
Locus_5069_Transcript_2/2_Conf_1.000	739	20	1.56E-89	XP_002639463.1	83	333.183	224	188	C. briggsae CBR-OBR-4 protein
Locus_507_Transcript_1/1_Conf_1.000	852	20	5.53E-103	NP_491370.1	84	378.252	273	231	Eukaryotic Initiation Factor family member (eif-3.H)
Locus_5070_Transcript_1/1_Conf_1.000	404	0							
Locus_5071_Transcript_1/1_Conf_1.000	507	0							
Locus_5072_Transcript_1/2_Conf_1.000	2697	20	1.10E-47	XP_002634045.1	61	196.823	239	146	Hypothetical protein CBG01584
Locus_5072_Transcript_2/2_Conf_1.000	2694	20	1.10E-47	XP_002634045.1	61	196.823	239	146	Hypothetical protein CBG01584
Locus_5073_Transcript_1/1_Conf_1.000	1471	20	4.62E-113	XP_002643397.1	71	412.92	408	292	Hypothetical protein CBG16012
Locus_5074_Transcript_1/1_Conf_1.000	2349	20	3.96E-131	XP_001895542.1	78	473.781	342	270	Biotin/lipoate A/B protein ligase family protein

Locus_5075_Transcript_1/1_Conf_1.000	2022	20	7.29E-163	NP_001024873.1	83	578.941	437	367	Nuclear Hormone Receptor family member (nhr-40)
Locus_5076_Transcript_1/1_Conf_1.000	585	20	7.34E-71	AAA97927.1	81	270.396	193	158	hum-3
Locus_5077_Transcript_1/1_Conf_1.000	1106	20	4.02E-121	NP_498559.1	81	439.113	331	269	hypothetical protein B0280.1
Locus_5078_Transcript_1/1_Conf_1.000	240	0							
Locus_5079_Transcript_1/2_Conf_0.500	977	20	4.72E-43	NP_001040990.1	56	179.489	280	158	hypothetical protein T23B5.1
Locus_5079_Transcript_2/2_Conf_0.500	977	20	4.72E-43	NP_001040990.1	56	179.489	280	158	hypothetical protein T23B5.1
Locus_508_Transcript_1/1_Conf_1.000	2300	20	2.46E-69	NP_001022696.1	56	268.47	504	283	hypothetical protein M88.5

Locus_5080_Transcript_1/1_Conf_1.000	280	0							
Locus_5081_Transcript_1/1_Conf_1.000	824	20	7.31E-49	NP_493396.1	62	198.364	259	163	hypothetical protein W04A4.5
Locus_5082_Transcript_1/1_Conf_1.000	160	0							
Locus_5083_Transcript_1/1_Conf_1.000	561	20	1.82E-49	NP_492376.1	67	199.134	198	134	MAFBx (F-box protein) homolog family member (mfb-1)
Locus_5084_Transcript_1/1_Conf_1.000	1201	20	2.16E-38	NP_510818.3	45	164.466	345	156	hypothetical protein F10D7.5
Locus_5085_Transcript_1/1_Conf_1.000	465	20	8.15E-20	XP_001900333.1	66	100.138	105	70	Anaphase promoting complex subunit 8 / cdc23 family protein
Locus_5086_Transcript_1/1_Conf_1.000	278	0							
Locus_5087_Transcript_1/1_Conf_1.000	613	20	5.58E-19	XP_001629955.1	86	98.2117	67	58	predicted protein
Locus_5088_Transcript_1/1_Conf_1.000	695	0							
Locus_5089_Transcript_1/1_Conf_1.000	1191	3	7.32E-47	NP_871624.2	50	192.586	362	183	hypothetical protein B0336.7
Locus_509_Transcript_1/1_Conf_1.000	461	5	2.39E-32	NP_505714.1	74	141.739	119	89	LiPid Depleted family member (lpd-9)
Locus_5090_Transcript_1/1_Conf_1.000	651	9	9.10E-106	NP_502119.2	95	386.726	215	205	hypothetical protein F54D1.6
Locus_5091_Transcript_1/2_Conf_1.000	721	20	1.21E-67	NP_492333.1	80	260.381	193	155	hypothetical protein F43G9.3
Locus_5091_Transcript_2/2_Conf_1.000	916	20	7.67E-85	NP_492333.1	82	318.161	226	186	hypothetical protein F43G9.3
Locus_5092_Transcript_1/1_Conf_1.000	269	20	8.08E-28	XP_002637628.1	84	126.716	88	74	Hypothetical protein CBG19373

Locus_5093_Transcript_1/1_Conf_1.000	945	3	1.79E-07	Q60YF6.3	49	61.2326	130	64	Mediator of RNA polymerase II transcription subunit 29
Locus_5094_Transcript_1/1_Conf_1.000	1093	20	6.47E-31	EFO19409.1	78	139.428	109	86	hypothetical protein LOAG_09084
Locus_5095_Transcript_1/1_Conf_1.000	479	4	5.03E-14	XP_002630619.1	67	80.8777	96	65	Hypothetical protein CBG02284
Locus_5096_Transcript_1/1_Conf_1.000	931	20	3.79E-87	XP_002633510.1	91	325.865	226	206	C. briggsae CBR-VHA-8 protein
Locus_5097_Transcript_1/1_Conf_1.000	524	0							
Locus_5098_Transcript_1/3_Conf_0.714	1618	20	2.07E-93	NP_492960.1	73	347.821	301	220	hypothetical protein C17D12.1
Locus_5098_Transcript_2/3_Conf_0.714	1614	20	2.06E-93	NP_492960.1	73	347.821	301	220	hypothetical protein C17D12.1
Locus_5098_Transcript_3/3_Conf_0.714	1614	20	2.06E-93	NP_492960.1	73	347.821	301	220	hypothetical protein C17D12.1
Locus_5099_Transcript_1/1_Conf_1.000	401	0							
Locus_51_Transcript_1/1_Conf_1.000	343	14	1.60E-15	XP_002634040.1	68	85.8853	119	81	C. briggsae CBR-VIT-6 protein
Locus_510_Transcript_1/1_Conf_1.000	3540	20	0	XP_002645914.1	71	1224.54	1162	831	Hypothetical protein CBG07670
Locus_5100_Transcript_1/1_Conf_1.000	324	0							
Locus_5101_Transcript_1/1_Conf_1.000	417	0							
Locus_5102_Transcript_1/1_Conf_1.000	215	0							
Locus_5103_Transcript_1/1_Conf_1.000	1367	20	2.77E-48	XP_001899202.1	55	197.593	319	177	RGL1
Locus_5104_Transcript_1/1_Conf_1.000	360	20	5.90E-47	NP_497894.1	84	190.274	113	96	hypothetical protein R07E5.13

Locus_5105_Transcript_1/1_Conf_1.000	495	20	1.36E-35	XP_002630954.1	67	152.525	158	107	C. briggsae CBR-TAG-184 protein
Locus_5106_Transcript_1/1_Conf_1.000	605	5	1.19E-10	NP_001021852.2	58	70.4774	73	43	hypothetical protein ZC434.9
Locus_5107_Transcript_1/1_Conf_1.000	138	9	5.56E-05	EFO27233.1	62	50.8322	45	28	CAMK/MLCK protein kinase
Locus_5108_Transcript_1/1_Conf_1.000	172	0							
Locus_5109_Transcript_1/1_Conf_1.000	247	20	1.79E-11	XP_002834351.1	100	72.4034	59	59	PREDICTED: hypothetical protein LOC100438152
Locus_511_Transcript_1/3_Conf_0.556	512	0							
Locus_511_Transcript_2/3_Conf_0.222	513	0							
Locus_511_Transcript_3/3_Conf_0.667	240	0							
Locus_5110_Transcript_1/1_Conf_1.000	452	2	4.02E-11	XP_002632149.1	54	71.2478	103	56	Hypothetical protein CBG07008
Locus_5111_Transcript_1/1_Conf_1.000	1614	20	1.08E-142	CAA84693.3	74	511.531	539	402	C. elegans protein D2045.2, partially confirmed by transcript evidence

Locus_5112_Transcript_1/1_Conf_1.000	358	20	8.57E-38	NP_492033.1	97	159.844	82	80	hypothetical protein M05B5.4
Locus_5113_Transcript_1/4_Conf_0.250	1233	0							
Locus_5113_Transcript_2/4_Conf_0.250	1275	0							
Locus_5113_Transcript_3/4_Conf_0.375	1742	0							
Locus_5113_Transcript_4/4_Conf_0.375	1742	0							
Locus_5114_Transcript_1/1_Conf_1.000	489	20	1.47E-29	NP_001022138.1	62	132.494	153	96	hypothetical protein F33G12.6
Locus_5115_Transcript_1/1_Conf_1.000	498	1	5.56E-05	XP_001440076.1	54	50.8322	111	61	hypothetical protein
Locus_5116_Transcript_1/1_Conf_1.000	582	0							
Locus_5117_Transcript_1/1_Conf_1.000	603	20	4.63E-55	NP_502998.2	75	218.009	196	147	Maternal Effect Lethal family member (mel-46)
Locus_5118_Transcript_1/1_Conf_1.000	930	20	6.78E-153	XP_002640032.1	91	544.273	311	286	Hypothetical protein CBG12504
Locus_5119_Transcript_1/1_Conf_1.000	778	20	1.16E-61	NP_001123010.1	65	240.736	269	177	related to yeast Vacuolar Protein Sorting factor family member (vps-39)
Locus_512_Transcript_1/5_Conf_0.667	1956	20	2.09E-66	XP_002642054.1	66	258.455	267	178	Hypothetical protein CBG17992
Locus_512_Transcript_2/5_Conf_0.667	2105	20	2.36E-79	XP_002642054.1	67	301.597	302	204	Hypothetical protein CBG17992
Locus_512_Transcript_3/5_Conf_0.667	2105	20	2.36E-79	XP_002642054.1	67	301.597	302	204	Hypothetical protein CBG17992
Locus_512_Transcript_4/5_Conf_0.667	2102	20	2.36E-79	XP_002642054.1	67	301.597	302	204	Hypothetical protein CBG17992
Locus_512_Transcript_5/5_Conf_0.667	2105	20	2.36E-79	XP_002642054.1	67	301.597	302	204	Hypothetical protein CBG17992
Locus_5120_Transcript_1/1_Conf_1.000	417	0							

Locus_5121_Transcript_1/4_Conf_0.556	546	20	1.04E-06	ZP_02693165.1	45	56.9954	155	71	hypothetical protein Epulo_08463
Locus_5121_Transcript_2/4_Conf_0.667	962	20	5.66E-09	XP_002630833.1	41	66.2402	264	109	C. briggsae CBR-VRK-1 protein
Locus_5121_Transcript_3/4_Conf_0.222	508	2	2.28E-04	NP_495185.1	69	48.9062	46	32	Vaccinia Related Kinase family member (vrk-1)
Locus_5121_Transcript_4/4_Conf_0.667	962								
Locus_5122_Transcript_1/1_Conf_1.000	432	20	2.25E-38	XP_002644784.1	74	161.77	131	97	Hypothetical protein CBG14799
Locus_5123_Transcript_1/1_Conf_1.000	347	0							
Locus_5124_Transcript_1/1_Conf_1.000	953	20	7.59E-91	XP_002630191.1	73	338.191	327	241	C. briggsae CBR-KAP-1 protein
Locus_5125_Transcript_1/1_Conf_1.000	367	20	8.51E-22	EFO17196.1	78	106.686	83	65	hypothetical protein LOAG_11307
Locus_5126_Transcript_1/1_Conf_1.000	2388	20	0	XP_002633792.1	85	1204.89	808	690	Hypothetical protein CBG03484

Locus_5127_Transcript_1/1_Conf_1.000	636	20	3.62E-88	NP_872179.1	91	328.176	198	182	Chaperonin Containing TCP-1 family member (cct-7)
Locus_5128_Transcript_1/1_Conf_1.000	685	20	1.48E-56	NP_492393.1	74	223.402	202	151	Heavy chain, Unconventional Myosin family member (hum-1)
Locus_5129_Transcript_1/1_Conf_1.000	1114	20	3.70E-114	NP_502795.2	69	416.001	370	258	Homolog of Hedgehog AcylTransferase family member (hhat-2)
Locus_513_Transcript_1/2_Conf_1.000	2102	20	0	NP_001022041.1	91	1107.43	691	632	UNCoordinated family member (unc-104)
Locus_513_Transcript_2/2_Conf_1.000	2108	20	0	NP_001022041.1	91	1102.43	693	632	UNCoordinated family member (unc-104)
Locus_5130_Transcript_1/1_Conf_1.000	491	0							
Locus_5131_Transcript_1/2_Conf_1.000	666	20	3.55E-44	XP_002640159.1	90	182.185	110	99	C. briggsae CBR-DAD-1 protein
Locus_5131_Transcript_2/2_Conf_1.000	204	0							

Locus_5132_Transcript_1/1_Conf_1.000	679	20	1.16E-29	EFO24192.1	57	134.035	190	110	hypothetical protein LOAG_04291
Locus_5133_Transcript_1/1_Conf_1.000	383	0							
Locus_5134_Transcript_1/1_Conf_1.000	1229	20	4.62E-68	NP_001022547.1	80	263.077	200	160	hypothetical protein F23H11.9
Locus_5135_Transcript_1/1_Conf_1.000	229	4	5.66E-13	XP_001891849.1	73	77.411	68	50	Retinoblastoma-associated protein A domain containing protein
Locus_5136_Transcript_1/1_Conf_1.000	695	20	6.11E-114	XP_002632905.1	92	414.075	228	211	Hypothetical protein CBG21657
Locus_5137_Transcript_1/1_Conf_1.000	532	0							
Locus_5138_Transcript_1/1_Conf_1.000	709	20	1.24E-85	XP_002631237.1	84	320.087	234	197	C. briggsae CBR-RSP-7 protein
Locus_5139_Transcript_1/1_Conf_1.000	907	20	2.82E-23	NP_001076697.1	55	113.62	200	110	Ref/ALY RNA export adaptor family member (aly-3)
Locus_514_Transcript_1/1_Conf_1.000	351	20	1.30E-17	NP_492539.1	67	92.8189	86	58	LEM domain protein family member (lem-3)
Locus_5140_Transcript_1/1_Conf_1.000	808	20	8.12E-61	XP_001898049.1	74	238.039	230	172	3' exoribonuclease family, domain 2 containing protein
Locus_5141_Transcript_1/2_Conf_1.000	1355	0							
Locus_5141_Transcript_2/2_Conf_1.000	797	0							
Locus_5142_Transcript_1/1_Conf_1.000	234	0							
Locus_5143_Transcript_1/1_Conf_1.000	1156	20	7.32E-113	NP_491924.1	74	411.764	354	264	hypothetical protein W02D3.4
Locus_5144_Transcript_1/1_Conf_1.000	212	20	1.85E-16	XP_002647661.1	98	88.9669	57	56	C. briggsae CBR-NCX-2 protein

Locus_5145_Transcript_1/1_Conf_1.000	1569	20	1.46E-104	XP_002639426.1	82	384.8	261	216	Hypothetical protein CBG04019
Locus_5146_Transcript_1/1_Conf_1.000	913	20	2.39E-54	XP_001902781.1	73	216.853	203	149	Ring canal kelch protein
Locus_5147_Transcript_1/2_Conf_1.000	853	0							
Locus_5147_Transcript_2/2_Conf_1.000	852	0							
Locus_5148_Transcript_1/1_Conf_1.000	283	6	1.08E-11	NP_507633.1	88	73.1738	36	32	hypothetical protein Y51A2D.14
Locus_5149_Transcript_1/1_Conf_1.000	947	20	3.34E-38	XP_002640137.1	76	163.31	132	101	C. briggsae CBR-CDC-25.1 protein
Locus_515_Transcript_1/1_Conf_1.000	803	5	9.28E-09	XP_001900765.1	56	65.0846	107	60	hypothetical protein Bm1_46515
Locus_5150_Transcript_1/1_Conf_1.000	493	0							
Locus_5151_Transcript_1/2_Conf_1.000	908	2	1.10E-43	NP_491566.1	62	181.415	223	140	hypothetical protein F48C1.6
Locus_5151_Transcript_2/2_Conf_1.000	908	2	1.10E-43	NP_491566.1	62	181.415	223	140	hypothetical protein F48C1.6
Locus_5152_Transcript_1/1_Conf_1.000	247	0							
Locus_5153_Transcript_1/1_Conf_1.000	417	0							
Locus_5154_Transcript_1/1_Conf_1.000	504	4	2.36E-22	NP_497264.1	58	108.612	173	101	hypothetical protein B0412.3
Locus_5155_Transcript_1/1_Conf_1.000	976	20	7.84E-131	NP_001022191.1	89	471.085	325	292	BCS1 (mitochondrial chaperone) homolog family member (bcs-1)
Locus_5156_Transcript_1/1_Conf_1.000	705	20	3.86E-55	NP_492377.1	73	218.779	191	141	SUPpressor family member (sup-17)
Locus_5157_Transcript_1/1_Conf_1.000	529	0							

Locus_5158_Transcript_1/1_Conf_1.000	778	20	1.19E-98	XP_002630624.1	92	363.614	205	190	C. briggsae CBR-PBS-3 protein
Locus_5159_Transcript_1/1_Conf_1.000	268	0							
Locus_516_Transcript_1/1_Conf_1.000	182	1	2.19E-04	XP_002647616.1	63	48.9062	44	28	Hypothetical protein CBG06707
Locus_5160_Transcript_1/1_Conf_1.000	1098	20	3.22E-171	NP_493572.2	91	605.52	344	314	hypothetical protein F39B2.8
Locus_5161_Transcript_1/2_Conf_1.000	852	20	7.19E-119	NP_509509.1	85	431.024	268	229	hypothetical protein D1009.1
Locus_5161_Transcript_2/2_Conf_1.000	1413	20	5.60E-177	XP_002645319.1	78	625.165	471	368	Hypothetical protein CBG00242
Locus_5162_Transcript_1/5_Conf_0.364	1230	0							
Locus_5162_Transcript_2/5_Conf_0.364	1438	0							
Locus_5162_Transcript_3/5_Conf_0.364	1046	0							
Locus_5162_Transcript_4/5_Conf_0.273	693	0							
Locus_5162_Transcript_5/5_Conf_0.364	1438	0							
Locus_5163_Transcript_1/1_Conf_1.000	572	0							
Locus_5164_Transcript_1/1_Conf_1.000	1329	20	4.09E-65	XP_002635088.1	55	253.447	381	212	C. briggsae CBR-ASP-6 protein

Locus_5165_Transcript_1/1_Conf_1.000	234	20	4.74E-28	XP_002048633.1	88	127.487	76	67	GJ11250
Locus_5166_Transcript_1/1_Conf_1.000	608	3	1.48E-08	XP_002633586.1	61	63.5438	92	57	C. briggsae CBR-SMG-3 protein
Locus_5167_Transcript_1/1_Conf_1.000	202	0							
Locus_5168_Transcript_1/1_Conf_1.000	823	20	1.41E-92	NP_001022714.1	81	343.584	262	214	ALIX (Apoptosis-linked gene 2 interacting protein X) homolog family member (alx-1)
Locus_5169_Transcript_1/2_Conf_1.000	1180	0							
Locus_5169_Transcript_2/2_Conf_1.000	1129	0							
Locus_517_Transcript_1/5_Conf_0.500	1547	7	2.72E-79	XP_002631173.1	70	300.827	279	198	Hypothetical protein CBG02959
Locus_517_Transcript_2/5_Conf_0.200	501	8	2.83E-04	CAA92456.3	41	48.521	158	66	C. elegans protein C53B4.4b, partially confirmed by transcript evidence
Locus_517_Transcript_3/5_Conf_0.500	1760	7	3.22E-79	XP_002631173.1	70	300.827	279	198	Hypothetical protein CBG02959
Locus_517_Transcript_4/5_Conf_0.400	812	8	9.08E-04	CAA92456.3	41	48.521	158	66	C. elegans protein C53B4.4b, partially confirmed by transcript evidence
Locus_517_Transcript_5/5_Conf_0.500	1673	7	3.03E-79	XP_002631173.1	70	300.827	279	198	Hypothetical protein CBG02959
Locus_5170_Transcript_1/1_Conf_1.000	1200	20	1.36E-24	XP_002635272.1	55	118.627	354	196	Hypothetical protein CBG11516
Locus_5171_Transcript_1/1_Conf_1.000	578	0							
Locus_5172_Transcript_1/1_Conf_1.000	397	0							
Locus_5173_Transcript_1/1_Conf_1.000	275	20	3.59E-36	AAD31839.1	85	154.451	91	78	AF132291_1ancylostoma-secreted protein 1 precursor
Locus_5174_Transcript_1/1_Conf_1.000	983	20	2.61E-158	CBI70492.1	94	562.377	328	309	vacuolar ATPase a subunit
Locus_5175_Transcript_1/3_Conf_0.667	1913	20	3.72E-68	XP_001899496.1	64	264.233	346	222	LIM-domain binding protein
Locus_5175_Transcript_2/3_Conf_0.667	1828	20	1.21E-68	XP_001899496.1	55	265.774	441	244	LIM-domain binding protein
Locus_5175_Transcript_3/3_Conf_0.667	1934	20	1.86E-67	XP_001899496.1	64	261.922	346	222	LIM-domain binding protein
Locus_5176_Transcript_1/1_Conf_1.000	407	0							
Locus_5177_Transcript_1/1_Conf_1.000	371	0							
Locus_5178_Transcript_1/1_Conf_1.000	1614	20	2.30E-68	XP_001892034.1	58	264.618	396	232	erythroblast macrophage protein EMP

Locus_5179_Transcript_1/1_Conf_1.000	460	20	4.84E-17	EFO16233.1	59	90.8929	122	73	variant SH3 domain-containing protein
Locus_518_Transcript_1/2_Conf_1.000	548	20	6.04E-55	XP_002639660.1	96	217.238	151	145	C. briggsae CBR-RPS-15 protein
Locus_518_Transcript_2/2_Conf_1.000	536	20	8.34E-51	XP_002639660.1	93	203.371	151	141	C. briggsae CBR-RPS-15 protein
Locus_5180_Transcript_1/1_Conf_1.000	425	20	1.16E-50	NP_491930.1	89	202.601	137	123	DiHydroOrotate Dehydrogenas family member (dhod-1)
Locus_5181_Transcript_1/1_Conf_1.000	560	0							
Locus_5182_Transcript_1/1_Conf_1.000	891	20	6.67E-54	NP_510298.1	87	215.312	141	124	AMP-Activated Kinase Beta subunit family member (aakb-1)
Locus_5183_Transcript_1/1_Conf_1.000	774	4	8.19E-84	NP_501169.1	80	314.309	232	187	hypothetical protein F42C5.9
Locus_5184_Transcript_1/1_Conf_1.000	1066	20	4.31E-141	NP_499987.2	86	505.368	322	278	hypothetical protein F56B3.8
Locus_5185_Transcript_1/2_Conf_1.000	978	20	1.37E-58	NP_504573.1	72	231.106	191	138	hypothetical protein Y38A10A.7

Locus_5185_Transcript_2/2_Conf_1.000	801	20	8.91E-36	XP_002639559.1	97	154.836	80	78	C. briggsae CBR-MEK-2 protein
Locus_5186_Transcript_1/1_Conf_1.000	773	0							
Locus_5187_Transcript_1/1_Conf_1.000	392	0							
Locus_5188_Transcript_1/1_Conf_1.000	2163	20	4.53E-118	ADK24110.1	55	430.254	759	418	Eps15 (endocytosis protein) homologous sequence protein 1, isoform b, confirmed by transcript evidence
Locus_5189_Transcript_1/1_Conf_1.000	206	0							
Locus_519_Transcript_1/1_Conf_1.000	634	0							
Locus_5190_Transcript_1/1_Conf_1.000	2178	1	7.54E-04	CAR63599.1	56	50.8322	78	44	hypothetical protein
Locus_5191_Transcript_1/1_Conf_1.000	1858	20	1.76E-115	EFO25151.1	58	421.394	631	370	MutS domain III family protein
Locus_5192_Transcript_1/1_Conf_1.000	445	0							
Locus_5193_Transcript_1/1_Conf_1.000	607	20	2.67E-50	NP_498260.2	93	202.216	116	109	DEAD boX helicase homolog family member (ddx-23)
Locus_5194_Transcript_1/1_Conf_1.000	597	20	7.73E-31	YP_003592777.1	57	137.502	198	113	alkaline phosphatase
Locus_5195_Transcript_1/1_Conf_1.000	603	20	2.91E-41	XP_002639088.1	70	172.17	165	116	C. briggsae CBR-TAG-83 protein
Locus_5196_Transcript_1/2_Conf_1.000	910	20	9.72E-32	EFO19475.1	73	141.739	124	91	adrenal gland protein AD-001
Locus_5196_Transcript_2/2_Conf_1.000	657	20	5.22E-32	EFO19475.1	73	141.739	124	91	adrenal gland protein AD-001

Locus_5197_Transcript_1/2_Conf_1.000	577	4	4.30E-28	Q20548.2	69	128.257	160	111	Probable RING finger protein 207 homolog
Locus_5197_Transcript_2/2_Conf_1.000	577	4	4.30E-28	Q20548.2	69	128.257	160	111	Probable RING finger protein 207 homolog
Locus_5198_Transcript_1/1_Conf_1.000	172	0							
Locus_5199_Transcript_1/1_Conf_1.000	1296	20	1.23E-159	NP_497264.1	78	567.385	454	356	hypothetical protein B0412.3
Locus_52_Transcript_1/1_Conf_1.000	428	20	1.69E-17	CAY80864.1	68	92.4337	74	51	Bat2p
Locus_520_Transcript_1/1_Conf_1.000	617	20	6.00E-45	XP_002647198.1	72	184.496	180	130	C. briggsae CBR-LACT-9 protein
Locus_5200_Transcript_1/1_Conf_1.000	657	20	5.77E-31	NP_501284.1	59	138.272	177	105	Temporarily Assigned Gene name family member (tag-321)
Locus_5201_Transcript_1/1_Conf_1.000	1060	20	2.04E-42	NP_001024128.1	62	177.563	319	200	EEA1 (Early Endosome Antigen, Rab effector) homolog family member (eea-1)
Locus_5202_Transcript_1/1_Conf_1.000	253	2	2.18E-04	XP_002167274.1	52	48.9062	76	40	PREDICTED: similar to Chromobox protein homolog 5
Locus_5203_Transcript_1/1_Conf_1.000	234	0							
Locus_5204_Transcript_1/1_Conf_1.000	1482	20	1.61E-105	EFO27140.1	67	387.882	397	269	mannose-6-phosphate isomerase
Locus_5205_Transcript_1/1_Conf_1.000	433	0							
Locus_5206_Transcript_1/1_Conf_1.000	142	0							
Locus_5207_Transcript_1/2_Conf_1.000	1141	20	2.22E-122	NP_493209.1	78	443.351	350	274	NuDiX family member (ndx-1)
Locus_5207_Transcript_2/2_Conf_1.000	1141	20	2.22E-122	NP_493209.1	78	443.351	350	274	NuDiX family member (ndx-1)
Locus_5208_Transcript_1/2_Conf_1.000	476	9	1.33E-14	EFO21491.1	59	82.8037	136	81	hypothetical protein LOAG_06999
Locus_5208_Transcript_2/2_Conf_1.000	288	0							
Locus_5209_Transcript_1/2_Conf_1.000	3271	20	6.74E-164	XP_002631594.1	80	583.178	481	387	C. briggsae CBR-ALH-7 protein
Locus_5209_Transcript_2/2_Conf_1.000	1687	20	4.56E-124		61	440.654	540	334	protein F43G9.7
Locus_521_Transcript_1/1_Conf_1.000	2381	20	0	NP_490886.2	69	734.561	780	544	hypothetical protein Y71G12B.11
Locus_5210_Transcript_1/1_Conf_1.000	566	20	5.80E-27	EFO25650.1	71	124.405	138	99	hypothetical protein LOAG_02839
Locus_5211_Transcript_1/1_Conf_1.000	1690	20	1.92E-97	XP_002632959.1	76	361.303	326	248	C. briggsae CBR-RAD-26 protein
Locus_5212_Transcript_1/1_Conf_1.000	598	0							

Locus_5213_Transcript_1/1_Conf_1.000	706	20	8.49E-103	NP_001022764.1	88	377.096	237	209	BTB and MATH domain containing family member (bath-43)
Locus_5214_Transcript_1/1_Conf_1.000	440	0							
Locus_5215_Transcript_1/1_Conf_1.000	777	20	1.17E-45	XP_002646524.1	90	187.578	109	99	C. briggsae CBR-SNR-2 protein
Locus_5216_Transcript_1/1_Conf_1.000	450	20	3.01E-83	XP_002763611.1	100	310.842	149	149	PREDICTED: 60S ribosomal protein L3-like isoform 1
Locus_5217_Transcript_1/1_Conf_1.000	338	20	3.25E-21	NP_508961.2	66	104.76	107	71	CYtochrome P450 family member (cyp-43A1)
Locus_5218_Transcript_1/1_Conf_1.000	1259	20	2.06E-71	NP_491343.1	64	274.248	408	264	Cell Division Cycle related family member (cdc-6)
Locus_5219_Transcript_1/1_Conf_1.000	679	20	1.66E-44	XP_002642246.1	81	183.341	161	131	Hypothetical protein CBG18231
Locus_522_Transcript_1/3_Conf_0.333	228	0							

Locus_522_Transcript_2/3_Conf_0.667	1607	20	3.27E-83	XP_002639488.1	57	313.923	487	282	C. briggsae CBR-NPP-2 protein
Locus_522_Transcript_3/3_Conf_0.667	1607	20	1.47E-83	XP_002639488.1	58	315.079	487	283	C. briggsae CBR-NPP-2 protein
Locus_5220_Transcript_1/6_Conf_0.688	4917	20	0	NP_001021830.1	83	940.258	693	582	ABC Transporter, Mitochondrial family member (abtm-1)
Locus_5220_Transcript_2/6_Conf_0.125	283	0							
Locus_5220_Transcript_3/6_Conf_0.125	283	0							
Locus_5220_Transcript_4/6_Conf_0.688	4917	20	0	NP_001021830.1	83	940.258	693	582	ABC Transporter, Mitochondrial family member (abtm-1)
Locus_5220_Transcript_5/6_Conf_0.688	4917	20	0	NP_001021830.1	83	940.258	693	582	ABC Transporter, Mitochondrial family member (abtm-1)
Locus_5220_Transcript_6/6_Conf_0.688	4917	20	0	NP_001021830.1	83	940.258	693	582	ABC Transporter, Mitochondrial family member (abtm-1)

Locus_5221_Transcript_1/2_Conf_1.000	1060	20	1.05E-155		88	553.903	353	312	IMP dehydrogenase (EC 1.1.1.205) T22D1.3
Locus_5221_Transcript_2/2_Conf_1.000	1415	20	0	XP_002633039.1	88	766.148	483	426	Hypothetical protein CBG05718
Locus_5222_Transcript_1/1_Conf_1.000	855	20	7.04E-98	NP_495552.2	81	361.303	237	193	Nematode AStacin protease family member (nas-7)
Locus_5223_Transcript_1/1_Conf_1.000	401	20	7.28E-61	NP_492363.1	91	236.498	131	120	yeast PRP (splicing factor) related family member (prp-4)
Locus_5224_Transcript_1/1_Conf_1.000	1437	20	7.55E-153	NP_492343.2	85	545.043	371	318	Silencing In Germline defective family member (sig-7)
Locus_5225_Transcript_1/1_Conf_1.000	1331	20	5.03E-156	XP_001901254.1	77	555.444	417	325	Regulator of nonsense transcripts 1 homolog
Locus_5226_Transcript_1/1_Conf_1.000	159	9	2.54E-13	XP_002646356.1	82	78.5666	51	42	Hypothetical protein CBG12070
Locus_5227_Transcript_1/1_Conf_1.000	313	4	2.23E-33	XP_002633326.1	83	145.206	100	83	Hypothetical protein CBG06063
Locus_5228_Transcript_1/1_Conf_1.000	1259	20	1.71E-33	XP_002639589.1	51	148.288	358	185	Hypothetical protein CBG04227
Locus_5229_Transcript_1/1_Conf_1.000	202	0							

Locus_523_Transcript_1/1_Conf_1.000	695	20	1.43E-62	EFO17307.1	74	243.432	230	171	hypothetical protein LOAG_11192
Locus_5230_Transcript_1/1_Conf_1.000	1028	20	2.37E-64	NP_497807.1	67	250.366	238	161	hypothetical protein T02C12.2
Locus_5231_Transcript_1/2_Conf_1.000	1861	20	0	NP_505977.1	91	961.059	585	533	PYruvate Carboxylase family member (pyc-1)
Locus_5231_Transcript_2/2_Conf_1.000	1834	20	0	NP_505977.1	92	968.763	576	533	PYruvate Carboxylase family member (pyc-1)
Locus_5232_Transcript_1/1_Conf_1.000	296	20	2.00E-18	XP_536549.2	97	95.5153	88	86	PREDICTED: similar to 40S ribosomal protein S25

Locus_5233_Transcript_1/1_Conf_1.000	1017	20	8.43E-124	XP_001088540.2	100	270.396	199	199	PREDICTED: hypothetical protein LOC700140
Locus_5234_Transcript_1/1_Conf_1.000	689	2	2.19E-07	NP_498866.1	61	60.077	72	44	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-96)
Locus_5235_Transcript_1/1_Conf_1.000	357	0							
Locus_5236_Transcript_1/1_Conf_1.000	829	20	1.30E-61	XP_002641966.1	71	240.736	202	144	Hypothetical protein CBG16672
Locus_5237_Transcript_1/2_Conf_1.000	1055	20	3.80E-49	NP_495976.1	76	199.904	167	127	hypothetical protein C01G6.4
Locus_5237_Transcript_2/2_Conf_1.000	1058	20	3.82E-49	NP_495976.1	76	199.904	167	127	hypothetical protein C01G6.4
Locus_5238_Transcript_1/1_Conf_1.000	318	20	4.33E-29	XP_001894880.1	76	130.954	104	80	hypothetical protein
Locus_5239_Transcript_1/1_Conf_1.000	923	5	3.77E-39	Q61T02.2	53	166.392	315	168	Lysine-specific demethylase rbr-2

Locus_524_Transcript_1/1_Conf_1.000	1241	20	0	NP_509693.1	88	658.677	407	360	hypothetical protein W07E11.1
Locus_5240_Transcript_1/1_Conf_1.000	250	0							
Locus_5241_Transcript_1/1_Conf_1.000	180	8	8.57E-17	NP_501908.2	86	90.1225	58	50	hypothetical protein Y43C5B.3
Locus_5242_Transcript_1/2_Conf_1.000	730	8	2.24E-16	NP_500566.1	48	90.1225	251	122	WAPL (Drosophila Wings APart-Like cohesin interactor) family member (wapl-1)
Locus_5242_Transcript_2/2_Conf_1.000	721	11	1.61E-19	NP_500566.1	47	100.523	248	119	WAPL (Drosophila Wings APart-Like cohesin interactor) family member (wapl-1)
Locus_5243_Transcript_1/3_Conf_0.500	695	20	6.28E-18	XP_002639457.1	75	95.1301	79	60	C. briggsae CBR-HRPF-1 protein
Locus_5243_Transcript_2/3_Conf_0.500	683	20	6.02E-18	XP_002639457.1	75	95.1301	79	60	C. briggsae CBR-HRPF-1 protein
Locus_5243_Transcript_3/3_Conf_0.500	683	20	6.02E-18	XP_002639457.1	75	95.1301	79	60	C. briggsae CBR-HRPF-1 protein
Locus_5244_Transcript_1/1_Conf_1.000	139	0							
Locus_5245_Transcript_1/1_Conf_1.000	794	20	3.13E-110	NP_505980.1	86	402.134	264	228	hypothetical protein D2023.6

Locus_5246_Transcript_1/1_Conf_1.000	1065	20	4.24E-80	NP_493639.1	71	302.753	329	236	hypothetical protein F23F1.5
Locus_5247_Transcript_1/2_Conf_1.000	728	20	2.97E-45	NP_501852.1	63	186.037	241	154	hypothetical protein T14G10.7
Locus_5247_Transcript_2/2_Conf_1.000	728	20	2.97E-45	NP_501852.1	63	186.037	241	154	hypothetical protein T14G10.7
Locus_5248_Transcript_1/1_Conf_1.000	523	1	4.23E-04	XP_002637717.1	42	48.1358	176	74	C. briggsae CBR-SDC-3 protein
Locus_5249_Transcript_1/1_Conf_1.000	867	20	3.32E-18	NP_497087.1	61	96.6709	122	75	hypothetical protein Y53F4B.3
Locus_525_Transcript_1/3_Conf_0.667	1811	20	1.94E-111	XP_002638547.1	71	407.912	380	273	Hypothetical protein CBG05583
Locus_525_Transcript_2/3_Conf_0.667	1429	20	5.79E-113	XP_002638547.1	70	412.535	390	276	Hypothetical protein CBG05583

Locus_525_Transcript_3/3_Conf_0.667	1802	20	1.93E-111	XP_002638547.1	71	407.912	383	272	Hypothetical protein CBG05583
Locus_5250_Transcript_1/1_Conf_1.000	516	20	7.83E-32	XP_002632939.1	74	140.198	119	89	Hypothetical protein CBG21694
Locus_5251_Transcript_1/1_Conf_1.000	810	2	1.76E-15	NP_001024867.1	56	87.4261	169	95	hypothetical protein T01B4.3
Locus_5252_Transcript_1/4_Conf_0.667	1401	20	2.56E-73	NP_504395.2	53	280.796	480	259	hypothetical protein Y47A7.1
Locus_5252_Transcript_2/4_Conf_0.667	1956	20	2.45E-91	NP_504395.2	52	341.273	645	340	hypothetical protein Y47A7.1
Locus_5252_Transcript_3/4_Conf_0.667	1956	20	4.18E-91	NP_504395.2	52	340.502	645	339	hypothetical protein Y47A7.1
Locus_5252_Transcript_4/4_Conf_0.667	1956	20	4.18E-91	NP_504395.2	52	340.502	645	339	hypothetical protein Y47A7.1
Locus_5253_Transcript_1/1_Conf_1.000	448	4	3.31E-05	XP_001888410.1	62	51.6026	53	33	predicted protein
Locus_5254_Transcript_1/1_Conf_1.000	341	0							
Locus_5255_Transcript_1/1_Conf_1.000	1262	20	3.72E-113	NP_741036.2	88	412.92	325	287	DNaJ domain (prokaryotic heat shock protein) family member (dnj-20)
Locus_5256_Transcript_1/1_Conf_1.000	918	4	2.62E-16	XP_002648995.1	53	90.5077	189	101	C. briggsae CBR-CID-1 protein
Locus_5257_Transcript_1/1_Conf_1.000	356	0							
Locus_5258_Transcript_1/1_Conf_1.000	1524	20	3.55E-164	NP_001022322.1	89	582.793	378	337	hypothetical protein T05H10.7
Locus_5259_Transcript_1/1_Conf_1.000	771	20	5.00E-33	XP_001896542.1	55	145.591	254	140	hypothetical protein Bm1_25410

Locus_526_Transcript_1/3_Conf_0.714	886	20	1.96E-67	EFO25012.1	74	235.343	197	146	hypothetical protein LOAG_03476
Locus_526_Transcript_2/3_Conf_0.286	842	20	2.44E-63	NP_498874.2	89	246.514	137	123	hypothetical protein F42H10.3
Locus_526_Transcript_3/3_Conf_0.714	791	20	9.44E-75	NP_498874.2	71	284.263	228	164	hypothetical protein F42H10.3
Locus_5260_Transcript_1/2_Conf_1.000	718	20	1.75E-42	XP_001893741.1	72	176.792	135	98	LIM domain containing protein
Locus_5260_Transcript_2/2_Conf_1.000	718	20	1.75E-42	XP_001893741.1	72	176.792	135	98	LIM domain containing protein
Locus_5261_Transcript_1/1_Conf_1.000	609	20	1.13E-80	XP_002629767.1	92	303.138	153	141	Hypothetical protein CBG01005
Locus_5262_Transcript_1/1_Conf_1.000	745	20	1.21E-97	XP_002629847.1	89	360.147	244	219	C. briggsae CBR-EAT-3 protein
Locus_5263_Transcript_1/1_Conf_1.000	251	9	5.18E-11	NP_001023416.1	66	70.8626	59	39	Helix Loop Helix family member (hlh-30)
Locus_5264_Transcript_1/1_Conf_1.000	775	0							
Locus_5265_Transcript_1/1_Conf_1.000	311	0							
Locus_5266_Transcript_1/1_Conf_1.000	519	0							

Locus_5267_Transcript_1/1_Conf_1.000	717	20	1.33E-74	XP_002631269.1	85	283.493	187	159	Hypothetical protein CBG03077
Locus_5268_Transcript_1/3_Conf_0.286	741	6	1.11E-34	XP_002636592.1	50	150.984	291	147	C. briggsae CBR-APE-1 protein
Locus_5268_Transcript_2/3_Conf_0.714	2045	20	2.32E-132	XP_002636592.1	66	477.633	524	346	C. briggsae CBR-APE-1 protein
Locus_5268_Transcript_3/3_Conf_0.714	2045	20	2.32E-132	XP_002636592.1	66	477.633	524	346	C. briggsae CBR-APE-1 protein
Locus_5269_Transcript_1/1_Conf_1.000	1287	20	2.32E-17	XP_002639309.1	67	94.7449	101	68	C. briggsae CBR-ICP-1 protein
Locus_527_Transcript_1/1_Conf_1.000	666	20	8.44E-46	XP_002643165.1	69	187.578	165	114	Hypothetical protein CBG15346
Locus_5270_Transcript_1/1_Conf_1.000	599	20	5.73E-26	XP_002630901.1	93	121.324	63	59	Hypothetical protein CBG02625
Locus_5271_Transcript_1/1_Conf_1.000	335	20	2.25E-38	NP_498053.2	81	161.77	111	91	hypothetical protein C27F2.9
Locus_5272_Transcript_1/1_Conf_1.000	656	0							
Locus_5273_Transcript_1/1_Conf_1.000	1697	20	0	XP_002639055.1	87	816.609	551	480	C. briggsae CBR-GCY-28 protein
Locus_5274_Transcript_1/1_Conf_1.000	1273	1	2.60E-21	EFO18350.1	64	107.842	114	74	hypothetical protein LOAG_10146
Locus_5275_Transcript_1/1_Conf_1.000	298	20	2.26E-46	XP_002631126.1	95	188.348	99	95	C. briggsae CBR-SHN-1 protein
Locus_5276_Transcript_1/1_Conf_1.000	1289	20	2.79E-71	XP_001900679.1	56	273.863	391	220	Endonuclease/Exonuclease/phosphatase family protein
Locus_5277_Transcript_1/1_Conf_1.000	3242	20	4.08E-129	EFO26197.1	74	467.618	375	278	zinc finger protein
Locus_5278_Transcript_1/1_Conf_1.000	659	6	2.50E-34	NP_001021024.1	60	149.443	156	95	IntraMembrane Protease (IMPAS) family member (imp-1)
Locus_5279_Transcript_1/1_Conf_1.000	229	0							
Locus_528_Transcript_1/2_Conf_1.000	1393	20	2.64E-46	NP_492005.1	69	191.045	192	133	hypothetical protein F22D6.2

Locus_528_Transcript_2/2_Conf_1.000	1378	20	1.10E-44	NP_492005.1	65	185.652	192	126	hypothetical protein F22D6.2
Locus_5280_Transcript_1/1_Conf_1.000	571	1	1.88E-04	EFN66680.1	45	49.6766	192	87	Ubiquitin associated and SH3 domain-containing protein B
Locus_5281_Transcript_1/1_Conf_1.000	320	0							
Locus_5282_Transcript_1/1_Conf_1.000	287	0							
Locus_5283_Transcript_1/1_Conf_1.000	756	0							
Locus_5284_Transcript_1/1_Conf_1.000	1128	20	2.22E-106	AAV41897.1	76	390.193	382	292	SAX-2
Locus_5285_Transcript_1/3_Conf_0.600	546	8	1.77E-22	XP_002646171.1	62	109.383	127	80	C. briggsae CBR-APB-3 protein
Locus_5285_Transcript_2/3_Conf_0.600	604	9	1.36E-22	XP_002646171.1	62	110.153	127	80	C. briggsae CBR-APB-3 protein
Locus_5285_Transcript_3/3_Conf_0.600	604	8	2.32E-22	XP_002646171.1	62	109.383	127	80	C. briggsae CBR-APB-3 protein
Locus_5286_Transcript_1/1_Conf_1.000	228	20	1.94E-29	NP_500082.1	88	132.109	75	66	CaLPain family member (clp-7)
Locus_5287_Transcript_1/1_Conf_1.000	368	0							
Locus_5288_Transcript_1/2_Conf_1.000	549	20	6.51E-89	XP_002639128.1	95	330.102	182	173	C. briggsae CBR-SPG-7 protein

Locus_5288_Transcript_2/2_Conf_1.000	231	20	1.43E-32	XP_002639128.1	97	142.51	76	74	C. briggsae CBR-SPG-7 protein
Locus_5289_Transcript_1/3_Conf_0.667	610	20	1.65E-31	XP_002647662.1	55	139.813	181	101	Hypothetical protein CBG06772
Locus_5289_Transcript_2/3_Conf_0.667	618	20	1.72E-31	NP_504413.1	55	139.813	159	89	hypothetical protein Y49G5A.1
Locus_5289_Transcript_3/3_Conf_0.667	618	20	2.93E-31	XP_002647662.1	55	139.043	180	100	Hypothetical protein CBG06772
Locus_529_Transcript_1/1_Conf_1.000	603	20	1.15E-29	EFO26691.1	89	133.65	89	80	dynein light chain 2B
Locus_5290_Transcript_1/1_Conf_1.000	1254	20	2.53E-162	NP_500894.1	77	576.244	426	329	INneXin family member (inx-7)
Locus_5291_Transcript_1/1_Conf_1.000	335	20	1.97E-34	XP_002637506.1	98	148.673	72	71	C. briggsae CBR-INX-10 protein
Locus_5292_Transcript_1/1_Conf_1.000	306	20	2.33E-27	EFO16836.1	74	125.176	100	74	autophagy protein Apg9 containing protein
Locus_5293_Transcript_1/1_Conf_1.000	978	20	5.23E-50	NP_001040678.1	88	202.601	117	103	hypothetical protein K11D2.4
Locus_5294_Transcript_1/1_Conf_1.000	962	20	1.71E-114	AAT28332.1	99	416.772	198	197	glutathione peroxidase
Locus_5295_Transcript_1/1_Conf_1.000	1306	20	1.33E-44	NP_506059.1	64	185.267	242	156	RNP (RRM RNA binding domain) containing family member (rnp-1)
Locus_5296_Transcript_1/1_Conf_1.000	451	0							
Locus_5297_Transcript_1/1_Conf_1.000	442	0							
Locus_5298_Transcript_1/1_Conf_1.000	182	0							
Locus_5299_Transcript_1/1_Conf_1.000	385	20	1.28E-25	EFO23813.1	66	119.398	109	73	cuticlin 1
Locus_53_Transcript_1/1_Conf_1.000	607	20	1.15E-61	ACS37721.1	83	239.965	142	118	C-type lectin-1

Locus_530_Transcript_1/1_Conf_1.000	1687	20	1.18E-30	EFO21568.1	48	139.428	321	157	hypothetical protein LOAG_06919
Locus_5300_Transcript_1/1_Conf_1.000	1078	20	4.94E-84	EFO18955.1	76	315.849	284	216	protein phosphatase 2C containing protein
Locus_5301_Transcript_1/1_Conf_1.000	497	20	1.23E-44	NP_493571.1	95	182.57	92	88	Ribosomal Protein, Small subunit family member (rps-26)
Locus_5302_Transcript_1/1_Conf_1.000	826	20	5.59E-81	XP_002642370.1	66	305.064	277	183	C. briggsae CBR-RAB-33 protein
Locus_5303_Transcript_1/1_Conf_1.000	577	20	1.79E-58	EFO21722.1	81	229.18	197	160	A-macroglobulin complement component family protein
Locus_5304_Transcript_1/1_Conf_1.000	811	20	2.12E-77	NP_741838.1	72	293.123	248	180	GLYcosylation related family member (gly-12)
Locus_5305_Transcript_1/1_Conf_1.000	622	20	1.31E-23	XP_001631156.1	63	113.62	150	95	predicted protein
Locus_5306_Transcript_1/1_Conf_1.000	1077	20	1.06E-78	NP_497264.1	66	298.13	349	233	hypothetical protein B0412.3
Locus_5307_Transcript_1/1_Conf_1.000	579	0							
Locus_5308_Transcript_1/1_Conf_1.000	799	20	9.29E-94	NP_504502.1	84	347.436	234	198	hypothetical protein F25B4.1
Locus_5309_Transcript_1/1_Conf_1.000	150	0							
Locus_531_Transcript_1/1_Conf_1.000	700	20	3.71E-58	EFO15889.1	66	228.794	236	156	hypothetical protein LOAG_12619
Locus_5310_Transcript_1/2_Conf_1.000	682	20	3.47E-74	NP_509589.1	75	281.952	209	158	hypothetical protein ZK899.2
Locus_5310_Transcript_2/2_Conf_1.000	682	20	1.01E-73	NP_509589.1	75	280.411	209	158	hypothetical protein ZK899.2
Locus_5311_Transcript_1/1_Conf_1.000	263	20	3.00E-14	XP_002638233.1	69	81.6481	82	57	Hypothetical protein CBG15892
Locus_5312_Transcript_1/1_Conf_1.000	301	0							

Locus_5313_Transcript_1/3_Conf_0.667	799	20	1.10E-94	NP_490891.1	88	350.517	269	237	hypothetical protein Y71G12B.8
Locus_5313_Transcript_2/3_Conf_0.667	799	20	1.10E-94	NP_490891.1	88	350.517	269	237	hypothetical protein Y71G12B.8
Locus_5313_Transcript_3/3_Conf_0.667	799	20	1.10E-94	NP_490891.1	88	350.517	269	237	hypothetical protein Y71G12B.8
Locus_5314_Transcript_1/1_Conf_1.000	199	8	6.01E-23	XP_002637217.1	90	110.538	64	58	Hypothetical protein CBG18883
Locus_5315_Transcript_1/1_Conf_1.000	944	20	3.83E-127	XP_002633092.1	90	458.759	279	252	Hypothetical protein CBG05779
Locus_5316_Transcript_1/1_Conf_1.000	420	20	1.88E-16	NP_491552.2	53	88.9669	143	76	LEThal family member (let-363)
Locus_5317_Transcript_1/1_Conf_1.000	1788	20	2.31E-157	NP_498283.1	70	560.451	564	400	hypothetical protein C28H8.3
Locus_5318_Transcript_1/1_Conf_1.000	756	0							
Locus_5319_Transcript_1/1_Conf_1.000	688	5	3.73E-15	XP_002647047.1	46	85.8853	247	115	Hypothetical protein CBG03565
Locus_532_Transcript_1/1_Conf_1.000	510	20	3.04E-25	NP_492974.2	74	118.242	87	65	Kex-2 Proprotein Convertase family member (kpc-1)
Locus_5320_Transcript_1/1_Conf_1.000	1678	20	3.18E-161	NP_001023664.1	86	573.163	414	359	Kinesin Light Chain family member (klc-2)
Locus_5321_Transcript_1/1_Conf_1.000	1072	2	4.84E-07	XP_001897538.1	46	60.077	174	81	hypothetical protein Bm1_30495
Locus_5322_Transcript_1/1_Conf_1.000	908	20	2.67E-90	EFO28128.1	74	336.265	309	230	hypothetical protein LOAG_00362
Locus_5323_Transcript_1/1_Conf_1.000	1079	2	2.05E-13	NP_740965.2	48	81.2629	265	129	hypothetical protein B0432.13

Locus_5324_Transcript_1/1_Conf_1.000	1783	20	0	NP_502054.2	88	870.922	572	506	ALdehyde deHydrogenase family member (alh-3)
Locus_5325_Transcript_1/1_Conf_1.000	1275	20	1.77E-86	NP_494438.2	75	324.324	271	204	hypothetical protein Y25C1A.7
Locus_5326_Transcript_1/2_Conf_1.000	308	20	9.82E-10	NP_498217.2	75	66.6254	56	42	abnormal embryonic PARtitioning of cytoplasm family member (par-3)
Locus_5326_Transcript_2/2_Conf_1.000	280	0							
Locus_5327_Transcript_1/4_Conf_0.583	714	7	1.25E-16	NP_493601.2	45	90.8929	242	111	FERM domain (protein4.1-ezrin-radixin-moesin) family member (frm-1)
Locus_5327_Transcript_2/4_Conf_0.583	723	4	2.51E-12	NP_493601.2	45	76.6406	243	110	FERM domain (protein4.1-ezrin-radixin-moesin) family member (frm-1)
Locus_5327_Transcript_3/4_Conf_0.250	748	5	3.18E-21	NP_493601.2	44	106.301	258	116	FERM domain (protein4.1-ezrin-radixin-moesin) family member (frm-1)
Locus_5327_Transcript_4/4_Conf_0.583	723	6	3.74E-16	NP_493601.2	45	89.3521	242	110	FERM domain (protein4.1-ezrin-radixin-moesin) family member (frm-1)
Locus_5328_Transcript_1/1_Conf_1.000	499	2	2.41E-08	NP_500336.1	65	62.003	64	42	Mitochondrial ATPase Inhibitor family member (mai-2)
Locus_5329_Transcript_1/2_Conf_1.000	432	20	3.46E-47		100	191.045	95	95	histone H4

Locus_5329_Transcript_2/2_Conf_1.000	432	20	3.46E-47		100	191.045	95	95	histone H4
Locus_533_Transcript_1/1_Conf_1.000	2216	20	0	NP_501213.1	81	966.837	722	591	PhosphoLipase C family member (plc-4)
Locus_5330_Transcript_1/1_Conf_1.000	190	0							
Locus_5331_Transcript_1/1_Conf_1.000	738	0							
Locus_5332_Transcript_1/1_Conf_1.000	330	0							
Locus_5333_Transcript_1/1_Conf_1.000	1354	20	0	NP_508999.2	95	668.692	367	349	protein KINase family member (kin-2)
Locus_5334_Transcript_1/1_Conf_1.000	1003	20	3.22E-26	XP_001899531.1	78	123.635	104	82	LD36024p

Locus_5335_Transcript_1/1_Conf_1.000	808	20	1.77E-140	NP_001024972.1	94	502.671	269	255	abnormal cell MIGration family member (mig-15)
Locus_5336_Transcript_1/1_Conf_1.000	557	3	1.21E-21	XP_002640682.1	56	106.686	187	105	Hypothetical protein CBG19744
Locus_5337_Transcript_1/1_Conf_1.000	1344	20	2.00E-168	NP_001024587.1	81	596.66	435	355	abnormal cell LINeage family member (lin-2)
Locus_5338_Transcript_1/1_Conf_1.000	618	20	2.30E-60	NP_496100.1	76	235.728	207	159	hypothetical protein Y53C12B.1
Locus_5339_Transcript_1/1_Conf_1.000	420	3	5.45E-32	ACJ65067.1	71	140.584	132	95	Lgc-53
Locus_534_Transcript_1/2_Conf_1.000	1804	9	8.23E-62	NP_741594.1	48	243.047	635	308	hypothetical protein H24G06.1
Locus_534_Transcript_2/2_Conf_1.000	1723	9	2.84E-64	NP_741594.1	50	251.136	611	306	hypothetical protein H24G06.1
Locus_5340_Transcript_1/1_Conf_1.000	321	20	4.46E-26	XP_002640628.1	73	120.939	99	73	C. briggsae CBR-EAT-18 protein
Locus_5341_Transcript_1/1_Conf_1.000	240	0							
Locus_5342_Transcript_1/2_Conf_1.000	1083	20	4.24E-71	NP_505573.1	74	160.999	136	101	Uridine DiPhosphatase family member (uda-1)
Locus_5342_Transcript_2/2_Conf_1.000	959	20	3.13E-76	NP_505573.1	75	289.656	266	202	Uridine DiPhosphatase family member (uda-1)

Locus_5343_Transcript_1/3_Conf_0.667	1700	20	6.56E-21	AAB04136.1	59	107.071	130	77	RNA helicase
Locus_5343_Transcript_2/3_Conf_0.667	1692	20	6.53E-21	AAB04136.1	59	107.071	130	77	RNA helicase
Locus_5343_Transcript_3/3_Conf_0.667	1692	20	6.53E-21	AAB04136.1	59	107.071	130	77	RNA helicase
Locus_5344_Transcript_1/1_Conf_1.000	632	0							
Locus_5345_Transcript_1/1_Conf_1.000	622	4	3.96E-12	XP_001893623.1	55	75.485	161	89	hypothetical protein Bm1_10755
Locus_5346_Transcript_1/1_Conf_1.000	354								
Locus_5347_Transcript_1/1_Conf_1.000	316	0							
Locus_5348_Transcript_1/1_Conf_1.000	165	0							
Locus_5349_Transcript_1/2_Conf_1.000	743	20	3.23E-26	NP_491477.2	67	122.865	126	85	IMportin Beta family member (imb-1)
Locus_5349_Transcript_2/2_Conf_1.000	743	20	3.23E-26	NP_491477.2	67	122.865	126	85	IMportin Beta family member (imb-1)
Locus_535_Transcript_1/3_Conf_0.600	924	20	1.64E-58	XP_002639611.1	67	230.72	238	160	C. briggsae CBR-PPK-1 protein
Locus_535_Transcript_2/3_Conf_0.400	971	20	1.76E-58	XP_002639611.1	67	230.72	238	160	C. briggsae CBR-PPK-1 protein
Locus_535_Transcript_3/3_Conf_0.600	1448	20	3.18E-58	XP_002639611.1	67	230.72	238	160	C. briggsae CBR-PPK-1 protein
Locus_5350_Transcript_1/1_Conf_1.000	803	20	3.32E-107	NP_001022275.1	83	392.119	266	223	abnormal cell MIGration family member (mig-14)
Locus_5351_Transcript_1/1_Conf_1.000	609	0							
Locus_5352_Transcript_1/1_Conf_1.000	318	2	1.71E-09	NP_496913.1	68	65.855	64	44	hypothetical protein W02B8.1
Locus_5353_Transcript_1/1_Conf_1.000	335	0							
Locus_5354_Transcript_1/1_Conf_1.000	1547	20	3.40E-114	Q61UC4.2	89	416.772	259	232	Raf homolog serine/threonine-protein kinase
Locus_5355_Transcript_1/1_Conf_1.000	404	20	6.03E-07	XP_002742168.1	57	57.3806	84	48	PREDICTED: hypothetical protein

Locus_5356_Transcript_1/3_Conf_0.667	538	20	4.12E-21	BAB68205.1	69	104.76	121	84	keratin-like protein
Locus_5356_Transcript_2/3_Conf_0.667	545	20	4.29E-21	BAB68205.1	69	104.76	121	84	keratin-like protein
Locus_5356_Transcript_3/3_Conf_0.333	322	3	1.70E-09	BAB68205.1	69	65.855	73	51	keratin-like protein
Locus_5357_Transcript_1/1_Conf_1.000	128	9	1.58E-07	AAN16458.1	87	59.3066	39	34	tyramine receptor long isoform SER-2
Locus_5358_Transcript_1/1_Conf_1.000	559	20	2.19E-39	XP_002635284.1	74	165.622	176	131	Hypothetical protein CBG11531
Locus_5359_Transcript_1/1_Conf_1.000	487	20	9.98E-10	XP_002646279.1	50	66.6254	165	84	C. briggsae CBR-COL-51 protein
Locus_536_Transcript_1/1_Conf_1.000	1183	20	6.77E-162	XP_002636692.1	82	574.704	395	327	Hypothetical protein CBG23406
Locus_5360_Transcript_1/2_Conf_1.000	489	0							
Locus_5360_Transcript_2/2_Conf_1.000	393	0							
Locus_5361_Transcript_1/1_Conf_1.000	449	20	7.59E-18	NP_502415.1	62	93.5893	108	68	hypothetical protein Y55D9A.2
Locus_5362_Transcript_1/1_Conf_1.000	168	0							
Locus_5363_Transcript_1/1_Conf_1.000	346	0							
Locus_5364_Transcript_1/1_Conf_1.000	633	0							
Locus_5365_Transcript_1/1_Conf_1.000	678	0							
Locus_5366_Transcript_1/1_Conf_1.000	958	20	5.01E-66	XP_001900961.1	65	255.758	240	158	Zinc finger, C2H2 type family protein
Locus_5367_Transcript_1/1_Conf_1.000	325	20	2.21E-17	EFO20157.1	74	92.0485	104	77	hypothetical protein LOAG_08332
Locus_5368_Transcript_1/1_Conf_1.000	806	20	4.40E-75	NP_502329.3	75	285.419	271	205	hypothetical protein C42C1.2
Locus_5369_Transcript_1/1_Conf_1.000	1613	20	7.20E-30	XP_002129449.1	49	136.732	298	147	PREDICTED: hypothetical protein
Locus_537_Transcript_1/1_Conf_1.000	1098	3	1.59E-77	CAR63557.1	80	294.278	306	246	hypothetical protein
Locus_5370_Transcript_1/2_Conf_1.000	893	0							
Locus_5370_Transcript_2/2_Conf_1.000	893	0							

Locus_5371_Transcript_1/1_Conf_1.000	295	0							
Locus_5372_Transcript_1/1_Conf_1.000	463	3	1.77E-06	XP_002129449.1	49	55.8398	130	64	PREDICTED: hypothetical protein
Locus_5373_Transcript_1/1_Conf_1.000	496	20	2.72E-68	XP_532633.2	95	261.151	148	142	PREDICTED: similar to 60S ribosomal protein L32
Locus_5374_Transcript_1/3_Conf_0.667	1546	20	4.17E-104	XP_002637782.1	71	383.259	378	270	Hypothetical protein CBG04567
Locus_5374_Transcript_2/3_Conf_0.667	1442	20	5.50E-103	NP_872134.1	70	379.407	339	239	hypothetical protein C54G10.4
Locus_5374_Transcript_3/3_Conf_0.667	1399	20	2.37E-103	NP_872134.1	71	380.563	359	256	hypothetical protein C54G10.4
Locus_5375_Transcript_1/1_Conf_1.000	1637	20	2.61E-152		70	543.502	517	365	hypothetical protein ZK1151.2a
Locus_5376_Transcript_1/1_Conf_1.000	238	0							
Locus_5377_Transcript_1/1_Conf_1.000	621	20	2.29E-52	A8WMY4.2	74	209.149	197	147	Nicotinic receptor-associated protein 1
Locus_5378_Transcript_1/1_Conf_1.000	823	20	1.64E-141	P01876.2	100	506.138	274	274	Ig alpha-1 chain C region
Locus_5379_Transcript_1/1_Conf_1.000	566	20	1.48E-30	XP_002645738.1	69	136.346	134	93	Hypothetical protein CBG07411
Locus_538_Transcript_1/1_Conf_1.000	224	0							
Locus_5380_Transcript_1/1_Conf_1.000	498	0							
Locus_5381_Transcript_1/1_Conf_1.000	470	0							
Locus_5382_Transcript_1/2_Conf_1.000	1687	20	8.64E-74	NP_872031.2	57	282.722	424	242	hypothetical protein Y39F10B.1
Locus_5382_Transcript_2/2_Conf_1.000	1660	20	8.46E-74	NP_872031.2	57	282.722	424	242	hypothetical protein Y39F10B.1
Locus_5383_Transcript_1/1_Conf_1.000	846	20	2.48E-63	XP_002646187.1	85	246.514	174	149	Hypothetical protein CBG24492
Locus_5384_Transcript_1/1_Conf_1.000	328	0							
Locus_5385_Transcript_1/2_Conf_1.000	471	20	7.01E-48	XP_001892004.1	98	193.356	103	101	histone H2B 2

Locus_5385_Transcript_2/2_Conf_1.000	471	20	7.01E-48	XP_001892004.1	98	193.356	103	101	histone H2B 2
Locus_5386_Transcript_1/1_Conf_1.000	492	20	5.23E-19	XP_001898723.1	58	97.4413	115	67	LD46868p
Locus_5387_Transcript_1/1_Conf_1.000	611	20	1.03E-41	NP_001022469.1	66	173.711	189	126	Eukaryotic Initiation Factor family member (eif-3.B)
Locus_5388_Transcript_1/1_Conf_1.000	328	20	7.53E-34	XP_001896464.1	97	146.747	70	68	PHD finger-like domain protein 5A
Locus_5389_Transcript_1/1_Conf_1.000	726	0							
Locus_539_Transcript_1/1_Conf_1.000	1757	7	1.66E-59	XP_002642111.1	51	235.343	497	256	C. briggsae CBR-ATF-7 protein
Locus_5390_Transcript_1/1_Conf_1.000	299	0							
Locus_5391_Transcript_1/1_Conf_1.000	793	0							
Locus_5392_Transcript_1/4_Conf_0.500	611	0							
Locus_5392_Transcript_2/4_Conf_0.250	654	0							
Locus_5392_Transcript_3/4_Conf_0.500	627	0							
Locus_5392_Transcript_4/4_Conf_0.500	611	0							
Locus_5393_Transcript_1/2_Conf_1.000	940	20	1.49E-22	NP_506340.1	48	111.309	224	109	FERM domain (protein4.1-ezrin-radixin-moesin) family member (frm-10)
Locus_5393_Transcript_2/2_Conf_1.000	181	0							
Locus_5394_Transcript_1/1_Conf_1.000	396	0							

Locus_5395_Transcript_1/1_Conf_1.000	698	20	1.12E-98	NP_493377.1	85	265.003	170	145	Valyl tRNA Synthetase family member (vrs-2)
Locus_5396_Transcript_1/1_Conf_1.000	738	0							
Locus_5397_Transcript_1/1_Conf_1.000	875	3	1.32E-14	XP_001900988.1	50	84.7297	222	112	hypothetical protein Bm1_47635
Locus_5398_Transcript_1/1_Conf_1.000	1081	20	3.45E-69	XP_002642651.1	77	266.544	243	188	C. briggsae CBR-MTX-2 protein
Locus_5399_Transcript_1/1_Conf_1.000	906	20	5.03E-97	NP_492687.1	78	358.607	282	220	Aryl Hydrocarbon receptor Associated protein family member (aha-1)
Locus_54_Transcript_1/1_Conf_1.000	296	0							

Locus_540_Transcript_1/1_Conf_1.000	1752	20	2.44E-103	XP_002640656.1	60	380.948	522	315	C. briggsae CBR-AEX-5 protein
Locus_5400_Transcript_1/1_Conf_1.000	533	20	4.20E-18	NP_497020.2	51	94.7449	184	94	Suppressor of PAr-Two defect family member (spat-1)
Locus_5401_Transcript_1/1_Conf_1.000	1047	20	1.01E-86	XP_002639396.1	96	324.709	205	198	Hypothetical protein CBG03984
Locus_5402_Transcript_1/1_Conf_1.000	1364	20	3.14E-68	XP_002644068.1	57	263.848	459	262	Hypothetical protein CBG17536
Locus_5403_Transcript_1/1_Conf_1.000	1218	20	8.59E-75	NP_501910.1	68	285.419	326	222	hypothetical protein R11A8.2
Locus_5404_Transcript_1/1_Conf_1.000	603	20	1.96E-37	XP_002641945.1	56	159.458	200	112	C. briggsae CBR-TAG-198 protein
Locus_5405_Transcript_1/1_Conf_1.000	416	4	5.72E-18	NP_505735.1	57	93.9745	136	78	hypothetical protein T28B11.1

Locus_5406_Transcript_1/1_Conf_1.000	490	20	1.27E-73	NP_502014.2	88	278.87	160	141	hypothetical protein T11G6.8
Locus_5407_Transcript_1/1_Conf_1.000	1341	20	0	EFO25450.1	91	731.095	423	389	cleavage stimulation factor
Locus_5408_Transcript_1/1_Conf_1.000	810	20	1.01E-103	NP_491953.1	90	380.563	227	206	Temporarily Assigned Gene name family member (tag-203)
Locus_5409_Transcript_1/1_Conf_1.000	1115	6	1.10E-33	A8X9H4.2	48	148.673	292	141	Chondroitin proteoglycan 4
Locus_541_Transcript_1/4_Conf_0.692	1542	20	0	ADK47524.1	92	576.244	320	297	enolase
Locus_541_Transcript_2/4_Conf_0.231	298	0							
Locus_541_Transcript_3/4_Conf_0.692	1542	20	0	ADK47524.1	92	576.244	320	297	enolase

Locus_541_Transcript_4/4_Conf_0.692	1542	20	0	ADK47524.1	92	576.244	320	297	enolase
Locus_5410_Transcript_1/1_Conf_1.000	378	0							
Locus_5411_Transcript_1/1_Conf_1.000	675	20	2.03E-18	EFO27874.1	54	96.6709	122	67	hypothetical protein LOAG_00617
Locus_5412_Transcript_1/1_Conf_1.000	1054	0							
Locus_5413_Transcript_1/1_Conf_1.000	309	0							
Locus_5414_Transcript_1/1_Conf_1.000	951	17	1.40E-44	XP_002643035.1	60	184.496	264	161	C. briggsae CBR-CLP-1 protein
Locus_5415_Transcript_1/1_Conf_1.000	650	13	2.95E-32	NP_492669.2	71	142.51	122	87	hypothetical protein Y106G6D.6
Locus_5416_Transcript_1/1_Conf_1.000	619	20	9.71E-43	NP_510540.1	66	177.178	204	136	hypothetical protein C33A11.1
Locus_5417_Transcript_1/1_Conf_1.000	541	20	1.17E-47	XP_002635582.1	82	192.971	159	131	C. briggsae CBR-TTR-33 protein
Locus_5418_Transcript_1/1_Conf_1.000	648	5	1.91E-39	ACI49189.1	70	166.392	155	110	hypothetical protein Csp3_JD02.017
Locus_5419_Transcript_1/1_Conf_1.000	335	0							
Locus_542_Transcript_1/1_Conf_1.000	624	20	1.55E-64	NP_494767.1	81	249.595	206	168	hypothetical protein H20J04.2
Locus_5420_Transcript_1/2_Conf_1.000	1458	20	0	XP_001899599.1	85	700.664	454	388	DNA-binding protein LAG-1
Locus_5420_Transcript_2/2_Conf_1.000	1458	20	0	XP_001899599.1	85	700.664	454	388	DNA-binding protein LAG-1
Locus_5421_Transcript_1/1_Conf_1.000	238	0							
Locus_5422_Transcript_1/1_Conf_1.000	1370	6	8.02E-72	NP_741168.1	53	275.789	439	237	hypothetical protein C05D10.1
Locus_5423_Transcript_1/1_Conf_1.000	1172	20	9.20E-87	NP_502294.1	73	325.094	298	219	hypothetical protein F11A10.5
Locus_5424_Transcript_1/1_Conf_1.000	506	2	5.83E-13	NP_001023217.1	57	77.411	113	65	hypothetical protein F53H1.4

Locus_5425_Transcript_1/1_Conf_1.000	1097	20	2.04E-109	XP_002637274.1	78	400.208	318	249	Hypothetical protein CBG18957
Locus_5426_Transcript_1/1_Conf_1.000	228	20	1.82E-11	XP_002636806.1	83	72.4034	48	40	Hypothetical protein CBG09248
Locus_5427_Transcript_1/1_Conf_1.000	166	0							
Locus_5428_Transcript_1/1_Conf_1.000	1038	0							
Locus_5429_Transcript_1/1_Conf_1.000	275	11	4.42E-10	EFO20463.1	64	67.781	87	56	hypothetical protein LOAG_08027
Locus_543_Transcript_1/2_Conf_1.000	1349	20	1.02E-79	XP_002646267.1	89	301.982	189	169	Hypothetical protein CBG11972
Locus_543_Transcript_2/2_Conf_1.000	1290	20	3.30E-80	XP_002646267.1	89	303.523	191	170	Hypothetical protein CBG11972
Locus_5430_Transcript_1/1_Conf_1.000	886	20	8.23E-89	ACI49172.1	72	331.257	285	206	hypothetical protein Csp3_JD01.004
Locus_5431_Transcript_1/1_Conf_1.000	525	20	6.76E-74	NP_741553.1	89	280.026	174	156	ALdehyde deHydrogenase family member (alh-4)
Locus_5432_Transcript_1/1_Conf_1.000	593	0							
Locus_5433_Transcript_1/1_Conf_1.000	615	0							
Locus_5434_Transcript_1/1_Conf_1.000	176	0							
Locus_5435_Transcript_1/1_Conf_1.000	786	0							
Locus_5436_Transcript_1/1_Conf_1.000	2264	20	8.10E-33	CAZ65529.1	42	147.132	766	325	C. elegans protein T28C6.7b, partially confirmed by transcript evidence

Locus_5437_Transcript_1/1_Conf_1.000	541	20	5.13E-27	XP_002629901.1	71	124.405	135	96	Hypothetical protein CBG21942
Locus_5438_Transcript_1/1_Conf_1.000	579	20	3.97E-13	NP_001041239.1	50	78.5666	216	108	abnormal DAuer Formation family member (daf-12)
Locus_5439_Transcript_1/2_Conf_1.000	484	0							
Locus_5439_Transcript_2/2_Conf_1.000	484	0							
Locus_544_Transcript_1/1_Conf_1.000	1344	0							
Locus_5440_Transcript_1/2_Conf_0.500	1395	20	1.28E-149	XP_001899556.1	86	534.258	359	310	GDP-mannose pyrophosphorylase B, isoform 2
Locus_5440_Transcript_2/2_Conf_0.500	1395	20	3.36E-150	XP_001899556.1	86	536.184	359	310	GDP-mannose pyrophosphorylase B, isoform 2
Locus_5441_Transcript_1/1_Conf_1.000	1026	20	5.42E-93	NP_499106.1	78	345.51	291	227	hypothetical protein ZK1098.4
Locus_5442_Transcript_1/1_Conf_1.000	890	0							
Locus_5443_Transcript_1/2_Conf_1.000	1062	20	2.57E-69	XP_002630380.1	83	266.929	221	184	C. briggsae CBR-VPS-32.1 protein
Locus_5443_Transcript_2/2_Conf_1.000	1059	20	2.56E-69	XP_002630380.1	83	266.929	221	184	C. briggsae CBR-VPS-32.1 protein
Locus_5444_Transcript_1/1_Conf_1.000	428	20	5.06E-30	NP_491765.2	64	134.035	142	92	hypothetical protein T27A3.2
Locus_5445_Transcript_1/1_Conf_1.000	467	0							
Locus_5446_Transcript_1/3_Conf_0.667	1158	4	3.72E-48	XP_002643393.1	49	196.823	428	211	Hypothetical protein CBG16006
Locus_5446_Transcript_2/3_Conf_0.667	1792	4	5.28E-69	XP_002643393.1	51	266.929	460	239	Hypothetical protein CBG16006
Locus_5446_Transcript_3/3_Conf_0.667	1792	4	2.01E-68	XP_002643393.1	51	265.003	460	239	Hypothetical protein CBG16006
Locus_5447_Transcript_1/1_Conf_1.000	352	0							
Locus_5448_Transcript_1/1_Conf_1.000	1149	4	7.92E-43	XP_002633035.1	58	179.104	339	197	Hypothetical protein CBG05711
Locus_5449_Transcript_1/1_Conf_1.000	196	20	4.48E-10	XP_002639044.1	75	67.781	48	36	Hypothetical protein CBG22296

Locus_545_Transcript_1/1_Conf_1.000	416	0							
Locus_5450_Transcript_1/1_Conf_1.000	737	11	5.95E-41	XP_002639670.1	61	171.785	191	117	Hypothetical protein CBG12388
Locus_5451_Transcript_1/1_Conf_1.000	1422	12	0	NP_001022641.1	89	712.99	472	421	LEThal family member (let-805)
Locus_5452_Transcript_1/1_Conf_1.000	1067	20	1.10E-11	NP_498678.3	42	75.485	194	83	abnormal cell LINeage family member (lin-13)
Locus_5453_Transcript_1/1_Conf_1.000	608	4	5.23E-30	XP_002639325.1	74	134.806	113	84	Hypothetical protein CBG03903
Locus_5454_Transcript_1/1_Conf_1.000	395								
Locus_5455_Transcript_1/1_Conf_1.000	347	20	2.81E-28	NP_500566.1	73	128.257	116	85	WAPL (Drosophila Wings APart-Like cohesin interactor) family member (wapl-1)
Locus_5456_Transcript_1/1_Conf_1.000	140	20	1.28E-17	CAI42449.1	100	92.8189	46	46	ubiquitously-expressed transcript
Locus_5457_Transcript_1/1_Conf_1.000	398	20	2.77E-68	NP_001022641.1	98	261.151	132	130	LEThal family member (let-805)

Locus_5458_Transcript_1/1_Conf_1.000	769	20	2.74E-116	NP_001021588.1	90	422.165	247	224	hypothetical protein R11A5.4
Locus_5459_Transcript_1/1_Conf_1.000	181	20	5.93E-18	XP_002639611.1	91	93.9745	60	55	C. briggsae CBR-PPK-1 protein
Locus_546_Transcript_1/1_Conf_1.000	788	0							
Locus_5460_Transcript_1/1_Conf_1.000	255	20	1.49E-29	XP_002708870.1	100	132.494	65	65	PREDICTED: ribosomal protein S8-like
Locus_5461_Transcript_1/1_Conf_1.000	405	0							
Locus_5462_Transcript_1/1_Conf_1.000	523	20	1.29E-69	XP_002642725.1	88	265.774	175	154	C. briggsae CBR-ABCF-3 protein
Locus_5463_Transcript_1/1_Conf_1.000	162	0							
Locus_5464_Transcript_1/1_Conf_1.000	792	1	2.02E-08	XP_001892596.1	45	63.929	239	109	hypothetical protein Bm1_05610
Locus_5465_Transcript_1/1_Conf_1.000	661	0							
Locus_5466_Transcript_1/1_Conf_1.000	1004	20	1.36E-109	NP_501361.1	82	400.593	278	228	Iron-Sulfur Protein family member (isp-1)
Locus_5467_Transcript_1/1_Conf_1.000	1128	20	3.00E-103	NP_499094.1	88	379.793	257	228	Vacuolar H ATPase family member (vha-14)
Locus_5468_Transcript_1/1_Conf_1.000	1042	20	6.02E-124	XP_002644545.1	85	448.358	312	268	C. briggsae CBR-ASB-2 protein
Locus_5469_Transcript_1/1_Conf_1.000	527	20	2.84E-72	NP_001122631.1	88	274.633	160	141	ELAV-Type RNA binding protein family member (etr-1)
Locus_547_Transcript_1/1_Conf_1.000	808	0							

Locus_5470_Transcript_1/1_Conf_1.000	353	5	4.46E-18	XP_001897390.1	68	94.3597	101	69	Presenilin spe-4
Locus_5471_Transcript_1/1_Conf_1.000	2010	20	6.31E-175	NP_505661.1	83	619.002	444	372	hypothetical protein K07C5.6
Locus_5472_Transcript_1/1_Conf_1.000	663	20	1.01E-75	NP_492486.2	80	286.96	220	178	hypothetical protein C12C8.2
Locus_5473_Transcript_1/1_Conf_1.000	848	0							
Locus_5474_Transcript_1/1_Conf_1.000	456	0							
Locus_5475_Transcript_1/1_Conf_1.000	217	0							
Locus_5476_Transcript_1/1_Conf_1.000	1858	20	1.76E-115	NP_493543.1	72	421.394	383	279	BTB and MATH domain containing family member (bath-40)
Locus_5477_Transcript_1/1_Conf_1.000	494	0							
Locus_5478_Transcript_1/5_Conf_0.692	3363	20	0	NP_001021395.1	85	1632.08	1134	974	Receptor Mediated Endocytosis family member (rme-8)
Locus_5478_Transcript_2/5_Conf_0.692	3363	20	0	NP_001021395.1	85	1632.08	1134	974	Receptor Mediated Endocytosis family member (rme-8)
Locus_5478_Transcript_3/5_Conf_0.615	3152	20	0	NP_001021395.1	86	1538.86	1064	922	Receptor Mediated Endocytosis family member (rme-8)
Locus_5478_Transcript_4/5_Conf_0.692	3363	20	0	NP_001021395.1	85	1632.08	1134	974	Receptor Mediated Endocytosis family member (rme-8)
Locus_5478_Transcript_5/5_Conf_0.692	3363	20	0	NP_001021395.1	85	1632.08	1134	974	Receptor Mediated Endocytosis family member (rme-8)
Locus_5479_Transcript_1/1_Conf_1.000	392	20	9.68E-42	EFO16124.1	81	172.94	129	105	protein-tyrosine phosphatase
Locus_548_Transcript_1/1_Conf_1.000	825	1	5.52E-04	AAP83584.1	41	49.2914	175	73	DNA-topoisomerase II
Locus_5480_Transcript_1/1_Conf_1.000	728	20	7.60E-25	NP_508544.2	77	118.242	103	80	hypothetical protein C15C7.1
Locus_5481_Transcript_1/1_Conf_1.000	579	1	3.37E-04	NP_506662.1	45	48.9062	133	60	hypothetical protein ZC412.3
Locus_5482_Transcript_1/1_Conf_1.000	323	0							

Locus_5483_Transcript_1/1_Conf_1.000	598	12	3.44E-63	XP_002641548.1	76	244.973	205	156	C. briggsae CBR-FEH-1 protein
Locus_5484_Transcript_1/1_Conf_1.000	747	20	9.40E-82	EFO18967.1	76	307.375	249	190	LIM domain-containing protein
Locus_5485_Transcript_1/2_Conf_1.000	422	3	2.02E-10	NP_490799.2	44	68.9366	139	62	SHC (Src Homology domain C-terminal) adaptor homolog family member (shc-1)
Locus_5485_Transcript_2/2_Conf_1.000	392	2	3.97E-11	XP_002638780.1	62	71.2478	80	50	C. briggsae CBR-SHC-1 protein
Locus_5486_Transcript_1/2_Conf_1.000	1374	20	1.06E-47	EFO24053.1	88	195.667	117	104	hypothetical protein LOAG_04430
Locus_5486_Transcript_2/2_Conf_1.000	1368	20	1.80E-47	EFO24053.1	94	194.897	106	100	hypothetical protein LOAG_04430
Locus_5487_Transcript_1/1_Conf_1.000	587	20	1.87E-74	NP_492952.1	87	282.337	172	150	hypothetical protein F15D3.6
Locus_5488_Transcript_1/1_Conf_1.000	1163	5	2.06E-30	NP_001041082.1	51	137.887	319	165	hypothetical protein C14C10.2
Locus_5489_Transcript_1/1_Conf_1.000	461	0							
Locus_549_Transcript_1/3_Conf_0.600	2239	20	2.23E-67	XP_002644641.1	62	261.922	375	234	C. briggsae CBR-APL-1 protein
Locus_549_Transcript_2/3_Conf_0.400	135	2	1.28E-09	XP_002630033.1	85	66.2402	42	36	C. briggsae CBR-PUF-12 protein

Locus_549_Transcript_3/3_Conf_0.400	3076	20	0	XP_002644641.1	70	701.819	696	490	C. briggsae CBR-APL-1 protein
Locus_5490_Transcript_1/1_Conf_1.000	267	20	8.38E-17	XP_002630362.1	75	90.1225	83	63	C. briggsae CBR-RPN-5 protein
Locus_5491_Transcript_1/1_Conf_1.000	442	20	1.44E-16	AAO63576.1	50	89.3521	133	67	secreted protein 4 precursor
Locus_5492_Transcript_1/1_Conf_1.000	604	0							
Locus_5493_Transcript_1/1_Conf_1.000	132	0							
Locus_5494_Transcript_1/1_Conf_1.000	447	2	1.06E-11	NP_498724.3	53	73.1738	152	82	Nuclear Pore complex Protein family member (npp-15)
Locus_5495_Transcript_1/1_Conf_1.000	831	0							
Locus_5496_Transcript_1/4_Conf_0.429	1171	20	2.63E-150	NP_499032.1	78	536.184	391	307	INtegrin Alpha family member (ina-1)
Locus_5496_Transcript_2/4_Conf_0.429	1410	20	8.12E-152	NP_499032.1	78	541.576	400	312	INtegrin Alpha family member (ina-1)
Locus_5496_Transcript_3/4_Conf_0.286	233	0							
Locus_5496_Transcript_4/4_Conf_0.429	1219	20	4.31E-151	NP_499032.1	77	538.88	400	311	INtegrin Alpha family member (ina-1)
Locus_5497_Transcript_1/1_Conf_1.000	660	4	1.24E-17	XP_001894367.1	51	93.9745	205	105	hypothetical protein Bm1_14505
Locus_5498_Transcript_1/2_Conf_1.000	2610	20	0	NP_001123198.1	68	679.093	776	531	GTPase Activating Protein family member (gap-2)
Locus_5498_Transcript_2/2_Conf_1.000	2556	20	0	NP_509597.1	69	681.789	759	525	GTPase Activating Protein family member (gap-2)

Locus_5499_Transcript_1/4_Conf_0.700	1711	20	0	NP_499487.1	96	871.307	524	504	hypothetical protein Y66D12A.15
Locus_5499_Transcript_2/4_Conf_0.700	1711	20	0	NP_499487.1	96	871.307	524	504	hypothetical protein Y66D12A.15

Locus_5499_Transcript_3/4_Conf_0.700	1711	20	0	NP_499487.1	96	871.307	524	504	hypothetical protein Y66D12A.15
Locus_5499_Transcript_4/4_Conf_0.700	1711	20	0	NP_499487.1	96	871.307	524	504	hypothetical protein Y66D12A.15
Locus_55_Transcript_1/2_Conf_0.889	705	5	5.84E-11	XP_002630572.1	46	72.0182	160	74	Hypothetical protein CBG13025
Locus_55_Transcript_2/2_Conf_0.889	705	5	5.84E-11	XP_002630572.1	46	72.0182	160	74	Hypothetical protein CBG13025
Locus_550_Transcript_1/1_Conf_1.000	201	0							

Locus_5500_Transcript_1/1_Conf_1.000	829	20	3.02E-42	XP_002642343.1	66	176.407	205	137	C. briggsae CBR-CNT-2 protein
Locus_5501_Transcript_1/1_Conf_1.000	1075	15	1.21E-74	XP_002639830.1	69	284.648	359	249	C. briggsae CBR-EXOC-7 protein
Locus_5502_Transcript_1/1_Conf_1.000	1085	7	6.43E-07	NP_509538.1	66	59.6918	68	45	Apical Junction Molecule family member (ajm-1)
Locus_5503_Transcript_1/1_Conf_1.000	599	0							
Locus_5504_Transcript_1/1_Conf_1.000	427	0							
Locus_5505_Transcript_1/1_Conf_1.000	764	20	3.70E-65	NP_490990.2	71	252.292	259	184	hypothetical protein Y23H5B.5
Locus_5506_Transcript_1/1_Conf_1.000	851	20	7.54E-44	NP_504952.1	67	181.8	276	186	hypothetical protein F19F10.9
Locus_5507_Transcript_1/1_Conf_1.000	1825	20	0	NP_508711.1	96	919.457	492	477	Vacuolar H ATPase family member (vha-12)
Locus_5508_Transcript_1/1_Conf_1.000	1377	20	1.09E-148	A8XXC7.2	81	477.248	323	264	WD repeat and FYVE domain-containing protein 2
Locus_5509_Transcript_1/1_Conf_1.000	144	0							
Locus_551_Transcript_1/1_Conf_1.000	1936	8	5.82E-53	XP_002632887.1	52	213.772	509	266	Hypothetical protein CBG15095
Locus_5510_Transcript_1/1_Conf_1.000	1544	0							
Locus_5511_Transcript_1/1_Conf_1.000	865	3	4.60E-20	NP_872067.1	54	102.834	222	122	hypothetical protein M176.11
Locus_5512_Transcript_1/1_Conf_1.000	435	0							
Locus_5513_Transcript_1/1_Conf_1.000	1300	1	1.75E-04	CAB55122.3	37	51.9878	331	124	C. elegans protein Y116A8C.16a, partially confirmed by transcript evidence
Locus_5514_Transcript_1/1_Conf_1.000	248	10	1.08E-08	NP_493100.1	57	63.1586	82	47	hypothetical protein F41D3.11
Locus_5515_Transcript_1/1_Conf_1.000	506	20	1.68E-52	XP_002642602.1	84	208.764	137	116	C. briggsae CBR-TTR-8 protein
Locus_5516_Transcript_1/2_Conf_0.667	167	0							
Locus_5516_Transcript_2/2_Conf_0.667	167	0							
Locus_5517_Transcript_1/1_Conf_1.000	327	0							

Locus_5518_Transcript_1/1_Conf_1.000	1317	20	0	XP_002641348.1	96	647.506	365	352	Hypothetical protein CBG13201
Locus_5519_Transcript_1/2_Conf_1.000	500	0							
Locus_5519_Transcript_2/2_Conf_1.000	487	4	3.32E-05	XP_001120514.1	66	51.6026	60	40	PREDICTED: hypothetical protein, partial
Locus_552_Transcript_1/2_Conf_0.500	737	5	3.48E-49	XP_002645475.1	92	199.134	139	129	Hypothetical protein CBG22717
Locus_552_Transcript_2/2_Conf_0.500	1899	20	7.93E-79	NP_001023574.1	90	299.671	192	173	homologous to Drosophila SQD (squid) protein family member (sqd-1)
Locus_5520_Transcript_1/1_Conf_1.000	837	2	1.39E-18	NP_510115.1	90	97.8265	55	50	Nuclear Hormone Receptor family member (nhr-17)
Locus_5521_Transcript_1/2_Conf_1.000	1643	1	9.09E-04	XP_756627.1	39	50.0618	243	95	hypothetical protein UM00480.1
Locus_5521_Transcript_2/2_Conf_1.000	1552	1	8.42E-04	XP_756627.1	39	50.0618	243	95	hypothetical protein UM00480.1
Locus_5522_Transcript_1/1_Conf_1.000	339	5	3.96E-11	NP_502366.1	71	71.2478	90	64	Dolichol Phosphate Mannosyltransferase family member (dpm-3)
Locus_5523_Transcript_1/1_Conf_1.000	164	0							
Locus_5524_Transcript_1/1_Conf_1.000	1171	20	1.19E-17	XP_001629578.1	45	95.5153	277	126	predicted protein
Locus_5525_Transcript_1/3_Conf_0.714	1372	0							
Locus_5525_Transcript_2/3_Conf_0.571	1404	0							
Locus_5525_Transcript_3/3_Conf_0.714	1377	0							

Locus_5526_Transcript_1/1_Conf_1.000	688	20	4.03E-94	ACH43609.1	100	348.206	175	175	putative 40S ribosomal protein S9
Locus_5527_Transcript_1/1_Conf_1.000	1403	20	1.86E-23	AAN11402.1	39	115.161	449	176	secreted-protein 1 precursor
Locus_5528_Transcript_1/1_Conf_1.000	1045	9	1.34E-30	NP_500018.3	95	138.272	80	76	PLeXin family member (plx-1)
Locus_5529_Transcript_1/1_Conf_1.000	527	20	4.71E-51	XP_002633191.1	94	204.142	128	121	C. briggsae CBR-DIF-1 protein
Locus_553_Transcript_1/1_Conf_1.000	183	2	3.60E-07	XP_002643084.1	68	58.151	58	40	C. briggsae CBR-TAG-174 protein
Locus_5530_Transcript_1/1_Conf_1.000	555	20	1.76E-12	NP_495338.1	55	76.2554	129	72	hypothetical protein C56C10.9
Locus_5531_Transcript_1/1_Conf_1.000	486	20	2.12E-52	XP_002646152.1	77	208.379	159	123	C. briggsae CBR-GPI-1 protein
Locus_5532_Transcript_1/1_Conf_1.000	1611	20	0	XP_002642367.1	83	738.799	548	456	Hypothetical protein CBG18370
Locus_5533_Transcript_1/1_Conf_1.000	473	0							
Locus_5534_Transcript_1/1_Conf_1.000	459	20	1.26E-49	XP_001106448.2	96	199.134	105	101	PREDICTED: 60S ribosomal protein L36-like
Locus_5535_Transcript_1/1_Conf_1.000	1116	20	7.95E-133	ABL61878.1	97	478.019	372	361	cytochrome b
Locus_5536_Transcript_1/1_Conf_1.000	357	0							
Locus_5537_Transcript_1/1_Conf_1.000	663	8	4.03E-24	XP_002648487.1	59	115.546	223	133	Hypothetical protein CBG24777
Locus_5538_Transcript_1/2_Conf_1.000	282	0							
Locus_5538_Transcript_2/2_Conf_1.000	283	0							
Locus_5539_Transcript_1/2_Conf_1.000	449	0							
Locus_5539_Transcript_2/2_Conf_1.000	401	0							
Locus_554_Transcript_1/1_Conf_1.000	498	2	3.04E-19	XP_002631443.1	75	98.2117	92	69	Hypothetical protein CBG03305
Locus_5540_Transcript_1/1_Conf_1.000	230	0							

Locus_5541_Transcript_1/1_Conf_1.000	333	2	9.54E-25	XP_001116236.1	93	86.2705	46	43	PREDICTED: hypothetical protein LOC718269
Locus_5542_Transcript_1/2_Conf_1.000	1183	20	9.15E-159	XP_001893248.1	83	564.303	395	329	Pre-B cell enhancing factor precursor
Locus_5542_Transcript_2/2_Conf_1.000	448	20	4.56E-47	XP_001893248.1	77	190.66	149	116	Pre-B cell enhancing factor precursor
Locus_5543_Transcript_1/2_Conf_1.000	1619	20	2.24E-55	EFO22579.1	52	221.476	457	238	hypothetical protein LOAG_05905
Locus_5543_Transcript_2/2_Conf_1.000	1619	20	6.50E-55	EFO22579.1	52	219.935	457	238	hypothetical protein LOAG_05905
Locus_5544_Transcript_1/1_Conf_1.000	295	0							
Locus_5545_Transcript_1/1_Conf_1.000	285	20	2.02E-26	NP_507688.2	95	122.094	70	67	CYtochrome P450 family member (cyp-42A1)
Locus_5546_Transcript_1/1_Conf_1.000	364	20	3.13E-32	XP_002635588.1	73	141.354	124	91	C. briggsae CBR-IMB-4 protein
Locus_5547_Transcript_1/1_Conf_1.000	312	20	9.43E-16	XP_001895783.1	64	86.6557	98	63	BTB/POZ domain containing protein 9
Locus_5548_Transcript_1/1_Conf_1.000	878	0							
Locus_5549_Transcript_1/1_Conf_1.000	850	20	3.16E-50	NP_496146.1	67	202.986	226	153	Ubiquitin Fusion Degradation (yeast UFD homolog) family member (ufd-3)
Locus_555_Transcript_1/1_Conf_1.000	674	7	1.24E-52	XP_002646995.1	68	210.305	199	137	C. briggsae CBR-LIN-66 protein
Locus_5550_Transcript_1/1_Conf_1.000	716	20	2.43E-28	NP_505643.1	57	129.798	205	117	LYSozyme family member (lys-2)
Locus_5551_Transcript_1/1_Conf_1.000	756	20	7.63E-39	NP_500698.1	67	164.851	171	115	Sperm-Specific family, class Q family member (ssq-2)

Locus_5552_Transcript_1/1_Conf_1.000	595	0							
Locus_5553_Transcript_1/1_Conf_1.000	854	20	1.09E-66	XP_001899907.1	71	257.684	223	160	MOZ/SAS family protein
Locus_5554_Transcript_1/1_Conf_1.000	588	1	9.72E-07	XP_002129638.1	42	57.3806	135	58	PREDICTED: similar to matrix metalloproteinase e
Locus_5555_Transcript_1/1_Conf_1.000	441	0							
Locus_5556_Transcript_1/1_Conf_1.000	961	20	2.43E-52	EFO20472.1	82	210.305	166	137	hypothetical protein LOAG_08015
Locus_5557_Transcript_1/1_Conf_1.000	971	20	1.31E-45	XP_001901812.1	56	187.963	267	150	RNase3 domain containing protein
Locus_5558_Transcript_1/1_Conf_1.000	1078	20	8.67E-97	XP_001897984.1	73	358.221	306	226	Leucine carboxyl methyltransferase family protein
Locus_5559_Transcript_1/1_Conf_1.000	180	0							
Locus_556_Transcript_1/2_Conf_1.000	3043	20	0	NP_001122729.1	74	795.808	739	554	Oxysterol Binding protein (OSBP) Related family member (obr-1)
Locus_556_Transcript_2/2_Conf_1.000	3209	20	0	XP_002641357.1	77	844.729	717	555	C. briggsae CBR-OBR-1 protein
Locus_5560_Transcript_1/1_Conf_1.000	265	0							
Locus_5561_Transcript_1/1_Conf_1.000	585	20	5.79E-84	CAJ57642.1	100	313.923	147	147	putative ubiquitin conjugating enzyme 2
Locus_5562_Transcript_1/2_Conf_1.000	992	20	2.68E-09	XP_002096947.1	57	67.3958	98	56	GE24773
Locus_5562_Transcript_2/2_Conf_1.000	899	20	2.27E-09	XP_002096947.1	57	67.3958	98	56	GE24773
Locus_5563_Transcript_1/1_Conf_1.000	2990	20	1.04E-179	NP_493625.4	56	635.565	1012	571	hypothetical protein F31C3.3
Locus_5564_Transcript_1/1_Conf_1.000	913	0							

Locus_5565_Transcript_1/1_Conf_1.000	466	0							
Locus_5566_Transcript_1/1_Conf_1.000	884	20	3.42E-103	Q20390.2	83	379.022	261	219	Palmitoyl-protein thioesterase 1
Locus_5567_Transcript_1/1_Conf_1.000	568	20	3.52E-88	ADI24632.1	87	327.791	186	163	Hypothetical protein C25H3.9a
Locus_5568_Transcript_1/1_Conf_1.000	3389	20	0	ACI49172.1	68	1056.97	1146	780	hypothetical protein Csp3_JD01.004
Locus_5569_Transcript_1/1_Conf_1.000	827	20	6.48E-29	NP_497279.2	57	132.109	235	135	EXOSome (multiexonuclease complex) component family member (exos-4.2)
Locus_557_Transcript_1/2_Conf_1.000	465	20	1.06E-46	NP_510575.1	80	122.094	83	67	yeast ERV (ER to Golgi transport Vesicle protein) homolog family member (erv-46)
Locus_557_Transcript_2/2_Conf_1.000	431	20	5.18E-51	NP_510575.1	80	203.756	143	115	yeast ERV (ER to Golgi transport Vesicle protein) homolog family member (erv-46)
Locus_5570_Transcript_1/1_Conf_1.000	601	20	2.74E-92	XP_001893622.1	91	341.658	199	183	Leucine Rich Repeat family protein

Locus_5571_Transcript_1/1_Conf_1.000	995	20	7.97E-70	NP_502172.1	78	268.47	195	153	human GAS41-Like family member (gfl-1)
Locus_5572_Transcript_1/3_Conf_0.667	888	20	1.63E-60	NP_500065.2	82	237.269	163	134	hypothetical protein F53H1.3
Locus_5572_Transcript_2/3_Conf_0.667	1017	20	2.05E-60	NP_500065.2	82	237.269	163	134	hypothetical protein F53H1.3
Locus_5572_Transcript_3/3_Conf_0.667	1004	20	2.00E-60	NP_500065.2	82	237.269	163	134	hypothetical protein F53H1.3
Locus_5573_Transcript_1/2_Conf_1.000	3530	20	2.23E-136	XP_002642010.1	90	491.886	286	260	C. briggsae CBR-NHL-2 protein
Locus_5573_Transcript_2/2_Conf_1.000	3175	20	1.97E-136	XP_002642010.1	90	491.886	286	260	C. briggsae CBR-NHL-2 protein
Locus_5574_Transcript_1/1_Conf_1.000	436	20	4.63E-60	XP_002638749.1	88	233.802	150	133	Hypothetical protein CBG18552
Locus_5575_Transcript_1/1_Conf_1.000	580	0							
Locus_5576_Transcript_1/2_Conf_1.000	1208	0							
Locus_5576_Transcript_2/2_Conf_1.000	1172	3	9.74E-04	NP_510818.3	52	49.2914	98	51	hypothetical protein F10D7.5
Locus_5577_Transcript_1/1_Conf_1.000	436	6	2.66E-15	XP_001900298.1	54	85.1149	133	72	putative WD-40 repeat protein
Locus_5578_Transcript_1/1_Conf_1.000	1062	20	2.24E-81	NP_498605.1	89	306.99	180	161	hypothetical protein B0361.10
Locus_5579_Transcript_1/2_Conf_1.000	1185	20	4.13E-151	NP_506018.1	88	538.88	357	316	hypothetical protein F10C2.5

Locus_5579_Transcript_2/2_Conf_1.000	1185	20	4.13E-151	NP_506018.1	88	538.88	357	316	hypothetical protein F10C2.5
Locus_558_Transcript_1/1_Conf_1.000	1252	20	1.44E-165	NP_497182.2	92	587.03	343	318	hypothetical protein Y50D7A.2
Locus_5580_Transcript_1/1_Conf_1.000	285	20	9.38E-24	XP_001897193.1	86	113.235	95	82	GH21176p
Locus_5581_Transcript_1/3_Conf_0.600	395	20	1.66E-12	NP_001129837.1	85	75.8702	48	41	hypothetical protein F35G12.4
Locus_5581_Transcript_2/3_Conf_0.600	484	20	1.65E-12	NP_001129837.1	85	75.8702	48	41	hypothetical protein F35G12.4
Locus_5581_Transcript_3/3_Conf_0.400	2234	20	0	A8Q2R5.2	75	770	671	505	WD repeat-containing protein 48 homolog
Locus_5582_Transcript_1/1_Conf_1.000	1083	10	5.78E-32	NP_504492.1	53	142.895	279	149	hypothetical protein C14C11.1
Locus_5583_Transcript_1/1_Conf_1.000	2257	20	2.85E-62	CAZ65529.1	47	244.973	702	336	C. elegans protein T28C6.7b, partially confirmed by transcript evidence
Locus_5584_Transcript_1/2_Conf_1.000	1248	5	7.35E-53	AAM12419.1	56	212.616	396	224	spliced leader 175 kDa protein
Locus_5584_Transcript_2/2_Conf_1.000	699	5	1.37E-36	XP_002632824.1	59	157.147	232	139	C. briggsae CBR-SNA-2 protein
Locus_5585_Transcript_1/1_Conf_1.000	440	4	3.03E-19	NP_492852.1	68	98.2117	99	68	hypothetical protein Y95D11A.1

Locus_5586_Transcript_1/1_Conf_1.000	718	20	9.82E-78	XP_002640810.1	84	293.893	198	167	C. briggsae CBR-PES-4 protein
Locus_5587_Transcript_1/1_Conf_1.000	1428	20	6.66E-93	XP_002641467.1	82	345.895	245	201	Hypothetical protein CBG09751
Locus_5588_Transcript_1/1_Conf_1.000	3075	20	0	NP_496534.1	60	727.243	1112	669	Nuclear Pore complex Protein family member (npp-3)
Locus_5589_Transcript_1/1_Conf_1.000	2239	20	2.75E-25	EFO28145.1	50	122.094	365	183	hypothetical protein LOAG_00351
Locus_559_Transcript_1/2_Conf_1.000	701	20	1.97E-51	NP_502790.1	87	206.453	131	114	NADH Ubiquinone Oxidoreductase family member (nuo-3)
Locus_559_Transcript_2/2_Conf_1.000	233	5	4.95E-09	NP_001122821.1	87	64.3142	40	35	NADH Ubiquinone Oxidoreductase family member (nuo-3)
Locus_5590_Transcript_1/1_Conf_1.000	1173	20	4.73E-91	NP_498395.1	77	339.347	324	251	hypothetical protein C16A3.6
Locus_5591_Transcript_1/1_Conf_1.000	463	0							
Locus_5592_Transcript_1/1_Conf_1.000	733	20	1.99E-105	BAC25813.1	100	385.956	214	214	unnamed protein product
Locus_5593_Transcript_1/1_Conf_1.000	929	20	8.35E-103	EFO22451.1	75	377.867	309	233	hypothetical protein LOAG_06034

Locus_5594_Transcript_1/3_Conf_0.333	696	20	1.76E-60	XP_002640329.1	80	236.498	177	142	Hypothetical protein CBG12877
Locus_5594_Transcript_2/3_Conf_0.667	2781	20	0	NP_491672.1	96	766.148	429	415	proteasome Regulatory Particle, ATPase-like family member (rpt-5)
Locus_5594_Transcript_3/3_Conf_0.667	2784	20	0	NP_491672.1	96	766.148	429	415	proteasome Regulatory Particle, ATPase-like family member (rpt-5)
Locus_5595_Transcript_1/1_Conf_1.000	535	20	8.08E-46	NP_499308.1	73	186.808	160	117	hypothetical protein D2045.5
Locus_5596_Transcript_1/1_Conf_1.000	1552	20	0	XP_002643479.1	88	861.677	526	468	C. briggsae CBR-FLNA-1 protein
Locus_5597_Transcript_1/1_Conf_1.000	165	0							
Locus_5598_Transcript_1/1_Conf_1.000	1084	4	4.43E-141	NP_505848.1	88	505.368	315	279	hypothetical protein T19B10.2
Locus_5599_Transcript_1/1_Conf_1.000	972	20	1.31E-69	XP_002633511.1	76	267.7	225	173	Hypothetical protein CBG05373
Locus_56_Transcript_1/3_Conf_0.714	2503	20	1.79E-113	NP_501082.2	51	415.231	809	418	hypothetical protein C25A8.4

Locus_56_Transcript_2/3_Conf_0.714	2503	20	1.52E-112	NP_501082.2	51	412.149	809	417	hypothetical protein C25A8.4
Locus_56_Transcript_3/3_Conf_0.714	2503	20	8.89E-113	NP_501082.2	51	412.92	809	417	hypothetical protein C25A8.4
Locus_560_Transcript_1/1_Conf_1.000	218	2	2.57E-10	XP_002647686.1	65	68.5514	78	51	Hypothetical protein CBG17874
Locus_5600_Transcript_1/1_Conf_1.000	351	16	9.22E-40	XP_002645128.1	85	166.392	107	92	C. briggsae CBR-NSY-4 protein
Locus_5601_Transcript_1/1_Conf_1.000	645	5	2.74E-14	NP_508012.2	65	82.8037	81	53	hypothetical protein Y44A6D.3
Locus_5602_Transcript_1/1_Conf_1.000	576	20	2.07E-06	XP_002190459.1	71	56.225	56	40	PREDICTED: DEK oncogene (DNA binding)
Locus_5603_Transcript_1/2_Conf_1.000	671	6	1.52E-10	NP_001023411.1	51	70.4774	137	71	Helix Loop Helix family member (hlh-30)
Locus_5603_Transcript_2/2_Conf_1.000	593	2	1.58E-04	NP_500461.1	47	50.0618	108	51	Helix Loop Helix family member (hlh-30)
Locus_5604_Transcript_1/2_Conf_1.000	1198	20	1.44E-167	XP_002640277.1	83	593.578	419	351	Hypothetical protein CBG12802

Locus_5604_Transcript_2/2_Conf_1.000	1192	20	7.07E-167	XP_002640277.1	83	591.267	417	349	Hypothetical protein CBG12802
Locus_5605_Transcript_1/2_Conf_1.000	1828	20	1.49E-34	NP_491344.1	44	152.525	521	233	Conserved Oligomeric Golgi (COG) Component family member (cogc-5)
Locus_5605_Transcript_2/2_Conf_1.000	1819	20	6.64E-35	NP_491344.1	44	153.68	518	233	Conserved Oligomeric Golgi (COG) Component family member (cogc-5)
Locus_5606_Transcript_1/1_Conf_1.000	150	0							

Locus_5607_Transcript_1/3_Conf_0.714	2137	20	1.49E-129	XP_001896367.1	62	468.389	521	327	ELM2 domain containing protein
Locus_5607_Transcript_2/3_Conf_0.714	2137	20	1.14E-129	XP_001896367.1	62	468.774	521	327	ELM2 domain containing protein
Locus_5607_Transcript_3/3_Conf_0.714	2137	20	1.49E-129	XP_001896367.1	62	468.389	521	327	ELM2 domain containing protein
Locus_5608_Transcript_1/1_Conf_1.000	531	0							
Locus_5609_Transcript_1/3_Conf_0.600	593	20	9.51E-18	CAR63567.1	77	93.9745	70	54	putative COLlagen
Locus_5609_Transcript_2/3_Conf_0.600	902	20	2.79E-15	CAR63567.1	79	87.0409	62	49	putative COLlagen
Locus_5609_Transcript_3/3_Conf_0.600	927	20	2.41E-17	CAR63567.1	77	93.9745	70	54	putative COLlagen
Locus_561_Transcript_1/1_Conf_1.000	1226	19	1.86E-77	XP_002634261.1	78	294.278	221	173	Hypothetical protein CBG01832
Locus_5610_Transcript_1/1_Conf_1.000	1451	20	0	XP_002642172.1	85	682.174	452	386	Hypothetical protein CBG18137

Locus_5611_Transcript_1/1_Conf_1.000	780	20	1.59E-26		57	124.02	127	73	protein F33E11.3
Locus_5612_Transcript_1/1_Conf_1.000	536	2	2.07E-25	NP_491390.2	54	119.013	179	97	hypothetical protein D1007.15
Locus_5613_Transcript_1/1_Conf_1.000	268	0							
Locus_5614_Transcript_1/1_Conf_1.000	177	0							
Locus_5615_Transcript_1/1_Conf_1.000	688	5	6.15E-18	XP_002630482.1	46	95.1301	229	106	Hypothetical protein CBG11218
Locus_5616_Transcript_1/1_Conf_1.000	422	3	8.19E-12	NP_001024778.2	56	73.559	125	70	neuRonal IGCAM family member (rig-1)
Locus_5617_Transcript_1/1_Conf_1.000	413	7	1.40E-56	CAD44145.2	87	222.246	138	121	C. elegans protein T21C9.3b, confirmed by transcript evidence
Locus_5618_Transcript_1/1_Conf_1.000	1383	20	6.10E-35	XP_793959.2	54	153.295	247	135	PREDICTED: similar to ENSANGP00000010363
Locus_5619_Transcript_1/1_Conf_1.000	1085	20	1.11E-83	XP_002631436.1	91	314.694	215	196	C. briggsae CBR-VHA-4 protein
Locus_562_Transcript_1/10_Conf_0.154	298	0							
Locus_562_Transcript_10/10_Conf_0.577	1820	20	8.49E-107		62	392.504	453	281	protein F28E10.3
Locus_562_Transcript_2/10_Conf_0.615	1865	20	8.77E-107		62	392.504	453	281	protein F28E10.3
Locus_562_Transcript_3/10_Conf_0.154	624	20	2.17E-58		70	229.18	219	155	protein F47C8.1
Locus_562_Transcript_4/10_Conf_0.577	1758	20	5.22E-94		63	347.051	394	249	Rte-1 element
Locus_562_Transcript_5/10_Conf_0.115	654	20	2.01E-60		70	236.113	227	159	protein F47C8.1
Locus_562_Transcript_6/10_Conf_0.077	440	20	3.01E-35	AAC72298.1	78	151.369	118	93	reverse transcriptase
Locus_562_Transcript_7/10_Conf_0.308	1069	20	1.20E-82		66	311.227	322	215	protein F47C8.1
Locus_562_Transcript_8/10_Conf_0.115	343	0							

Locus_562_Transcript_9/10_Conf_0.423	2038	20	9.77E-107		62	392.504	453	281	protein F28E10.3
Locus_5620_Transcript_1/3_Conf_0.667	731	20	9.99E-33	NP_493619.1	61	144.436	198	122	hypothetical protein F33H2.2
Locus_5620_Transcript_2/3_Conf_0.667	734	20	8.54E-32	NP_493619.1	61	141.354	198	121	hypothetical protein F33H2.2
Locus_5620_Transcript_3/3_Conf_0.667	734	20	1.01E-32	NP_493619.1	61	144.436	198	122	hypothetical protein F33H2.2
Locus_5621_Transcript_1/1_Conf_1.000	1232	10	2.82E-57	NP_510823.1	75	227.254	175	132	OSMotic avoidance abnormal family member (osm-11)
Locus_5622_Transcript_1/1_Conf_1.000	340	0							
Locus_5623_Transcript_1/2_Conf_1.000	859	20	1.68E-107	NP_502119.2	80	393.275	275	221	hypothetical protein F54D1.6
Locus_5623_Transcript_2/2_Conf_1.000	721	20	1.29E-93	NP_502119.2	81	346.665	238	195	hypothetical protein F54D1.6
Locus_5624_Transcript_1/1_Conf_1.000	763	20	2.00E-103	XP_002634283.1	85	379.407	245	209	C. briggsae CBR-HRS-1 protein
Locus_5625_Transcript_1/1_Conf_1.000	329	0							
Locus_5626_Transcript_1/1_Conf_1.000	1046	20	1.26E-129	XP_002640711.1	96	467.233	259	251	Hypothetical protein CBG19778
Locus_5627_Transcript_1/1_Conf_1.000	886	0							
Locus_5628_Transcript_1/1_Conf_1.000	1070	5	8.57E-89	XP_002630376.1	67	331.643	356	240	Hypothetical protein CBG04315
Locus_5629_Transcript_1/1_Conf_1.000	154	0							
Locus_563_Transcript_1/1_Conf_1.000	1007	20	1.86E-90	NP_505145.1	92	337.035	197	182	Suppressor/Enhancer of Lin-12 family member (sel-9)
Locus_5630_Transcript_1/1_Conf_1.000	969	20	6.32E-32	XP_001899729.1	52	142.51	276	144	Posterior Sex Combs gene.
Locus_5631_Transcript_1/1_Conf_1.000	239	20	7.56E-18	XP_002640883.1	80	93.5893	68	55	Hypothetical protein CBG15774
Locus_5632_Transcript_1/2_Conf_1.000	318	0							
Locus_5632_Transcript_2/2_Conf_1.000	375	0							

Locus_5633_Transcript_1/1_Conf_1.000	1378	20	1.69E-61	NP_497866.2	65	241.506	285	186	Defective in Cullin Neddylation family member (dcn-1)
Locus_5634_Transcript_1/1_Conf_1.000	214	0							
Locus_5635_Transcript_1/1_Conf_1.000	734	5	3.14E-26	NP_001021652.1	52	122.865	251	133	FANCI (Fanconi anemia complex component I) homolog family member (fnci-1)
Locus_5636_Transcript_1/1_Conf_1.000	334	0							
Locus_5637_Transcript_1/1_Conf_1.000	544	20	2.17E-73	NP_504512.1	89	278.485	172	154	hypothetical protein F44E7.2
Locus_5638_Transcript_1/1_Conf_1.000	1206	20	0	XP_002636771.1	93	682.174	402	376	C. briggsae CBR-ATN-1 protein
Locus_5639_Transcript_1/1_Conf_1.000	688	20	5.88E-61	NP_499913.1	73	238.039	228	168	Sphingosine Phosphate Lyase family member (spl-1)
Locus_564_Transcript_1/7_Conf_0.500	1048	8	1.82E-27	ADN00784.1	71	127.872	105	75	parasitic stage specific protein 2
Locus_564_Transcript_2/7_Conf_0.222	479	11	3.58E-28	ADN00784.1	71	127.872	105	75	parasitic stage specific protein 2
Locus_564_Transcript_3/7_Conf_0.667	1535	13	3.15E-27	ADN00784.1	71	127.872	105	75	parasitic stage specific protein 2
Locus_564_Transcript_4/7_Conf_0.667	1547	13	3.16E-27	ADN00784.1	71	127.872	105	75	parasitic stage specific protein 2
Locus_564_Transcript_5/7_Conf_0.611	1547	8	3.16E-27	ADN00784.1	71	127.872	105	75	parasitic stage specific protein 2
Locus_564_Transcript_6/7_Conf_0.167	549	16	1.05E-38	ADN00784.1	73	163.31	122	90	parasitic stage specific protein 2
Locus_564_Transcript_7/7_Conf_0.667	1547	13	3.16E-27	ADN00784.1	71	127.872	105	75	parasitic stage specific protein 2

Locus_5640_Transcript_1/1_Conf_1.000	744	20	5.28E-85	XP_002635306.1	82	318.161	239	196	C. briggsae CBR-ATGR-18 protein
Locus_5641_Transcript_1/1_Conf_1.000	794	20	3.60E-90	XP_001899472.1	82	335.495	261	216	Patatin-like phospholipase family protein
Locus_5642_Transcript_1/1_Conf_1.000	160	0							
Locus_5643_Transcript_1/1_Conf_1.000	778	20	9.19E-59	XP_002634987.1	75	231.106	208	158	Hypothetical protein CBG13527
Locus_5644_Transcript_1/3_Conf_0.667	362	20	1.16E-18	XP_001892049.1	74	96.2857	67	50	Variant SH3 domain containing protein
Locus_5644_Transcript_2/3_Conf_0.667	377	20	1.18E-18	XP_001892049.1	74	96.2857	67	50	Variant SH3 domain containing protein
Locus_5644_Transcript_3/3_Conf_0.667	362	20	1.16E-18	XP_001892049.1	74	96.2857	67	50	Variant SH3 domain containing protein
Locus_5645_Transcript_1/1_Conf_1.000	682	20	2.03E-90	XP_001894987.1	93	335.88	202	189	RE32166p
Locus_5646_Transcript_1/1_Conf_1.000	368	20	1.22E-52	CAR63541.1	96	209.149	112	108	putative Ribosomal Protein
Locus_5647_Transcript_1/1_Conf_1.000	1754	20	0	NP_495453.1	87	872.463	558	488	lysyl (K) tRNA Synthetase family member (krs-1)
Locus_5648_Transcript_1/2_Conf_1.000	654	0							
Locus_5648_Transcript_2/2_Conf_1.000	658	0							
Locus_5649_Transcript_1/1_Conf_1.000	1467	20	8.08E-134	EFO18685.1	86	481.871	337	293	DNA topoisomerase I
Locus_565_Transcript_1/1_Conf_1.000	262	0							
Locus_5650_Transcript_1/1_Conf_1.000	464	0							

Locus_5651_Transcript_1/1_Conf_1.000	575	20	5.88E-38	NP_508239.1	88	160.999	102	90	Temporarily Assigned Gene name family member (tag-303)
Locus_5652_Transcript_1/1_Conf_1.000	470	20	3.30E-13	EFO27956.1	74	78.1814	58	43	leucine Rich Repeat family protein
Locus_5653_Transcript_1/1_Conf_1.000	614	20	6.17E-18	XP_001900211.1	50	94.7449	202	102	Peptidase family M13 containing protein
Locus_5654_Transcript_1/2_Conf_1.000	1361	20	4.35E-107	XP_001899430.1	66	285.034	264	175	Nuclear hormone receptor family member nhr-3
Locus_5654_Transcript_2/2_Conf_1.000	1282	20	1.83E-123	NP_510423.1	72	447.203	434	316	Nuclear Hormone Receptor family member (nhr-3)
Locus_5655_Transcript_1/1_Conf_1.000	193	0							
Locus_5656_Transcript_1/1_Conf_1.000	1536	7	3.25E-40	NP_501316.2	52	171.014	366	192	hypothetical protein C49H3.6
Locus_5657_Transcript_1/1_Conf_1.000	1587	20	1.08E-163	NP_491363.1	88	581.252	385	340	Dynein Heavy Chain family member (dhc-1)
Locus_5658_Transcript_1/1_Conf_1.000	155	20	4.65E-15	NP_001182573.1	100	84.3445	39	39	pyruvate kinase isozymes M1/M2 isoform 1

Locus_5659_Transcript_1/1_Conf_1.000	863	9	4.88E-30	AAA20077.1	65	135.961	155	102	CDS structure deduced from alignment with C. elegans ced-9 gene
Locus_566_Transcript_1/6_Conf_0.762	616	20	3.10E-37	P27613.1	76	132.494	104	80	Globin-like host-protective antigen
Locus_566_Transcript_2/6_Conf_0.476	599	20	2.94E-30	P27613.1	77	135.576	104	81	Globin-like host-protective antigen
Locus_566_Transcript_3/6_Conf_0.571	599	20	1.50E-35	P27613.1	77	135.576	104	81	Globin-like host-protective antigen
Locus_566_Transcript_4/6_Conf_0.524	600	20	2.98E-30	P27613.1	77	135.576	104	81	Globin-like host-protective antigen
Locus_566_Transcript_5/6_Conf_0.762	537	20	1.04E-36	P27613.1	80	130.183	98	79	Globin-like host-protective antigen
Locus_566_Transcript_6/6_Conf_0.762	616	20	3.73E-38	P27613.1	77	135.576	104	81	Globin-like host-protective antigen
Locus_5660_Transcript_1/1_Conf_1.000	1283	20	1.83E-06	XP_001897358.1	40	58.5362	212	86	hypothetical protein
Locus_5661_Transcript_1/1_Conf_1.000	502	0							

Locus_5662_Transcript_1/1_Conf_1.000	402	20	1.09E-24	NP_491926.1	79	116.316	106	84	Lipid Binding Protein family member (lbp-6)
Locus_5663_Transcript_1/1_Conf_1.000	462	0							
Locus_5664_Transcript_1/1_Conf_1.000	1066	5	2.99E-25	XP_002639089.1	42	120.553	382	161	C. briggsae CBR-TAG-163 protein
Locus_5665_Transcript_1/2_Conf_1.000	515	0							
Locus_5665_Transcript_2/2_Conf_1.000	473	0							
Locus_5666_Transcript_1/1_Conf_1.000	982	20	1.03E-45	NP_496406.2	51	188.348	326	169	hypothetical protein T06D8.9
Locus_5667_Transcript_1/1_Conf_1.000	164	0							
Locus_5668_Transcript_1/2_Conf_1.000	476	4	9.54E-05	AAY29120.1	52	50.0618	136	71	cement precursor protein 3B variant 1
Locus_5668_Transcript_2/2_Conf_1.000	428	0							
Locus_5669_Transcript_1/1_Conf_1.000	662	20	8.29E-30	XP_002642918.1	56	134.42	224	126	Hypothetical protein CBG15194
Locus_567_Transcript_1/1_Conf_1.000	650	20	1.42E-26	NP_501527.1	79	123.635	89	71	COLlagen family member (col-3)
Locus_5670_Transcript_1/1_Conf_1.000	318	20	1.95E-13	XP_002640077.1	90	78.9518	63	57	Hypothetical protein CBG12562
Locus_5671_Transcript_1/1_Conf_1.000	1203	20	9.49E-127	XP_002639344.1	86	457.988	321	279	C. briggsae CBR-TMD-1 protein

Locus_5672_Transcript_1/2_Conf_1.000	1506	20	2.55E-98	NP_502122.1	80	363.999	290	233	DNaJ domain (prokaryotic heat shock protein) family member (dnj-1)
Locus_5672_Transcript_2/2_Conf_1.000	1518	20	2.58E-98	NP_502122.1	80	363.999	290	233	DNaJ domain (prokaryotic heat shock protein) family member (dnj-1)
Locus_5673_Transcript_1/4_Conf_0.222	244	2	5.29E-06	XP_002646454.1	66	52.7582	56	37	Hypothetical protein CBG18864
Locus_5673_Transcript_2/4_Conf_0.333	1011	20	6.57E-35	XP_002646454.1	72	152.525	137	99	Hypothetical protein CBG18864
Locus_5673_Transcript_3/4_Conf_0.444	597	7	5.04E-06	XP_002646454.1	60	55.0694	68	41	Hypothetical protein CBG18864
Locus_5673_Transcript_4/4_Conf_0.444	824	20	1.52E-46	NP_493447.2	73	190.66	183	135	hypothetical protein Y71A12C.2
Locus_5674_Transcript_1/2_Conf_1.000	820	20	1.12E-57	XP_002646753.1	77	227.639	184	142	Hypothetical protein CBG13150
Locus_5674_Transcript_2/2_Conf_1.000	820	20	1.12E-57	XP_002646753.1	77	227.639	184	142	Hypothetical protein CBG13150
Locus_5675_Transcript_1/1_Conf_1.000	1459	20	2.17E-147	NP_501256.1	83	526.939	359	298	hypothetical protein F33D4.4
Locus_5676_Transcript_1/1_Conf_1.000	865	20	1.31E-107	NP_001024749.1	83	393.66	287	239	High temperature-Induced Dauer formation family member (hid-1)
Locus_5677_Transcript_1/1_Conf_1.000	2622	20	0	EFO19478.1	85	1247.65	875	748	U5 snRNP-associated protein
Locus_5678_Transcript_1/1_Conf_1.000	505	4	7.13E-11	EFO26249.1	74	70.4774	62	46	hypothetical protein LOAG_02232

Locus_5679_Transcript_1/1_Conf_1.000	1125	20	8.08E-08	XP_002629684.1	59	62.7734	79	47	C. briggsae CBR-ERGO-1.1 protein
Locus_568_Transcript_1/1_Conf_1.000	1376	20	1.14E-41	XP_001901854.1	50	175.637	258	130	Zinc finger, C2H2 type family protein
Locus_5680_Transcript_1/1_Conf_1.000	2813	20	0	NP_496945.3	63	815.839	994	636	XRN (mouse/S. cerevisiae) ribonuclease related family member (xrn-1)
Locus_5681_Transcript_1/1_Conf_1.000	1147	20	5.35E-116	XP_002630350.1	78	422.165	351	276	Hypothetical protein CBG04280
Locus_5682_Transcript_1/1_Conf_1.000	407	20	1.55E-71	XP_002714405.1	100	271.937	132	132	PREDICTED: tubulin, beta 5-like
Locus_5683_Transcript_1/1_Conf_1.000	225	5	2.47E-16	NP_001041092.2	94	88.5817	52	49	Motor AXon guidance family member (max-1)
Locus_5684_Transcript_1/1_Conf_1.000	1553	20	0	XP_002629737.1	88	642.114	399	354	Hypothetical protein CBG00970
Locus_5685_Transcript_1/1_Conf_1.000	1447	6	3.11E-130	NP_001123061.1	67	469.929	485	325	hypothetical protein Y69H2.15
Locus_5686_Transcript_1/1_Conf_1.000	1147	20	4.68E-120	XP_002639984.1	75	435.647	319	242	C. briggsae CBR-CHP-1 protein
Locus_5687_Transcript_1/1_Conf_1.000	257	0							

Locus_5688_Transcript_1/1_Conf_1.000	1064	20	5.30E-107	XP_002643153.1	77	392.119	368	286	C. briggsae CBR-RHA-2 protein
Locus_5689_Transcript_1/1_Conf_1.000	214	0							
Locus_569_Transcript_1/2_Conf_1.000	796	20	1.10E-62	NP_497181.2	91	244.202	145	133	hypothetical protein Y50D7A.3
Locus_569_Transcript_2/2_Conf_1.000	873	20	5.04E-123	NP_497181.2	83	444.891	308	256	hypothetical protein Y50D7A.3
Locus_5690_Transcript_1/1_Conf_1.000	580	11	1.66E-19	NP_503758.4	45	99.7525	181	82	KETtiN (Drosophila actin-binding) homolog family member (ketn-1)
Locus_5691_Transcript_1/2_Conf_1.000	351	2	6.25E-04	XP_001900384.1	49	47.3654	87	43	Protein kinase domain containing protein
Locus_5691_Transcript_2/2_Conf_1.000	300	0							
Locus_5692_Transcript_1/1_Conf_1.000	1870	20	9.02E-27	AAO63577.1	52	126.716	200	105	secreted protein 5 precursor
Locus_5693_Transcript_1/1_Conf_1.000	532	5	6.29E-06	XP_001897921.1	53	54.299	128	68	RhoGEF domain containing protein

Locus_5694_Transcript_1/1_Conf_1.000	1302	20	1.69E-132	NP_502171.1	83	477.248	325	272	hypothetical protein M04B2.4
Locus_5695_Transcript_1/1_Conf_1.000	664	20	1.52E-47	NP_492692.1	72	193.356	172	125	hypothetical protein Y106G6E.4
Locus_5696_Transcript_1/1_Conf_1.000	334	1	8.06E-04	EFO13988.1	51	46.9802	77	40	ephrin EFN-4
Locus_5697_Transcript_1/1_Conf_1.000	317	5	1.23E-15	XP_001891653.1	60	86.2705	101	61	2700029M09Rik protein
Locus_5698_Transcript_1/1_Conf_1.000	490	3	1.21E-07	XP_002634680.1	77	59.6918	44	34	Hypothetical protein CBG19666
Locus_5699_Transcript_1/2_Conf_1.000	1055	4	4.25E-08	XP_002632110.1	55	63.5438	144	80	Hypothetical protein CBG06964
Locus_5699_Transcript_2/2_Conf_1.000	1058	4	4.27E-08	XP_002632110.1	55	63.5438	144	80	Hypothetical protein CBG06964
Locus_57_Transcript_1/3_Conf_0.778	1445	19	1.14E-15	XP_001892587.1	77	89.3521	74	57	hypothetical protein Bm1_05565
Locus_57_Transcript_2/3_Conf_0.778	1440	4	7.37E-15	XP_001892587.1	76	86.6557	73	56	hypothetical protein Bm1_05565
Locus_57_Transcript_3/3_Conf_0.778	1445	19	1.14E-15	XP_001892587.1	77	89.3521	74	57	hypothetical protein Bm1_05565
Locus_570_Transcript_1/1_Conf_1.000	1915	20	0	XP_002639664.1	90	1063.52	639	579	C. briggsae CBR-HUM-1 protein
Locus_5700_Transcript_1/1_Conf_1.000	248	20	1.77E-35	CAR63700.1	96	152.14	82	79	hypothetical protein
Locus_5701_Transcript_1/1_Conf_1.000	1635	20	3.81E-111	XP_002639727.1	69	406.757	436	303	Hypothetical protein CBG12454
Locus_5702_Transcript_1/2_Conf_1.000	640	0							
Locus_5702_Transcript_2/2_Conf_1.000	625	1	7.72E-04	NP_001036881.1	41	46.2098	118	49	annexin B13
Locus_5703_Transcript_1/1_Conf_1.000	651	20	1.67E-83	NP_509898.1	90	312.768	184	166	ACOnitase family member (aco-1)
Locus_5704_Transcript_1/1_Conf_1.000	994	20	2.34E-37	NP_498151.2	53	160.614	212	114	hypothetical protein Y32H12A.8

Locus_5705_Transcript_1/1_Conf_1.000	414	20	8.50E-30	EFO21331.1	80	133.265	102	82	expressed sequence
Locus_5706_Transcript_1/1_Conf_1.000	420	0							
Locus_5707_Transcript_1/1_Conf_1.000	971	20	1.22E-67	NP_493616.1	66	261.151	333	220	hypothetical protein F33H2.5
Locus_5708_Transcript_1/1_Conf_1.000	144	1	8.31E-04	XP_002642902.1	66	46.9802	48	32	Hypothetical protein CBG15176
Locus_5709_Transcript_1/1_Conf_1.000	434	0							
Locus_571_Transcript_1/1_Conf_1.000	1622	20	0	XP_002641813.1	94	667.537	389	366	C. briggsae CBR-INF-1 protein
Locus_5710_Transcript_1/1_Conf_1.000	1132	20	0	XP_002931172.1	100	754.592	373	373	PREDICTED: actin, cytoplasmic 2-like
Locus_5711_Transcript_1/4_Conf_0.222	403	20	7.80E-39	AAN11401.1	74	163.31	134	100	metalloprotease 1 precursor
Locus_5711_Transcript_2/4_Conf_0.667	1213	20	1.05E-149	AAN11401.1	78	534.258	405	316	metalloprotease 1 precursor
Locus_5711_Transcript_3/4_Conf_0.667	1213	20	1.80E-149	AAN11401.1	77	533.487	405	313	metalloprotease 1 precursor

Locus_5711_Transcript_4/4_Conf_0.667	1213	20	2.35E-149	AAN11401.1	77	533.102	405	315	metalloprotease 1 precursor
Locus_5712_Transcript_1/1_Conf_1.000	1117	20	1.19E-136	XP_002635531.1	86	490.73	319	276	Hypothetical protein CBG08841
Locus_5713_Transcript_1/1_Conf_1.000	509	0							
Locus_5714_Transcript_1/1_Conf_1.000	1420	20	4.61E-179	XP_002647109.1	88	632.098	398	351	Hypothetical protein CBG20301
Locus_5715_Transcript_1/1_Conf_1.000	286	0							
Locus_5716_Transcript_1/1_Conf_1.000	224	0							
Locus_5717_Transcript_1/1_Conf_1.000	944	20	6.56E-111	NP_501576.2	84	404.831	284	240	Mitochondrial Processing Peptidase Beta family member (mppb-1)
Locus_5718_Transcript_1/1_Conf_1.000	1984	20	4.26E-91	EFO23961.1	65	340.502	402	265	hypothetical protein LOAG_04523
Locus_5719_Transcript_1/1_Conf_1.000	548	20	1.89E-32	XP_002631685.1	73	142.51	107	79	Hypothetical protein CBG20878
Locus_572_Transcript_1/1_Conf_1.000	509	0							
Locus_5720_Transcript_1/1_Conf_1.000	229	7	3.21E-16	XP_001894589.1	69	88.1965	75	52	DnaJ domain containing protein
Locus_5721_Transcript_1/1_Conf_1.000	678	0							
Locus_5722_Transcript_1/3_Conf_0.667	606	20	1.20E-34	NP_001022362.1	66	150.214	155	103	hypothetical protein T24F1.3
Locus_5722_Transcript_2/3_Conf_0.667	633	20	7.81E-35	NP_001022362.1	65	150.984	155	102	hypothetical protein T24F1.3

Locus_5722_Transcript_3/3_Conf_0.667	633	20	1.33E-34	NP_001022362.1	66	150.214	155	103	hypothetical protein T24F1.3
Locus_5723_Transcript_1/1_Conf_1.000	584	20	2.75E-70	CBW44402.1	86	268.47	194	167	C. elegans protein Y59A8B.22c, partially confirmed by transcript evidence
Locus_5724_Transcript_1/1_Conf_1.000	744	20	2.74E-41	NP_502144.1	54	172.94	256	140	hypothetical protein T01G1.3
Locus_5725_Transcript_1/1_Conf_1.000	533	20	6.05E-25	NP_505963.3	61	117.472	145	89	hypothetical protein T04F3.1
Locus_5726_Transcript_1/1_Conf_1.000	379	20	1.64E-12	NP_001021200.1	62	75.8702	64	40	tryptophanyl (W) tRNA Synthetase family member (wrs-2)
Locus_5727_Transcript_1/1_Conf_1.000	1055	20	2.16E-153	AAC38987.1	89	546.199	351	315	P-glycoprotein
Locus_5728_Transcript_1/1_Conf_1.000	734	20	3.89E-93	NP_492379.1	81	345.125	246	200	hypothetical protein F36A2.2
Locus_5729_Transcript_1/2_Conf_1.000	3238	20	0	XP_002631481.1	90	1717.98	1082	980	Hypothetical protein CBG20636

Locus_5729_Transcript_2/2_Conf_1.000	3234	20	0	XP_002631481.1	90	1466.06	936	843	Hypothetical protein CBG20636
Locus_573_Transcript_1/3_Conf_0.750	3823	20	0	EFO20496.1	72	977.622	929	676	hypothetical protein LOAG_07994
Locus_573_Transcript_2/3_Conf_0.750	3823	20	0	EFO20496.1	72	977.622	929	676	hypothetical protein LOAG_07994
Locus_573_Transcript_3/3_Conf_0.750	3823	20	0	EFO20496.1	72	977.622	929	676	hypothetical protein LOAG_07994
Locus_5730_Transcript_1/1_Conf_1.000	413	20	3.12E-48	A8XP97.2	81	194.512	139	113	Voltage-dependent calcium channel unc-36
Locus_5731_Transcript_1/1_Conf_1.000	588	20	5.42E-66	NP_498541.1	86	254.218	153	133	UBiquitin Conjugating enzyme family member (ubc-18)
Locus_5732_Transcript_1/2_Conf_0.500	2382	20	1.28E-177	NP_001129765.1	73	628.246	500	369	hypothetical protein F16A11.1
Locus_5732_Transcript_2/2_Conf_0.500	2382	20	3.36E-178	NP_001129765.1	73	630.172	500	369	hypothetical protein F16A11.1
Locus_5733_Transcript_1/1_Conf_1.000	335	20	1.09E-08	NP_001123161.1	58	63.1586	77	45	hypothetical protein K03A11.6
Locus_5734_Transcript_1/2_Conf_1.000	481	0							
Locus_5734_Transcript_2/2_Conf_1.000	481	0							

Locus_5735_Transcript_1/2_Conf_1.000	264	18	2.07E-15	XP_002642178.1	65	85.5001	86	56	C. briggsae CBR-UBXN-4 protein
Locus_5735_Transcript_2/2_Conf_1.000	264	19	1.59E-15	XP_002642178.1	65	85.8853	86	56	C. briggsae CBR-UBXN-4 protein
Locus_5736_Transcript_1/1_Conf_1.000	1530	20	9.46E-24	EFO25952.1	51	116.316	170	87	hypothetical protein LOAG_02532
Locus_5737_Transcript_1/2_Conf_1.000	568	0							
Locus_5737_Transcript_2/2_Conf_1.000	424	0							
Locus_5738_Transcript_1/1_Conf_1.000	145	20	3.25E-16	XP_002640875.1	93	88.1965	47	44	C. briggsae CBR-UNC-71 protein
Locus_5739_Transcript_1/1_Conf_1.000	235	20	7.85E-15	CAZ65483.1	85	83.5741	67	57	C. elegans protein F02H6.5b, confirmed by transcript evidence
Locus_574_Transcript_1/1_Conf_1.000	1462	20	0	XP_001894819.1	99	757.673	376	375	actin
Locus_5740_Transcript_1/1_Conf_1.000	192	20	1.60E-07	XP_001623630.1	70	59.3066	64	45	predicted protein
Locus_5741_Transcript_1/1_Conf_1.000	143	0							

Locus_5742_Transcript_1/1_Conf_1.000	535	2	8.09E-05	XP_002953870.1	51	49.2914	70	36	hypothetical protein VOLCADRAFT_118487
Locus_5743_Transcript_1/1_Conf_1.000	360	1	2.27E-06	NP_001122488.1	54	55.4546	102	56	hypothetical protein F56H1.7
Locus_5744_Transcript_1/4_Conf_0.250	224	0							
Locus_5744_Transcript_2/4_Conf_0.375	295	0							
Locus_5744_Transcript_3/4_Conf_0.500	375	0							
Locus_5744_Transcript_4/4_Conf_0.625	396	0							
Locus_5745_Transcript_1/1_Conf_1.000	366	13	3.03E-11	XP_001899331.1	73	71.633	64	47	FYVE zinc finger family protein
Locus_5746_Transcript_1/1_Conf_1.000	493	8	5.18E-51	NP_508552.1	71	203.756	161	115	hypothetical protein F40F4.6
Locus_5747_Transcript_1/1_Conf_1.000	766	20	8.12E-28	XP_002641869.1	55	128.257	248	138	C. briggsae CBR-TEN-1 protein
Locus_5748_Transcript_1/1_Conf_1.000	362	20	1.79E-11	ADD20274.1	70	72.4034	61	43	heterochromatin-associated protein hP1
Locus_5749_Transcript_1/6_Conf_0.111	137	0							
Locus_5749_Transcript_2/6_Conf_0.556	683	0							
Locus_5749_Transcript_3/6_Conf_0.500	351	0							
Locus_5749_Transcript_4/6_Conf_0.333	683	0							
Locus_5749_Transcript_5/6_Conf_0.556	519	0							
Locus_5749_Transcript_6/6_Conf_0.556	683	0							
Locus_575_Transcript_1/1_Conf_1.000	683	0							
Locus_5750_Transcript_1/1_Conf_1.000	524	4	8.72E-42	XP_002634224.1	80	173.326	130	105	Hypothetical protein CBG01794
Locus_5751_Transcript_1/5_Conf_0.364	1686	20	2.10E-120	NP_740922.1	64	437.573	426	273	CEll Death abnormality family member (ced-1)

Locus_5751_Transcript_2/5_Conf_0.364	1245	20	5.88E-119	NP_740922.1	66	432.18	400	264	CEll Death abnormality family member (ced-1)
Locus_5751_Transcript_3/5_Conf_0.273	698	0							
Locus_5751_Transcript_4/5_Conf_0.364	1623	20	1.75E-116	NP_001021772.1	68	424.476	386	264	CEll Death abnormality family member (ced-1)
Locus_5751_Transcript_5/5_Conf_0.545	1800	20	4.29E-119	NP_740922.1	61	433.335	447	276	CEll Death abnormality family member (ced-1)
Locus_5752_Transcript_1/2_Conf_1.000	561	20	3.93E-44	XP_002633663.1	69	181.415	175	121	Hypothetical protein CBG03338
Locus_5752_Transcript_2/2_Conf_1.000	557	20	1.28E-38	XP_002633663.1	74	107.457	90	67	Hypothetical protein CBG03338
Locus_5753_Transcript_1/1_Conf_1.000	833	20	7.45E-57	XP_002639338.1	66	224.942	216	143	Hypothetical protein CBG03917
Locus_5754_Transcript_1/1_Conf_1.000	753	0							

Locus_5755_Transcript_1/1_Conf_1.000	922	20	1.44E-30	NP_741494.1	55	137.887	273	151	Temporarily Assigned Gene name family member (tag-115)
Locus_5756_Transcript_1/1_Conf_1.000	5390	20	0	XP_002646579.1	65	901.738	1087	712	C. briggsae CBR-CRML-1 protein
Locus_5757_Transcript_1/1_Conf_1.000	431	5	4.13E-24	AAV50097.1	69	114.39	143	100	intersectin 2
Locus_5758_Transcript_1/1_Conf_1.000	361	20	2.67E-15	EFO22120.1	61	85.1149	110	68	hypothetical protein LOAG_06363
Locus_5759_Transcript_1/2_Conf_1.000	687	20	1.11E-43	ABA00169.1	70	180.644	166	117	Plexin protein 1
Locus_5759_Transcript_2/2_Conf_1.000	687	20	1.11E-43	ABA00169.1	70	180.644	166	117	Plexin protein 1
Locus_576_Transcript_1/1_Conf_1.000	238	20	2.67E-39	AAH65733.1	100	164.851	79	79	IGH@ protein
Locus_5760_Transcript_1/1_Conf_1.000	179	5	1.61E-12	XP_002642067.1	81	75.8702	58	47	Hypothetical protein CBG18006
Locus_5761_Transcript_1/1_Conf_1.000	646	20	5.52E-23	XP_001899289.1	53	111.694	210	112	hypothetical protein
Locus_5762_Transcript_1/1_Conf_1.000	128	0							
Locus_5763_Transcript_1/1_Conf_1.000	638	2	1.84E-07	XP_002637126.1	55	60.077	133	74	Hypothetical protein CBG09628
Locus_5764_Transcript_1/1_Conf_1.000	422	20	6.87E-43	XP_002631614.1	79	176.792	130	103	C. briggsae CBR-MAC-1 protein
Locus_5765_Transcript_1/1_Conf_1.000	863	20	5.45E-106	NP_504635.1	84	388.267	277	235	GAstrulation Defective family member (gad-1)
Locus_5766_Transcript_1/1_Conf_1.000	769	8	8.49E-17	XP_002634977.1	46	91.6633	249	115	Hypothetical protein CBG13513
Locus_5767_Transcript_1/2_Conf_1.000	480	0							
Locus_5767_Transcript_2/2_Conf_1.000	232	2	1.26E-04	XP_528085.1	55	49.6766	54	30	PREDICTED: tumor necrosis factor receptor superfamily, member 10c

Locus_5768_Transcript_1/1_Conf_1.000	1659	20	2.77E-125	XP_002638998.1	63	453.751	523	332	Hypothetical protein CBG22244
Locus_5769_Transcript_1/1_Conf_1.000	178	0							
Locus_577_Transcript_1/1_Conf_1.000	3139	20	0	ABO07440.1	99	1347.8	843	837	paramyosin
Locus_5770_Transcript_1/1_Conf_1.000	288	20	5.48E-24	NP_001033541.1	71	114.005	94	67	TransThyretin-Related family domain family member (ttr-36)
Locus_5771_Transcript_1/1_Conf_1.000	256	0							
Locus_5772_Transcript_1/1_Conf_1.000	464	20	1.02E-78	XP_002637229.1	97	295.819	154	150	C. briggsae CBR-TAG-59 protein
Locus_5773_Transcript_1/1_Conf_1.000	682	20	4.10E-75	NP_505154.1	76	285.034	217	167	More Of MS family member (mom-2)

Locus_5774_Transcript_1/1_Conf_1.000	605	20	1.23E-15	ZP_07335120.1	57	87.0409	145	83	adenylate cyclase
Locus_5775_Transcript_1/2_Conf_1.000	1354	20	3.34E-163	NP_740905.1	85	579.326	425	362	EATing: abnormal pharyngeal pumping family member (eat-16)
Locus_5775_Transcript_2/2_Conf_1.000	1354	20	3.34E-163	NP_740905.1	85	579.326	425	362	EATing: abnormal pharyngeal pumping family member (eat-16)
Locus_5776_Transcript_1/1_Conf_1.000	425	0							
Locus_5777_Transcript_1/1_Conf_1.000	351	0							
Locus_5778_Transcript_1/1_Conf_1.000	1120	0							
Locus_5779_Transcript_1/1_Conf_1.000	456	0							
Locus_578_Transcript_1/2_Conf_1.000	625	20	1.15E-75	ABR87130.1	92	286.574	193	179	large subunit ribosomal protein 1
Locus_578_Transcript_2/2_Conf_1.000	483	20	3.66E-28	ABR87128.1	88	127.872	76	67	large subunit ribosomal protein 1
Locus_5780_Transcript_1/2_Conf_1.000	1311	15	2.39E-09	XP_002634943.1	48	68.1662	128	62	Hypothetical protein CBG22545
Locus_5780_Transcript_2/2_Conf_1.000	771	0							
Locus_5781_Transcript_1/1_Conf_1.000	776	20	3.98E-38	NP_505071.1	72	162.54	142	103	hypothetical protein ZC513.5
Locus_5782_Transcript_1/1_Conf_1.000	132	0							

Locus_5783_Transcript_1/2_Conf_1.000	1225	20	3.64E-73	XP_001896695.1	60	280.026	386	233	Hr1 repeat family protein
Locus_5783_Transcript_2/2_Conf_1.000	1213	20	3.35E-71	XP_001896695.1	59	273.478	385	228	Hr1 repeat family protein
Locus_5784_Transcript_1/1_Conf_1.000	972	20	6.84E-10	XP_002125751.1	36	69.3218	294	107	PREDICTED: similar to Thrombospondin type 1 domain containing protein
Locus_5785_Transcript_1/2_Conf_1.000	937	6	1.49E-14	XP_002638931.1	44	84.7297	307	136	Hypothetical protein CBG22158
Locus_5785_Transcript_2/2_Conf_1.000	937	6	3.00E-15	XP_002638931.1	44	87.0409	307	136	Hypothetical protein CBG22158
Locus_5786_Transcript_1/1_Conf_1.000	746	2	2.87E-06	NP_001022555.1	74	56.6102	43	32	Homeobox family member (ceh-20)
Locus_5787_Transcript_1/3_Conf_0.286	277	0							
Locus_5787_Transcript_2/3_Conf_0.286	741	16	2.31E-24	XP_002642356.1	50	116.701	208	105	Hypothetical protein CBG18353
Locus_5787_Transcript_3/3_Conf_0.714	984	16	1.71E-24	XP_002642356.1	49	117.857	219	109	Hypothetical protein CBG18353
Locus_5788_Transcript_1/1_Conf_1.000	950	20	1.05E-31	EFO28280.1	83	141.739	100	83	hypothetical protein LOAG_00204
Locus_5789_Transcript_1/1_Conf_1.000	259	0							
Locus_579_Transcript_1/1_Conf_1.000	306	0							
Locus_5790_Transcript_1/1_Conf_1.000	321	0							
Locus_5791_Transcript_1/1_Conf_1.000	1072	20	1.11E-120	NP_504235.2	73	437.573	385	284	Drosophila SOS homolog family member (sos-1)
Locus_5792_Transcript_1/1_Conf_1.000	274	0							
Locus_5793_Transcript_1/1_Conf_1.000	1868	0							
Locus_5794_Transcript_1/1_Conf_1.000	1441	0							
Locus_5795_Transcript_1/1_Conf_1.000	187	20	2.73E-23	CAR63675.1	93	111.694	61	57	hypothetical protein

Locus_5796_Transcript_1/2_Conf_1.000	1037	7	4.46E-10	CAL56095.1	50	70.0922	160	81	DNA-directed RNA polymerase (ISS)
Locus_5796_Transcript_2/2_Conf_1.000	1037	2	2.89E-09	CAL56095.1	51	67.3958	160	82	DNA-directed RNA polymerase (ISS)
Locus_5797_Transcript_1/2_Conf_1.000	1089	20	3.17E-62	XP_002632974.1	57	243.432	390	224	Hypothetical protein CBG21734
Locus_5797_Transcript_2/2_Conf_1.000	1089	20	2.43E-62	XP_002632974.1	56	243.817	390	222	Hypothetical protein CBG21734
Locus_5798_Transcript_1/3_Conf_0.400	516	20	2.98E-23	NP_001026796.1	56	111.694	171	97	hypothetical protein C06G8.3
Locus_5798_Transcript_2/3_Conf_0.400	573	20	2.55E-49	XP_002648032.1	83	198.749	153	128	Hypothetical protein CBG24005
Locus_5798_Transcript_3/3_Conf_0.600	1024	20	7.56E-79	NP_500517.1	66	298.516	323	216	hypothetical protein F30B5.7
Locus_5799_Transcript_1/1_Conf_1.000	1110	0							
Locus_58_Transcript_1/1_Conf_1.000	744	20	4.57E-121	NP_507683.2	93	437.958	246	230	tryptophanyl (W) tRNA Synthetase family member (wrs-1)
Locus_580_Transcript_1/1_Conf_1.000	738	20	2.36E-37	XP_002639986.1	66	159.844	204	135	Hypothetical protein CBG10814
Locus_5800_Transcript_1/1_Conf_1.000	749	0							
Locus_5801_Transcript_1/1_Conf_1.000	1044	20	1.04E-83	XP_001902233.1	68	314.694	327	225	ThiF family protein
Locus_5802_Transcript_1/3_Conf_0.667	676	0							
Locus_5802_Transcript_2/3_Conf_0.667	664	0							
Locus_5802_Transcript_3/3_Conf_0.667	676	0							
Locus_5803_Transcript_1/1_Conf_1.000	200	0							

Locus_5804_Transcript_1/1_Conf_1.000	1058	0							
Locus_5805_Transcript_1/1_Conf_1.000	1052	20	5.83E-58	NP_497831.1	62	229.18	333	209	CCDC (human Coiled Coil Domain Containing) homolog family member (ccdc-55)
Locus_5806_Transcript_1/1_Conf_1.000	566	20	1.74E-31	EFO23470.1	71	139.428	128	92	hypothetical protein LOAG_05017
Locus_5807_Transcript_1/1_Conf_1.000	1569	20	3.68E-148	NP_490712.1	76	529.635	422	322	hypothetical protein C53D5.1
Locus_5808_Transcript_1/1_Conf_1.000	865	0							
Locus_5809_Transcript_1/2_Conf_1.000	2110	20	5.89E-46	EFO24874.1	50	190.66	716	365	kinesin motor domain-containing protein
Locus_5809_Transcript_2/2_Conf_1.000	2104	20	2.23E-45	EFO24874.1	52	188.734	622	328	kinesin motor domain-containing protein
Locus_581_Transcript_10/13_Conf_0.469	1897	20	5.96E-135	XP_002637289.1	64	486.108	574	370	Hypothetical protein CBG18976
Locus_581_Transcript_11/13_Conf_0.188	877	20	5.44E-69	XP_002637289.1	71	265.388	248	177	Hypothetical protein CBG18976
Locus_581_Transcript_12/13_Conf_0.188	1288	20	5.23E-86	XP_002637289.1	62	322.783	421	264	Hypothetical protein CBG18976
Locus_581_Transcript_13/13_Conf_0.469	1897	20	1.33E-134	XP_002637289.1	64	484.952	574	370	Hypothetical protein CBG18976
Locus_581_Transcript_2/13_Conf_1.000	144	0							
Locus_581_Transcript_3/13_Conf_1.000	151	0							
Locus_581_Transcript_4/13_Conf_0.406	1897	20	1.02E-134	XP_002637289.1	64	485.337	574	371	Hypothetical protein CBG18976
Locus_581_Transcript_5/13_Conf_0.469	1897	20	4.57E-135	XP_002637289.1	64	486.493	574	371	Hypothetical protein CBG18976
Locus_581_Transcript_6/13_Conf_0.062	342	20	2.82E-20	XP_002637289.1	73	101.679	90	66	Hypothetical protein CBG18976
Locus_581_Transcript_7/13_Conf_0.438	1900	20	1.74E-134	XP_002637289.1	64	484.567	574	370	Hypothetical protein CBG18976
Locus_581_Transcript_8/13_Conf_0.469	1909	20	1.34E-134	XP_002637289.1	64	484.952	574	370	Hypothetical protein CBG18976
Locus_581_Transcript_9/13_Conf_0.125	430	20	3.27E-21	XP_002637289.1	71	104.76	117	84	Hypothetical protein CBG18976
Locus_5810_Transcript_1/1_Conf_1.000	566	0							
Locus_5811_Transcript_1/1_Conf_1.000	825	20	1.82E-39	ACO15788.1	48	167.162	321	156	Hypothetical protein Y55F3BL.1
Locus_5812_Transcript_1/1_Conf_1.000	309	20	1.95E-42	NP_493658.2	89	175.252	102	91	hypothetical protein C50D2.8
Locus_5813_Transcript_1/1_Conf_1.000	853	20	1.97E-100	XP_002646710.1	80	369.777	265	214	C. briggsae CBR-MAOC-1 protein

Locus_5814_Transcript_1/1_Conf_1.000	907	0							
Locus_5815_Transcript_1/1_Conf_1.000	1054	20	7.84E-87	EFO20564.1	70	325.094	338	238	hypothetical protein LOAG_07924
Locus_5816_Transcript_1/1_Conf_1.000	618	20	2.47E-46	XP_002630829.1	74	189.119	170	126	C. briggsae CBR-VPS-35 protein
Locus_5817_Transcript_1/1_Conf_1.000	582	20	6.53E-72	NP_495666.3	81	273.863	186	151	Temporarily Assigned Gene name family member (tag-341)
Locus_5818_Transcript_1/1_Conf_1.000	362	20	6.09E-52	XP_002639368.1	88	206.838	120	106	C. briggsae CBR-GNRR-1 protein
Locus_5819_Transcript_1/5_Conf_0.200	258	2	1.18E-10	XP_002634825.1	64	69.707	73	47	Hypothetical protein CBG13933
Locus_5819_Transcript_2/5_Conf_0.600	2449	20	2.84E-47	XP_002634825.1	47	195.282	540	258	Hypothetical protein CBG13933
Locus_5819_Transcript_3/5_Conf_0.500	1407	20	3.28E-44	XP_002634825.1	48	184.111	510	249	Hypothetical protein CBG13933
Locus_5819_Transcript_4/5_Conf_0.200	616	0							
Locus_5819_Transcript_5/5_Conf_0.600	2449	20	2.84E-47	XP_002634825.1	48	195.282	536	261	Hypothetical protein CBG13933
Locus_582_Transcript_1/1_Conf_1.000	1462	20	0	XP_001899189.1	98	801.201	431	425	tubulin alpha chain - mouse

Locus_5820_Transcript_1/1_Conf_1.000	439	20	3.41E-71	EFO25124.1	97	270.781	136	133	bromodomain containing protein
Locus_5821_Transcript_1/1_Conf_1.000	1095	20	2.41E-110	NP_490766.2	76	403.29	363	279	hypothetical protein Y65B4A.8
Locus_5822_Transcript_1/1_Conf_1.000	156	0							
Locus_5823_Transcript_1/2_Conf_1.000	205	0							
Locus_5823_Transcript_2/2_Conf_1.000	186	0							
Locus_5824_Transcript_1/1_Conf_1.000	959	6	1.58E-11	EFO21616.1	76	74.7146	51	39	hypothetical protein LOAG_06869
Locus_5825_Transcript_1/3_Conf_0.714	634	20	3.59E-72	XP_002640528.1	94	275.018	145	137	C. briggsae CBR-MAG-1 protein

Locus_5825_Transcript_2/3_Conf_0.714	634	20	3.59E-72	XP_002640528.1	94	275.018	145	137	C. briggsae CBR-MAG-1 protein
Locus_5825_Transcript_3/3_Conf_0.714	634	20	3.59E-72	XP_002640528.1	94	275.018	145	137	C. briggsae CBR-MAG-1 protein
Locus_5826_Transcript_1/1_Conf_1.000	655	20	7.94E-41	XP_002638953.1	60	171.014	225	137	C. briggsae CBR-PPFR-1 protein
Locus_5827_Transcript_1/1_Conf_1.000	617	0							
Locus_5828_Transcript_1/2_Conf_1.000	2161	20	1.59E-155	XP_002630265.1	74	554.673	498	372	C. briggsae CBR-RAN-3 protein
Locus_5828_Transcript_2/2_Conf_1.000	1602	20	1.49E-152	XP_002630265.1	75	544.273	476	360	C. briggsae CBR-RAN-3 protein
Locus_5829_Transcript_1/1_Conf_1.000	781	0							
Locus_583_Transcript_1/1_Conf_1.000	190	0							

Locus_5830_Transcript_1/1_Conf_1.000	788	20	2.73E-74	EFO15724.1	82	282.722	192	159	hypothetical protein LOAG_12785
Locus_5831_Transcript_1/1_Conf_1.000	778	20	1.04E-78	NP_495878.1	92	297.36	178	164	RER (Retention in Endoplasmic Reticulum) homolog family member (rer-1)
Locus_5832_Transcript_1/1_Conf_1.000	859	20	2.99E-80	NP_508729.2	86	302.753	232	200	hypothetical protein C52B9.4
Locus_5833_Transcript_1/1_Conf_1.000	631	20	4.76E-85	NP_497420.1	88	317.775	209	184	hypothetical protein Y67D2.6
Locus_5834_Transcript_1/1_Conf_1.000	322	4	9.59E-20	XP_002640750.1	75	94.7449	86	65	Hypothetical protein CBG24187
Locus_5835_Transcript_1/2_Conf_1.000	569	20	1.83E-36	XP_002632946.1	87	155.992	91	80	Hypothetical protein CBG21702
Locus_5835_Transcript_2/2_Conf_1.000	568	20	4.82E-37	XP_002632946.1	88	157.918	92	81	Hypothetical protein CBG21702
Locus_5836_Transcript_1/1_Conf_1.000	1196	20	1.85E-90	NP_001022690.2	66	337.421	372	249	hypothetical protein M01F1.9
Locus_5837_Transcript_1/1_Conf_1.000	1514	20	0	NP_492851.1	90	767.303	437	397	yeast PRP (splicing factor) related family member (prp-17)
Locus_5838_Transcript_1/1_Conf_1.000	590	20	1.99E-60	XP_002646611.1	84	235.728	166	140	Hypothetical protein CBG20496
Locus_5839_Transcript_1/1_Conf_1.000	1372	20	8.66E-50	XP_001900673.1	57	202.601	394	228	cutaneous T-cell lymphoma tumor antigen se70-2
Locus_584_Transcript_1/1_Conf_1.000	593	14	6.39E-06	XP_002615609.1	44	54.6842	191	85	hypothetical protein CLUG_04491
Locus_5840_Transcript_1/1_Conf_1.000	450	20	3.59E-52	NP_001122835.1	86	207.608	151	130	UNCoordinated family member (unc-22)

Locus_5841_Transcript_1/1_Conf_1.000	627	20	4.57E-72	NP_510828.1	95	274.633	151	144	Myosin Light Chain family member (mlc-2)
Locus_5842_Transcript_1/1_Conf_1.000	612	20	9.07E-70	XP_001608164.1	100	266.929	137	137	PREDICTED: hypothetical protein isoform 1
Locus_5843_Transcript_1/1_Conf_1.000	736	20	4.13E-34	XP_002642801.1	53	149.058	226	122	C. briggsae CBR-CUA-1 protein
Locus_5844_Transcript_2/4_Conf_0.429	537	0							
Locus_5844_Transcript_3/4_Conf_0.286	679	0							
Locus_5844_Transcript_4/4_Conf_0.429	546	0							
Locus_5845_Transcript_1/1_Conf_1.000	910	1	8.57E-04	XP_001863637.1	36	48.9062	259	94	conserved hypothetical protein
Locus_5846_Transcript_1/1_Conf_1.000	511	20	1.90E-43	NP_503392.2	70	178.718	170	120	hypothetical protein Y50D4A.4
Locus_5847_Transcript_1/1_Conf_1.000	1128	0							
Locus_5848_Transcript_1/1_Conf_1.000	404	0							

Locus_5849_Transcript_1/1_Conf_1.000	1248	20	2.26E-94	NP_494763.1	83	350.517	241	201	Spliceosome-Associated Protein family member (sap-1)
Locus_585_Transcript_1/1_Conf_1.000	1411	6	1.06E-26	XP_002640792.1	40	125.946	493	198	Hypothetical protein CBG15667
Locus_5850_Transcript_1/1_Conf_1.000	1407	20	5.18E-82	NP_502405.1	58	309.686	396	230	hypothetical protein K08E7.1
Locus_5851_Transcript_1/3_Conf_0.667	983	20	5.09E-45	3KRN	65	186.037	210	137	CrystalStructure Of C. Elegans Cell-Death-Related Nuclease 5(Crn-5)
Locus_5851_Transcript_2/3_Conf_0.667	781	20	2.62E-45	3KRN	64	186.422	210	136	CrystalStructure Of C. Elegans Cell-Death-Related Nuclease 5(Crn-5)
Locus_5851_Transcript_3/3_Conf_0.667	983	20	1.13E-44	3KRN	64	184.882	210	136	CrystalStructure Of C. Elegans Cell-Death-Related Nuclease 5(Crn-5)
Locus_5852_Transcript_1/1_Conf_1.000	290	1	1.66E-04	NP_491250.1	72	49.2914	62	45	hypothetical protein C50F2.3
Locus_5853_Transcript_1/1_Conf_1.000	472	1	3.64E-04	EFO17906.1	42	48.1358	140	60	hypothetical protein LOAG_10592
Locus_5854_Transcript_1/1_Conf_1.000	2165	0							
Locus_5855_Transcript_1/1_Conf_1.000	215	4	2.41E-08	NP_509687.1	60	62.003	63	38	hypothetical protein ZC373.2
Locus_5856_Transcript_1/1_Conf_1.000	379	20	7.60E-10	EFO27824.1	55	67.0106	87	48	hypothetical protein LOAG_00660
Locus_5857_Transcript_1/1_Conf_1.000	478	0							
Locus_5858_Transcript_1/1_Conf_1.000	352	20	9.27E-24	XP_002642390.1	74	113.235	117	87	Hypothetical protein CBG18394
Locus_5859_Transcript_1/1_Conf_1.000	305	0							
Locus_586_Transcript_1/2_Conf_1.000	593	0							
Locus_586_Transcript_2/2_Conf_1.000	491	0							
Locus_5860_Transcript_1/2_Conf_1.000	1491	20	6.26E-57	NP_001122591.1	51	226.483	383	196	hypothetical protein C23H3.3
Locus_5860_Transcript_2/2_Conf_1.000	1437	20	2.04E-57	XP_002632139.1	56	228.024	362	204	Hypothetical protein CBG06998
Locus_5861_Transcript_1/2_Conf_1.000	1368	20	1.53E-30	EFO20174.1	53	138.658	224	120	hypothetical protein LOAG_08316

Locus_5861_Transcript_2/2_Conf_1.000	382	0							
Locus_5862_Transcript_1/1_Conf_1.000	211	0							
Locus_5863_Transcript_1/6_Conf_0.643	1713	20	2.18E-173	NP_741561.1	82	613.609	443	364	hypothetical protein Y57E12AL.1
Locus_5863_Transcript_2/6_Conf_0.571	1652	20	3.54E-173	NP_741561.1	82	612.838	436	361	hypothetical protein Y57E12AL.1
Locus_5863_Transcript_3/6_Conf_0.571	1634	20	7.28E-171	NP_741561.1	81	605.134	436	355	hypothetical protein Y57E12AL.1
Locus_5863_Transcript_4/6_Conf_0.643	1685	20	5.61E-174	NP_741561.1	82	615.535	443	364	hypothetical protein Y57E12AL.1
Locus_5863_Transcript_5/6_Conf_0.643	1688	20	2.14E-173	NP_741561.1	82	613.609	443	364	hypothetical protein Y57E12AL.1
Locus_5863_Transcript_6/6_Conf_0.643	1685	20	2.13E-173	NP_741561.1	82	613.609	443	364	hypothetical protein Y57E12AL.1
Locus_5864_Transcript_1/1_Conf_1.000	380	2	4.32E-05	EFO21827.1	62	51.2174	53	33	hypothetical protein LOAG_06660
Locus_5865_Transcript_1/2_Conf_1.000	671	20	1.37E-27	XP_002637373.1	79	127.102	82	65	Hypothetical protein CBG19074
Locus_5865_Transcript_2/2_Conf_1.000	671	20	1.37E-27	XP_002637373.1	79	127.102	82	65	Hypothetical protein CBG19074
Locus_5866_Transcript_1/1_Conf_1.000	493	20	5.30E-88	XP_002639940.1	96	326.635	164	159	Hypothetical protein CBG08279
Locus_5867_Transcript_1/1_Conf_1.000	940	1	4.82E-05	XP_002642207.1	46	53.1434	158	74	C. briggsae CBR-KBP-2 protein
Locus_5868_Transcript_1/1_Conf_1.000	401	0							
Locus_5869_Transcript_1/2_Conf_1.000	1988	20	3.60E-106	NP_001022928.1	64	390.578	443	284	Rab Escort Protein homolog family member (rep-1)
Locus_5869_Transcript_2/2_Conf_1.000	1973	20	5.49E-107	NP_001022928.1	64	393.275	438	284	Rab Escort Protein homolog family member (rep-1)
Locus_587_Transcript_1/1_Conf_1.000	366	20	4.09E-16	NP_500824.1	60	87.8113	119	72	FEMinization of XX and XO animals family member (fem-1)
Locus_5870_Transcript_1/1_Conf_1.000	539	20	2.47E-58	EFO18399.1	81	228.409	159	130	geranylgeranyl pyrophosphate synthetase

Locus_5871_Transcript_1/1_Conf_1.000	627	20	1.98E-67	XP_002648826.1	78	259.225	207	162	C. briggsae CBR-GIP-2 protein
Locus_5872_Transcript_1/1_Conf_1.000	575	0							
Locus_5873_Transcript_1/1_Conf_1.000	1915	20	6.86E-38	NP_490662.1	45	163.696	449	205	hypothetical protein Y74C9A.4
Locus_5874_Transcript_1/1_Conf_1.000	844	20	1.09E-95	NP_741437.1	80	353.984	268	215	DEnse Body family member (deb-1)
Locus_5875_Transcript_1/1_Conf_1.000	718	0							
Locus_5876_Transcript_1/1_Conf_1.000	291	20	2.90E-25	XP_002630908.1	72	118.242	96	70	Hypothetical protein CBG02632
Locus_5877_Transcript_1/1_Conf_1.000	384	0							
Locus_5878_Transcript_1/1_Conf_1.000	503	4	2.01E-34	XP_002648378.1	91	148.673	99	91	Hypothetical protein CBG24627
Locus_5879_Transcript_1/1_Conf_1.000	456	0							
Locus_588_Transcript_1/1_Conf_1.000	893	20	1.82E-35	ADD38287.1	82	154.066	111	92	yippee-like 5
Locus_5880_Transcript_1/1_Conf_1.000	183	5	1.28E-04	NP_497046.1	72	49.6766	37	27	UNCoordinated family member (unc-52)
Locus_5881_Transcript_1/2_Conf_1.000	354	20	2.27E-22	NP_496850.2	73	108.612	106	78	hypothetical protein Y48E1B.5
Locus_5881_Transcript_2/2_Conf_1.000	354	20	2.97E-22	NP_496850.2	73	108.227	106	78	hypothetical protein Y48E1B.5
Locus_5882_Transcript_1/1_Conf_1.000	567	20	6.94E-44	XP_002629858.1	88	180.644	117	104	Hypothetical protein CBG21892
Locus_5883_Transcript_1/2_Conf_1.000	270	0							
Locus_5883_Transcript_2/2_Conf_1.000	570	4	7.84E-27	NP_494791.1	63	124.02	121	77	hypothetical protein T05C1.1
Locus_5884_Transcript_1/2_Conf_1.000	428	20	1.24E-60	NP_498711.1	88	235.728	142	125	TYRosinase family member (tyr-1)
Locus_5884_Transcript_2/2_Conf_1.000	428	20	1.24E-60	NP_498711.1	88	235.728	142	125	TYRosinase family member (tyr-1)
Locus_5885_Transcript_1/1_Conf_1.000	279	0							
Locus_5886_Transcript_1/1_Conf_1.000	427	19	5.82E-10	AAO63578.1	49	67.3958	113	56	secreted protein 6 precursor
Locus_5887_Transcript_1/1_Conf_1.000	631	0							

Locus_5888_Transcript_1/1_Conf_1.000	2375	12	6.58E-33	NP_493601.2	39	147.517	593	235	FERM domain (protein4.1-ezrin-radixin-moesin) family member (frm-1)
Locus_5889_Transcript_1/1_Conf_1.000	410	20	3.15E-32	NP_509145.2	68	141.354	135	93	AuTophaGy (yeast Atg homolog) family member (atg-2)
Locus_589_Transcript_1/1_Conf_1.000	447	0							
Locus_5890_Transcript_1/1_Conf_1.000	786	20	2.09E-66	NP_500504.1	78	256.529	212	166	RNP (RRM RNA binding domain) containing family member (rnp-2)
Locus_5891_Transcript_1/1_Conf_1.000	640	0							
Locus_5892_Transcript_1/1_Conf_1.000	512	20	4.64E-66	XP_002641985.1	83	253.832	173	145	Hypothetical protein CBG09207
Locus_5893_Transcript_1/1_Conf_1.000	2295	20	0	XP_002645186.1	70	687.567	739	524	Hypothetical protein CBG16916
Locus_5894_Transcript_1/1_Conf_1.000	139	0							
Locus_5895_Transcript_1/1_Conf_1.000	742	20	3.07E-85	NP_498730.1	81	318.931	219	179	LEThal family member (let-754)
Locus_5896_Transcript_1/1_Conf_1.000	954	0							
Locus_5897_Transcript_1/1_Conf_1.000	130	0							
Locus_5898_Transcript_1/1_Conf_1.000	944	0							

Locus_5899_Transcript_1/1_Conf_1.000	361	20	8.25E-41	BAE31040.1	100	169.859	81	81	unnamed protein product
Locus_59_Transcript_1/3_Conf_0.400	1403	20	5.89E-78	XP_001892703.1	78	296.204	231	182	Uncharacterized protein family UPF0005 containing protein
Locus_59_Transcript_2/3_Conf_0.400	1125	0							
Locus_59_Transcript_3/3_Conf_0.600	1444	20	2.33E-77	XP_001892703.1	79	294.278	229	181	Uncharacterized protein family UPF0005 containing protein
Locus_590_Transcript_1/1_Conf_1.000	134	0							
Locus_5900_Transcript_1/1_Conf_1.000	542	20	3.51E-68	NP_496205.2	82	261.151	182	151	PhosphoLipase C family member (plc-3)
Locus_5901_Transcript_1/1_Conf_1.000	337	20	9.42E-29	NP_001022673.1	80	129.798	90	72	NADC (Na+-coupled dicarboxylate transporter) family member (nac-3)
Locus_5902_Transcript_1/2_Conf_1.000	538	20	1.47E-10	XP_784255.2	61	69.707	86	53	PREDICTED: similar to Msx-2 interacting nuclear target protein
Locus_5902_Transcript_2/2_Conf_1.000	544	20	4.92E-09	XP_784255.2	60	64.6994	88	53	PREDICTED: similar to Msx-2 interacting nuclear target protein
Locus_5903_Transcript_1/1_Conf_1.000	1052	20	4.47E-167	XP_002633820.1	93	591.652	350	327	Hypothetical protein CBG19850
Locus_5904_Transcript_1/1_Conf_1.000	760	20	5.01E-22	AAO63576.1	55	108.997	168	94	secreted protein 4 precursor

Locus_5905_Transcript_1/1_Conf_1.000	949	20	2.80E-101	NP_492283.1	73	372.859	310	227	hypothetical protein F02E9.7
Locus_5906_Transcript_1/1_Conf_1.000	1284	2	2.80E-47	NP_506277.1	60	194.126	240	146	High Incidence of Males (increased X chromosome loss) family member (him-17)
Locus_5907_Transcript_1/1_Conf_1.000	449	20	1.33E-46	NP_497589.3	91	189.119	111	102	hypothetical protein Y71H2B.5
Locus_5908_Transcript_1/2_Conf_1.000	1815	20	3.41E-140	XP_002646134.1	74	503.442	447	333	Hypothetical protein CBG08013
Locus_5908_Transcript_2/2_Conf_1.000	1662	20	1.06E-124	XP_002646134.1	83	451.825	325	270	Hypothetical protein CBG08013
Locus_5909_Transcript_1/1_Conf_1.000	365	20	8.78E-43	XP_002642916.1	83	176.407	118	98	C. briggsae CBR-TAG-168 protein
Locus_591_Transcript_1/1_Conf_1.000	2233	20	0	XP_002645529.1	90	1018.07	645	583	C. briggsae CBR-SDHA-1 protein
Locus_5910_Transcript_1/2_Conf_1.000	470	20	2.99E-14	XP_001512056.1	53	81.6481	174	93	PREDICTED: hypothetical protein, partial
Locus_5910_Transcript_2/2_Conf_1.000	462	20	1.23E-07	CAG11756.1	70	59.6918	65	46	unnamed protein product
Locus_5911_Transcript_1/1_Conf_1.000	1319	20	1.59E-61	NP_493587.1	86	241.506	150	130	UBiquitin Conjugating enzyme family member (ubc-16)
Locus_5912_Transcript_1/1_Conf_1.000	1024	20	5.48E-37	CBI63237.1	59	159.458	335	198	C. elegans protein Y111B2A.4a, partially confirmed by transcript evidence
Locus_5913_Transcript_1/1_Conf_1.000	1357	20	2.15E-77	XP_001901579.1	65	294.278	319	210	Piwi domain containing protein
Locus_5914_Transcript_1/1_Conf_1.000	274	20	1.51E-26	CAA10033.1	83	122.479	89	74	DYS-1 protein

Locus_5915_Transcript_1/2_Conf_1.000	355	20	1.02E-38	XP_001895467.1	82	162.925	120	99	DEAD/DEAH box helicase family protein
Locus_5915_Transcript_2/2_Conf_1.000	355	20	1.02E-38	XP_001895467.1	82	162.925	120	99	DEAD/DEAH box helicase family protein
Locus_5916_Transcript_1/1_Conf_1.000	168	0							
Locus_5917_Transcript_1/2_Conf_1.000	316	20	5.66E-37	NP_001023110.1	83	157.147	105	88	Homolog Of ELAC2 (cancer susceptibility locus) family member (hoe-1)
Locus_5917_Transcript_2/2_Conf_1.000	316	20	5.66E-37	NP_001023110.1	83	157.147	105	88	Homolog Of ELAC2 (cancer susceptibility locus) family member (hoe-1)
Locus_5918_Transcript_1/1_Conf_1.000	813	1	1.36E-07	XP_001897896.1	45	61.2326	259	117	RNA binding motif protein 21
Locus_5919_Transcript_1/1_Conf_1.000	889	0							
Locus_592_Transcript_1/1_Conf_1.000	218	20	1.96E-26	NP_001023936.1	90	122.094	72	65	hypothetical protein F46B6.6
Locus_5920_Transcript_1/1_Conf_1.000	261	20	7.65E-10	NP_493426.2	70	67.0106	54	38	TAF (TBP-associated transcription factor) family member (taf-1)
Locus_5921_Transcript_1/1_Conf_1.000	324	0							
Locus_5922_Transcript_1/1_Conf_1.000	1550	0							
Locus_5923_Transcript_1/1_Conf_1.000	242	20	1.73E-22	XP_002636587.1	77	108.997	77	60	C. briggsae CBR-TRE-3 protein
Locus_5924_Transcript_1/1_Conf_1.000	175	0							
Locus_5925_Transcript_1/1_Conf_1.000	206	0							
Locus_5926_Transcript_1/1_Conf_1.000	650	0							
Locus_5927_Transcript_1/1_Conf_1.000	691	20	8.87E-57	NP_505743.1	75	224.172	216	162	hypothetical protein F28H7.3

Locus_5928_Transcript_1/2_Conf_1.000	3240	20	0	AAB99830.2	90	1746.48	969	875	thrombospondin
Locus_5928_Transcript_2/2_Conf_1.000	3176	20	0	AAB99830.2	90	1744.55	968	874	thrombospondin
Locus_5929_Transcript_1/1_Conf_1.000	1174	20	5.18E-122	NP_508618.2	72	442.195	372	271	CRAL/TRIO and GOLD domain suppressor of activated Ras family member (cgr-1)
Locus_593_Transcript_1/1_Conf_1.000	559	20	1.17E-08	XP_002731776.1	63	63.5438	85	54	PREDICTED: CASP-like transcription factor
Locus_5930_Transcript_1/1_Conf_1.000	1411	20	1.79E-74	NP_501296.1	60	284.648	463	280	hypothetical protein C33H5.17

Locus_5931_Transcript_1/1_Conf_1.000	651	20	1.75E-40	XP_002641488.1	92	169.859	101	93	Hypothetical protein CBG09779
Locus_5932_Transcript_1/1_Conf_1.000	671	20	7.65E-79	XP_002641616.1	80	297.36	224	180	C. briggsae CBR-ALX-1 protein
Locus_5933_Transcript_1/1_Conf_1.000	1959	20	7.25E-160	NP_498059.2	66	568.926	615	412	hypothetical protein C27F2.8
Locus_5934_Transcript_1/1_Conf_1.000	1040	20	6.01E-116	XP_001897557.1	80	421.779	297	240	Tyrosine-protein kinase abl-1
Locus_5935_Transcript_1/1_Conf_1.000	707	0							
Locus_5936_Transcript_1/1_Conf_1.000	179	17	5.02E-06	ACZ54691.1	73	54.299	38	28	Uncoordinated protein 82, isoform f
Locus_5937_Transcript_1/1_Conf_1.000	624	20	2.31E-76	XP_002641247.1	87	288.886	188	164	Hypothetical protein CBG09115
Locus_5938_Transcript_1/1_Conf_1.000	1412	5	3.22E-07	XP_002402770.1	43	61.2326	175	76	conserved hypothetical protein
Locus_5939_Transcript_1/1_Conf_1.000	397	0							
Locus_594_Transcript_1/1_Conf_1.000	514	20	1.88E-30	NP_741323.1	69	135.576	122	85	hypothetical protein K08D12.3
Locus_5940_Transcript_1/1_Conf_1.000	917	20	2.34E-41	XP_002641848.1	77	173.711	131	102	Hypothetical protein CBG16522
Locus_5941_Transcript_1/1_Conf_1.000	2012	20	0	NP_497939.2	76	775.778	696	530	Suppressor/Enhancer of Lin-12 family member (sel-2)
Locus_5942_Transcript_1/1_Conf_1.000	382	0							
Locus_5943_Transcript_1/1_Conf_1.000	213	0							
Locus_5944_Transcript_1/1_Conf_1.000	569	20	3.14E-12	EFO23513.1	69	75.485	62	43	CMGC/CDK/CRK7 protein kinase
Locus_5945_Transcript_1/1_Conf_1.000	484	0							
Locus_5946_Transcript_1/1_Conf_1.000	144	0							
Locus_5947_Transcript_1/1_Conf_1.000	324	0							
Locus_5948_Transcript_1/3_Conf_0.286	303	5	1.68E-17	XP_002641479.1	71	92.4337	77	55	Hypothetical protein CBG09770

Locus_5948_Transcript_2/3_Conf_0.429	1039	20	2.70E-116	NP_741113.3	84	422.935	311	263	hypothetical protein C32A3.3
Locus_5948_Transcript_3/3_Conf_0.571	1256	20	4.34E-138	XP_002641479.1	83	495.738	366	305	Hypothetical protein CBG09770
Locus_5949_Transcript_1/1_Conf_1.000	1229	20	1.51E-127	CAD28559.2	72	460.685	405	295	metalloprotease I
Locus_595_Transcript_1/1_Conf_1.000	1948	20	0	NP_001024192.1	94	1025	570	541	Receptor Mediated Endocytosis family member (rme-1)
Locus_5950_Transcript_1/1_Conf_1.000	321	0							
Locus_5951_Transcript_1/1_Conf_1.000	1230	20	5.64E-82	XP_002631148.1	84	309.301	213	179	C. briggsae CBR-RAGA-1 protein
Locus_5952_Transcript_1/1_Conf_1.000	3073	20	0	XP_001895334.1	58	790.03	1069	625	Protein kinase domain containing protein
Locus_5953_Transcript_1/1_Conf_1.000	405	0							
Locus_5954_Transcript_1/1_Conf_1.000	571	0							
Locus_5955_Transcript_1/1_Conf_1.000	347	2	7.43E-05	XP_002632142.1	48	50.447	137	67	Hypothetical protein CBG07001
Locus_5956_Transcript_1/2_Conf_1.000	2726	20	1.04E-53	NP_741547.1	65	216.853	235	153	hypothetical protein R01B10.6
Locus_5956_Transcript_2/2_Conf_1.000	2605	20	2.12E-48	NP_504568.1	64	199.134	290	186	JAMP (JNK1-Associated Membrane Protein) homolog family member (jamp-1)
Locus_5957_Transcript_1/1_Conf_1.000	245	0							
Locus_5958_Transcript_1/1_Conf_1.000	178	0							
Locus_5959_Transcript_1/1_Conf_1.000	170	0							
Locus_596_Transcript_1/1_Conf_1.000	897	20	2.95E-150	NP_495019.1	95	535.413	298	286	Masculinisation Of Germline family member (mog-5)
Locus_5960_Transcript_1/1_Conf_1.000	326	0							
Locus_5961_Transcript_1/2_Conf_1.000	2162	13	1.96E-12	XP_002641123.1	38	79.337	495	193	Hypothetical protein CBG08972

Locus_5961_Transcript_2/2_Conf_1.000	2162	13	1.96E-12	XP_002641123.1	38	79.337	495	193	Hypothetical protein CBG08972
Locus_5962_Transcript_1/1_Conf_1.000	615	5	6.07E-05	XP_001662306.1	53	51.6026	66	35	cysteine-rich venom protein, putative
Locus_5963_Transcript_1/1_Conf_1.000	515	0							
Locus_5964_Transcript_1/2_Conf_1.000	513	0							
Locus_5964_Transcript_2/2_Conf_1.000	406	0							
Locus_5965_Transcript_1/1_Conf_1.000	851	20	3.34E-92	NP_001021185.2	81	342.428	232	188	PaXiLlin homolo family member (pxl-1)
Locus_5966_Transcript_1/1_Conf_1.000	334	0							
Locus_5967_Transcript_1/3_Conf_0.667	948	20	7.09E-113	NP_507943.1	83	411.379	298	249	hypothetical protein B0250.5
Locus_5967_Transcript_2/3_Conf_0.667	1062	20	1.44E-112	NP_507943.1	83	410.609	298	249	hypothetical protein B0250.5
Locus_5967_Transcript_3/3_Conf_0.667	1062	20	8.43E-113	NP_507943.1	83	411.379	298	249	hypothetical protein B0250.5
Locus_5968_Transcript_1/1_Conf_1.000	1118	20	7.23E-118	EFO24874.1	79	428.328	340	271	kinesin motor domain-containing protein
Locus_5969_Transcript_1/1_Conf_1.000	440	20	1.04E-35	XP_002635001.1	86	152.91	96	83	Hypothetical protein CBG13541
Locus_597_Transcript_1/2_Conf_1.000	655	1	3.48E-12	EFO23299.1	53	75.8702	140	75	hypothetical protein LOAG_05186
Locus_597_Transcript_2/2_Conf_1.000	640	1	6.59E-13	EFO23299.1	55	78.1814	135	75	hypothetical protein LOAG_05186
Locus_5970_Transcript_1/1_Conf_1.000	146	0							
Locus_5971_Transcript_1/1_Conf_1.000	578	0							
Locus_5972_Transcript_1/1_Conf_1.000	530	13	2.50E-07	NP_001076676.1	48	58.9214	130	63	hypothetical protein F13E9.14
Locus_5973_Transcript_1/1_Conf_1.000	1206	20	1.20E-12	NP_502137.1	48	78.9518	185	89	hypothetical protein F54E12.2

Locus_5974_Transcript_1/1_Conf_1.000	474	0							
Locus_5975_Transcript_1/1_Conf_1.000	185								
Locus_5976_Transcript_1/1_Conf_1.000	187	20	1.23E-23	NP_001129905.1	90	112.849	61	55	hypothetical protein T03D8.6
Locus_5977_Transcript_1/1_Conf_1.000	703	20	2.20E-50		96	202.986	198	191	URF 2
Locus_5978_Transcript_1/1_Conf_1.000	1164	0							
Locus_5979_Transcript_1/1_Conf_1.000	770	2	6.96E-11	XP_002644947.1	58	72.0182	124	73	Hypothetical protein CBG10904
Locus_598_Transcript_1/1_Conf_1.000	786	20	1.12E-19	EFO24565.1	51	101.293	211	109	hypothetical protein LOAG_03922
Locus_5980_Transcript_1/1_Conf_1.000	362	20	2.84E-33	XP_001898731.1	68	144.821	119	81	Tyrosyl-DNA phosphodiesterase family protein
Locus_5981_Transcript_1/2_Conf_1.000	481	5	1.66E-17	XP_002641872.1	54	92.4337	158	86	C. briggsae CBR-LIM-8 protein
Locus_5981_Transcript_2/2_Conf_1.000	474	5	1.09E-16	XP_002641872.1	55	89.7373	150	83	C. briggsae CBR-LIM-8 protein
Locus_5982_Transcript_1/1_Conf_1.000	240	2	1.13E-13	NP_498270.1	71	79.7221	77	55	hypothetical protein F01F1.3
Locus_5983_Transcript_1/1_Conf_1.000	485	0							
Locus_5984_Transcript_1/1_Conf_1.000	636	20	1.53E-70	XP_002639544.1	82	269.626	184	152	Hypothetical protein CBG04173
Locus_5985_Transcript_1/1_Conf_1.000	230	2	1.00E-09	NP_001076661.1	60	66.6254	76	46	hypothetical protein C10C6.7
Locus_5986_Transcript_1/1_Conf_1.000	219	20	9.39E-32	AAA27981.1	100	139.813	68	68	clathrin-associated protein homologue
Locus_5987_Transcript_1/1_Conf_1.000	180	20	7.03E-11	XP_002641457.1	72	70.4774	58	42	C. briggsae CBR-TOP-3 protein
Locus_5988_Transcript_1/1_Conf_1.000	1279	20	1.22E-135	XP_002641208.1	74	487.649	428	319	C. briggsae CBR-DPF-4 protein
Locus_5989_Transcript_1/1_Conf_1.000	1232	20	4.31E-90	NP_490882.3	88	336.265	195	172	UBiquitin Conjugating enzyme family member (ubc-3)
Locus_599_Transcript_1/1_Conf_1.000	1005	20	2.56E-31	EFO27395.1	56	140.584	291	165	hypothetical protein LOAG_01089
Locus_5990_Transcript_1/1_Conf_1.000	1369	20	1.82E-116	NP_506229.1	69	424.091	395	273	hypothetical protein F54F3.3

Locus_5991_Transcript_1/1_Conf_1.000	597	20	2.22E-70	XP_002714405.1	100	268.855	130	130	PREDICTED: tubulin, beta 5-like
Locus_5992_Transcript_1/1_Conf_1.000	499	20	2.32E-27	NP_001033395.1	86	125.176	76	66	Sensory AXon guidance family member (sax-7)
Locus_5993_Transcript_1/1_Conf_1.000	245	20	1.32E-22	XP_002634349.1	96	109.383	54	52	Hypothetical protein CBG17698
Locus_5994_Transcript_1/2_Conf_1.000	304	4	5.78E-10	NP_504792.1	62	67.3958	88	55	hypothetical protein Y57E12AL.6
Locus_5994_Transcript_2/2_Conf_1.000	539	4	1.97E-31	NP_504792.1	72	139.043	129	94	hypothetical protein Y57E12AL.6
Locus_5995_Transcript_1/1_Conf_1.000	813	0							
Locus_5996_Transcript_1/1_Conf_1.000	149	0							
Locus_5997_Transcript_1/1_Conf_1.000	459	20	8.73E-51	NP_493580.1	80	202.986	146	117	hypothetical protein K11B4.1
Locus_5998_Transcript_1/1_Conf_1.000	773	20	1.33E-102	NP_506303.1	84	376.711	257	218	hypothetical protein C50B6.7

Locus_5999_Transcript_1/2_Conf_1.000	399	10	3.30E-29	XP_002723896.1	95	131.339	81	77	PREDICTED: hypothetical protein
Locus_5999_Transcript_2/2_Conf_1.000	399	10	1.25E-28	XP_002723896.1	95	129.413	81	77	PREDICTED: hypothetical protein
Locus_6_Transcript_1/3_Conf_0.667	507	20	1.51E-40	XP_001901336.1	90	169.088	98	89	DNA-directed RNA polymerases I, II, and III 14.4 kDa polypeptide
Locus_6_Transcript_2/3_Conf_0.667	497	20	1.41E-40	XP_001901336.1	90	169.088	98	89	DNA-directed RNA polymerases I, II, and III 14.4 kDa polypeptide
Locus_6_Transcript_3/3_Conf_0.667	517	20	1.57E-40	XP_001901336.1	90	169.088	98	89	DNA-directed RNA polymerases I, II, and III 14.4 kDa polypeptide
Locus_60_Transcript_1/1_Conf_1.000	1691	20	0	ABC86837.1	94	808.52	507	479	depsiphilin
Locus_600_Transcript_1/1_Conf_1.000	758	20	7.56E-71	XP_002637003.1	87	271.166	187	164	C. briggsae CBR-EIF-3.K protein
Locus_6000_Transcript_1/1_Conf_1.000	259	0							
Locus_6001_Transcript_1/1_Conf_1.000	355	1	1.53E-10	ACV31095.1	78	69.3218	46	36	Hypothetical protein C25H3.17

Locus_6002_Transcript_1/1_Conf_1.000	1851	20	2.03E-55	EFO25299.1	47	221.861	633	303	piwi domain-containing protein
Locus_6003_Transcript_1/1_Conf_1.000	1497	20	0		93	862.448	464	432	splice form 1 - Caenorhabditis elegans
Locus_6004_Transcript_1/1_Conf_1.000	317	20	3.94E-22	XP_002635866.1	68	107.842	109	75	Hypothetical protein CBG01082
Locus_6005_Transcript_1/1_Conf_1.000	167	3	5.09E-06	XP_002630376.1	69	54.299	55	38	Hypothetical protein CBG04315
Locus_6006_Transcript_1/1_Conf_1.000	1594	20	9.12E-86	XP_002634702.1	72	322.398	266	192	C. briggsae CBR-TAG-182 protein
Locus_6007_Transcript_1/2_Conf_1.000	560	20	1.74E-36	NP_504599.2	66	155.992	180	119	Myotonic dystrophy-Related, Cdc42-binding Kinase homolog family member (mrck-1)
Locus_6007_Transcript_2/2_Conf_1.000	545	20	2.50E-37	NP_504599.2	66	158.688	175	117	Myotonic dystrophy-Related, Cdc42-binding Kinase homolog family member (mrck-1)
Locus_6008_Transcript_1/1_Conf_1.000	776	0							

Locus_6009_Transcript_1/1_Conf_1.000	544	20	8.85E-51	NP_498128.1	93	203.371	113	106	CLocK (biological timing) abnormality family member (clk-1)
Locus_601_Transcript_1/1_Conf_1.000	3462	20	0	NP_491363.1	91	1976.06	1165	1066	Dynein Heavy Chain family member (dhc-1)
Locus_6010_Transcript_1/1_Conf_1.000	939	20	2.09E-16	XP_969818.1	56	90.8929	142	80	PREDICTED: similar to AGAP008118-PA
Locus_6011_Transcript_1/2_Conf_1.000	1690	20	8.35E-85	XP_002630905.1	72	319.316	282	204	C. briggsae CBR-SET-4 protein
Locus_6011_Transcript_2/2_Conf_1.000	1690	20	8.35E-85	XP_002630905.1	72	319.316	282	204	C. briggsae CBR-SET-4 protein
Locus_6012_Transcript_1/1_Conf_1.000	468	0							
Locus_6013_Transcript_1/1_Conf_1.000	315	4	9.41E-08	XP_001899300.1	67	60.077	70	47	Negative elongation factor B homolog

Locus_6014_Transcript_1/1_Conf_1.000	1575	20	0	XP_002644583.1	82	729.554	508	419	C. briggsae CBR-GLIT-1 protein
Locus_6015_Transcript_1/1_Conf_1.000	449	5	4.43E-34	NP_491893.1	71	147.517	146	105	BAG1 (human) homolog family member (bag-1)
Locus_6016_Transcript_1/2_Conf_1.000	580	20	2.99E-61	XP_002631151.1	87	238.424	165	144	Hypothetical protein CBG02935
Locus_6016_Transcript_2/2_Conf_1.000	710	20	4.77E-53	XP_002631151.1	87	211.846	165	144	Hypothetical protein CBG02935
Locus_6017_Transcript_1/2_Conf_1.000	1093	20	1.62E-98	XP_002639122.1	86	363.999	261	227	Hypothetical protein CBG14941
Locus_6017_Transcript_2/2_Conf_1.000	1020	20	1.46E-98	XP_002639122.1	86	363.999	261	227	Hypothetical protein CBG14941
Locus_6018_Transcript_1/2_Conf_1.000	781	2	2.56E-08	NP_492595.1	46	63.5438	153	71	hypothetical protein F26E4.4
Locus_6018_Transcript_2/2_Conf_1.000	1397	4	2.11E-27	NP_492595.1	44	128.257	395	175	hypothetical protein F26E4.4
Locus_6019_Transcript_1/1_Conf_1.000	357	0							
Locus_602_Transcript_1/1_Conf_1.000	1097	20	1.10E-70	NP_001122975.1	63	271.552	336	212	hypothetical protein K10C8.3
Locus_6020_Transcript_1/1_Conf_1.000	149	0							

Locus_6021_Transcript_1/1_Conf_1.000	505	0							
Locus_6022_Transcript_1/1_Conf_1.000	442	20	2.42E-80	XP_533842.2	98	301.212	147	145	PREDICTED: similar to ribosomal protein L18a
Locus_6023_Transcript_1/1_Conf_1.000	195	0							
Locus_6024_Transcript_1/3_Conf_0.500	752	20	1.56E-84	EFO26720.1	78	316.62	234	183	hypothetical protein LOAG_01771
Locus_6024_Transcript_2/3_Conf_0.500	803	20	2.92E-87	EFO26720.1	77	325.865	248	191	hypothetical protein LOAG_01771
Locus_6024_Transcript_3/3_Conf_0.333	1379	20	1.18E-155	XP_002640277.1	84	554.288	400	338	Hypothetical protein CBG12802
Locus_6025_Transcript_1/1_Conf_1.000	853	20	2.08E-25	EFO24662.1	75	120.553	110	83	hypothetical protein LOAG_03822
Locus_6026_Transcript_1/1_Conf_1.000	550	20	1.68E-36	NP_493125.2	65	155.992	166	109	hypothetical protein T09E11.9
Locus_6027_Transcript_1/1_Conf_1.000	850	0							
Locus_6028_Transcript_1/1_Conf_1.000	1006	20	2.56E-31	NP_001021834.1	80	140.584	88	71	hypothetical protein Y87G2A.18
Locus_6029_Transcript_1/2_Conf_1.000	1561	5	9.00E-30	NP_508196.1	56	136.346	319	180	STAUfen (dsRNA binding protein) homolog family member (stau-1)
Locus_6029_Transcript_2/2_Conf_1.000	1556	5	8.95E-30	NP_508196.1	56	136.346	319	180	STAUfen (dsRNA binding protein) homolog family member (stau-1)
Locus_603_Transcript_1/1_Conf_1.000	655	20	5.44E-82	NP_491242.2	81	307.76	220	180	hypothetical protein T03F1.7

Locus_6030_Transcript_1/2_Conf_1.000	1519	20	1.14E-146	XP_002641256.1	72	524.628	504	363	Hypothetical protein CBG05167
Locus_6030_Transcript_2/2_Conf_1.000	1519	20	1.14E-146	XP_002641256.1	72	524.628	504	363	Hypothetical protein CBG05167
Locus_6031_Transcript_1/1_Conf_1.000	200	0							
Locus_6032_Transcript_1/1_Conf_1.000	1603	20	1.34E-153	NP_001040704.1	74	547.74	445	333	DNaJ domain (prokaryotic heat shock protein) family member (dnj-27)
Locus_6033_Transcript_1/1_Conf_1.000	667	20	1.32E-107	NP_497139.1	92	392.889	217	201	Paralysed Arrest at Two-fold family member (pat-4)
Locus_6034_Transcript_1/5_Conf_0.600	1611	20	5.62E-83	NP_498281.2	59	313.153	375	223	hypothetical protein C28H8.9
Locus_6034_Transcript_2/5_Conf_0.500	1562	20	2.35E-54	XP_002641182.1	74	218.009	155	116	Hypothetical protein CBG09043
Locus_6034_Transcript_3/5_Conf_0.500	1710	20	6.09E-83	NP_498281.2	59	313.153	375	223	hypothetical protein C28H8.9
Locus_6034_Transcript_4/5_Conf_0.200	757	20	2.77E-81	NP_504559.1	96	305.834	157	152	AdaPtin, Small chain (clathrin associated complex) family member (aps-1)
Locus_6034_Transcript_5/5_Conf_0.500	1653	20	5.82E-83	NP_498281.2	59	313.153	375	223	hypothetical protein C28H8.9
Locus_6035_Transcript_1/2_Conf_1.000	1379	20	3.37E-102	NP_508025.1	61	376.711	447	275	hypothetical protein F31D4.2
Locus_6035_Transcript_2/2_Conf_1.000	1379	20	4.40E-102	NP_508025.1	61	376.326	447	275	hypothetical protein F31D4.2

Locus_6036_Transcript_1/1_Conf_1.000	427	20	1.41E-56	NP_493413.1	89	222.246	134	120	NuDiX family member (ndx-4)
Locus_6037_Transcript_1/1_Conf_1.000	444	20	1.63E-36	AAK29933.3	77	155.606	127	99	Rab connectin related protein 2, partially confirmed by transcript evidence
Locus_6038_Transcript_1/1_Conf_1.000	518	0							
Locus_6039_Transcript_1/2_Conf_1.000	2680	20	0	NP_494939.1	76	940.643	769	589	PhosphoLipase D family member (pld-1)
Locus_6039_Transcript_2/2_Conf_1.000	595	2	3.93E-11	XP_002630650.1	52	72.0182	127	67	C. briggsae CBR-PLD-1 protein
Locus_604_Transcript_1/2_Conf_1.000	594	12	4.21E-05	XP_002644369.1	56	51.9878	83	47	C. briggsae CBR-VIT-4 protein
Locus_604_Transcript_2/2_Conf_1.000	594	12	4.21E-05	XP_002644369.1	56	51.9878	83	47	C. briggsae CBR-VIT-4 protein
Locus_6040_Transcript_1/1_Conf_1.000	1435	20	3.29E-15	XP_002755952.1	46	87.8113	443	205	PREDICTED: myosin-11
Locus_6041_Transcript_1/2_Conf_1.000	802	20	1.59E-117	CAR63542.1	91	426.402	265	242	putative Pre-mRNA splicing protein
Locus_6041_Transcript_2/2_Conf_1.000	802	20	9.94E-120	CAR63542.1	91	433.721	265	242	putative Pre-mRNA splicing protein
Locus_6042_Transcript_1/1_Conf_1.000	941	20	6.63E-55	XP_002633449.1	57	218.779	319	185	C. briggsae CBR-SPT-5 protein
Locus_6043_Transcript_1/1_Conf_1.000	1802	20	2.52E-111	NP_497803.1	60	407.527	553	333	hypothetical protein C36E8.1
Locus_6044_Transcript_1/2_Conf_1.000	647	20	3.46E-25	CAD21647.3	65	119.013	138	91	C. elegans protein T03F6.6, confirmed by transcript evidence
Locus_6044_Transcript_2/2_Conf_1.000	327	20	1.25E-12	CAD21647.3	66	76.2554	86	57	C. elegans protein T03F6.6, confirmed by transcript evidence

Locus_6045_Transcript_1/1_Conf_1.000	604	7	3.33E-45	XP_002639766.1	66	185.267	203	135	C. briggsae CBR-SEC-8 protein
Locus_6046_Transcript_1/2_Conf_1.000	2391	20	0	NP_503512.1	85	875.544	535	458	GLYcosylation related family member (gly-7)
Locus_6046_Transcript_2/2_Conf_1.000	2391	20	0	NP_503512.1	85	875.544	535	458	GLYcosylation related family member (gly-7)
Locus_6047_Transcript_1/2_Conf_1.000	1746	20	1.19E-41	NP_741137.1	53	176.022	331	176	SKP2 (S phase Kinase associated Protein Two) homolog family member (skpt-1)
Locus_6047_Transcript_2/2_Conf_1.000	1746	20	1.19E-41	NP_741137.1	53	176.022	331	177	SKP2 (S phase Kinase associated Protein Two) homolog family member (skpt-1)
Locus_6048_Transcript_1/1_Conf_1.000	582	20	3.85E-56	XP_002647989.1	77	221.476	167	130	C. briggsae CBR-LPD-5 protein
Locus_6049_Transcript_1/1_Conf_1.000	697	20	5.48E-62	NP_502014.2	66	241.506	234	156	hypothetical protein T11G6.8
Locus_605_Transcript_1/1_Conf_1.000	1332	20	0	XP_002638488.1	94	807.749	443	418	C. briggsae CBR-SEC-23 protein
Locus_6050_Transcript_1/1_Conf_1.000	205	0							
Locus_6051_Transcript_1/1_Conf_1.000	335	0							

Locus_6052_Transcript_1/2_Conf_1.000	538	20	9.35E-74	NP_001040633.1	83	279.641	178	148	hypothetical protein B0261.4
Locus_6052_Transcript_2/2_Conf_1.000	538	20	9.35E-74	NP_001040633.1	83	279.641	178	148	hypothetical protein B0261.4
Locus_6053_Transcript_1/1_Conf_1.000	642	20	1.28E-72	XP_002632892.1	82	276.559	213	175	Hypothetical protein CBG15100
Locus_6054_Transcript_1/1_Conf_1.000	222	0							
Locus_6055_Transcript_1/1_Conf_1.000	1361	20	2.06E-128	NP_491552.2	66	463.766	507	337	LEThal family member (let-363)
Locus_6056_Transcript_1/1_Conf_1.000	1663	20	4.08E-68	NP_498027.2	60	263.848	335	201	Temporarily Assigned Gene name family member (tag-340)
Locus_6057_Transcript_1/1_Conf_1.000	1670	20	4.76E-08	NP_823528.1	39	64.3142	301	119	hypothetical protein SAV_2352
Locus_6058_Transcript_1/1_Conf_1.000	330	20	8.30E-33	XP_002646441.1	88	143.28	88	78	Hypothetical protein CBG18827

Locus_6059_Transcript_1/1_Conf_1.000	577	20	2.81E-112	XP_002834824.1	100	407.912	191	191	PREDICTED: LOW QUALITY PROTEIN: guanine nucleotide-binding protein subunit beta-2-like 1-like
Locus_606_Transcript_1/1_Conf_1.000	852	3	3.20E-26	NP_509267.2	50	123.25	271	138	hypothetical protein F48E3.4
Locus_6060_Transcript_1/1_Conf_1.000	587	20	1.59E-49	XP_002640081.1	89	199.519	124	111	C. briggsae CBR-RPS-17 protein
Locus_6061_Transcript_1/1_Conf_1.000	872	20	2.35E-80	NP_499291.1	73	303.138	272	201	Uridine MonoPhosphate Synthetase family member (umps-1)
Locus_6062_Transcript_1/1_Conf_1.000	515	20	5.84E-40	XP_002640655.1	84	167.162	125	106	Hypothetical protein CBG19713
Locus_6063_Transcript_1/1_Conf_1.000	401	2	1.26E-04	NP_496786.2	55	49.6766	67	37	hypothetical protein F29C12.3
Locus_6064_Transcript_1/3_Conf_0.500	2033	2	3.20E-33	XP_002631528.1	72	148.288	159	116	Hypothetical protein CBG20694
Locus_6064_Transcript_2/3_Conf_0.500	906	1	4.48E-37	XP_002631528.1	69	159.458	185	128	Hypothetical protein CBG20694
Locus_6064_Transcript_3/3_Conf_0.667	2042	2	3.22E-33	XP_002631528.1	72	148.288	159	116	Hypothetical protein CBG20694
Locus_6065_Transcript_1/1_Conf_1.000	654	0							
Locus_6066_Transcript_1/1_Conf_1.000	822	20	5.02E-82	ACI49151.1	78	308.531	232	183	hypothetical protein Cbre_JD20.006
Locus_6067_Transcript_1/1_Conf_1.000	215	0							
Locus_6068_Transcript_1/1_Conf_1.000	804	0							
Locus_6069_Transcript_1/1_Conf_1.000	793	3	2.47E-06	NP_501541.2	52	56.9954	184	96	hypothetical protein C09G9.5
Locus_607_Transcript_1/6_Conf_0.125	612	0							
Locus_607_Transcript_5/6_Conf_0.321	544	0							
Locus_6070_Transcript_1/2_Conf_0.571	473	7	1.24E-36	NP_740819.2	70	155.992	157	110	hypothetical protein F32B5.6
Locus_6070_Transcript_2/2_Conf_0.571	829	8	6.23E-72	NP_740819.2	70	275.018	274	194	hypothetical protein F32B5.6
Locus_6071_Transcript_1/1_Conf_1.000	311	20	6.11E-20	NP_001022386.1	68	100.523	103	71	hypothetical protein W02B12.12
Locus_6072_Transcript_1/1_Conf_1.000	337	0							
Locus_6073_Transcript_1/1_Conf_1.000	1752	20	2.83E-160	NP_490931.1	86	570.081	356	309	hypothetical protein Y37E3.11

Locus_6074_Transcript_1/1_Conf_1.000	477	3	1.67E-17	XP_002636192.1	56	92.4337	159	90	Hypothetical protein CBG12107
Locus_6075_Transcript_1/1_Conf_1.000	328	9	1.21E-07	CAO00417.1	67	59.6918	58	39	two-domain activation associated secreted protein ASP4 precursor
Locus_6076_Transcript_1/1_Conf_1.000	435	20	2.47E-37	XP_002641005.1	96	158.303	85	82	C. briggsae CBR-SNR-6 protein
Locus_6077_Transcript_1/1_Conf_1.000	510	20	3.35E-32	EFO19245.1	71	141.354	121	87	AGC/PDK1 protein kinase
Locus_6078_Transcript_2/3_Conf_0.714	310	0							
Locus_6078_Transcript_3/3_Conf_0.714	235	0							
Locus_6079_Transcript_1/1_Conf_1.000	431	0							
Locus_608_Transcript_1/1_Conf_1.000	917	20	5.67E-88	EFO22999.1	75	328.561	257	193	hypothetical protein LOAG_05485
Locus_6080_Transcript_1/1_Conf_1.000	642	20	2.26E-61	CAQ48388.2	74	239.195	203	152	C. elegans protein C26H9A.1b, confirmed by transcript evidence
Locus_6081_Transcript_1/1_Conf_1.000	941	20	1.00E-127	NP_498093.1	89	460.685	309	278	Glycyl tRNA Synthetase family member (grs-1)
Locus_6082_Transcript_1/1_Conf_1.000	1370	20	9.57E-41	NP_491704.1	62	172.555	221	138	VAP (VAMP-associated protein) Related family member (vpr-1)
Locus_6083_Transcript_1/1_Conf_1.000	1546	2	2.04E-34	XP_001897733.1	51	151.754	246	126	hypothetical protein Bm1_31440
Locus_6084_Transcript_1/1_Conf_1.000	713	0							
Locus_6085_Transcript_1/1_Conf_1.000	360	20	6.53E-38	AAC38987.1	97	160.229	92	90	P-glycoprotein

Locus_6086_Transcript_1/1_Conf_1.000	355	20	1.24E-36	NP_001022869.1	77	155.992	124	96	hypothetical protein Y42G9A.4
Locus_6087_Transcript_1/1_Conf_1.000	395	5	2.56E-13	NP_510311.2	65	78.5666	141	92	hypothetical protein T21H8.1
Locus_6088_Transcript_1/1_Conf_1.000	142	0							
Locus_6089_Transcript_1/1_Conf_1.000	712	3	2.41E-28	NP_491606.2	56	129.798	238	134	hypothetical protein C09D4.4
Locus_609_Transcript_1/1_Conf_1.000	321	2	4.63E-15	XP_001232842.1	71	84.3445	80	57	PREDICTED: hypothetical protein
Locus_6090_Transcript_1/1_Conf_1.000	605	4	3.97E-14	XP_002641242.1	56	82.0333	136	77	Hypothetical protein CBG09110
Locus_6091_Transcript_1/1_Conf_1.000	209	20	1.47E-13	CAR97821.1	78	79.337	66	52	C. elegans protein F11C1.5d, partially confirmed by transcript evidence
Locus_6092_Transcript_1/1_Conf_1.000	270	20	7.02E-40	XP_002642413.1	96	166.777	89	86	Hypothetical protein CBG06810
Locus_6093_Transcript_1/1_Conf_1.000	381	20	6.59E-30	XP_001898426.1	67	133.65	134	90	Bromodomain containing protein
Locus_6094_Transcript_1/1_Conf_1.000	287	0							
Locus_6095_Transcript_1/1_Conf_1.000	842	10	3.02E-21	XP_001886292.1	47	106.686	227	107	predicted protein
Locus_6096_Transcript_1/1_Conf_1.000	1453	20	0	NP_492730.2	86	781.941	485	421	hypothetical protein Y106G6H.5
Locus_6097_Transcript_1/1_Conf_1.000	639	5	8.77E-66	NP_504033.2	74	253.832	227	169	hypothetical protein T27C4.1
Locus_6098_Transcript_1/6_Conf_0.667	2903	20	0	NP_490938.3	61	681.404	978	600	AFaDin (actin filament binding protein) homolog family member (afd-1)
Locus_6098_Transcript_2/6_Conf_0.667	2903	20	0	NP_490938.3	61	680.633	978	599	AFaDin (actin filament binding protein) homolog family member (afd-1)

Locus_6098_Transcript_3/6_Conf_0.667	2903	20	0	NP_490938.3	61	681.404	978	600	AFaDin (actin filament binding protein) homolog family member (afd-1)
Locus_6098_Transcript_4/6_Conf_0.667	2903	20	0	NP_490938.3	61	681.404	978	600	AFaDin (actin filament binding protein) homolog family member (afd-1)
Locus_6098_Transcript_5/6_Conf_0.533	2610	20	0	NP_490938.3	62	664.455	906	565	AFaDin (actin filament binding protein) homolog family member (afd-1)
Locus_6098_Transcript_6/6_Conf_0.667	2903	20	0	NP_490938.3	61	681.404	978	600	AFaDin (actin filament binding protein) homolog family member (afd-1)
Locus_6099_Transcript_1/1_Conf_1.000	434	20	2.33E-27	XP_002633403.1	62	125.176	130	81	Hypothetical protein CBG06165
Locus_61_Transcript_1/1_Conf_1.000	3571	20	0	NP_741632.2	86	1571.6	1194	1034	SMAll family member (sma-1)
Locus_610_Transcript_1/2_Conf_1.000	1193	20	1.91E-79	EFO20642.1	76	300.827	235	180	hypothetical protein LOAG_07844
Locus_610_Transcript_2/2_Conf_1.000	1305	20	2.17E-79	EFO20642.1	76	300.827	235	180	hypothetical protein LOAG_07844
Locus_6100_Transcript_1/1_Conf_1.000	168	1	4.14E-16	CAR63626.1	90	87.8113	53	48	hypothetical protein
Locus_6101_Transcript_1/2_Conf_1.000	486	0							
Locus_6101_Transcript_2/2_Conf_1.000	642	0							
Locus_6102_Transcript_1/1_Conf_1.000	339	20	2.14E-57	XP_002801893.1	100	224.942	113	113	PREDICTED: translocon-associated protein subunit beta-like isoform 2
Locus_6103_Transcript_1/1_Conf_1.000	240	0							
Locus_6104_Transcript_1/1_Conf_1.000	1091	20	8.19E-127	NP_001023928.1	77	457.988	356	275	hypothetical protein F44E7.4

Locus_6105_Transcript_1/1_Conf_1.000	604	20	2.20E-97	XP_002644536.1	98	358.607	201	198	C. briggsae CBR-DPY-23 protein
Locus_6106_Transcript_1/1_Conf_1.000	1415	20	1.81E-159	XP_002629880.1	83	567	391	327	Hypothetical protein CBG21917
Locus_6107_Transcript_1/1_Conf_1.000	828	20	7.90E-59	NP_001083402.1	74	231.491	211	157	RAB21, member RAS oncogene family
Locus_6108_Transcript_1/1_Conf_1.000	1405	20	4.62E-06	XP_002712937.1	49	57.3806	130	64	PREDICTED: nuclear matrix transcription factor 4 isoform 1
Locus_6109_Transcript_1/1_Conf_1.000	307	0							
Locus_611_Transcript_1/1_Conf_1.000	859	7	1.67E-22	A8X0L9.2	52	110.923	234	123	Tat-binding homolog 7
Locus_6110_Transcript_1/1_Conf_1.000	690	12	1.09E-38	NP_498612.1	55	164.081	226	125	hypothetical protein F56C9.7

Locus_6111_Transcript_1/1_Conf_1.000	538	4	1.20E-20	XP_002635869.1	60	103.219	133	80	Hypothetical protein CBG01085
Locus_6112_Transcript_1/1_Conf_1.000	466	20	2.06E-39	EFO21364.1	74	165.236	131	98	dCMP deaminase
Locus_6113_Transcript_1/1_Conf_1.000	225	20	1.22E-23	NP_491275.2	87	112.849	74	65	hypothetical protein F47B3.6
Locus_6114_Transcript_1/1_Conf_1.000	177	0							
Locus_6115_Transcript_1/2_Conf_1.000	486	20	2.45E-24	NP_498400.1	94	115.161	70	66	hypothetical protein C16A3.1
Locus_6115_Transcript_2/2_Conf_1.000	588	20	3.93E-24	NP_498400.1	94	115.161	70	66	hypothetical protein C16A3.1
Locus_6116_Transcript_1/1_Conf_1.000	510	0							
Locus_6117_Transcript_1/1_Conf_1.000	849	20	2.18E-67	XP_001895891.1	66	259.996	282	187	ubiquitin-conjugating enzyme E2Q
Locus_6118_Transcript_1/1_Conf_1.000	395	0							
Locus_6119_Transcript_1/1_Conf_1.000	193	8	1.11E-08	XP_002638736.1	68	63.1586	57	39	C. briggsae CBR-EGO-1 protein
Locus_612_Transcript_1/2_Conf_1.000	1411	20	4.21E-116	NP_001023759.2	75	422.935	340	255	hypothetical protein DC2.3
Locus_612_Transcript_2/2_Conf_1.000	1411	20	3.56E-115	NP_001023759.2	74	419.853	340	254	hypothetical protein DC2.3
Locus_6120_Transcript_1/2_Conf_1.000	1796	20	8.41E-83	NP_498020.1	98	312.768	169	166	ARp2/3 compleX component family member (arx-6)

Locus_6120_Transcript_2/2_Conf_1.000	1796	20	8.41E-83	NP_498020.1	98	312.768	169	166	ARp2/3 compleX component family member (arx-6)
Locus_6121_Transcript_1/1_Conf_1.000	479	20	1.05E-11	EFO18092.1	64	73.1738	90	58	hypothetical protein LOAG_10406
Locus_6122_Transcript_1/1_Conf_1.000	1035	20	3.31E-122	EFO24060.1	81	442.58	304	248	hypothetical protein LOAG_04426
Locus_6123_Transcript_1/1_Conf_1.000	136	0							
Locus_6124_Transcript_1/2_Conf_1.000	564	0							
Locus_6124_Transcript_2/2_Conf_1.000	995	20	5.58E-31	XP_002632984.1	62	139.428	156	98	Hypothetical protein CBG21747
Locus_6125_Transcript_1/1_Conf_1.000	497	7	9.66E-74	CAD44145.2	87	279.256	166	146	C. elegans protein T21C9.3b, confirmed by transcript evidence
Locus_6126_Transcript_1/1_Conf_1.000	1173	20	1.15E-129	NP_741303.2	90	467.618	299	271	hypothetical protein F38A1.8
Locus_6127_Transcript_1/1_Conf_1.000	1294	20	1.05E-134	NP_500157.2	77	484.567	385	299	Cleavage and Polyadenylation Specificity Factor family member (cpsf-1)
Locus_6128_Transcript_1/1_Conf_1.000	901	20	5.49E-96	EFO25036.1	76	355.14	248	190	CUP-2 protein
Locus_6129_Transcript_1/2_Conf_1.000	1436	2	7.33E-15	XP_002636412.1	41	86.6557	279	115	Hypothetical protein CBG23065
Locus_6129_Transcript_2/2_Conf_1.000	1436	2	7.33E-15	XP_002636412.1	41	86.6557	279	115	Hypothetical protein CBG23065

Locus_613_Transcript_1/3_Conf_0.667	1684	20	0	NP_505733.1	98	645.58	315	311	yeast Glc Seven-like Phosphatases family member (gsp-1)
Locus_613_Transcript_2/3_Conf_0.667	1744	20	0	NP_505733.1	98	645.58	315	311	yeast Glc Seven-like Phosphatases family member (gsp-1)
Locus_613_Transcript_3/3_Conf_0.667	1672	20	0	NP_505733.1	98	645.58	315	311	yeast Glc Seven-like Phosphatases family member (gsp-1)

Locus_6130_Transcript_1/1_Conf_1.000	356	20	3.15E-48	NP_001022190.1	91	194.512	118	108	hypothetical protein F53A10.2
Locus_6131_Transcript_1/1_Conf_1.000	320	20	9.31E-32	NP_001024956.1	80	139.813	103	83	hypothetical protein Y26E6A.3
Locus_6132_Transcript_1/4_Conf_0.375	712	8	3.70E-45	CAR63526.1	93	185.652	105	98	hypothetical protein
Locus_6132_Transcript_2/4_Conf_0.625	1542	20	9.77E-154	CAR63526.1	94	548.125	341	322	hypothetical protein
Locus_6132_Transcript_3/4_Conf_0.625	1617	20	1.04E-153	CAR63526.1	94	548.125	341	322	hypothetical protein
Locus_6132_Transcript_4/4_Conf_0.625	1617	20	1.04E-153	CAR63526.1	94	548.125	341	322	hypothetical protein
Locus_6133_Transcript_1/1_Conf_1.000	306	0							
Locus_6134_Transcript_1/2_Conf_0.500	1172	0							
Locus_6134_Transcript_2/2_Conf_0.875	1172	0							
Locus_6135_Transcript_1/1_Conf_1.000	922	20	1.92E-67	ADI24626.1	87	260.381	174	152	Dehydrogenases, short chain protein 27, partially confirmed by transcript evidence
Locus_6136_Transcript_1/1_Conf_1.000	584	20	2.68E-41	NP_001076703.1	75	172.17	146	110	hypothetical protein T11G6.2
Locus_6137_Transcript_1/1_Conf_1.000	1270	20	1.42E-128	NP_506418.1	80	464.151	344	276	Seven WD repeats, AN11 family member (swan-1)
Locus_6138_Transcript_1/1_Conf_1.000	1135	20	1.13E-150	AAO62949.1	90	537.339	335	303	neuronal acetylcholinesterase precursor

Locus_6139_Transcript_1/1_Conf_1.000	1177	20	9.81E-121	CBB16332.1	75	437.958	395	299	C. elegans protein Y47D3A.29b, partially confirmed by transcript evidence
Locus_614_Transcript_1/2_Conf_1.000	1301	5	3.74E-23	NP_001033342.1	47	114.005	326	155	hypothetical protein ZK177.4
Locus_614_Transcript_2/2_Conf_1.000	1301	5	3.74E-23	NP_001033342.1	47	114.005	326	155	hypothetical protein ZK177.4
Locus_6140_Transcript_1/1_Conf_1.000	1665	20	0	NP_001122812.1	78	778.474	598	472	TBC (Tre-2/Bub2/Cdc16) domain family member (tbc-9)
Locus_6141_Transcript_1/1_Conf_1.000	1284	20	8.58E-97	NP_498746.1	67	358.607	372	250	hypothetical protein F44B9.5
Locus_6142_Transcript_1/2_Conf_1.000	311	0							
Locus_6142_Transcript_2/2_Conf_1.000	287	0							
Locus_6143_Transcript_1/1_Conf_1.000	925	3	1.31E-23	NP_872046.1	43	114.775	340	148	hypothetical protein ZK131.11
Locus_6144_Transcript_1/1_Conf_1.000	1201	20	1.88E-167	NP_495750.1	94	593.193	337	318	Chaperonin Containing TCP-1 family member (cct-4)
Locus_6145_Transcript_1/1_Conf_1.000	390	20	5.70E-26	XP_001897340.1	67	120.553	128	87	BTB/POZ domain containing protein
Locus_6146_Transcript_1/1_Conf_1.000	870	20	2.05E-92	XP_002642445.1	78	343.199	288	225	Hypothetical protein CBG06850
Locus_6147_Transcript_1/1_Conf_1.000	326	20	1.62E-52	XP_002747844.1	97	208.764	103	100	PREDICTED: 60S ribosomal protein L37a-like

Locus_6148_Transcript_1/1_Conf_1.000	1322	4	1.32E-07	NP_506662.1	47	62.3882	219	103	hypothetical protein ZC412.3
Locus_6149_Transcript_1/1_Conf_1.000	880	8	2.04E-15	XP_001902629.1	55	87.4261	226	126	Zinc finger, C2H2 type family protein
Locus_615_Transcript_1/1_Conf_1.000	899	20	1.67E-28	XP_001895197.1	64	130.954	151	97	Piwi domain containing protein
Locus_6150_Transcript_1/1_Conf_1.000	633	4	7.57E-30	XP_001900891.1	64	134.42	195	125	Prion-like-
Locus_6151_Transcript_1/1_Conf_1.000	501	20	2.14E-44	CAD11604.1	81	181.8	116	95	cystathionine beta-synthase
Locus_6152_Transcript_1/1_Conf_1.000	326	0							
Locus_6153_Transcript_1/1_Conf_1.000	241	20	3.48E-39	ACT66687.1	100	164.466	80	80	glutathione S-transferase pi
Locus_6154_Transcript_1/1_Conf_1.000	1436	20	1.76E-101	XP_001898939.1	65	374.4	414	273	Immunoglobulin I-set domain containing protein
Locus_6155_Transcript_1/1_Conf_1.000	1424	20	1.60E-147	NP_492149.1	84	527.324	369	312	Temporarily Assigned Gene name family member (tag-173)
Locus_6156_Transcript_1/1_Conf_1.000	375	20	2.00E-18	XP_002644331.1	82	95.5153	76	63	Hypothetical protein CBG14140
Locus_6157_Transcript_1/1_Conf_1.000	638	20	5.81E-62	NP_496426.1	73	241.121	199	147	hypothetical protein B0491.1

Locus_6158_Transcript_1/1_Conf_1.000	627	0							
Locus_6159_Transcript_1/1_Conf_1.000	744	9	1.92E-10	XP_001901704.1	59	70.4774	94	56	hypothetical protein
Locus_616_Transcript_1/1_Conf_1.000	1270	20	6.13E-39	XP_001895592.1	59	166.392	270	160	RIKEN cDNA 2810405J04
Locus_6160_Transcript_1/1_Conf_1.000	490	20	1.68E-41	XP_002637289.1	73	172.17	155	114	Hypothetical protein CBG18976
Locus_6161_Transcript_1/1_Conf_1.000	622	20	4.80E-42	XP_001902295.1	70	174.866	177	125	T-complex protein 11 containing protein
Locus_6162_Transcript_1/1_Conf_1.000	225	20	8.73E-30	XP_001900704.1	90	133.265	73	66	Protein kinase domain containing protein
Locus_6163_Transcript_1/1_Conf_1.000	704	20	2.35E-52	XP_001901522.1	78	209.534	149	117	EBF3-S
Locus_6164_Transcript_1/3_Conf_0.400	380	0							
Locus_6164_Transcript_2/3_Conf_0.400	456	3	6.58E-06	XP_002644494.1	57	53.9138	78	45	Hypothetical protein CBG14382
Locus_6164_Transcript_3/3_Conf_0.400	552	20	1.18E-45	NP_741765.1	71	186.422	180	128	tubulin folding COfactor E-Like protein family member (coel-1)
Locus_6165_Transcript_1/1_Conf_1.000	1271	20	1.23E-172	NP_491027.1	89	610.527	372	333	hypothetical protein F32B5.1
Locus_6166_Transcript_1/1_Conf_1.000	539	20	2.09E-65	XP_002641725.1	85	251.906	179	153	Hypothetical protein CBG10062
Locus_6167_Transcript_1/1_Conf_1.000	848	20	1.09E-135	NP_510438.1	97	486.878	277	269	CalSeQuestrin family member (csq-1)
Locus_6168_Transcript_1/3_Conf_0.667	2082	20	5.14E-119	NP_741593.1	58	433.335	623	366	hypothetical protein H24G06.1
Locus_6168_Transcript_2/3_Conf_0.667	1936	20	1.55E-122	NP_741593.1	59	444.891	622	371	hypothetical protein H24G06.1
Locus_6168_Transcript_3/3_Conf_0.667	2031	20	2.82E-122	NP_741593.1	60	444.121	606	366	hypothetical protein H24G06.1
Locus_6169_Transcript_1/1_Conf_1.000	217	0							
Locus_617_Transcript_1/1_Conf_1.000	184	0							

Locus_6170_Transcript_1/1_Conf_1.000	786	3	4.14E-14	XP_002639978.1	65	82.8037	131	86	C. briggsae CBR-FHOD-1 protein
Locus_6171_Transcript_1/1_Conf_1.000	323	0							
Locus_6172_Transcript_1/1_Conf_1.000	621	4	6.31E-18	EFO24663.1	74	94.7449	98	73	swan
Locus_6173_Transcript_1/2_Conf_1.000	680	20	4.52E-50	XP_001900652.1	70	201.83	226	159	Leucine Rich Repeat family protein
Locus_6173_Transcript_2/2_Conf_1.000	680	20	1.01E-49	XP_001900652.1	69	200.675	226	158	Leucine Rich Repeat family protein
Locus_6174_Transcript_1/1_Conf_1.000	750	20	1.43E-53	AAX29951.1	100	213.772	100	100	beta-2-microglobulin
Locus_6175_Transcript_1/1_Conf_1.000	789	20	5.04E-52	XP_002642969.1	66	208.764	225	150	Hypothetical protein CBG15253
Locus_6176_Transcript_1/1_Conf_1.000	591	3	9.15E-37	NP_504540.2	62	157.147	193	121	hypothetical protein C04E6.11
Locus_6177_Transcript_1/1_Conf_1.000	334	4	1.37E-11	XP_002639436.1	81	72.7886	64	52	Hypothetical protein CBG04029
Locus_6178_Transcript_1/1_Conf_1.000	1837	20	0	ACI49195.1	99	707.597	355	353	hypothetical protein Csp3_JD03.004
Locus_6179_Transcript_1/1_Conf_1.000	259	0							
Locus_618_Transcript_1/1_Conf_1.000	470	20	1.37E-43	XP_002640960.1	91	179.104	110	101	Hypothetical protein CBG11702

Locus_6180_Transcript_1/1_Conf_1.000	268	14	2.00E-10	EFO22013.1	77	68.9366	54	42	ATP synthase subunit epsilon
Locus_6181_Transcript_1/1_Conf_1.000	487	20	5.42E-40	CAX65081.1	78	167.162	129	101	C. elegans protein Y105E8A.7e, confirmed by transcript evidence
Locus_6182_Transcript_1/1_Conf_1.000	684	20	1.68E-84	NP_505885.2	97	316.235	169	164	CalciNeurin B family member (cnb-1)
Locus_6183_Transcript_1/1_Conf_1.000	490	3	4.03E-11	XP_002631220.1	50	71.2478	132	67	C. briggsae CBR-NPP-19 protein
Locus_6184_Transcript_1/1_Conf_1.000	423	0							
Locus_6185_Transcript_1/1_Conf_1.000	2050	20	6.74E-31	XP_001902695.1	54	140.584	188	103	cytoplasmic polyadenylation element binding protein CPEB2, putative
Locus_6186_Transcript_1/3_Conf_0.714	1097	3	9.46E-06	XP_973428.1	41	55.8398	225	94	PREDICTED: similar to SJCHGC06573 protein
Locus_6186_Transcript_2/3_Conf_0.714	1160	0							
Locus_6186_Transcript_3/3_Conf_0.714	1160	2	2.98E-05	XP_973428.1	39	54.299	236	93	PREDICTED: similar to SJCHGC06573 protein
Locus_6187_Transcript_1/1_Conf_1.000	395	20	1.88E-40	EFO25784.1	75	168.703	138	104	hypothetical protein LOAG_02706
Locus_6188_Transcript_1/1_Conf_1.000	465	1	1.88E-08	CAH23216.1	50	62.3882	133	67	putative L3 ES protein
Locus_6189_Transcript_1/1_Conf_1.000	432	0							
Locus_619_Transcript_1/2_Conf_1.000	1711	9	8.69E-05	XP_002664701.1	44	53.5286	166	74	PREDICTED: HLA-B-associated transcript 3-like
Locus_619_Transcript_2/2_Conf_1.000	1462	0							
Locus_6190_Transcript_1/1_Conf_1.000	548	20	1.39E-51	NP_497419.1	75	206.068	149	113	hypothetical protein Y67D2.3
Locus_6191_Transcript_1/1_Conf_1.000	336	20	1.15E-18	XP_001953272.1	67	96.2857	108	73	GF17288

Locus_6192_Transcript_1/1_Conf_1.000	534	20	4.76E-30	NP_500308.2	62	134.42	178	111	hypothetical protein T26C12.3
Locus_6193_Transcript_1/1_Conf_1.000	1227	20	2.78E-89	NP_500410.2	65	333.569	388	253	UDP-GlucuronosylTransferase family member (ugt-45)
Locus_6194_Transcript_1/2_Conf_1.000	1249	20	4.19E-32	XP_002401494.1	67	143.665	162	109	F-box containing protein, putative
Locus_6194_Transcript_2/2_Conf_1.000	339	2	1.72E-06	XP_002640966.1	72	55.8398	51	37	Hypothetical protein CBG11709
Locus_6195_Transcript_1/1_Conf_1.000	395	1	4.84E-04	NP_508284.1	46	47.7506	67	31	hypothetical protein F09E10.6
Locus_6196_Transcript_1/1_Conf_1.000	833	20	1.38E-10	XP_002644140.1	95	71.2478	41	39	C. briggsae CBR-SDN-1 protein
Locus_6197_Transcript_1/1_Conf_1.000	2054	20	0	XP_002630402.1	83	762.296	533	445	Hypothetical protein CBG04341
Locus_6198_Transcript_1/1_Conf_1.000	880	20	2.20E-110	ACJ65179.1	93	402.905	220	205	Hypothetical protein Y67D8C.10d
Locus_6199_Transcript_1/1_Conf_1.000	1023	0							
Locus_62_Transcript_1/1_Conf_1.000	1496	20	0	NP_501802.2	84	681.789	469	395	hypothetical protein C47E12.3
Locus_620_Transcript_1/1_Conf_1.000	1790	20	0	XP_002647028.1	85	840.106	552	473	C. briggsae CBR-EMB-8 protein

Locus_6200_Transcript_1/1_Conf_1.000	301	3	9.49E-37	NP_501647.2	87	156.377	102	89	hypothetical protein T20D3.11
Locus_6201_Transcript_1/1_Conf_1.000	536	20	4.31E-31	NP_001021859.1	66	137.887	168	111	Variable ABnormal morphology family member (vab-10)
Locus_6202_Transcript_1/1_Conf_1.000	613	0							
Locus_6203_Transcript_1/1_Conf_1.000	503	20	2.64E-18	NP_001122441.1	61	95.1301	95	58	hypothetical protein F02E9.10
Locus_6204_Transcript_1/1_Conf_1.000	1443	20	1.11E-111	EFO23151.1	69	408.297	360	251	transcriptional regulator
Locus_6205_Transcript_1/1_Conf_1.000	243	0							
Locus_6206_Transcript_1/1_Conf_1.000	605	0							
Locus_6207_Transcript_1/1_Conf_1.000	400	0							
Locus_6208_Transcript_1/1_Conf_1.000	473	20	3.47E-55	NP_505616.2	86	217.624	152	132	CULlin family member (cul-5)
Locus_6209_Transcript_1/1_Conf_1.000	825	20	2.38E-31	XP_002639510.1	67	140.198	134	91	C. briggsae CBR-YOP-1 protein
Locus_621_Transcript_1/2_Conf_1.000	947	1	1.90E-25	CAR63707.1	61	120.939	151	93	hypothetical protein
Locus_621_Transcript_2/2_Conf_1.000	964	1	1.83E-15	CAR63707.1	55	87.8113	130	72	hypothetical protein
Locus_6210_Transcript_1/1_Conf_1.000	1477	0							

Locus_6211_Transcript_1/1_Conf_1.000	576	20	2.55E-105	NP_501715.1	98	384.8	191	189	Acetylcholine-gated Chloride Channel family member (acc-1)
Locus_6212_Transcript_1/1_Conf_1.000	153	0							
Locus_6213_Transcript_1/1_Conf_1.000	432	0							
Locus_6214_Transcript_1/1_Conf_1.000	868	0							
Locus_6215_Transcript_1/3_Conf_0.667	768	20	2.05E-79	NP_506260.1	76	299.671	261	199	hypothetical protein W07G4.4
Locus_6215_Transcript_2/3_Conf_0.667	768	20	2.05E-79	NP_506260.1	76	299.671	261	199	hypothetical protein W07G4.4
Locus_6215_Transcript_3/3_Conf_0.667	768	20	2.05E-79	NP_506260.1	76	299.671	261	199	hypothetical protein W07G4.4
Locus_6216_Transcript_1/2_Conf_0.500	966	0							
Locus_6216_Transcript_2/2_Conf_0.833	651	0							
Locus_6217_Transcript_1/1_Conf_1.000	1805	20	3.36E-47	EFA03559.1	64	194.512	265	171	hypothetical protein TcasGA2_TC013564
Locus_6218_Transcript_1/1_Conf_1.000	1287	20	3.51E-82	ACI49105.1	67	310.071	322	217	hypothetical protein Cbre_JD13.007
Locus_6219_Transcript_1/1_Conf_1.000	681	20	2.59E-45	NP_492839.4	71	186.037	240	172	Leucine-rich repeats, Ras-like domain, Kinase family member (lrk-1)
Locus_622_Transcript_1/1_Conf_1.000	169	20	2.51E-21	XP_002640076.1	92	105.145	55	51	Hypothetical protein CBG12561
Locus_6220_Transcript_1/1_Conf_1.000	261	0							
Locus_6221_Transcript_1/1_Conf_1.000	575	3	1.07E-31	NP_505169.2	65	140.198	140	92	hypothetical protein F52E1.9
Locus_6222_Transcript_1/1_Conf_1.000	964	5	1.90E-04	XP_001494660.2	41	51.2174	257	106	PREDICTED: similar to Fibrous sheath CABYR binding protein
Locus_6223_Transcript_1/2_Conf_1.000	286	0							
Locus_6223_Transcript_2/2_Conf_1.000	277	0							
Locus_6224_Transcript_1/1_Conf_1.000	819	8	1.13E-09	Q61QK6.2	90	68.1662	42	38	Protein melted homolog

Locus_6225_Transcript_1/1_Conf_1.000	1254	20	0	NP_001022939.1	97	739.954	418	409	hypothetical protein Y71H2B.10
Locus_6226_Transcript_1/3_Conf_0.667	680	20	2.35E-115	A8WJR8.2	99	418.698	225	223	Dual specificity tyrosine-phosphorylation-regulated kinase mbk-2
Locus_6226_Transcript_2/3_Conf_0.667	758	20	1.23E-129	A8WJR8.2	98	466.463	251	246	Dual specificity tyrosine-phosphorylation-regulated kinase mbk-2
Locus_6226_Transcript_3/3_Conf_0.667	680	20	2.35E-115	A8WJR8.2	99	418.698	225	223	Dual specificity tyrosine-phosphorylation-regulated kinase mbk-2
Locus_6227_Transcript_1/1_Conf_1.000	423	11	2.62E-18	NP_001022851.1	58	95.1301	133	78	GLYcosylation related family member (gly-5)

Locus_6228_Transcript_1/1_Conf_1.000	601	20	3.91E-14	NP_740774.1	59	82.0333	82	49	hypothetical protein Y48G1A.4
Locus_6229_Transcript_1/1_Conf_1.000	607	20	5.21E-46	NP_495103.1	69	187.963	195	135	ZYGote defective: embryonic lethal family member (zyg-1)
Locus_623_Transcript_1/1_Conf_1.000	2625	20	0	NP_001040817.1	68	715.687	703	484	NHL (ring finger b-box coiled coil) domain containing family member (nhl-3)
Locus_6230_Transcript_1/2_Conf_1.000	430	0							
Locus_6230_Transcript_2/2_Conf_1.000	470	0							
Locus_6231_Transcript_1/1_Conf_1.000	755	2	2.22E-06	EFO24024.1	61	56.9954	76	47	CMGC/DYRK/HIPK protein kinase
Locus_6232_Transcript_1/1_Conf_1.000	663	7	8.43E-14	EFO27864.1	51	81.2629	145	74	hypothetical protein LOAG_00607
Locus_6233_Transcript_1/1_Conf_1.000	585	20	1.34E-56	XP_002630082.1	83	223.016	160	133	Hypothetical protein CBG13461
Locus_6234_Transcript_1/1_Conf_1.000	464	20	2.71E-39	XP_002631669.1	93	164.851	98	92	C. briggsae CBR-MOG-4 protein
Locus_6235_Transcript_1/1_Conf_1.000	1235	20	1.69E-102	NP_501452.1	68	377.481	410	279	Acyl CoA DeHydrogenase family member (acdh-13)
Locus_6236_Transcript_1/1_Conf_1.000	1758	20	3.56E-78	EFO23262.1	52	297.36	557	295	hypothetical protein LOAG_05225
Locus_6237_Transcript_1/1_Conf_1.000	591	2	9.87E-07	XP_002634618.1	50	57.3806	174	87	Hypothetical protein CBG18472
Locus_6238_Transcript_1/1_Conf_1.000	304	0							
Locus_6239_Transcript_1/1_Conf_1.000	338	0							
Locus_624_Transcript_1/3_Conf_0.250	1124	20	7.91E-64	NP_492709.2	67	248.825	245	166	hypothetical protein ZC434.4
Locus_624_Transcript_2/3_Conf_0.250	125	0							

Locus_624_Transcript_3/3_Conf_0.625	349	20	1.49E-13	AAD51334.1	61	79.337	83	51	Kunitz type serine protease inhibitor
Locus_6240_Transcript_1/1_Conf_1.000	568	4	8.28E-13	XP_002634109.1	56	77.411	124	70	C. briggsae CBR-CSN-3 protein
Locus_6241_Transcript_1/1_Conf_1.000	147	0							
Locus_6242_Transcript_1/1_Conf_1.000	370	20	2.45E-48	ACX53263.1	92	194.897	116	107	glutathione S-transferase-3
Locus_6243_Transcript_1/4_Conf_0.250	876	0							
Locus_6243_Transcript_2/4_Conf_0.250	551	7	2.88E-28	NP_491629.1	73	128.642	108	79	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-52)
Locus_6243_Transcript_3/4_Conf_0.250	941	0							
Locus_6243_Transcript_4/4_Conf_0.500	493	7	2.50E-29	NP_491629.1	68	131.724	124	85	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-52)
Locus_6244_Transcript_1/1_Conf_1.000	593	4	6.82E-16	NP_495920.1	64	87.8113	89	57	hypothetical protein F44G4.3
Locus_6245_Transcript_1/1_Conf_1.000	351	20	6.40E-33	XP_001513459.1	100	143.665	68	68	PREDICTED: similar to insulinoma protein (rig), partial
Locus_6246_Transcript_1/1_Conf_1.000	128	0							
Locus_6247_Transcript_1/1_Conf_1.000	425	20	1.35E-06	XP_003064014.1	53	56.225	106	57	predicted protein
Locus_6248_Transcript_1/1_Conf_1.000	1381	20	1.75E-82	NP_510459.1	65	311.227	374	244	EPsiN (endocytic protein) homolog family member (epn-1)
Locus_6249_Transcript_1/1_Conf_1.000	967	8	1.30E-45	NP_505068.1	55	187.963	265	146	hypothetical protein F43H9.4
Locus_625_Transcript_1/1_Conf_1.000	1397	7	3.20E-92	XP_002639943.1	67	343.584	377	255	C. briggsae CBR-MDT-28 protein
Locus_6250_Transcript_1/1_Conf_1.000	477	20	1.60E-44	NP_001024594.1	73	182.185	134	98	Invertebrate LYSozyme family member (ilys-5)
Locus_6251_Transcript_1/2_Conf_0.500	656	3	1.72E-19	NP_503096.1	56	100.138	163	92	Temporarily Assigned Gene name family member (tag-141)
Locus_6251_Transcript_2/2_Conf_0.750	992	20	5.18E-37	XP_002632379.1	51	159.458	285	147	C. briggsae CBR-TAG-141 protein
Locus_6252_Transcript_1/2_Conf_1.000	397	0							

Locus_6252_Transcript_2/2_Conf_1.000	396	0								
Locus_6253_Transcript_1/1_Conf_1.000	401	20	1.17E-42	XP_002740677.1	79	176.022	133	106	PREDICTED: cyclin-dependent kinase 2-like	
Locus_6254_Transcript_1/1_Conf_1.000	479	1	4.71E-04	XP_002121584.1	41	47.7506	121	50	PREDICTED: similar to F36H2.3	
Locus_6255_Transcript_1/1_Conf_1.000	1418	20	7.01E-103	NP_001122517.1	62	379.022	440	277	hypothetical protein T08G11.4	
Locus_6256_Transcript_1/3_Conf_0.714	988	0								
Locus_6256_Transcript_2/3_Conf_0.714	988	1	7.52E-04	YP_001857748.1	48	49.2914	60	29	hypothetical protein Bphy_1520	
Locus_6256_Transcript_3/3_Conf_0.714	988	0								
Locus_6257_Transcript_1/1_Conf_1.000	538	20	1.00E-67	NP_492274.3	84	259.61	178	151	hypothetical protein T19A6.1	
Locus_6258_Transcript_1/1_Conf_1.000	341	1	6.30E-25	XP_002345943.1	100	117.087	55	55	PREDICTED: hypothetical protein	
Locus_6259_Transcript_1/1_Conf_1.000	381	0								
Locus_626_Transcript_1/1_Conf_1.000	311	0								
Locus_6260_Transcript_1/1_Conf_1.000	773	20	1.48E-85	CAR63564.1	90	320.087	186	169	hypothetical protein	
Locus_6261_Transcript_1/1_Conf_1.000	616	2	4.33E-19	EFO18701.1	63	98.5969	82	52	hypothetical protein LOAG_09794	
Locus_6262_Transcript_1/1_Conf_1.000	1053	20	2.51E-101	NP_508993.2	71	373.244	356	255	fatty Acid CoA Synthetase family member (acs-17)	
Locus_6263_Transcript_1/6_Conf_0.438	990	2	1.26E-29	XP_002642371.1	65	103.219	92	60	Hypothetical protein CBG18375	
Locus_6263_Transcript_2/6_Conf_0.188	806	9	6.13E-85	XP_002642371.1	79	318.161	269	215	Hypothetical protein CBG18375	
Locus_6263_Transcript_3/6_Conf_0.125	486	0								

Locus_6263_Transcript_4/6_Conf_0.312	477	2	3.25E-21	XP_002642371.1	78	104.76	69	54	Hypothetical protein CBG18375
Locus_6263_Transcript_5/6_Conf_0.562	1589	9	8.69E-119	XP_002642371.1	76	400.593	351	267	Hypothetical protein CBG18375
Locus_6263_Transcript_6/6_Conf_0.438	978	2	4.31E-30	XP_002642371.1	65	103.219	92	60	Hypothetical protein CBG18375
Locus_6264_Transcript_1/1_Conf_1.000	1016	20	2.57E-71	EFO27594.1	74	273.478	191	142	CXXC zinc finger family protein
Locus_6265_Transcript_1/1_Conf_1.000	438	0							
Locus_6266_Transcript_1/1_Conf_1.000	446	0							
Locus_6267_Transcript_1/1_Conf_1.000	1112	20	2.31E-108	XP_002631581.1	76	396.741	335	257	Hypothetical protein CBG20759
Locus_6268_Transcript_1/1_Conf_1.000	350	0							
Locus_6269_Transcript_1/3_Conf_0.714	1191	6	3.10E-21	XP_002642656.1	47	107.457	380	180	Hypothetical protein CBG00040
Locus_6269_Transcript_2/3_Conf_0.714	1191	6	3.10E-21	XP_002642656.1	48	107.457	365	176	Hypothetical protein CBG00040
Locus_6269_Transcript_3/3_Conf_0.714	1191	6	4.05E-21	XP_002642656.1	47	107.071	380	180	Hypothetical protein CBG00040
Locus_627_Transcript_1/1_Conf_1.000	853	20	7.58E-52	NP_001022932.1	70	208.379	240	170	SMN (Survival of Motor Neuron protein) Related family member (smr-1)
Locus_6270_Transcript_1/1_Conf_1.000	225	0							
Locus_6271_Transcript_1/1_Conf_1.000	792	20	2.68E-77	NP_495177.2	76	292.738	263	200	hypothetical protein F59G1.4
Locus_6272_Transcript_1/1_Conf_1.000	493	0							
Locus_6273_Transcript_1/1_Conf_1.000	276	20	2.58E-10	NP_496323.1	60	68.5514	85	51	SET (trithorax/polycomb) domain containing family member (set-14)

Locus_6274_Transcript_1/1_Conf_1.000	437	20	8.24E-33	EFO27859.1	84	143.28	88	74	hypothetical protein LOAG_00621
Locus_6275_Transcript_1/2_Conf_1.000	274	0							
Locus_6275_Transcript_2/2_Conf_1.000	271	0							
Locus_6276_Transcript_1/1_Conf_1.000	342	20	2.22E-49	XP_002639673.1	97	198.364	106	103	Hypothetical protein CBG12391
Locus_6277_Transcript_1/1_Conf_1.000	959	20	8.92E-148	XP_002643079.1	87	527.324	319	280	C. briggsae CBR-ABCE-1 protein
Locus_6278_Transcript_1/1_Conf_1.000	391	5	4.68E-20	EFO23406.1	71	100.908	99	71	hypothetical protein LOAG_05080
Locus_6279_Transcript_1/1_Conf_1.000	1584	20	2.56E-64	XP_001899505.1	50	251.136	470	238	p70
Locus_628_Transcript_1/1_Conf_1.000	299	0							
Locus_6280_Transcript_1/2_Conf_1.000	456	2	1.72E-30	NP_505746.2	71	135.576	135	96	hypothetical protein F28H7.8
Locus_6280_Transcript_2/2_Conf_1.000	447	4	5.23E-35	NP_505746.2	75	150.599	132	99	hypothetical protein F28H7.8
Locus_6281_Transcript_1/1_Conf_1.000	462	20	1.70E-25	NP_508934.1	98	119.013	57	56	hypothetical protein T23F2.3
Locus_6282_Transcript_1/1_Conf_1.000	1045	20	7.42E-114	NP_509670.2	83	414.846	312	262	hypothetical protein C17G1.7
Locus_6283_Transcript_1/1_Conf_1.000	877	20	5.23E-88	NP_492451.2	78	328.561	287	224	hypothetical protein ZK858.6
Locus_6284_Transcript_1/1_Conf_1.000	455	20	7.75E-31	NP_502573.1	70	136.732	121	85	hypothetical protein Y62E10A.6
Locus_6285_Transcript_1/1_Conf_1.000	833	4	6.79E-34	XP_002646138.1	49	148.673	278	137	Hypothetical protein CBG08018
Locus_6286_Transcript_1/1_Conf_1.000	316	4	9.99E-34	NP_490674.3	79	146.362	105	83	hypothetical protein Y48G1C.8
Locus_6287_Transcript_1/1_Conf_1.000	383	0							
Locus_6288_Transcript_1/1_Conf_1.000	155	0							
Locus_6289_Transcript_1/1_Conf_1.000	950	20	1.61E-56	NP_001024415.2	62	224.172	245	154	TetraSPanin family member (tsp-21)

Locus_629_Transcript_1/1_Conf_1.000	660	20	6.78E-32	XP_002639453.1	67	141.354	138	93	Hypothetical protein CBG04048
Locus_6290_Transcript_1/1_Conf_1.000	820	20	2.10E-64	XP_002634989.1	88	249.98	147	130	Hypothetical protein CBG13529
Locus_6291_Transcript_1/3_Conf_0.600	1015	20	8.86E-56	XP_002639565.1	89	221.861	139	125	Hypothetical protein CBG04196
Locus_6291_Transcript_2/3_Conf_0.600	643	20	1.12E-68	XP_002639565.1	89	263.462	167	149	Hypothetical protein CBG04196
Locus_6291_Transcript_3/3_Conf_0.600	1099	20	1.22E-69	XP_002639565.1	89	268.085	167	150	Hypothetical protein CBG04196
Locus_6292_Transcript_1/1_Conf_1.000	312	0							
Locus_6293_Transcript_1/1_Conf_1.000	544	18	1.73E-38	NP_493277.2	86	162.54	116	100	hypothetical protein C47B2.9
Locus_6294_Transcript_1/1_Conf_1.000	191	0							
Locus_6295_Transcript_1/1_Conf_1.000	549	5	9.58E-24	NP_001021818.1	76	113.62	135	103	hypothetical protein Y71G12B.11
Locus_6296_Transcript_1/1_Conf_1.000	170	0							
Locus_6297_Transcript_1/1_Conf_1.000	399	0							
Locus_6298_Transcript_1/1_Conf_1.000	2837	20	0	XP_002633378.1	82	1070.84	775	640	C. briggsae CBR-SEC-24.1 protein

Locus_6299_Transcript_1/1_Conf_1.000	575	20	2.37E-71	NP_495838.2	85	271.937	191	164	PYRimidine biosynthesis family member (pyr-1)
Locus_63_Transcript_1/1_Conf_1.000	1079	20	1.54E-77	NP_492437.1	94	294.278	160	151	Sorting NeXin family member (snx-3)
Locus_630_Transcript_1/3_Conf_0.375	155	6	2.23E-09	XP_002634040.1	78	65.4698	51	40	C. briggsae CBR-VIT-6 protein
Locus_630_Transcript_2/3_Conf_0.625	173	8	1.98E-10	XP_002634040.1	78	68.9366	56	44	C. briggsae CBR-VIT-6 protein
Locus_630_Transcript_3/3_Conf_0.750	180	8	1.57E-10	XP_002634040.1	77	69.3218	58	45	C. briggsae CBR-VIT-6 protein
Locus_6300_Transcript_1/1_Conf_1.000	649	20	7.79E-25	XP_394749.3	89	117.857	66	59	PREDICTED: similar to jumeau CG4029-PA
Locus_6301_Transcript_1/1_Conf_1.000	374	20	8.38E-49	XP_002634876.1	88	196.438	125	111	Hypothetical protein CBG10542

Locus_6302_Transcript_1/1_Conf_1.000	1047	20	4.49E-135	XP_002641834.1	84	485.337	336	283	C. briggsae CBR-RFL-1 protein
Locus_6303_Transcript_1/1_Conf_1.000	417	1	1.66E-04	AAD13339.1	53	49.2914	100	53	ancylostoma-secreted protein 1 precursor
Locus_6304_Transcript_1/1_Conf_1.000	1176	1	1.16E-04	XP_001902660.1	47	52.373	122	58	hypothetical protein Bm1_56010
Locus_6305_Transcript_1/1_Conf_1.000	329	20	4.59E-15	EFN88165.1	73	84.3445	82	60	Pantothenate kinase 4
Locus_6306_Transcript_1/1_Conf_1.000	396	1	2.91E-17	ADA77640.2	54	91.6633	106	58	Hypothetical protein ZC404.15
Locus_6307_Transcript_1/2_Conf_1.000	300	20	8.28E-49	ADN23570.1	100	196.438	99	99	ubiquitin
Locus_6307_Transcript_2/2_Conf_1.000	179	20	1.96E-26	XP_002347402.1	100	122.094	59	59	PREDICTED: similar to Os05g0242100
Locus_6308_Transcript_1/2_Conf_1.000	1204	0							
Locus_6308_Transcript_2/2_Conf_1.000	697	0							
Locus_6309_Transcript_1/1_Conf_1.000	279	15	1.77E-43	NP_510226.1	97	178.718	85	83	hypothetical protein C49F8.3
Locus_631_Transcript_1/1_Conf_1.000	1009	20	5.06E-112	XP_002639548.1	80	408.683	319	256	C. briggsae CBR-LPD-6 protein
Locus_6310_Transcript_1/1_Conf_1.000	130	0							
Locus_6311_Transcript_1/1_Conf_1.000	901	0							
Locus_6312_Transcript_1/1_Conf_1.000	330	2	1.74E-06	NP_501888.2	50	55.8398	109	55	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-55)
Locus_6313_Transcript_1/1_Conf_1.000	1025	20	1.06E-72	XP_002644744.1	66	278.1	307	204	C. briggsae CBR-SYM-3 protein
Locus_6314_Transcript_1/1_Conf_1.000	762	2	4.13E-24	EFO16535.1	54	115.931	224	122	hypothetical protein LOAG_11971
Locus_6315_Transcript_1/1_Conf_1.000	274	20	3.59E-36	NP_499157.2	87	154.451	90	79	hypothetical protein T05G5.8
Locus_6316_Transcript_1/2_Conf_1.000	430	20	1.19E-55	ACD86935.1	99	219.164	107	106	ubiquitin/60s ribosomal protein L40 fusion

Locus_6316_Transcript_2/2_Conf_1.000	430	20	1.19E-55	ACD86935.1	99	219.164	107	106	ubiquitin/60s ribosomal protein L40 fusion
Locus_6317_Transcript_1/1_Conf_1.000	318	0							
Locus_6318_Transcript_1/1_Conf_1.000	156	0							
Locus_6319_Transcript_1/1_Conf_1.000	337	0							
Locus_632_Transcript_1/1_Conf_1.000	768	20	2.61E-58	NP_501277.1	69	229.565	206	144	hypothetical protein C46A5.1
Locus_6320_Transcript_1/1_Conf_1.000	437	20	3.02E-35	NP_496721.2	80	151.369	110	89	Carnitine Palmitoyl Transferase family member (cpt-1)
Locus_6321_Transcript_1/1_Conf_1.000	246	20	2.03E-23	NP_493945.1	83	112.079	79	66	hypothetical protein Y57G7A.10
Locus_6322_Transcript_1/1_Conf_1.000	652	20	1.74E-48	ABD39381.1	76	196.438	170	130	putative galectin protein 10
Locus_6323_Transcript_1/1_Conf_1.000	484	0							
Locus_6324_Transcript_1/1_Conf_1.000	130	20	5.06E-14	NP_494571.1	100	80.8777	42	42	AdaPtin, Delta chain (clathrin associated complex) family member (apd-3)
Locus_6325_Transcript_1/1_Conf_1.000	387	18	2.66E-23	XP_002633945.1	81	111.694	79	64	C. briggsae CBR-ELO-1 protein
Locus_6326_Transcript_1/1_Conf_1.000	531	0							
Locus_6327_Transcript_1/1_Conf_1.000	315	0							
Locus_6328_Transcript_1/1_Conf_1.000	145	20	1.91E-16	XP_002647014.1	91	88.9669	46	42	Hypothetical protein CBG23800
Locus_6329_Transcript_1/1_Conf_1.000	387	0							

Locus_633_Transcript_1/4_Conf_0.556	540	20	3.66E-30	AAL09375.1	88	103.605	62	55	AF305957_1vitellogenin
Locus_633_Transcript_2/4_Conf_0.556	540	20	1.96E-24	AAL09375.1	80	84.3445	66	53	AF305957_1vitellogenin
Locus_633_Transcript_3/4_Conf_0.444	436	20	2.41E-39	AAL09375.1	91	134.035	79	72	AF305957_1vitellogenin
Locus_633_Transcript_4/4_Conf_0.444	394	19	2.80E-34	AAL09375.1	90	110.153	65	59	AF305957_1vitellogenin
Locus_6330_Transcript_1/1_Conf_1.000	964	20	3.47E-107	CAX65065.1	68	392.504	354	241	C. elegans protein K01A6.2c, partially confirmed by transcript evidence
Locus_6331_Transcript_1/1_Conf_1.000	467	20	2.14E-28	EFO17782.1	71	128.642	117	84	hypothetical protein LOAG_10716
Locus_6332_Transcript_1/1_Conf_1.000	618	20	9.34E-62	NP_504486.4	70	240.35	216	153	Adenylyl CYclase family member (acy-4)
Locus_6333_Transcript_1/1_Conf_1.000	397	9	2.70E-47	AAT02161.1	85	191.43	118	101	hypothetical protein L3ni22
Locus_6334_Transcript_1/1_Conf_1.000	366	0							
Locus_6335_Transcript_1/1_Conf_1.000	902	20	8.55E-65	NP_001021463.1	61	251.521	303	187	SUppressor of activated let-60 Ras family member (sur-2)
Locus_6336_Transcript_1/1_Conf_1.000	1483	20	3.81E-131	NP_001122780.1	68	473.011	452	309	hypothetical protein F41H10.6
Locus_6337_Transcript_1/1_Conf_1.000	330	20	1.99E-10	XP_002640972.1	60	68.9366	95	57	Hypothetical protein CBG11719
Locus_6338_Transcript_1/1_Conf_1.000	577	20	2.12E-43	NP_495253.2	76	179.104	139	106	Neuronal Membrane GlycoProtein family member (nmgp-1)
Locus_6339_Transcript_1/2_Conf_1.000	393	0							
Locus_6339_Transcript_2/2_Conf_1.000	587	0							
Locus_634_Transcript_1/1_Conf_1.000	329	20	1.47E-21	NP_501808.1	86	105.916	89	77	hypothetical protein F44D12.3

Locus_6340_Transcript_1/1_Conf_1.000	637	6	1.15E-09	ADM53754.1	47	67.3958	157	75	Hypothetical protein Y51H7C.5
Locus_6341_Transcript_1/3_Conf_0.571	1155	20	9.70E-65	XP_002642926.1	75	251.906	208	158	Hypothetical protein CBG15202
Locus_6341_Transcript_2/3_Conf_0.571	1167	20	9.86E-65	XP_002642926.1	75	251.906	208	158	Hypothetical protein CBG15202
Locus_6341_Transcript_3/3_Conf_0.286	712	14	1.27E-53	NP_001021233.1	65	213.772	217	143	hypothetical protein D2045.9
Locus_6342_Transcript_1/1_Conf_1.000	357	0							
Locus_6343_Transcript_1/1_Conf_1.000	149	0							
Locus_6344_Transcript_1/3_Conf_0.600	582	20	7.58E-20	XP_002646157.1	53	100.908	156	83	C. briggsae CBR-PNG-1 protein
Locus_6344_Transcript_2/3_Conf_0.600	590	20	5.87E-20	XP_002646157.1	53	101.293	156	83	C. briggsae CBR-PNG-1 protein
Locus_6344_Transcript_3/3_Conf_0.600	578	20	7.34E-20	XP_002646157.1	53	100.908	156	83	C. briggsae CBR-PNG-1 protein
Locus_6345_Transcript_1/4_Conf_0.333	232	0							
Locus_6345_Transcript_2/4_Conf_0.444	721	0							
Locus_6345_Transcript_3/4_Conf_0.556	704	0							
Locus_6345_Transcript_4/4_Conf_0.556	721	0							
Locus_6346_Transcript_1/1_Conf_1.000	844	8	2.62E-73	XP_002636989.1	77	279.641	227	175	C. briggsae CBR-TRY-10 protein
Locus_6347_Transcript_1/4_Conf_0.250	318	20	3.18E-56	CAA23781.1	100	221.09	106	106	unnamed protein product
Locus_6347_Transcript_2/4_Conf_0.500	1085	20	8.67E-129	P20039.1	95	464.537	258	247	HLA class II histocompatibility antigen
Locus_6347_Transcript_3/4_Conf_0.500	1042	20	2.14E-129	XP_002343977.1	99	466.463	248	247	PREDICTED: similar to HLA class II histocompatibility antigen, DRB1-7 beta chain isoform 1

Locus_6347_Transcript_4/4_Conf_0.500	1055	20	4.39E-130	XP_002343977.1	100	468.774	248	248	PREDICTED: similar to HLA class II histocompatibility antigen, DRB1-7 beta chain isoform 1
Locus_6348_Transcript_1/1_Conf_1.000	317	0							
Locus_6349_Transcript_1/1_Conf_1.000	883	20	1.46E-37	XP_002634401.1	62	160.999	190	119	C. briggsae CBR-PQN-55 protein
Locus_635_Transcript_1/1_Conf_1.000	3098	20	0	NP_507684.4	82	1447.57	1056	872	abnormal EMBroygenesis family member (emb-4)
Locus_6350_Transcript_1/1_Conf_1.000	883	20	5.84E-103	NP_491513.2	83	378.252	257	214	Formin HOmology Domain family member (fhod-1)
Locus_6351_Transcript_1/1_Conf_1.000	411	0							
Locus_6352_Transcript_1/1_Conf_1.000	1684	20	0	XP_001891652.1	92	940.258	560	516	myosin heavy chain, nonmuscle type 1

Locus_6353_Transcript_1/1_Conf_1.000	183	20	1.27E-20	XP_002819595.1	100	102.834	56	56	PREDICTED: glycosylphosphatidylinositol anchor attachment 1 protein-like isoform 2
Locus_6354_Transcript_1/1_Conf_1.000	532	0							
Locus_6355_Transcript_1/4_Conf_0.200	634	3	4.93E-13	CAA85490.2	67	78.5666	79	53	C. elegans protein C14B1.9, confirmed by transcript evidence
Locus_6355_Transcript_2/4_Conf_0.200	676	3	5.71E-13	CAA85490.2	67	78.5666	79	53	C. elegans protein C14B1.9, confirmed by transcript evidence
Locus_6355_Transcript_3/4_Conf_0.700	2307	3	7.06E-16	CAA85490.2	42	90.8929	259	111	C. elegans protein C14B1.9, confirmed by transcript evidence
Locus_6355_Transcript_4/4_Conf_0.700	2307	3	7.06E-16	CAA85490.2	42	90.8929	259	111	C. elegans protein C14B1.9, confirmed by transcript evidence
Locus_6356_Transcript_1/1_Conf_1.000	1269	20	3.31E-93	NP_497756.2	67	346.665	387	260	hypothetical protein F34D10.2
Locus_6357_Transcript_1/1_Conf_1.000	372	20	4.77E-36	XP_001893740.1	72	154.066	126	91	ATP-dependent helicase DDX1
Locus_6358_Transcript_1/1_Conf_1.000	1173	20	9.56E-84	XP_002633876.1	70	315.079	296	210	C. briggsae CBR-UNC-5 protein
Locus_6359_Transcript_1/1_Conf_1.000	1977	20	0	NP_001040977.1	81	835.869	593	485	Carnitine Palmitoyl Transferase family member (cpt-2)
Locus_636_Transcript_1/1_Conf_1.000	528	20	3.95E-45	XP_002646754.1	90	184.496	131	119	C. briggsae CBR-RPB-4 protein
Locus_6360_Transcript_1/2_Conf_1.000	320	0							
Locus_6360_Transcript_2/2_Conf_1.000	320	0							
Locus_6361_Transcript_1/1_Conf_1.000	582	20	1.91E-55	CAR63581.1	92	219.164	145	134	putative COLlagen
Locus_6362_Transcript_1/1_Conf_1.000	304	20	1.16E-18	XP_002644368.1	60	96.2857	99	60	C. briggsae CBR-CHT-1 protein
Locus_6363_Transcript_1/1_Conf_1.000	514	20	2.01E-40	NP_001071986.1	84	168.703	113	96	transcription factor protein
Locus_6364_Transcript_1/1_Conf_1.000	1227	20	1.73E-123	XP_002630374.1	73	447.203	410	302	Hypothetical protein CBG04313

Locus_6365_Transcript_1/1_Conf_1.000	1388	20	2.64E-54	XP_001899295.1	67	217.624	257	174	AT08590p
Locus_6366_Transcript_1/2_Conf_1.000	354	0							
Locus_6366_Transcript_2/2_Conf_1.000	299	0							
Locus_6367_Transcript_1/1_Conf_1.000	644	0							
Locus_6368_Transcript_1/1_Conf_1.000	135	0							
Locus_6369_Transcript_1/1_Conf_1.000	683	20	4.44E-37	EFO28162.1	84	158.688	101	85	PAB-dependent Poly(A) specific ribonuclease subunit
Locus_637_Transcript_1/1_Conf_1.000	1247	20	1.03E-131	XP_002638689.1	75	474.552	397	299	Hypothetical protein CBG11884
Locus_6370_Transcript_1/1_Conf_1.000	740	20	7.36E-31	XP_002629815.1	63	138.272	162	103	C. briggsae CBR-ARC-1 protein
Locus_6371_Transcript_1/1_Conf_1.000	645	20	2.65E-25	NP_491382.1	55	119.398	151	84	hypothetical protein Y119C1B.5
Locus_6372_Transcript_1/1_Conf_1.000	289	0							
Locus_6373_Transcript_1/2_Conf_1.000	848	0							
Locus_6373_Transcript_2/2_Conf_1.000	848	0							
Locus_6374_Transcript_1/1_Conf_1.000	637	20	3.88E-74	Q612R3.2	90	281.567	191	173	Pre-mRNA-splicing factor syf-2
Locus_6375_Transcript_1/1_Conf_1.000	327	3	2.27E-22	NP_496707.1	76	108.612	68	52	hypothetical protein Y38E10A.24
Locus_6376_Transcript_1/1_Conf_1.000	436	0							
Locus_6377_Transcript_1/1_Conf_1.000	374	20	2.07E-39	XP_002634452.1	87	165.236	105	92	Hypothetical protein CBG04467
Locus_6378_Transcript_1/1_Conf_1.000	483	5	2.14E-36	CAX65056.1	66	155.221	160	107	C. elegans protein F25C8.3d, partially confirmed by transcript evidence
Locus_6379_Transcript_1/1_Conf_1.000	1037	20	3.44E-103	NP_509242.1	77	379.407	311	241	hypothetical protein C07D8.6
Locus_638_Transcript_1/1_Conf_1.000	676	20	1.48E-53	NP_509508.1	82	213.386	141	117	Neuropeptide-Like Protein family member (nlp-14)
Locus_6380_Transcript_1/3_Conf_0.667	922	20	1.43E-46	NP_499473.2	56	191.045	252	142	hypothetical protein Y47D3B.11

Locus_6380_Transcript_2/3_Conf_0.667	923	20	1.87E-46	NP_499473.2	56	190.66	252	142	hypothetical protein Y47D3B.11
Locus_6380_Transcript_3/3_Conf_0.667	923	20	1.43E-46	NP_499473.2	56	191.045	252	142	hypothetical protein Y47D3B.11
Locus_6381_Transcript_1/1_Conf_1.000	132	0							
Locus_6382_Transcript_1/1_Conf_1.000	744	20	6.73E-56	NP_502170.3	63	221.476	255	163	TWiK family of potassium channels family member (twk-25)
Locus_6383_Transcript_1/1_Conf_1.000	435	20	6.79E-11	NP_500024.1	90	70.4774	42	38	AuTophaGy (yeast Atg homolog) family member (atg-3)
Locus_6384_Transcript_1/1_Conf_1.000	237	2	2.14E-04	XP_002639618.1	66	48.9062	50	33	Hypothetical protein CBG12331
Locus_6385_Transcript_1/1_Conf_1.000	569	20	1.26E-61	XP_002640720.1	76	239.58	194	149	C. briggsae CBR-TAG-301 protein
Locus_6386_Transcript_1/1_Conf_1.000	409	0							
Locus_6387_Transcript_1/1_Conf_1.000	597	20	7.01E-24	XP_002636443.1	95	114.39	64	61	Hypothetical protein CBG23104
Locus_6388_Transcript_1/1_Conf_1.000	484	20	1.74E-70	XP_002636769.1	94	268.47	142	134	C. briggsae CBR-EGL-10 protein
Locus_6389_Transcript_1/1_Conf_1.000	1203	20	1.28E-131	XP_002643608.1	74	474.167	381	285	Hypothetical protein CBG16342
Locus_639_Transcript_1/1_Conf_1.000	790	20	8.71E-121	NP_001180485.1	100	437.187	232	232	60S ribosomal protein L7
Locus_6390_Transcript_1/1_Conf_1.000	143	0							
Locus_6391_Transcript_1/1_Conf_1.000	355	0							
Locus_6392_Transcript_1/1_Conf_1.000	501	3	1.60E-07	XP_002642798.1	41	59.3066	154	64	C. briggsae CBR-ZTF-8 protein
Locus_6393_Transcript_1/1_Conf_1.000	301	5	1.02E-06	NP_496328.2	65	56.6102	64	42	hypothetical protein R06F6.8

Locus_6394_Transcript_1/1_Conf_1.000	230	0							
Locus_6395_Transcript_1/1_Conf_1.000	1223	20	1.17E-71	NP_491478.1	66	275.018	307	204	hypothetical protein F28B3.5
Locus_6396_Transcript_1/1_Conf_1.000	767	20	2.05E-47	XP_001898097.1	62	193.356	229	142	Asparaginase family protein
Locus_6397_Transcript_1/1_Conf_1.000	1988	20	5.33E-126	XP_001897054.1	63	456.447	560	355	Fes/CIP4 homology domain containing protein
Locus_6398_Transcript_1/2_Conf_1.000	711	20	6.08E-56	NP_001040796.1	72	221.476	222	161	hypothetical protein R12C12.6
Locus_6398_Transcript_2/2_Conf_1.000	711	20	4.65E-56	NP_001040796.1	72	221.861	222	161	hypothetical protein R12C12.6
Locus_6399_Transcript_1/4_Conf_0.250	1819	20	1.34E-136	XP_001896629.1	74	491.5	448	332	U-box domain containing protein
Locus_6399_Transcript_2/4_Conf_0.250	1861	20	7.34E-138	XP_001896629.1	74	495.738	448	332	U-box domain containing protein
Locus_6399_Transcript_3/4_Conf_0.375	2212	20	6.01E-158	XP_001896629.1	69	562.762	578	403	U-box domain containing protein
Locus_6399_Transcript_4/4_Conf_0.375	2212	20	3.19E-159	XP_001896629.1	69	567	578	403	U-box domain containing protein
Locus_64_Transcript_1/5_Conf_0.429	625	20	1.13E-14	XP_002698332.1	75	83.9593	72	54	PREDICTED: hypothetical protein
Locus_64_Transcript_2/5_Conf_0.571	934	20	4.74E-21	XP_002631414.1	75	106.301	93	70	C. briggsae CBR-DNJ-23 protein
Locus_64_Transcript_3/5_Conf_0.571	608	20	2.52E-16	XP_002698332.1	75	89.3521	76	57	PREDICTED: hypothetical protein
Locus_64_Transcript_4/5_Conf_0.143	913	20	3.35E-40	XP_001364158.1	61	169.859	253	156	PREDICTED: similar to DnaJ protein SB73
Locus_64_Transcript_5/5_Conf_0.643	638	20	2.83E-16	XP_002698332.1	75	89.3521	76	57	PREDICTED: hypothetical protein
Locus_640_Transcript_1/9_Conf_0.135	729	1	1.50E-04	AAP94887.1	59	50.8322	77	46	MFP3
Locus_640_Transcript_2/9_Conf_0.189	368	4	1.72E-06	NP_505347.1	49	55.8398	71	35	hypothetical protein C25E10.10
Locus_640_Transcript_3/9_Conf_0.378	448	4	1.75E-06	NP_505347.1	49	55.8398	71	35	hypothetical protein C25E10.10
Locus_640_Transcript_4/9_Conf_0.432	1477	12	1.44E-05	NP_505347.1	49	55.8398	71	35	hypothetical protein C25E10.10
Locus_640_Transcript_5/9_Conf_0.324	421	4	1.77E-06	NP_505347.1	49	55.8398	71	35	hypothetical protein C25E10.10
Locus_640_Transcript_6/9_Conf_0.378	445	4	1.76E-06	NP_505347.1	49	55.8398	71	35	hypothetical protein C25E10.10

Locus_640_Transcript_7/9_Conf_0.432	1480	12	1.45E-05	NP_505347.1	49	55.8398	71	35	hypothetical protein C25E10.10
Locus_640_Transcript_8/9_Conf_0.270	394	4	1.77E-06	NP_505347.1	49	55.8398	71	35	hypothetical protein C25E10.10
Locus_640_Transcript_9/9_Conf_0.378	404	4	1.75E-06	NP_505347.1	49	55.8398	71	35	hypothetical protein C25E10.10
Locus_6400_Transcript_1/1_Conf_1.000	895	1	6.37E-04	NP_506414.1	44	49.2914	149	67	hypothetical protein F53C11.4
Locus_6401_Transcript_1/1_Conf_1.000	180	5	8.89E-06	XP_001898505.1	74	53.5286	43	32	ALKBH protein
Locus_6402_Transcript_1/1_Conf_1.000	799	20	1.56E-40	NP_498848.2	63	170.629	212	135	histone METhyltransferase-like family member (met-2)
Locus_6403_Transcript_1/1_Conf_1.000	840	20	2.08E-46	A8XEZ1.3	60	190.274	265	160	Cell death abnormality protein 12
Locus_6404_Transcript_1/1_Conf_1.000	1256	4	1.35E-14	XP_002637928.1	41	85.5001	251	105	Hypothetical protein CBG04740
Locus_6405_Transcript_1/1_Conf_1.000	473	0							
Locus_6406_Transcript_1/1_Conf_1.000	1391	20	8.26E-133	NP_001021564.1	86	478.404	381	328	hypothetical protein K10C3.5
Locus_6407_Transcript_1/1_Conf_1.000	406	0							
Locus_6408_Transcript_1/1_Conf_1.000	855	4	2.25E-11	XP_002642002.1	61	73.9442	101	62	C. briggsae CBR-MTM-3 protein
Locus_6409_Transcript_1/1_Conf_1.000	455	0							
Locus_641_Transcript_1/1_Conf_1.000	422	0							

Locus_6410_Transcript_1/1_Conf_1.000	1122	20	3.65E-85	XP_001902701.1	87	319.701	230	201	I/LWEQ domain containing protein
Locus_6411_Transcript_1/1_Conf_1.000	233	20	6.02E-23	NP_490842.1	96	110.538	60	58	SUMO (ubiquitin-related) homolog family member (smo-1)
Locus_6412_Transcript_1/2_Conf_1.000	1385	20	2.04E-123	NP_496557.1	90	447.203	262	237	hypothetical protein Y17G7B.4
Locus_6412_Transcript_2/2_Conf_1.000	1385	20	2.04E-123	NP_496557.1	90	447.203	262	237	hypothetical protein Y17G7B.4
Locus_6413_Transcript_1/1_Conf_1.000	529	0							
Locus_6414_Transcript_1/1_Conf_1.000	277	14	6.80E-11	XP_002644932.1	61	70.4774	80	49	Hypothetical protein CBG10877
Locus_6415_Transcript_1/1_Conf_1.000	1629	20	5.47E-110	NP_493307.3	60	402.905	558	339	hypothetical protein F22G12.5
Locus_6416_Transcript_1/1_Conf_1.000	147	0							
Locus_6417_Transcript_1/1_Conf_1.000	498	5	1.04E-19	XP_002647027.1	50	99.7525	163	82	Hypothetical protein CBG03541
Locus_6418_Transcript_1/1_Conf_1.000	1228	20	1.00E-155	NP_499637.2	79	554.288	412	328	hypothetical protein Y111B2A.8
Locus_6419_Transcript_1/2_Conf_1.000	1260	20	2.77E-100	NP_492022.3	83	370.163	261	217	hypothetical protein H37N21.1
Locus_6419_Transcript_2/2_Conf_1.000	1248	20	5.02E-102	NP_492022.3	84	375.941	257	217	hypothetical protein H37N21.1

Locus_642_Transcript_1/8_Conf_0.237	1521	20	0	ACU00668.1	98	823.928	449	444	heat shock protein 90
Locus_642_Transcript_2/8_Conf_0.237	1563	20	0	ACU00668.1	98	834.713	466	461	heat shock protein 90
Locus_642_Transcript_3/8_Conf_0.184	802	20	7.14E-110	ACU00668.1	98	400.979	209	206	heat shock protein 90
Locus_642_Transcript_4/8_Conf_0.184	760	20	6.38E-110	ACU00668.1	98	400.979	209	206	heat shock protein 90
Locus_642_Transcript_5/8_Conf_0.316	1156	20	4.22E-169	ACU00668.1	98	598.586	371	366	heat shock protein 90
Locus_642_Transcript_6/8_Conf_0.316	1114	20	5.80E-168	ACU00668.1	98	594.734	365	361	heat shock protein 90
Locus_642_Transcript_7/8_Conf_0.421	2269	20	0	ACU00668.1	98	1197.19	707	698	heat shock protein 90
Locus_642_Transcript_8/8_Conf_0.421	2269	20	0	ACU00668.1	98	1189.87	707	698	heat shock protein 90

Locus_6420_Transcript_1/1_Conf_1.000	1421	20	1.19E-126	EFO17442.1	82	457.988	351	288	rad51
Locus_6421_Transcript_1/1_Conf_1.000	528	20	1.22E-54	AAV28323.2	74	216.083	169	126	Hypothetical protein T15B7.1
Locus_6422_Transcript_1/1_Conf_1.000	778	4	9.98E-05	NP_001022715.1	54	51.6026	77	42	ALIX (Apoptosis-linked gene 2 interacting protein X) homolog family member (alx-1)
Locus_6423_Transcript_1/1_Conf_1.000	561	20	2.54E-59	XP_001892087.1	86	231.876	141	122	hypothetical protein
Locus_6424_Transcript_1/1_Conf_1.000	139	0							
Locus_6425_Transcript_1/1_Conf_1.000	547	20	1.89E-40	XP_002643588.1	64	169.088	170	110	Hypothetical protein CBG16310
Locus_6426_Transcript_1/1_Conf_1.000	1368	20	1.79E-71	AAI42660.1	71	274.633	244	174	MYST3 protein
Locus_6427_Transcript_1/1_Conf_1.000	940	20	4.11E-97	XP_001895541.1	75	358.992	295	222	CG6179-PA
Locus_6428_Transcript_1/1_Conf_1.000	347	1	5.15E-06	XP_001902020.1	63	54.299	63	40	PRP39 pre-mRNA processing factor 39 homolog
Locus_6429_Transcript_1/1_Conf_1.000	363	0							
Locus_643_Transcript_1/1_Conf_1.000	1546	5	3.62E-15	XP_001899830.1	61	87.8113	88	54	Associated with TFs and helicases family protein
Locus_6430_Transcript_1/1_Conf_1.000	1667	20	1.62E-40	XP_002636574.1	58	172.17	295	172	Hypothetical protein CBG23268

Locus_6431_Transcript_1/1_Conf_1.000	1292	20	8.79E-150	NP_502179.1	81	534.643	398	326	Slit-Robo GAP homolog family member (srgp-1)
Locus_6432_Transcript_1/1_Conf_1.000	912	20	3.25E-152	XP_002634958.1	97	541.962	303	294	Hypothetical protein CBG13493
Locus_6433_Transcript_1/1_Conf_1.000	476	2	1.25E-04	EFO16985.1	51	49.6766	99	51	hypothetical protein LOAG_11519
Locus_6434_Transcript_1/1_Conf_1.000	578	19	1.09E-47	XP_002636620.1	87	193.356	118	103	Hypothetical protein CBG23324
Locus_6435_Transcript_1/1_Conf_1.000	609	20	3.51E-74	NP_497801.1	94	281.567	135	127	hypothetical protein Y1A5A.1
Locus_6436_Transcript_1/6_Conf_0.409	200	0							
Locus_6436_Transcript_3/6_Conf_0.136	169	0							
Locus_6436_Transcript_4/6_Conf_0.409	284	0							
Locus_6436_Transcript_5/6_Conf_0.182	391	0							
Locus_6437_Transcript_1/1_Conf_1.000	484	4	4.81E-12	XP_002630639.1	52	74.3294	149	78	Hypothetical protein CBG02308
Locus_6438_Transcript_1/1_Conf_1.000	1061	20	8.91E-22	EFO25960.1	50	108.997	261	132	hypothetical protein LOAG_02517

Locus_6439_Transcript_1/1_Conf_1.000	953	20	5.70E-46	NP_001129817.1	72	189.119	193	140	CLeaR family member (clr-1)
Locus_644_Transcript_1/3_Conf_0.600	324	20	2.78E-28	NP_505384.2	69	128.257	108	75	ASpartyl Protease family member (asp-2)
Locus_644_Transcript_2/3_Conf_0.400	153	20	2.55E-13	XP_002637505.1	86	78.5666	46	40	C. briggsae CBR-ASP-2 protein
Locus_644_Transcript_3/3_Conf_0.800	597	20	2.47E-53	NP_505384.2	72	212.231	170	124	ASpartyl Protease family member (asp-2)
Locus_6440_Transcript_1/1_Conf_1.000	479	0							
Locus_6441_Transcript_1/2_Conf_1.000	1007	20	1.04E-125	XP_002636421.1	81	454.136	333	272	C. briggsae CBR-PPTR-2 protein
Locus_6441_Transcript_2/2_Conf_1.000	829	4	2.85E-08	XP_002636421.1	57	63.5438	98	56	C. briggsae CBR-PPTR-2 protein
Locus_6442_Transcript_1/2_Conf_1.000	471	20	4.57E-31	XP_001900251.1	75	137.502	114	86	Pecanex-like protein 1
Locus_6442_Transcript_2/2_Conf_1.000	423	20	4.60E-31	XP_001900251.1	75	137.502	114	86	Pecanex-like protein 1
Locus_6443_Transcript_1/1_Conf_1.000	152	0							
Locus_6444_Transcript_1/1_Conf_1.000	452	20	3.50E-23	CAR63624.1	88	111.309	68	60	putative CU (copper) Chaperonin
Locus_6445_Transcript_1/1_Conf_1.000	2348	20	0	NP_001024216.1	77	663.685	520	401	GLYcosylation related family member (gly-4)
Locus_6446_Transcript_1/1_Conf_1.000	1325	2	4.12E-17	EFO22800.1	52	93.9745	153	81	hypothetical protein LOAG_05685
Locus_6447_Transcript_1/1_Conf_1.000	830	0							
Locus_6448_Transcript_1/1_Conf_1.000	301	0							
Locus_6449_Transcript_1/1_Conf_1.000	782	0							
Locus_645_Transcript_1/1_Conf_1.000	1992	20	1.13E-83	NP_498275.2	79	315.849	247	197	hypothetical protein F01F1.1
Locus_6450_Transcript_1/1_Conf_1.000	207	0							

Locus_6451_Transcript_1/1_Conf_1.000	694	20	1.29E-71	XP_001902350.1	81	273.478	230	188	Myosin XVIIIA
Locus_6452_Transcript_1/1_Conf_1.000	923	20	2.30E-129	XP_002640077.1	91	466.077	310	284	Hypothetical protein CBG12562
Locus_6453_Transcript_1/1_Conf_1.000	718	20	7.33E-49	NP_741658.1	67	197.978	197	132	hypothetical protein Y39B6A.39
Locus_6454_Transcript_1/1_Conf_1.000	418	20	7.40E-29	XP_002630899.1	68	130.183	113	77	Hypothetical protein CBG02621
Locus_6455_Transcript_1/1_Conf_1.000	411	20	1.59E-34	EFO26815.1	67	137.502	126	85	hypothetical protein LOAG_01669
Locus_6456_Transcript_1/2_Conf_1.000	526	0							
Locus_6456_Transcript_2/2_Conf_1.000	511	0							
Locus_6457_Transcript_1/1_Conf_1.000	379	0							
Locus_6458_Transcript_1/1_Conf_1.000	244	0							
Locus_6459_Transcript_1/1_Conf_1.000	773	20	1.05E-14	XP_002643138.1	92	84.7297	52	48	Hypothetical protein CBG15316
Locus_646_Transcript_1/2_Conf_1.000	605	0							
Locus_646_Transcript_2/2_Conf_1.000	609	0							
Locus_6460_Transcript_1/1_Conf_1.000	564	4	3.41E-19	EFO22637.1	50	98.5969	184	93	hypothetical protein LOAG_05847
Locus_6461_Transcript_1/2_Conf_1.000	410	0							
Locus_6461_Transcript_2/2_Conf_1.000	1094	20	2.22E-39	XP_002637143.1	60	167.548	224	136	Hypothetical protein CBG09645

Locus_6462_Transcript_1/1_Conf_1.000	373	4	6.27E-12	CAR63558.1	97	73.9442	41	40	hypothetical protein
Locus_6463_Transcript_1/1_Conf_1.000	270	20	3.73E-33	NP_509949.1	88	144.436	89	79	SideroFleXiN (mitochondrial iron transporter) family member (sfxn-1.5)
Locus_6464_Transcript_1/1_Conf_1.000	128	0							
Locus_6465_Transcript_1/2_Conf_1.000	954	20	8.20E-77	XP_002633289.1	74	291.582	259	192	Hypothetical protein CBG06018
Locus_6465_Transcript_2/2_Conf_1.000	948	20	8.19E-77	XP_002633289.1	74	291.582	259	192	Hypothetical protein CBG06018
Locus_6466_Transcript_1/2_Conf_1.000	574	0							
Locus_6466_Transcript_2/2_Conf_1.000	574	0							
Locus_6467_Transcript_1/2_Conf_1.000	1243	20	3.59E-84	XP_002632395.1	67	316.62	314	212	C. briggsae CBR-ITSN-1 protein
Locus_6467_Transcript_2/2_Conf_1.000	1243	20	3.59E-84	XP_002632395.1	67	316.62	314	212	C. briggsae CBR-ITSN-1 protein
Locus_6468_Transcript_1/1_Conf_1.000	177	2	1.01E-06	XP_002642439.1	75	56.6102	44	33	Hypothetical protein CBG06843
Locus_6469_Transcript_1/1_Conf_1.000	314	20	1.45E-16	XP_001894239.1	69	89.3521	78	54	Peptidase M16 inactive domain containing protein
Locus_647_Transcript_1/1_Conf_1.000	923	20	1.35E-121	XP_002640679.1	89	440.269	259	232	C. briggsae CBR-PBS-5 protein
Locus_6470_Transcript_1/1_Conf_1.000	132	0							

Locus_6471_Transcript_1/1_Conf_1.000	354	20	2.18E-57	EAW56803.1	100	224.942	108	108	eukaryotic translation initiation factor 3, subunit 12, isoform CRA_a
Locus_6472_Transcript_1/1_Conf_1.000	701	20	2.38E-97	NP_504837.1	88	358.992	231	205	hypothetical protein C05C8.2
Locus_6473_Transcript_1/1_Conf_1.000	716	20	1.19E-83	EFO26364.1	87	313.538	219	191	pontin
Locus_6474_Transcript_1/1_Conf_1.000	759	2	2.85E-09	EFO19794.1	47	66.6254	231	109	hypothetical protein LOAG_08700
Locus_6475_Transcript_1/2_Conf_1.000	531	20	1.13E-47	1TW9	76	192.971	139	106	Glutathione Transferase-2
Locus_6475_Transcript_2/2_Conf_1.000	530	20	1.71E-48	1TW9	76	195.667	139	107	Glutathione Transferase-2
Locus_6476_Transcript_1/1_Conf_1.000	1002	20	8.70E-48	XP_002640031.1	73	195.282	196	144	Hypothetical protein CBG12503
Locus_6477_Transcript_1/1_Conf_1.000	156	0							
Locus_6478_Transcript_1/1_Conf_1.000	399	20	5.21E-67	YP_001700362.1	96	256.914	132	127	cytochrome c oxidase subunit II
Locus_6479_Transcript_1/2_Conf_1.000	950	6	1.80E-07	EFO25761.1	57	61.2326	101	58	hypothetical protein LOAG_02722

Locus_6479_Transcript_2/2_Conf_1.000	950	6	1.80E-07	EFO25761.1	57	61.2326	101	58	hypothetical protein LOAG_02722
Locus_648_Transcript_1/2_Conf_1.000	1072	0							
Locus_648_Transcript_2/2_Conf_1.000	637	0							
Locus_6480_Transcript_1/1_Conf_1.000	382	20	3.26E-37	NP_741249.1	86	157.918	103	89	hypothetical protein C02F5.7
Locus_6481_Transcript_1/3_Conf_0.500	662	0							
Locus_6481_Transcript_2/3_Conf_0.667	896	0							
Locus_6481_Transcript_3/3_Conf_0.667	851	0							
Locus_6482_Transcript_1/1_Conf_1.000	312	0							
Locus_6483_Transcript_1/1_Conf_1.000	974	20	2.46E-76		71	290.041	312	224	hypothetical protein R13H4.4 - Caenorhabditis elegans
Locus_6484_Transcript_1/1_Conf_1.000	1867	20	5.29E-19	EFO19565.1	59	100.908	99	59	hypothetical protein LOAG_08928
Locus_6485_Transcript_1/2_Conf_1.000	926	20	3.96E-121	XP_002646071.1	95	438.728	246	234	C. briggsae CBR-EIF-6 protein
Locus_6485_Transcript_2/2_Conf_1.000	926	20	3.96E-121	XP_002646071.1	95	438.728	246	234	C. briggsae CBR-EIF-6 protein
Locus_6486_Transcript_1/1_Conf_1.000	284	0							
Locus_6487_Transcript_1/3_Conf_0.667	629	0							
Locus_6487_Transcript_2/3_Conf_0.667	641	0							
Locus_6487_Transcript_3/3_Conf_0.667	635	0							
Locus_6488_Transcript_1/1_Conf_1.000	266	0							
Locus_6489_Transcript_1/3_Conf_0.600	659	20	2.82E-78	NP_497230.2	85	295.434	230	197	hypothetical protein W06E11.7
Locus_6489_Transcript_2/3_Conf_0.600	664	20	7.48E-79	NP_497230.2	85	297.36	231	198	hypothetical protein W06E11.7
Locus_6489_Transcript_3/3_Conf_0.600	664	20	7.48E-79	NP_497230.2	85	297.36	231	198	hypothetical protein W06E11.7

Locus_649_Transcript_1/1_Conf_1.000	968	20	1.23E-120	XP_002639257.1	80	437.187	301	241	C. briggsae CBR-FCE-1 protein
Locus_6490_Transcript_1/1_Conf_1.000	441	20	6.44E-41	NP_001021001.1	73	170.244	146	107	hypothetical protein C17E4.11
Locus_6491_Transcript_1/2_Conf_1.000	993	1	9.92E-04	NP_495617.1	54	48.9062	70	38	hypothetical protein B0495.2
Locus_6491_Transcript_2/2_Conf_1.000	1143	20	3.10E-23	XP_001894905.1	62	114.005	129	81	Protein kinase domain containing protein
Locus_6492_Transcript_1/2_Conf_1.000	909	20	1.31E-44	XP_002630112.1	89	184.496	109	98	Hypothetical protein CBG00513
Locus_6492_Transcript_2/2_Conf_1.000	709	20	3.38E-91	XP_002630112.1	83	338.576	235	197	Hypothetical protein CBG00513
Locus_6493_Transcript_1/1_Conf_1.000	678	20	2.10E-47	XP_001900963.1	77	192.971	131	102	Zinc finger, C2H2 type family protein
Locus_6494_Transcript_1/1_Conf_1.000	684	0							
Locus_6495_Transcript_1/1_Conf_1.000	320	0							
Locus_6496_Transcript_1/3_Conf_0.600	514	5	1.31E-15	NP_490938.3	55	86.2705	169	93	AFaDin (actin filament binding protein) homolog family member (afd-1)
Locus_6496_Transcript_2/3_Conf_0.600	514	5	3.56E-21	NP_490938.3	55	104.76	169	93	AFaDin (actin filament binding protein) homolog family member (afd-1)
Locus_6496_Transcript_3/3_Conf_0.600	514	5	1.31E-15	NP_490938.3	55	86.2705	169	93	AFaDin (actin filament binding protein) homolog family member (afd-1)
Locus_6497_Transcript_1/1_Conf_1.000	948	20	4.24E-49	XP_002647074.1	82	199.519	200	165	C. briggsae CBR-CCDC-47 protein
Locus_6498_Transcript_1/1_Conf_1.000	304	0							
Locus_6499_Transcript_1/1_Conf_1.000	888	20	1.44E-32	NP_740784.1	79	144.436	146	116	hypothetical protein Y92H12BL.5
Locus_65_Transcript_1/1_Conf_1.000	1058	20	2.85E-20	XP_002634864.1	45	103.99	350	160	Hypothetical protein CBG13985
Locus_650_Transcript_1/1_Conf_1.000	1106	11	2.81E-90	XP_002643974.1	70	336.65	364	258	Hypothetical protein CBG17350

Locus_6500_Transcript_1/4_Conf_0.700	1314	20	5.28E-49	XP_002637569.1	52	199.904	393	205	C. briggsae CBR-MDF-1 protein
Locus_6500_Transcript_2/4_Conf_0.700	1314	20	8.42E-47	XP_002637569.1	52	192.586	395	207	C. briggsae CBR-MDF-1 protein
Locus_6500_Transcript_3/4_Conf_0.700	1314	20	1.44E-46	XP_002637569.1	51	191.815	395	205	C. briggsae CBR-MDF-1 protein
Locus_6500_Transcript_4/4_Conf_0.700	1314	20	1.44E-46	XP_002637569.1	51	191.815	395	205	C. briggsae CBR-MDF-1 protein
Locus_6501_Transcript_1/3_Conf_0.222	268	0							
Locus_6501_Transcript_2/3_Conf_0.556	899	0							
Locus_6501_Transcript_3/3_Conf_0.556	633	0							
Locus_6502_Transcript_1/1_Conf_1.000	662	20	2.38E-69	XP_002632485.1	74	265.774	221	164	C. briggsae CBR-NHR-5 protein
Locus_6503_Transcript_1/1_Conf_1.000	768	20	4.73E-76	NP_500272.2	97	288.5	150	146	UBiquitin Conjugating enzyme family member (ubc-13)
Locus_6504_Transcript_1/1_Conf_1.000	730	20	5.06E-77	XP_001899513.1	75	291.582	243	183	AIDA-1b
Locus_6505_Transcript_1/1_Conf_1.000	254	0							

Locus_6506_Transcript_1/1_Conf_1.000	982	20	2.65E-110	XP_001897993.1	86	402.905	256	222	F-box-like/WD-repeat protein ebi
Locus_6507_Transcript_1/1_Conf_1.000	413	20	8.52E-38	XP_002631238.1	98	159.844	98	97	Hypothetical protein CBG03041
Locus_6508_Transcript_1/1_Conf_1.000	777	0							
Locus_6509_Transcript_1/1_Conf_1.000	1968	20	0	NP_497134.1	93	1148.27	610	573	hypothetical protein W05G11.6
Locus_651_Transcript_1/1_Conf_1.000	2032	20	0	XP_002630114.1	91	1110.9	677	621	C. briggsae CBR-PYR-1 protein
Locus_6510_Transcript_1/1_Conf_1.000	171	0							
Locus_6511_Transcript_1/1_Conf_1.000	542	20	1.81E-56	XP_002631495.1	77	222.246	180	140	Hypothetical protein CBG20655
Locus_6512_Transcript_1/1_Conf_1.000	430	20	1.68E-25	XP_001896542.1	71	119.013	107	76	hypothetical protein Bm1_25410

Locus_6513_Transcript_1/1_Conf_1.000	387	4	7.03E-08	XP_002634312.1	71	60.4622	102	73	Hypothetical protein CBG17653
Locus_6514_Transcript_1/1_Conf_1.000	401	0							
Locus_6515_Transcript_1/2_Conf_1.000	350	0							
Locus_6515_Transcript_2/2_Conf_1.000	594	0							
Locus_6516_Transcript_1/1_Conf_1.000	801	20	3.14E-65	ACB13196.1	65	252.677	261	171	metalloproteinase
Locus_6517_Transcript_1/3_Conf_0.714	745	20	2.43E-35	NP_001041127.1	85	123.635	91	78	hypothetical protein F57A8.2
Locus_6517_Transcript_2/3_Conf_0.714	708	20	4.63E-40	NP_001041127.1	81	168.703	140	114	hypothetical protein F57A8.2
Locus_6517_Transcript_3/3_Conf_0.714	708	20	4.63E-40	NP_001041127.1	81	168.703	140	114	hypothetical protein F57A8.2
Locus_6518_Transcript_1/1_Conf_1.000	753	20	7.70E-92	XP_002640801.1	83	340.887	252	211	Hypothetical protein CBG15682
Locus_6519_Transcript_1/1_Conf_1.000	412	5	1.73E-14	XP_002634119.1	60	82.4185	143	86	Hypothetical protein CBG01673
Locus_652_Transcript_1/1_Conf_1.000	1113	4	1.14E-22	XP_002642990.1	60	112.079	177	107	Hypothetical protein CBG15276
Locus_6520_Transcript_1/1_Conf_1.000	286	12	1.31E-17	A8X6H1.2	75	92.8189	77	58	cGMP-dependent protein kinase egl-4
Locus_6521_Transcript_1/1_Conf_1.000	664	20	3.37E-63	NP_510184.1	80	245.358	182	146	hypothetical protein F09A5.4
Locus_6522_Transcript_1/1_Conf_1.000	662	3	4.87E-22	NP_493601.2	49	108.612	205	101	FERM domain (protein4.1-ezrin-radixin-moesin) family member (frm-1)
Locus_6523_Transcript_1/1_Conf_1.000	256	5	6.97E-11	XP_002640260.1	65	70.4774	73	48	Hypothetical protein CBG12785
Locus_6524_Transcript_1/1_Conf_1.000	526	7	6.19E-35	NP_500156.2	65	150.599	160	104	XPC (Xeroderma Pigmentosum group C) DNA repair gene homolog family member (xpc-1)
Locus_6525_Transcript_1/1_Conf_1.000	451	20	7.24E-53	XP_002633385.1	91	209.92	148	136	Hypothetical protein CBG06141

Locus_6526_Transcript_1/1_Conf_1.000	544	20	3.56E-84	AAK31527.3	90	314.309	185	168	Neuronal symmetry protein 1, partially confirmed by transcript evidence
Locus_6527_Transcript_1/1_Conf_1.000	419	0							
Locus_6528_Transcript_1/1_Conf_1.000	383	20	4.41E-34	EFO26258.1	74	147.517	127	95	hypothetical protein LOAG_02227
Locus_6529_Transcript_1/1_Conf_1.000	323	20	1.10E-32	XP_002639452.1	79	142.895	99	79	Hypothetical protein CBG04047
Locus_653_Transcript_1/1_Conf_1.000	1105	20	5.98E-133	NP_491004.1	84	478.404	335	283	Fructose-1,6-BiPhosphatase family member (fbp-1)
Locus_6530_Transcript_1/3_Conf_0.714	710	20	6.85E-68	XP_002639600.1	79	261.151	207	165	C. briggsae CBR-ATP-3 protein
Locus_6530_Transcript_2/3_Conf_0.714	710	20	1.53E-67	XP_002639600.1	79	259.996	207	165	C. briggsae CBR-ATP-3 protein

Locus_6530_Transcript_3/3_Conf_0.714	710	20	1.53E-67	XP_002639600.1	79	259.996	207	165	C. briggsae CBR-ATP-3 protein
Locus_6531_Transcript_1/1_Conf_1.000	194	20	6.03E-31	XP_002832350.1	100	137.117	64	64	PREDICTED: LOW QUALITY PROTEIN: filamin-A-like
Locus_6532_Transcript_1/1_Conf_1.000	134	0							
Locus_6533_Transcript_1/1_Conf_1.000	749	0							
Locus_6534_Transcript_1/1_Conf_1.000	296	0							
Locus_6535_Transcript_1/1_Conf_1.000	151	9	1.90E-08	CAB60377.4	74	62.3882	39	29	C. elegans protein Y46G5A.29, partially confirmed by transcript evidence
Locus_6536_Transcript_1/1_Conf_1.000	1121	20	1.70E-167	XP_002643348.1	89	593.193	371	331	Hypothetical protein CBG15945
Locus_6537_Transcript_1/1_Conf_1.000	312	20	1.27E-36	XP_002634847.1	75	155.992	116	88	Hypothetical protein CBG13964

Locus_6538_Transcript_1/1_Conf_1.000	721	11	1.51E-17	NP_492859.1	50	93.9745	131	66	hypothetical protein Y52B11A.8
Locus_6539_Transcript_1/1_Conf_1.000	473	4	6.36E-41	NP_499683.1	92	170.244	147	136	hypothetical protein Y37D8A.16
Locus_654_Transcript_1/1_Conf_1.000	605	20	1.49E-45	NP_001021553.1	79	186.422	149	119	DeoxyUTPase family member (dut-1)
Locus_6540_Transcript_1/1_Conf_1.000	539	6	8.30E-22	XP_002636434.1	67	107.071	105	71	Hypothetical protein CBG23095
Locus_6541_Transcript_1/1_Conf_1.000	539	20	4.81E-62	NP_492812.2	92	240.736	138	127	hypothetical protein B0205.6
Locus_6542_Transcript_1/2_Conf_1.000	940	6	3.82E-51	XP_002639860.1	66	146.362	150	100	Hypothetical protein CBG12214
Locus_6542_Transcript_2/2_Conf_1.000	936	6	1.33E-55	XP_002639860.1	60	221.09	291	175	Hypothetical protein CBG12214
Locus_6543_Transcript_1/1_Conf_1.000	504	20	1.10E-11	Q7ZWS2.2	57	73.1738	122	70	Cytosolic 5'-nucleotidase III-like protein A
Locus_6544_Transcript_1/1_Conf_1.000	707	20	2.92E-103	XP_002643185.1	92	378.637	212	197	Hypothetical protein CBG24154
Locus_6545_Transcript_1/1_Conf_1.000	685	20	2.19E-84	NP_509394.1	83	315.849	206	171	hypothetical protein M60.7
Locus_6546_Transcript_1/1_Conf_1.000	651	5	1.02E-48	AAL09380.1	85	197.208	119	102	AF305962_1putative protein hc43.4

Locus_6547_Transcript_1/5_Conf_0.571	960	18	3.67E-08	XP_002738326.1	41	63.5438	142	59	PREDICTED: neurogenic locus notch homolog protein 2-like
Locus_6547_Transcript_2/5_Conf_0.214	939	20	4.98E-10	EFO20860.1	43	69.707	186	80	hypothetical protein LOAG_07630
Locus_6547_Transcript_3/5_Conf_0.714	1703	20	5.04E-21	NP_001021459.2	36	107.457	481	174	hypothetical protein F36H2.3
Locus_6547_Transcript_4/5_Conf_0.714	1881	20	8.24E-20	EFO20860.1	39	103.605	477	187	hypothetical protein LOAG_07630
Locus_6547_Transcript_5/5_Conf_0.714	1860	20	8.12E-20	NP_001021459.2	36	103.605	481	174	hypothetical protein F36H2.3
Locus_6548_Transcript_1/1_Conf_1.000	541	20	4.56E-84	XP_002636692.1	91	313.923	180	164	Hypothetical protein CBG23406
Locus_6549_Transcript_1/1_Conf_1.000	727	20	8.53E-85	XP_001894578.1	82	317.39	227	188	RuvB-like 1

Locus_655_Transcript_1/1_Conf_1.000	891	20	3.47E-119	XP_001140124.1	99	432.18	246	244	PREDICTED: similar to Ferritin heavy chain (Ferritin H subunit) (Proliferation-inducing gene 15 protein)
Locus_6550_Transcript_1/1_Conf_1.000	679	0							
Locus_6551_Transcript_1/1_Conf_1.000	611	20	1.49E-32	NP_497850.2	65	143.28	178	116	hypothetical protein F43C1.3
Locus_6552_Transcript_1/1_Conf_1.000	266	20	2.88E-33	NP_510447.1	87	144.821	87	76	hypothetical protein C05G5.1
Locus_6553_Transcript_1/1_Conf_1.000	346	20	5.14E-14	XP_002639864.1	75	80.8777	69	52	C. briggsae CBR-AHA-1 protein
Locus_6554_Transcript_1/1_Conf_1.000	244	20	1.33E-14	XP_002638796.1	69	82.8037	82	57	Hypothetical protein CBG05151
Locus_6555_Transcript_1/1_Conf_1.000	470	0							

Locus_6556_Transcript_1/1_Conf_1.000	202	4	4.45E-10	NP_492694.1	88	67.781	44	39	CaSeiN Kinase family member (csnk-1)
Locus_6557_Transcript_1/1_Conf_1.000	846	20	1.90E-47	NP_493357.2	76	193.741	208	160	hypothetical protein C01A2.4
Locus_6558_Transcript_1/1_Conf_1.000	374	0							
Locus_6559_Transcript_1/1_Conf_1.000	478	20	2.82E-49	NP_501503.1	75	197.978	159	120	hypothetical protein F21D5.5
Locus_656_Transcript_1/1_Conf_1.000	1621	20	0	NP_498646.1	96	772.696	410	396	Conserved Germline Helicase family member (cgh-1)
Locus_6560_Transcript_1/1_Conf_1.000	1823	20	4.52E-128	EFO24175.1	61	456.833	591	361	hypothetical protein LOAG_04314

Locus_6561_Transcript_1/1_Conf_1.000	423	20	1.99E-34	NP_498632.1	79	148.673	102	81	hypothetical protein T20B12.7
Locus_6562_Transcript_1/1_Conf_1.000	421	0							
Locus_6563_Transcript_1/2_Conf_1.000	1527	20	1.10E-56	NP_498099.1	58	225.713	332	195	Caffeine Induced Death (S. pombe Cid) homolog family member (cid-1)
Locus_6563_Transcript_2/2_Conf_1.000	1637	20	1.20E-56	NP_498099.1	58	225.713	332	195	Caffeine Induced Death (S. pombe Cid) homolog family member (cid-1)
Locus_6564_Transcript_1/1_Conf_1.000	1848	20	2.36E-104	EFO19265.1	60	384.415	512	311	hypothetical protein LOAG_09228
Locus_6565_Transcript_1/1_Conf_1.000	1113	20	9.21E-73	NP_510385.1	72	278.485	240	174	hypothetical protein C11H1.3
Locus_6566_Transcript_1/1_Conf_1.000	466	2	2.00E-26	XP_002637429.1	58	122.094	158	92	Hypothetical protein CBG19140
Locus_6567_Transcript_1/1_Conf_1.000	890	20	2.12E-76	XP_001902331.1	85	290.041	196	168	RNA polymerase Rpb7, N-terminal domain containing protein
Locus_6568_Transcript_1/1_Conf_1.000	1331	20	2.96E-140	NP_871868.1	74	503.056	442	331	hypothetical protein F36A2.9

Locus_6569_Transcript_1/1_Conf_1.000	1033	20	9.48E-154	XP_002632369.1	89	547.354	344	308	C. briggsae CBR-PMP-4 protein
Locus_657_Transcript_1/1_Conf_1.000	257	2	4.65E-23	NP_500609.1	86	110.923	80	69	hypothetical protein F29B9.11
Locus_6570_Transcript_1/1_Conf_1.000	573	20	4.68E-19	XP_002644813.1	65	98.2117	144	94	Hypothetical protein CBG14831
Locus_6571_Transcript_1/1_Conf_1.000	376	0							
Locus_6572_Transcript_1/1_Conf_1.000	1185	0							
Locus_6573_Transcript_1/1_Conf_1.000	354	20	5.39E-40	XP_002632111.1	83	167.162	120	100	Hypothetical protein CBG06965
Locus_6574_Transcript_1/1_Conf_1.000	300	0							
Locus_6575_Transcript_1/1_Conf_1.000	279	20	6.95E-40	1TW9	93	166.777	93	87	Glutathione Transferase-2
Locus_6576_Transcript_1/1_Conf_1.000	480	20	1.14E-42	NP_001022050.1	74	176.022	158	117	hypothetical protein D1069.3
Locus_6577_Transcript_1/1_Conf_1.000	268	0							
Locus_6578_Transcript_1/1_Conf_1.000	949	20	1.21E-104	XP_002642649.1	79	384.03	296	235	Hypothetical protein CBG00031
Locus_6579_Transcript_1/1_Conf_1.000	873	20	1.00E-46	XP_001895786.1	60	191.43	289	174	Fringe-like family protein
Locus_658_Transcript_1/1_Conf_1.000	1111	20	1.51E-67	XP_002636702.1	71	261.151	251	179	C. briggsae CBR-RAD-50 protein
Locus_6580_Transcript_1/1_Conf_1.000	250	2	3.24E-13	XP_002647590.1	66	78.1814	72	48	Hypothetical protein CBG06678
Locus_6581_Transcript_1/1_Conf_1.000	328	0							

Locus_6582_Transcript_1/1_Conf_1.000	362	20	8.23E-49	XP_002636649.1	87	196.438	122	107	Hypothetical protein CBG23360
Locus_6583_Transcript_1/1_Conf_1.000	2337	0							
Locus_6584_Transcript_1/1_Conf_1.000	432	0							
Locus_6585_Transcript_1/1_Conf_1.000	219	20	2.10E-23	XP_002825864.1	100	112.079	54	54	PREDICTED: isocitrate dehydrogenase
Locus_6586_Transcript_1/1_Conf_1.000	2393	20	5.33E-99	XP_001891601.1	53	367.081	745	397	Centromere/kinetochore Zw10 family protein
Locus_6587_Transcript_1/1_Conf_1.000	554	0							
Locus_6588_Transcript_1/1_Conf_1.000	678	20	1.60E-63	NP_491980.1	69	246.514	225	156	hypothetical protein T10B11.6
Locus_6589_Transcript_1/1_Conf_1.000	667	2	2.74E-20	NP_492020.1	100	102.834	43	43	hypothetical protein K10D3.4
Locus_659_Transcript_1/1_Conf_1.000	637	5	2.02E-30	XP_002641414.1	84	136.346	79	67	Hypothetical protein CBG13281
Locus_6590_Transcript_1/2_Conf_1.000	1106	20	5.77E-144	NP_000993.1	100	514.998	317	317	60S acidic ribosomal protein P0
Locus_6590_Transcript_2/2_Conf_1.000	920	20	2.91E-108	XP_862838.1	100	395.971	255	255	PREDICTED: similar to acidic ribosomal phosphoprotein P0 isoform 3
Locus_6591_Transcript_1/1_Conf_1.000	294	0							

Locus_6592_Transcript_1/1_Conf_1.000	652	20	9.68E-124	NP_492694.1	99	446.432	217	215	CaSeiN Kinase family member (csnk-1)
Locus_6593_Transcript_1/1_Conf_1.000	234	0							
Locus_6594_Transcript_1/1_Conf_1.000	418	20	3.09E-51	NP_492738.1	82	204.527	138	114	hypothetical protein Y106G6H.14
Locus_6595_Transcript_1/1_Conf_1.000	171	0							
Locus_6596_Transcript_1/1_Conf_1.000	668	0							
Locus_6597_Transcript_1/1_Conf_1.000	466	6	3.32E-05	NP_001075187.1	56	51.6026	81	46	family with sequence similarity 8, member A1
Locus_6598_Transcript_1/1_Conf_1.000	934	20	5.30E-97	NP_510177.1	83	358.607	271	227	hypothetical protein F17H10.1
Locus_6599_Transcript_1/1_Conf_1.000	879	20	1.26E-73	XP_002647283.1	72	280.796	277	201	Hypothetical protein CBG06323
Locus_66_Transcript_1/2_Conf_1.000	352	15	1.34E-14	NP_495283.2	68	82.8037	74	51	C-type LECtin family member (clec-88)
Locus_66_Transcript_2/2_Conf_1.000	364	15	1.32E-14	NP_495283.2	68	82.8037	74	51	C-type LECtin family member (clec-88)

Locus_660_Transcript_1/2_Conf_1.000	1725	20	3.67E-112	XP_002642056.1	84	410.223	280	237	C. briggsae CBR-RPS-0 protein
Locus_660_Transcript_2/2_Conf_1.000	1725	20	3.67E-112	XP_002642056.1	84	410.223	280	237	C. briggsae CBR-RPS-0 protein
Locus_6600_Transcript_1/1_Conf_1.000	353	0							
Locus_6601_Transcript_1/1_Conf_1.000	1064	20	4.98E-89	CBW38507.1	72	332.413	302	218	calcium-activated apyrase
Locus_6602_Transcript_1/2_Conf_1.000	1556	20	1.10E-120	XP_002631928.1	84	438.343	287	243	Hypothetical protein CBG07920
Locus_6602_Transcript_2/2_Conf_1.000	1550	20	1.10E-120	XP_002631928.1	84	438.343	287	243	Hypothetical protein CBG07920

Locus_6603_Transcript_1/1_Conf_1.000	1627	20	8.12E-122	XP_969056.1	65	442.195	480	315	PREDICTED: similar to ubiquitin specific peptidase 14
Locus_6604_Transcript_1/2_Conf_1.000	969	20	6.66E-82	EFO24805.1	84	308.531	220	185	ubiquitin conjugating enzyme 6
Locus_6604_Transcript_2/2_Conf_1.000	347	0							
Locus_6605_Transcript_1/1_Conf_1.000	994	20	7.40E-92	NP_492685.2	80	341.658	236	191	hypothetical protein C25A1.12
Locus_6606_Transcript_1/1_Conf_1.000	522	0							
Locus_6607_Transcript_1/1_Conf_1.000	382	20	1.24E-28	NP_499781.1	94	129.413	69	65	hypothetical protein T27E9.2
Locus_6608_Transcript_1/1_Conf_1.000	208	1	2.34E-11	NP_001021186.1	86	72.0182	36	31	PaXiLlin homolo family member (pxl-1)
Locus_6609_Transcript_1/2_Conf_1.000	829	20	1.57E-99	XP_002633512.1	77	366.696	279	215	C. briggsae CBR-DYCI-1 protein
Locus_6609_Transcript_2/2_Conf_1.000	829	20	1.57E-99	XP_002633512.1	77	366.696	279	215	C. briggsae CBR-DYCI-1 protein
Locus_661_Transcript_1/1_Conf_1.000	1277	20	4.35E-101	XP_002639326.1	92	372.859	211	195	C. briggsae CBR-RAB-11.1 protein
Locus_6610_Transcript_1/1_Conf_1.000	707	0							

Locus_6611_Transcript_1/1_Conf_1.000	269	20	5.39E-40	NP_001024394.1	98	167.162	89	88	GLutamate Transporter family member (glt-1)
Locus_6612_Transcript_1/1_Conf_1.000	339	2	4.69E-04	NP_498926.2	50	47.7506	132	67	hypothetical protein ZK370.4
Locus_6613_Transcript_1/3_Conf_0.714	836	0							
Locus_6613_Transcript_2/3_Conf_0.429	1441	20	7.82E-41	NP_493453.1	54	172.94	264	145	hypothetical protein F47G4.4
Locus_6613_Transcript_3/3_Conf_0.714	1589	20	8.89E-41	NP_493453.1	54	172.94	264	145	hypothetical protein F47G4.4
Locus_6614_Transcript_1/1_Conf_1.000	362	4	3.15E-24	XP_002644930.1	74	114.775	85	63	C. briggsae CBR-SMF-1 protein
Locus_6615_Transcript_1/1_Conf_1.000	694	20	9.51E-83	EFO18010.1	90	310.457	183	166	n-terminal acetyltransferase complex ard1 subunit
Locus_6616_Transcript_1/1_Conf_1.000	484	20	2.79E-52	XP_002638821.1	77	207.994	158	123	Hypothetical protein CBG22025
Locus_6617_Transcript_1/2_Conf_1.000	713	20	6.67E-79	XP_002639371.1	90	297.745	166	150	Hypothetical protein CBG03955
Locus_6617_Transcript_2/2_Conf_1.000	673	20	2.18E-81	XP_002639371.1	90	305.834	171	155	Hypothetical protein CBG03955
Locus_6618_Transcript_1/1_Conf_1.000	441	2	3.02E-06	NP_509418.2	61	55.0694	94	58	hypothetical protein F40B5.2
Locus_6619_Transcript_1/1_Conf_1.000	829	20	1.59E-67	NP_001021638.1	68	260.381	264	180	hypothetical protein T23G11.6

Locus_662_Transcript_1/1_Conf_1.000	1142	20	1.67E-69	XP_002636320.1	85	267.7	168	144	Hypothetical protein CBG08613
Locus_6620_Transcript_1/1_Conf_1.000	822	20	1.59E-11	EFA07557.1	42	74.3294	252	106	serine protease P135
Locus_6621_Transcript_1/1_Conf_1.000	180	0							
Locus_6622_Transcript_1/1_Conf_1.000	1137	20	1.07E-132	NP_498118.1	82	477.633	330	273	Gro-1 OPeron gene family member (gop-2)
Locus_6623_Transcript_1/1_Conf_1.000	543	0							
Locus_6624_Transcript_1/1_Conf_1.000	240	20	7.74E-39	NP_116024.1	100	163.31	79	79	transmembrane protein 147
Locus_6625_Transcript_1/1_Conf_1.000	189	0							
Locus_6626_Transcript_1/1_Conf_1.000	405	20	1.84E-56	EFO26908.1	87	221.861	135	118	hypothetical protein LOAG_01583
Locus_6627_Transcript_1/1_Conf_1.000	340	10	1.36E-27	XP_002636230.1	70	125.946	112	79	Hypothetical protein CBG12154
Locus_6628_Transcript_1/2_Conf_1.000	1493	20	0	XP_002632895.1	84	727.628	489	415	Hypothetical protein CBG15103
Locus_6628_Transcript_2/2_Conf_1.000	457	20	1.36E-43	XP_001893128.1	78	179.104	122	96	Aminopeptidase P, N-terminal domain containing protein
Locus_6629_Transcript_1/1_Conf_1.000	177	1	1.08E-08	AAD51334.1	76	63.1586	39	30	Kunitz type serine protease inhibitor

Locus_663_Transcript_1/2_Conf_1.000	976	20	3.58E-67	EFO22193.1	100	259.61	126	126	ADP-ribosylation factor 1
Locus_663_Transcript_2/2_Conf_1.000	976	20	3.59E-67	EFO22193.1	100	259.61	126	126	ADP-ribosylation factor 1
Locus_6630_Transcript_1/1_Conf_1.000	1004	3	1.90E-10	ACE00317.1	48	71.2478	178	87	hypothetical protein
Locus_6631_Transcript_1/2_Conf_1.000	1076	20	2.43E-99	XP_002633457.1	71	366.696	326	234	Hypothetical protein CBG06225

Locus_6631_Transcript_2/2_Conf_1.000	1375	20	2.04E-99	XP_002633457.1	69	367.466	343	239	Hypothetical protein CBG06225
Locus_6632_Transcript_1/1_Conf_1.000	687	20	6.47E-76	NP_505219.1	95	287.73	216	206	hypothetical protein F41E6.9
Locus_6633_Transcript_1/1_Conf_1.000	602	0							
Locus_6634_Transcript_1/1_Conf_1.000	571	20	7.58E-30	XP_002641347.1	72	134.035	101	73	C. briggsae CBR-PEN-2 protein
Locus_6635_Transcript_1/1_Conf_1.000	412	20	2.56E-34	NP_498593.1	68	148.288	140	96	hypothetical protein R151.10
Locus_6636_Transcript_1/1_Conf_1.000	1642	20	8.13E-45	XP_001121003.1	58	186.422	278	162	PREDICTED: similar to Protein tyrosine phosphatase 69D CG10975-PB, isoform B
Locus_6637_Transcript_1/1_Conf_1.000	1338	0							
Locus_6638_Transcript_1/1_Conf_1.000	238	0							
Locus_6639_Transcript_1/1_Conf_1.000	165	0							
Locus_664_Transcript_1/1_Conf_1.000	177	20	9.43E-21	ACV20956.1	98	103.219	51	50	large subunit ribosomal protein 29
Locus_6640_Transcript_1/1_Conf_1.000	849	20	2.52E-23	EFO27046.1	60	113.62	168	101	hypothetical protein LOAG_01444

Locus_6641_Transcript_1/1_Conf_1.000	607	20	2.01E-98	NP_001040704.1	91	362.073	201	183	DNaJ domain (prokaryotic heat shock protein) family member (dnj-27)
Locus_6642_Transcript_1/1_Conf_1.000	845	20	1.98E-113	NP_499300.1	89	412.92	259	232	hypothetical protein M03C11.7
Locus_6643_Transcript_1/1_Conf_1.000	1045	20	8.12E-145	NP_492591.1	84	517.694	333	282	SUppressor of activated let-60 Ras family member (sur-6)
Locus_6644_Transcript_1/1_Conf_1.000	1099	20	4.48E-64	NP_492228.1	58	249.595	365	213	MAternally affected Uncoordination family member (mau-2)
Locus_6645_Transcript_1/1_Conf_1.000	200	3	1.49E-05	NP_741793.1	66	52.7582	54	36	hypothetical protein T23F2.2
Locus_6646_Transcript_1/1_Conf_1.000	635	20	8.03E-56	XP_002646099.1	86	220.705	176	152	C. briggsae CBR-NHX-8 protein
Locus_6647_Transcript_1/1_Conf_1.000	488	20	5.44E-32	NP_495687.1	81	140.584	110	90	APurinic/apyrimidinic endoNuclease family member (apn-1)
Locus_6648_Transcript_1/1_Conf_1.000	335	20	1.28E-25	XP_002641403.1	75	119.398	90	68	Hypothetical protein CBG13266
Locus_6649_Transcript_1/1_Conf_1.000	371	0							
Locus_665_Transcript_1/1_Conf_1.000	1102	20	4.66E-61	CAA60046.1	65	239.58	311	205	cytoplasmic intermediate filament protein
Locus_6650_Transcript_1/1_Conf_1.000	426	7	1.86E-24	XP_002646458.1	61	115.546	141	87	Hypothetical protein CBG18870

Locus_6651_Transcript_1/1_Conf_1.000	1537	3	2.34E-30	NP_491674.2	45	138.272	520	235	hypothetical protein F56H1.5
Locus_6652_Transcript_1/4_Conf_0.500	766	6	8.63E-46	NP_741957.1	77	187.963	205	159	hypothetical protein T23E7.2
Locus_6652_Transcript_2/4_Conf_0.500	905	7	3.28E-56	XP_002643698.1	72	223.016	227	164	Hypothetical protein CBG01887
Locus_6652_Transcript_3/4_Conf_0.500	1273	7	1.66E-76	NP_741957.1	82	291.197	295	244	hypothetical protein T23E7.2
Locus_6652_Transcript_4/4_Conf_0.500	751	6	1.17E-47	NP_741957.1	79	194.126	200	159	hypothetical protein T23E7.2
Locus_6653_Transcript_1/1_Conf_1.000	391	5	1.96E-26	NP_492018.1	69	122.094	123	85	UNCoordinated family member (unc-14)
Locus_6654_Transcript_1/1_Conf_1.000	578	20	7.95E-91	XP_528436.2	100	336.65	168	168	PREDICTED: similar to 60S ribosomal protein L12
Locus_6655_Transcript_1/1_Conf_1.000	439	0							
Locus_6656_Transcript_1/1_Conf_1.000	850	20	1.06E-21	EFO24421.1	70	108.227	78	55	hypothetical protein LOAG_04066
Locus_6657_Transcript_1/1_Conf_1.000	1175	20	1.63E-75	XP_002643218.1	61	287.73	342	210	Hypothetical protein CBG08083
Locus_6658_Transcript_1/1_Conf_1.000	349	0							
Locus_6659_Transcript_1/1_Conf_1.000	313	20	4.22E-24	ACN10033.1	87	114.39	73	64	60S ribosomal protein L38
Locus_666_Transcript_1/1_Conf_1.000	1937	20	0	XP_002632236.1	86	875.544	564	489	C. briggsae CBR-ALH-6 protein
Locus_6660_Transcript_1/1_Conf_1.000	1197	20	3.11E-146	XP_002635317.1	80	522.702	353	285	C. briggsae CBR-TAG-196 protein

Locus_6661_Transcript_1/1_Conf_1.000	147	20	7.47E-13	EFO26471.1	81	77.0258	49	40	hypothetical protein LOAG_02007
Locus_6662_Transcript_1/1_Conf_1.000	527	20	5.80E-25	NP_508584.3	61	117.472	139	85	hypothetical protein ZK563.5
Locus_6663_Transcript_1/1_Conf_1.000	174	0							
Locus_6664_Transcript_1/1_Conf_1.000	516	20	4.86E-66	XP_002646370.1	87	253.832	170	149	Hypothetical protein CBG12088
Locus_6665_Transcript_1/1_Conf_1.000	447	7	6.02E-15	XP_002633498.1	65	83.9593	132	86	Hypothetical protein CBG06270
Locus_6666_Transcript_1/2_Conf_1.000	2057	20	5.13E-180	NP_504828.1	72	635.95	689	497	hypothetical protein C13F10.4
Locus_6666_Transcript_2/2_Conf_1.000	3029	20	0	NP_504828.1	75	1050.43	1014	762	hypothetical protein C13F10.4
Locus_6667_Transcript_1/1_Conf_1.000	954	20	1.06E-100	XP_002642966.1	92	370.933	227	209	Hypothetical protein CBG15250
Locus_6668_Transcript_1/1_Conf_1.000	207	0							
Locus_6669_Transcript_1/1_Conf_1.000	470	20	4.27E-45	CAI19674.1	100	184.111	119	119	S100 calcium binding protein A1
Locus_667_Transcript_1/1_Conf_1.000	789	20	4.00E-41	CAR63644.1	90	172.555	104	94	hypothetical protein
Locus_6670_Transcript_1/1_Conf_1.000	273	0							
Locus_6671_Transcript_1/3_Conf_0.286	539	20	5.20E-24	XP_002633511.1	58	114.39	165	96	Hypothetical protein CBG05373
Locus_6671_Transcript_2/3_Conf_0.571	995	20	3.47E-57	NP_501039.1	59	226.483	330	197	hypothetical protein C17H12.2
Locus_6671_Transcript_3/3_Conf_0.571	663	20	1.17E-31	XP_002633511.1	58	140.584	211	123	Hypothetical protein CBG05373

Locus_6672_Transcript_1/1_Conf_1.000	1136	20	3.44E-06	NP_001158439.1	62	57.3806	67	42	forkhead box N1
Locus_6673_Transcript_1/1_Conf_1.000	671	20	1.26E-81	NP_509937.1	89	306.605	179	161	hypothetical protein F52D10.2
Locus_6674_Transcript_1/1_Conf_1.000	584	0							
Locus_6675_Transcript_1/1_Conf_1.000	836	2	3.18E-23	NP_491096.1	56	113.235	146	82	Zinc finger Transcription Factor family member (ztf-23)
Locus_6676_Transcript_1/1_Conf_1.000	275	0							
Locus_6677_Transcript_1/1_Conf_1.000	1125	20	4.72E-16	XP_002647607.1	48	90.1225	293	141	C. briggsae CBR-FRM-10 protein
Locus_6678_Transcript_1/1_Conf_1.000	273	20	3.73E-17	XP_002639283.1	65	91.2781	92	60	C. briggsae CBR-NAS-5 protein
Locus_6679_Transcript_1/2_Conf_1.000	357	20	1.73E-38	XP_002646110.1	94	162.155	86	81	Hypothetical protein CBG07988
Locus_6679_Transcript_2/2_Conf_1.000	357	20	2.25E-38	XP_002646110.1	93	161.77	86	80	Hypothetical protein CBG07988
Locus_668_Transcript_1/3_Conf_0.667	1018	6	7.37E-18	XP_002634397.1	51	95.9005	186	95	Hypothetical protein CBG04400
Locus_668_Transcript_2/3_Conf_0.667	1060	6	7.80E-18	XP_002634397.1	51	95.9005	186	95	Hypothetical protein CBG04400
Locus_668_Transcript_3/3_Conf_0.667	1066	6	7.88E-18	XP_002634397.1	51	95.9005	186	95	Hypothetical protein CBG04400

Locus_6680_Transcript_1/1_Conf_1.000	328	20	4.12E-40	NP_490960.1	92	167.548	93	86	hypothetical protein Y39G10AR.8
Locus_6681_Transcript_1/1_Conf_1.000	1135	13	5.82E-30	XP_002639466.1	48	136.346	377	184	C. briggsae CBR-MTK-1 protein
Locus_6682_Transcript_1/1_Conf_1.000	188	0							
Locus_6683_Transcript_1/1_Conf_1.000	664	2	3.10E-08	XP_001897181.1	51	62.7734	167	86	hypothetical protein Bm1_28665
Locus_6684_Transcript_1/1_Conf_1.000	208	0							
Locus_6685_Transcript_1/1_Conf_1.000	172	20	4.55E-23	XP_002752963.1	100	110.923	56	56	PREDICTED: endoplasmin-like

Locus_6686_Transcript_1/1_Conf_1.000	2283	20	0	XP_002640044.1	83	806.209	570	474	C. briggsae CBR-GON-2 protein
Locus_6687_Transcript_1/1_Conf_1.000	452	20	2.26E-38	ACI49192.1	76	161.77	123	94	hypothetical protein Csp3_JD03.001
Locus_6688_Transcript_1/1_Conf_1.000	550	20	2.16E-92	XP_002636622.1	97	341.658	181	177	C. briggsae CBR-SMA-1 protein
Locus_6689_Transcript_1/1_Conf_1.000	732	20	1.52E-113	NP_492097.1	93	412.92	231	217	hypothetical protein ZK524.4
Locus_669_Transcript_1/1_Conf_1.000	958	20	6.03E-120	XP_002637229.1	80	434.876	318	255	C. briggsae CBR-TAG-59 protein
Locus_6690_Transcript_1/1_Conf_1.000	646	3	9.05E-42	NP_495433.1	65	174.096	172	112	hypothetical protein C15F1.2
Locus_6691_Transcript_1/1_Conf_1.000	776	20	3.78E-105	NP_001122569.1	84	385.185	258	219	hypothetical protein ZK849.2
Locus_6692_Transcript_1/1_Conf_1.000	886	12	1.06E-35	ACI49247.1	62	154.836	216	134	hypothetical protein Csp3_JD06.013
Locus_6693_Transcript_1/1_Conf_1.000	256	0							
Locus_6694_Transcript_1/1_Conf_1.000	1234	0							
Locus_6695_Transcript_1/1_Conf_1.000	610	20	1.12E-104	XP_512797.2	100	382.874	192	192	PREDICTED: similar to ribosomal protein L18
Locus_6696_Transcript_1/3_Conf_0.500	346	0							
Locus_6696_Transcript_2/3_Conf_0.500	387	0							
Locus_6696_Transcript_3/3_Conf_0.500	353	0							
Locus_6697_Transcript_1/1_Conf_1.000	186	2	1.72E-09	NP_495901.1	71	65.855	56	40	hypothetical protein T21B10.3

Locus_6698_Transcript_1/1_Conf_1.000	617	20	1.33E-68	NP_502420.2	81	263.077	205	167	hypothetical protein C26H9A.2
Locus_6699_Transcript_1/1_Conf_1.000	591	2	1.09E-05	NP_500390.1	53	53.9138	104	56	hypothetical protein CC8.1
Locus_67_Transcript_1/3_Conf_0.667	963	20	7.15E-28	NP_741576.1	66	129.028	169	112	AuTophaGy (yeast Atg homolog) family member (atg-18)
Locus_67_Transcript_2/3_Conf_0.667	972	20	7.27E-28	NP_741576.1	66	129.028	169	112	AuTophaGy (yeast Atg homolog) family member (atg-18)
Locus_67_Transcript_3/3_Conf_0.667	972	20	7.27E-28	NP_741576.1	66	129.028	169	112	AuTophaGy (yeast Atg homolog) family member (atg-18)
Locus_670_Transcript_1/1_Conf_1.000	2223	5	2.82E-30	XP_002643154.1	47	138.658	430	205	Hypothetical protein CBG15334
Locus_6700_Transcript_1/2_Conf_1.000	815	7	2.02E-27	XP_002631928.1	86	127.102	82	71	Hypothetical protein CBG07920
Locus_6700_Transcript_2/2_Conf_1.000	340	14	2.16E-33	XP_002631928.1	85	145.206	95	81	Hypothetical protein CBG07920
Locus_6701_Transcript_1/2_Conf_1.000	940	20	6.03E-40	NP_497731.1	53	169.088	292	155	Nuclear Hormone Receptor family member (nhr-6)
Locus_6701_Transcript_2/2_Conf_1.000	832	20	1.32E-45	NP_497731.1	52	187.578	282	147	Nuclear Hormone Receptor family member (nhr-6)
Locus_6702_Transcript_1/1_Conf_1.000	266	1	8.96E-27	ABM85051.1	100	123.25	55	55	parathymosin
Locus_6703_Transcript_1/1_Conf_1.000	984	0							
Locus_6704_Transcript_1/1_Conf_1.000	239	1	1.64E-04	AAD13339.1	56	49.2914	55	31	ancylostoma-secreted protein 1 precursor
Locus_6705_Transcript_1/1_Conf_1.000	634	20	1.97E-62	NP_510787.2	81	242.662	160	130	hypothetical protein T08G2.2

Locus_6706_Transcript_1/1_Conf_1.000	616	0							
Locus_6707_Transcript_1/1_Conf_1.000	320	2	1.27E-04	NP_495712.1	50	49.6766	106	53	abnormal EMBroygenesis family member (emb-27)
Locus_6708_Transcript_1/1_Conf_1.000	198	2	2.22E-09	NP_001040757.1	75	65.4698	69	52	hypothetical protein EEED8.10
Locus_6709_Transcript_1/1_Conf_1.000	464	20	2.79E-52	XP_002639502.1	75	207.994	153	115	Hypothetical protein CBG04103
Locus_671_Transcript_1/1_Conf_1.000	154	0							
Locus_6710_Transcript_1/1_Conf_1.000	1348	0							
Locus_6711_Transcript_1/1_Conf_1.000	675	20	5.42E-80	NP_502775.2	86	301.212	184	160	hypothetical protein Y57G11C.31
Locus_6712_Transcript_1/2_Conf_0.500	940	20	3.14E-105	XP_002641673.1	85	385.956	264	227	C. briggsae CBR-ECH-6 protein
Locus_6712_Transcript_2/2_Conf_0.500	940	20	4.84E-106	XP_002641673.1	85	388.652	264	227	C. briggsae CBR-ECH-6 protein
Locus_6713_Transcript_1/1_Conf_1.000	134	0							
Locus_6714_Transcript_1/1_Conf_1.000	379	0							
Locus_6715_Transcript_1/1_Conf_1.000	978	20	6.80E-66	XP_002633541.1	77	255.373	212	165	C. briggsae CBR-DNJ-11 protein
Locus_6716_Transcript_1/1_Conf_1.000	1706	20	6.32E-165	XP_002630808.1	77	585.489	485	375	Hypothetical protein CBG02508

Locus_6717_Transcript_1/1_Conf_1.000	883	20	7.35E-114	XP_002634965.1	88	414.461	254	224	Hypothetical protein CBG13501
Locus_6718_Transcript_1/1_Conf_1.000	426	20	1.73E-46	XP_002646732.1	79	188.734	143	114	Hypothetical protein CBG13117
Locus_6719_Transcript_1/1_Conf_1.000	224	20	1.11E-08	XP_001892755.1	75	63.1586	52	39	TBC domain containing protein
Locus_672_Transcript_1/4_Conf_0.222	316	20	6.93E-27		76	123.635	103	79	hypothetical protein C25H3.4 - Caenorhabditis elegans
Locus_672_Transcript_2/4_Conf_0.667	1624	20	1.38E-113	AAK31455.4	62	414.846	514	321	Hypothetical protein C25H3.4
Locus_672_Transcript_3/4_Conf_0.667	1624	20	2.36E-113	AAK31455.4	62	414.075	514	321	Hypothetical protein C25H3.4
Locus_672_Transcript_4/4_Conf_0.667	1624	20	1.06E-113	AAK31455.4	62	415.231	514	321	Hypothetical protein C25H3.4
Locus_6720_Transcript_1/1_Conf_1.000	637	0							
Locus_6721_Transcript_1/1_Conf_1.000	818	20	2.37E-84	XP_002646101.1	77	316.235	228	177	Hypothetical protein CBG07973
Locus_6722_Transcript_1/1_Conf_1.000	658	20	4.88E-30	XP_001899346.1	57	135.191	185	106	Hsp20/alpha crystallin family protein
Locus_6723_Transcript_1/2_Conf_1.000	1264	20	3.80E-57	NP_497575.2	63	226.868	312	199	Homeobox family member (ceh-44)

Locus_6723_Transcript_2/2_Conf_1.000	534	20	3.20E-18	NP_497575.2	65	95.1301	143	93	Homeobox family member (ceh-44)
Locus_6724_Transcript_1/1_Conf_1.000	1324	20	7.24E-30	NP_741539.2	49	136.346	428	213	hypothetical protein C18C4.5
Locus_6725_Transcript_1/1_Conf_1.000	630	20	6.71E-55	XP_002632404.1	72	217.624	211	153	Hypothetical protein CBG00428
Locus_6726_Transcript_1/1_Conf_1.000	466	20	1.85E-72	XP_002633699.1	92	275.018	155	143	Hypothetical protein CBG03382
Locus_6727_Transcript_1/1_Conf_1.000	1516	20	6.93E-11	XP_002618430.1	51	73.559	147	75	hypothetical protein CLUG_01889
Locus_6728_Transcript_1/1_Conf_1.000	400	20	1.99E-50	XP_002634510.1	82	201.83	132	109	Hypothetical protein CBG08301
Locus_6729_Transcript_1/1_Conf_1.000	204	20	1.24E-28	NP_741697.2	88	129.413	68	60	Protein PHosphatase family member (pph-5)
Locus_673_Transcript_1/2_Conf_1.000	487	2	1.59E-07	CAR63546.1	48	59.3066	123	60	hypothetical protein
Locus_673_Transcript_2/2_Conf_1.000	343	2	1.23E-07	CAR63546.1	52	59.6918	96	50	hypothetical protein

Locus_6730_Transcript_1/1_Conf_1.000	389	20	2.56E-34	XP_002631067.1	74	148.288	118	88	C. briggsae CBR-TRR-1 protein
Locus_6731_Transcript_1/1_Conf_1.000	210	5	3.16E-08	XP_002637665.1	75	61.6178	45	34	C. briggsae CBR-APT-10 protein
Locus_6732_Transcript_1/1_Conf_1.000	480	1	1.91E-05	EFO19799.1	54	52.373	74	40	hypothetical protein LOAG_08693
Locus_6733_Transcript_1/1_Conf_1.000	162	0							
Locus_6734_Transcript_1/2_Conf_1.000	1088	20	2.59E-48	EFO15646.1	81	197.208	140	114	hypothetical protein LOAG_12863
Locus_6734_Transcript_2/2_Conf_1.000	887	9	1.59E-15	XP_002637541.1	83	87.8113	61	51	C. briggsae CBR-HUM-2 protein
Locus_6735_Transcript_1/1_Conf_1.000	704	20	9.03E-20	XP_001898015.1	56	101.293	148	84	FtsJ-like methyltransferase family protein
Locus_6736_Transcript_1/1_Conf_1.000	2089	20	0	NP_493657.2	83	712.22	504	423	hypothetical protein C50D2.7
Locus_6737_Transcript_1/1_Conf_1.000	535	0							
Locus_6738_Transcript_1/1_Conf_1.000	524	20	1.26E-40	Q09600.2	67	169.474	174	118	Vacuolar protein sorting-associated protein 11 homolog
Locus_6739_Transcript_1/1_Conf_1.000	139	0							
Locus_674_Transcript_1/1_Conf_1.000	1380	20	3.02E-143	EFO23198.1	78	513.072	420	331	dolichyl-di-phosphooligosaccharide-protein glycotransferase
Locus_6740_Transcript_1/1_Conf_1.000	646	20	1.65E-35	XP_002633290.1	63	153.295	184	116	Hypothetical protein CBG06019

Locus_6741_Transcript_1/1_Conf_1.000	1074	20	7.95E-34	NP_502425.2	54	149.058	320	173	hypothetical protein C27D8.4
Locus_6742_Transcript_1/1_Conf_1.000	530	3	1.02E-08	NP_490722.2	48	63.5438	179	87	hypothetical protein Y48G1A.1
Locus_6743_Transcript_1/2_Conf_1.000	1057	20	0	XP_002646949.1	97	640.573	350	341	C. briggsae CBR-APD-3 protein
Locus_6743_Transcript_2/2_Conf_1.000	1057	20	0	XP_002646949.1	97	640.573	350	341	C. briggsae CBR-APD-3 protein
Locus_6744_Transcript_1/2_Conf_1.000	381	20	9.89E-10	XP_002635041.1	53	66.6254	81	43	Hypothetical protein CBG13587
Locus_6744_Transcript_2/2_Conf_1.000	342	20	2.93E-09	XP_001896707.1	63	65.0846	65	41	Zinc knuckle family protein
Locus_6745_Transcript_1/1_Conf_1.000	658	5	2.01E-92	NP_001040851.1	85	342.428	217	185	UNCoordinated family member (unc-36)
Locus_6746_Transcript_1/1_Conf_1.000	133	2	6.37E-17	BAD92214.1	100	90.5077	44	44	ribosomal protein L4 variant
Locus_6747_Transcript_1/2_Conf_1.000	729	20	7.39E-36	NP_498217.2	55	154.836	254	141	abnormal embryonic PARtitioning of cytoplasm family member (par-3)
Locus_6747_Transcript_2/2_Conf_1.000	606	7	1.09E-19	NP_498217.2	48	100.523	212	102	abnormal embryonic PARtitioning of cytoplasm family member (par-3)
Locus_6748_Transcript_1/1_Conf_1.000	425	0							
Locus_6749_Transcript_1/1_Conf_1.000	594	0							
Locus_675_Transcript_1/1_Conf_1.000	1082	3	3.75E-15	XP_002631375.1	44	87.0409	327	144	Hypothetical protein CBG03217

Locus_6750_Transcript_1/1_Conf_1.000	325	20	3.27E-45	NP_508504.2	90	184.496	108	98	Non-muscle MYosin family member (nmy-1)
Locus_6751_Transcript_1/2_Conf_1.000	882	20	2.65E-63	NP_509962.1	76	246.514	218	166	Glutathione S-Transferase family member (gst-42)
Locus_6751_Transcript_2/2_Conf_1.000	880	20	2.63E-63	NP_509962.1	76	246.514	218	166	Glutathione S-Transferase family member (gst-42)
Locus_6752_Transcript_1/1_Conf_1.000	570	0							
Locus_6753_Transcript_1/1_Conf_1.000	1838	20	5.69E-151	XP_001898046.1	77	539.265	459	354	interferon-induced double-stranded RNA-activated protein kinase inhibitor
Locus_6754_Transcript_1/1_Conf_1.000	448	0							
Locus_6755_Transcript_1/1_Conf_1.000	417	4	7.45E-05	XP_002630769.1	47	50.447	108	51	Hypothetical protein CBG02464
Locus_6756_Transcript_1/1_Conf_1.000	500	0							
Locus_6757_Transcript_1/1_Conf_1.000	696	20	3.34E-43	NP_741586.1	61	179.104	220	136	SPAStin (human neurodegeneration-associated AAA ATPase) related family member (spas-1)
Locus_6758_Transcript_1/1_Conf_1.000	748	3	1.43E-21	NP_510840.2	51	107.457	229	118	hypothetical protein F31A3.5
Locus_6759_Transcript_1/1_Conf_1.000	488	20	6.86E-35	XP_001897214.1	76	150.214	111	85	Transcription initiation factor IIA, gamma subunit, helical domain containing protein
Locus_676_Transcript_1/2_Conf_1.000	4384	20	0	XP_002631075.1	69	478.789	493	345	Hypothetical protein CBG02847
Locus_676_Transcript_2/2_Conf_1.000	4380	20	0	XP_002631075.1	70	865.529	823	583	Hypothetical protein CBG02847
Locus_6760_Transcript_1/1_Conf_1.000	515	0							
Locus_6761_Transcript_1/1_Conf_1.000	311	20	1.84E-24	XP_001894880.1	89	115.546	75	67	hypothetical protein
Locus_6762_Transcript_1/1_Conf_1.000	323	0							
Locus_6763_Transcript_1/1_Conf_1.000	202	0							
Locus_6764_Transcript_1/1_Conf_1.000	438	20	9.03E-48	XP_002631150.1	79	192.971	136	108	Hypothetical protein CBG02934
Locus_6765_Transcript_1/1_Conf_1.000	390	20	5.90E-23	XP_001901686.1	68	110.538	124	85	Cohesin subunit SA-1

Locus_6766_Transcript_1/1_Conf_1.000	1070	20	1.18E-29	XP_002645186.1	49	135.191	361	180	Hypothetical protein CBG16916
Locus_6767_Transcript_1/1_Conf_1.000	714	20	3.61E-40	XP_001895119.1	57	169.088	239	137	eIF4-gamma/eIF5/eIF2-epsilon family protein
Locus_6768_Transcript_1/1_Conf_1.000	233	0							
Locus_6769_Transcript_1/1_Conf_1.000	391	0							
Locus_677_Transcript_1/3_Conf_0.667	721	20	4.30E-81	EFO21976.1	79	305.064	238	190	hypothetical protein LOAG_06510
Locus_677_Transcript_2/3_Conf_0.667	721	20	4.30E-81	EFO21976.1	79	305.064	238	190	hypothetical protein LOAG_06510
Locus_677_Transcript_3/3_Conf_0.667	721	20	4.30E-81	EFO21976.1	79	305.064	238	190	hypothetical protein LOAG_06510
Locus_6770_Transcript_1/1_Conf_1.000	142	0							
Locus_6771_Transcript_1/1_Conf_1.000	468	4	2.99E-14	NP_506247.1	52	81.6481	167	87	hypothetical protein R186.7
Locus_6772_Transcript_1/1_Conf_1.000	1308	20	3.04E-81	NP_498411.1	60	306.99	443	269	related to yeast Vacuolar Protein Sorting factor family member (vps-16)

Locus_6773_Transcript_1/1_Conf_1.000	1338	20	4.25E-78	XP_002639286.1	54	296.59	468	253	C. briggsae CBR-MOM-4 protein
Locus_6774_Transcript_1/1_Conf_1.000	577	20	3.85E-61	NP_496178.1	80	238.039	191	154	PUF (Pumilio/FBF) domain-containing family member (puf-12)
Locus_6775_Transcript_1/1_Conf_1.000	603	20	6.94E-43	AAP36640.1	100	177.563	96	96	Homo sapiens matrix Gla protein
Locus_6776_Transcript_1/1_Conf_1.000	663	20	1.09E-45	XP_002631042.1	93	187.193	106	99	C. briggsae CBR-MAX-2 protein
Locus_6777_Transcript_1/1_Conf_1.000	233	20	3.66E-12	EFN62114.1	84	74.7146	46	39	Metastasis-associated protein MTA1

Locus_6778_Transcript_1/1_Conf_1.000	756	20	8.30E-94	NP_495679.1	83	347.436	237	197	hypothetical protein C08B11.3
Locus_6779_Transcript_1/1_Conf_1.000	716	20	9.64E-110	XP_002645511.1	95	400.208	237	226	C. briggsae CBR-TAG-123 protein
Locus_678_Transcript_1/1_Conf_1.000	309	4	5.34E-24	XP_002633595.1	71	114.005	100	71	Hypothetical protein CBG05472
Locus_6780_Transcript_1/1_Conf_1.000	286	4	1.84E-11	NP_492341.1	61	72.4034	102	63	hypothetical protein F43G9.12
Locus_6781_Transcript_1/1_Conf_1.000	169	0							
Locus_6782_Transcript_1/1_Conf_1.000	655	20	1.58E-81	Q61QK6.2	83	306.22	218	182	Protein melted homolog
Locus_6783_Transcript_1/1_Conf_1.000	1713	20	6.64E-138	NP_504828.1	67	495.738	581	394	hypothetical protein C13F10.4
Locus_6784_Transcript_1/1_Conf_1.000	616	11	1.53E-32	XP_002630779.1	71	143.28	204	145	Hypothetical protein CBG02475
Locus_6785_Transcript_1/1_Conf_1.000	647	0							
Locus_6786_Transcript_1/1_Conf_1.000	2080	20	1.29E-162	NP_501320.2	68	578.17	635	436	eXPOrtin (nuclear export receptor) family member (xpo-3)
Locus_6787_Transcript_1/1_Conf_1.000	517	2	4.18E-09	NP_501033.1	49	64.6994	138	68	Suppressor with Morphological effect on Genitalia family member (smg-7)
Locus_6788_Transcript_1/1_Conf_1.000	273	20	1.24E-12	EFO26611.1	59	76.2554	93	55	hypothetical protein LOAG_01867
Locus_6789_Transcript_1/2_Conf_1.000	1787	20	2.88E-75	XP_001895294.1	59	287.73	360	213	Endonuclease/Exonuclease/phosphatase family protein
Locus_6789_Transcript_2/2_Conf_1.000	1616	20	2.53E-75	XP_001895294.1	59	287.73	360	213	Endonuclease/Exonuclease/phosphatase family protein
Locus_679_Transcript_1/1_Conf_1.000	929	0							
Locus_6790_Transcript_1/2_Conf_1.000	887	20	1.31E-102	NP_498052.1	90	377.096	237	215	hypothetical protein C27F2.5

Locus_6790_Transcript_2/2_Conf_1.000	887	20	1.31E-102	NP_498052.1	90	377.096	237	215	hypothetical protein C27F2.5
Locus_6791_Transcript_1/1_Conf_1.000	320	20	2.14E-36	EFO25190.1	94	155.221	106	100	hypothetical protein LOAG_03297
Locus_6792_Transcript_1/1_Conf_1.000	204	4	2.87E-17	XP_002641184.1	81	91.6633	66	54	Hypothetical protein CBG09045
Locus_6793_Transcript_1/1_Conf_1.000	403	4	9.24E-32	XP_002643061.1	79	139.813	93	74	Hypothetical protein CBG22978
Locus_6794_Transcript_1/1_Conf_1.000	329	0							
Locus_6795_Transcript_1/1_Conf_1.000	496	6	4.57E-07	EFO24754.1	52	57.7658	101	53	hypothetical protein LOAG_03725
Locus_6796_Transcript_1/1_Conf_1.000	2008	20	1.88E-86	NP_507625.2	54	325.094	600	326	hypothetical protein Y51A2D.7
Locus_6797_Transcript_1/1_Conf_1.000	646	2	9.12E-18	XP_002641661.1	53	94.3597	223	120	Hypothetical protein CBG09989
Locus_6798_Transcript_1/1_Conf_1.000	1487	20	1.84E-125	NP_506580.1	70	454.136	400	282	Temporarily Assigned Gene name family member (tag-114)
Locus_6799_Transcript_1/1_Conf_1.000	160	0							

Locus_68_Transcript_1/1_Conf_1.000	1070	20	3.68E-124	NP_495526.1	90	449.129	311	282	BRF (transcription factor) homolog family member (brf-1)
Locus_680_Transcript_1/1_Conf_1.000	995	0							
Locus_6800_Transcript_1/1_Conf_1.000	342	20	1.88E-40	ACX53263.1	83	168.703	115	96	glutathione S-transferase-3
Locus_6801_Transcript_1/1_Conf_1.000	229	0							
Locus_6802_Transcript_1/1_Conf_1.000	283	0							
Locus_6803_Transcript_1/1_Conf_1.000	975	20	1.53E-126	XP_002646072.1	89	456.833	277	247	C. briggsae CBR-PBS-2 protein
Locus_6804_Transcript_1/1_Conf_1.000	491	20	6.83E-35	CAZ65501.2	67	150.214	154	104	C. elegans protein F46C3.3c, partially confirmed by transcript evidence
Locus_6805_Transcript_1/1_Conf_1.000	551	20	2.89E-12	XP_002639902.1	52	75.485	117	61	Hypothetical protein CBG08226

Locus_6806_Transcript_1/1_Conf_1.000	763	20	9.13E-56	XP_002632596.1	62	221.09	254	159	Hypothetical protein CBG23720
Locus_6807_Transcript_1/1_Conf_1.000	858	20	2.10E-41	XP_002637083.1	65	173.711	277	181	Hypothetical protein CBG09582
Locus_6808_Transcript_1/1_Conf_1.000	143	4	2.17E-17	NP_509299.1	95	92.0485	47	45	hypothetical protein C53C9.2
Locus_6809_Transcript_1/1_Conf_1.000	2474	20	0	NP_494706.1	74	812.757	741	553	Temporarily Assigned Gene name family member (tag-218)
Locus_681_Transcript_1/1_Conf_1.000	1971	12	6.95E-102	XP_001902665.1	59	376.326	584	347	hypothetical protein Bm1_56035
Locus_6810_Transcript_1/1_Conf_1.000	330	0							
Locus_6811_Transcript_1/1_Conf_1.000	440	0							
Locus_6812_Transcript_1/1_Conf_1.000	423	0							
Locus_6813_Transcript_1/1_Conf_1.000	497	20	2.34E-19	XP_002647213.1	81	98.5969	69	56	Hypothetical protein CBG22395
Locus_6814_Transcript_1/1_Conf_1.000	848	20	1.20E-134	CAR63671.1	93	483.411	283	264	hypothetical protein
Locus_6815_Transcript_1/1_Conf_1.000	199	0							
Locus_6816_Transcript_1/2_Conf_1.000	1164	20	5.74E-73	EFO26307.1	58	279.256	379	222	hypothetical protein LOAG_02179
Locus_6816_Transcript_2/2_Conf_1.000	1164	20	5.74E-73	EFO26307.1	58	279.256	379	222	hypothetical protein LOAG_02179
Locus_6817_Transcript_1/1_Conf_1.000	406	20	1.19E-63	XP_002643626.1	100	245.743	134	134	Hypothetical protein CBG16368
Locus_6818_Transcript_1/1_Conf_1.000	414	4	2.84E-09	EFO23348.1	52	65.0846	123	64	hypothetical protein LOAG_05138

Locus_6819_Transcript_1/1_Conf_1.000	241	5	2.19E-17	XP_002641966.1	72	92.0485	74	54	Hypothetical protein CBG16672
Locus_682_Transcript_1/1_Conf_1.000	251	0							
Locus_6820_Transcript_1/1_Conf_1.000	933	20	7.84E-16	XP_001891682.1	52	88.9669	153	80	MRG family protein
Locus_6821_Transcript_1/1_Conf_1.000	194	0							
Locus_6822_Transcript_1/1_Conf_1.000	855	4	1.11E-26	NP_501353.2	44	124.79	309	139	hypothetical protein Y42H9AR.4
Locus_6823_Transcript_1/1_Conf_1.000	503	20	2.54E-37	AAO18223.1	95	158.303	108	103	FMRFamide-like propeptide
Locus_6824_Transcript_1/1_Conf_1.000	799	0							
Locus_6825_Transcript_1/1_Conf_1.000	408	20	5.34E-48	EFO26660.1	95	193.741	105	100	ELC-1 protein
Locus_6826_Transcript_1/1_Conf_1.000	1878	20	3.86E-94	XP_001898111.1	73	350.517	317	233	tumor suppressor.
Locus_6827_Transcript_1/1_Conf_1.000	341	0							
Locus_6828_Transcript_1/1_Conf_1.000	524	16	1.41E-07	XP_001901397.1	56	59.6918	97	55	hypothetical protein Bm1_49650
Locus_6829_Transcript_1/1_Conf_1.000	329	0							
Locus_683_Transcript_1/1_Conf_1.000	777	0							
Locus_6830_Transcript_1/1_Conf_1.000	1381	20	2.01E-62	EFO18349.1	53	244.588	471	254	cation efflux family protein
Locus_6831_Transcript_1/1_Conf_1.000	757	20	1.49E-26	EFO19591.1	53	124.02	242	130	hypothetical protein LOAG_08901
Locus_6832_Transcript_1/1_Conf_1.000	370	20	8.49E-17	XP_002632195.1	60	90.1225	120	73	Hypothetical protein CBG07061

Locus_6833_Transcript_1/1_Conf_1.000	313	20	3.92E-54	NP_001076604.1	100	214.157	104	104	NSF (N-ethylmaleimide sensitive secretion factor) homolog family member (nsf-1)
Locus_6834_Transcript_1/1_Conf_1.000	671	20	1.35E-83	XP_002641314.1	87	313.153	208	182	Hypothetical protein CBG24614
Locus_6835_Transcript_1/2_Conf_1.000	1203	20	2.82E-54	NP_001122489.1	72	217.238	174	126	hypothetical protein F57C9.4
Locus_6835_Transcript_2/2_Conf_1.000	1515	20	3.88E-54	NP_001122489.1	72	217.238	174	126	hypothetical protein F57C9.4
Locus_6836_Transcript_1/1_Conf_1.000	592	20	6.68E-88	XP_002646151.1	95	327.02	169	161	C. briggsae CBR-UBC-14 protein
Locus_6837_Transcript_1/1_Conf_1.000	645	5	4.35E-36	XP_002639422.1	72	155.221	135	98	C. briggsae CBR-NOAH-1 protein
Locus_6838_Transcript_1/1_Conf_1.000	805	3	7.14E-40	XP_002643513.1	57	121.324	202	116	Hypothetical protein CBG16187
Locus_6839_Transcript_1/1_Conf_1.000	1587	20	1.67E-156	NP_506445.2	83	557.37	367	308	Serine Palmitoyl Transferase famiLy family member (sptl-3)
Locus_684_Transcript_1/1_Conf_1.000	372	20	2.81E-12	NP_491944.2	74	75.0998	93	69	hypothetical protein C37A2.7
Locus_6840_Transcript_1/1_Conf_1.000	500	2	1.73E-06	CAR63610.1	55	55.8398	98	54	putative IQ calmodulin-binding motif domain protein
Locus_6841_Transcript_1/1_Conf_1.000	976	0							
Locus_6842_Transcript_1/1_Conf_1.000	1168	20	8.40E-157	NP_492974.2	89	557.755	377	337	Kex-2 Proprotein Convertase family member (kpc-1)
Locus_6843_Transcript_1/2_Conf_1.000	505	6	1.57E-50	NP_502119.2	87	202.216	156	136	hypothetical protein F54D1.6
Locus_6843_Transcript_2/2_Conf_1.000	548	6	1.10E-64	NP_502119.2	88	249.595	183	162	hypothetical protein F54D1.6

Locus_6844_Transcript_1/1_Conf_1.000	834	20	2.92E-93	NP_498042.1	77	345.895	278	215	hypothetical protein C26E6.12
Locus_6845_Transcript_1/2_Conf_1.000	2149	20	0	XP_002640683.1	72	699.123	680	492	C. briggsae CBR-HMP-2 protein
Locus_6845_Transcript_2/2_Conf_1.000	2149	20	0	XP_002640683.1	72	699.123	680	492	C. briggsae CBR-HMP-2 protein
Locus_6846_Transcript_1/1_Conf_1.000	584	20	1.25E-22	XP_002632629.1	64	110.153	118	76	Hypothetical protein CBG21543

Locus_6847_Transcript_1/1_Conf_1.000	765	20	1.53E-34	NP_508944.1	66	150.599	208	138	SULfate Permease family member (sulp-2)
Locus_6848_Transcript_1/1_Conf_1.000	318	0							
Locus_6849_Transcript_1/3_Conf_0.571	492	0							
Locus_6849_Transcript_2/3_Conf_0.714	854	20	1.10E-42	NP_496363.1	88	177.948	107	95	LEThal family member (let-858)
Locus_6849_Transcript_3/3_Conf_0.714	854	20	1.10E-42	NP_496363.1	88	177.948	107	95	LEThal family member (let-858)
Locus_685_Transcript_1/1_Conf_1.000	694	2	2.73E-13	NP_497898.1	64	79.7221	116	75	hypothetical protein R07E5.7
Locus_6850_Transcript_1/1_Conf_1.000	411	20	1.40E-40	XP_002821646.1	100	169.088	84	84	PREDICTED: protein phosphatase 1 regulatory subunit 14B-like
Locus_6851_Transcript_1/1_Conf_1.000	331	4	2.19E-17	NP_495565.2	70	92.0485	96	68	A Kinase Anchor protein family member (aka-1)
Locus_6852_Transcript_1/2_Conf_1.000	369	20	2.38E-27	EFO20609.1	70	125.176	121	85	importin-beta domain-containing protein
Locus_6852_Transcript_2/2_Conf_1.000	369	20	2.38E-27	EFO20609.1	70	125.176	121	85	importin-beta domain-containing protein
Locus_6853_Transcript_1/1_Conf_1.000	683	20	1.73E-57	CAR63681.1	89	226.483	149	133	putative Temporarily Assigned Gene name family member
Locus_6854_Transcript_1/1_Conf_1.000	861	20	7.85E-113	XP_002637127.1	85	410.994	284	242	Hypothetical protein CBG09629
Locus_6855_Transcript_1/2_Conf_1.000	592	20	6.48E-75	NP_495708.1	81	283.878	197	161	hypothetical protein F10B5.2
Locus_6855_Transcript_2/2_Conf_1.000	601	20	3.04E-75	NP_495708.1	81	285.034	199	162	hypothetical protein F10B5.2
Locus_6856_Transcript_1/1_Conf_1.000	309	2	2.76E-04	NP_495437.2	56	48.521	67	38	hypothetical protein C52E12.4

Locus_6857_Transcript_1/1_Conf_1.000	270	0							
Locus_6858_Transcript_1/1_Conf_1.000	866	20	7.04E-53	NP_507155.1	56	211.846	245	138	hypothetical protein F26D2.13
Locus_6859_Transcript_1/1_Conf_1.000	1213	20	8.41E-123	NP_510450.1	87	444.891	320	279	hypothetical protein C05G5.4
Locus_686_Transcript_1/1_Conf_1.000	369	0							
Locus_6860_Transcript_1/1_Conf_1.000	1113	20	6.94E-129	NP_871953.1	85	464.922	292	251	hypothetical protein T05H10.6
Locus_6861_Transcript_1/1_Conf_1.000	208	0							
Locus_6862_Transcript_1/1_Conf_1.000	543	20	1.32E-62	NP_001022442.1	80	242.662	176	141	hypothetical protein Y46G5A.35
Locus_6863_Transcript_1/1_Conf_1.000	887	20	2.17E-89	AAA96224.2	68	333.183	295	201	Hypothetical protein T07H6.4
Locus_6864_Transcript_1/1_Conf_1.000	421	20	4.74E-52	P51547.1	92	207.223	113	105	Extracellular superoxide dismutase [Cu-Zn]
Locus_6865_Transcript_1/1_Conf_1.000	265	2	9.96E-10	XP_001901651.1	84	66.6254	45	38	hypothetical protein Bm1_50915
Locus_6866_Transcript_1/2_Conf_1.000	648	20	4.40E-36	AAN05752.1	69	155.221	153	106	heat shock protein 20
Locus_6866_Transcript_2/2_Conf_1.000	667	20	4.64E-36	AAN05752.1	69	155.221	153	106	heat shock protein 20
Locus_6867_Transcript_1/1_Conf_1.000	371	20	2.39E-19	NP_505778.1	97	98.5969	68	66	EndoMitotic Oocytes family member (emo-1)
Locus_6868_Transcript_1/1_Conf_1.000	244	20	5.72E-34	NP_508756.2	94	147.132	79	75	Lateral Signaling Target family member (lst-2)

Locus_6869_Transcript_1/1_Conf_1.000	172	20	2.68E-07	XP_001898157.1	62	58.5362	48	30	EGF-like domain containing protein
Locus_687_Transcript_1/1_Conf_1.000	661	20	4.35E-63	NP_740937.1	73	244.973	219	162	AdaPtin, Gamma chain (clathrin associated complex) family member (apg-1)
Locus_6870_Transcript_1/1_Conf_1.000	750	20	1.57E-60	XP_001901409.1	75	236.884	172	129	TM2 domain containing protein
Locus_6871_Transcript_1/1_Conf_1.000	821	3	6.42E-13	NP_490864.2	53	78.9518	146	78	hypothetical protein Y92H12A.3
Locus_6872_Transcript_1/1_Conf_1.000	1030	20	4.54E-148	NP_492146.1	91	528.48	332	304	hypothetical protein F27D4.1
Locus_6873_Transcript_1/1_Conf_1.000	244	20	4.52E-39	NP_001122684.1	100	164.081	81	81	UNCoordinated family member (unc-103)

Locus_6874_Transcript_1/1_Conf_1.000	348	13	6.62E-46	NP_498645.1	82	186.808	116	96	MUscle Positioning family member (mup-4)
Locus_6875_Transcript_1/1_Conf_1.000	169	20	5.40E-24	XP_002639165.1	98	114.005	55	54	C. briggsae CBR-RPL-24.2 protein
Locus_6876_Transcript_1/1_Conf_1.000	1018	20	5.24E-40	XP_001893474.1	48	169.474	324	157	Rap/ran-GAP family protein
Locus_6877_Transcript_1/2_Conf_1.000	1476	5	8.10E-41	NP_001041154.2	51	172.94	314	163	hypothetical protein R31.2
Locus_6877_Transcript_2/2_Conf_1.000	1410	5	4.31E-36	XP_002636623.1	62	157.147	174	108	Hypothetical protein CBG23327
Locus_6878_Transcript_1/1_Conf_1.000	389	0							
Locus_6879_Transcript_1/1_Conf_1.000	634	20	1.16E-46	XP_002647555.1	66	190.274	228	152	Hypothetical protein CBG06641
Locus_688_Transcript_1/1_Conf_1.000	623	20	1.63E-90	XP_002642599.1	95	335.88	186	177	C. briggsae CBR-RPL-9 protein
Locus_6880_Transcript_1/1_Conf_1.000	1154	20	3.51E-107	XP_002646111.1	71	392.889	384	273	C. briggsae CBR-PAD-1 protein
Locus_6881_Transcript_1/1_Conf_1.000	593	20	1.76E-80	XP_002645216.1	88	302.368	181	160	Hypothetical protein CBG00074
Locus_6882_Transcript_1/1_Conf_1.000	262	0							
Locus_6883_Transcript_1/2_Conf_1.000	766	20	1.35E-115	CAR63545.1	89	419.853	254	227	putative Hsp90 protein

Locus_6883_Transcript_2/2_Conf_1.000	389	20	4.97E-54	CAR63545.1	89	213.772	129	116	putative Hsp90 protein
Locus_6884_Transcript_1/1_Conf_1.000	1249	20	3.50E-79	NP_499802.2	75	300.056	271	204	hypothetical protein Y76A2B.6
Locus_6885_Transcript_1/1_Conf_1.000	1245	0							
Locus_6886_Transcript_1/1_Conf_1.000	664	20	1.74E-43	XP_002647987.1	78	179.874	146	115	Hypothetical protein CBG23928
Locus_6887_Transcript_1/1_Conf_1.000	697	3	2.85E-18	NP_490661.1	68	96.2857	120	82	Neuropeptide-Like Protein family member (nlp-40)
Locus_6888_Transcript_1/1_Conf_1.000	199	0							
Locus_6889_Transcript_1/1_Conf_1.000	181	20	4.70E-15	NP_001180506.1	100	84.3445	41	41	40S ribosomal protein S2
Locus_689_Transcript_1/1_Conf_1.000	1539	20	2.04E-42	NP_505233.2	62	178.333	226	142	hypothetical protein ZC190.4
Locus_6890_Transcript_1/1_Conf_1.000	727	20	1.25E-27	XP_002643195.1	74	127.487	102	76	C. briggsae CBR-TAG-303 protein
Locus_6891_Transcript_1/1_Conf_1.000	232	0							
Locus_6892_Transcript_1/1_Conf_1.000	577	20	9.77E-73	NP_001040648.2	82	276.559	183	151	hypothetical protein F02E9.9
Locus_6893_Transcript_1/1_Conf_1.000	624	20	7.00E-49	XP_001900859.1	72	197.593	206	150	Leucine Rich Repeat family protein
Locus_6894_Transcript_1/1_Conf_1.000	370	20	2.02E-18	NP_493275.1	66	95.5153	125	83	SELB (SelB homolog) translation factor for selenocysteine incorporation family member (selb-1)
Locus_6895_Transcript_1/1_Conf_1.000	523	0							
Locus_6896_Transcript_1/1_Conf_1.000	174	0							
Locus_6897_Transcript_1/1_Conf_1.000	150	5	2.47E-16	NP_001024902.1	92	88.5817	50	46	hypothetical protein T10B10.4

Locus_6898_Transcript_1/1_Conf_1.000	280	20	1.51E-18	EFO20414.1	76	95.9005	75	57	hypothetical protein LOAG_08075
Locus_6899_Transcript_1/1_Conf_1.000	1274	20	2.20E-28	NP_001040680.1	64	131.339	153	98	UNCoordinated family member (unc-57)
Locus_69_Transcript_1/1_Conf_1.000	1164	20	1.29E-32	EFO22902.1	46	145.206	290	134	rnf126-prov protein
Locus_690_Transcript_1/3_Conf_0.286	307	0							
Locus_690_Transcript_2/3_Conf_0.714	1605	20	9.12E-118	CAR63572.1	85	428.713	386	329	putative Prion-like-(q/n-rich)-domain-bearing protein protein 51
Locus_690_Transcript_3/3_Conf_0.714	1605	20	1.08E-118	CAR63572.1	85	431.795	386	330	putative Prion-like-(q/n-rich)-domain-bearing protein protein 51
Locus_6900_Transcript_1/1_Conf_1.000	351	0							
Locus_6901_Transcript_1/1_Conf_1.000	749	2	1.81E-16	NP_506154.1	64	90.5077	157	101	hypothetical protein C14C10.6
Locus_6902_Transcript_1/1_Conf_1.000	237	0							
Locus_6903_Transcript_1/1_Conf_1.000	377	20	3.39E-50	CAA10033.1	87	201.06	125	109	DYS-1 protein
Locus_6904_Transcript_1/1_Conf_1.000	334	0							
Locus_6905_Transcript_1/2_Conf_1.000	593	3	3.28E-10	NP_498558.1	49	68.9366	129	64	hypothetical protein B0280.10
Locus_6905_Transcript_2/2_Conf_1.000	667	3	4.38E-10	NP_498558.1	49	68.9366	129	64	hypothetical protein B0280.10

Locus_6906_Transcript_1/1_Conf_1.000	2267	20	0	NP_501283.1	82	870.152	657	541	yeast SEC homolog family member (sec-10)
Locus_6907_Transcript_1/1_Conf_1.000	452	20	7.75E-47	EFO22906.1	88	189.889	113	100	hypothetical protein LOAG_05578
Locus_6908_Transcript_1/2_Conf_1.000	1249	20	1.71E-25	NP_502785.2	67	121.709	137	92	hypothetical protein Y57G11C.9
Locus_6908_Transcript_2/2_Conf_1.000	1243	20	1.69E-25	NP_502785.2	67	121.709	137	92	hypothetical protein Y57G11C.9
Locus_6909_Transcript_1/1_Conf_1.000	966	20	7.86E-67	NP_001123010.1	64	258.455	301	193	related to yeast Vacuolar Protein Sorting factor family member (vps-39)
Locus_691_Transcript_1/3_Conf_0.625	2370	20	2.23E-73	DAA04553.1	58	281.952	600	348	TPA_exp: ANC-1
Locus_691_Transcript_2/3_Conf_0.375	2810	20	3.05E-117	NP_491353.2	59	427.943	919	547	abnormal nuclear ANChorage family member (anc-1)
Locus_691_Transcript_3/3_Conf_0.625	2962	20	1.96E-130	DAA04553.1	57	471.855	966	554	TPA_exp: ANC-1

Locus_6910_Transcript_1/3_Conf_0.714	668	20	5.23E-88	NP_740947.2	92	327.791	212	196	hypothetical protein Y105E8A.19
Locus_6910_Transcript_2/3_Conf_0.714	668	20	5.23E-88	NP_740947.2	92	327.791	212	196	hypothetical protein Y105E8A.19
Locus_6910_Transcript_3/3_Conf_0.714	668	20	5.23E-88	NP_740947.2	92	327.791	212	196	hypothetical protein Y105E8A.19
Locus_6911_Transcript_1/1_Conf_1.000	1434	20	2.94E-173	XP_002642675.1	75	612.838	460	349	C. briggsae CBR-TAG-282 protein
Locus_6912_Transcript_1/1_Conf_1.000	1485	20	0	XP_001897051.1	85	749.199	496	425	RNA polymerase Rpb1, domain 1 family protein

Locus_6913_Transcript_1/1_Conf_1.000	2157	20	3.74E-104	EFO23880.1	61	384.03	487	300	transportin-SR
Locus_6914_Transcript_1/1_Conf_1.000	579	20	3.30E-68	NP_506714.1	79	261.536	186	147	hypothetical protein C01G10.9
Locus_6915_Transcript_1/1_Conf_1.000	1410	20	8.24E-104	EFO23138.1	70	382.104	402	283	CPSF A subunit region family protein
Locus_6916_Transcript_1/1_Conf_1.000	624	20	1.12E-54	XP_001901976.1	68	216.853	212	146	Protein kinase domain containing protein
Locus_6917_Transcript_1/1_Conf_1.000	991	10	5.56E-23	NP_741460.2	77	112.849	90	70	WASP (actin cytoskeleton modulator) homolog family member (wsp-1)
Locus_6918_Transcript_1/1_Conf_1.000	387	20	1.07E-64	NP_740855.2	98	249.21	128	126	hypothetical protein F46F11.1
Locus_6919_Transcript_1/1_Conf_1.000	1217	20	5.21E-64	AAY58318.1	55	249.595	342	191	C-type lectin precursor
Locus_692_Transcript_1/1_Conf_1.000	129	0							
Locus_6920_Transcript_1/2_Conf_1.000	856	12	4.23E-10	XP_002588239.1	68	69.707	90	62	hypothetical protein BRAFLDRAFT_86686
Locus_6920_Transcript_2/2_Conf_1.000	808	8	5.53E-09	XP_002588239.1	62	65.855	104	65	hypothetical protein BRAFLDRAFT_86686
Locus_6921_Transcript_1/1_Conf_1.000	455	20	1.05E-35	CAA72916.2	65	152.91	151	99	serine protease inhibitor-like protein

Locus_6922_Transcript_1/1_Conf_1.000	221	20	2.40E-19	AAB50206.1	79	98.5969	64	51	unknown
Locus_6923_Transcript_1/1_Conf_1.000	269	0							
Locus_6924_Transcript_1/1_Conf_1.000	197	0							
Locus_6925_Transcript_1/1_Conf_1.000	237	20	7.31E-21	NP_492593.2	79	103.605	64	51	hypothetical protein F26E4.3
Locus_6926_Transcript_1/1_Conf_1.000	406	20	4.27E-29	XP_001902803.1	85	130.954	89	76	Hypothetical HIT-like protein F21C3.3
Locus_6927_Transcript_1/1_Conf_1.000	314	20	1.07E-27	EFN83990.1	75	126.331	104	79	DNA damage-binding protein 1
Locus_6928_Transcript_1/1_Conf_1.000	547	3	2.66E-10	EFO20474.1	50	68.9366	162	82	SNARE domain-containing protein
Locus_6929_Transcript_1/1_Conf_1.000	176	0							
Locus_693_Transcript_1/1_Conf_1.000	309	0							
Locus_6930_Transcript_1/1_Conf_1.000	220	4	9.14E-11	EFO24279.1	72	70.0922	50	36	hypothetical protein LOAG_04211

Locus_6931_Transcript_1/1_Conf_1.000	140	0							
Locus_6932_Transcript_1/1_Conf_1.000	495	2	3.06E-11	XP_002631386.1	48	71.633	137	66	Hypothetical protein CBG03228
Locus_6933_Transcript_1/2_Conf_1.000	309	2	1.32E-06	NP_494766.1	72	56.225	51	37	hypothetical protein H20J04.3
Locus_6933_Transcript_2/2_Conf_1.000	315	2	6.75E-06	NP_494766.1	69	53.9138	56	39	hypothetical protein H20J04.3
Locus_6934_Transcript_1/1_Conf_1.000	449	20	1.69E-17	XP_001899578.1	57	92.4337	152	87	Hyaluronidase family protein
Locus_6935_Transcript_1/1_Conf_1.000	482	20	4.20E-45	EFO20390.1	77	184.111	160	124	subtilase
Locus_6936_Transcript_1/1_Conf_1.000	458	0							
Locus_6937_Transcript_1/1_Conf_1.000	178	0							
Locus_6938_Transcript_1/2_Conf_1.000	1739	20	1.28E-96	NP_001040987.1	79	358.607	226	180	ALP/Enigma encoding family member (alp-1)
Locus_6938_Transcript_2/2_Conf_1.000	1739	20	1.28E-96	NP_001040987.1	79	358.607	226	180	ALP/Enigma encoding family member (alp-1)
Locus_6939_Transcript_1/1_Conf_1.000	1155	6	8.17E-80	NP_500907.1	66	301.982	345	228	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-22)
Locus_694_Transcript_1/1_Conf_1.000	817	20	1.19E-35	XP_002630316.1	96	154.451	87	84	Hypothetical protein CBG04239
Locus_6940_Transcript_1/3_Conf_0.714	1419	20	3.57E-139	XP_002639103.1	75	499.59	424	318	C. briggsae CBR-TAG-345 protein
Locus_6940_Transcript_2/3_Conf_0.714	1419	20	2.09E-139	XP_002639103.1	75	500.36	424	319	C. briggsae CBR-TAG-345 protein

Locus_6940_Transcript_3/3_Conf_0.714	1419	20	2.09E-139	XP_002639103.1	75	500.36	424	319	C. briggsae CBR-TAG-345 protein
Locus_6941_Transcript_1/1_Conf_1.000	195	20	2.21E-25	NP_500306.1	98	118.627	64	63	hypothetical protein T26C12.1
Locus_6942_Transcript_1/1_Conf_1.000	369	0							
Locus_6943_Transcript_1/1_Conf_1.000	404	0							
Locus_6944_Transcript_1/1_Conf_1.000	499	2	2.02E-39	NP_505312.1	69	165.236	165	115	hypothetical protein T19A5.1
Locus_6945_Transcript_1/1_Conf_1.000	396	20	3.68E-12	XP_001896161.1	51	74.7146	129	67	tRNA intron endonuclease family protein
Locus_6946_Transcript_1/1_Conf_1.000	1402	5	9.91E-09	NP_506662.1	39	66.2402	244	97	hypothetical protein ZC412.3
Locus_6947_Transcript_1/3_Conf_0.333	357	14	1.05E-35	NP_491391.3	76	152.91	107	82	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-24)
Locus_6947_Transcript_2/3_Conf_0.667	718	13	7.87E-35	NP_491391.3	78	151.369	103	81	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-24)
Locus_6947_Transcript_3/3_Conf_0.667	680	13	7.01E-35	NP_491391.3	78	151.369	103	81	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-24)
Locus_6948_Transcript_1/1_Conf_1.000	334	20	1.02E-14	XP_002639918.1	67	83.1889	109	74	C. briggsae CBR-NMY-2 protein

Locus_6949_Transcript_1/1_Conf_1.000	197	20	7.39E-13	XP_002923753.1	100	77.0258	35	35	PREDICTED: rRNA 2'-O-methyltransferase fibrillarin-like
Locus_695_Transcript_1/1_Conf_1.000	1751	20	0	XP_002641757.1	86	644.81	444	384	Hypothetical protein CBG10097
Locus_6950_Transcript_1/1_Conf_1.000	506	20	1.20E-42	XP_001898472.1	68	176.022	167	114	Trehalase family protein
Locus_6951_Transcript_1/1_Conf_1.000	622	0							
Locus_6952_Transcript_1/1_Conf_1.000	218	20	1.66E-25	NP_001122677.1	92	119.013	56	52	PaXiLlin homolo family member (pxl-1)
Locus_6953_Transcript_1/2_Conf_1.000	503	20	2.08E-31	NP_495010.2	78	138.658	111	87	hypothetical protein F09E5.2
Locus_6953_Transcript_2/2_Conf_1.000	698	20	4.96E-63	NP_495010.2	73	244.973	213	157	hypothetical protein F09E5.2
Locus_6954_Transcript_1/1_Conf_1.000	569	0							
Locus_6955_Transcript_1/1_Conf_1.000	858	20	2.17E-30	EFO27189.1	78	137.117	103	81	hypothetical protein LOAG_01295

Locus_6956_Transcript_1/1_Conf_1.000	572	20	8.24E-85	NP_001122711.1	86	316.62	192	167	CBP/p300 homolog family member (cbp-1)
Locus_6957_Transcript_1/1_Conf_1.000	1386	20	1.05E-135	NP_497949.1	86	488.034	314	272	hypothetical protein T23F11.1
Locus_6958_Transcript_1/2_Conf_1.000	1226	4	1.11E-13	XP_002641036.1	54	82.4185	211	115	C. briggsae CBR-EPC-1 protein
Locus_6958_Transcript_2/2_Conf_1.000	454	0							
Locus_6959_Transcript_1/1_Conf_1.000	221	0							
Locus_696_Transcript_1/4_Conf_0.625	2348	20	9.34E-157	XP_002632235.1	60	558.91	755	454	Hypothetical protein CBG07108
Locus_696_Transcript_2/4_Conf_0.625	2351	20	9.35E-157	XP_002632235.1	60	558.91	755	454	Hypothetical protein CBG07108
Locus_696_Transcript_3/4_Conf_0.625	2351	20	5.49E-157	XP_002632235.1	60	559.681	755	454	Hypothetical protein CBG07108
Locus_696_Transcript_4/4_Conf_0.625	2351	20	9.35E-157	XP_002632235.1	60	558.91	755	454	Hypothetical protein CBG07108
Locus_6960_Transcript_1/1_Conf_1.000	996	20	2.24E-88	NP_501500.1	67	330.102	331	222	hypothetical protein F21D5.1
Locus_6961_Transcript_1/1_Conf_1.000	658	20	2.74E-73	NP_504842.1	81	278.87	192	157	hypothetical protein C05C8.1
Locus_6962_Transcript_1/1_Conf_1.000	331	0							
Locus_6963_Transcript_1/1_Conf_1.000	340	0							

Locus_6964_Transcript_1/1_Conf_1.000	346	16	2.73E-07	NP_496959.1	78	58.5362	41	32	EATing: abnormal pharyngeal pumping family member (eat-2)
Locus_6965_Transcript_1/2_Conf_1.000	394	20	3.01E-30	XP_002641403.1	68	134.806	131	90	Hypothetical protein CBG13266
Locus_6965_Transcript_2/2_Conf_1.000	394	20	6.70E-30	XP_002641403.1	67	133.65	131	89	Hypothetical protein CBG13266
Locus_6966_Transcript_1/1_Conf_1.000	559	3	1.02E-28	NP_001021864.1	59	130.183	175	104	human KRIT 1 (Krev interaction trapped/cerebral cavernous malformation 1) homolog family member (kri-1)
Locus_6967_Transcript_1/1_Conf_1.000	563	20	1.53E-72	NP_499089.1	95	275.789	148	141	aspartyl(D) tRNA Synthetase family member (drs-1)
Locus_6968_Transcript_1/1_Conf_1.000	375	0							
Locus_6969_Transcript_1/1_Conf_1.000	1055	20	2.19E-105	NP_490765.1	81	386.726	277	227	hypothetical protein Y65B4A.1
Locus_697_Transcript_1/1_Conf_1.000	290	6	1.15E-05	XP_002639634.1	70	53.1434	51	36	C. briggsae CBR-CLE-1 protein
Locus_6970_Transcript_1/1_Conf_1.000	543	0							
Locus_6971_Transcript_1/1_Conf_1.000	247	0							
Locus_6972_Transcript_1/1_Conf_1.000	758	20	1.46E-98	XP_002636819.1	86	363.229	243	211	C. briggsae CBR-DHS-17 protein
Locus_6973_Transcript_1/1_Conf_1.000	1111	20	3.12E-105	NP_498078.2	82	386.341	284	233	hypothetical protein C45G9.2
Locus_6974_Transcript_1/1_Conf_1.000	161	10	3.20E-16	XP_002638706.1	91	88.1965	48	44	Hypothetical protein CBG00285
Locus_6975_Transcript_1/2_Conf_1.000	2156	20	8.33E-96	ADE60688.1	49	356.295	744	371	Larp (rna binding la related protein) homolog protein 1, isoform b, partially confirmed by transcript evidence
Locus_6975_Transcript_2/2_Conf_1.000	2099	20	4.72E-96	ADE60688.1	51	357.066	725	370	Larp (rna binding la related protein) homolog protein 1, isoform b, partially confirmed by transcript evidence

Locus_6976_Transcript_1/1_Conf_1.000	1239	20	1.45E-85	NP_499392.1	64	321.242	418	269	OXidative stress Induced family member (oxi-1)
Locus_6977_Transcript_1/1_Conf_1.000	468	4	1.09E-24	XP_001895501.1	65	116.316	146	96	PAN domain containing protein
Locus_6978_Transcript_1/2_Conf_1.000	1921	6	5.66E-24	NP_510744.1	46	117.472	415	194	hypothetical protein F52G3.1
Locus_6978_Transcript_2/2_Conf_1.000	1870	4	1.22E-23	NP_510744.1	46	116.316	408	190	hypothetical protein F52G3.1
Locus_6979_Transcript_1/1_Conf_1.000	495	20	9.38E-61	NP_490755.1	86	236.113	165	143	Heavy chain, Unconventional Myosin family member (hum-7)
Locus_698_Transcript_1/1_Conf_1.000	1002	20	8.07E-78	NP_504700.2	70	295.049	327	229	hypothetical protein W02F12.5
Locus_6980_Transcript_1/1_Conf_1.000	594	0							
Locus_6981_Transcript_1/1_Conf_1.000	566	20	7.26E-62	NP_001023252.1	82	240.35	189	155	Transbilayer Amphipath Transporters (subfamily IV P-type ATPase) family member (tat-2)
Locus_6982_Transcript_1/2_Conf_1.000	1494	3	8.88E-11	XP_001894599.1	50	73.1738	151	76	Zinc finger, C2H2 type family protein
Locus_6982_Transcript_2/2_Conf_1.000	1485	3	5.71E-10	XP_001894599.1	58	70.4774	87	51	Zinc finger, C2H2 type family protein
Locus_6983_Transcript_1/1_Conf_1.000	385	20	5.36E-40	XP_001891916.1	90	167.162	83	75	cysteine-rich protein 1
Locus_6984_Transcript_1/1_Conf_1.000	1421	20	1.90E-124	XP_002638998.1	67	450.669	485	328	Hypothetical protein CBG22244
Locus_6985_Transcript_1/1_Conf_1.000	517	0							
Locus_6986_Transcript_1/1_Conf_1.000	700	20	2.41E-57	XP_002644345.1	85	226.098	150	128	C. briggsae CBR-LBP-3 protein
Locus_6987_Transcript_1/1_Conf_1.000	644	0							
Locus_6988_Transcript_1/1_Conf_1.000	331	4	3.62E-20	XP_002641171.1	68	101.293	110	75	C. briggsae CBR-DCT-6 protein
Locus_6989_Transcript_1/1_Conf_1.000	1475	11	6.91E-117	NP_001129817.1	67	425.631	433	291	CLeaR family member (clr-1)
Locus_699_Transcript_1/1_Conf_1.000	621	0							
Locus_6990_Transcript_1/2_Conf_1.000	507	1	9.87E-08	CAR63546.1	61	60.077	73	45	hypothetical protein

Locus_6990_Transcript_2/2_Conf_1.000	523	2	1.15E-09	CAR63546.1	58	66.6254	92	54	hypothetical protein
Locus_6991_Transcript_1/1_Conf_1.000	408	0							
Locus_6992_Transcript_1/1_Conf_1.000	336	20	8.27E-17	XP_002634761.1	65	90.1225	96	63	C. briggsae CBR-TTR-20 protein
Locus_6993_Transcript_1/1_Conf_1.000	702	20	8.75E-15	XP_001898381.1	56	84.7297	187	106	Plus-3 domain containing protein
Locus_6994_Transcript_1/1_Conf_1.000	1890	20	8.66E-102	XP_001897613.1	62	375.941	492	308	SPRY domain containing protein
Locus_6995_Transcript_1/1_Conf_1.000	931	8	2.03E-48	XP_001901365.1	54	197.208	311	168	hypothetical protein
Locus_6996_Transcript_1/1_Conf_1.000	1821	3	4.34E-127	NP_001021809.1	60	459.914	618	372	Branching AbnorMal family member (bam-2)
Locus_6997_Transcript_1/1_Conf_1.000	374	20	2.69E-55	NP_001122835.1	92	218.009	124	115	UNCoordinated family member (unc-22)
Locus_6998_Transcript_1/1_Conf_1.000	393	1	2.83E-04	XP_001440076.1	54	48.521	106	58	hypothetical protein
Locus_6999_Transcript_1/1_Conf_1.000	712	0							
Locus_7_Transcript_1/1_Conf_1.000	1110	20	6.72E-108	NP_498722.1	82	395.201	267	220	GLYcosylation related family member (gly-3)
Locus_70_Transcript_1/4_Conf_0.700	1934	20	4.46E-162	EFO20898.1	90	576.244	370	334	ankyrin repeat-containing protein
Locus_70_Transcript_2/4_Conf_0.200	547	20	1.10E-56	CBK19467.1	83	223.016	159	133	C. elegans protein R11A8.7e, partially confirmed by transcript evidence
Locus_70_Transcript_3/4_Conf_0.700	1934	20	4.46E-162	EFO20898.1	90	576.244	370	334	ankyrin repeat-containing protein
Locus_70_Transcript_4/4_Conf_0.700	1934	20	4.46E-162	EFO20898.1	90	576.244	370	334	ankyrin repeat-containing protein

Locus_700_Transcript_1/1_Conf_1.000	1156	0							
Locus_7000_Transcript_1/1_Conf_1.000	336	20	1.83E-48	NP_506125.1	93	195.282	108	101	EGg Laying defective family member (egl-10)
Locus_7001_Transcript_1/4_Conf_0.333	185	0							
Locus_7001_Transcript_2/4_Conf_0.333	171	0							
Locus_7001_Transcript_3/4_Conf_0.333	173	0							
Locus_7001_Transcript_4/4_Conf_0.500	162	0							
Locus_7002_Transcript_1/1_Conf_1.000	819	0							
Locus_7003_Transcript_1/1_Conf_1.000	251	0							
Locus_7004_Transcript_1/1_Conf_1.000	642	20	8.96E-34	AAK57805.1	65	147.517	170	112	putative retinol-binding protein
Locus_7005_Transcript_1/1_Conf_1.000	529	19	2.26E-16	NP_498982.1	57	88.9669	183	105	hypothetical protein R08D7.1
Locus_7006_Transcript_1/1_Conf_1.000	3202	20	9.39E-86	XP_001895110.1	55	323.553	493	274	ARID/BRIGHT DNA binding domain containing protein
Locus_7007_Transcript_1/1_Conf_1.000	331	20	2.05E-15	XP_853757.1	71	85.5001	85	61	PREDICTED: similar to UPF0197 protein C11orf10 homolog isoform 2
Locus_7008_Transcript_1/1_Conf_1.000	376	20	1.49E-13	XP_001861443.1	54	79.337	108	59	set domain protein
Locus_7009_Transcript_1/1_Conf_1.000	425	3	1.35E-06	NP_499532.2	55	56.225	89	49	hypothetical protein C18D11.3
Locus_701_Transcript_1/2_Conf_1.000	546	0							
Locus_701_Transcript_2/2_Conf_1.000	552	0							
Locus_7010_Transcript_1/1_Conf_1.000	290	0							
Locus_7011_Transcript_1/1_Conf_1.000	478	20	5.70E-42	ADN00783.1	86	173.711	107	93	collagen protein
Locus_7012_Transcript_1/1_Conf_1.000	230	0							
Locus_7013_Transcript_1/1_Conf_1.000	880	20	5.92E-31	NP_741223.1	52	139.043	262	137	hypothetical protein F56C9.10

Locus_7014_Transcript_1/1_Conf_1.000	159	1	2.15E-04	NP_496764.1	79	48.9062	39	31	hypothetical protein Y38F1A.6
Locus_7015_Transcript_1/1_Conf_1.000	457	20	6.53E-30	EFO27449.1	79	133.65	106	84	hypothetical protein LOAG_01039
Locus_7016_Transcript_1/1_Conf_1.000	1130	7	4.56E-35	XP_001894177.1	50	153.295	358	182	GYF domain containing protein
Locus_7017_Transcript_1/1_Conf_1.000	1049	9	5.50E-08	NP_001021459.2	39	63.1586	270	106	hypothetical protein F36H2.3
Locus_7018_Transcript_1/3_Conf_0.571	2056	20	4.23E-158	EFO22782.1	68	563.148	603	411	hypothetical protein LOAG_05703
Locus_7018_Transcript_2/3_Conf_0.714	3071	20	1.61E-159	EFO22782.1	57	568.54	853	491	hypothetical protein LOAG_05703
Locus_7018_Transcript_3/3_Conf_0.714	3071	20	1.61E-159	EFO22782.1	57	568.54	853	491	hypothetical protein LOAG_05703
Locus_7019_Transcript_1/1_Conf_1.000	344	2	3.70E-04	NP_500403.2	69	48.1358	39	27	hypothetical protein Y37E11AM.3
Locus_702_Transcript_1/1_Conf_1.000	502	0							
Locus_7020_Transcript_1/1_Conf_1.000	134	7	4.28E-05	XP_001895616.1	70	51.2174	44	31	CG8232-PA
Locus_7021_Transcript_1/1_Conf_1.000	1407	20	2.45E-23	XP_001891682.1	44	114.775	374	168	MRG family protein
Locus_7022_Transcript_1/1_Conf_1.000	418	0							
Locus_7023_Transcript_1/1_Conf_1.000	266	20	4.58E-39	NP_499055.1	90	164.081	87	79	hypothetical protein C40H1.6

Locus_7024_Transcript_1/1_Conf_1.000	278	20	5.56E-13	NP_509645.1	66	77.411	75	50	DumPY : shorter than wild-type family member (dpy-22)
Locus_7025_Transcript_1/1_Conf_1.000	1410	20	1.04E-114	XP_001898527.1	85	418.313	349	297	Hsp90 co-chaperone Cdc37
Locus_7026_Transcript_1/1_Conf_1.000	1899	20	0	NP_501797.1	83	761.525	523	436	DiHydroPyrimidinase family member (dhp-2)
Locus_7027_Transcript_1/2_Conf_1.000	1777	20	2.55E-124	NP_505950.1	87	450.669	308	269	mammalian SKIP (Ski interacting protein) homolog family member (skp-1)
Locus_7027_Transcript_2/2_Conf_1.000	1777	20	5.14E-125	NP_505950.1	87	452.981	308	269	mammalian SKIP (Ski interacting protein) homolog family member (skp-1)
Locus_7028_Transcript_1/1_Conf_1.000	637	0							
Locus_7029_Transcript_1/1_Conf_1.000	743	0							
Locus_703_Transcript_1/1_Conf_1.000	3203	20	0	NP_001023909.2	69	899.042	945	654	SMEK (Dictyostelium Suppressor of MEK null) homolog family member (smk-1)
Locus_7030_Transcript_1/1_Conf_1.000	420	0							
Locus_7031_Transcript_1/1_Conf_1.000	674	1	8.73E-06	NP_490861.3	46	54.6842	181	85	hypothetical protein Y92H12A.5
Locus_7032_Transcript_1/1_Conf_1.000	279	0							
Locus_7033_Transcript_1/1_Conf_1.000	794	20	1.34E-52	NP_498248.2	62	210.69	270	169	hypothetical protein Y37B11A.2

Locus_7034_Transcript_1/1_Conf_1.000	1332	20	5.87E-96	Q61CA3.2	78	355.91	271	212	Serine/threonine-protein phosphatase Pgam5
Locus_7035_Transcript_1/1_Conf_1.000	415	0							
Locus_7036_Transcript_1/1_Conf_1.000	241	0							
Locus_7037_Transcript_1/1_Conf_1.000	226	0							
Locus_7038_Transcript_1/1_Conf_1.000	182	20	4.10E-27	XP_002639744.1	91	124.405	57	52	C. briggsae CBR-LAM-3 protein
Locus_7039_Transcript_1/1_Conf_1.000	670	6	4.73E-12	XP_002641929.1	47	75.485	171	82	Hypothetical protein CBG16628
Locus_704_Transcript_1/1_Conf_1.000	1158	20	1.23E-75	P34563.1	96	288.115	157	151	Eukaryotic translation initiation factor 5A-1
Locus_7040_Transcript_1/2_Conf_1.000	444	3	1.07E-11	CAA99805.3	51	73.1738	123	63	C. elegans protein C54D10.4, confirmed by transcript evidence
Locus_7040_Transcript_2/2_Conf_1.000	737	3	2.44E-10	CAA99805.3	52	70.0922	123	65	C. elegans protein C54D10.4, confirmed by transcript evidence
Locus_7041_Transcript_1/1_Conf_1.000	1493	20	2.39E-157	XP_002629982.1	69	560.066	502	349	Hypothetical protein CBG13344
Locus_7042_Transcript_1/1_Conf_1.000	283	6	2.25E-17	XP_002634542.1	67	92.0485	93	63	Hypothetical protein CBG08339
Locus_7043_Transcript_1/1_Conf_1.000	808	20	9.46E-110	XP_002637057.1	82	400.593	266	220	C. briggsae CBR-DAF-36 protein
Locus_7044_Transcript_1/1_Conf_1.000	2122	20	0	NP_502420.2	74	695.656	668	498	hypothetical protein C26H9A.2
Locus_7045_Transcript_1/1_Conf_1.000	745	20	9.69E-63	EFO19115.1	63	244.202	246	155	SPE-10 protein

Locus_7046_Transcript_1/1_Conf_1.000	734	20	2.25E-24	XP_001896246.1	73	116.701	110	81	hypothetical protein Bm1_23945
Locus_7047_Transcript_1/1_Conf_1.000	1307	20	1.18E-101	XP_002643347.1	95	374.785	205	196	C. briggsae CBR-RAB-6.2 protein
Locus_7048_Transcript_1/1_Conf_1.000	230	2	1.65E-04	NP_492267.1	54	49.2914	64	35	CYtochrome P450 family member (cyp-36A1)
Locus_7049_Transcript_1/1_Conf_1.000	996	20	4.71E-171	NP_500284.2	94	604.749	332	315	Enhancer of EfL-1 mutant phenotype family member (eel-1)
Locus_705_Transcript_1/1_Conf_1.000	560	8	1.99E-24	NP_498724.3	59	115.931	198	117	Nuclear Pore complex Protein family member (npp-15)
Locus_7050_Transcript_1/1_Conf_1.000	580	20	1.06E-66	XP_002642172.1	87	256.529	166	146	Hypothetical protein CBG18137
Locus_7051_Transcript_1/1_Conf_1.000	295	0							
Locus_7052_Transcript_1/1_Conf_1.000	333	0							

Locus_7053_Transcript_1/2_Conf_1.000	2710	20	0	NP_490716.1	75	935.25	808	611	eXPOrtin (nuclear export receptor) family member (xpo-2)
Locus_7053_Transcript_2/2_Conf_1.000	2710	20	0	NP_490716.1	75	934.865	808	611	eXPOrtin (nuclear export receptor) family member (xpo-2)
Locus_7054_Transcript_1/1_Conf_1.000	1441	20	1.25E-46	EFO23215.1	66	192.2	195	130	hypothetical protein LOAG_05271
Locus_7055_Transcript_1/1_Conf_1.000	752	16	9.27E-45	NP_001021024.1	60	184.496	257	156	IntraMembrane Protease (IMPAS) family member (imp-1)
Locus_7056_Transcript_1/1_Conf_1.000	676	20	2.78E-84	XP_002641561.1	95	315.464	171	164	C. briggsae CBR-MLC-4 protein
Locus_7057_Transcript_1/1_Conf_1.000	2231	20	9.99E-169	NP_741778.1	75	598.586	526	397	TBC (Tre-2/Bub2/Cdc16) domain family member (tbc-7)
Locus_7058_Transcript_1/1_Conf_1.000	424	20	5.74E-74	XP_002914026.1	100	280.026	140	140	PREDICTED: polyadenylate-binding protein 1-like
Locus_7059_Transcript_1/1_Conf_1.000	343	0							
Locus_706_Transcript_1/1_Conf_1.000	349	0							

Locus_7060_Transcript_1/2_Conf_1.000	2186	20	4.52E-49	NP_001024042.1	40	201.06	671	275	plant Late Embryo Abundant (LEA) related family member (lea-1)
Locus_7060_Transcript_2/2_Conf_1.000	2120	20	7.74E-46	NP_001024042.1	39	190.274	663	259	plant Late Embryo Abundant (LEA) related family member (lea-1)
Locus_7061_Transcript_1/1_Conf_1.000	589	0							
Locus_7062_Transcript_1/1_Conf_1.000	910	20	1.19E-29	NP_497899.1	48	134.806	311	152	Caenorhabditis KU family member (cku-80)
Locus_7063_Transcript_1/1_Conf_1.000	796	3	1.28E-10	EFO20340.1	47	71.2478	221	105	hypothetical protein LOAG_08148
Locus_7064_Transcript_1/1_Conf_1.000	949	20	1.56E-152	NP_001022641.1	89	543.117	316	284	LEThal family member (let-805)
Locus_7065_Transcript_1/1_Conf_1.000	243	0							
Locus_7066_Transcript_1/1_Conf_1.000	170	0							
Locus_7067_Transcript_1/1_Conf_1.000	535	20	2.70E-25	XP_002631178.1	62	118.627	132	82	C. briggsae CBR-MAT-2 protein
Locus_7068_Transcript_1/1_Conf_1.000	946	20	1.68E-106	XP_001895342.1	90	390.193	316	287	CLC chloride channel protein
Locus_7069_Transcript_1/1_Conf_1.000	781	0							
Locus_707_Transcript_1/1_Conf_1.000	1835	20	1.83E-141	NP_496328.2	63	507.679	643	408	hypothetical protein R06F6.8
Locus_7070_Transcript_1/1_Conf_1.000	701	20	2.77E-37	XP_002642051.1	55	159.458	235	131	Hypothetical protein CBG17988
Locus_7071_Transcript_1/1_Conf_1.000	2394	20	2.85E-84	XP_001893145.1	66	318.161	343	229	hypothetical protein
Locus_7072_Transcript_1/1_Conf_1.000	210	0							

Locus_7073_Transcript_1/1_Conf_1.000	304	0							
Locus_7074_Transcript_1/1_Conf_1.000	569	20	1.26E-61	XP_002642872.1	78	239.58	176	138	Hypothetical protein CBG15142
Locus_7075_Transcript_1/1_Conf_1.000	264	1	1.49E-05	NP_001041196.1	45	52.7582	85	39	hypothetical protein Y50D4A.1
Locus_7076_Transcript_1/1_Conf_1.000	468	5	5.62E-21	EFO18382.1	58	103.99	154	90	hypothetical protein LOAG_10114
Locus_7077_Transcript_1/1_Conf_1.000	582	20	7.08E-26	XP_001894111.1	71	120.939	123	88	IWS1 C-terminus family protein
Locus_7078_Transcript_1/1_Conf_1.000	587	20	1.58E-73	NP_496353.1	89	279.256	167	149	hypothetical protein R03D7.1
Locus_7079_Transcript_1/1_Conf_1.000	307	0							
Locus_708_Transcript_1/2_Conf_1.000	1801	20	4.42E-15	EFO16453.1	56	87.8113	137	77	UBX domain-containing protein
Locus_708_Transcript_2/2_Conf_1.000	1801	20	4.42E-15	EFO16453.1	56	87.8113	137	77	UBX domain-containing protein
Locus_7080_Transcript_1/1_Conf_1.000	517	20	4.27E-46	XP_002640548.1	80	187.578	171	137	Hypothetical protein CBG15812
Locus_7081_Transcript_1/1_Conf_1.000	330	20	1.16E-26	XP_001898915.1	90	122.865	96	87	Uncoordinated protein 44, isoform e

Locus_7082_Transcript_1/1_Conf_1.000	199	20	9.27E-24	ACI49074.1	89	113.235	66	59	hypothetical protein Cbre_JD10.006
Locus_7083_Transcript_1/1_Conf_1.000	374	0							
Locus_7084_Transcript_1/1_Conf_1.000	372	20	1.38E-51	EFO18771.1	88	205.682	122	108	fumarylacetoacetate hydrolase domain containing 1
Locus_7085_Transcript_1/1_Conf_1.000	253	0							
Locus_7086_Transcript_1/2_Conf_1.000	191	0							
Locus_7086_Transcript_2/2_Conf_1.000	200	0							
Locus_7087_Transcript_1/1_Conf_1.000	467	20	7.11E-32	XP_001202573.1	71	140.198	157	112	PREDICTED: similar to damaged-DNA recognition protein 1, partial
Locus_7088_Transcript_1/1_Conf_1.000	180	0							
Locus_7089_Transcript_1/1_Conf_1.000	404	5	3.17E-40	NP_497814.3	84	167.933	138	116	UNCoordinated family member (unc-79)
Locus_709_Transcript_1/2_Conf_1.000	959	0							
Locus_709_Transcript_2/2_Conf_1.000	953	0							
Locus_7090_Transcript_1/1_Conf_1.000	246	0							
Locus_7091_Transcript_1/1_Conf_1.000	314	8	1.44E-40	ABS45067.1	84	169.088	100	84	latrophilin-like protein 2
Locus_7092_Transcript_1/1_Conf_1.000	542	20	4.58E-68	AAS49411.1	88	260.766	147	130	putative neuromuscular acetylcholinesterase
Locus_7093_Transcript_1/1_Conf_1.000	395	0							
Locus_7094_Transcript_1/1_Conf_1.000	348	0							
Locus_7095_Transcript_1/2_Conf_1.000	438	0							
Locus_7095_Transcript_2/2_Conf_1.000	405	0							
Locus_7096_Transcript_1/2_Conf_1.000	1185	4	4.31E-07	CAR63632.1	60	60.4622	87	53	hypothetical protein
Locus_7096_Transcript_2/2_Conf_1.000	639	1	1.74E-13	CAR63632.1	59	80.1073	114	68	hypothetical protein
Locus_7097_Transcript_1/1_Conf_1.000	477	0							
Locus_7098_Transcript_1/1_Conf_1.000	631	20	1.45E-33	NP_493385.2	64	146.747	208	135	hypothetical protein Y87G2A.13

Locus_7099_Transcript_1/1_Conf_1.000	1244	20	5.01E-78	XP_001894589.1	71	296.204	280	200	DnaJ domain containing protein
Locus_71_Transcript_1/1_Conf_1.000	1124	20	2.93E-34	ACO09264.1	60	150.599	240	144	Acidic leucine-rich nuclear phosphoprotein 32 family member A
Locus_710_Transcript_1/4_Conf_0.500	1004	20	1.02E-88	NP_001040945.1	88	331.257	195	173	human HnRNP A1 homolog family member (hrp-1)
Locus_710_Transcript_2/4_Conf_0.625	1020	20	1.05E-88	NP_001040945.1	88	331.257	195	173	human HnRNP A1 homolog family member (hrp-1)
Locus_710_Transcript_3/4_Conf_0.625	1041	20	4.51E-87	NP_001040945.1	89	325.865	191	170	human HnRNP A1 homolog family member (hrp-1)
Locus_710_Transcript_4/4_Conf_0.625	1029	20	1.06E-88	NP_001040945.1	88	331.257	195	173	human HnRNP A1 homolog family member (hrp-1)
Locus_7100_Transcript_1/1_Conf_1.000	574	20	4.07E-39	XP_002630213.1	67	164.851	191	128	Hypothetical protein CBG00623
Locus_7101_Transcript_1/1_Conf_1.000	481	20	1.38E-72	NP_001040755.1	91	275.404	156	142	UBiquitin Conjugating enzyme family member (ubc-6)
Locus_7102_Transcript_1/1_Conf_1.000	1504	0							
Locus_7103_Transcript_1/1_Conf_1.000	469	20	5.07E-30	ACI49105.1	81	134.035	103	84	hypothetical protein Cbre_JD13.007
Locus_7104_Transcript_1/1_Conf_1.000	133	0							
Locus_7105_Transcript_1/1_Conf_1.000	477	0							
Locus_7106_Transcript_1/1_Conf_1.000	1908	20	6.37E-169	AAS49411.1	71	598.971	551	392	putative neuromuscular acetylcholinesterase

Locus_7107_Transcript_1/1_Conf_1.000	325	20	1.68E-41	BAG57092.1	100	172.17	79	79	unnamed protein product
Locus_7108_Transcript_1/1_Conf_1.000	1408	0							
Locus_7109_Transcript_1/1_Conf_1.000	474	0							
Locus_711_Transcript_1/1_Conf_1.000	1161	20	1.99E-25	XP_002641700.1	72	121.324	115	83	C. briggsae CBR-HLH-11 protein
Locus_7110_Transcript_1/1_Conf_1.000	908	20	2.37E-46	XP_001901856.1	88	190.274	130	115	Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit,epsilon isoform
Locus_7111_Transcript_1/2_Conf_1.000	427	0							
Locus_7111_Transcript_2/2_Conf_1.000	431	0							
Locus_7112_Transcript_1/1_Conf_1.000	532	0							
Locus_7113_Transcript_1/1_Conf_1.000	1769	20	9.94E-129	EFO20039.1	64	465.307	611	394	GRP1 binding protein
Locus_7114_Transcript_1/1_Conf_1.000	640	20	2.64E-62	NP_499704.1	75	242.276	216	162	CYtochrome P450 family member (cyp-13A11)
Locus_7115_Transcript_1/1_Conf_1.000	277	0							
Locus_7116_Transcript_1/1_Conf_1.000	1312	20	0	NP_497970.1	81	642.499	427	349	Adenylyl CYclase family member (acy-1)
Locus_7117_Transcript_1/1_Conf_1.000	1157	20	4.95E-85	NP_001041112.1	70	319.316	326	231	hypothetical protein F33E11.6
Locus_7118_Transcript_1/1_Conf_1.000	417	0							
Locus_7119_Transcript_1/1_Conf_1.000	354	20	1.04E-59	NP_497814.3	96	232.646	117	113	UNCoordinated family member (unc-79)
Locus_712_Transcript_1/2_Conf_1.000	1111	0							
Locus_712_Transcript_2/2_Conf_1.000	1111	0							

Locus_7120_Transcript_1/1_Conf_1.000	501	0							
Locus_7121_Transcript_1/3_Conf_0.714	455	20	7.51E-26	CBA11992.1	59	120.168	144	85	endonuclease-reverse transcriptase HmRTE-e01
Locus_7121_Transcript_2/3_Conf_0.429	455	20	1.91E-21	CBA11992.1	59	105.531	144	86	endonuclease-reverse transcriptase HmRTE-e01
Locus_7121_Transcript_3/3_Conf_0.714	455	20	6.79E-27	CBA11992.1	59	123.635	144	85	endonuclease-reverse transcriptase HmRTE-e01
Locus_7122_Transcript_1/1_Conf_1.000	1181	20	3.81E-64	NP_500304.3	70	249.98	206	146	hypothetical protein Y67D8A.1
Locus_7123_Transcript_1/1_Conf_1.000	637	20	8.82E-119	XP_002644713.1	94	429.869	212	200	C. briggsae CBR-UNC-97 protein
Locus_7124_Transcript_1/1_Conf_1.000	386	6	8.26E-41	XP_002639325.1	78	169.859	128	101	Hypothetical protein CBG03903
Locus_7125_Transcript_1/1_Conf_1.000	1149	20	8.26E-16	XP_001883167.1	48	89.3521	175	85	SET domain-containing protein
Locus_7126_Transcript_1/1_Conf_1.000	960	5	8.69E-143	NP_510486.2	86	510.76	319	277	hypothetical protein F20D1.3
Locus_7127_Transcript_1/1_Conf_1.000	1261	20	6.65E-70	NP_498223.2	88	269.24	184	163	Regulator of CalciNeurin family member (rcn-1)
Locus_7128_Transcript_1/1_Conf_1.000	1840	20	0	XP_002644321.1	94	647.892	362	343	C. briggsae CBR-PCCB-1 protein
Locus_7129_Transcript_1/1_Conf_1.000	232	0							

Locus_713_Transcript_1/1_Conf_1.000	481	20	1.45E-37	XP_002643164.1	90	159.073	96	87	C. briggsae CBR-HIPR-1 protein
Locus_7130_Transcript_1/1_Conf_1.000	1028	20	3.80E-54	EFO26993.1	71	216.468	254	181	hypothetical protein LOAG_01489
Locus_7131_Transcript_1/2_Conf_1.000	291	0							
Locus_7131_Transcript_2/2_Conf_1.000	921	0							
Locus_7132_Transcript_1/1_Conf_1.000	540	20	2.46E-29	XP_002642209.1	70	132.109	110	77	C. briggsae CBR-ROM-1 protein
Locus_7133_Transcript_1/1_Conf_1.000	362	0							
Locus_7134_Transcript_1/1_Conf_1.000	449	5	1.34E-14	XP_002629878.1	62	82.8037	98	61	Hypothetical protein CBG21915
Locus_7135_Transcript_1/1_Conf_1.000	413	20	1.89E-45	XP_002630183.1	85	185.267	120	103	C. briggsae CBR-FLI-1 protein
Locus_7136_Transcript_1/1_Conf_1.000	1900	20	2.05E-34	NP_490825.3	51	152.14	223	114	hypothetical protein Y48G8AL.10
Locus_7137_Transcript_1/1_Conf_1.000	536	20	1.98E-68	XP_002638874.1	83	261.922	179	149	Hypothetical protein CBG22093
Locus_7138_Transcript_1/1_Conf_1.000	580	0							
Locus_7139_Transcript_1/4_Conf_0.667	1488	20	7.08E-85	NP_001022032.1	58	319.316	507	299	TRRAP-like (transcription/transformation domain-associated protein) family member (trr-1)

Locus_7139_Transcript_2/4_Conf_0.222	696	20	1.19E-40	NP_001022032.1	60	170.629	234	142	TRRAP-like (transcription/transformation domain-associated protein) family member (trr-1)
Locus_7139_Transcript_3/4_Conf_0.667	1489	20	1.02E-83	NP_001022032.1	58	315.464	507	298	TRRAP-like (transcription/transformation domain-associated protein) family member (trr-1)
Locus_7139_Transcript_4/4_Conf_0.444	1368	20	1.12E-81	NP_001022032.1	60	308.531	456	275	TRRAP-like (transcription/transformation domain-associated protein) family member (trr-1)
Locus_714_Transcript_1/1_Conf_1.000	472	20	1.21E-41	NP_505420.1	77	132.88	110	85	hypothetical protein K07B1.7
Locus_7140_Transcript_1/1_Conf_1.000	157	20	5.87E-10	XP_002639473.1	74	67.3958	50	37	C. briggsae CBR-RNT-1 protein
Locus_7141_Transcript_1/1_Conf_1.000	879								
Locus_7142_Transcript_1/1_Conf_1.000	1314	20	5.65E-160	NP_492650.1	82	568.54	374	308	Nuclear Pore complex Protein family member (npp-17)
Locus_7143_Transcript_1/1_Conf_1.000	1221	20	1.27E-126	NP_492732.2	76	457.603	392	298	yeast SEC homolog family member (sec-8)
Locus_7144_Transcript_1/1_Conf_1.000	143	0							
Locus_7145_Transcript_1/1_Conf_1.000	374	20	3.52E-47	XP_002640000.1	88	191.045	115	102	Hypothetical protein CBG10830
Locus_7146_Transcript_1/1_Conf_1.000	319	0							
Locus_7147_Transcript_1/1_Conf_1.000	1389	0							
Locus_7148_Transcript_1/1_Conf_1.000	823	20	2.34E-71	XP_002648140.1	70	273.092	260	182	Hypothetical protein CBG24216
Locus_7149_Transcript_1/1_Conf_1.000	291	7	2.08E-07	XP_001894678.1	51	58.9214	79	41	hypothetical protein Bm1_16105

Locus_715_Transcript_1/1_Conf_1.000	2166	20	2.31E-138	XP_002634680.1	65	497.664	589	385	Hypothetical protein CBG19666
Locus_7150_Transcript_1/1_Conf_1.000	563	0							
Locus_7151_Transcript_1/1_Conf_1.000	187	0							
Locus_7152_Transcript_1/1_Conf_1.000	1240	20	1.12E-170	NP_508537.1	87	603.979	413	361	SPeCtrin family member (spc-1)
Locus_7153_Transcript_1/1_Conf_1.000	288	0							
Locus_7154_Transcript_1/2_Conf_1.000	1134	20	8.76E-119	NP_001023639.1	81	431.409	313	255	hypothetical protein C10F3.4
Locus_7154_Transcript_2/2_Conf_1.000	1925	20	1.02E-166	XP_002636829.1	78	591.652	453	357	Hypothetical protein CBG09277
Locus_7155_Transcript_1/1_Conf_1.000	133	0							
Locus_7156_Transcript_1/1_Conf_1.000	1084	20	4.25E-59	EFO25446.1	59	233.032	325	192	CK1/DUAL protein kinase
Locus_7157_Transcript_1/1_Conf_1.000	1062	16	2.41E-168	CBK19475.1	87	595.89	358	312	C. elegans protein T12G3.2e, confirmed by transcript evidence
Locus_7158_Transcript_1/1_Conf_1.000	2538	20	0	XP_002644612.1	72	797.734	762	551	C. briggsae CBR-PES-22 protein

Locus_7159_Transcript_1/1_Conf_1.000	845	20	1.27E-51	NP_502291.1	61	207.608	267	163	hypothetical protein F11A10.7
Locus_716_Transcript_1/1_Conf_1.000	635	0							
Locus_7160_Transcript_1/1_Conf_1.000	1109	20	2.94E-71	NP_506709.1	68	273.478	249	171	OTUBain deubiquitylating protease homolog family member (otub-1)
Locus_7161_Transcript_1/1_Conf_1.000	788	20	3.02E-65	XP_002646659.1	68	252.677	270	186	C. briggsae CBR-NURF-1 protein
Locus_7162_Transcript_1/1_Conf_1.000	1088	20	8.30E-63	EFO20377.1	63	245.358	294	188	plk/plk-unclassified protein kinase
Locus_7163_Transcript_1/1_Conf_1.000	448	0							
Locus_7164_Transcript_1/1_Conf_1.000	302	3	1.48E-05	EFO23400.1	54	52.7582	100	54	hypothetical protein LOAG_05084
Locus_7165_Transcript_1/1_Conf_1.000	150	20	1.77E-14	XP_002825167.1	100	82.4185	39	39	PREDICTED: heat shock protein HSP 90-alpha
Locus_7166_Transcript_1/1_Conf_1.000	219	0							
Locus_7167_Transcript_1/1_Conf_1.000	265	3	2.54E-05	NP_499134.2	53	51.9878	88	47	GEX Interacting protein family member (gei-13)
Locus_7168_Transcript_1/1_Conf_1.000	552	20	3.26E-11	EFO16473.1	86	72.0182	93	80	zinc finger protein
Locus_7169_Transcript_1/1_Conf_1.000	148	0							

Locus_717_Transcript_1/1_Conf_1.000	2244	20	0	NP_001024107.1	95	756.903	413	396	hypothetical protein T05H4.6
Locus_7170_Transcript_1/1_Conf_1.000	374	20	1.02E-62	P02751.4	100	242.662	119	119	Fibronectin
Locus_7171_Transcript_1/1_Conf_1.000	713	5	3.27E-09	NP_001122637.1	48	66.2402	215	104	hypothetical protein T12C9.7
Locus_7172_Transcript_1/1_Conf_1.000	552	20	1.01E-36	NP_001022657.1	64	156.762	164	106	hypothetical protein K02F3.12
Locus_7173_Transcript_1/1_Conf_1.000	410	20	1.28E-25	XP_002637141.1	58	119.398	143	83	C. briggsae CBR-VPS-54 protein
Locus_7174_Transcript_1/1_Conf_1.000	526	20	5.96E-46	NP_496343.1	69	187.193	191	132	PaTched Related family member (ptr-8)
Locus_7175_Transcript_1/1_Conf_1.000	338	20	2.84E-25	NP_498092.4	69	118.242	120	83	hypothetical protein Y54H5A.4
Locus_7176_Transcript_1/1_Conf_1.000	544	4	1.43E-16	XP_002639215.1	56	89.7373	155	88	C. briggsae CBR-NPP-14 protein
Locus_7177_Transcript_1/1_Conf_1.000	163	0							
Locus_7178_Transcript_1/1_Conf_1.000	435	0							
Locus_7179_Transcript_1/1_Conf_1.000	419	0							

Locus_718_Transcript_1/1_Conf_1.000	435	20	4.47E-71	NP_491363.1	97	270.396	144	140	Dynein Heavy Chain family member (dhc-1)
Locus_7180_Transcript_1/1_Conf_1.000	1285	20	2.64E-138	NP_508026.1	79	496.508	402	319	FK506-Binding protein family member (fkb-6)
Locus_7181_Transcript_1/1_Conf_1.000	479	5	1.56E-23	NP_491337.1	59	112.464	133	79	EXOCyst component family member (exoc-7)
Locus_7182_Transcript_1/3_Conf_0.600	737	20	2.65E-65	NP_500086.1	69	252.677	226	158	Nuclear Pore complex Protein family member (npp-20)
Locus_7182_Transcript_2/3_Conf_0.400	449	20	4.42E-42	NP_500086.1	69	174.096	148	103	Nuclear Pore complex Protein family member (npp-20)

Locus_7182_Transcript_3/3_Conf_0.600	864	20	6.14E-65	NP_500086.1	69	251.906	226	158	Nuclear Pore complex Protein family member (npp-20)
Locus_7183_Transcript_1/1_Conf_1.000	364	0							
Locus_7184_Transcript_1/2_Conf_1.000	393	20	1.53E-50	XP_002634173.1	88	202.216	130	115	C. briggsae CBR-HOE-1 protein
Locus_7184_Transcript_2/2_Conf_1.000	393	20	1.53E-50	XP_002634173.1	88	202.216	130	115	C. briggsae CBR-HOE-1 protein
Locus_7185_Transcript_1/2_Conf_1.000	915	2	5.44E-06	EFO25449.1	51	56.225	116	60	hypothetical protein LOAG_03032
Locus_7185_Transcript_2/2_Conf_1.000	764	3	3.89E-06	EFO25449.1	51	56.225	116	60	hypothetical protein LOAG_03032
Locus_7186_Transcript_1/1_Conf_1.000	549	20	3.06E-46	XP_002642216.1	76	188.348	171	130	C. briggsae CBR-ULA-1 protein
Locus_7187_Transcript_1/2_Conf_1.000	732	0							
Locus_7187_Transcript_2/2_Conf_1.000	628	0							
Locus_7188_Transcript_1/1_Conf_1.000	549	20	6.17E-47	ACI49253.1	74	190.66	158	117	hypothetical protein Csp3_JD07.003
Locus_7189_Transcript_1/1_Conf_1.000	1116	20	1.31E-135	XP_002648365.1	81	487.263	371	303	C. briggsae CBR-DNJ-9 protein
Locus_719_Transcript_1/1_Conf_1.000	461	0							
Locus_7190_Transcript_1/1_Conf_1.000	364	20	8.50E-38	NP_497892.1	86	159.844	93	80	PeRoxireDoXin family member (prdx-3)
Locus_7191_Transcript_1/1_Conf_1.000	444	2	3.43E-10	XP_002641308.1	55	68.1662	110	61	Hypothetical protein CBG24608
Locus_7192_Transcript_1/1_Conf_1.000	1201	20	1.11E-151	NP_491792.1	81	540.806	395	320	phenylalanyl (F) tRNA Synthetase family member (frs-1)
Locus_7193_Transcript_1/2_Conf_1.000	993	20	2.12E-30	EFO16980.1	61	137.502	194	119	hypothetical protein LOAG_11522

Locus_7193_Transcript_2/2_Conf_1.000	770	20	1.35E-30	EFO16980.1	61	137.502	194	119	hypothetical protein LOAG_11522
Locus_7194_Transcript_1/1_Conf_1.000	777	4	1.86E-51	NP_510540.1	65	206.838	264	172	hypothetical protein C33A11.1
Locus_7195_Transcript_1/1_Conf_1.000	559	3	2.43E-30	XP_002636924.1	60	135.576	164	99	C. briggsae CBR-ACL-6 protein
Locus_7196_Transcript_1/1_Conf_1.000	873	15	6.55E-22	NP_500721.1	69	108.997	121	84	hypothetical protein C02B10.2
Locus_7197_Transcript_1/1_Conf_1.000	665	0							
Locus_7198_Transcript_1/1_Conf_1.000	159	0							
Locus_7199_Transcript_1/1_Conf_1.000	1208	4	1.99E-07	NP_504527.2	41	61.6178	347	145	hypothetical protein F26F12.3
Locus_72_Transcript_1/1_Conf_1.000	3001	20	0	NP_502196.1	77	1226.85	924	716	Methionyl tRNA Synthetase family member (mrs-1)
Locus_720_Transcript_1/1_Conf_1.000	459	20	3.09E-64	XP_520919.2	99	247.669	142	141	PREDICTED: similar to ribosomal protein L28
Locus_7200_Transcript_1/1_Conf_1.000	865	5	4.39E-71	XP_002642699.1	80	272.322	205	166	C. briggsae CBR-TAG-250 protein
Locus_7201_Transcript_1/1_Conf_1.000	732	0							
Locus_7202_Transcript_1/1_Conf_1.000	899	20	4.75E-116	ABY74339.1	89	421.779	250	224	SPARC precursor
Locus_7203_Transcript_1/2_Conf_1.000	336	8	1.56E-15	XP_002633360.1	76	85.8853	63	48	C. briggsae CBR-PRX-2 protein
Locus_7203_Transcript_2/2_Conf_1.000	334	0							
Locus_7204_Transcript_1/3_Conf_0.667	1477	20	4.42E-55	EFO25376.1	53	220.32	423	228	hypothetical protein LOAG_03111
Locus_7204_Transcript_2/3_Conf_0.667	1441	20	7.29E-55	EFO25376.1	53	219.55	423	227	hypothetical protein LOAG_03111
Locus_7204_Transcript_3/3_Conf_0.667	1477	20	3.39E-55	EFO25376.1	53	220.705	423	228	hypothetical protein LOAG_03111
Locus_7205_Transcript_1/1_Conf_1.000	519	0							
Locus_7206_Transcript_1/3_Conf_0.200	250	0							
Locus_7206_Transcript_2/3_Conf_0.400	497	0							
Locus_7206_Transcript_3/3_Conf_0.700	1128	20	7.06E-28	XP_001899178.1	61	129.413	163	101	hypothetical protein

Locus_7207_Transcript_1/1_Conf_1.000	288	20	2.38E-27	XP_002634722.1	75	125.176	88	66	Hypothetical protein CBG24065
Locus_7208_Transcript_1/1_Conf_1.000	500	11	6.48E-54	NP_496839.1	74	213.386	163	122	hypothetical protein F45H10.3
Locus_7209_Transcript_1/1_Conf_1.000	543	20	9.74E-66	XP_002643274.1	88	253.062	176	155	C. briggsae CBR-MRP-2 protein
Locus_721_Transcript_1/1_Conf_1.000	1729	20	4.05E-127	NP_497103.1	69	459.914	493	345	hypothetical protein Y53F4B.18
Locus_7210_Transcript_1/1_Conf_1.000	420	20	2.21E-33	XP_002631488.1	64	145.206	146	94	C. briggsae CBR-PTR-8 protein
Locus_7211_Transcript_1/1_Conf_1.000	281	0							
Locus_7212_Transcript_1/1_Conf_1.000	199	5	4.46E-18	NP_001129755.1	94	94.3597	50	47	GLoBin family member (glb-8)
Locus_7213_Transcript_1/1_Conf_1.000	228	0							
Locus_7214_Transcript_1/2_Conf_1.000	701	4	4.39E-59	NP_505032.1	61	231.876	265	163	hypothetical protein F40A3.6
Locus_7214_Transcript_2/2_Conf_1.000	662	4	1.66E-62	NP_505032.1	65	243.047	252	164	hypothetical protein F40A3.6
Locus_7215_Transcript_1/1_Conf_1.000	709	20	2.21E-50	XP_002634804.1	73	202.986	189	139	Hypothetical protein CBG13909
Locus_7216_Transcript_1/1_Conf_1.000	1522	20	4.39E-114	XP_002634131.1	75	416.387	357	271	Hypothetical protein CBG01690
Locus_7217_Transcript_1/1_Conf_1.000	1017	20	7.37E-18	XP_002634379.1	48	95.9005	218	105	Hypothetical protein CBG17732
Locus_7218_Transcript_1/1_Conf_1.000	784	5	1.12E-11	NP_871663.1	44	74.7146	231	103	hypothetical protein ZK688.5
Locus_7219_Transcript_1/2_Conf_1.000	502	4	3.44E-18	XP_002642801.1	64	94.7449	117	75	C. briggsae CBR-CUA-1 protein

Locus_7219_Transcript_2/2_Conf_1.000	705	20	7.01E-73	XP_002642801.1	77	277.715	240	186	C. briggsae CBR-CUA-1 protein
Locus_722_Transcript_1/1_Conf_1.000	187	20	3.34E-21	EFO23627.1	88	104.76	62	55	elongation factor Tu domain-containing protein
Locus_7220_Transcript_1/2_Conf_1.000	1853	20	9.62E-106	EFO27328.1	64	389.037	448	291	calpain D
Locus_7220_Transcript_2/2_Conf_1.000	1858	20	9.97E-111	EFO27328.1	65	405.601	461	301	calpain D
Locus_7221_Transcript_1/1_Conf_1.000	151	0							
Locus_7222_Transcript_1/2_Conf_1.000	852	20	1.22E-126	XP_002641359.1	92	456.833	253	233	C. briggsae CBR-RSKS-1 protein
Locus_7222_Transcript_2/2_Conf_1.000	1365	20	1.48E-126	NP_499447.1	76	457.603	356	271	RSK-pSeventy (RSK-p70 kinase) homolog family member (rsks-1)
Locus_7223_Transcript_1/1_Conf_1.000	347	0							
Locus_7224_Transcript_1/1_Conf_1.000	810	0							
Locus_7225_Transcript_1/3_Conf_0.667	1930	20	0	CAB01686.2	71	655.21	639	460	C. elegans protein C35C5.6, partially confirmed by transcript evidence
Locus_7225_Transcript_2/3_Conf_0.667	1930	20	0	CAB01686.2	71	655.21	639	460	C. elegans protein C35C5.6, partially confirmed by transcript evidence
Locus_7225_Transcript_3/3_Conf_0.333	688	20	2.90E-76	CAB01686.2	84	288.886	221	187	C. elegans protein C35C5.6, partially confirmed by transcript evidence
Locus_7226_Transcript_1/1_Conf_1.000	860	20	3.33E-55	XP_002630541.1	82	219.55	168	139	Hypothetical protein CBG12982
Locus_7227_Transcript_1/1_Conf_1.000	218	0							
Locus_7228_Transcript_1/1_Conf_1.000	603	4	3.23E-32	XP_002630724.1	56	142.124	191	107	Hypothetical protein CBG02408

Locus_7229_Transcript_1/2_Conf_1.000	1887	20	0	EFO23157.1	92	1036.17	627	583	U5 small nuclear ribonucleoprotein helicase
Locus_7229_Transcript_2/2_Conf_1.000	1022	20	9.28E-162	EFO23157.1	90	573.933	338	306	U5 small nuclear ribonucleoprotein helicase
Locus_723_Transcript_1/1_Conf_1.000	609	20	4.02E-62	EFO16136.1	100	241.506	115	115	heterotrimeric G protein alpha subunit
Locus_7230_Transcript_1/1_Conf_1.000	400	1	2.61E-34	CAR63592.1	74	148.288	118	88	hypothetical protein
Locus_7231_Transcript_1/1_Conf_1.000	461	20	3.10E-56	XP_001158172.1	99	221.09	106	105	PREDICTED: similar to MAT8 protein isoform 8
Locus_7232_Transcript_1/1_Conf_1.000	212	0							
Locus_7233_Transcript_1/1_Conf_1.000	526	20	2.06E-30	NP_494756.1	72	135.576	131	95	hypothetical protein C01F1.1
Locus_7234_Transcript_1/1_Conf_1.000	908	20	9.55E-72	NP_509790.2	74	274.633	270	202	hypothetical protein F13E6.5
Locus_7235_Transcript_1/3_Conf_0.333	610	20	1.48E-48	XP_002639833.1	69	196.438	188	131	C. briggsae CBR-MET-1 protein
Locus_7235_Transcript_2/3_Conf_0.778	1115	20	7.59E-51	XP_002639833.1	68	205.682	202	138	C. briggsae CBR-MET-1 protein
Locus_7235_Transcript_3/3_Conf_0.778	1176	20	1.94E-68	XP_002639833.1	56	264.233	392	222	C. briggsae CBR-MET-1 protein

Locus_7236_Transcript_1/1_Conf_1.000	258	20	1.49E-21	EFO18882.1	76	105.916	86	66	hypothetical protein LOAG_09612
Locus_7237_Transcript_1/1_Conf_1.000	810	20	1.43E-57	XP_002636834.1	90	227.254	138	125	Hypothetical protein CBG09283
Locus_7238_Transcript_1/1_Conf_1.000	600	5	3.76E-33	NP_499878.3	55	145.206	214	118	COP-9 SigNalosome subunit family member (csn-3)
Locus_7239_Transcript_1/2_Conf_1.000	590	0							
Locus_7239_Transcript_2/2_Conf_1.000	590	0							
Locus_724_Transcript_1/1_Conf_1.000	1251	3	4.09E-11	XP_002642878.1	42	73.9442	333	141	Hypothetical protein CBG15148
Locus_7240_Transcript_1/1_Conf_1.000	934	9	1.13E-14	XP_001895525.1	50	85.1149	167	85	MIF4G domain containing protein
Locus_7241_Transcript_1/1_Conf_1.000	2556	20	0	XP_002637095.1	73	695.271	689	505	C. briggsae CBR-CASH-1 protein
Locus_7242_Transcript_1/1_Conf_1.000	1294	20	4.85E-140	NP_500340.1	86	502.286	354	307	hypothetical protein C04C3.3
Locus_7243_Transcript_1/1_Conf_1.000	220	0							
Locus_7244_Transcript_1/1_Conf_1.000	1153	20	2.76E-128	NP_498204.1	77	462.996	360	278	hypothetical protein C05D2.10
Locus_7245_Transcript_1/1_Conf_1.000	145	0							

Locus_7246_Transcript_1/1_Conf_1.000	552	20	1.52E-101	AAB99830.2	94	372.089	184	174	thrombospondin
Locus_7247_Transcript_1/1_Conf_1.000	1089	14	7.32E-51	P0C5E7.1	57	205.682	343	196	Phosphatidylinositol 3-kinase age-1
Locus_7248_Transcript_1/1_Conf_1.000	883	20	1.36E-51	NP_490762.1	82	207.608	210	174	hypothetical protein Y65B4A.3
Locus_7249_Transcript_1/1_Conf_1.000	233	20	1.17E-26	NP_741342.2	89	122.865	76	68	MAD (yeast Mitosis Arrest DeFicient) related family member (mdf-2)
Locus_725_Transcript_1/2_Conf_1.000	3231	20	0	NP_001129788.1	69	1075.46	1084	748	abnormal GONad development family member (gon-2)
Locus_725_Transcript_2/2_Conf_1.000	3219	20	0	NP_001129788.1	68	1070.84	1080	745	abnormal GONad development family member (gon-2)
Locus_7250_Transcript_1/1_Conf_1.000	969	20	2.46E-68	XP_001895121.1	73	263.462	226	167	hypothetical protein
Locus_7251_Transcript_1/1_Conf_1.000	767	5	3.42E-18	XP_002644049.1	54	96.2857	181	98	C. briggsae CBR-CLC-1 protein
Locus_7252_Transcript_1/2_Conf_1.000	599	20	3.82E-46	NP_001022376.1	90	188.348	108	98	hypothetical protein T27F7.3

Locus_7252_Transcript_2/2_Conf_1.000	485	20	1.59E-41	ACI49017.1	90	104.76	60	54	hypothetical protein Cbre_JD04.002
Locus_7253_Transcript_1/1_Conf_1.000	344	11	1.18E-34	NP_501890.1	76	149.443	116	89	hypothetical protein R09E10.5
Locus_7254_Transcript_1/1_Conf_1.000	1483	20	9.68E-135	XP_002633395.1	70	484.952	504	353	C. briggsae CBR-KIN-4 protein
Locus_7255_Transcript_1/1_Conf_1.000	919	20	4.15E-38	XP_001897556.1	64	162.925	190	123	Tyrosine-protein kinase abl-1
Locus_7256_Transcript_1/1_Conf_1.000	691	0							
Locus_7257_Transcript_1/1_Conf_1.000	818	20	2.92E-50	XP_001900655.1	66	202.986	188	125	Skb1 methyltransferase family protein
Locus_7258_Transcript_1/1_Conf_1.000	347	20	1.03E-30	NP_498641.1	74	136.346	113	84	hypothetical protein H14A12.3
Locus_7259_Transcript_1/1_Conf_1.000	248	0							
Locus_726_Transcript_1/1_Conf_1.000	1114	20	1.16E-75	NP_509227.2	60	288.115	374	227	hypothetical protein K03A1.2
Locus_7260_Transcript_1/1_Conf_1.000	450	20	8.32E-33	EFO25368.1	68	143.28	143	98	cytochrome P450
Locus_7261_Transcript_1/1_Conf_1.000	316	0							
Locus_7262_Transcript_1/1_Conf_1.000	547	20	3.77E-65	NP_497726.2	91	251.136	143	131	hypothetical protein M01F1.7

Locus_7263_Transcript_1/1_Conf_1.000	606	20	8.84E-62	NP_001040875.1	74	240.35	212	158	hypothetical protein T23G5.2
Locus_7264_Transcript_1/1_Conf_1.000	301	0							
Locus_7265_Transcript_1/1_Conf_1.000	377	0							
Locus_7266_Transcript_1/1_Conf_1.000	930	20	2.24E-55	NP_495987.1	74	220.32	235	174	hypothetical protein D2013.6
Locus_7267_Transcript_1/1_Conf_1.000	375	0							
Locus_7268_Transcript_1/1_Conf_1.000	1575	20	3.10E-70	NP_498631.2	78	270.781	246	193	Myc and Mondo-Like family member (mml-1)
Locus_7269_Transcript_1/1_Conf_1.000	307	16	5.36E-24	CBL87054.2	72	114.005	102	74	C. elegans protein F54E4.1, partially confirmed by transcript evidence
Locus_727_Transcript_1/1_Conf_1.000	244	0							
Locus_7270_Transcript_1/1_Conf_1.000	165	3	1.21E-15	NP_001023496.1	88	86.2705	54	48	L1 CAM ADhesion molecule homolog family member (lad-2)
Locus_7271_Transcript_1/1_Conf_1.000	608	20	3.72E-52	XP_001901281.1	66	208.379	208	138	Myb-like DNA-binding domain containing protein
Locus_7272_Transcript_1/1_Conf_1.000	626	20	4.85E-50	NP_496299.1	65	201.445	196	129	beta-LACTamase domain containing family member (lact-3)
Locus_7273_Transcript_1/1_Conf_1.000	405	6	2.87E-25	XP_002646949.1	75	118.242	126	95	C. briggsae CBR-APD-3 protein
Locus_7274_Transcript_1/1_Conf_1.000	947	1	1.37E-07	CAR63629.1	52	61.6178	104	55	hypothetical protein
Locus_7275_Transcript_1/1_Conf_1.000	1214	20	1.85E-170	NP_500304.3	84	603.208	407	343	hypothetical protein Y67D8A.1
Locus_7276_Transcript_1/1_Conf_1.000	280	0							
Locus_7277_Transcript_1/1_Conf_1.000	474	3	7.81E-07	NP_493601.2	47	56.9954	141	67	FERM domain (protein4.1-ezrin-radixin-moesin) family member (frm-1)
Locus_7278_Transcript_1/1_Conf_1.000	1030	20	8.18E-73	XP_002631068.1	81	278.485	183	150	C. briggsae CBR-NEP-1 protein
Locus_7279_Transcript_1/2_Conf_1.000	318	0							
Locus_7279_Transcript_2/2_Conf_1.000	265	0							
Locus_728_Transcript_1/4_Conf_0.700	2835	20	0	XP_002637629.1	78	848.966	617	486	C. briggsae CBR-ZTF-7 protein
Locus_728_Transcript_2/4_Conf_0.700	2832	20	0	XP_002637629.1	78	853.588	616	486	C. briggsae CBR-ZTF-7 protein

Locus_728_Transcript_3/4_Conf_0.700	2832	20	0	XP_002637629.1	78	853.588	616	486	C. briggsae CBR-ZTF-7 protein
Locus_728_Transcript_4/4_Conf_0.700	2832	20	0	XP_002637629.1	78	853.588	616	486	C. briggsae CBR-ZTF-7 protein
Locus_7280_Transcript_1/1_Conf_1.000	991	20	3.09E-90	NP_504045.1	72	336.265	325	235	hypothetical protein R08E5.3
Locus_7281_Transcript_1/1_Conf_1.000	620	20	7.18E-46	CAO00417.1	70	187.578	175	123	two-domain activation associated secreted protein ASP4 precursor
Locus_7282_Transcript_1/1_Conf_1.000	1920	20	5.90E-114	NP_001003994.1	58	416.387	600	348	MORC family CW-type zinc finger 2
Locus_7283_Transcript_1/1_Conf_1.000	358	20	6.38E-17	XP_001901741.1	71	90.5077	74	53	Eukaryotic-type DNA primase, large subunit family protein
Locus_7284_Transcript_1/1_Conf_1.000	2314	20	2.57E-175	NP_492758.1	76	620.542	530	404	hypothetical protein F25H2.2
Locus_7285_Transcript_1/1_Conf_1.000	154	0							
Locus_7286_Transcript_1/1_Conf_1.000	1274	20	2.48E-72	XP_002631278.1	61	277.33	341	210	C. briggsae CBR-PQN-47 protein
Locus_7287_Transcript_1/3_Conf_0.400	305	0							
Locus_7287_Transcript_2/3_Conf_0.600	566	20	1.64E-21	XP_001895408.1	68	106.301	102	70	Helix-loop-helix DNA-binding domain containing protein
Locus_7287_Transcript_3/3_Conf_0.600	567	16	1.45E-10	XP_001369674.1	54	50.447	112	61	PREDICTED: similar to max isoform 1
Locus_7288_Transcript_1/1_Conf_1.000	444	20	2.60E-42	XP_002631150.1	74	174.866	149	111	Hypothetical protein CBG02934
Locus_7289_Transcript_1/1_Conf_1.000	564	20	4.57E-48	XP_537270.1	78	194.512	164	129	PREDICTED: similar to haloacid dehalogenase-like hydrolase domain containing 2

Locus_729_Transcript_1/1_Conf_1.000	996	20	2.99E-133	NP_501211.1	92	479.174	282	262	hypothetical protein R05G6.7
Locus_7290_Transcript_1/1_Conf_1.000	493	4	2.35E-19	NP_741449.1	56	98.5969	153	87	hypothetical protein C06A6.2
Locus_7291_Transcript_1/1_Conf_1.000	1647	20	6.03E-173	XP_002641548.1	84	612.068	412	350	C. briggsae CBR-FEH-1 protein
Locus_7292_Transcript_1/1_Conf_1.000	438	20	6.24E-57	NP_001041140.1	88	223.402	131	116	hypothetical protein F58H1.7
Locus_7293_Transcript_1/1_Conf_1.000	1267	6	7.19E-56	XP_002642052.1	62	222.631	274	171	Hypothetical protein CBG17990
Locus_7294_Transcript_1/1_Conf_1.000	734	20	5.17E-37	NP_510460.2	63	158.688	174	111	MiniBrain Kinase (Drosophila) homolog family member (mbk-1)
Locus_7295_Transcript_1/1_Conf_1.000	1153	20	3.60E-19	XP_002636474.1	48	100.523	352	169	C. briggsae CBR-IMA-1 protein
Locus_7296_Transcript_1/1_Conf_1.000	1444	20	1.85E-82	XP_002642257.1	75	311.227	273	207	C. briggsae CBR-SET-16 protein
Locus_7297_Transcript_1/1_Conf_1.000	373	20	6.02E-39	XP_002635565.1	94	163.696	123	116	Hypothetical protein CBG20548
Locus_7298_Transcript_1/1_Conf_1.000	404	20	1.09E-40	EFO19039.1	81	169.474	134	109	Tln1 protein

Locus_7299_Transcript_1/1_Conf_1.000	414	20	1.83E-24	BAJ10384.1	71	115.546	91	65	aurora kinase
Locus_73_Transcript_1/5_Conf_0.429	432	0							
Locus_73_Transcript_2/5_Conf_0.190	1164	20	2.99E-130	NP_501838.2	74	469.544	368	274	hypothetical protein C04G2.9
Locus_73_Transcript_3/5_Conf_0.190	1164	20	2.99E-130	NP_501838.2	74	469.544	368	274	hypothetical protein C04G2.9
Locus_73_Transcript_4/5_Conf_0.095	553	20	2.14E-71	P51535.1	92	271.937	154	142	Myoglobin
Locus_73_Transcript_5/5_Conf_0.619	795	20	6.07E-37	XP_002634040.1	58	158.688	236	139	C. briggsae CBR-VIT-6 protein
Locus_730_Transcript_1/1_Conf_1.000	2820	20	0	NP_001040989.1	86	1228.39	873	754	hypothetical protein T14G10.5

Locus_7300_Transcript_1/3_Conf_0.667	1230	20	3.13E-157	NP_500191.3	86	559.296	393	338	ParaPleGiN AAA protease family member (ppgn-1)
Locus_7300_Transcript_2/3_Conf_0.667	1215	20	4.01E-157	NP_500191.3	86	558.91	393	338	ParaPleGiN AAA protease family member (ppgn-1)
Locus_7300_Transcript_3/3_Conf_0.667	1215	20	3.07E-157	NP_500191.3	86	559.296	393	338	ParaPleGiN AAA protease family member (ppgn-1)
Locus_7301_Transcript_1/1_Conf_1.000	466	6	3.90E-30	NP_741868.1	87	134.42	82	72	Apical Junction Molecule family member (ajm-1)
Locus_7302_Transcript_1/1_Conf_1.000	1582	20	0	XP_002638687.1	79	640.958	471	375	Hypothetical protein CBG11882
Locus_7303_Transcript_1/1_Conf_1.000	739	20	1.73E-72	XP_002636543.1	75	276.559	244	184	Hypothetical protein CBG23230

Locus_7304_Transcript_1/1_Conf_1.000	239	3	3.89E-06	NP_741355.2	64	54.6842	62	40	hypothetical protein Y67D8A.2
Locus_7305_Transcript_1/1_Conf_1.000	2327	20	1.72E-86	XP_002648991.1	67	325.479	318	214	C. briggsae CBR-ULP-1 protein
Locus_7306_Transcript_1/1_Conf_1.000	1815	20	0	NP_499949.2	84	801.201	550	463	Gut on EXterior family member (gex-2)
Locus_7307_Transcript_1/1_Conf_1.000	1176	20	6.39E-104	NP_492254.1	96	382.104	186	180	protein KINase family member (kin-10)

Locus_7308_Transcript_1/3_Conf_0.400	274	0							
Locus_7308_Transcript_2/3_Conf_0.400	447	2	6.24E-04	XP_002091979.1	72	47.3654	61	44	GE11922
Locus_7308_Transcript_3/3_Conf_0.400	1159	20	8.59E-37	XP_002647311.1	56	159.073	346	195	Hypothetical protein CBG06352
Locus_7309_Transcript_1/1_Conf_1.000	484	20	6.23E-36	NP_491096.1	70	153.68	129	91	Zinc finger Transcription Factor family member (ztf-23)
Locus_731_Transcript_1/3_Conf_0.667	780	20	2.17E-108	NP_498642.1	92	395.971	229	212	FUMarase family member (fum-1)
Locus_731_Transcript_2/3_Conf_0.667	834	20	2.81E-112	NP_498642.1	93	409.068	247	230	FUMarase family member (fum-1)
Locus_731_Transcript_3/3_Conf_0.667	834	20	2.81E-112	NP_498642.1	93	409.068	247	230	FUMarase family member (fum-1)
Locus_7310_Transcript_1/1_Conf_1.000	333	0							
Locus_7311_Transcript_1/1_Conf_1.000	163	0							
Locus_7312_Transcript_1/1_Conf_1.000	360	13	7.00E-32	A8Y3Q1.2	79	140.198	104	83	Putative 28S ribosomal protein S5

Locus_7313_Transcript_1/1_Conf_1.000	712	20	4.64E-64	XP_001898420.1	71	248.44	215	154	ATP-dependent DNA helicase, RecQ family protein
Locus_7314_Transcript_1/1_Conf_1.000	518	20	9.46E-70	ACR27076.1	100	266.159	122	122	transforming growth protein 2-like protein
Locus_7315_Transcript_1/1_Conf_1.000	1258	20	1.97E-114	EFO20863.1	72	417.157	418	301	hypothetical protein LOAG_07626
Locus_7316_Transcript_1/2_Conf_1.000	768	0							
Locus_7316_Transcript_2/2_Conf_1.000	720	0							
Locus_7317_Transcript_1/1_Conf_1.000	446	20	4.00E-59	AAX43301.1	100	230.72	115	115	ribosomal protein L30
Locus_7318_Transcript_1/1_Conf_1.000	300	0							
Locus_7319_Transcript_1/1_Conf_1.000	664	20	3.81E-107	NP_499860.1	94	391.349	208	197	TPA (tetradecanoyl phorbol acetate) resistant family member (tpa-1)
Locus_732_Transcript_1/1_Conf_1.000	971	20	1.90E-28	EFO24421.1	50	130.954	244	124	hypothetical protein LOAG_04066
Locus_7320_Transcript_1/1_Conf_1.000	1063	20	0	ACZ64269.1	96	666.381	352	338	astacin metalloprotease b
Locus_7321_Transcript_1/1_Conf_1.000	305	0							
Locus_7322_Transcript_1/1_Conf_1.000	392	0							
Locus_7323_Transcript_1/2_Conf_1.000	1246	4	9.98E-18	XP_002640607.1	53	95.9005	182	97	Hypothetical protein CBG08718
Locus_7323_Transcript_2/2_Conf_1.000	388	0							
Locus_7324_Transcript_1/1_Conf_1.000	306	0							
Locus_7325_Transcript_1/1_Conf_1.000	286	5	9.40E-16	NP_502089.1	69	86.6557	84	58	PreFolDin (molecular chaperone) family member (pfd-1)

Locus_7326_Transcript_1/1_Conf_1.000	189	2	5.71E-05	EFO20005.1	75	50.8322	37	28	RhoGAP domain-containing protein
Locus_7327_Transcript_1/1_Conf_1.000	1004	20	4.07E-138	XP_002641056.1	85	495.352	320	273	Hypothetical protein CBG22467
Locus_7328_Transcript_1/1_Conf_1.000	1009	20	4.99E-43	EFO22115.1	57	179.489	308	176	hypothetical protein LOAG_06367
Locus_7329_Transcript_1/1_Conf_1.000	1296	5	9.42E-51	XP_002646407.1	61	205.682	230	142	Hypothetical protein CBG15386
Locus_733_Transcript_1/2_Conf_1.000	3295	20	0	NP_001020999.1	56	734.561	1096	617	abnormal cell LINeage family member (lin-41)
Locus_733_Transcript_2/2_Conf_1.000	3235	20	0	NP_001020999.1	57	744.577	1077	618	abnormal cell LINeage family member (lin-41)
Locus_7330_Transcript_1/2_Conf_1.000	715	7	6.86E-15	NP_499074.2	46	85.1149	241	113	abnormal EMBroygenesis family member (emb-30)
Locus_7330_Transcript_2/2_Conf_1.000	547	7	1.50E-13	XP_002641754.1	47	79.7221	188	90	C. briggsae CBR-EMB-30 protein
Locus_7331_Transcript_1/1_Conf_1.000	197	0							
Locus_7332_Transcript_1/1_Conf_1.000	1152	20	1.06E-103	NP_493980.1	82	381.333	308	253	hypothetical protein H17B01.4
Locus_7333_Transcript_1/1_Conf_1.000	736	20	7.06E-26	NP_001122423.1	75	121.709	86	65	hypothetical protein C25A1.16
Locus_7334_Transcript_1/1_Conf_1.000	744	0							
Locus_7335_Transcript_1/1_Conf_1.000	376	20	1.39E-19	NP_508184.2	90	99.3673	55	50	AdaPtin, Mu/medium chain (clathrin associated complex) family member (apm-3)

Locus_7336_Transcript_1/1_Conf_1.000	723	20	8.21E-72	NP_499667.1	83	274.248	184	153	ARp2/3 compleX component family member (arx-5)
Locus_7337_Transcript_1/1_Conf_1.000	429	1	9.57E-05	EFO27420.1	54	50.0618	68	37	TK/FER protein kinase
Locus_7338_Transcript_1/1_Conf_1.000	681	20	2.04E-74	XP_002646580.1	82	282.722	205	170	C. briggsae CBR-XPA-1 protein
Locus_7339_Transcript_1/1_Conf_1.000	207	2	1.47E-05	NP_497647.1	72	52.7582	44	32	hypothetical protein Y55D5A.3
Locus_734_Transcript_1/1_Conf_1.000	915	0							
Locus_7340_Transcript_1/1_Conf_1.000	333	6	4.56E-15	XP_001899397.1	62	84.3445	108	68	hypothetical protein Bm1_39710
Locus_7341_Transcript_1/1_Conf_1.000	176	0							
Locus_7342_Transcript_1/1_Conf_1.000	594	20	1.07E-24	XP_002637561.1	79	117.087	98	78	Hypothetical protein CBG19294
Locus_7343_Transcript_1/2_Conf_1.000	643	20	2.44E-31	NP_500284.2	63	139.428	217	138	Enhancer of EfL-1 mutant phenotype family member (eel-1)
Locus_7343_Transcript_2/2_Conf_1.000	637	20	7.40E-33	NP_500284.2	64	144.436	215	138	Enhancer of EfL-1 mutant phenotype family member (eel-1)
Locus_7344_Transcript_1/1_Conf_1.000	390	0							
Locus_7345_Transcript_1/1_Conf_1.000	996	20	4.41E-52	XP_002646168.1	70	209.534	215	151	Hypothetical protein CBG23731
Locus_7346_Transcript_1/1_Conf_1.000	751	20	9.46E-90	NP_497347.3	79	333.954	249	199	hypothetical protein Y119D3B.16
Locus_7347_Transcript_1/1_Conf_1.000	683	20	5.41E-43	XP_002642660.1	58	178.333	200	116	Hypothetical protein CBG12241
Locus_7348_Transcript_1/1_Conf_1.000	559	0							
Locus_7349_Transcript_1/2_Conf_1.000	557	20	4.25E-75	NP_495662.2	85	284.263	184	157	PaTChed family member (ptc-1)

Locus_7349_Transcript_2/2_Conf_1.000	557	20	4.25E-75	NP_495662.2	85	284.263	184	157	PaTChed family member (ptc-1)
Locus_735_Transcript_1/1_Conf_1.000	229	0							
Locus_7350_Transcript_1/1_Conf_1.000	1715	20	0	EFO23679.1	70	641.728	608	431	hypothetical protein LOAG_04806
Locus_7351_Transcript_1/1_Conf_1.000	459	1	9.46E-05	EFA84537.1	76	50.0618	38	29	putative transmembrane protein
Locus_7352_Transcript_1/2_Conf_1.000	651	3	6.35E-83	NP_498952.1	83	310.842	212	176	hypothetical protein F44E2.4
Locus_7352_Transcript_2/2_Conf_1.000	651	3	6.35E-83	NP_498952.1	83	310.842	212	176	hypothetical protein F44E2.4
Locus_7353_Transcript_1/1_Conf_1.000	159	3	7.64E-10	NP_001122554.1	82	67.0106	50	41	hypothetical protein Y71G12A.2
Locus_7354_Transcript_1/1_Conf_1.000	361	0							
Locus_7355_Transcript_1/1_Conf_1.000	1080	20	2.42E-139	XP_002639071.1	83	499.59	344	288	C. briggsae CBR-TOM-1 protein
Locus_7356_Transcript_1/1_Conf_1.000	1389	9	9.33E-60	NP_499134.2	75	235.728	197	149	GEX Interacting protein family member (gei-13)
Locus_7357_Transcript_1/1_Conf_1.000	173	20	2.76E-20	XP_002643051.1	87	101.679	57	50	C. briggsae CBR-DPF-6 protein
Locus_7358_Transcript_1/1_Conf_1.000	493	20	2.19E-33	XP_001892233.1	87	145.206	89	78	mothers against decapentaplegic homolog 3

Locus_7359_Transcript_1/1_Conf_1.000	715	20	8.46E-98	XP_002640509.1	86	360.533	238	207	C. briggsae CBR-RGA-2 protein
Locus_736_Transcript_1/1_Conf_1.000	1126	20	0	NP_497787.1	95	690.649	375	358	Paralysed Arrest at Two-fold family member (pat-3)
Locus_7360_Transcript_1/2_Conf_1.000	375	0							
Locus_7360_Transcript_2/2_Conf_1.000	381	0							
Locus_7361_Transcript_1/1_Conf_1.000	329	0							
Locus_7362_Transcript_1/1_Conf_1.000	1421	20	3.78E-56	XP_002634601.1	55	223.787	363	203	C. briggsae CBR-DCAP-1 protein
Locus_7363_Transcript_1/2_Conf_1.000	1002	20	5.69E-132	NP_498822.2	82	474.937	335	276	abnormal cell MIGration family member (mig-10)
Locus_7363_Transcript_2/2_Conf_1.000	1002	20	5.69E-132	NP_498822.2	82	474.937	335	276	abnormal cell MIGration family member (mig-10)
Locus_7364_Transcript_1/2_Conf_1.000	647	20	1.67E-13	XP_002646166.1	70	58.5362	54	38	Hypothetical protein CBG23728
Locus_7364_Transcript_2/2_Conf_1.000	532	20	3.22E-18	NP_492164.1	67	95.1301	129	87	hypothetical protein F30F8.3
Locus_7365_Transcript_1/1_Conf_1.000	536	20	1.38E-53	NP_502166.1	86	212.616	138	119	MBF (multiprotein bridging factor) transcriptional coactivator family member (mbf-1)
Locus_7366_Transcript_1/1_Conf_1.000	436	0							
Locus_7367_Transcript_1/1_Conf_1.000	391	20	3.47E-15	NP_497059.1	60	84.7297	129	78	TACC (transforming acid coiled coil) protein family member (tac-1)
Locus_7368_Transcript_1/2_Conf_1.000	1947	20	3.46E-146	XP_002630713.1	71	523.472	532	381	Hypothetical protein CBG02397
Locus_7368_Transcript_2/2_Conf_1.000	1903	20	9.85E-146	XP_002630713.1	70	521.931	517	366	Hypothetical protein CBG02397

Locus_7369_Transcript_1/1_Conf_1.000	1143	20	6.20E-56	EFO20168.1	53	222.631	366	197	PHD-finger family protein
Locus_737_Transcript_1/2_Conf_1.000	602	20	7.88E-15	XP_002435868.1	73	84.3445	72	53	ubiquitin specific protease, putative
Locus_737_Transcript_2/2_Conf_1.000	533	20	1.96E-07	CBH11658.1	74	59.3066	51	38	ubiquitin hydrolase, putative
Locus_7370_Transcript_1/1_Conf_1.000	304	0							
Locus_7371_Transcript_1/1_Conf_1.000	527	2	1.88E-07	XP_002647571.1	53	59.3066	95	51	Hypothetical protein CBG06657
Locus_7372_Transcript_1/1_Conf_1.000	423	0							
Locus_7373_Transcript_1/1_Conf_1.000	277	20	4.10E-32	3HOF	100	140.969	68	68	Structure Of Macrophage Migration Inhibitory Factor (Mif) With Caffeic Acid At 1.9a Resolution
Locus_7374_Transcript_1/1_Conf_1.000	311	20	5.32E-40	NP_001076680.1	87	167.162	103	90	hypothetical protein F13H10.3
Locus_7375_Transcript_1/1_Conf_1.000	1417	20	2.00E-174	NP_499157.2	80	616.69	475	383	hypothetical protein T05G5.8
Locus_7376_Transcript_1/1_Conf_1.000	375	20	5.07E-38	XP_001899898.1	77	160.614	119	92	LMBR1-like conserved region family protein
Locus_7377_Transcript_1/1_Conf_1.000	804	20	2.73E-117	XP_001898305.1	85	425.631	268	229	Transmembrane 9 superfamily protein member 2 precursor, putative

Locus_7378_Transcript_1/1_Conf_1.000	564	20	8.53E-79	XP_002637342.1	93	296.59	187	174	C. briggsae CBR-UNC-70 protein
Locus_7379_Transcript_1/1_Conf_1.000	585	0							
Locus_738_Transcript_1/1_Conf_1.000	347	12	7.17E-16	NP_502675.4	62	87.0409	106	66	hypothetical protein Y37A1A.3
Locus_7380_Transcript_1/1_Conf_1.000	290	0							
Locus_7381_Transcript_1/1_Conf_1.000	791	0							
Locus_7382_Transcript_1/1_Conf_1.000	457	20	1.67E-09	NP_494315.1	58	65.855	100	58	hypothetical protein F22E5.8
Locus_7383_Transcript_1/1_Conf_1.000	1653	20	5.91E-144	XP_002645201.1	78	515.768	411	324	C. briggsae CBR-BCAT-1 protein
Locus_7384_Transcript_1/1_Conf_1.000	285	20	3.81E-25	NP_509879.2	76	117.857	96	73	hypothetical protein C03A3.2
Locus_7385_Transcript_1/1_Conf_1.000	315	18	1.11E-08	NP_740774.1	69	63.1586	86	60	hypothetical protein Y48G1A.4
Locus_7386_Transcript_1/2_Conf_1.000	1130	20	2.37E-108	XP_002638797.1	75	396.741	315	238	Hypothetical protein CBG05152
Locus_7386_Transcript_2/2_Conf_1.000	1087	20	2.23E-108	XP_002638797.1	75	396.741	315	238	Hypothetical protein CBG05152
Locus_7387_Transcript_1/1_Conf_1.000	721	20	1.63E-88	NP_496708.2	79	329.717	239	189	hypothetical protein Y46G5A.2
Locus_7388_Transcript_1/1_Conf_1.000	1313	20	1.11E-131	NP_506513.1	78	474.552	345	272	TRNA Methylase family member (trm-1)
Locus_7389_Transcript_1/1_Conf_1.000	320	20	4.03E-43	NP_001021405.1	87	177.563	106	93	asparagiNyl tRNA Synthetase family member (nrs-1)
Locus_739_Transcript_1/1_Conf_1.000	722	20	6.62E-90	EFO24963.1	80	334.339	240	192	hypothetical protein LOAG_03520
Locus_7390_Transcript_1/1_Conf_1.000	158	0							
Locus_7391_Transcript_1/1_Conf_1.000	250	0							

Locus_7392_Transcript_1/1_Conf_1.000	500	20	1.01E-30	NP_492783.1	77	136.346	104	81	Temporarily Assigned Gene name family member (tag-264)
Locus_7393_Transcript_1/1_Conf_1.000	228	0							
Locus_7394_Transcript_1/1_Conf_1.000	359	20	7.49E-42	XP_002629939.1	85	173.326	115	98	Hypothetical protein CBG03659
Locus_7395_Transcript_1/1_Conf_1.000	1286	20	5.87E-138	NP_506417.1	85	495.352	323	275	Seven WD repeats, AN11 family member (swan-2)
Locus_7396_Transcript_1/1_Conf_1.000	154	6	1.83E-11	NP_001021110.1	86	72.4034	50	43	CAlSYntenin/Alcadein homolog family member (casy-1)
Locus_7397_Transcript_1/1_Conf_1.000	664	1	3.79E-06	ACI49256.1	48	55.8398	140	68	hypothetical protein Csp3_JD07.006
Locus_7398_Transcript_1/2_Conf_1.000	673	20	3.18E-40	NP_500284.2	60	169.088	220	134	Enhancer of EfL-1 mutant phenotype family member (eel-1)
Locus_7398_Transcript_2/2_Conf_1.000	741	20	6.92E-45	XP_002633684.1	60	184.882	246	149	C. briggsae CBR-EEL-1 protein
Locus_7399_Transcript_1/1_Conf_1.000	1225	20	1.37E-112	NP_001020973.1	74	410.994	408	303	hypothetical protein B0414.8
Locus_74_Transcript_1/1_Conf_1.000	1095	20	1.34E-68	XP_002645928.1	80	264.618	186	150	C. briggsae CBR-TAG-97 protein
Locus_740_Transcript_1/3_Conf_0.500	420	0							
Locus_740_Transcript_2/3_Conf_0.667	942	20	6.97E-20	EFO19007.1	48	102.449	245	118	hypothetical protein LOAG_09488
Locus_740_Transcript_3/3_Conf_0.500	421	0							

Locus_7400_Transcript_1/2_Conf_1.000	701	20	2.60E-19	EFO16251.1	92	99.7525	54	50	hypothetical protein LOAG_12257
Locus_7400_Transcript_2/2_Conf_1.000	608	20	2.20E-20	CAO82046.4	86	102.834	60	52	C. elegans protein F43D9.3b, confirmed by transcript evidence
Locus_7401_Transcript_1/1_Conf_1.000	1411	6	5.97E-62	NP_741405.1	55	243.047	459	255	SKiNhead family member (skn-1)
Locus_7402_Transcript_1/1_Conf_1.000	1232	20	1.94E-74	NP_491320.1	83	284.263	183	152	hypothetical protein R12E2.13
Locus_7403_Transcript_1/1_Conf_1.000	548	20	1.41E-11	AAD51334.1	65	73.1738	61	40	Kunitz type serine protease inhibitor
Locus_7404_Transcript_1/1_Conf_1.000	141	0							
Locus_7405_Transcript_1/1_Conf_1.000	506	3	4.03E-22	ACI49066.1	70	107.842	117	83	hypothetical protein Cbre_JD09.010
Locus_7406_Transcript_1/2_Conf_1.000	652	4	3.90E-32	EFO22827.1	63	142.124	172	109	hypothetical protein LOAG_05660
Locus_7406_Transcript_2/2_Conf_1.000	912	4	3.45E-53	EFO22827.1	61	213.001	267	165	hypothetical protein LOAG_05660
Locus_7407_Transcript_1/1_Conf_1.000	1416	3	3.93E-29	NP_492328.1	52	134.035	232	122	yeast Enhancer of DeCapping homolog family member (edc-3)
Locus_7408_Transcript_1/1_Conf_1.000	754	7	7.06E-45	NP_001023039.1	84	184.882	131	111	EXCretory canal abnormal family member (exc-5)
Locus_7409_Transcript_1/1_Conf_1.000	734	20	2.70E-86	AAP36551.1	100	322.398	178	178	Homo sapiens FXYD domain containing ion transport regulator 5
Locus_741_Transcript_1/1_Conf_1.000	670	20	2.43E-117	XP_002799759.1	100	425.246	211	211	PREDICTED: 40S ribosomal protein S2-like
Locus_7410_Transcript_1/3_Conf_0.714	899	20	4.53E-50	XP_002633239.1	62	202.601	311	193	C. briggsae CBR-DNC-1 protein
Locus_7410_Transcript_2/3_Conf_0.714	899	20	1.32E-49	XP_002633239.1	62	201.06	311	193	C. briggsae CBR-DNC-1 protein

Locus_7410_Transcript_3/3_Conf_0.714	899	20	1.32E-49	XP_002633239.1	62	201.06	311	193	C. briggsae CBR-DNC-1 protein
Locus_7411_Transcript_1/2_Conf_1.000	624	0							
Locus_7411_Transcript_2/2_Conf_1.000	615	0							
Locus_7412_Transcript_1/1_Conf_1.000	1586	20	1.39E-94	NP_503136.2	58	351.673	501	294	hypothetical protein Y38C9A.1
Locus_7413_Transcript_1/1_Conf_1.000	268	3	3.19E-08	NP_494366.2	81	61.6178	44	36	hypothetical protein F08D12.1
Locus_7414_Transcript_1/1_Conf_1.000	446	0							
Locus_7415_Transcript_1/1_Conf_1.000	439	2	2.40E-08	XP_001898153.1	70	62.003	58	41	RNA polymerase II:SUBUNIT=110kD.
Locus_7416_Transcript_1/1_Conf_1.000	487	14	6.23E-20	XP_002645614.1	60	100.523	123	75	Hypothetical protein CBG05337
Locus_7417_Transcript_1/1_Conf_1.000	406	0							
Locus_7418_Transcript_1/1_Conf_1.000	854	20	1.11E-127	XP_002636822.1	99	460.299	248	246	C. briggsae CBR-RPT-2 protein
Locus_7419_Transcript_1/1_Conf_1.000	609	2	6.96E-14	NP_508128.1	74	81.2629	83	62	hypothetical protein F13C5.5
Locus_742_Transcript_1/1_Conf_1.000	1034	20	3.00E-91	NP_001129807.1	70	339.732	316	222	hypothetical protein C08H9.2
Locus_7420_Transcript_1/1_Conf_1.000	777	20	6.77E-78	XP_002593329.1	79	294.664	235	186	hypothetical protein BRAFLDRAFT_119583

Locus_7421_Transcript_1/1_Conf_1.000	821	20	2.76E-40	EFO26611.1	57	169.859	242	139	hypothetical protein LOAG_01867
Locus_7422_Transcript_1/1_Conf_1.000	141	0							
Locus_7423_Transcript_1/1_Conf_1.000	274	0							
Locus_7424_Transcript_1/1_Conf_1.000	973	20	4.52E-54	NP_501489.2	79	216.083	169	134	hypothetical protein F08B4.5
Locus_7425_Transcript_1/1_Conf_1.000	1527	20	5.93E-127	NP_498138.2	70	459.144	400	282	hypothetical protein F52C9.3
Locus_7426_Transcript_1/1_Conf_1.000	253	20	9.67E-45	XP_002818294.1	100	182.956	84	84	PREDICTED: collagen alpha-2(I) chain-like
Locus_7427_Transcript_1/1_Conf_1.000	745	20	4.18E-82	XP_002634568.1	90	308.531	180	163	Hypothetical protein CBG08374
Locus_7428_Transcript_1/1_Conf_1.000	546	20	2.40E-11	EFO24929.1	64	72.4034	77	50	hypothetical protein LOAG_03556
Locus_7429_Transcript_1/2_Conf_0.500	1720	20	2.62E-110	XP_002630825.1	56	404.06	681	383	Hypothetical protein CBG02527
Locus_7429_Transcript_2/2_Conf_0.500	1720	20	2.62E-110	XP_002630825.1	56	404.06	681	383	Hypothetical protein CBG02527
Locus_743_Transcript_1/1_Conf_1.000	788	20	3.82E-60	XP_002635477.1	82	235.728	200	165	Hypothetical protein CBG08772
Locus_7430_Transcript_1/1_Conf_1.000	568	20	1.14E-54	XP_002640720.1	77	216.468	190	148	C. briggsae CBR-TAG-301 protein

Locus_7431_Transcript_1/1_Conf_1.000	313	20	2.15E-44	NP_492363.1	95	181.8	103	98	yeast PRP (splicing factor) related family member (prp-4)
Locus_7432_Transcript_1/1_Conf_1.000	632	20	4.22E-41	XP_001899546.1	68	171.785	167	115	hypothetical protein
Locus_7433_Transcript_1/1_Conf_1.000	498	20	3.09E-72	NP_492593.2	87	274.248	165	144	hypothetical protein F26E4.3
Locus_7434_Transcript_1/1_Conf_1.000	841	20	7.19E-23	XP_002634943.1	49	112.079	212	104	Hypothetical protein CBG22545
Locus_7435_Transcript_1/1_Conf_1.000	407	0							
Locus_7436_Transcript_1/2_Conf_1.000	540	20	1.02E-67	NP_500987.3	88	259.61	149	132	hypothetical protein Y73B6BL.1
Locus_7436_Transcript_2/2_Conf_1.000	417	2	4.33E-37	NP_500987.3	63	157.532	149	94	hypothetical protein Y73B6BL.1
Locus_7437_Transcript_1/1_Conf_1.000	160	0							
Locus_7438_Transcript_1/1_Conf_1.000	776	20	4.91E-121	NP_001129749.1	95	437.958	262	249	abnormal cell LINeage family member (lin-10)
Locus_7439_Transcript_1/1_Conf_1.000	328	20	2.60E-26	XP_002631178.1	71	121.709	108	77	C. briggsae CBR-MAT-2 protein
Locus_744_Transcript_1/1_Conf_1.000	1468	20	1.64E-118	XP_001894786.1	76	431.024	335	256	DnaJ homolog subfamily B member 4
Locus_7440_Transcript_1/1_Conf_1.000	673	0							
Locus_7441_Transcript_1/1_Conf_1.000	138	13	3.47E-15	EFO15646.1	91	84.7297	45	41	hypothetical protein LOAG_12863
Locus_7442_Transcript_1/1_Conf_1.000	487	5	2.89E-25	NP_001123108.1	70	118.242	135	95	hypothetical protein C14H10.3
Locus_7443_Transcript_1/1_Conf_1.000	355	20	1.41E-56	EFO26612.1	93	222.246	118	110	hypothetical protein LOAG_01868

Locus_7444_Transcript_1/1_Conf_1.000	922	20	2.94E-100	XP_002637600.1	80	369.392	294	238	C. briggsae CBR-SULP-8 protein
Locus_7445_Transcript_1/1_Conf_1.000	721	20	2.20E-93	NP_491261.1	90	345.895	198	180	Proteasome Beta Subunit family member (pbs-4)
Locus_7446_Transcript_1/1_Conf_1.000	206	0							
Locus_7447_Transcript_1/1_Conf_1.000	528	20	1.26E-75	NP_497920.3	90	285.804	150	135	hypothetical protein M88.7
Locus_7448_Transcript_1/1_Conf_1.000	501	20	1.77E-06	XP_001839086.2	54	55.8398	118	64	hypothetical protein CC1G_10651
Locus_7449_Transcript_1/1_Conf_1.000	1222	20	2.88E-171	NP_499556.1	82	605.905	407	337	NitFhit family member (nft-1)
Locus_745_Transcript_1/1_Conf_1.000	350	0							
Locus_7450_Transcript_1/1_Conf_1.000	391	19	5.17E-19	NP_498112.1	60	97.4413	134	81	PRotein arginine MethylTransferase family member (prmt-5)
Locus_7451_Transcript_1/1_Conf_1.000	1220	20	1.15E-103	CAQ58114.2	76	381.333	311	238	C. elegans protein H21P03.3c, partially confirmed by transcript evidence
Locus_7452_Transcript_1/1_Conf_1.000	722	4	4.78E-64	XP_002636230.1	71	248.44	246	176	Hypothetical protein CBG12154

Locus_7453_Transcript_1/1_Conf_1.000	465	20	5.63E-29	EFO18511.1	72	130.568	104	75	zinc finger in N-recognin family protein
Locus_7454_Transcript_1/1_Conf_1.000	798	20	1.44E-86	NP_508216.1	81	323.553	249	202	Sorting NeXin family member (snx-1)
Locus_7455_Transcript_1/1_Conf_1.000	912	20	4.61E-90	XP_002646678.1	84	335.495	217	184	Hypothetical protein CBG11120
Locus_7456_Transcript_1/1_Conf_1.000	843	0							
Locus_7457_Transcript_1/1_Conf_1.000	707	20	2.00E-19	EFO23663.1	72	100.138	111	80	myosin xviiia
Locus_7458_Transcript_1/1_Conf_1.000	331	6	2.05E-23	EFO20439.1	66	112.079	112	74	hypothetical protein LOAG_08053
Locus_7459_Transcript_1/1_Conf_1.000	189	0							
Locus_746_Transcript_1/1_Conf_1.000	620	20	1.32E-23	XP_001895452.1	59	113.62	169	101	DNA mismatch repair protein MutL containing protein
Locus_7460_Transcript_1/1_Conf_1.000	639	5	5.41E-07	NP_498661.1	74	58.5362	62	46	LiPid Depleted family member (lpd-7)
Locus_7461_Transcript_1/1_Conf_1.000	667	0							
Locus_7462_Transcript_1/1_Conf_1.000	297	0							

Locus_7463_Transcript_1/1_Conf_1.000	341	20	5.16E-19	NP_501593.1	93	97.4413	48	45	RNA Polymerase II (B) subunit family member (rpb-12)
Locus_7464_Transcript_1/1_Conf_1.000	368	20	4.65E-36	XP_002648989.1	85	154.066	109	93	C. briggsae CBR-GRS-1 protein
Locus_7465_Transcript_1/1_Conf_1.000	1626	20	1.30E-103	XP_002641128.1	61	381.719	472	291	Hypothetical protein CBG08978
Locus_7466_Transcript_1/1_Conf_1.000	1068	20	1.25E-55	XP_002031100.1	70	221.476	227	161	GM24211
Locus_7467_Transcript_1/1_Conf_1.000	1585	20	9.09E-70	XP_001899173.1	52	269.24	550	288	ENTH domain containing protein
Locus_7468_Transcript_1/1_Conf_1.000	1030	20	1.93E-98	NP_506927.2	83	363.614	293	246	HAlF transporter (PGP related) family member (haf-3)
Locus_7469_Transcript_1/2_Conf_1.000	638	3	1.01E-05	EFO26068.1	39	54.299	207	82	hypothetical protein LOAG_02419
Locus_7469_Transcript_2/2_Conf_1.000	638	4	7.71E-06	AAI39651.1	41	54.6842	180	75	Si:busm1-142b24.1 protein
Locus_747_Transcript_1/1_Conf_1.000	357	0							
Locus_7470_Transcript_1/1_Conf_1.000	577	20	5.41E-39	XP_002636914.1	62	164.466	191	119	Hypothetical protein CBG09378
Locus_7471_Transcript_1/1_Conf_1.000	601	20	1.57E-47	NP_491262.2	81	192.971	160	131	hypothetical protein T20F5.3
Locus_7472_Transcript_1/1_Conf_1.000	289	20	8.44E-33	EFO16727.1	81	143.28	95	77	hypothetical protein LOAG_11776
Locus_7473_Transcript_1/1_Conf_1.000	139	0							
Locus_7474_Transcript_1/1_Conf_1.000	458	20	2.19E-09	CBW48565.1	67	65.4698	74	50	Hypothetical protein Y111B2A.22d

Locus_7475_Transcript_1/1_Conf_1.000	226	20	1.31E-09	EFO27829.1	64	66.2402	74	48	hypothetical protein LOAG_00642
Locus_7476_Transcript_1/2_Conf_1.000	1632	20	1.24E-61	XP_002629747.1	66	242.276	271	181	Hypothetical protein CBG00981
Locus_7476_Transcript_2/2_Conf_1.000	929	20	6.32E-26	XP_002629747.1	63	122.479	138	87	Hypothetical protein CBG00981
Locus_7477_Transcript_1/1_Conf_1.000	1120	10	3.72E-05	XP_002043842.1	39	53.9138	222	87	GM17783
Locus_7478_Transcript_1/1_Conf_1.000	1732	20	0	XP_002638790.1	95	706.442	405	386	Hypothetical protein CBG05145
Locus_7479_Transcript_1/1_Conf_1.000	1867	20	4.14E-56	XP_002634522.1	57	224.172	323	187	Hypothetical protein CBG08316

Locus_748_Transcript_1/1_Conf_1.000	3305	20	0	EFO24929.1	63	928.702	1141	729	hypothetical protein LOAG_03556
Locus_7480_Transcript_1/1_Conf_1.000	562	20	3.35E-19	EFO16288.1	73	98.5969	84	62	hypothetical protein LOAG_12221
Locus_7481_Transcript_1/1_Conf_1.000	1183	20	4.03E-114	NP_493376.1	96	416.001	215	207	Aboc, EXpulsion defective family member (aex-6)
Locus_7482_Transcript_1/1_Conf_1.000	754	20	1.91E-58	XP_002642487.1	81	229.95	150	122	Hypothetical protein CBG06906
Locus_7483_Transcript_1/1_Conf_1.000	268	0							

Locus_7484_Transcript_1/2_Conf_1.000	1507	20	5.98E-31	EFO21559.1	52	140.198	360	190	hypothetical protein LOAG_06930
Locus_7484_Transcript_2/2_Conf_1.000	1461	20	5.73E-31	EFO21559.1	52	140.198	360	190	hypothetical protein LOAG_06930
Locus_7485_Transcript_1/1_Conf_1.000	168	20	9.22E-16	NP_490714.1	83	86.6557	55	46	hypothetical protein C53D5.5
Locus_7486_Transcript_1/1_Conf_1.000	327	20	4.26E-45	NP_001122528.1	87	184.111	108	95	Cation transporting ATPase family member (catp-1)
Locus_7487_Transcript_1/2_Conf_1.000	673	0							
Locus_7487_Transcript_2/2_Conf_1.000	545	0							
Locus_7488_Transcript_1/1_Conf_1.000	452	0							
Locus_7489_Transcript_1/1_Conf_1.000	364	20	4.48E-63	XP_573067.2	98	243.817	119	117	PREDICTED: ribosomal protein S10-like
Locus_749_Transcript_1/1_Conf_1.000	1536	20	0	XP_001898544.1	83	724.161	511	429	Probable methylenetetrahydrofolate reductase
Locus_7490_Transcript_1/1_Conf_1.000	290	0							
Locus_7491_Transcript_1/1_Conf_1.000	746	20	1.11E-58	NP_492616.1	66	230.72	248	164	Nematode AStacin protease family member (nas-5)
Locus_7492_Transcript_1/1_Conf_1.000	1178	20	3.57E-155	AAW82658.1	95	552.362	317	303	cyclophilin
Locus_7493_Transcript_1/1_Conf_1.000	232	1	1.93E-04	XP_002633725.1	52	35.4242	61	32	Hypothetical protein CBG03410

Locus_7494_Transcript_1/1_Conf_1.000	373	20	2.52E-53	A8X3A7.2	87	211.46	124	109	Integrin alpha pat-2
Locus_7495_Transcript_1/1_Conf_1.000	717	20	1.69E-45	NP_498418.2	67	186.808	179	120	hypothetical protein T26A5.5
Locus_7496_Transcript_1/1_Conf_1.000	790	20	1.66E-87	ABW16951.1	97	326.635	165	161	E2 ubiquitin conjugating enzyme
Locus_7497_Transcript_1/1_Conf_1.000	359	0							
Locus_7498_Transcript_1/1_Conf_1.000	580	20	1.76E-45	XP_002634139.1	76	186.037	194	148	Hypothetical protein CBG01700
Locus_7499_Transcript_1/1_Conf_1.000	383	0							
Locus_75_Transcript_1/2_Conf_1.000	379	0							
Locus_75_Transcript_2/2_Conf_1.000	225	0							
Locus_750_Transcript_1/1_Conf_1.000	398	0							

Locus_7500_Transcript_1/1_Conf_1.000	950	20	3.25E-158	XP_002640630.1	97	561.992	301	292	C. briggsae CBR-APG-1 protein
Locus_7501_Transcript_1/1_Conf_1.000	629	20	1.46E-94	NP_499324.1	90	349.362	207	187	4-HydroxyPhenylpyruvate Dioxygenase (HPD) family member (hpd-1)
Locus_7502_Transcript_1/1_Conf_1.000	251	20	2.39E-32	XP_002642075.1	90	141.739	83	75	C. briggsae CBR-TAG-243 protein
Locus_7503_Transcript_1/1_Conf_1.000	255	3	1.88E-40	XP_002647011.1	94	168.703	84	79	Hypothetical protein CBG23797
Locus_7504_Transcript_1/1_Conf_1.000	280	2	3.60E-04	CBN75987.1	62	48.1358	53	33	conserved unknown protein
Locus_7505_Transcript_1/1_Conf_1.000	357	20	2.51E-13	AAZ67091.1	60	78.5666	99	60	transposase
Locus_7506_Transcript_1/1_Conf_1.000	919	0							
Locus_7507_Transcript_1/1_Conf_1.000	1172	0							
Locus_7508_Transcript_1/1_Conf_1.000	426	20	1.11E-77	NP_497235.2	99	292.352	141	140	G-protein-coupled Receptor Kinase family member (grk-2)
Locus_7509_Transcript_1/1_Conf_1.000	547	0							
Locus_751_Transcript_1/1_Conf_1.000	831	20	5.51E-60	NP_495670.1	71	235.343	261	187	hypothetical protein ZK669.4
Locus_7510_Transcript_1/1_Conf_1.000	271	0							
Locus_7511_Transcript_1/1_Conf_1.000	802	20	7.58E-19	XP_001901969.1	51	98.5969	212	110	hypothetical protein
Locus_7512_Transcript_1/1_Conf_1.000	428	9	9.57E-21	NP_503523.2	58	103.219	126	74	hypothetical protein Y32G9A.8

Locus_7513_Transcript_1/1_Conf_1.000	1119	20	3.83E-135	XP_002646930.1	81	485.723	369	302	Hypothetical protein CBG19635
Locus_7514_Transcript_1/1_Conf_1.000	786	10	8.36E-07	XP_002634943.1	48	58.5362	132	64	Hypothetical protein CBG22545
Locus_7515_Transcript_1/1_Conf_1.000	832	20	2.64E-62	XP_002637746.1	61	243.047	306	189	C. briggsae CBR-TAG-333 protein
Locus_7516_Transcript_1/1_Conf_1.000	1129	0							
Locus_7517_Transcript_1/1_Conf_1.000	666	20	1.16E-87	XP_002645390.1	85	326.635	225	192	C. briggsae CBR-SEC-15 protein
Locus_7518_Transcript_1/1_Conf_1.000	1098	20	5.48E-62	XP_001898944.1	57	242.662	361	207	Protein kinase domain containing protein
Locus_7519_Transcript_1/2_Conf_1.000	608	20	2.56E-77	BAC01801.1	99	291.967	157	156	immunoglobulin lambda light chain VLJ region
Locus_7519_Transcript_2/2_Conf_1.000	598	20	1.10E-77	ACF34413.1	96	293.123	154	148	immunoglobulin light chain
Locus_752_Transcript_1/1_Conf_1.000	578	20	1.28E-72	XP_001892288.1	78	276.174	192	151	UPF0017 protein CG3488
Locus_7520_Transcript_1/1_Conf_1.000	462	20	2.08E-31	NP_506713.1	73	138.658	123	90	hypothetical protein C01G10.10
Locus_7521_Transcript_1/1_Conf_1.000	1396	11	2.33E-34	NP_497280.1	66	151.369	145	96	hypothetical protein T24C4.2
Locus_7522_Transcript_1/1_Conf_1.000	312	0							

Locus_7523_Transcript_1/3_Conf_0.400	791	20	1.98E-48	XP_002632461.1	66	196.823	262	174	C. briggsae CBR-MEL-46 protein
Locus_7523_Transcript_2/3_Conf_0.600	2560	20	8.96E-68	NP_502998.2	46	263.462	828	387	Maternal Effect Lethal family member (mel-46)
Locus_7523_Transcript_3/3_Conf_0.600	2558	20	8.95E-68	NP_502998.2	46	263.462	828	387	Maternal Effect Lethal family member (mel-46)
Locus_7524_Transcript_1/1_Conf_1.000	659	20	9.38E-82	NP_001021395.1	84	306.99	201	170	Receptor Mediated Endocytosis family member (rme-8)
Locus_7525_Transcript_1/1_Conf_1.000	421	6	1.70E-33	XP_002639089.1	73	145.591	142	104	C. briggsae CBR-TAG-163 protein
Locus_7526_Transcript_1/1_Conf_1.000	1416	20	3.02E-130	NP_505415.2	74	469.929	438	326	COenzyme Q (ubiquinone) biosynthesis family member (coq-6)
Locus_7527_Transcript_1/1_Conf_1.000	387	0							
Locus_7528_Transcript_1/4_Conf_0.500	1636	20	0	XP_002634760.1	98	1042.72	545	539	C. briggsae CBR-RPB-1 protein
Locus_7528_Transcript_2/4_Conf_0.625	1953	20	0	XP_002634760.1	98	1196.42	651	639	C. briggsae CBR-RPB-1 protein

Locus_7528_Transcript_3/4_Conf_0.500	1965	20	0	XP_002634760.1	94	1167.53	659	626	C. briggsae CBR-RPB-1 protein
Locus_7528_Transcript_4/4_Conf_0.625	2214	20	0	XP_002634760.1	95	1311.21	742	709	C. briggsae CBR-RPB-1 protein
Locus_7529_Transcript_1/5_Conf_0.636	1349	20	1.80E-92	XP_002642319.1	73	344.354	291	214	C. briggsae CBR-TAG-331 protein
Locus_7529_Transcript_2/5_Conf_0.636	1350	20	1.80E-92	XP_002642319.1	73	344.354	291	214	C. briggsae CBR-TAG-331 protein
Locus_7529_Transcript_3/5_Conf_0.636	1476	20	2.03E-92	XP_002642319.1	73	344.354	291	214	C. briggsae CBR-TAG-331 protein
Locus_7529_Transcript_4/5_Conf_0.636	1350	20	2.69E-96	NP_499375.1	68	357.066	360	245	RiNg Finger protein family member (rnf-113)
Locus_7529_Transcript_5/5_Conf_0.636	1350	20	1.80E-92	XP_002642319.1	73	344.354	291	214	C. briggsae CBR-TAG-331 protein
Locus_753_Transcript_1/1_Conf_1.000	567	4	8.46E-50	NP_500037.2	73	200.29	177	130	hypothetical protein Y55F3AR.1

Locus_7530_Transcript_1/1_Conf_1.000	1072	20	6.58E-97	XP_001894445.1	68	358.607	357	245	amine oxidase, flavin-containing family protein
Locus_7531_Transcript_1/2_Conf_1.000	2656	20	4.37E-166	XP_001899928.1	63	590.112	788	504	hypothetical protein Bm1_42320
Locus_7531_Transcript_2/2_Conf_1.000	2566	20	1.44E-166	XP_001899928.1	63	591.652	801	509	hypothetical protein Bm1_42320
Locus_7532_Transcript_1/1_Conf_1.000	209	20	7.04E-16	XP_002636002.1	75	87.0409	66	50	Hypothetical protein CBG01236
Locus_7533_Transcript_1/1_Conf_1.000	1124	20	2.43E-105	NP_496089.3	69	386.726	379	264	ARF-related in C-term (ARD family) family member (arc-1)
Locus_7534_Transcript_1/1_Conf_1.000	612	20	2.64E-61	XP_002640467.1	84	238.81	168	142	C. briggsae CBR-PFD-3 protein
Locus_7535_Transcript_1/1_Conf_1.000	570	20	4.00E-47	NP_500082.1	76	191.43	152	116	CaLPain family member (clp-7)
Locus_7536_Transcript_1/1_Conf_1.000	594	20	7.38E-26	XP_002641410.1	89	120.939	68	61	C. briggsae CBR-TIN-10 protein

Locus_7537_Transcript_1/2_Conf_1.000	1762	20	2.47E-79	XP_001891652.1	76	301.212	305	234	myosin heavy chain, nonmuscle type 1
Locus_7537_Transcript_2/2_Conf_1.000	1756	20	7.64E-81	XP_001891652.1	77	306.22	303	234	myosin heavy chain, nonmuscle type 1
Locus_7538_Transcript_1/1_Conf_1.000	318	1	5.69E-05	CAR63546.1	53	50.8322	98	52	hypothetical protein

Locus_7539_Transcript_1/1_Conf_1.000	1307	20	4.00E-49	NP_502599.2	62	200.29	296	184	TBC (Tre-2/Bub2/Cdc16) domain family member (tbc-9)
Locus_754_Transcript_1/3_Conf_0.667	1840	20	1.50E-159	NP_505653.1	71	567.77	564	403	hypothetical protein B0024.11
Locus_754_Transcript_2/3_Conf_0.667	1840	20	5.69E-159	NP_505653.1	71	565.844	564	402	hypothetical protein B0024.11
Locus_754_Transcript_3/3_Conf_0.667	1840	20	1.50E-159	NP_505653.1	71	567.77	564	403	hypothetical protein B0024.11
Locus_7540_Transcript_1/1_Conf_1.000	452	0							
Locus_7541_Transcript_1/1_Conf_1.000	184	0							
Locus_7542_Transcript_1/1_Conf_1.000	1227	20	7.51E-119	XP_002639561.1	74	431.795	367	272	Hypothetical protein CBG04192
Locus_7543_Transcript_1/1_Conf_1.000	701	20	1.91E-46	NP_505751.1	68	189.889	198	136	hypothetical protein D1054.3
Locus_7544_Transcript_1/1_Conf_1.000	500	0							
Locus_7545_Transcript_1/2_Conf_1.000	245	0							
Locus_7545_Transcript_2/2_Conf_1.000	257	0							
Locus_7546_Transcript_1/1_Conf_1.000	1153	20	1.03E-66	NP_495959.1	82	258.455	179	147	Phosphatase Interacting with RNA/RNP family member (pir-1)
Locus_7547_Transcript_1/1_Conf_1.000	830	20	2.20E-101	CAD28559.2	76	372.859	277	211	metalloprotease I
Locus_7548_Transcript_1/1_Conf_1.000	629	20	2.54E-22	NP_492739.1	65	109.383	113	74	hypothetical protein Y106G6H.15
Locus_7549_Transcript_1/1_Conf_1.000	648	20	1.06E-61	XP_002631164.1	73	172.94	142	105	Hypothetical protein CBG02950
Locus_755_Transcript_1/1_Conf_1.000	1179	20	5.71E-161	A8WTI8.2	91	571.622	367	335	Elongation factor G
Locus_7550_Transcript_1/1_Conf_1.000	357	0							
Locus_7551_Transcript_1/1_Conf_1.000	480	4	4.38E-10	AAA50679.3	60	67.781	129	78	Bard homolog (tumor suppressor gene bard1) protein 1, partially confirmed by transcript evidence

Locus_7552_Transcript_1/1_Conf_1.000	1329	20	0	ABS45069.1	100	781.941	413	413	slowpoke potassium channel family member SLO-1
Locus_7553_Transcript_1/1_Conf_1.000	1498	20	1.01E-139	XP_002640865.1	79	501.516	385	306	Hypothetical protein CBG15756
Locus_7554_Transcript_1/2_Conf_1.000	648	20	3.79E-96	XP_002631515.1	91	354.755	198	181	Hypothetical protein CBG20679
Locus_7554_Transcript_2/2_Conf_1.000	648	20	3.79E-96	XP_002631515.1	91	354.755	198	181	Hypothetical protein CBG20679
Locus_7555_Transcript_1/1_Conf_1.000	641	15	3.00E-82	NP_001122770.1	86	308.531	210	182	hypothetical protein F13E9.11
Locus_7556_Transcript_1/1_Conf_1.000	412	0							
Locus_7557_Transcript_1/1_Conf_1.000	734	20	2.19E-11	CAZ39166.1	65	73.559	69	45	C. elegans protein T20D3.3c, confirmed by transcript evidence
Locus_7558_Transcript_1/1_Conf_1.000	398	6	4.34E-21	XP_002639073.1	64	104.375	119	77	C. briggsae CBR-PQN-52 protein
Locus_7559_Transcript_1/1_Conf_1.000	532	6	1.31E-19	NP_501035.1	62	99.7525	129	80	hypothetical protein H34C03.2
Locus_756_Transcript_1/1_Conf_1.000	1890	20	3.77E-89	NP_499364.1	61	333.954	388	238	hypothetical protein W09D10.1
Locus_7560_Transcript_1/1_Conf_1.000	627	0							
Locus_7561_Transcript_1/1_Conf_1.000	390	0							
Locus_7562_Transcript_1/1_Conf_1.000	675	20	2.71E-55	CAB60494.2	67	219.164	222	149	C. elegans protein Y39C12A.1, partially confirmed by transcript evidence
Locus_7563_Transcript_1/2_Conf_1.000	1479	20	5.41E-61	XP_002643057.1	54	239.965	374	205	C. briggsae CBR-APC-2 protein
Locus_7563_Transcript_2/2_Conf_1.000	1479	20	7.06E-61	XP_002643057.1	54	239.58	374	204	C. briggsae CBR-APC-2 protein
Locus_7564_Transcript_1/1_Conf_1.000	1056	20	8.67E-102	ABC69942.1	70	374.785	369	260	STIP
Locus_7565_Transcript_1/1_Conf_1.000	387	20	2.58E-10	NP_508439.2	53	68.5514	113	61	hypothetical protein C43H6.1

Locus_7566_Transcript_1/1_Conf_1.000	425	20	1.53E-26	EFO27261.1	88	122.479	79	70	APB-1 protein
Locus_7567_Transcript_1/2_Conf_0.846	822	0							
Locus_7567_Transcript_2/2_Conf_0.615	120	0							
Locus_7568_Transcript_1/1_Conf_1.000	247	20	6.97E-32	NP_502298.2	95	140.198	72	69	Dynein Light Chain family member (dlc-2)
Locus_7569_Transcript_1/2_Conf_1.000	1229	20	3.63E-89	XP_002644425.1	70	333.183	280	197	Hypothetical protein CBG14281
Locus_7569_Transcript_2/2_Conf_1.000	1073	20	1.85E-91	XP_002644425.1	70	340.502	286	201	Hypothetical protein CBG14281
Locus_757_Transcript_1/1_Conf_1.000	3219	20	5.00E-95	XP_002630387.1	51	354.369	866	444	Hypothetical protein CBG04326
Locus_7570_Transcript_1/1_Conf_1.000	621	3	3.71E-10	XP_002630813.1	50	68.9366	188	94	Hypothetical protein CBG02513
Locus_7571_Transcript_1/1_Conf_1.000	530	20	2.02E-57	NP_508464.2	79	225.328	170	135	hypothetical protein F52H2.7

Locus_7572_Transcript_1/1_Conf_1.000	1506	20	0	NP_500051.2	81	660.988	484	395	hypothetical protein Y104H12D.3
Locus_7573_Transcript_1/1_Conf_1.000	248	0							
Locus_7574_Transcript_1/1_Conf_1.000	284	3	5.00E-17	XP_002635262.1	81	90.8929	65	53	Hypothetical protein CBG11506
Locus_7575_Transcript_1/1_Conf_1.000	1014	20	6.56E-59	NP_492123.2	64	232.261	274	178	hypothetical protein D2030.8
Locus_7576_Transcript_1/1_Conf_1.000	794	20	6.60E-68	XP_002642974.1	69	261.536	265	183	Hypothetical protein CBG15258
Locus_7577_Transcript_1/1_Conf_1.000	486	3	3.21E-08	XP_001901749.1	55	61.6178	96	53	hypothetical protein Bm1_51405
Locus_7578_Transcript_1/1_Conf_1.000	838	20	9.22E-63	NP_492422.2	73	244.588	230	169	SYNtaxin family member (syn-13)
Locus_7579_Transcript_1/1_Conf_1.000	375	0							
Locus_758_Transcript_1/1_Conf_1.000	1268	20	0	NP_492905.1	86	643.269	411	357	hypothetical protein H25P06.1

Locus_7580_Transcript_1/1_Conf_1.000	446	20	1.81E-35	EFO21791.1	72	152.14	151	109	hypothetical protein LOAG_06693
Locus_7581_Transcript_1/1_Conf_1.000	283	0							
Locus_7582_Transcript_1/1_Conf_1.000	552	20	2.02E-45	XP_002631190.1	65	185.652	173	114	Hypothetical protein CBG02979
Locus_7583_Transcript_1/1_Conf_1.000	626	0							
Locus_7584_Transcript_1/1_Conf_1.000	352	20	7.58E-26	XP_001963617.1	85	120.168	77	66	GF20488
Locus_7585_Transcript_1/1_Conf_1.000	290	0							
Locus_7586_Transcript_1/1_Conf_1.000	846	20	3.32E-84	NP_495670.1	88	315.849	198	175	hypothetical protein ZK669.4
Locus_7587_Transcript_1/1_Conf_1.000	567	5	2.54E-62	XP_002637803.1	87	241.891	133	117	C. briggsae CBR-RIL-1 protein
Locus_7588_Transcript_1/1_Conf_1.000	1158	20	2.50E-145	XP_002647642.1	79	519.62	366	290	Hypothetical protein CBG06741
Locus_7589_Transcript_1/1_Conf_1.000	726	20	1.52E-41	EFO25430.1	69	173.711	168	117	hypothetical protein LOAG_03054
Locus_759_Transcript_1/1_Conf_1.000	419	7	1.44E-24	XP_002638694.1	63	115.931	138	88	C. briggsae CBR-CHS-1 protein
Locus_7590_Transcript_1/1_Conf_1.000	443	0							
Locus_7591_Transcript_1/1_Conf_1.000	676	0							

Locus_7592_Transcript_1/1_Conf_1.000	679	20	5.71E-53	NP_491075.2	70	211.46	200	141	hypothetical protein Y71F9AL.1
Locus_7593_Transcript_1/1_Conf_1.000	386	4	7.31E-05	EFO22388.1	71	50.447	38	27	hypothetical protein LOAG_06099
Locus_7594_Transcript_1/1_Conf_1.000	495	20	1.15E-50	NP_490687.1	83	202.601	134	112	PaTched Related family member (ptr-11)
Locus_7595_Transcript_1/1_Conf_1.000	1820	20	2.24E-107	O18023.4	63	394.43	517	330	Ig-like and fibronectin type-III domain-containing protein C25G4.10
Locus_7596_Transcript_1/1_Conf_1.000	266	20	7.12E-16	XP_002944626.1	81	87.0409	58	47	PREDICTED: LYR motif-containing protein 5A
Locus_7597_Transcript_1/1_Conf_1.000	418	0							
Locus_7598_Transcript_1/1_Conf_1.000	240	20	7.53E-18	NP_740774.1	80	93.5893	78	63	hypothetical protein Y48G1A.4
Locus_7599_Transcript_1/1_Conf_1.000	1010	20	1.38E-109	NP_496879.1	76	400.593	331	252	yeast BUB homolog family member (bub-3)

Locus_76_Transcript_1/1_Conf_1.000	1532	20	0	AAT28330.1	94	934.865	500	470	catalase
Locus_760_Transcript_1/1_Conf_1.000	829	20	2.13E-96	NP_499964.1	94	356.295	204	192	Ribosomal Protein, Large subunit family member (rpl-15)
Locus_7600_Transcript_1/1_Conf_1.000	1543	20	1.87E-96	NP_001036083.1	63	357.836	475	302	poly [ADP-ribose] polymerase 2 isoform 2
Locus_7601_Transcript_1/1_Conf_1.000	210	4	4.87E-09	NP_500403.2	65	64.3142	64	42	hypothetical protein Y37E11AM.3
Locus_7602_Transcript_1/1_Conf_1.000	1119	0							
Locus_7603_Transcript_1/1_Conf_1.000	270	2	1.38E-11	XP_002637757.1	69	72.7886	62	43	Hypothetical protein CBG04540
Locus_7604_Transcript_1/1_Conf_1.000	608	20	6.85E-22	XP_002637325.1	55	107.842	202	112	C. briggsae CBR-SPE-39 protein
Locus_7605_Transcript_1/1_Conf_1.000	296	20	2.78E-44	AAA18259.1	96	181.415	95	92	protein kinase C
Locus_7606_Transcript_1/1_Conf_1.000	885	20	9.21E-48	NP_508182.1	88	194.897	104	92	SphingoMyelin Synthase family member (sms-2)
Locus_7607_Transcript_1/1_Conf_1.000	352	0							
Locus_7608_Transcript_1/1_Conf_1.000	217	0							
Locus_7609_Transcript_1/1_Conf_1.000	453	0							

Locus_761_Transcript_1/1_Conf_1.000	704	20	5.05E-63	XP_002632404.1	76	244.973	217	166	Hypothetical protein CBG00428
Locus_7610_Transcript_1/1_Conf_1.000	411	5	7.72E-31	NP_492455.1	75	136.732	135	102	hypothetical protein F25H5.6
Locus_7611_Transcript_1/1_Conf_1.000	1590	20	9.24E-30	EFO22136.1	48	136.346	282	137	hypothetical protein LOAG_06352
Locus_7612_Transcript_1/2_Conf_1.000	454	20	1.28E-41	NP_499775.1	84	172.555	126	107	hypothetical protein F45G2.8
Locus_7612_Transcript_2/2_Conf_1.000	968	20	6.70E-42	XP_002642810.1	76	175.637	152	117	Hypothetical protein CBG21206
Locus_7613_Transcript_1/1_Conf_1.000	1373	20	5.24E-172	NP_502812.1	81	608.601	452	369	glutamyl(E)/glutaminyl(Q) tRNA Synthetase family member (ers-1)
Locus_7614_Transcript_1/1_Conf_1.000	1223	20	1.34E-51	XP_001893816.1	59	208.379	299	177	Protein kinase domain containing protein
Locus_7615_Transcript_1/1_Conf_1.000	870	20	6.11E-12	XP_001902481.1	52	75.8702	112	59	PHD-finger family protein
Locus_7616_Transcript_1/1_Conf_1.000	217	0							
Locus_7617_Transcript_1/1_Conf_1.000	520	0							
Locus_7618_Transcript_1/1_Conf_1.000	896	0							
Locus_7619_Transcript_1/1_Conf_1.000	792	20	2.54E-27	XP_002643058.1	49	126.716	271	133	C. briggsae CBR-DCR-1 protein
Locus_762_Transcript_1/1_Conf_1.000	1407	20	3.19E-140	NP_001021565.1	74	503.056	473	354	hypothetical protein K10C3.5

Locus_7620_Transcript_1/1_Conf_1.000	1219	20	5.54E-90	NP_497972.1	92	335.88	192	177	R-RAS related family member (ras-2)
Locus_7621_Transcript_1/1_Conf_1.000	698	20	8.13E-82	XP_001891630.1	86	307.375	212	183	Rho-GTPase-activating
Locus_7622_Transcript_1/2_Conf_1.000	1992	20	0	NP_501878.1	91	959.903	598	545	hypothetical protein F01G10.1
Locus_7622_Transcript_2/2_Conf_1.000	1992	20	0	NP_501878.1	90	958.362	598	544	hypothetical protein F01G10.1
Locus_7623_Transcript_1/1_Conf_1.000	516	0							
Locus_7624_Transcript_1/1_Conf_1.000	247	2	1.12E-05	NP_496395.1	75	53.1434	45	34	LIn-26 Related family member (lir-3)
Locus_7625_Transcript_1/1_Conf_1.000	567	20	6.05E-56	XP_002639922.1	77	220.705	186	144	Hypothetical protein CBG08254
Locus_7626_Transcript_1/1_Conf_1.000	1075	20	7.46E-24	XP_001894716.1	52	115.931	238	125	Bromodomain containing protein
Locus_7627_Transcript_1/1_Conf_1.000	370	0							
Locus_7628_Transcript_1/1_Conf_1.000	136	0							
Locus_7629_Transcript_1/2_Conf_1.000	662	6	2.19E-14	CBW48395.1	47	83.1889	153	73	Hypothetical protein F54C8.6d
Locus_7629_Transcript_2/2_Conf_1.000	595	6	1.31E-14	CBW48395.1	47	83.5741	167	80	Hypothetical protein F54C8.6d
Locus_763_Transcript_1/2_Conf_1.000	2856	20	0	XP_002648178.1	67	794.267	852	571	C. briggsae CBR-RPN-2 protein
Locus_763_Transcript_2/2_Conf_1.000	2856	20	0	XP_002648178.1	67	794.267	852	571	C. briggsae CBR-RPN-2 protein
Locus_7630_Transcript_1/1_Conf_1.000	149	0							
Locus_7631_Transcript_1/1_Conf_1.000	467	4	5.62E-37	XP_002641228.1	76	157.147	140	107	C. briggsae CBR-IDA-1 protein

Locus_7632_Transcript_1/1_Conf_1.000	648	20	1.08E-42	CAD44516.1	69	177.178	211	147	VAB-10B protein
Locus_7633_Transcript_1/1_Conf_1.000	605	0							
Locus_7634_Transcript_1/1_Conf_1.000	1214	20	1.25E-09	XP_002593043.1	43	68.9366	250	108	hypothetical protein BRAFLDRAFT_120702
Locus_7635_Transcript_1/3_Conf_0.600	432	20	1.15E-34	NP_499768.2	84	149.443	97	82	Nematode AStacin protease family member (nas-1)
Locus_7635_Transcript_2/3_Conf_0.600	562	20	2.01E-56	NP_499768.2	90	222.246	130	117	Nematode AStacin protease family member (nas-1)
Locus_7635_Transcript_3/3_Conf_0.600	463	20	1.18E-34	NP_499768.2	84	149.443	97	82	Nematode AStacin protease family member (nas-1)
Locus_7636_Transcript_1/1_Conf_1.000	271	20	7.74E-47	NP_001171651.1	100	189.889	89	89	glucose-6-phosphate isomerase isoform 1
Locus_7637_Transcript_1/1_Conf_1.000	889	2	1.89E-08	XP_001895354.1	53	64.3142	95	51	SAP domain containing protein
Locus_7638_Transcript_1/1_Conf_1.000	265	0							
Locus_7639_Transcript_1/1_Conf_1.000	633	3	3.62E-40	NP_001076704.1	74	168.703	152	113	hypothetical protein T12A7.2
Locus_764_Transcript_1/2_Conf_1.000	499	20	1.15E-34	EFO15898.1	100	149.443	72	72	hypothetical protein LOAG_12610
Locus_764_Transcript_2/2_Conf_1.000	337	20	1.15E-34	EFO15898.1	100	149.443	72	72	hypothetical protein LOAG_12610
Locus_7640_Transcript_1/1_Conf_1.000	514	20	3.66E-42	NP_490985.1	96	174.481	90	87	hypothetical protein Y74C10AL.2
Locus_7641_Transcript_1/1_Conf_1.000	167	0							
Locus_7642_Transcript_1/1_Conf_1.000	555	3	7.37E-19	NP_505214.2	61	97.4413	134	83	hypothetical protein C10B5.3

Locus_7643_Transcript_1/1_Conf_1.000	865	20	5.33E-93	NP_001021171.1	87	345.125	233	205	PDF Receptor homolog family member (pdfr-1)
Locus_7644_Transcript_1/2_Conf_1.000	662	20	1.11E-66	EFO18438.1	72	256.914	202	146	zinc finger protein
Locus_7644_Transcript_2/2_Conf_1.000	503	20	1.86E-64	EFO18438.1	79	248.44	168	133	zinc finger protein
Locus_7645_Transcript_1/1_Conf_1.000	1358	20	0	XP_002642598.1	86	643.269	445	383	C. briggsae CBR-LPD-7 protein
Locus_7646_Transcript_1/1_Conf_1.000	605	20	9.59E-77	AAK62032.1	78	290.041	200	157	metalloprotease 1 precursor
Locus_7647_Transcript_1/1_Conf_1.000	264	0							
Locus_7648_Transcript_1/1_Conf_1.000	469	0							
Locus_7649_Transcript_1/1_Conf_1.000	284	0							
Locus_765_Transcript_1/1_Conf_1.000	471	0							
Locus_7650_Transcript_1/1_Conf_1.000	182	0							
Locus_7651_Transcript_1/1_Conf_1.000	396	20	4.03E-43	EFO27558.1	90	177.563	98	89	hypothetical protein LOAG_00922

Locus_7652_Transcript_1/1_Conf_1.000	560	3	5.24E-25	NP_871894.1	58	117.857	156	92	hypothetical protein Y48G1C.10
Locus_7653_Transcript_1/1_Conf_1.000	147	0							
Locus_7654_Transcript_1/1_Conf_1.000	545	20	5.70E-74	NP_001122835.1	89	280.411	181	162	UNCoordinated family member (unc-22)
Locus_7655_Transcript_1/1_Conf_1.000	178	20	5.92E-15	NP_901429.1	84	83.9593	57	48	hydroxymethylglutaryl-CoA lyase
Locus_7656_Transcript_1/1_Conf_1.000	692	2	9.29E-14	XP_002637429.1	46	81.2629	243	114	Hypothetical protein CBG19140
Locus_7657_Transcript_1/1_Conf_1.000	253	20	5.50E-32	NP_491780.1	92	140.584	84	78	hypothetical protein T09B4.9
Locus_7658_Transcript_2/3_Conf_0.400	108	0							
Locus_7658_Transcript_3/3_Conf_0.880	127	0							
Locus_7659_Transcript_1/1_Conf_1.000	359	20	5.39E-24	NP_004065.1	100	114.005	54	54	cytochrome c oxidase subunit 8A, mitochondrial precursor
Locus_766_Transcript_1/1_Conf_1.000	1246	0							
Locus_7660_Transcript_1/1_Conf_1.000	796	20	4.46E-64	XP_002646315.1	85	248.825	180	153	C. briggsae CBR-MSH-2 protein
Locus_7661_Transcript_1/1_Conf_1.000	422	20	8.65E-54	NP_500135.1	95	213.001	140	134	hypothetical protein Y41D4A.8
Locus_7662_Transcript_1/1_Conf_1.000	534	20	1.32E-72	XP_002643655.1	80	275.789	175	140	Hypothetical protein CBG16407

Locus_7663_Transcript_1/1_Conf_1.000	784	7	1.50E-40	XP_002638694.1	80	170.629	142	115	C. briggsae CBR-CHS-1 protein
Locus_7664_Transcript_1/1_Conf_1.000	872	20	3.77E-62	XP_002639468.1	76	242.662	249	190	Hypothetical protein CBG04063
Locus_7665_Transcript_1/1_Conf_1.000	757	2	2.65E-07	XP_002634335.1	51	60.077	112	58	C. briggsae CBR-SGO-1 protein
Locus_7666_Transcript_1/1_Conf_1.000	633	6	4.92E-21	NP_496175.1	59	105.145	167	99	Dorsal Intercalation and Elongation defect family member (die-1)
Locus_7667_Transcript_1/1_Conf_1.000	263	0							
Locus_7668_Transcript_1/1_Conf_1.000	185	0							
Locus_7669_Transcript_1/1_Conf_1.000	907	20	4.88E-84	NP_496290.2	90	315.464	213	192	hypothetical protein C14A4.11
Locus_767_Transcript_1/6_Conf_0.500	527	0							
Locus_767_Transcript_2/6_Conf_0.500	569	0							
Locus_767_Transcript_3/6_Conf_0.643	789	0							
Locus_767_Transcript_4/6_Conf_0.643	789	0							
Locus_767_Transcript_5/6_Conf_0.643	779	0							
Locus_767_Transcript_6/6_Conf_0.643	779	0							
Locus_7670_Transcript_1/1_Conf_1.000	624	20	2.18E-42	NP_501803.1	86	176.022	114	99	hypothetical protein C47E12.2
Locus_7671_Transcript_1/1_Conf_1.000	280	0							
Locus_7672_Transcript_1/1_Conf_1.000	831	20	2.24E-53	EFO27237.1	64	213.386	261	169	autophagy protein Apg5 containing protein
Locus_7673_Transcript_1/1_Conf_1.000	309	20	1.11E-37	EFO15860.1	81	159.458	102	83	mannosidase

Locus_7674_Transcript_1/1_Conf_1.000	325	4	2.61E-26	NP_507807.1	68	121.709	107	73	hypothetical protein Y43F8C.7
Locus_7675_Transcript_1/1_Conf_1.000	402	20	2.77E-36	NP_497467.1	92	154.836	81	75	human DDP related family member (ddp-1)
Locus_7676_Transcript_1/1_Conf_1.000	129	20	9.25E-08	XP_001898759.1	91	60.077	34	31	collagen col-34
Locus_7677_Transcript_1/1_Conf_1.000	261	0							
Locus_7678_Transcript_1/1_Conf_1.000	1061	20	1.01E-49	NP_494168.1	59	201.83	246	147	hypothetical protein F07E5.5
Locus_7679_Transcript_1/1_Conf_1.000	685	20	8.97E-62	XP_001893093.1	75	240.736	204	154	Leucine Rich Repeat family protein
Locus_768_Transcript_1/2_Conf_1.000	256	20	1.35E-22	NP_502076.2	83	109.383	68	57	hypothetical protein T05E11.6
Locus_768_Transcript_2/2_Conf_1.000	724	20	3.65E-104	XP_002633281.1	95	381.719	226	216	Hypothetical protein CBG06010
Locus_7680_Transcript_1/1_Conf_1.000	225	4	6.71E-14	NP_500551.2	72	80.4925	73	53	hypothetical protein F55F10.1
Locus_7681_Transcript_1/1_Conf_1.000	632	20	4.08E-44	XP_001900929.1	67	181.8	164	111	Zinc finger DHHC domain containing protein 2
Locus_7682_Transcript_1/1_Conf_1.000	1089	20	4.67E-106	NP_497086.1	80	389.037	269	216	fatty acid ELOngation family member (elo-9)
Locus_7683_Transcript_1/3_Conf_0.714	1240	10	9.53E-37	XP_002646603.1	78	159.073	157	123	Hypothetical protein CBG20487
Locus_7683_Transcript_2/3_Conf_0.714	1244	10	9.57E-37	XP_002646603.1	78	159.073	157	123	Hypothetical protein CBG20487
Locus_7683_Transcript_3/3_Conf_0.714	1244	10	9.57E-37	XP_002646603.1	78	159.073	157	123	Hypothetical protein CBG20487
Locus_7684_Transcript_1/1_Conf_1.000	717	20	2.35E-63	NP_510091.2	76	246.128	211	162	hypothetical protein T18D3.3

Locus_7685_Transcript_1/1_Conf_1.000	1160	0							
Locus_7686_Transcript_1/1_Conf_1.000	209	12	2.96E-14	NP_497506.3	76	81.6481	69	53	hypothetical protein Y48G9A.3
Locus_7687_Transcript_1/2_Conf_1.000	937	16	9.50E-62	AAK93964.1	87	241.506	139	122	AF395836_1putative chitinase
Locus_7687_Transcript_2/2_Conf_1.000	937	16	9.50E-62	AAK93964.1	87	241.506	139	122	AF395836_1putative chitinase
Locus_7688_Transcript_1/1_Conf_1.000	360	0							
Locus_7689_Transcript_1/2_Conf_1.000	1431	20	5.39E-26	XP_001898684.1	77	123.635	87	67	ring finger-H2 protein
Locus_7689_Transcript_2/2_Conf_1.000	1419	20	5.33E-26	XP_001898684.1	77	123.635	87	67	ring finger-H2 protein
Locus_769_Transcript_1/2_Conf_1.000	998	20	3.29E-140	NP_498081.2	90	502.286	324	293	ALdehyde deHydrogenase family member (alh-1)
Locus_769_Transcript_2/2_Conf_1.000	998	20	3.29E-140	NP_498081.2	90	502.286	324	293	ALdehyde deHydrogenase family member (alh-1)
Locus_7690_Transcript_1/2_Conf_1.000	335	2	9.52E-05	XP_002631178.1	48	50.0618	103	50	C. briggsae CBR-MAT-2 protein

Locus_7690_Transcript_2/2_Conf_1.000	792	12	1.71E-15	XP_002631178.1	47	87.4261	225	106	C. briggsae CBR-MAT-2 protein
Locus_7691_Transcript_1/1_Conf_1.000	138	0							
Locus_7692_Transcript_1/1_Conf_1.000	603	20	5.35E-19	XP_002646918.1	57	98.2117	137	79	Hypothetical protein CBG19620
Locus_7693_Transcript_1/1_Conf_1.000	284	20	2.10E-15	XP_002731916.1	100	85.5001	40	40	PREDICTED: Ab1-108-like
Locus_7694_Transcript_1/1_Conf_1.000	539	20	5.38E-21	XP_001898220.1	58	104.375	187	109	multidrug Resistance Protein family member (mrp-5)
Locus_7695_Transcript_1/1_Conf_1.000	1522	0							
Locus_7696_Transcript_1/1_Conf_1.000	633	20	7.28E-49	XP_002601552.1	76	197.593	163	124	hypothetical protein BRAFLDRAFT_115609
Locus_7697_Transcript_1/1_Conf_1.000	643	20	1.56E-70	XP_002639255.1	71	269.626	227	162	C. briggsae CBR-OCRL-1 protein
Locus_7698_Transcript_1/1_Conf_1.000	669	9	2.42E-16	NP_491045.1	54	89.7373	183	100	hypothetical protein W03D8.10
Locus_7699_Transcript_1/2_Conf_1.000	2581	20	1.33E-119	EFO23614.1	60	435.647	578	348	hypothetical protein LOAG_04870
Locus_7699_Transcript_2/2_Conf_1.000	1684	20	1.94E-33	XP_001897063.1	53	148.673	315	167	Bromodomain containing protein
Locus_77_Transcript_1/3_Conf_0.286	1433	4	3.56E-78	XP_002639057.1	68	296.975	320	220	Hypothetical protein CBG14867

Locus_77_Transcript_2/3_Conf_0.714	3285	20	0	XP_002639057.1	70	834.328	890	623	Hypothetical protein CBG14867
Locus_77_Transcript_3/3_Conf_0.571	2050	20	1.66E-138	XP_002639057.1	68	498.049	528	361	Hypothetical protein CBG14867
Locus_770_Transcript_1/1_Conf_1.000	1075	20	7.54E-101	NP_490988.2	80	371.703	279	225	Eukaryotic Initiation Factor family member (eif-3.I)
Locus_7700_Transcript_1/1_Conf_1.000	598	0							
Locus_7701_Transcript_1/1_Conf_1.000	506	6	1.81E-14	XP_001898639.1	65	82.4185	88	58	Conserved hypothetical protein
Locus_7702_Transcript_1/1_Conf_1.000	392	4	9.15E-08	NP_871894.1	50	60.077	130	66	hypothetical protein Y48G1C.10
Locus_7703_Transcript_1/1_Conf_1.000	719	20	4.54E-91	XP_002641406.1	80	338.191	243	196	Hypothetical protein CBG13269
Locus_7704_Transcript_1/1_Conf_1.000	564	20	7.60E-19	NP_001021028.1	63	97.4413	164	104	CYclin E family member (cye-1)
Locus_7705_Transcript_1/1_Conf_1.000	311	20	2.03E-15	XP_001899951.1	74	85.5001	66	49	Veph-A
Locus_7706_Transcript_1/1_Conf_1.000	1154	20	0	NP_503059.2	87	638.262	384	337	hypothetical protein ZK550.3
Locus_7707_Transcript_1/1_Conf_1.000	373	0							
Locus_7708_Transcript_1/1_Conf_1.000	758	20	9.92E-55	NP_497173.1	74	217.624	193	144	MaX-Like family member (mxl-2)

Locus_7709_Transcript_1/1_Conf_1.000	671	20	1.24E-36	XP_002643105.1	70	157.147	145	102	C. briggsae CBR-PHP-3 protein
Locus_771_Transcript_1/2_Conf_1.000	622	20	3.20E-54	XP_002633339.1	69	215.312	197	137	Hypothetical protein CBG06078
Locus_771_Transcript_2/2_Conf_1.000	622	20	1.88E-54	XP_002633339.1	69	216.083	197	137	Hypothetical protein CBG06078
Locus_7710_Transcript_1/1_Conf_1.000	155	0							
Locus_7711_Transcript_1/1_Conf_1.000	3350	20	0	NP_498785.1	98	2165.58	1115	1098	yeast PRP (splicing factor) related family member (prp-8)

Locus_7712_Transcript_1/1_Conf_1.000	368	20	5.85E-47	BAG72555.2	100	190.274	92	92	filamin A alpha
Locus_7713_Transcript_1/1_Conf_1.000	768	20	1.20E-79	XP_002643175.1	95	300.442	167	159	C. briggsae CBR-PSD-1 protein
Locus_7714_Transcript_1/1_Conf_1.000	568	20	4.78E-61	ACI49202.1	82	237.654	189	156	hypothetical protein Csp3_JD04.001
Locus_7715_Transcript_1/1_Conf_1.000	175	4	1.37E-19	A8XQD5.2	91	99.3673	57	52	Serine/threonine-protein kinase dkf-2
Locus_7716_Transcript_1/1_Conf_1.000	936	20	6.90E-129	NP_001021220.1	83	464.537	313	261	hypothetical protein C46F11.2
Locus_7717_Transcript_1/1_Conf_1.000	233	20	2.21E-17	XP_002632141.1	76	92.0485	71	54	C. briggsae CBR-TRE-5 protein

Locus_7718_Transcript_1/1_Conf_1.000	271	0							
Locus_7719_Transcript_1/1_Conf_1.000	315	20	1.07E-11	XP_002641902.1	82	73.1738	74	61	Hypothetical protein CBG16598
Locus_772_Transcript_1/3_Conf_0.667	697	20	8.19E-58	NP_741466.1	72	227.639	201	146	SaPosin-like Protein family member (spp-10)
Locus_772_Transcript_2/3_Conf_0.667	718	20	3.17E-60	NP_741465.1	66	235.728	237	158	SaPosin-like Protein family member (spp-10)
Locus_772_Transcript_3/3_Conf_0.667	718	20	3.17E-60	NP_741465.1	66	235.728	237	158	SaPosin-like Protein family member (spp-10)
Locus_7720_Transcript_1/1_Conf_1.000	804	0							
Locus_7721_Transcript_1/1_Conf_1.000	134	0							
Locus_7722_Transcript_1/1_Conf_1.000	352	0							
Locus_7723_Transcript_1/1_Conf_1.000	415	0							
Locus_7724_Transcript_1/1_Conf_1.000	920	0							
Locus_7725_Transcript_1/1_Conf_1.000	726	20	6.01E-30	XP_002637262.1	63	135.191	134	85	C. briggsae CBR-ACL-9 protein
Locus_7726_Transcript_1/1_Conf_1.000	1582	20	6.82E-17	XP_002630594.1	43	93.5893	270	118	C. briggsae CBR-AKA-1 protein
Locus_7727_Transcript_1/1_Conf_1.000	508	20	4.98E-68	XP_001900116.1	89	260.381	165	148	SMC proteins Flexible Hinge Domain containing protein
Locus_7728_Transcript_1/1_Conf_1.000	377	15	7.17E-39	XP_002804494.1	94	154.451	100	94	PREDICTED: hypothetical protein LOC698789
Locus_7729_Transcript_1/1_Conf_1.000	874	20	1.79E-11	XP_001898275.1	43	74.3294	308	133	GRIP domain containing protein

Locus_773_Transcript_1/1_Conf_1.000	2088	20	0	EFO26258.1	74	744.191	676	501	hypothetical protein LOAG_02227
Locus_7730_Transcript_1/1_Conf_1.000	294	20	1.13E-29	NP_510494.2	88	132.88	89	79	hypothetical protein C18B12.6
Locus_7731_Transcript_1/1_Conf_1.000	361	0							
Locus_7732_Transcript_1/1_Conf_1.000	315	20	2.46E-32	NP_506242.2	78	141.739	103	81	hypothetical protein R186.6
Locus_7733_Transcript_1/1_Conf_1.000	250	20	2.09E-28	XP_002634371.1	86	128.642	82	71	C. briggsae CBR-RIG-4 protein
Locus_7734_Transcript_1/1_Conf_1.000	154	0							
Locus_7735_Transcript_1/2_Conf_1.000	881	20	3.37E-18	XP_002072569.1	47	96.6709	194	92	GK13666
Locus_7735_Transcript_2/2_Conf_1.000	869	20	3.32E-18	XP_002072569.1	47	96.6709	194	92	GK13666
Locus_7736_Transcript_1/1_Conf_1.000	508	0							
Locus_7737_Transcript_1/1_Conf_1.000	449	0							
Locus_7738_Transcript_1/1_Conf_1.000	401	20	9.62E-21	BAB68205.1	70	103.219	112	79	keratin-like protein
Locus_7739_Transcript_1/1_Conf_1.000	865	0							

Locus_774_Transcript_1/2_Conf_1.000	1496	5	5.70E-42	NP_741151.1	85	176.792	120	103	MeDiaTor family member (mdt-15)
Locus_774_Transcript_2/2_Conf_1.000	1433	5	1.12E-39	NP_741151.1	95	169.088	90	86	MeDiaTor family member (mdt-15)
Locus_7740_Transcript_1/1_Conf_1.000	1324	20	1.96E-160	CAJ43810.1	77	570.081	427	333	astacin-like metalloprotease
Locus_7741_Transcript_1/1_Conf_1.000	379	3	1.86E-24	XP_002632304.1	63	115.546	118	75	Hypothetical protein CBG07208
Locus_7742_Transcript_1/1_Conf_1.000	275	20	6.16E-20	NP_503171.1	74	100.523	85	63	hypothetical protein F33E11.3
Locus_7743_Transcript_1/1_Conf_1.000	1665	20	2.53E-110	EFO26375.1	64	404.06	554	360	hypothetical protein LOAG_02108
Locus_7744_Transcript_1/1_Conf_1.000	615	20	4.14E-62	NP_510264.1	73	241.506	190	139	Carbonic AnHydrase family member (cah-4)

Locus_7745_Transcript_1/2_Conf_1.000	794	20	5.38E-86	NP_502083.1	86	321.627	217	188	Alcohol/Ribitol Dehydrogenase family member (ard-1)
Locus_7745_Transcript_2/2_Conf_1.000	794	20	5.38E-86	NP_502083.1	86	321.627	217	188	Alcohol/Ribitol Dehydrogenase family member (ard-1)
Locus_7746_Transcript_1/1_Conf_1.000	1203	2	2.68E-04	XP_001299868.1	47	51.2174	134	64	hypothetical protein
Locus_7747_Transcript_1/2_Conf_1.000	974	20	9.23E-124	ABQ88321.1	84	447.588	296	250	transposase
Locus_7747_Transcript_2/2_Conf_1.000	264	20	1.18E-11	ABQ88321.1	72	72.7886	58	42	transposase

Locus_7748_Transcript_1/1_Conf_1.000	1879	20	0	CAA60047.1	96	962.214	529	512	cytoplasmic intermediate filament protein
Locus_7749_Transcript_1/1_Conf_1.000	1855	20	8.29E-166	NP_001021778.1	84	588.571	391	332	C-terminal Src Kinase family member (csk-1)
Locus_775_Transcript_1/1_Conf_1.000	569	20	4.64E-48	NP_740944.1	96	194.512	110	106	Ribosomal Protein, Small subunit family member (rps-20)
Locus_7750_Transcript_1/1_Conf_1.000	231	0							
Locus_7751_Transcript_1/1_Conf_1.000	646	20	1.44E-63	XP_002635372.1	75	246.514	213	161	C. briggsae CBR-RPM-1 protein
Locus_7752_Transcript_1/1_Conf_1.000	627	0							
Locus_7753_Transcript_1/1_Conf_1.000	730	20	2.89E-48	XP_002630311.1	58	196.052	243	143	C. briggsae CBR-CTNS-1 protein
Locus_7754_Transcript_1/3_Conf_0.667	1055	20	1.02E-86	NP_494280.3	79	324.709	310	245	MNAT (menage a trois) TFIIH subunit family member (mnat-1)

Locus_7754_Transcript_2/3_Conf_0.667	1083	20	7.93E-85	NP_494280.3	79	263.077	198	157	MNAT (menage a trois) TFIIH subunit family member (mnat-1)
Locus_7754_Transcript_3/3_Conf_0.667	1060	20	1.03E-86	NP_494280.3	79	324.709	310	245	MNAT (menage a trois) TFIIH subunit family member (mnat-1)
Locus_7755_Transcript_1/2_Conf_1.000	440	2	5.35E-08	NP_001023436.1	59	60.8474	136	81	hypothetical protein Y37E11AL.3
Locus_7755_Transcript_2/2_Conf_1.000	440	2	5.35E-08	NP_001023436.1	59	60.8474	136	81	hypothetical protein Y37E11AL.3
Locus_7756_Transcript_1/1_Conf_1.000	553	20	3.22E-51	XP_002632168.1	75	204.912	184	139	C. briggsae CBR-PQN-85 protein
Locus_7757_Transcript_1/1_Conf_1.000	253	20	4.21E-32	AAK31527.3	90	140.969	81	73	Neuronal symmetry protein 1, partially confirmed by transcript evidence
Locus_7758_Transcript_1/1_Conf_1.000	840	20	2.02E-33	CAO00417.1	48	147.132	283	137	two-domain activation associated secreted protein ASP4 precursor
Locus_7759_Transcript_1/1_Conf_1.000	1416	0							
Locus_776_Transcript_1/1_Conf_1.000	886	20	6.13E-68	EFO14607.1	67	261.922	222	150	TRE-2 protein
Locus_7760_Transcript_1/1_Conf_1.000	131	20	2.52E-05	XP_002809331.1	100	51.9878	41	41	PREDICTED: LOW QUALITY PROTEIN: interferon regulatory factor 2-binding protein 2-like
Locus_7761_Transcript_1/2_Conf_1.000	395	5	5.52E-08	EFO18202.1	88	60.8474	36	32	hypothetical protein LOAG_10292

Locus_7761_Transcript_2/2_Conf_1.000	389	5	5.38E-08	EFO18202.1	88	60.8474	36	32	hypothetical protein LOAG_10292
Locus_7762_Transcript_1/1_Conf_1.000	679	20	6.96E-59	NP_491663.1	79	231.106	177	140	hypothetical protein T19B4.3
Locus_7763_Transcript_1/1_Conf_1.000	322	0							
Locus_7764_Transcript_1/1_Conf_1.000	428	0							
Locus_7765_Transcript_1/1_Conf_1.000	625	20	8.42E-103	XP_001473838.1	99	376.711	203	202	PREDICTED: similar to ribosomal protein L15 isoform 1
Locus_7766_Transcript_1/1_Conf_1.000	413	20	7.99E-28	NP_495790.1	70	126.716	132	93	beta-LACTamase domain containing family member (lact-4)
Locus_7767_Transcript_1/1_Conf_1.000	162	0							
Locus_7768_Transcript_1/1_Conf_1.000	319	4	1.15E-05	A8Y236.2	48	53.1434	80	39	Putative polypeptide N-acetylgalactosaminyltransferase 10
Locus_7769_Transcript_1/1_Conf_1.000	2564	20	2.31E-31	CAR63726.1	79	142.51	158	125	hypothetical protein
Locus_777_Transcript_1/1_Conf_1.000	1870	20	0	NP_496508.1	99	692.96	340	338	G Protein, Beta subunit family member (gpb-1)
Locus_7770_Transcript_1/1_Conf_1.000	727	20	1.21E-38	NP_502448.1	81	164.081	107	87	hypothetical protein ZK896.9
Locus_7771_Transcript_1/1_Conf_1.000	676	0							
Locus_7772_Transcript_1/3_Conf_0.333	787	20	1.18E-69	NP_498146.1	79	267.314	193	153	DeHydrogenases, Short chain family member (dhs-9)

Locus_7772_Transcript_2/3_Conf_0.333	441	20	2.28E-46	NP_498146.1	78	188.348	136	107	DeHydrogenases, Short chain family member (dhs-9)
Locus_7772_Transcript_3/3_Conf_0.667	1203	20	9.22E-114	NP_498146.1	78	414.846	321	252	DeHydrogenases, Short chain family member (dhs-9)
Locus_7773_Transcript_1/2_Conf_1.000	1932	20	0	EFO21446.1	86	726.087	511	441	hypothetical protein LOAG_07043
Locus_7773_Transcript_2/2_Conf_1.000	1932	20	0	EFO21446.1	86	726.087	511	441	hypothetical protein LOAG_07043
Locus_7774_Transcript_1/1_Conf_1.000	1098	4	2.87E-103	NP_491469.2	85	379.793	256	219	hypothetical protein F25F8.1
Locus_7775_Transcript_1/3_Conf_0.611	156	0							
Locus_7775_Transcript_2/3_Conf_0.722	139	0							
Locus_7775_Transcript_3/3_Conf_0.778	122	0							
Locus_7776_Transcript_1/1_Conf_1.000	247	3	8.56E-14	NP_495495.1	65	80.1073	81	53	hypothetical protein E04F6.6
Locus_7777_Transcript_1/1_Conf_1.000	1158	20	2.23E-85	XP_002639094.1	64	320.472	351	227	Hypothetical protein CBG14913
Locus_7778_Transcript_1/1_Conf_1.000	157	0							
Locus_7779_Transcript_1/1_Conf_1.000	360	0							
Locus_778_Transcript_1/1_Conf_1.000	155	20	1.11E-08	XP_002632600.1	92	63.1586	51	47	Hypothetical protein CBG21499
Locus_7780_Transcript_1/1_Conf_1.000	720	20	4.46E-70	XP_002642216.1	74	268.47	240	179	C. briggsae CBR-ULA-1 protein
Locus_7781_Transcript_1/1_Conf_1.000	704	0							
Locus_7782_Transcript_1/1_Conf_1.000	369	7	3.68E-20	NP_001041091.2	72	101.293	99	72	Motor AXon guidance family member (max-1)
Locus_7783_Transcript_1/1_Conf_1.000	317	20	5.63E-53	XP_002801758.1	98	210.305	102	100	PREDICTED: 60S ribosomal protein L37-like
Locus_7784_Transcript_1/1_Conf_1.000	615	20	3.89E-44	XP_002647583.1	66	181.8	198	131	C. briggsae CBR-CHK-1 protein
Locus_7785_Transcript_1/1_Conf_1.000	380	2	2.21E-17	XP_002636950.1	57	92.0485	119	68	C. briggsae CBR-HIM-17 protein
Locus_7786_Transcript_1/1_Conf_1.000	232	0							

Locus_7787_Transcript_1/3_Conf_0.600	1384	20	0	NP_491013.1	83	671.389	452	376	Cysteinyl tRNA Synthetase family member (crs-1)
Locus_7787_Transcript_2/3_Conf_0.600	959	20	3.82E-82	XP_001897270.1	76	309.301	278	214	cysteinyl tRNA synthetase protein 1, isoform b
Locus_7787_Transcript_3/3_Conf_0.600	1721	20	0	NP_491013.1	79	729.169	537	429	Cysteinyl tRNA Synthetase family member (crs-1)
Locus_7788_Transcript_1/1_Conf_1.000	1009	20	6.51E-51	A8XZU0.2	71	205.682	199	142	Probable cytosolic Fe-S cluster assembly factor oxy-4
Locus_7789_Transcript_1/1_Conf_1.000	751	20	1.65E-17	AAY66873.1	62	93.9745	114	71	FUN14 family protein
Locus_779_Transcript_1/2_Conf_1.000	1103	20	2.45E-94	NP_492310.1	68	350.132	355	243	hypothetical protein K02B12.7
Locus_779_Transcript_2/2_Conf_1.000	1588	20	1.35E-105	NP_492310.1	65	388.267	424	278	hypothetical protein K02B12.7
Locus_7790_Transcript_1/2_Conf_1.000	1055	7	1.82E-51	NP_493473.2	59	207.608	289	173	hypothetical protein C37A5.7
Locus_7790_Transcript_2/2_Conf_1.000	950	3	3.26E-33	NP_493473.2	50	146.747	289	147	hypothetical protein C37A5.7
Locus_7791_Transcript_1/1_Conf_1.000	495	0							
Locus_7792_Transcript_1/1_Conf_1.000	150	0							
Locus_7793_Transcript_1/1_Conf_1.000	802	20	4.48E-104	NP_499587.1	90	381.719	225	204	hypothetical protein Y75B8A.14
Locus_7794_Transcript_1/2_Conf_1.000	231	20	6.90E-11	XP_001894671.1	67	70.4774	70	47	Protein kinase domain containing protein
Locus_7794_Transcript_2/2_Conf_1.000	231	20	5.28E-11	XP_001894671.1	67	70.8626	70	47	Protein kinase domain containing protein
Locus_7795_Transcript_1/1_Conf_1.000	469	20	4.84E-73	NP_501418.1	91	276.944	156	143	SQuashed Vulva family member (sqv-1)

Locus_7796_Transcript_1/1_Conf_1.000	782	20	3.20E-43	NP_001020983.1	89	179.489	115	103	TOLl (Drosophila) family member (tol-1)
Locus_7797_Transcript_1/2_Conf_1.000	908	20	3.27E-88	NP_499493.1	82	329.331	231	190	hypothetical protein Y66D12A.9
Locus_7797_Transcript_2/2_Conf_1.000	908	20	3.27E-88	NP_499493.1	82	329.331	231	190	hypothetical protein Y66D12A.9
Locus_7798_Transcript_1/1_Conf_1.000	172	0							
Locus_7799_Transcript_1/1_Conf_1.000	433	20	4.10E-40	2OS5	89	167.548	104	93	Macrophage Migration Inhibitory Factor
Locus_78_Transcript_1/3_Conf_0.400	512	20	4.23E-35		85	150.984	105	90	hypothetical protein T22B7.
Locus_78_Transcript_2/3_Conf_0.600	581	20	3.21E-47		85	191.815	128	110	hypothetical protein T22B7.3
Locus_78_Transcript_3/3_Conf_0.600	1266	20	4.00E-123	NP_508952.2	87	446.047	281	247	hypothetical protein T22B7.3
Locus_780_Transcript_1/2_Conf_1.000	1869	20	0	XP_002647383.1	88	768.844	505	445	C. briggsae CBR-CGP-1 protein
Locus_780_Transcript_2/2_Conf_1.000	1863	20	0	XP_002647383.1	88	773.852	503	445	C. briggsae CBR-CGP-1 protein

Locus_7800_Transcript_1/2_Conf_1.000	1383	20	1.13E-89	XP_002639203.1	74	335.109	307	229	C. briggsae CBR-MEC-8 protein
Locus_7800_Transcript_2/2_Conf_1.000	1448	20	1.20E-89	XP_002639203.1	74	335.109	307	229	C. briggsae CBR-MEC-8 protein
Locus_7801_Transcript_1/1_Conf_1.000	234	0							
Locus_7802_Transcript_1/1_Conf_1.000	160	0							
Locus_7803_Transcript_1/1_Conf_1.000	573	0							
Locus_7804_Transcript_1/1_Conf_1.000	842	20	9.67E-36	XP_001898512.1	66	154.836	168	111	Protein kinase domain containing protein
Locus_7805_Transcript_1/1_Conf_1.000	824	20	1.79E-71	NP_740841.1	75	273.478	269	204	protein KINase family member (kin-32)
Locus_7806_Transcript_1/1_Conf_1.000	858	20	2.24E-43	XP_001900229.1	62	180.259	233	146	FAT domain containing protein
Locus_7807_Transcript_1/1_Conf_1.000	169	0							
Locus_7808_Transcript_1/2_Conf_1.000	2094	20	0	XP_002633289.1	68	660.988	650	448	Hypothetical protein CBG06018
Locus_7808_Transcript_2/2_Conf_1.000	2094	20	0	XP_002633289.1	68	660.988	650	448	Hypothetical protein CBG06018
Locus_7809_Transcript_1/1_Conf_1.000	544	0							
Locus_781_Transcript_1/1_Conf_1.000	1322	20	2.38E-174	NP_500998.1	84	616.305	431	365	hypothetical protein C43G2.1

Locus_7810_Transcript_1/3_Conf_0.600	505	20	5.41E-43	NP_001024914.1	70	177.178	167	118	hypothetical protein T14G8.3
Locus_7810_Transcript_2/3_Conf_0.600	505	20	7.06E-43	NP_001024914.1	70	176.792	167	117	hypothetical protein T14G8.3
Locus_7810_Transcript_3/3_Conf_0.600	505	20	7.06E-43	NP_001024914.1	70	176.792	167	117	hypothetical protein T14G8.3
Locus_7811_Transcript_1/1_Conf_1.000	466	20	1.58E-39	BAG59908.1	100	165.622	83	83	unnamed protein product
Locus_7812_Transcript_1/1_Conf_1.000	323	0							
Locus_7813_Transcript_1/1_Conf_1.000	381	0							
Locus_7814_Transcript_1/1_Conf_1.000	3628	20	0	NP_491855.1	61	732.25	1097	676	Nuclear Pore complex Protein family member (npp-12)
Locus_7815_Transcript_1/1_Conf_1.000	708	20	1.67E-106	ACK44110.1	96	389.423	201	194	manganese superoxide dismutase precursor
Locus_7816_Transcript_1/1_Conf_1.000	604	20	2.06E-95	XP_002640056.1	99	352.058	195	194	Hypothetical protein CBG12532
Locus_7817_Transcript_1/1_Conf_1.000	228	0							
Locus_7818_Transcript_1/1_Conf_1.000	336	2	3.61E-04	CBM41222.1	44	48.1358	92	41	C. elegans protein T10G3.3b, partially confirmed by transcript evidence
Locus_7819_Transcript_1/2_Conf_1.000	1053	5	3.35E-29	XP_002639130.1	44	133.65	384	172	Hypothetical protein CBG14950
Locus_7819_Transcript_2/2_Conf_1.000	451	6	3.29E-13	ABD94095.1	48	78.1814	146	71	Hypothetical protein W05F2.4a
Locus_782_Transcript_1/1_Conf_1.000	331	20	2.05E-23	ACI49074.1	68	112.079	110	75	hypothetical protein Cbre_JD10.006
Locus_7820_Transcript_1/1_Conf_1.000	263	2	7.90E-15	NP_492351.1	82	83.5741	52	43	hypothetical protein K07A12.7

Locus_7821_Transcript_1/1_Conf_1.000	493	20	1.77E-75	NP_504661.1	96	285.034	164	159	Daf-12, REdundant with family member (dre-1)
Locus_7822_Transcript_1/1_Conf_1.000	890	20	4.91E-49	EFO15488.1	61	199.134	242	148	hypothetical protein LOAG_13022
Locus_7823_Transcript_1/1_Conf_1.000	659	2	2.13E-09	XP_001891619.1	60	66.6254	147	89	PH domain containing protein
Locus_7824_Transcript_1/1_Conf_1.000	459	20	3.21E-53	NP_501505.1	88	211.075	124	110	hypothetical protein F21D5.8
Locus_7825_Transcript_1/1_Conf_1.000	1268	20	4.19E-80	XP_002647044.1	57	303.138	458	264	C. briggsae CBR-ELPC-2 protein
Locus_7826_Transcript_1/1_Conf_1.000	501	0							
Locus_7827_Transcript_1/2_Conf_1.000	1528	20	1.53E-90	EFO25005.1	57	338.191	447	259	hypothetical protein LOAG_03478
Locus_7827_Transcript_2/2_Conf_1.000	1363	20	9.12E-68	EFO25005.1	70	262.307	225	159	hypothetical protein LOAG_03478
Locus_7828_Transcript_1/1_Conf_1.000	731	20	1.48E-68	XP_001899812.1	74	263.462	232	173	hypothetical protein Bm1_41765
Locus_7829_Transcript_1/1_Conf_1.000	718	20	9.78E-94	XP_002639432.1	81	347.051	239	195	C. briggsae CBR-TYR-4 protein
Locus_783_Transcript_1/1_Conf_1.000	644	20	3.98E-66	XP_002629858.1	92	254.988	150	138	Hypothetical protein CBG21892
Locus_7830_Transcript_1/1_Conf_1.000	176	0							
Locus_7831_Transcript_1/1_Conf_1.000	529	0							
Locus_7832_Transcript_1/2_Conf_1.000	318	9	1.15E-05	XP_809492.1	67	53.1434	65	44	vesicular transport-associated repeat protein
Locus_7832_Transcript_2/2_Conf_1.000	264	6	4.33E-05	XP_001640051.1	62	51.2174	72	45	predicted protein
Locus_7833_Transcript_1/1_Conf_1.000	672	0							
Locus_7834_Transcript_1/1_Conf_1.000	685	20	7.30E-80	XP_002636225.1	79	300.827	225	179	Hypothetical protein CBG12149
Locus_7835_Transcript_1/1_Conf_1.000	452	20	3.71E-57	XP_001899521.1	94	224.172	117	110	Disorganized muscle protein 1
Locus_7836_Transcript_1/1_Conf_1.000	808	0							
Locus_7837_Transcript_1/1_Conf_1.000	701	20	1.12E-46	EFO21887.1	91	190.66	104	95	SCPL-2 protein

Locus_7838_Transcript_1/1_Conf_1.000	773	2	1.79E-06	XP_002404556.1	48	57.3806	201	98	nuclear hormone receptor 48, putative
Locus_7839_Transcript_1/1_Conf_1.000	817	20	6.49E-66	CAX32485.1	71	254.988	271	194	C. elegans protein T20D3.11b, partially confirmed by transcript evidence
Locus_784_Transcript_1/1_Conf_1.000	2055	20	0	NP_505508.1	79	781.556	552	440	hypothetical protein F40F9.6
Locus_7840_Transcript_1/1_Conf_1.000	788	15	4.42E-16	XP_002637665.1	42	89.3521	258	109	C. briggsae CBR-APT-10 protein
Locus_7841_Transcript_1/1_Conf_1.000	900	20	1.23E-71	AAC47112.1	66	274.248	287	190	sel-1
Locus_7842_Transcript_1/1_Conf_1.000	293	20	2.80E-20	NP_492590.1	71	101.679	96	69	hypothetical protein K02A11.3
Locus_7843_Transcript_1/1_Conf_1.000	1209	20	6.27E-86	NP_001022524.1	73	322.398	264	193	CoBaLamin deficiency, C complementation group (human) homolog family member (cblc-1)
Locus_7844_Transcript_1/1_Conf_1.000	505	0							
Locus_7845_Transcript_1/1_Conf_1.000	306	0							
Locus_7846_Transcript_1/1_Conf_1.000	278	0							
Locus_7847_Transcript_1/1_Conf_1.000	861	20	6.56E-43	NP_508196.1	57	178.718	238	136	STAUfen (dsRNA binding protein) homolog family member (stau-1)
Locus_7848_Transcript_1/2_Conf_1.000	1431	0							
Locus_7848_Transcript_2/2_Conf_1.000	696	0							
Locus_7849_Transcript_1/1_Conf_1.000	373	0							
Locus_785_Transcript_1/7_Conf_0.444	908	0							
Locus_785_Transcript_2/7_Conf_0.500	957	0							
Locus_785_Transcript_3/7_Conf_0.389	851	0							
Locus_785_Transcript_4/7_Conf_0.167	674	0							
Locus_785_Transcript_5/7_Conf_0.167	674	0							
Locus_785_Transcript_6/7_Conf_0.500	978	0							

Locus_785_Transcript_7/7_Conf_0.556	978	0							
Locus_7850_Transcript_1/1_Conf_1.000	250	0							
Locus_7851_Transcript_1/2_Conf_1.000	1185	20	1.30E-112	AAA68954.1	80	410.994	330	264	UNC-76
Locus_7851_Transcript_2/2_Conf_1.000	1194	20	8.53E-112	AAA68954.1	79	408.297	332	265	UNC-76
Locus_7852_Transcript_1/1_Conf_1.000	580	20	6.03E-62	ADM53749.1	76	240.736	181	138	Hypothetical protein F45F2.9b
Locus_7853_Transcript_1/2_Conf_1.000	754	20	1.31E-98	NP_741467.1	86	233.802	161	139	hypothetical protein C09G4.2
Locus_7853_Transcript_2/2_Conf_1.000	746	20	5.08E-104	NP_741467.1	86	381.333	249	216	hypothetical protein C09G4.2
Locus_7854_Transcript_1/2_Conf_1.000	1061	20	2.09E-79	NP_491513.2	85	300.442	213	182	Formin HOmology Domain family member (fhod-1)
Locus_7854_Transcript_2/2_Conf_1.000	871	20	1.69E-78	NP_491513.2	89	296.975	193	172	Formin HOmology Domain family member (fhod-1)
Locus_7855_Transcript_1/1_Conf_1.000	416	0							
Locus_7856_Transcript_1/1_Conf_1.000	1203	20	0	ACN93882.1	94	737.643	401	378	putative glutamate-cysteine ligase catalytic subunit
Locus_7857_Transcript_1/1_Conf_1.000	228	20	4.47E-26	NP_504502.1	88	120.939	76	67	hypothetical protein F25B4.1
Locus_7858_Transcript_1/2_Conf_1.000	342	0							
Locus_7858_Transcript_2/2_Conf_1.000	342	0							

Locus_7859_Transcript_1/2_Conf_1.000	596	20	1.26E-17	EFN84094.1	54	93.5893	174	95	Dehydrogenase/reductase SDR family member 7
Locus_7859_Transcript_2/2_Conf_1.000	947	20	1.61E-24	NP_001085784.1	53	117.857	267	143	dehydrogenase/reductase (SDR family) member 7
Locus_786_Transcript_1/2_Conf_1.000	1234	20	1.51E-42	EFO20187.1	54	178.333	322	176	nuclear factor I
Locus_786_Transcript_2/2_Conf_1.000	1207	20	2.75E-41	XP_001902121.1	61	174.096	234	143	MH1 domain containing protein
Locus_7860_Transcript_1/1_Conf_1.000	785	5	7.59E-85	NP_492783.1	79	317.775	229	182	Temporarily Assigned Gene name family member (tag-264)
Locus_7861_Transcript_1/1_Conf_1.000	294	0							
Locus_7862_Transcript_1/1_Conf_1.000	382	3	1.99E-10	AAA96289.2	80	68.9366	55	44	Hypothetical protein D1014.2
Locus_7863_Transcript_1/1_Conf_1.000	325	20	6.61E-38	NP_496205.2	86	160.229	108	93	PhosphoLipase C family member (plc-3)
Locus_7864_Transcript_1/1_Conf_1.000	1270	20	1.21E-111	EFO18387.1	76	407.912	359	273	hypothetical protein LOAG_10109
Locus_7865_Transcript_1/1_Conf_1.000	578	20	3.05E-58	NP_491282.1	89	228.409	141	126	CalPoNin family member (cpn-3)
Locus_7866_Transcript_1/2_Conf_1.000	1210	20	3.11E-85	XP_002631227.1	66	320.087	384	257	Hypothetical protein CBG03025
Locus_7866_Transcript_2/2_Conf_1.000	747	20	1.98E-47	NP_496307.1	68	193.356	247	168	hypothetical protein C09G5.2
Locus_7867_Transcript_1/1_Conf_1.000	603	0							
Locus_7868_Transcript_1/1_Conf_1.000	265	0							

Locus_7869_Transcript_1/2_Conf_1.000	3179	20	2.38E-73	EFO21171.1	54	282.337	446	244	PHD-finger family protein
Locus_7869_Transcript_2/2_Conf_1.000	3159	20	2.36E-73	EFO21171.1	54	282.337	446	244	PHD-finger family protein
Locus_787_Transcript_1/3_Conf_0.571	1915	20	3.07E-46	XP_001895704.1	38	191.43	652	251	Chitin binding Peritrophin-A domain containing protein
Locus_787_Transcript_2/3_Conf_0.714	2120	20	3.47E-46	XP_001895704.1	38	191.43	652	251	Chitin binding Peritrophin-A domain containing protein

Locus_787_Transcript_3/3_Conf_0.714	1947	20	1.31E-44	XP_001895704.1	40	186.037	695	279	Chitin binding Peritrophin-A domain containing protein
Locus_7870_Transcript_1/1_Conf_1.000	324	13	5.45E-16	XP_002646301.1	74	87.4261	91	68	C. briggsae CBR-UNC-11 protein
Locus_7871_Transcript_1/1_Conf_1.000	599	4	8.61E-06	NP_495677.1	47	54.299	200	94	ZYGote defective: embryonic lethal family member (zyg-11)
Locus_7872_Transcript_1/1_Conf_1.000	2232	20	6.05E-174	NP_001022570.1	63	615.92	670	424	CYLinDromatosis (human disease gene) homolog family member (cyld-1)
Locus_7873_Transcript_1/1_Conf_1.000	654	0							
Locus_7874_Transcript_1/1_Conf_1.000	179	20	6.78E-11	EFO23362.1	75	70.4774	49	37	CAP-Gly domain-containing protein
Locus_7875_Transcript_1/1_Conf_1.000	1130	0							
Locus_7876_Transcript_1/2_Conf_1.000	581	0							
Locus_7876_Transcript_2/2_Conf_1.000	581	0							
Locus_7877_Transcript_1/1_Conf_1.000	306	0							
Locus_7878_Transcript_1/1_Conf_1.000	229	20	1.81E-27	NP_497480.2	89	125.561	76	68	POLH (DNA polymerase eta) homolog family member (polh-1)
Locus_7879_Transcript_1/1_Conf_1.000	200	0							
Locus_788_Transcript_1/2_Conf_1.000	1107	20	6.36E-50	AAB09129.2	72	202.601	184	134	Hypothetical protein M02B7.4
Locus_788_Transcript_2/2_Conf_1.000	1107	20	6.37E-50	AAB09129.2	72	202.601	184	134	Hypothetical protein M02B7.4
Locus_7880_Transcript_1/1_Conf_1.000	287	0							
Locus_7881_Transcript_1/1_Conf_1.000	812	20	2.24E-111	NP_497625.3	91	405.986	243	223	hypothetical protein Y71H2AM.1
Locus_7882_Transcript_1/1_Conf_1.000	629	20	1.63E-61	XP_002639893.1	87	239.58	151	132	Hypothetical protein CBG08215
Locus_7883_Transcript_1/1_Conf_1.000	667	0							
Locus_7884_Transcript_1/1_Conf_1.000	811	20	1.26E-21	AAO63577.1	46	107.842	242	112	secreted protein 5 precursor
Locus_7885_Transcript_1/1_Conf_1.000	203	0							

Locus_7886_Transcript_1/2_Conf_1.000	870	20	5.78E-87	XP_002635267.1	78	325.094	264	207	C. briggsae CBR-LETM-1 protein
Locus_7886_Transcript_2/2_Conf_1.000	824	20	3.71E-85	NP_506382.1	82	318.931	234	194	LETM1 (Leucine zipper, EF-hand, TransMembrane mitochondrial protein) homolog family member (letm-1)
Locus_7887_Transcript_1/2_Conf_1.000	2062	20	0	XP_002644202.1	83	850.121	629	526	Hypothetical protein CBG17192
Locus_7887_Transcript_2/2_Conf_1.000	1073	20	4.50E-138	XP_002644202.1	83	495.352	358	299	Hypothetical protein CBG17192
Locus_7888_Transcript_1/1_Conf_1.000	699	4	1.34E-07	EFO17538.1	45	60.8474	192	88	hypothetical protein LOAG_10961
Locus_7889_Transcript_1/1_Conf_1.000	339	20	3.44E-39	XP_002636622.1	84	164.466	112	95	C. briggsae CBR-SMA-1 protein
Locus_789_Transcript_1/1_Conf_1.000	159	0							
Locus_7890_Transcript_1/1_Conf_1.000	188	2	6.76E-06	NP_001022051.1	81	53.9138	43	35	SREBP Cleavage activating Protein (SCAP) homolog family member (scp-1)
Locus_7891_Transcript_1/1_Conf_1.000	501	20	2.37E-35	EFO23330.1	98	151.754	78	77	GTP-binding regulatory protein alpha chain
Locus_7892_Transcript_1/1_Conf_1.000	870	20	9.25E-77	EFO24390.1	72	291.197	258	187	hypothetical protein LOAG_04097
Locus_7893_Transcript_1/1_Conf_1.000	150	0							
Locus_7894_Transcript_1/1_Conf_1.000	193	5	1.65E-12	NP_001122450.1	89	75.8702	46	41	hypothetical protein F10G8.8
Locus_7895_Transcript_1/2_Conf_1.000	491	20	1.13E-29	NP_507487.1	75	132.88	142	107	P-GlycoProtein related family member (pgp-9)
Locus_7895_Transcript_2/2_Conf_1.000	1094	20	5.91E-117	NP_507487.1	83	425.246	345	289	P-GlycoProtein related family member (pgp-9)

Locus_7896_Transcript_1/1_Conf_1.000	657	20	3.02E-72	XP_002634540.1	81	275.404	186	151	C. briggsae CBR-EGL-21 protein
Locus_7897_Transcript_1/1_Conf_1.000	1350	20	3.50E-104	XP_002645345.1	90	383.259	309	280	C. briggsae CBR-TNT-2 protein
Locus_7898_Transcript_1/1_Conf_1.000	312	20	1.14E-45	NP_001022869.1	91	186.037	103	94	hypothetical protein Y42G9A.4
Locus_7899_Transcript_1/1_Conf_1.000	140	0							
Locus_79_Transcript_1/1_Conf_1.000	302	20	5.96E-31	XP_002640973.1	88	137.117	98	87	C. briggsae CBR-SNF-6 protein
Locus_790_Transcript_1/4_Conf_0.200	867	20	1.12E-90	XP_002642802.1	94	337.421	178	168	C. briggsae CBR-ABCF-2 protein
Locus_790_Transcript_2/4_Conf_0.200	825	20	1.12E-89	XP_002642802.1	94	333.954	175	165	C. briggsae CBR-ABCF-2 protein
Locus_790_Transcript_3/4_Conf_0.400	2206	20	0	XP_002642802.1	94	1036.17	568	539	C. briggsae CBR-ABCF-2 protein
Locus_790_Transcript_4/4_Conf_0.400	2206	20	0	XP_002642802.1	94	1037.33	570	540	C. briggsae CBR-ABCF-2 protein

Locus_7900_Transcript_1/1_Conf_1.000	1068	20	2.56E-117	XP_002633370.1	81	426.402	321	261	Hypothetical protein CBG06117
Locus_7901_Transcript_1/1_Conf_1.000	405	0							
Locus_7902_Transcript_1/2_Conf_1.000	491	0							
Locus_7902_Transcript_2/2_Conf_1.000	491	0							
Locus_7903_Transcript_1/1_Conf_1.000	368	0							
Locus_7904_Transcript_1/1_Conf_1.000	797	20	3.41E-72	XP_002629818.1	83	275.789	184	153	Hypothetical protein CBG01062
Locus_7905_Transcript_1/1_Conf_1.000	1636	20	2.67E-72	EFO22647.1	57	277.715	435	251	DEAD/DEAH box helicase
Locus_7906_Transcript_1/1_Conf_1.000	1309	20	0	ACI02330.1	92	727.628	409	379	aspartic protease 1
Locus_7907_Transcript_1/1_Conf_1.000	365	20	5.36E-16	XP_001894880.1	75	87.4261	74	56	hypothetical protein
Locus_7908_Transcript_1/1_Conf_1.000	479	20	1.70E-70	XP_002832118.1	98	268.47	141	139	PREDICTED: histone H3.3-like, partial

Locus_7909_Transcript_1/1_Conf_1.000	1077	20	1.66E-39	ACI49198.1	94	167.933	118	112	hypothetical protein Csp3_JD03.007
Locus_791_Transcript_1/3_Conf_0.714	2639	20	0	XP_002642195.1	89	1264.98	805	723	C. briggsae CBR-UNC-116 protein
Locus_791_Transcript_2/3_Conf_0.714	2648	20	0	XP_002642195.1	89	1264.98	806	723	C. briggsae CBR-UNC-116 protein

Locus_791_Transcript_3/3_Conf_0.714	2648	20	0	XP_002642195.1	89	1264.98	806	723	C. briggsae CBR-UNC-116 protein
Locus_7910_Transcript_1/1_Conf_1.000	423	20	3.08E-35	NP_499963.1	79	151.369	101	80	hypothetical protein K11H12.1
Locus_7911_Transcript_1/1_Conf_1.000	1254	20	4.18E-149	NP_493388.1	81	532.332	409	332	UNCoordinated family member (unc-59)
Locus_7912_Transcript_1/1_Conf_1.000	610	0							
Locus_7913_Transcript_1/1_Conf_1.000	846	20	4.26E-31	EFO20247.1	64	139.428	167	108	transcription initiation factor IID
Locus_7914_Transcript_1/1_Conf_1.000	578	0							
Locus_7915_Transcript_1/1_Conf_1.000	252	3	6.13E-07	AAF60449.3	61	57.3806	84	52	Hypothetical protein Y17G9B.8
Locus_7916_Transcript_1/1_Conf_1.000	974	20	6.93E-79	XP_001899472.1	73	298.516	276	204	Patatin-like phospholipase family protein
Locus_7917_Transcript_1/1_Conf_1.000	218	0							
Locus_7918_Transcript_1/2_Conf_1.000	979	20	3.27E-60	XP_001893007.1	79	236.498	184	147	DJ-1 family protein
Locus_7918_Transcript_2/2_Conf_1.000	680	20	1.18E-74	NP_493695.1	87	283.493	175	153	hypothetical protein B0432.3

Locus_7919_Transcript_1/1_Conf_1.000	597	20	1.41E-32	XP_002644685.1	78	143.28	161	126	C. briggsae CBR-SYN-1 protein
Locus_792_Transcript_1/1_Conf_1.000	1419	20	6.18E-91	EFO27641.1	63	339.347	477	304	symplekin
Locus_7920_Transcript_1/1_Conf_1.000	882	20	7.91E-92	NP_001021719.1	79	341.273	251	199	hypothetical protein Y110A7A.9
Locus_7921_Transcript_1/1_Conf_1.000	220	19	1.15E-13	NP_495353.1	70	79.7221	71	50	hypothetical protein T19D12.9
Locus_7922_Transcript_1/1_Conf_1.000	362	20	2.85E-25	AAC70065.1	66	118.242	121	81	MutS homolog
Locus_7923_Transcript_1/3_Conf_0.714	1051	20	6.31E-12	XP_002648823.1	40	76.2554	250	100	Hypothetical protein CBG16936
Locus_7923_Transcript_2/3_Conf_0.714	1051	20	2.17E-12	XP_002648823.1	38	77.7962	259	100	Hypothetical protein CBG16936
Locus_7923_Transcript_3/3_Conf_0.714	1051	20	6.31E-12	XP_002648823.1	38	76.2554	256	98	Hypothetical protein CBG16936
Locus_7924_Transcript_1/1_Conf_1.000	634	20	1.51E-70	XP_002629723.1	75	269.626	197	149	C. briggsae CBR-UGT-58 protein
Locus_7925_Transcript_1/1_Conf_1.000	619	4	1.32E-23	NP_496091.1	70	113.62	99	70	Neuropeptide-Like Protein family member (nlp-11)
Locus_7926_Transcript_1/1_Conf_1.000	693	20	5.10E-44	ABF69526.1	80	181.8	140	113	unknown
Locus_7927_Transcript_1/1_Conf_1.000	192	0							
Locus_7928_Transcript_1/1_Conf_1.000	508	20	1.46E-35	XP_002639165.1	82	152.525	117	96	C. briggsae CBR-RPL-24.2 protein
Locus_7929_Transcript_1/1_Conf_1.000	549	0							

Locus_793_Transcript_1/1_Conf_1.000	5511	20	0	NP_506153.1	71	1993.01	1833	1318	hypothetical protein C14C10.5
Locus_7930_Transcript_1/3_Conf_0.400	455	0							
Locus_7930_Transcript_2/3_Conf_0.400	745	20	1.79E-16	NP_001076697.1	58	90.5077	153	89	Ref/ALY RNA export adaptor family member (aly-3)
Locus_7930_Transcript_3/3_Conf_0.600	963	20	4.34E-25	NP_001076697.1	60	119.783	179	108	Ref/ALY RNA export adaptor family member (aly-3)
Locus_7931_Transcript_1/1_Conf_1.000	853	8	4.79E-22	NP_001023856.1	51	109.383	224	116	hypothetical protein F26F12.3
Locus_7932_Transcript_1/1_Conf_1.000	1048	20	7.49E-98	XP_002633628.1	76	361.688	288	219	Hypothetical protein CBG05511
Locus_7933_Transcript_1/1_Conf_1.000	414	0							
Locus_7934_Transcript_1/1_Conf_1.000	995	20	1.09E-34	XP_002639861.1	73	151.754	126	93	C. briggsae CBR-CSNK-1 protein
Locus_7935_Transcript_1/2_Conf_1.000	887	20	3.39E-42	XP_001898751.1	65	176.407	201	131	UBX domain containing protein
Locus_7935_Transcript_2/2_Conf_1.000	887	20	7.07E-40	EFO17525.1	64	168.703	188	121	hypothetical protein LOAG_10973
Locus_7936_Transcript_1/1_Conf_1.000	1537	10	2.24E-57	XP_002639135.1	49	228.024	528	260	C. briggsae CBR-SEP-1 protein
Locus_7937_Transcript_1/1_Conf_1.000	290	8	2.47E-08	NP_495685.1	65	62.003	94	62	hypothetical protein C08B11.8

Locus_7938_Transcript_1/1_Conf_1.000	1237	20	1.43E-117	NP_496403.1	86	427.557	258	224	Cytochrome C Heme-Lyase family member (cchl-1)
Locus_7939_Transcript_1/1_Conf_1.000	632	0							
Locus_794_Transcript_1/1_Conf_1.000	2028	20	2.13E-154	XP_001900974.1	75	550.821	465	352	hnRNP-R, Q splicing factor family protein
Locus_7940_Transcript_1/1_Conf_1.000	213	20	3.82E-30	XP_002630350.1	94	134.42	71	67	Hypothetical protein CBG04280
Locus_7941_Transcript_1/1_Conf_1.000	139	0							
Locus_7942_Transcript_1/1_Conf_1.000	1230	9	1.41E-32	XP_001900721.1	51	145.206	279	145	hypothetical protein
Locus_7943_Transcript_1/1_Conf_1.000	456	0							
Locus_7944_Transcript_1/3_Conf_0.667	2189	20	1.36E-162	XP_002633518.1	67	578.17	586	397	Hypothetical protein CBG05381
Locus_7944_Transcript_2/3_Conf_0.333	558	20	8.88E-49	XP_002633518.1	80	196.823	134	108	Hypothetical protein CBG05381
Locus_7944_Transcript_3/3_Conf_0.667	2189	20	3.04E-162	XP_002633518.1	67	577.015	586	397	Hypothetical protein CBG05381
Locus_7945_Transcript_1/1_Conf_1.000	257	0							
Locus_7946_Transcript_1/1_Conf_1.000	133	0							
Locus_7947_Transcript_1/1_Conf_1.000	1100	5	1.50E-35	NP_491011.1	54	154.836	274	150	hypothetical protein Y23H5A.3
Locus_7948_Transcript_1/1_Conf_1.000	367	0							
Locus_7949_Transcript_1/1_Conf_1.000	134	0							
Locus_795_Transcript_1/3_Conf_0.571	1410	0							
Locus_795_Transcript_2/3_Conf_0.714	1703	0							
Locus_795_Transcript_3/3_Conf_0.571	1410	0							
Locus_7950_Transcript_1/1_Conf_1.000	578	0							
Locus_7951_Transcript_1/1_Conf_1.000	240	0							
Locus_7952_Transcript_1/1_Conf_1.000	2500	2	2.57E-11	NP_491665.1	44	75.8702	241	108	Nuclear Pore complex Protein family member (npp-7)

Locus_7953_Transcript_1/1_Conf_1.000	382	20	3.15E-48	CAR63533.1	98	194.512	101	99	putative Vitellogenin-linked Transcript family member
Locus_7954_Transcript_1/1_Conf_1.000	701	20	9.19E-41	XP_002639642.1	65	171.014	178	116	Hypothetical protein CBG12356
Locus_7955_Transcript_1/1_Conf_1.000	718	0							
Locus_7956_Transcript_1/1_Conf_1.000	528	0							
Locus_7957_Transcript_1/3_Conf_0.667	2046	20	2.45E-65	NP_490809.2	49	254.988	562	279	SPindle Defective family member (spd-1)
Locus_7957_Transcript_2/3_Conf_0.667	1845	20	1.82E-72	NP_490809.2	54	278.485	512	279	SPindle Defective family member (spd-1)
Locus_7957_Transcript_3/3_Conf_0.667	1995	20	2.37E-65	NP_490809.2	49	254.988	562	279	SPindle Defective family member (spd-1)
Locus_7958_Transcript_1/1_Conf_1.000	198	2	9.95E-10	XP_002638852.1	70	66.6254	65	46	Hypothetical protein CBG22064
Locus_7959_Transcript_1/1_Conf_1.000	1032	20	2.46E-93	XP_002630650.1	77	346.665	284	221	C. briggsae CBR-PLD-1 protein
Locus_796_Transcript_1/6_Conf_0.800	2035	20	2.32E-116	EFO27998.1	77	424.476	366	283	DnaJ chaperonine
Locus_796_Transcript_2/6_Conf_0.800	2035	20	6.10E-117	EFO27998.1	77	426.402	366	283	DnaJ chaperonine
Locus_796_Transcript_3/6_Conf_0.800	2035	20	6.10E-117	EFO27998.1	77	426.402	366	283	DnaJ chaperonine
Locus_796_Transcript_4/6_Conf_0.800	2035	20	6.10E-117	EFO27998.1	77	426.402	366	283	DnaJ chaperonine
Locus_796_Transcript_5/6_Conf_0.800	2035	20	6.10E-117	EFO27998.1	77	426.402	366	283	DnaJ chaperonine
Locus_796_Transcript_6/6_Conf_0.800	2035	20	6.10E-117	EFO27998.1	77	426.402	366	283	DnaJ chaperonine
Locus_7960_Transcript_1/1_Conf_1.000	129	0							

Locus_7961_Transcript_1/1_Conf_1.000	1051	20	2.36E-67	ADI24655.1	65	260.381	237	156	Hypothetical protein F52C9.1
Locus_7962_Transcript_1/1_Conf_1.000	675	0							
Locus_7963_Transcript_1/2_Conf_1.000	380	0							
Locus_7963_Transcript_2/2_Conf_1.000	332	0							
Locus_7964_Transcript_1/1_Conf_1.000	1569	20	3.31E-56	EFO22562.1	50	224.172	414	211	hypothetical protein LOAG_05922
Locus_7965_Transcript_1/1_Conf_1.000	240	13	2.42E-24	CAR63681.1	84	115.161	78	66	putative Temporarily Assigned Gene name family member
Locus_7966_Transcript_1/1_Conf_1.000	193	0							
Locus_7967_Transcript_1/1_Conf_1.000	330	20	1.16E-18	XP_002809274.1	100	96.2857	54	54	PREDICTED: LOW QUALITY PROTEIN: heterogeneous nuclear ribonucleoprotein U-like
Locus_7968_Transcript_1/1_Conf_1.000	602	20	1.29E-33	XP_002636713.1	58	146.747	177	103	Hypothetical protein CBG23432
Locus_7969_Transcript_1/2_Conf_0.750	496	0							
Locus_7969_Transcript_2/2_Conf_0.875	381	0							
Locus_797_Transcript_1/1_Conf_1.000	1429	20	2.66E-41	XP_002637617.1	51	174.481	317	163	Hypothetical protein CBG19360
Locus_7970_Transcript_1/1_Conf_1.000	469	20	6.81E-51	EFO26835.1	83	203.371	136	114	hypothetical protein LOAG_01645
Locus_7971_Transcript_1/1_Conf_1.000	463	0							
Locus_7972_Transcript_1/1_Conf_1.000	192	0							
Locus_7973_Transcript_1/1_Conf_1.000	499	2	4.26E-05	NP_001122827.1	52	51.2174	105	55	Suppressor with Morphological effect on Genitalia family member (smg-3)

Locus_7974_Transcript_1/1_Conf_1.000	611	20	4.61E-50	XP_002642650.1	69	201.445	203	142	Hypothetical protein CBG00032
Locus_7975_Transcript_1/1_Conf_1.000	730	20	3.46E-118	XP_002637342.1	92	428.328	241	224	C. briggsae CBR-UNC-70 protein
Locus_7976_Transcript_1/1_Conf_1.000	500	20	4.82E-41	XP_002641443.1	94	170.629	93	88	Hypothetical protein CBG13312
Locus_7977_Transcript_1/1_Conf_1.000	458	0							
Locus_7978_Transcript_1/1_Conf_1.000	456	0							
Locus_7979_Transcript_1/1_Conf_1.000	1791	20	5.92E-20	XP_001304086.1	44	103.99	569	256	hypothetical protein
Locus_798_Transcript_1/1_Conf_1.000	229	0							
Locus_7980_Transcript_1/1_Conf_1.000	889	20	8.98E-43	XP_001895635.1	57	178.333	292	168	hypothetical protein Bm1_20905

Locus_7981_Transcript_1/2_Conf_1.000	899	20	9.92E-76	XP_001902483.1	86	280.026	181	157	Rnp
Locus_7981_Transcript_2/2_Conf_1.000	2706	20	2.49E-116	XP_001902483.1	87	424.861	272	237	Rnp
Locus_7982_Transcript_1/1_Conf_1.000	760	2	5.03E-06	XP_002640813.1	51	55.8398	93	48	Hypothetical protein CBG15698
Locus_7983_Transcript_1/1_Conf_1.000	356	0							
Locus_7984_Transcript_1/2_Conf_1.000	1041	0							
Locus_7984_Transcript_2/2_Conf_1.000	1041	0							
Locus_7985_Transcript_1/1_Conf_1.000	629	20	8.69E-39	XP_002631393.1	67	164.081	182	122	C. briggsae CBR-TAG-169 protein
Locus_7986_Transcript_1/2_Conf_1.000	562	0							
Locus_7986_Transcript_2/2_Conf_1.000	562	0							
Locus_7987_Transcript_1/1_Conf_1.000	805	20	9.44E-94	XP_002641346.1	82	347.436	236	195	Hypothetical protein CBG13199

Locus_7988_Transcript_1/1_Conf_1.000	228	20	2.13E-44	3K6S	100	181.8	75	75	Structure Of Integrin Alphaxbeta2 Ectodomain
Locus_7989_Transcript_1/1_Conf_1.000	218	0							
Locus_799_Transcript_1/1_Conf_1.000	558	20	1.58E-21	ABJ99064.1	64	106.301	149	96	Hypothetical protein W03A3.2
Locus_7990_Transcript_1/1_Conf_1.000	1009	20	1.87E-90	ACI49253.1	79	337.035	262	208	hypothetical protein Csp3_JD07.003
Locus_7991_Transcript_1/1_Conf_1.000	381	20	6.31E-65	NP_001040798.1	99	249.98	126	125	PhosphoDiEsterase family member (pde-4)
Locus_7992_Transcript_1/1_Conf_1.000	599	7	4.33E-74	ABM91438.1	88	281.182	171	152	defective mitochondrial respiration family member protein 1
Locus_7993_Transcript_1/1_Conf_1.000	457	20	1.26E-73	XP_002763539.1	100	278.87	138	138	PREDICTED: 60S ribosomal protein L3-like isoform 2
Locus_7994_Transcript_1/1_Conf_1.000	731	20	2.65E-09	XP_001580142.1	52	66.6254	120	63	small GTP-binding protein
Locus_7995_Transcript_1/1_Conf_1.000	957	20	1.39E-124	NP_001122555.1	87	450.284	321	282	PhosphoDiEsterase family member (pde-6)

Locus_7996_Transcript_1/1_Conf_1.000	721	20	1.64E-64	NP_495324.2	66	249.98	240	159	human WRN (Werner's syndrome) related family member (wrn-1)
Locus_7997_Transcript_1/1_Conf_1.000	302	0							
Locus_7998_Transcript_1/1_Conf_1.000	340	0							
Locus_7999_Transcript_1/1_Conf_1.000	1083	20	2.01E-109	NP_490891.1	77	400.208	384	296	hypothetical protein Y71G12B.8
Locus_8_Transcript_1/2_Conf_1.000	155	3	3.81E-09	XP_001891902.1	80	64.6994	45	36	rRNA promoter binding protein
Locus_8_Transcript_2/2_Conf_1.000	175	3	3.73E-09	XP_001891902.1	80	64.6994	45	36	rRNA promoter binding protein
Locus_80_Transcript_1/2_Conf_1.000	2194	20	1.66E-68	NP_498382.2	63	218.009	243	155	hypothetical protein F47D12.9
Locus_80_Transcript_2/2_Conf_1.000	2156	20	2.61E-73	NP_498382.2	54	281.567	490	269	hypothetical protein F47D12.9
Locus_800_Transcript_1/4_Conf_0.250	165	0							
Locus_800_Transcript_2/4_Conf_0.250	207	0							
Locus_800_Transcript_3/4_Conf_0.375	302	0							
Locus_800_Transcript_4/4_Conf_0.375	302	0							
Locus_8000_Transcript_1/1_Conf_1.000	279	20	1.19E-23	XP_002636179.1	91	112.849	67	61	Hypothetical protein CBG01436
Locus_8001_Transcript_1/1_Conf_1.000	977	20	8.15E-112	XP_002636654.1	84	407.912	304	256	C. briggsae CBR-CLH-6 protein

Locus_8002_Transcript_1/1_Conf_1.000	1796	20	8.16E-70	ACZ54694.1	58	269.626	438	256	Nuclear pore complex protein protein 10, isoform b, partially confirmed by transcript evidence
Locus_8003_Transcript_1/1_Conf_1.000	532	20	1.65E-22	NP_501199.1	54	109.383	181	98	hypothetical protein F55G1.9
Locus_8004_Transcript_1/1_Conf_1.000	350	0							
Locus_8005_Transcript_1/1_Conf_1.000	691	20	4.33E-112	XP_002643213.1	93	407.912	230	214	C. briggsae CBR-DGK-1 protein
Locus_8006_Transcript_1/1_Conf_1.000	182	2	2.19E-04	XP_001893253.1	66	48.9062	60	40	hypothetical protein Bm1_08910
Locus_8007_Transcript_1/1_Conf_1.000	307	20	7.02E-16	XP_002640572.1	70	87.0409	91	64	C. briggsae CBR-DNJ-27 protein
Locus_8008_Transcript_1/1_Conf_1.000	473	0							
Locus_8009_Transcript_1/1_Conf_1.000	765	2	8.42E-17	XP_002635239.1	49	91.6633	209	104	Hypothetical protein CBG11483
Locus_801_Transcript_1/2_Conf_1.000	1202	12	1.11E-26	CBH29664.1	56	125.561	167	95	C. elegans protein F49E2.5k, confirmed by transcript evidence
Locus_801_Transcript_2/2_Conf_1.000	256	11	6.49E-25	CBH29664.1	85	117.087	87	74	C. elegans protein F49E2.5k, confirmed by transcript evidence
Locus_8010_Transcript_1/1_Conf_1.000	846	0							
Locus_8011_Transcript_1/1_Conf_1.000	1492	0							
Locus_8012_Transcript_1/1_Conf_1.000	433	20	1.84E-40	NP_001033512.1	71	168.703	130	93	Lipid Binding Protein family member (lbp-9)

Locus_8013_Transcript_1/2_Conf_1.000	1406	20	1.33E-53	ACI48997.1	57	215.312	355	205	hypothetical protein Cbre_JD01.004
Locus_8013_Transcript_2/2_Conf_1.000	1199	20	1.65E-30	ACI48997.1	52	138.272	286	151	hypothetical protein Cbre_JD01.004
Locus_8014_Transcript_1/1_Conf_1.000	1281	20	1.09E-75	NP_493579.1	54	288.5	363	197	hypothetical protein F39B2.1
Locus_8015_Transcript_1/1_Conf_1.000	652	0							
Locus_8016_Transcript_1/1_Conf_1.000	257	0							
Locus_8017_Transcript_1/1_Conf_1.000	290	20	6.70E-22	EFO26876.1	73	107.071	89	65	hypothetical protein LOAG_01599
Locus_8018_Transcript_1/1_Conf_1.000	687	0							
Locus_8019_Transcript_1/1_Conf_1.000	350								
Locus_802_Transcript_1/1_Conf_1.000	572	20	1.61E-72	NP_502794.1	98	275.789	154	151	Ribosomal Protein, Small subunit family member (rps-18)
Locus_8020_Transcript_1/1_Conf_1.000	400	2	2.08E-07	XP_002644748.1	71	58.9214	57	41	Hypothetical protein CBG14752
Locus_8021_Transcript_1/1_Conf_1.000	143	0							
Locus_8022_Transcript_1/1_Conf_1.000	518	20	5.25E-28	XP_002639581.1	68	127.487	135	93	C. briggsae CBR-NXT-1 protein

Locus_8023_Transcript_1/1_Conf_1.000	622	20	3.46E-16	XP_002645688.1	77	88.9669	57	44	C. briggsae CBR-ELT-3 protein
Locus_8024_Transcript_1/1_Conf_1.000	181	4	5.75E-13	XP_002644617.1	77	77.411	54	42	C. briggsae CBR-CALU-1 protein
Locus_8025_Transcript_1/1_Conf_1.000	1058	20	4.07E-59	NP_497624.2	72	233.032	187	136	hypothetical protein Y71H2AM.2
Locus_8026_Transcript_1/1_Conf_1.000	618	20	7.67E-48	XP_002641294.1	78	194.126	147	116	Hypothetical protein CBG05209
Locus_8027_Transcript_1/1_Conf_1.000	584	20	2.58E-60	CBK19514.1	77	235.343	193	150	C. elegans protein Y73F8A.24b, partially confirmed by transcript evidence
Locus_8028_Transcript_1/1_Conf_1.000	694	0							
Locus_8029_Transcript_1/1_Conf_1.000	259	0							
Locus_803_Transcript_1/1_Conf_1.000	422	20	2.61E-42	NP_510575.1	81	174.866	133	108	yeast ERV (ER to Golgi transport Vesicle protein) homolog family member (erv-46)
Locus_8030_Transcript_1/1_Conf_1.000	333	0							
Locus_8031_Transcript_1/3_Conf_0.600	1069	20	6.94E-14	XP_002640100.1	85	82.8037	71	61	Hypothetical protein CBG12588
Locus_8031_Transcript_2/3_Conf_0.400	675	0							
Locus_8031_Transcript_3/3_Conf_0.600	860	20	3.05E-16	XP_002640100.1	79	90.1225	86	68	Hypothetical protein CBG12588
Locus_8032_Transcript_1/2_Conf_1.000	863	20	1.35E-72	XP_001639978.1	66	277.33	258	172	predicted protein

Locus_8032_Transcript_2/2_Conf_1.000	503	20	1.44E-40	NP_001135503.1	65	169.088	160	104	hydroxyacylglutathione hydrolase, mitochondrial
Locus_8033_Transcript_1/1_Conf_1.000	579	0							
Locus_8034_Transcript_1/1_Conf_1.000	227	20	1.14E-21	AAR86713.1	77	106.301	75	58	LIN-45 isoform 3
Locus_8035_Transcript_1/1_Conf_1.000	595	13	2.13E-57	NP_001022814.1	73	225.713	196	144	ODoRant response abnormal family member (odr-4)
Locus_8036_Transcript_1/1_Conf_1.000	2429	20	1.28E-124	XP_002636412.1	54	452.21	854	466	Hypothetical protein CBG23065
Locus_8037_Transcript_1/2_Conf_1.000	767	20	1.33E-54	XP_002634394.1	90	217.238	126	114	C. briggsae CBR-UNC-43 protein
Locus_8037_Transcript_2/2_Conf_1.000	721	20	1.81E-71	XP_002634394.1	91	273.092	158	145	C. briggsae CBR-UNC-43 protein

Locus_8038_Transcript_1/1_Conf_1.000	385	20	1.67E-25	CAR97823.1	64	119.013	125	81	C. elegans protein F26H11.2i, partially confirmed by transcript evidence
Locus_8039_Transcript_1/1_Conf_1.000	1031	4	6.60E-06	CBH16810.1	46	56.225	150	70	hypothetical protein, conserved, (fragment)
Locus_804_Transcript_1/1_Conf_1.000	458	0							
Locus_8040_Transcript_1/1_Conf_1.000	794	5	1.33E-60	NP_001024958.1	68	237.269	276	188	hypothetical protein Y34B4A.4
Locus_8041_Transcript_1/2_Conf_1.000	749	20	4.64E-97	BAF62082.1	81	358.221	249	203	inositol-1(or 4)-monophosphatase
Locus_8041_Transcript_2/2_Conf_1.000	613	20	1.22E-74	BAF62083.1	79	283.108	203	161	inositol-1(or 4)-monophosphatase
Locus_8042_Transcript_1/1_Conf_1.000	869	20	5.82E-39	NP_871685.1	71	165.622	139	100	hypothetical protein Y71H2AR.3
Locus_8043_Transcript_1/1_Conf_1.000	128	0							
Locus_8044_Transcript_1/2_Conf_1.000	292	20	7.89E-23	CAX51690.1	82	110.153	79	65	C. elegans protein ZK1098.10e, partially confirmed by transcript evidence
Locus_8044_Transcript_2/2_Conf_1.000	292	20	7.89E-23	CAX51690.1	82	110.153	79	65	C. elegans protein ZK1098.10e, partially confirmed by transcript evidence
Locus_8045_Transcript_1/1_Conf_1.000	284	0							
Locus_8046_Transcript_1/2_Conf_1.000	844	20	6.67E-77	NP_001021702.1	75	291.582	264	200	EXOCyst component family member (exoc-8)
Locus_8046_Transcript_2/2_Conf_1.000	844	20	6.67E-77	NP_001021702.1	75	291.582	264	200	EXOCyst component family member (exoc-8)
Locus_8047_Transcript_1/1_Conf_1.000	488	0							
Locus_8048_Transcript_1/1_Conf_1.000	292	5	1.22E-07	NP_001032983.1	65	59.6918	67	44	hypothetical protein W05F2.4
Locus_8049_Transcript_1/1_Conf_1.000	410	0							

Locus_805_Transcript_1/1_Conf_1.000	1228	20	2.14E-81	CAB58173.1	75	307.375	285	215	putative nucleosome binding protein
Locus_8050_Transcript_1/2_Conf_1.000	507	13	4.01E-09	NP_493130.2	65	64.6994	81	53	hypothetical protein T09E11.6
Locus_8050_Transcript_2/2_Conf_1.000	342	0							
Locus_8051_Transcript_1/1_Conf_1.000	1353	20	3.87E-111	XP_002631410.1	87	406.371	270	236	C. briggsae CBR-CLH-5 protein
Locus_8052_Transcript_1/1_Conf_1.000	934	20	2.27E-31	EFO24018.1	49	140.584	322	158	hypothetical protein LOAG_04470
Locus_8053_Transcript_1/1_Conf_1.000	990	2	6.82E-13	XP_002646310.1	42	79.337	303	128	C. briggsae CBR-LIN-59 protein
Locus_8054_Transcript_1/1_Conf_1.000	589	20	3.41E-52	NP_501835.2	80	208.379	161	130	DIS3 (yeast disjunction abnormal) exonuclease homolog family member (dis-3)
Locus_8055_Transcript_1/1_Conf_1.000	344	20	9.70E-21	NP_001041064.1	67	103.219	110	74	Nuclear Hormone Receptor family member (nhr-11)
Locus_8056_Transcript_1/1_Conf_1.000	305	3	6.58E-22	XP_002630273.1	70	107.071	96	68	Hypothetical protein CBG00701
Locus_8057_Transcript_1/1_Conf_1.000	1107	20	1.44E-118	NP_001024629.1	83	430.639	303	252	TBC (Tre-2/Bub2/Cdc16) domain family member (tbc-11)
Locus_8058_Transcript_1/1_Conf_1.000	538	20	3.11E-69	XP_002648832.1	83	264.618	179	149	Hypothetical protein CBG16947
Locus_8059_Transcript_1/2_Conf_1.000	342	20	4.37E-13	ZP_06975916.1	46	77.7962	106	49	hypothetical protein Krac_1188

Locus_8059_Transcript_2/2_Conf_1.000	243	20	5.57E-13	ZP_06975916.1	52	77.411	75	39	hypothetical protein Krac_1188
Locus_806_Transcript_1/1_Conf_1.000	553	6	9.18E-06	XP_002633233.1	47	53.9138	98	47	Hypothetical protein CBG05953
Locus_8060_Transcript_1/1_Conf_1.000	441	0							
Locus_8061_Transcript_1/1_Conf_1.000	320	0							
Locus_8062_Transcript_1/1_Conf_1.000	133	0							
Locus_8063_Transcript_1/1_Conf_1.000	1761	20	4.11E-50	NP_001040717.1	72	204.142	170	123	hypothetical protein ZC328.3
Locus_8064_Transcript_1/1_Conf_1.000	1314	20	2.27E-76	XP_002639475.1	55	290.812	448	250	Hypothetical protein CBG04073
Locus_8065_Transcript_1/1_Conf_1.000	482	20	4.48E-47	NP_496500.1	82	190.66	130	107	hypothetical protein VF13D12L.3
Locus_8066_Transcript_1/1_Conf_1.000	762	20	2.32E-59	XP_002637192.1	91	233.032	136	125	Hypothetical protein CBG09713
Locus_8067_Transcript_1/1_Conf_1.000	613	20	3.62E-18	XP_002110470.1	76	95.5153	63	48	hypothetical protein TRIADDRAFT_22842

Locus_8068_Transcript_1/1_Conf_1.000	677	20	4.73E-84	XP_002633628.1	92	314.694	185	171	Hypothetical protein CBG05511
Locus_8069_Transcript_1/1_Conf_1.000	191	2	3.12E-11	NP_505848.1	83	71.633	48	40	hypothetical protein T19B10.2
Locus_807_Transcript_1/2_Conf_1.000	804	0							
Locus_807_Transcript_2/2_Conf_1.000	794	0							
Locus_8070_Transcript_1/1_Conf_1.000	522	20	1.44E-44	XP_002645875.1	67	182.57	178	121	Hypothetical protein CBG07619
Locus_8071_Transcript_1/1_Conf_1.000	358	19	1.79E-19	XP_001902614.1	65	98.9821	113	74	Elongation factor Tu GTP binding domain containing protein
Locus_8072_Transcript_1/1_Conf_1.000	164	0							
Locus_8073_Transcript_1/1_Conf_1.000	1021	4	1.64E-33	XP_002640038.1	51	147.902	314	163	Hypothetical protein CBG12510
Locus_8074_Transcript_1/1_Conf_1.000	886	0							
Locus_8075_Transcript_1/1_Conf_1.000	671	20	7.48E-42	NP_490871.1	93	174.481	89	83	hypothetical protein Y73E7A.6
Locus_8076_Transcript_1/1_Conf_1.000	541	4	3.69E-09	CAR63553.1	47	65.0846	167	79	putative major allergen
Locus_8077_Transcript_1/1_Conf_1.000	148	18	3.14E-11	EAW82497.1	100	71.633	48	48	tetracycline transporter-like protein, isoform CRA_b
Locus_8078_Transcript_1/1_Conf_1.000	340	4	2.66E-07	NP_001040915.1	69	58.5362	52	36	hypothetical protein C27D8.3
Locus_8079_Transcript_1/1_Conf_1.000	246	20	1.72E-30	XP_002633475.1	83	135.576	81	68	C. briggsae CBR-NLR-1 protein
Locus_808_Transcript_1/1_Conf_1.000	922	20	1.07E-118	NP_741632.2	81	430.639	304	248	SMAll family member (sma-1)
Locus_8080_Transcript_1/1_Conf_1.000	193	0							

Locus_8081_Transcript_1/1_Conf_1.000	247	0							
Locus_8082_Transcript_1/1_Conf_1.000	940								
Locus_8083_Transcript_1/1_Conf_1.000	672	20	2.70E-23	XP_002631601.1	56	112.849	191	107	Hypothetical protein CBG20782
Locus_8084_Transcript_1/1_Conf_1.000	939	20	1.47E-78	NP_506083.1	74	297.36	305	228	hypothetical protein F55C5.8
Locus_8085_Transcript_1/1_Conf_1.000	351	20	2.51E-45	NP_001125384.1	100	184.882	113	113	ubiquitin-like protein fubi and ribosomal protein S30 precursor
Locus_8086_Transcript_1/1_Conf_1.000	642	20	2.49E-84	XP_002641730.1	88	315.464	197	175	Hypothetical protein CBG10069
Locus_8087_Transcript_1/1_Conf_1.000	1259	20	4.16E-64		54	249.98	423	232	R01H10.1 protein (clone R01H10)
Locus_8088_Transcript_1/1_Conf_1.000	1251	20	1.08E-128	NP_001024720.1	82	464.537	379	313	Na/H eXchanger family member (nhx-5)
Locus_8089_Transcript_1/1_Conf_1.000	517	20	1.37E-52	NP_001041127.1	88	209.149	129	114	hypothetical protein F57A8.2
Locus_809_Transcript_1/4_Conf_0.538	463	10	9.96E-34	XP_002581843.1	61	146.362	157	97	hypothetical protein
Locus_809_Transcript_2/4_Conf_0.615	663	13	1.74E-51	XP_001896587.1	57	206.453	246	141	hypothetical protein Bm1_25640
Locus_809_Transcript_3/4_Conf_0.615	663	13	2.96E-51	XP_001896587.1	57	205.682	246	141	hypothetical protein Bm1_25640
Locus_809_Transcript_4/4_Conf_0.769	885	13	3.04E-75	XP_002581843.1	61	286.189	316	195	hypothetical protein
Locus_8090_Transcript_1/2_Conf_1.000	941	20	1.68E-82	NP_492139.3	66	310.457	326	216	hypothetical protein T23G11.7
Locus_8090_Transcript_2/2_Conf_1.000	917	20	1.04E-81	NP_492139.3	66	307.76	314	210	hypothetical protein T23G11.7
Locus_8091_Transcript_1/1_Conf_1.000	414	0							
Locus_8092_Transcript_1/1_Conf_1.000	297	20	1.09E-24	ABQ88321.1	74	116.316	98	73	transposase
Locus_8093_Transcript_1/2_Conf_1.000	1631	20	0	XP_002642444.1	88	758.444	458	407	Hypothetical protein CBG06849
Locus_8093_Transcript_2/2_Conf_1.000	1631	20	0	XP_002642444.1	88	758.444	458	407	Hypothetical protein CBG06849

Locus_8094_Transcript_1/1_Conf_1.000	375	20	1.75E-30	CAV31772.1	74	135.576	115	86	C. elegans protein F25H5.3e, partially confirmed by transcript evidence
Locus_8095_Transcript_1/1_Conf_1.000	755	20	8.25E-86	XP_002647214.1	87	320.857	200	175	Hypothetical protein CBG22398
Locus_8096_Transcript_1/1_Conf_1.000	1108	20	2.98E-132	NP_491666.2	78	476.093	357	282	hypothetical protein T19B4.1
Locus_8097_Transcript_1/3_Conf_0.625	1200	20	4.26E-111	AAK62032.1	68	405.986	413	283	metalloprotease 1 precursor
Locus_8097_Transcript_2/3_Conf_0.750	1498	20	2.43E-117	AAN11401.1	65	427.172	440	287	metalloprotease 1 precursor
Locus_8097_Transcript_3/3_Conf_0.625	951	20	1.13E-94	AAK62032.1	70	350.903	330	231	metalloprotease 1 precursor
Locus_8098_Transcript_1/1_Conf_1.000	182	0							
Locus_8099_Transcript_1/1_Conf_1.000	1253	20	7.91E-39	NP_498253.1	51	166.007	421	217	High Incidence of Males (increased X chromosome loss) family member (him-10)
Locus_81_Transcript_1/1_Conf_1.000	1055	4	2.47E-40	XP_002633516.1	65	170.629	205	134	Hypothetical protein CBG05378
Locus_810_Transcript_1/1_Conf_1.000	652	15	4.76E-38	NP_001022833.1	88	161.77	135	119	hypothetical protein Y37D8A.25
Locus_8100_Transcript_1/2_Conf_1.000	675	3	4.22E-16	EFO27562.1	64	88.9669	99	64	hypothetical protein LOAG_00926
Locus_8100_Transcript_2/2_Conf_1.000	1228	20	1.27E-33	EFO27562.1	55	148.673	249	139	hypothetical protein LOAG_00926
Locus_8101_Transcript_1/1_Conf_1.000	291	0							
Locus_8102_Transcript_1/1_Conf_1.000	472	20	2.12E-36	NP_507905.2	69	155.221	152	105	hypothetical protein Y113G7B.24
Locus_8103_Transcript_1/1_Conf_1.000	580	20	1.45E-31	BAE41498.1	73	139.813	110	81	unnamed protein product
Locus_8104_Transcript_1/1_Conf_1.000	1261	20	4.05E-51	NP_741830.1	56	206.838	420	237	hypothetical protein F46H5.7

Locus_8105_Transcript_1/1_Conf_1.000	614	20	5.77E-16	BAF63671.1	53	88.1965	179	95	protein disulfide isomerase-2
Locus_8106_Transcript_1/1_Conf_1.000	1093	20	1.37E-81	NP_506707.2	96	307.76	181	174	RAP homolog (vertebrate Rap GTPase family) family member (rap-2)
Locus_8107_Transcript_1/1_Conf_1.000	171	0							
Locus_8108_Transcript_1/2_Conf_1.000	2081	0							
Locus_8108_Transcript_2/2_Conf_1.000	2072	0							
Locus_8109_Transcript_1/1_Conf_1.000	935	20	1.69E-119	NP_496299.1	79	433.335	311	248	beta-LACTamase domain containing family member (lact-3)
Locus_811_Transcript_1/1_Conf_1.000	420	20	2.69E-47	NP_501886.1	80	191.43	137	110	THymidine Kinase family member (thk-1)
Locus_8110_Transcript_1/1_Conf_1.000	213	18	1.56E-07	AAD51334.1	86	59.3066	36	31	Kunitz type serine protease inhibitor
Locus_8111_Transcript_1/1_Conf_1.000	182	0							
Locus_8112_Transcript_1/1_Conf_1.000	865	20	2.00E-23	XP_002645934.1	53	114.005	206	110	Hypothetical protein CBG07699
Locus_8113_Transcript_1/1_Conf_1.000	529	20	7.18E-55	XP_002641774.1	85	216.853	140	120	C. briggsae CBR-TTR-5 protein
Locus_8114_Transcript_1/1_Conf_1.000	639	20	6.33E-40	ADK91433.1	69	167.933	145	101	c-type lectin 1
Locus_8115_Transcript_1/1_Conf_1.000	865	20	9.93E-132	NP_741507.1	92	473.781	290	268	hypothetical protein H24K24.3
Locus_8116_Transcript_1/1_Conf_1.000	965	2	3.94E-10	XP_002645111.1	50	70.0922	146	73	Hypothetical protein CBG16801
Locus_8117_Transcript_1/1_Conf_1.000	183	7	4.84E-20	XP_002647883.1	88	100.908	61	54	Hypothetical protein CBG23714

Locus_8118_Transcript_1/1_Conf_1.000	136	0							
Locus_8119_Transcript_1/1_Conf_1.000	403	10	1.53E-18	XP_002647546.1	61	95.9005	113	69	C. briggsae CBR-PME-5 protein
Locus_812_Transcript_1/4_Conf_0.625	1256	20	5.54E-101	XP_002629984.1	75	372.474	313	236	C. briggsae CBR-UBH-4 protein
Locus_812_Transcript_2/4_Conf_0.375	651	20	6.81E-69	XP_002629984.1	76	264.233	217	166	C. briggsae CBR-UBH-4 protein
Locus_812_Transcript_3/4_Conf_0.625	1268	20	5.62E-101	XP_002629984.1	75	372.474	313	236	C. briggsae CBR-UBH-4 protein
Locus_812_Transcript_4/4_Conf_0.375	868	20	4.38E-95	XP_002629984.1	76	352.058	289	220	C. briggsae CBR-UBH-4 protein
Locus_8120_Transcript_1/1_Conf_1.000	1350	0							
Locus_8121_Transcript_1/1_Conf_1.000	256	1	8.82E-06	EDL12487.1	70	53.5286	55	39	eukaryotic translation initiation factor 5A, isoform CRA_i
Locus_8122_Transcript_1/1_Conf_1.000	390	20	2.65E-23	NP_001021054.1	68	111.694	125	86	Suppressor with Morphological effect on Genitalia family member (smg-1)
Locus_8123_Transcript_1/1_Conf_1.000	422	0							

Locus_8124_Transcript_1/1_Conf_1.000	1935	20	2.64E-130	AAC28740.1	59	470.7	657	388	putative zinc metallopeptidase
Locus_8125_Transcript_1/1_Conf_1.000	330	0							
Locus_8126_Transcript_1/1_Conf_1.000	367	0							
Locus_8127_Transcript_1/1_Conf_1.000	347	20	3.77E-41	XP_002640078.1	85	171.014	107	92	Hypothetical protein CBG12563
Locus_8128_Transcript_1/1_Conf_1.000	364	3	4.26E-05	NP_001024412.1	52	51.2174	76	40	hypothetical protein C17G1.4
Locus_8129_Transcript_1/1_Conf_1.000	537	20	3.59E-33	EFO24135.1	76	144.821	121	92	hypothetical protein LOAG_04354
Locus_813_Transcript_1/1_Conf_1.000	276	0							
Locus_8130_Transcript_1/3_Conf_0.571	812	20	9.12E-105	AAN11401.1	77	384.03	269	208	metalloprotease 1 precursor
Locus_8130_Transcript_2/3_Conf_0.714	1002	20	2.74E-118	AAN11401.1	74	429.483	327	243	metalloprotease 1 precursor
Locus_8130_Transcript_3/3_Conf_0.714	1002	20	6.11E-118	AAN11401.1	74	428.328	327	242	metalloprotease 1 precursor
Locus_8131_Transcript_1/2_Conf_1.000	427	20	1.05E-51	EFO26601.1	76	206.068	140	107	CK1/WORM6 protein kinase
Locus_8131_Transcript_2/2_Conf_1.000	747	20	1.18E-108	XP_002640076.1	84	396.741	250	212	Hypothetical protein CBG12561
Locus_8132_Transcript_1/1_Conf_1.000	153	0							
Locus_8133_Transcript_1/2_Conf_1.000	904	0							
Locus_8133_Transcript_2/2_Conf_1.000	904	0							
Locus_8134_Transcript_1/1_Conf_1.000	454	20	2.57E-42	CAA92791.2	71	174.866	150	107	C. elegans protein C33A12.6, partially confirmed by transcript evidence

Locus_8135_Transcript_1/1_Conf_1.000	325	11	2.61E-18	XP_001900506.1	70	95.1301	89	63	CG7038-PA
Locus_8136_Transcript_1/1_Conf_1.000	298	0							
Locus_8137_Transcript_1/1_Conf_1.000	439	2	1.66E-09	EFO28054.1	59	65.855	101	60	hypothetical protein LOAG_00426
Locus_8138_Transcript_1/2_Conf_1.000	1637	20	1.52E-168	A8XJW8.2	81	597.43	482	392	Serine/threonine-protein kinase cst-1
Locus_8138_Transcript_2/2_Conf_1.000	1099	20	2.75E-138	A8XJW8.2	88	496.123	328	289	Serine/threonine-protein kinase cst-1
Locus_8139_Transcript_1/1_Conf_1.000	527	20	8.30E-56	NP_505698.2	78	219.935	175	138	hypothetical protein C35A5.8
Locus_814_Transcript_1/1_Conf_1.000	1197	20	3.83E-120	NP_741296.1	79	436.032	348	277	hypothetical protein K11H12.8
Locus_8140_Transcript_1/3_Conf_0.600	439	20	2.56E-26	EFO17754.1	68	121.709	126	86	RNA pol II accessory factor
Locus_8140_Transcript_2/3_Conf_0.600	480	20	2.56E-26	EFO17754.1	68	121.709	126	86	RNA pol II accessory factor
Locus_8140_Transcript_3/3_Conf_0.600	481	20	2.56E-26	EFO17754.1	68	121.709	126	86	RNA pol II accessory factor
Locus_8141_Transcript_1/2_Conf_1.000	311	20	1.50E-34	NP_500412.1	77	149.058	103	80	Variable ABnormal morphology family member (vab-2)
Locus_8141_Transcript_2/2_Conf_1.000	298	20	2.43E-32	NP_500412.1	78	141.739	97	76	Variable ABnormal morphology family member (vab-2)
Locus_8142_Transcript_1/1_Conf_1.000	198	7	4.60E-23	XP_002633317.1	86	110.923	65	56	Hypothetical protein CBG06054
Locus_8143_Transcript_1/1_Conf_1.000	239	20	9.56E-13	XP_002632532.1	89	76.6406	39	35	C. briggsae CBR-DPY-4 protein
Locus_8144_Transcript_1/1_Conf_1.000	1020	20	2.12E-81	EFO16147.1	79	306.99	236	188	major facilitator superfamily transporter
Locus_8145_Transcript_1/1_Conf_1.000	249	3	1.36E-11	XP_002639131.1	71	72.7886	66	47	Hypothetical protein CBG14951

Locus_8146_Transcript_1/1_Conf_1.000	217	20	9.73E-18	XP_001902041.1	80	93.2041	67	54	Protein kinase domain containing protein
Locus_8147_Transcript_1/1_Conf_1.000	737	5	1.92E-23	Q09261.2	67	113.62	189	128	Uncharacterized protein C32A3.2
Locus_8148_Transcript_1/1_Conf_1.000	325	5	1.34E-14	XP_002644049.1	67	82.8037	91	61	C. briggsae CBR-CLC-1 protein
Locus_8149_Transcript_1/1_Conf_1.000	497	0							
Locus_815_Transcript_1/2_Conf_1.000	1588	20	2.26E-153	XP_002631561.1	81	546.969	364	296	C. briggsae CBR-GLN-2 protein
Locus_815_Transcript_2/2_Conf_1.000	1528	20	2.16E-153	XP_002631561.1	81	546.969	364	296	C. briggsae CBR-GLN-2 protein
Locus_8150_Transcript_1/2_Conf_1.000	593	4	1.97E-31	XP_002647590.1	67	139.428	179	121	Hypothetical protein CBG06678
Locus_8150_Transcript_2/2_Conf_1.000	593	4	8.86E-32	XP_002647590.1	67	140.584	179	121	Hypothetical protein CBG06678
Locus_8151_Transcript_1/1_Conf_1.000	346	0							
Locus_8152_Transcript_1/1_Conf_1.000	788	20	1.74E-20	XP_002132160.1	51	103.99	209	108	PREDICTED: similar to coiled-coil domain containing 53
Locus_8153_Transcript_1/1_Conf_1.000	183	0							
Locus_8154_Transcript_1/1_Conf_1.000	417	0							
Locus_8155_Transcript_1/1_Conf_1.000	830	20	1.50E-33	CAR63677.1	84	147.517	139	118	putative SPErmatogenesis family member
Locus_8156_Transcript_1/1_Conf_1.000	244	0							
Locus_8157_Transcript_1/1_Conf_1.000	1034	0							

Locus_8158_Transcript_1/3_Conf_0.500	554	20	3.01E-57	NP_493024.1	86	224.942	138	119	UBiquitin Conjugating enzyme family member (ubc-12)
Locus_8158_Transcript_2/3_Conf_0.667	682	20	1.05E-70	NP_493024.1	85	270.396	180	154	UBiquitin Conjugating enzyme family member (ubc-12)
Locus_8158_Transcript_3/3_Conf_0.667	683	20	1.05E-70	NP_493024.1	85	270.396	180	154	UBiquitin Conjugating enzyme family member (ubc-12)
Locus_8159_Transcript_1/1_Conf_1.000	2330	20	0	NP_500130.1	93	979.548	572	532	hypothetical protein Y41D4A.4
Locus_816_Transcript_1/1_Conf_1.000	793	4	4.98E-07	AAF68853.2	40	59.3066	267	107	AF162774_1Nopp140-like nucleolar protein
Locus_8160_Transcript_1/1_Conf_1.000	637	0							
Locus_8161_Transcript_1/1_Conf_1.000	568	3	3.25E-17	XP_002645238.1	60	92.0485	120	73	C. briggsae CBR-SCD-1 protein
Locus_8162_Transcript_1/1_Conf_1.000	1430	20	1.24E-123	NP_499891.1	79	447.973	367	291	Paralysed Arrest at Two-fold family member (pat-6)
Locus_8163_Transcript_1/1_Conf_1.000	637	0							

Locus_8164_Transcript_1/1_Conf_1.000	675	9	6.50E-25	NP_492047.1	63	118.242	106	67	Chondroitin ProteoGlycan family member (cpg-3)
Locus_8165_Transcript_1/1_Conf_1.000	379	20	9.27E-16	XP_002647707.1	63	86.6557	60	38	Hypothetical protein CBG17896
Locus_8166_Transcript_1/1_Conf_1.000	957	20	6.71E-95	NP_501775.1	67	351.673	344	233	Nuclear Hormone Receptor family member (nhr-4)
Locus_8167_Transcript_1/3_Conf_0.333	292	3	5.83E-26	NP_499012.2	76	120.553	99	76	hypothetical protein F02A9.4
Locus_8167_Transcript_2/3_Conf_0.333	730	20	3.27E-84	XP_002642413.1	81	315.464	232	190	Hypothetical protein CBG06810
Locus_8167_Transcript_3/3_Conf_0.667	1184	20	5.81E-113	NP_499012.2	73	412.149	385	284	hypothetical protein F02A9.4
Locus_8168_Transcript_1/1_Conf_1.000	232	20	8.42E-17	XP_002641573.1	77	90.1225	66	51	C. briggsae CBR-TTLL-4 protein
Locus_8169_Transcript_1/1_Conf_1.000	282	0							
Locus_817_Transcript_1/5_Conf_0.333	2033	20	2.08E-141	XP_001893221.1	78	507.679	402	316	splicing factor, CC1-like family protein
Locus_817_Transcript_2/5_Conf_0.222	279	0							
Locus_817_Transcript_3/5_Conf_0.222	286	4	2.32E-06	XP_002639234.1	68	55.4546	76	52	Hypothetical protein CBG03790
Locus_817_Transcript_4/5_Conf_0.222	286	4	2.32E-06	XP_002639234.1	68	55.4546	76	52	Hypothetical protein CBG03790

Locus_817_Transcript_5/5_Conf_0.444	2013	20	2.05E-141	XP_001893221.1	78	507.679	402	316	splicing factor, CC1-like family protein
Locus_8170_Transcript_1/1_Conf_1.000	530	20	1.35E-69	XP_002646472.1	87	265.774	176	154	C. briggsae CBR-NSF-1 protein
Locus_8171_Transcript_1/1_Conf_1.000	1095	20	3.98E-113	XP_002631003.1	75	412.535	364	273	Hypothetical protein CBG02750
Locus_8172_Transcript_1/1_Conf_1.000	2235	20	0	NP_502064.1	71	680.248	637	454	AuTophaGy (yeast Atg homolog) family member (atg-7)
Locus_8173_Transcript_1/1_Conf_1.000	141	20	1.56E-07	NP_509407.1	63	59.3066	49	31	Activated in Blocked Unfolded protein response family member (abu-9)
Locus_8174_Transcript_1/1_Conf_1.000	333	0							
Locus_8175_Transcript_1/1_Conf_1.000	145	0							
Locus_8176_Transcript_1/1_Conf_1.000	455	0							
Locus_8177_Transcript_1/1_Conf_1.000	406	0							
Locus_8178_Transcript_1/1_Conf_1.000	463	5	2.02E-18	NP_495016.1	52	95.5153	159	83	hypothetical protein EEED8.16
Locus_8179_Transcript_1/2_Conf_1.000	525	0							
Locus_8179_Transcript_2/2_Conf_1.000	512	0							
Locus_818_Transcript_1/1_Conf_1.000	1390	20	5.31E-47	XP_001898350.1	66	193.356	214	143	Temporarily assigned gene name protein 44, isoform c

Locus_8180_Transcript_1/1_Conf_1.000	2611	20	0	XP_001899737.1	75	900.197	759	571	SMC proteins Flexible Hinge Domain containing protein
Locus_8181_Transcript_1/2_Conf_1.000	349	0							
Locus_8181_Transcript_2/2_Conf_1.000	277	0							
Locus_8182_Transcript_1/1_Conf_1.000	996	20	9.27E-26	NP_499543.2	51	122.094	279	145	hypothetical protein Y56A3A.11
Locus_8183_Transcript_1/1_Conf_1.000	204	0							
Locus_8184_Transcript_1/1_Conf_1.000	668	20	2.29E-59	EFO24227.1	70	232.646	199	141	hypothetical protein LOAG_04258
Locus_8185_Transcript_1/2_Conf_1.000	1113	6	3.51E-64	ACV31098.1	68	249.98	324	221	Temporarily assigned gene name protein 250, isoform a, confirmed by transcript evidence
Locus_8185_Transcript_2/2_Conf_1.000	1101	6	2.23E-63	ACV31098.1	67	247.284	325	219	Temporarily assigned gene name protein 250, isoform a, confirmed by transcript evidence
Locus_8186_Transcript_1/1_Conf_1.000	425	4	3.63E-36	XP_002638375.1	73	154.451	141	104	Hypothetical protein CBG18580
Locus_8187_Transcript_1/1_Conf_1.000	448	20	6.61E-38	NP_504245.3	82	160.229	134	111	hypothetical protein Y61A9LA.10
Locus_8188_Transcript_1/1_Conf_1.000	232	0							
Locus_8189_Transcript_1/1_Conf_1.000	765	0							
Locus_819_Transcript_1/1_Conf_1.000	455	0							
Locus_8190_Transcript_1/1_Conf_1.000	188	20	6.52E-17	NP_741529.1	91	90.5077	62	57	hypothetical protein C37H5.6
Locus_8191_Transcript_1/1_Conf_1.000	925	20	2.89E-63	NP_509119.3	61	246.514	319	196	Nuclear Hormone Receptor family member (nhr-173)
Locus_8192_Transcript_1/1_Conf_1.000	318	4	6.94E-11	EFO27060.1	88	70.4774	44	39	hypothetical protein LOAG_01427
Locus_8193_Transcript_1/1_Conf_1.000	195	0							
Locus_8194_Transcript_1/1_Conf_1.000	386	0							
Locus_8195_Transcript_1/1_Conf_1.000	157	0							
Locus_8196_Transcript_1/1_Conf_1.000	634	0							

Locus_8197_Transcript_1/2_Conf_1.000	383	16	4.87E-33	XP_001895776.1	74	144.05	127	94	PDZ domain containing protein
Locus_8197_Transcript_2/2_Conf_1.000	122	11	8.44E-09	XP_002633733.1	89	63.5438	39	35	Hypothetical protein CBG03418
Locus_8198_Transcript_1/1_Conf_1.000	323	0							
Locus_8199_Transcript_1/1_Conf_1.000	257	4	4.52E-10	NP_496498.1	67	67.781	73	49	hypothetical protein C47D12.8
Locus_82_Transcript_1/1_Conf_1.000	225	20	3.00E-30	EFO21255.1	95	134.806	66	63	hypothetical protein LOAG_07233
Locus_820_Transcript_1/1_Conf_1.000	1135	20	3.17E-169	NP_499743.2	91	598.971	366	336	hypothetical protein Y43F4B.7
Locus_8200_Transcript_1/1_Conf_1.000	229	4	9.98E-18	XP_002638921.1	73	93.2041	75	55	Hypothetical protein CBG22147
Locus_8201_Transcript_1/1_Conf_1.000	565	0							
Locus_8202_Transcript_1/1_Conf_1.000	864	2	3.41E-23	NP_500834.1	49	113.235	249	124	hypothetical protein C39H7.4
Locus_8203_Transcript_1/2_Conf_1.000	471	20	5.75E-42	ACI49049.1	67	173.711	154	104	hypothetical protein Cbre_JD08.001
Locus_8203_Transcript_2/2_Conf_1.000	471	20	5.75E-42	ACI49049.1	67	173.711	154	104	hypothetical protein Cbre_JD08.001
Locus_8204_Transcript_1/1_Conf_1.000	1468	20	1.91E-50	EFO26149.1	52	204.912	496	262	rad50 family protein
Locus_8205_Transcript_1/1_Conf_1.000	294	20	1.21E-39	EFO21605.1	92	166.007	99	92	hypothetical protein LOAG_06883
Locus_8206_Transcript_1/1_Conf_1.000	677	20	2.65E-18	XP_001898812.1	59	96.2857	128	76	Autophagy protein Apg6 containing protein

Locus_8207_Transcript_1/1_Conf_1.000	779	20	8.88E-62	NP_508504.2	82	241.121	258	212	Non-muscle MYosin family member (nmy-1)
Locus_8208_Transcript_1/1_Conf_1.000	773	20	9.31E-72	XP_002637243.1	65	274.248	293	192	Hypothetical protein CBG18919
Locus_8209_Transcript_1/1_Conf_1.000	777	20	9.00E-14	EFN79173.1	45	81.6481	181	83	Chromobox protein-like protein 5
Locus_821_Transcript_1/3_Conf_0.600	516	20	3.46E-88	ACS37721.1	98	327.405	153	150	C-type lectin-1
Locus_821_Transcript_2/3_Conf_0.600	504	20	8.81E-86	ACS37721.1	96	319.316	153	147	C-type lectin-1
Locus_821_Transcript_3/3_Conf_0.600	504	20	1.41E-83	ACS37721.1	94	311.997	153	144	C-type lectin-1
Locus_8210_Transcript_1/1_Conf_1.000	787	0							
Locus_8211_Transcript_1/1_Conf_1.000	154	0							
Locus_8212_Transcript_1/1_Conf_1.000	491	4	1.12E-45	NP_001022641.1	76	186.037	142	109	LEThal family member (let-805)

Locus_8213_Transcript_1/1_Conf_1.000	926	2	6.00E-69	XP_002639154.1	74	265.388	250	186	Hypothetical protein CBG14981
Locus_8214_Transcript_1/4_Conf_0.250	438	5	8.82E-11	XP_002649011.1	51	70.0922	145	74	Hypothetical protein CBG21458
Locus_8214_Transcript_2/4_Conf_0.333	438	5	3.96E-11	XP_002649011.1	51	71.2478	145	75	Hypothetical protein CBG21458
Locus_8214_Transcript_3/4_Conf_0.500	794	20	5.67E-19	NP_494220.2	42	98.9821	291	124	hypothetical protein F54A3.1
Locus_8214_Transcript_4/4_Conf_0.583	1145	20	6.06E-19	NP_494220.2	43	99.7525	293	128	hypothetical protein F54A3.1
Locus_8215_Transcript_1/1_Conf_1.000	757	20	2.22E-38	EFO25502.1	56	163.31	274	156	F/Y-rich family protein
Locus_8216_Transcript_1/1_Conf_1.000	277	0							
Locus_8217_Transcript_1/1_Conf_1.000	1137	20	1.75E-42	NP_500514.1	59	177.948	242	144	hypothetical protein F30B5.4
Locus_8218_Transcript_1/3_Conf_0.571	823	20	8.56E-82	NP_498415.2	80	307.76	205	166	LEThal family member (let-721)
Locus_8218_Transcript_2/3_Conf_0.714	1893	20	0	XP_002634690.1	86	897.886	562	486	C. briggsae CBR-LET-721 protein

Locus_8218_Transcript_3/3_Conf_0.571	823	20	2.94E-82	NP_498415.2	80	309.301	205	166	LEThal family member (let-721)
Locus_8219_Transcript_1/1_Conf_1.000	203	20	5.99E-23	NP_492127.1	83	110.538	66	55	Low-density lipoprotein Receptor Related family member (lrp-1)
Locus_822_Transcript_1/1_Conf_1.000	846	20	6.07E-78	NP_510144.1	73	295.049	265	194	Branched Chain AminoTransferase family member (bcat-1)
Locus_8220_Transcript_1/1_Conf_1.000	368	5	1.23E-20	NP_508500.1	71	102.834	122	87	VANG (Van Gogh/Strabismus planar polarity protein) homolog family member (vang-1)
Locus_8221_Transcript_1/2_Conf_1.000	1606	20	2.19E-95	EFO23215.1	55	354.369	574	318	hypothetical protein LOAG_05271
Locus_8221_Transcript_2/2_Conf_1.000	1594	20	4.67E-90	NP_501725.2	55	336.65	538	300	hypothetical protein ZK1251.9
Locus_8222_Transcript_1/1_Conf_1.000	577	20	2.67E-54	NP_505112.1	79	215.312	163	129	hypothetical protein F20D6.11
Locus_8223_Transcript_1/1_Conf_1.000	384	0							
Locus_8224_Transcript_1/1_Conf_1.000	143	0							
Locus_8225_Transcript_1/1_Conf_1.000	429	0							
Locus_8226_Transcript_1/2_Conf_1.000	356	20	7.54E-34	XP_002630143.1	85	146.747	87	74	Hypothetical protein CBG00545
Locus_8226_Transcript_2/2_Conf_1.000	360	20	7.48E-34	XP_002630143.1	85	146.747	87	74	Hypothetical protein CBG00545
Locus_8227_Transcript_1/1_Conf_1.000	437	11	1.08E-24	EFO27980.1	75	116.316	112	84	hypothetical protein LOAG_00505
Locus_8228_Transcript_1/1_Conf_1.000	344	0							
Locus_8229_Transcript_1/1_Conf_1.000	568	2	2.32E-23	XP_002640320.1	65	112.464	151	99	C. briggsae CBR-DNJ-4 protein

Locus_823_Transcript_1/1_Conf_1.000	1374	20	8.67E-58	EFO22339.1	59	229.18	300	177	protein-tyrosine phosphatase
Locus_8230_Transcript_1/1_Conf_1.000	701	0							
Locus_8231_Transcript_1/1_Conf_1.000	199	20	2.36E-27	XP_002640690.1	95	125.176	65	62	Hypothetical protein CBG19753
Locus_8232_Transcript_1/1_Conf_1.000	462	20	3.08E-59	XP_002646888.1	86	231.106	149	129	C. briggsae CBR-PTC-3 protein
Locus_8233_Transcript_1/1_Conf_1.000	798	5	2.77E-05	Q62635.1	54	53.5286	103	56	Mucin-2
Locus_8234_Transcript_1/1_Conf_1.000	339	20	1.34E-59	NP_505734.2	100	232.261	113	113	Protein PHosphatase family member (pph-1)
Locus_8235_Transcript_1/3_Conf_0.400	606	20	2.32E-70	NP_001122565.1	81	268.855	197	160	Variable ABnormal morphology family member (vab-10)
Locus_8235_Transcript_2/3_Conf_0.400	762	20	9.71E-74	XP_002640549.1	86	280.796	209	180	C. briggsae CBR-VAB-10 protein
Locus_8235_Transcript_3/3_Conf_0.600	1034	20	2.96E-139	NP_001021857.1	87	499.204	346	303	Variable ABnormal morphology family member (vab-10)
Locus_8236_Transcript_1/2_Conf_1.000	1104	20	1.21E-117	XP_002637723.1	94	427.557	237	223	C. briggsae CBR-FIB-1 protein

Locus_8236_Transcript_2/2_Conf_1.000	1173	20	1.32E-117	XP_002637723.1	94	427.557	237	223	C. briggsae CBR-FIB-1 protein
Locus_8237_Transcript_1/1_Conf_1.000	502	20	1.05E-91	2QUJ	100	338.961	167	167	CrystalStructures Of Human Tryptophanyl-Trna Synthetase In Complex With Trpamp
Locus_8238_Transcript_1/1_Conf_1.000	417	0							
Locus_8239_Transcript_1/1_Conf_1.000	1101	20	2.51E-123	NP_499913.1	81	446.432	327	267	Sphingosine Phosphate Lyase family member (spl-1)
Locus_824_Transcript_1/4_Conf_0.200	395	4	1.15E-13	XP_002630872.1	64	79.7221	88	57	Hypothetical protein CBG02589
Locus_824_Transcript_2/4_Conf_0.600	582	4	1.81E-13	XP_002630872.1	64	79.7221	88	57	Hypothetical protein CBG02589
Locus_824_Transcript_3/4_Conf_0.400	530	4	1.37E-13	XP_002630872.1	64	79.7221	88	57	Hypothetical protein CBG02589
Locus_824_Transcript_4/4_Conf_0.600	640	4	2.27E-13	XP_002630872.1	64	79.7221	88	57	Hypothetical protein CBG02589
Locus_8240_Transcript_1/1_Conf_1.000	643	20	2.77E-51	NP_502576.1	89	205.682	141	126	RAB family member (rab-19)
Locus_8241_Transcript_1/1_Conf_1.000	535	2	3.00E-08	XP_002642044.1	75	62.003	48	36	Hypothetical protein CBG17981

Locus_8242_Transcript_1/1_Conf_1.000	625	20	1.19E-64	BAG53869.1	100	249.98	129	129	unnamed protein product
Locus_8243_Transcript_1/2_Conf_1.000	856	20	1.12E-111	XP_002645468.1	79	407.142	276	219	Hypothetical protein CBG22707
Locus_8243_Transcript_2/2_Conf_1.000	1471	20	5.41E-146	NP_001123112.1	64	522.316	540	348	hypothetical protein C17H11.6
Locus_8244_Transcript_1/1_Conf_1.000	1058	2	3.38E-13	XP_002638647.1	53	80.4925	160	86	C. briggsae CBR-REPS-1 protein
Locus_8245_Transcript_1/1_Conf_1.000	320	20	5.26E-43	XP_002928912.1	100	177.178	106	106	PREDICTED: tubulin beta chain-like
Locus_8246_Transcript_1/2_Conf_1.000	736	0							
Locus_8246_Transcript_2/2_Conf_1.000	736	0							
Locus_8247_Transcript_1/1_Conf_1.000	289	0							
Locus_8248_Transcript_1/1_Conf_1.000	1637	12	4.57E-56	NP_001021044.1	51	223.787	485	251	hypothetical protein C45G3.5
Locus_8249_Transcript_1/1_Conf_1.000	875	5	4.27E-05	XP_001944113.1	43	53.1434	182	80	PREDICTED: similar to splicing factor, arginine/serine-rich 16
Locus_825_Transcript_1/2_Conf_1.000	1007	20	1.87E-82	CBW38507.1	72	310.457	285	206	calcium-activated apyrase
Locus_825_Transcript_2/2_Conf_1.000	431	3	3.76E-09	CBW38507.1	72	64.6994	62	45	calcium-activated apyrase
Locus_8250_Transcript_1/1_Conf_1.000	241	3	1.05E-11	XP_002489033.1	76	73.1738	47	36	hypothetical protein SORBIDRAFT_0351s002020
Locus_8251_Transcript_1/2_Conf_1.000	1257	20	3.74E-89	NP_491448.2	68	333.183	335	231	hypothetical protein M04F3.5
Locus_8251_Transcript_2/2_Conf_1.000	1367	20	2.47E-89	NP_491448.2	69	333.954	335	232	hypothetical protein M04F3.5

Locus_8252_Transcript_1/1_Conf_1.000	431	20	6.60E-22	XP_002816802.1	69	107.071	103	72	PREDICTED: protein CutA-like isoform 3
Locus_8253_Transcript_1/1_Conf_1.000	377	0							
Locus_8254_Transcript_1/1_Conf_1.000	1217	20	3.68E-110	NP_490930.1	85	402.905	308	263	hypothetical protein Y37E3.10
Locus_8255_Transcript_1/1_Conf_1.000	401	20	1.43E-40	NP_001122905.1	74	169.088	133	99	hypothetical protein F09G2.8
Locus_8256_Transcript_1/1_Conf_1.000	526	20	5.96E-46	XP_002632331.1	72	187.193	162	118	C. briggsae CBR-ROM-4 protein
Locus_8257_Transcript_1/2_Conf_1.000	689	20	6.94E-62	XP_002636565.1	73	241.121	214	158	Hypothetical protein CBG23257
Locus_8257_Transcript_2/2_Conf_1.000	652	20	6.83E-61	XP_002636565.1	72	237.654	214	156	Hypothetical protein CBG23257
Locus_8258_Transcript_1/1_Conf_1.000	465								
Locus_8259_Transcript_1/1_Conf_1.000	613	20	8.51E-60	CAR63645.1	79	233.802	166	132	hypothetical protein

Locus_826_Transcript_1/1_Conf_1.000	518	20	2.41E-57	NP_001021661.1	96	224.942	125	120	AFaDin (actin filament binding protein) homolog family member (afd-1)
Locus_8260_Transcript_1/1_Conf_1.000	138	0							
Locus_8261_Transcript_1/1_Conf_1.000	276	0							
Locus_8262_Transcript_1/1_Conf_1.000	964	20	9.58E-57	XP_002630381.1	94	224.942	128	121	C. briggsae CBR-ICD-1 protein
Locus_8263_Transcript_1/1_Conf_1.000	223	20	3.95E-14	CBK19482.1	72	81.2629	73	53	C. elegans protein Y116A8C.13b, partially confirmed by transcript evidence
Locus_8264_Transcript_1/1_Conf_1.000	190	20	6.48E-25	XP_002640347.1	95	117.087	63	60	C. briggsae CBR-HAF-9 protein
Locus_8265_Transcript_1/1_Conf_1.000	735	20	3.53E-118	XP_002639586.1	92	428.328	241	222	C. briggsae CBR-ARX-1 protein
Locus_8266_Transcript_1/1_Conf_1.000	1485	20	0	NP_001122838.1	90	680.248	439	399	hypothetical protein B0399.1
Locus_8267_Transcript_1/1_Conf_1.000	204	0							
Locus_8268_Transcript_1/1_Conf_1.000	302	0							

Locus_8269_Transcript_1/1_Conf_1.000	669	20	3.60E-28	EFO26050.1	57	129.028	225	130	PEK/PEK protein kinase
Locus_827_Transcript_1/1_Conf_1.000	1090	20	2.30E-129	NP_001033540.1	86	466.463	284	245	hypothetical protein F08C6.2
Locus_8270_Transcript_1/1_Conf_1.000	977	8	7.03E-47	XP_002634253.1	57	192.2	276	159	Hypothetical protein CBG01824
Locus_8271_Transcript_1/1_Conf_1.000	1242	7	1.03E-06	NP_001022708.1	45	59.3066	247	113	Inhibitor of NFKappaB Kinase Epsilon subunit homolog family member (ikke-1)
Locus_8272_Transcript_1/1_Conf_1.000	822	0							
Locus_8273_Transcript_1/1_Conf_1.000	456	0							
Locus_8274_Transcript_1/1_Conf_1.000	381	0							
Locus_8275_Transcript_1/1_Conf_1.000	233	0							

Locus_8276_Transcript_1/1_Conf_1.000	713	20	8.86E-23	NP_491676.2	59	111.309	190	113	hypothetical protein T22E7.1
Locus_8277_Transcript_1/1_Conf_1.000	687	20	7.68E-61	XP_002643159.1	71	237.654	230	164	C. briggsae CBR-VPS-33.1 protein
Locus_8278_Transcript_1/1_Conf_1.000	443	20	2.14E-44	NP_510443.4	84	181.8	113	96	Temporarily Assigned Gene name family member (tag-53)
Locus_8279_Transcript_1/1_Conf_1.000	190	0							
Locus_828_Transcript_1/1_Conf_1.000	1254	20	3.32E-53	XP_002630959.1	58	213.772	234	138	C. briggsae CBR-DIE-1 protein
Locus_8280_Transcript_1/1_Conf_1.000	399	20	7.59E-34	XP_002633337.1	71	146.747	132	95	C. briggsae CBR-KLP-12 protein
Locus_8281_Transcript_1/1_Conf_1.000	169	0							
Locus_8282_Transcript_1/2_Conf_1.000	640	20	9.12E-47	NP_501598.2	64	190.66	214	137	Prolyl Carboxy Peptidase like family member (pcp-3)
Locus_8282_Transcript_2/2_Conf_1.000	592	20	3.36E-39	NP_501598.2	62	165.236	198	123	Prolyl Carboxy Peptidase like family member (pcp-3)

Locus_8283_Transcript_1/1_Conf_1.000	184	0							
Locus_8284_Transcript_1/1_Conf_1.000	210	20	5.94E-15	NP_001024837.1	81	83.9593	70	57	Gut granule LOss family member (glo-1)
Locus_8285_Transcript_1/1_Conf_1.000	238	0							
Locus_8286_Transcript_1/1_Conf_1.000	1547	20	6.74E-179	XP_002640548.1	81	631.713	516	422	Hypothetical protein CBG15812
Locus_8287_Transcript_1/2_Conf_1.000	1007	0							
Locus_8287_Transcript_2/2_Conf_1.000	920	0							
Locus_8288_Transcript_1/1_Conf_1.000	1441	20	1.21E-25	EFO19124.1	69	122.479	112	78	origin recognition complex subunit 1
Locus_8289_Transcript_1/1_Conf_1.000	354	0							
Locus_829_Transcript_1/1_Conf_1.000	678	7	9.49E-24	NP_001129836.1	62	114.39	132	83	Nuclear Hormone Receptor family member (nhr-6)
Locus_8290_Transcript_1/1_Conf_1.000	277	0							
Locus_8291_Transcript_1/1_Conf_1.000	571	20	1.36E-87	XP_002633641.1	92	325.865	189	174	C. briggsae CBR-KCC-3 protein
Locus_8292_Transcript_1/1_Conf_1.000	144	0							
Locus_8293_Transcript_1/1_Conf_1.000	289	5	4.66E-07	XP_002647600.1	52	57.7658	88	46	Hypothetical protein CBG06690
Locus_8294_Transcript_1/1_Conf_1.000	470	20	1.12E-53	ABY68595.1	100	212.616	105	105	myosin light chain 6
Locus_8295_Transcript_1/1_Conf_1.000	303	20	5.94E-31	NP_506060.2	87	137.117	80	70	hypothetical protein ZK836.2
Locus_8296_Transcript_1/3_Conf_0.571	652	4	1.48E-47	NP_872015.1	89	193.356	116	104	hypothetical protein R12C12.9
Locus_8296_Transcript_2/3_Conf_0.571	770	4	4.62E-47	NP_872015.1	82	192.2	141	116	hypothetical protein R12C12.9
Locus_8296_Transcript_3/3_Conf_0.714	995	4	3.82E-72	NP_495203.1	81	276.174	249	202	hypothetical protein R12C12.9
Locus_8297_Transcript_1/1_Conf_1.000	219	0							
Locus_8298_Transcript_1/1_Conf_1.000	457	20	7.72E-31	ACM46026.1	65	136.732	132	87	Temporarily assigned gene name protein 233, isoform a, partially confirmed by transcript evidence

Locus_8299_Transcript_1/1_Conf_1.000	858	20	3.72E-22	XP_002637261.1	62	109.768	135	84	C. briggsae CBR-ACL-8 protein
Locus_83_Transcript_1/1_Conf_1.000	163	1	3.91E-06	CAR63637.1	67	54.6842	52	35	hypothetical protein
Locus_830_Transcript_1/1_Conf_1.000	1535	20	1.33E-134	NP_001033386.1	86	484.567	340	294	similar to Transporter Of divalent Cations family member (toc-1)
Locus_8300_Transcript_1/1_Conf_1.000	154	0							
Locus_8301_Transcript_1/1_Conf_1.000	672	20	2.03E-87	NP_001021852.2	82	325.865	224	184	hypothetical protein ZC434.9
Locus_8302_Transcript_1/1_Conf_1.000	204	0							
Locus_8303_Transcript_1/1_Conf_1.000	1179	5	4.99E-48	NP_497319.1	63	196.438	398	251	hypothetical protein Y46E12BL.2
Locus_8304_Transcript_1/1_Conf_1.000	638	20	5.89E-14	XP_002740228.1	52	81.6481	161	84	PREDICTED: transducin (beta)-like 1 X-linked receptor 1-like
Locus_8305_Transcript_1/1_Conf_1.000	513	20	6.72E-20	NP_501726.1	89	100.523	56	50	hypothetical protein K01H12.1
Locus_8306_Transcript_1/1_Conf_1.000	1799	20	2.49E-34	XP_002637479.1	45	151.754	516	237	Hypothetical protein CBG19196
Locus_8307_Transcript_1/1_Conf_1.000	523	20	2.02E-14	XP_002166584.1	52	82.4185	155	82	PREDICTED: similar to harbinger transposase derived 1
Locus_8308_Transcript_1/2_Conf_1.000	349	0							
Locus_8308_Transcript_2/2_Conf_1.000	228	0							

Locus_8309_Transcript_1/1_Conf_1.000	176	0							
Locus_831_Transcript_1/1_Conf_1.000	1453	20	5.64E-172	XP_002641924.1	96	608.601	329	319	Hypothetical protein CBG16623
Locus_8310_Transcript_1/1_Conf_1.000	1432	11	3.42E-97	ADI24669.1	69	360.147	393	272	Hypothetical protein ZK355.2a
Locus_8311_Transcript_1/1_Conf_1.000	279	5	5.92E-15	XP_002646401.1	74	83.9593	91	68	C. briggsae CBR-DYS-1 protein
Locus_8312_Transcript_1/3_Conf_0.667	563	0							
Locus_8312_Transcript_2/3_Conf_0.667	563	0							
Locus_8312_Transcript_3/3_Conf_0.667	560	0							
Locus_8313_Transcript_1/1_Conf_1.000	334	0							
Locus_8314_Transcript_1/1_Conf_1.000	1290	20	4.24E-136	EFO27607.1	80	489.189	341	273	histone deacetylase 3
Locus_8315_Transcript_1/1_Conf_1.000	537	20	3.38E-15	XP_001896288.1	49	85.1149	167	82	mbt repeat family protein
Locus_8316_Transcript_1/1_Conf_1.000	394	20	9.39E-16	NP_502032.2	50	86.6557	140	71	RB (Retinoblastoma Binding protein) Related family member (rbr-2)
Locus_8317_Transcript_1/1_Conf_1.000	800	20	5.50E-62	XP_001891671.1	64	241.891	266	172	RhoGEF domain containing protein
Locus_8318_Transcript_1/1_Conf_1.000	456	20	1.55E-47	NP_001021638.1	78	192.2	151	119	hypothetical protein T23G11.6
Locus_8319_Transcript_1/1_Conf_1.000	505	0							
Locus_832_Transcript_1/1_Conf_1.000	982	20	5.62E-52	XP_001900183.1	63	209.149	231	147	ERG2 and Sigma1 receptor like protein
Locus_8320_Transcript_1/1_Conf_1.000	296	0							
Locus_8321_Transcript_1/1_Conf_1.000	276	0							

Locus_8322_Transcript_1/1_Conf_1.000	584	20	2.65E-73	NP_001024865.1	84	278.485	194	163	DumPY : shorter than wild-type family member (dpy-23)
Locus_8323_Transcript_1/1_Conf_1.000	1060	20	2.73E-71	NP_001024128.1	67	273.478	302	204	EEA1 (Early Endosome Antigen, Rab effector) homolog family member (eea-1)
Locus_8324_Transcript_1/1_Conf_1.000	900	20	1.30E-105	NP_001076711.1	81	387.111	274	224	hypothetical protein T20D3.5
Locus_8325_Transcript_1/1_Conf_1.000	1414	20	3.24E-108	NP_502137.1	66	396.741	445	296	hypothetical protein F54E12.2
Locus_8326_Transcript_1/1_Conf_1.000	381	0							
Locus_8327_Transcript_1/1_Conf_1.000	362	20	1.66E-41	NP_741369.1	86	172.17	120	104	hypothetical protein Y24D9A.8
Locus_8328_Transcript_1/2_Conf_1.000	1735	20	1.16E-89	NP_506685.2	54	335.495	537	295	hypothetical protein T01C3.1
Locus_8328_Transcript_2/2_Conf_1.000	1761	20	9.05E-90	NP_506685.2	54	335.88	551	301	hypothetical protein T01C3.1
Locus_8329_Transcript_1/1_Conf_1.000	133	0							
Locus_833_Transcript_1/2_Conf_1.000	295	0							
Locus_833_Transcript_2/2_Conf_1.000	721	2	9.76E-17	NP_509050.1	55	91.2781	206	115	hypothetical protein W05H9.1
Locus_8330_Transcript_1/1_Conf_1.000	204	6	7.33E-05	AAD31839.1	68	50.447	38	26	AF132291_1ancylostoma-secreted protein 1 precursor

Locus_8331_Transcript_1/1_Conf_1.000	170	20	8.04E-28	BAG63035.1	100	126.716	56	56	unnamed protein product
Locus_8332_Transcript_1/1_Conf_1.000	265	4	2.45E-16	NP_492856.1	87	88.5817	54	47	hypothetical protein Y52B11A.4
Locus_8333_Transcript_1/1_Conf_1.000	802	20	3.13E-73	CAB05153.2	71	279.256	264	190	C. elegans protein C49C3.1, partially confirmed by transcript evidence
Locus_8334_Transcript_1/1_Conf_1.000	284	4	6.13E-07	XP_002641312.1	94	57.3806	34	32	C. briggsae CBR-UNC-50 protein
Locus_8335_Transcript_1/1_Conf_1.000	320	0							
Locus_8336_Transcript_1/1_Conf_1.000	506	5	1.02E-57	XP_002643839.1	78	226.098	167	131	Hypothetical protein CBG02063
Locus_8337_Transcript_1/1_Conf_1.000	358	0							
Locus_8338_Transcript_1/1_Conf_1.000	716	0							
Locus_8339_Transcript_1/2_Conf_1.000	1372	20	1.46E-97	NP_001024379.1	96	361.303	187	181	P21-Activated Kinase family member (pak-1)
Locus_8339_Transcript_2/2_Conf_1.000	633	0							

Locus_834_Transcript_1/1_Conf_1.000	2867	20	0	XP_002636072.1	95	1456.43	840	798	Hypothetical protein CBG01313
Locus_8340_Transcript_1/1_Conf_1.000	439	14	6.31E-17	CAR63608.1	67	90.5077	73	49	hypothetical protein
Locus_8341_Transcript_1/1_Conf_1.000	402	0							
Locus_8342_Transcript_1/1_Conf_1.000	369	0							
Locus_8343_Transcript_1/1_Conf_1.000	957	1	2.89E-05	NP_500284.2	43	53.9138	232	101	Enhancer of EfL-1 mutant phenotype family member (eel-1)
Locus_8344_Transcript_1/1_Conf_1.000	1494	20	5.47E-69	EFO20206.1	53	266.544	424	226	hypothetical protein LOAG_08284
Locus_8345_Transcript_1/1_Conf_1.000	364	0							
Locus_8346_Transcript_1/1_Conf_1.000	959	20	1.65E-109	NP_001021765.1	87	400.208	254	223	hypothetical protein Y47G6A.22
Locus_8347_Transcript_1/1_Conf_1.000	224	0							
Locus_8348_Transcript_1/1_Conf_1.000	363	7	1.08E-24	NP_509919.2	70	116.316	120	85	hypothetical protein T25C12.3
Locus_8349_Transcript_1/1_Conf_1.000	445	0							
Locus_835_Transcript_1/1_Conf_1.000	452	20	1.51E-58	CAA21686.2	83	228.794	151	126	C. elegans protein Y54E2A.4, partially confirmed by transcript evidence
Locus_8350_Transcript_1/1_Conf_1.000	545	0							

Locus_8351_Transcript_1/1_Conf_1.000	1471	2	5.03E-51	EFO25215.1	72	206.838	187	136	hypothetical protein LOAG_03273
Locus_8352_Transcript_1/1_Conf_1.000	2354	3	2.85E-04	XP_002048623.1	38	52.373	286	111	GJ11255
Locus_8353_Transcript_1/1_Conf_1.000	469	0							
Locus_8354_Transcript_1/1_Conf_1.000	247	20	3.83E-30	AAZ82849.1	85	134.42	82	70	Cam kinase kinase protein 1, isoform b
Locus_8355_Transcript_1/1_Conf_1.000	260	20	4.35E-13	XP_002435696.1	68	77.7962	85	58	ABC transporter, putative
Locus_8356_Transcript_1/1_Conf_1.000	1217	20	2.56E-95	XP_002640701.1	79	353.599	309	245	C. briggsae CBR-MTX-1 protein
Locus_8357_Transcript_1/1_Conf_1.000	460	20	3.13E-24	NP_505980.1	77	114.775	97	75	hypothetical protein D2023.6
Locus_8358_Transcript_1/1_Conf_1.000	336	0							
Locus_8359_Transcript_1/1_Conf_1.000	421	4	2.38E-11	XP_001891718.1	55	72.0182	114	63	hypothetical protein Bm1_01005
Locus_836_Transcript_1/1_Conf_1.000	481	0							
Locus_8360_Transcript_1/1_Conf_1.000	847	20	1.04E-77	XP_002643992.1	77	294.278	275	213	Hypothetical protein CBG17372
Locus_8361_Transcript_1/1_Conf_1.000	1580	20	1.12E-144	CAP30936.1	74	518.079	524	388	C. briggsae CBR-BMK-1 protein
Locus_8362_Transcript_3/3_Conf_0.571	275	20	1.02E-14	Q16937.1	61	83.1889	72	44	Ancylostoma secreted protein
Locus_8363_Transcript_1/1_Conf_1.000	600	20	4.29E-37	XP_001899812.1	62	158.303	208	129	hypothetical protein Bm1_41765
Locus_8364_Transcript_1/1_Conf_1.000	182	0							

Locus_8365_Transcript_1/1_Conf_1.000	158	20	1.44E-08	XP_002748197.1	100	62.7734	38	38	PREDICTED: probable ATP-dependent RNA helicase DDX5 isoform 4
Locus_8366_Transcript_1/1_Conf_1.000	194	1	9.70E-05	XP_001894296.1	65	50.0618	63	41	hypothetical protein
Locus_8367_Transcript_1/2_Conf_1.000	604	20	6.02E-71	XP_002630890.1	80	270.781	200	160	Hypothetical protein CBG02611
Locus_8367_Transcript_2/2_Conf_1.000	604	20	1.34E-70	XP_002630890.1	80	269.626	200	160	Hypothetical protein CBG02611
Locus_8368_Transcript_1/1_Conf_1.000	497	20	2.03E-47	EFO18549.1	77	191.815	160	124	hypothetical protein LOAG_09946
Locus_8369_Transcript_1/1_Conf_1.000	742	20	8.97E-69	NP_496154.1	76	264.233	198	152	hypothetical protein R53.5
Locus_837_Transcript_1/1_Conf_1.000	398	20	2.38E-19	CBW44358.1	87	98.5969	62	54	C. elegans protein C01G10.11f, partially confirmed by transcript evidence
Locus_8370_Transcript_1/1_Conf_1.000	283	0							
Locus_8371_Transcript_1/1_Conf_1.000	448	20	1.56E-63	NP_001022715.1	93	245.358	147	138	ALIX (Apoptosis-linked gene 2 interacting protein X) homolog family member (alx-1)
Locus_8372_Transcript_1/1_Conf_1.000	1155	0							
Locus_8373_Transcript_1/3_Conf_0.667	525	4	1.53E-09	NP_499522.2	53	66.2402	107	57	GBF1(Golgi-specific Brefeldin-A-resistant Factor 1) homolog family member (gbf-1)
Locus_8373_Transcript_2/3_Conf_0.667	525	4	3.42E-09	NP_499522.2	53	65.0846	107	57	GBF1(Golgi-specific Brefeldin-A-resistant Factor 1) homolog family member (gbf-1)
Locus_8373_Transcript_3/3_Conf_0.667	525	4	3.42E-09	NP_499522.2	53	65.0846	107	57	GBF1(Golgi-specific Brefeldin-A-resistant Factor 1) homolog family member (gbf-1)
Locus_8374_Transcript_1/2_Conf_1.000	291	0							
Locus_8374_Transcript_2/2_Conf_1.000	291	0							
Locus_8375_Transcript_1/1_Conf_1.000	142	0							
Locus_8376_Transcript_1/1_Conf_1.000	533	14	2.73E-09	AAI34162.1	43	65.4698	172	74	Zgc:162945 protein
Locus_8377_Transcript_1/1_Conf_1.000	1301	20	9.09E-70	NP_498555.1	55	268.855	373	208	hypothetical protein B0280.9
Locus_8378_Transcript_1/1_Conf_1.000	220	0							
Locus_8379_Transcript_1/1_Conf_1.000	715	20	1.15E-70	NP_493375.2	74	270.396	227	168	AuTophaGy (yeast Atg homolog) family member (atg-4.1)

Locus_838_Transcript_1/1_Conf_1.000	1102	20	1.11E-46	NP_001021419.1	66	191.815	192	127	hypothetical protein F27C1.2
Locus_8380_Transcript_1/1_Conf_1.000	444	0							
Locus_8381_Transcript_1/1_Conf_1.000	669	20	1.74E-115	NP_498808.2	98	419.083	222	218	hypothetical protein C02F5.3
Locus_8382_Transcript_1/1_Conf_1.000	242	20	3.62E-12	XP_002637016.1	85	74.7146	47	40	C. briggsae CBR-TTR-27 protein
Locus_8383_Transcript_1/1_Conf_1.000	1016	20	2.94E-67	NP_499760.1	81	259.996	208	169	Quinoid DihyroPteridine Reductase family member (qdpr-1)
Locus_8384_Transcript_1/3_Conf_0.600	277	20	3.37E-18	XP_002639974.1	68	94.7449	80	55	C. briggsae CBR-PHAT-2 protein
Locus_8384_Transcript_2/3_Conf_0.600	413	20	4.68E-28	NP_491507.1	60	127.487	142	86	hypothetical protein C46H11.7
Locus_8384_Transcript_3/3_Conf_0.600	413	20	4.68E-28	NP_491507.1	60	127.487	142	86	hypothetical protein C46H11.7
Locus_8385_Transcript_1/1_Conf_1.000	274	20	1.01E-38	XP_001891673.1	95	162.925	90	86	hypothetical protein Bm1_00760
Locus_8386_Transcript_1/1_Conf_1.000	508	0							
Locus_8387_Transcript_1/2_Conf_1.000	780	20	4.22E-120	XP_002631757.1	90	434.876	254	230	Hypothetical protein CBG20965
Locus_8387_Transcript_2/2_Conf_1.000	780	20	4.22E-120	XP_002631757.1	90	434.876	254	230	Hypothetical protein CBG20965
Locus_8388_Transcript_1/1_Conf_1.000	821	20	4.60E-11	XP_002642235.1	63	72.7886	84	53	C. briggsae CBR-BRD-1 protein
Locus_8389_Transcript_1/1_Conf_1.000	573	20	5.66E-57	NP_501190.1	70	224.172	200	140	Temporarily Assigned Gene name family member (tag-224)
Locus_839_Transcript_1/1_Conf_1.000	295	0							
Locus_8390_Transcript_1/2_Conf_1.000	832	6	6.31E-56	NP_001023468.1	52	221.861	330	174	hypothetical protein Y45F10B.13
Locus_8390_Transcript_2/2_Conf_1.000	796	6	4.62E-61	NP_001023468.1	59	238.81	294	175	hypothetical protein Y45F10B.13
Locus_8391_Transcript_1/1_Conf_1.000	1789	20	1.17E-92	NP_500332.1	64	345.51	427	275	Vacuolar H ATPase family member (vha-19)
Locus_8392_Transcript_1/1_Conf_1.000	223	0							
Locus_8393_Transcript_1/2_Conf_1.000	827	2	1.89E-12	XP_001902674.1	68	77.411	76	52	hypothetical protein

Locus_8393_Transcript_2/2_Conf_1.000	505	2	5.83E-13	XP_001902674.1	68	77.411	76	52	hypothetical protein
Locus_8394_Transcript_1/1_Conf_1.000	923	20	1.64E-42	XP_002644147.1	85	177.563	140	119	Hypothetical protein CBG04517
Locus_8395_Transcript_1/1_Conf_1.000	344	0							
Locus_8396_Transcript_1/1_Conf_1.000	1729	20	1.94E-137	XP_002647576.1	75	494.197	398	301	Hypothetical protein CBG06663
Locus_8397_Transcript_1/1_Conf_1.000	195	20	1.76E-14	BAJ04734.1	100	82.4185	60	60	T-cell receptor beta chain
Locus_8398_Transcript_1/1_Conf_1.000	392	5	2.72E-52	NP_001129755.1	90	207.994	130	118	GLoBin family member (glb-8)
Locus_8399_Transcript_1/1_Conf_1.000	858	2	4.88E-06	EFO26249.1	41	56.225	135	56	hypothetical protein LOAG_02232
Locus_84_Transcript_1/1_Conf_1.000	400	0							
Locus_840_Transcript_1/1_Conf_1.000	1447	20	2.11E-94	AAX47336.1	62	350.903	489	307	beta-catenin
Locus_8400_Transcript_1/1_Conf_1.000	969	9	6.46E-69	AAT12422.1	70	265.388	322	227	hypothetical protein isoform a
Locus_8401_Transcript_1/1_Conf_1.000	180	0							
Locus_8402_Transcript_1/1_Conf_1.000	1397	20	2.56E-166	NP_001041102.1	78	589.726	442	348	hypothetical protein F21A3.2
Locus_8403_Transcript_1/1_Conf_1.000	365	0							
Locus_8404_Transcript_1/1_Conf_1.000	448	20	5.73E-66	NP_494213.2	88	253.447	149	132	hypothetical protein Y59C2A.1
Locus_8405_Transcript_1/1_Conf_1.000	542	0							

Locus_8406_Transcript_1/1_Conf_1.000	978	20	5.89E-102	XP_002648981.1	79	375.17	276	219	Hypothetical protein CBG21312
Locus_8407_Transcript_1/1_Conf_1.000	566	20	4.56E-56	NP_498409.1	86	221.09	148	128	hypothetical protein C05D11.10
Locus_8408_Transcript_1/1_Conf_1.000	213	0							
Locus_8409_Transcript_1/1_Conf_1.000	189	9	5.50E-16	NP_503758.4	79	87.4261	63	50	KETtiN (Drosophila actin-binding) homolog family member (ketn-1)
Locus_841_Transcript_1/1_Conf_1.000	573	20	1.22E-43	EFO19802.1	82	179.874	117	96	MSP domain-containing protein
Locus_8410_Transcript_1/1_Conf_1.000	273	20	3.99E-19	NP_492913.1	68	97.8265	91	62	PNG (Peptide:N-Glycanase) homolog family member (png-1)
Locus_8411_Transcript_1/1_Conf_1.000	2769	20	0	NP_499680.1	70	901.738	892	631	UNCoordinated family member (unc-71)
Locus_8412_Transcript_1/1_Conf_1.000	609	20	4.77E-55	XP_002430642.1	72	218.009	200	144	dual specificity mitogen-activated protein kinase kinase, putative
Locus_8413_Transcript_1/1_Conf_1.000	521	20	4.69E-32	NP_508937.1	72	140.969	122	89	hypothetical protein C54G7.2
Locus_8414_Transcript_1/1_Conf_1.000	623	4	8.78E-28	XP_001897082.1	56	127.487	173	98	hypothetical protein Bm1_28160
Locus_8415_Transcript_1/1_Conf_1.000	136	0							
Locus_8416_Transcript_1/1_Conf_1.000	593	20	2.72E-81	XP_001639298.1	89	305.064	192	171	predicted protein
Locus_8417_Transcript_1/1_Conf_1.000	1250	20	2.27E-78	NP_502544.1	57	297.36	417	240	abnormal cell LINeage family member (lin-54)
Locus_8418_Transcript_1/1_Conf_1.000	302	0							
Locus_8419_Transcript_1/1_Conf_1.000	277	0							

Locus_842_Transcript_1/3_Conf_0.667	677	20	1.58E-79	NP_498081.2	93	299.671	173	161	ALdehyde deHydrogenase family member (alh-1)
Locus_842_Transcript_2/3_Conf_0.667	668	20	1.99E-79	NP_498081.2	92	299.286	173	160	ALdehyde deHydrogenase family member (alh-1)
Locus_842_Transcript_3/3_Conf_0.667	677	20	2.06E-79	NP_498081.2	92	299.286	173	160	ALdehyde deHydrogenase family member (alh-1)
Locus_8420_Transcript_1/1_Conf_1.000	200	0							
Locus_8421_Transcript_1/1_Conf_1.000	690	20	2.20E-39	NP_001041033.1	64	166.392	192	123	beta-LACTamase domain containing family member (lact-9)
Locus_8422_Transcript_1/1_Conf_1.000	679	20	4.51E-58	NP_001024434.1	69	228.409	222	155	hypothetical protein C26B9.1
Locus_8423_Transcript_1/1_Conf_1.000	682	20	6.00E-34	XP_002645176.1	81	148.288	109	89	C. briggsae CBR-VEM-1 protein
Locus_8424_Transcript_1/1_Conf_1.000	1136	20	5.27E-31	XP_002639002.1	53	139.813	280	150	Hypothetical protein CBG22248
Locus_8425_Transcript_1/1_Conf_1.000	252	0							
Locus_8426_Transcript_1/1_Conf_1.000	2612	20	0	NP_740830.2	60	788.875	931	566	hypothetical protein Y47G6A.29
Locus_8427_Transcript_1/1_Conf_1.000	203	3	4.01E-27	AAM82167.1	92	124.405	67	62	gamma-butyrobetaine,2-oxoglutarate dioxygenase
Locus_8428_Transcript_1/1_Conf_1.000	158	0							
Locus_8429_Transcript_1/1_Conf_1.000	186	0							
Locus_843_Transcript_1/5_Conf_0.692	2784	20	0	ABA00169.1	78	1233.01	942	739	Plexin protein 1

Locus_843_Transcript_2/5_Conf_0.692	2784	20	0	ABA00169.1	78	1233.01	942	739	Plexin protein 1
Locus_843_Transcript_3/5_Conf_0.692	2784	20	0	ABA00169.1	78	1233.01	942	739	Plexin protein 1
Locus_843_Transcript_4/5_Conf_0.692	2784	20	0	ABA00169.1	78	1233.01	942	739	Plexin protein 1
Locus_843_Transcript_5/5_Conf_0.692	2784	20	0	ABA00169.1	78	1233.01	942	739	Plexin protein 1
Locus_8430_Transcript_1/1_Conf_1.000	482	8	1.36E-11	ACP34146.1	60	72.7886	125	76	Hypothetical protein F56B3.4a
Locus_8431_Transcript_1/1_Conf_1.000	1026	20	1.25E-89	NP_493283.3	73	334.339	310	228	hypothetical protein W05B5.2
Locus_8432_Transcript_1/1_Conf_1.000	265	0							
Locus_8433_Transcript_1/1_Conf_1.000	714	0							
Locus_8434_Transcript_1/1_Conf_1.000	174	0							
Locus_8435_Transcript_1/1_Conf_1.000	654	3	2.72E-49	NP_497970.1	65	199.134	232	152	Adenylyl CYclase family member (acy-1)

Locus_8436_Transcript_1/1_Conf_1.000	743	20	1.81E-69	NP_502083.1	74	266.544	250	187	Alcohol/Ribitol Dehydrogenase family member (ard-1)
Locus_8437_Transcript_1/1_Conf_1.000	1805	20	0	NP_001022257.1	72	640.573	602	434	hypothetical protein M106.4
Locus_8438_Transcript_1/2_Conf_1.000	1553	20	1.98E-45	NP_505976.2	71	188.348	172	123	hypothetical protein D2023.3
Locus_8438_Transcript_2/2_Conf_1.000	1384	20	1.71E-45	NP_505976.2	71	188.348	172	123	hypothetical protein D2023.3
Locus_8439_Transcript_1/1_Conf_1.000	705	20	2.09E-93	Q27539.2	91	345.895	210	192	ATP-dependent Clp protease proteolytic subunit 1
Locus_844_Transcript_1/1_Conf_1.000	538	0							

Locus_8440_Transcript_1/1_Conf_1.000	244	7	4.41E-10	NP_503178.1	68	67.781	58	40	AuTophaGy (yeast Atg homolog) family member (atg-9)
Locus_8441_Transcript_1/1_Conf_1.000	131	0							
Locus_8442_Transcript_1/1_Conf_1.000	182	2	2.95E-09	EFO23249.1	80	65.0846	40	32	hypothetical protein LOAG_05238
Locus_8443_Transcript_1/1_Conf_1.000	581	20	1.82E-50	XP_002640505.1	77	202.601	153	118	Hypothetical protein CBG13644
Locus_8444_Transcript_1/1_Conf_1.000	417	8	2.32E-06	XP_001344986.1	50	55.4546	122	62	PREDICTED: zinc finger protein-like
Locus_8445_Transcript_1/1_Conf_1.000	494	9	4.39E-50	NP_502314.1	74	200.675	167	124	hypothetical protein F35G2.1
Locus_8446_Transcript_1/2_Conf_1.000	654	20	3.82E-35	AAL09376.1	98	152.14	96	95	AF305958_1putative protein hc28.3
Locus_8446_Transcript_2/2_Conf_1.000	510	20	1.90E-35	AAL09376.1	98	152.14	96	95	AF305958_1putative protein hc28.3
Locus_8447_Transcript_1/1_Conf_1.000	558	0							
Locus_8448_Transcript_1/2_Conf_1.000	953	5	9.74E-38	EFO24641.1	48	161.77	327	159	hypothetical protein LOAG_03848
Locus_8448_Transcript_2/2_Conf_1.000	953	5	6.75E-39	EFO24641.1	49	165.622	318	158	hypothetical protein LOAG_03848
Locus_8449_Transcript_1/1_Conf_1.000	412	0							
Locus_845_Transcript_1/3_Conf_0.714	1488	0							
Locus_845_Transcript_2/3_Conf_0.714	1602	0							
Locus_845_Transcript_3/3_Conf_0.714	1587	0							
Locus_8450_Transcript_1/1_Conf_1.000	683	0							
Locus_8451_Transcript_1/1_Conf_1.000	1118	20	1.82E-44	XP_002634200.1	54	184.496	333	181	C. briggsae CBR-NOL-9 protein
Locus_8452_Transcript_1/1_Conf_1.000	448	0							
Locus_8453_Transcript_1/1_Conf_1.000	349	4	1.13E-29	NP_501852.1	78	132.88	114	89	hypothetical protein T14G10.7
Locus_8454_Transcript_1/1_Conf_1.000	333	8	5.38E-16	NP_001022317.1	63	87.4261	111	71	abnormal cell MIGration family member (mig-5)
Locus_8455_Transcript_1/1_Conf_1.000	1873	20	2.58E-90	XP_002641350.1	54	337.806	586	322	Hypothetical protein CBG13203
Locus_8456_Transcript_1/1_Conf_1.000	498	20	1.49E-58	XP_002642846.1	88	228.794	143	126	C. briggsae CBR-PPK-2 protein
Locus_8457_Transcript_1/1_Conf_1.000	272	2	4.56E-31	XP_002640091.1	91	137.502	71	65	Hypothetical protein CBG12578
Locus_8458_Transcript_1/1_Conf_1.000	581	20	1.40E-42	XP_002637561.1	62	176.407	193	121	Hypothetical protein CBG19294

Locus_8459_Transcript_1/1_Conf_1.000	843	10	1.40E-58	XP_002646355.1	65	230.72	287	187	Hypothetical protein CBG12069
Locus_846_Transcript_1/6_Conf_0.267	1282	20	9.56E-05	ACD88885.1	62	48.521	59	37	propionyl-coenzyme A carboxylase beta subunit
Locus_846_Transcript_2/6_Conf_0.200	1204	20	8.80E-05	ACD88885.1	62	48.521	59	37	propionyl-coenzyme A carboxylase beta subunit
Locus_846_Transcript_3/6_Conf_0.400	1797	0							
Locus_846_Transcript_4/6_Conf_0.267	662	0							
Locus_846_Transcript_5/6_Conf_0.467	1917	20	3.21E-06	NP_999066.1	40	51.9878	216	87	propionyl-CoA carboxylase beta chain, mitochondrial precursor
Locus_846_Transcript_6/6_Conf_0.400	1882	20	6.55E-09	XP_002636628.1	75	67.3958	53	40	Hypothetical protein CBG23332
Locus_8460_Transcript_1/1_Conf_1.000	221	20	1.36E-22	XP_002634980.1	84	109.383	73	62	C. briggsae CBR-ARK-1 protein
Locus_8461_Transcript_1/1_Conf_1.000	328	0							
Locus_8462_Transcript_1/1_Conf_1.000	941	20	1.05E-92	NP_498798.2	87	344.354	212	186	hypothetical protein C30A5.3
Locus_8463_Transcript_1/1_Conf_1.000	215	0							
Locus_8464_Transcript_1/1_Conf_1.000	540	3	3.23E-13	XP_002636882.1	56	78.5666	151	86	Hypothetical protein CBG09343
Locus_8465_Transcript_1/1_Conf_1.000	545	20	6.35E-49	XP_002636807.1	71	197.208	177	127	Hypothetical protein CBG09249
Locus_8466_Transcript_1/1_Conf_1.000	690	20	3.99E-49	NP_495988.1	82	198.749	139	114	Eukaryotic Initiation Factor family member (eif-3.F)

Locus_8467_Transcript_1/1_Conf_1.000	691	20	3.85E-60	P02452.5	100	235.343	121	121	Collagen alpha-1(I) chain
Locus_8468_Transcript_1/4_Conf_0.667	670	20	1.61E-44	XP_002634876.1	60	183.341	222	134	Hypothetical protein CBG10542
Locus_8468_Transcript_2/4_Conf_0.667	691	20	3.74E-47	XP_002634876.1	59	192.2	232	139	Hypothetical protein CBG10542
Locus_8468_Transcript_3/4_Conf_0.667	670	20	5.53E-45	XP_002634876.1	60	184.882	222	134	Hypothetical protein CBG10542
Locus_8468_Transcript_4/4_Conf_0.667	670	20	7.23E-45	XP_002634876.1	60	184.496	222	134	Hypothetical protein CBG10542
Locus_8469_Transcript_1/1_Conf_1.000	443	20	2.53E-45	XP_002634584.1	77	184.882	147	114	Hypothetical protein CBG08395
Locus_847_Transcript_1/1_Conf_1.000	739	3	1.80E-61	XP_002637472.1	69	239.965	249	173	Hypothetical protein CBG19188
Locus_8470_Transcript_1/1_Conf_1.000	360	20	2.83E-41	XP_002645846.1	80	171.4	111	89	Hypothetical protein CBG07580
Locus_8471_Transcript_1/1_Conf_1.000	202	0							

Locus_8472_Transcript_1/1_Conf_1.000	525	20	9.26E-23	NP_500844.1	55	110.153	170	95	BEClin (human autophagy) homolog family member (bec-1)
Locus_8473_Transcript_1/1_Conf_1.000	481	20	6.44E-62	NP_492686.1	88	239.965	151	133	hypothetical protein C25A1.13
Locus_8474_Transcript_1/1_Conf_1.000	383	0							
Locus_8475_Transcript_1/1_Conf_1.000	465	0							
Locus_8476_Transcript_1/1_Conf_1.000	579	20	3.25E-15	XP_002639397.1	46	85.5001	180	83	Hypothetical protein CBG03985
Locus_8477_Transcript_1/3_Conf_0.500	874	20	1.43E-93	EFO19444.1	78	347.051	284	224	Cullin 3

Locus_8477_Transcript_2/3_Conf_0.333	1631	20	1.96E-83	EFO19444.1	79	314.694	254	203	Cullin 3
Locus_8477_Transcript_3/3_Conf_0.667	2101	20	0	EFO19444.1	73	783.867	706	522	Cullin 3
Locus_8478_Transcript_1/1_Conf_1.000	613	20	1.01E-52	EFO28302.1	69	210.305	192	134	hypothetical protein LOAG_00195
Locus_8479_Transcript_1/1_Conf_1.000	153	0							
Locus_848_Transcript_1/1_Conf_1.000	459	0							
Locus_8480_Transcript_1/1_Conf_1.000	584	20	1.08E-50	XP_002644307.1	87	203.371	133	116	Hypothetical protein CBG14099
Locus_8481_Transcript_1/1_Conf_1.000	291	0							

Locus_8482_Transcript_1/1_Conf_1.000	1411	20	0	AAP36911.1	100	788.104	388	388	Homo sapiens GNAS complex locus
Locus_8483_Transcript_1/1_Conf_1.000	846	20	2.55E-76	XP_002635156.1	71	289.656	265	189	Hypothetical protein CBG11386
Locus_8484_Transcript_1/1_Conf_1.000	322	20	7.12E-24	ABC25099.1	88	113.62	62	55	transcription regulator
Locus_8485_Transcript_1/1_Conf_1.000	832	20	3.58E-51	XP_002639652.1	85	206.068	134	115	C. briggsae CBR-MFB-1 protein
Locus_8486_Transcript_1/1_Conf_1.000	1366	20	0	XP_002632951.1	89	650.203	405	363	C. briggsae CBR-RPN-7 protein
Locus_8487_Transcript_1/1_Conf_1.000	188	0							
Locus_8488_Transcript_1/1_Conf_1.000	1258	20	1.13E-61	NP_001129849.1	54	241.891	385	209	Choline Kinase A family member (cka-1)
Locus_8489_Transcript_1/1_Conf_1.000	425	20	7.32E-37	NP_500284.2	60	156.762	171	103	Enhancer of EfL-1 mutant phenotype family member (eel-1)

Locus_849_Transcript_1/2_Conf_1.000	1567	20	2.62E-162	XP_002640294.1	96	576.63	336	324	C. briggsae CBR-KIN-3 protein
Locus_849_Transcript_2/2_Conf_1.000	1502	20	2.49E-162	XP_002640294.1	96	576.63	336	324	C. briggsae CBR-KIN-3 protein
Locus_8490_Transcript_1/1_Conf_1.000	1361	20	0	NP_491711.2	84	669.463	453	382	hypothetical protein C34G6.1
Locus_8491_Transcript_1/1_Conf_1.000	1126	20	2.99E-103	EFO17909.1	75	379.793	375	283	hypothetical protein LOAG_10587
Locus_8492_Transcript_1/1_Conf_1.000	1077	20	1.83E-54	XP_002646916.1	76	217.624	162	124	C. briggsae CBR-UBC-15 protein
Locus_8493_Transcript_1/3_Conf_0.286	399	20	1.39E-19	NP_499684.1	80	99.3673	70	56	hypothetical protein Y37D8A.17
Locus_8493_Transcript_2/3_Conf_0.571	793	20	1.30E-31	NP_499684.1	72	140.969	118	86	hypothetical protein Y37D8A.17
Locus_8493_Transcript_3/3_Conf_0.714	990	20	2.56E-60	NP_499684.1	73	236.884	235	172	hypothetical protein Y37D8A.17
Locus_8494_Transcript_1/2_Conf_1.000	218	0							
Locus_8494_Transcript_2/2_Conf_1.000	242	0							

Locus_8495_Transcript_1/1_Conf_1.000	755	20	1.09E-53	NP_499472.1	63	214.157	270	172	Sterol regulatory element Binding Protein family member (sbp-1)
Locus_8496_Transcript_1/1_Conf_1.000	1267	20	2.05E-119	XP_002633848.1	85	433.721	309	265	C. briggsae CBR-CSN-5 protein
Locus_8497_Transcript_1/1_Conf_1.000	561	3	4.54E-08	NP_492036.2	50	61.6178	142	71	hypothetical protein C01H6.2
Locus_8498_Transcript_1/1_Conf_1.000	1576	18	4.38E-24	NP_499886.1	41	117.472	346	142	hypothetical protein R02D3.7
Locus_8499_Transcript_1/1_Conf_1.000	990	20	1.59E-94	EFO21654.1	70	350.517	329	232	hypothetical protein LOAG_06832
Locus_85_Transcript_1/3_Conf_0.286	588	20	3.41E-44	NP_491529.2	91	181.8	114	104	hypothetical protein Y110A7A.6
Locus_85_Transcript_2/3_Conf_0.714	733	20	4.82E-43	XP_002638373.1	94	178.718	91	86	C. briggsae CBR-CYN-3 protein
Locus_85_Transcript_3/3_Conf_0.714	649	20	1.89E-79	XP_002638373.1	94	299.286	171	161	C. briggsae CBR-CYN-3 protein
Locus_850_Transcript_1/3_Conf_0.714	2467	20	0	NP_740855.2	78	999.194	816	641	hypothetical protein F46F11.1
Locus_850_Transcript_2/3_Conf_0.714	2467	20	0	NP_740855.2	78	999.194	816	641	hypothetical protein F46F11.1
Locus_850_Transcript_3/3_Conf_0.714	2467	20	0	NP_740855.2	78	999.194	816	641	hypothetical protein F46F11.1
Locus_8500_Transcript_1/2_Conf_1.000	377	20	2.59E-58	XP_002343536.1	99	228.024	118	117	PREDICTED: similar to Os05g0242100
Locus_8500_Transcript_2/2_Conf_1.000	378	20	1.98E-50	XP_002343536.1	92	201.83	109	101	PREDICTED: similar to Os05g0242100

Locus_8501_Transcript_1/2_Conf_1.000	2158	20	7.23E-15	XP_001900806.1	43	87.4261	296	130	Topors protein
Locus_8501_Transcript_2/2_Conf_1.000	2143	20	7.17E-15	XP_001900806.1	43	87.4261	296	130	Topors protein
Locus_8502_Transcript_1/1_Conf_1.000	707	20	3.13E-89	NP_741143.1	82	332.028	232	192	hypothetical protein F09F7.4
Locus_8503_Transcript_1/1_Conf_1.000	513	20	4.93E-47	XP_002641224.1	75	190.66	169	127	Hypothetical protein CBG09088
Locus_8504_Transcript_1/1_Conf_1.000	423	20	5.59E-45	NP_491529.2	96	183.726	101	97	hypothetical protein Y110A7A.6
Locus_8505_Transcript_1/1_Conf_1.000	1068	20	1.80E-70	AAC47126.1	86	270.781	178	154	cyclophilin isoform 5
Locus_8506_Transcript_1/1_Conf_1.000	143	0							
Locus_8507_Transcript_1/1_Conf_1.000	533	20	4.96E-19	NP_502368.1	70	97.8265	97	68	Gut on EXterior family member (gex-3)
Locus_8508_Transcript_1/1_Conf_1.000	430	0							
Locus_8509_Transcript_1/1_Conf_1.000	662	20	5.90E-52	AAG29103.2	67	207.994	188	126	AF273084_1zinc metallopeptidase 1
Locus_851_Transcript_1/1_Conf_1.000	919	20	1.30E-116	EFO22550.1	80	423.705	307	248	TATA binding protein associated factor

Locus_8510_Transcript_1/1_Conf_1.000	223	4	8.50E-17	XP_002642787.1	85	90.1225	61	52	C. briggsae CBR-GOP-3 protein
Locus_8511_Transcript_1/1_Conf_1.000	829	4	4.84E-24	XP_002639112.1	50	115.931	286	144	Hypothetical protein CBG14931
Locus_8512_Transcript_1/1_Conf_1.000	295	0							
Locus_8513_Transcript_1/1_Conf_1.000	353	20	8.58E-62	XP_533657.2	99	239.58	117	116	PREDICTED: similar to ribosomal protein S19
Locus_8514_Transcript_1/1_Conf_1.000	498	2	1.46E-05	XP_002643186.1	51	52.7582	58	30	C. briggsae CBR-ADR-2 protein
Locus_8515_Transcript_1/1_Conf_1.000	670	0							
Locus_8516_Transcript_1/1_Conf_1.000	513	0							
Locus_8517_Transcript_1/1_Conf_1.000	178	20	1.56E-15	NP_505174.3	86	85.8853	58	50	hypothetical protein F52E1.13
Locus_8518_Transcript_1/1_Conf_1.000	925	20	3.03E-12	NP_001023625.1	51	77.0258	256	132	hypothetical protein ZK809.5
Locus_8519_Transcript_1/1_Conf_1.000	704	0							

Locus_852_Transcript_1/1_Conf_1.000	783	20	5.37E-123	XP_002641343.1	92	444.506	260	240	C. briggsae CBR-DPY-18 protein
Locus_8520_Transcript_1/1_Conf_1.000	1461	20	2.60E-116	XP_002643548.1	69	423.705	495	342	Hypothetical protein CBG16244
Locus_8521_Transcript_1/1_Conf_1.000	320	20	9.06E-11	ACS37721.1	65	70.0922	79	52	C-type lectin-1
Locus_8522_Transcript_1/1_Conf_1.000	335	20	1.19E-39	XP_002662404.1	80	166.007	109	88	PREDICTED: raptor-like
Locus_8523_Transcript_1/1_Conf_1.000	232	0							
Locus_8524_Transcript_1/1_Conf_1.000	197	0							
Locus_8525_Transcript_1/1_Conf_1.000	741	20	5.35E-122	XP_001158457.1	100	441.039	234	234	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma laminin-binding protein) (NEM/1CHD4) (Multidrug resistance-associated protein MGr1-Ag) isoform 2
Locus_8526_Transcript_1/2_Conf_1.000	1126	20	2.89E-98	NP_495993.2	76	363.229	277	211	hypothetical protein F42A8.3
Locus_8526_Transcript_2/2_Conf_1.000	1125	20	3.78E-98	NP_495993.2	77	362.844	272	210	hypothetical protein F42A8.3
Locus_8527_Transcript_1/2_Conf_1.000	1234	20	1.23E-44	AAA67723.1	66	185.267	259	173	ribonucleoprotein

Locus_8528_Transcript_1/1_Conf_1.000	2160	20	0	XP_001899924.1	77	677.167	604	469	symbol
Locus_8529_Transcript_1/2_Conf_1.000	1271	20	9.91E-114	XP_002644745.1	95	414.846	244	232	C. briggsae CBR-SFT-4 protein
Locus_8529_Transcript_2/2_Conf_1.000	1132	20	1.43E-129	XP_002644745.1	93	467.233	277	260	C. briggsae CBR-SFT-4 protein
Locus_853_Transcript_1/3_Conf_0.714	1269	20	3.46E-58	NP_001022851.1	82	230.335	135	112	GLYcosylation related family member (gly-5)
Locus_853_Transcript_2/3_Conf_0.714	2265	20	0	NP_001022852.1	90	795.808	467	422	GLYcosylation related family member (gly-5)
Locus_853_Transcript_3/3_Conf_0.714	2264	20	0	NP_001022852.1	90	795.808	467	422	GLYcosylation related family member (gly-5)
Locus_8530_Transcript_1/1_Conf_1.000	321	2	1.95E-05	NP_001021809.1	58	52.373	73	43	Branching AbnorMal family member (bam-2)

Locus_8531_Transcript_1/1_Conf_1.000	1575	20	3.62E-111	NP_494807.1	59	406.757	541	322	Variable ABnormal morphology family member (vab-1)
Locus_8532_Transcript_1/1_Conf_1.000	1113	20	9.98E-27	XP_002601395.1	65	125.561	173	114	hypothetical protein BRAFLDRAFT_130395
Locus_8533_Transcript_1/1_Conf_1.000	329	20	1.51E-50	EFO19620.1	90	202.216	109	99	histone acetyltransferase
Locus_8534_Transcript_1/1_Conf_1.000	174	0							
Locus_8535_Transcript_1/1_Conf_1.000	407	3	1.58E-15	XP_002644589.1	55	85.8853	129	72	C. briggsae CBR-LON-2 protein
Locus_8536_Transcript_1/1_Conf_1.000	320	0							
Locus_8537_Transcript_1/1_Conf_1.000	397	14	2.23E-09	XP_001894326.1	57	65.4698	95	55	DEK protein
Locus_8538_Transcript_1/1_Conf_1.000	1172	0							
Locus_8539_Transcript_1/1_Conf_1.000	1208	20	1.01E-35	NP_001024508.1	47	155.606	334	158	hypothetical protein D1009.3
Locus_854_Transcript_1/1_Conf_1.000	2399	20	1.73E-73	XP_001896545.1	48	282.337	517	249	hypothetical protein Bm1_25425
Locus_8540_Transcript_1/1_Conf_1.000	623	2	2.25E-07	XP_002638582.1	66	59.6918	50	33	Hypothetical protein CBG05629
Locus_8541_Transcript_1/1_Conf_1.000	368	6	1.27E-17	NP_499447.1	74	92.8189	101	75	RSK-pSeventy (RSK-p70 kinase) homolog family member (rsks-1)
Locus_8542_Transcript_1/1_Conf_1.000	530	4	7.03E-10	NP_501107.1	48	67.3958	165	80	hypothetical protein ZC477.5
Locus_8543_Transcript_1/2_Conf_1.000	1331	20	6.53E-63	NP_491059.2	77	246.128	201	156	hypothetical protein Y71F9AL.10

Locus_8543_Transcript_2/2_Conf_1.000	1292	20	6.91E-62	NP_491059.2	73	242.662	198	146	hypothetical protein Y71F9AL.10
Locus_8544_Transcript_1/1_Conf_1.000	199	0							
Locus_8545_Transcript_1/1_Conf_1.000	885	20	6.52E-86	XP_002642853.1	90	321.627	221	200	C. briggsae CBR-CKR-2 protein
Locus_8546_Transcript_1/1_Conf_1.000	744	20	8.15E-86	NP_510666.1	83	320.857	248	207	hypothetical protein F01G12.6
Locus_8547_Transcript_1/1_Conf_1.000	518	0							
Locus_8548_Transcript_1/1_Conf_1.000	301	3	1.13E-21	NP_508552.1	69	106.301	100	69	hypothetical protein F40F4.6
Locus_8549_Transcript_1/1_Conf_1.000	2448	6	4.26E-27	EFO27105.1	41	128.257	531	220	hypothetical protein LOAG_01374
Locus_855_Transcript_1/1_Conf_1.000	1172	20	0	NP_492711.1	88	641.343	387	341	glutamyl(E)/glutaminyl(Q) tRNA Synthetase family member (ers-2)
Locus_8550_Transcript_1/1_Conf_1.000	360	4	8.87E-19	NP_502082.1	64	96.6709	113	73	Phasmid Socket Absent family member (psa-4)
Locus_8551_Transcript_1/1_Conf_1.000	132	8	2.59E-10	NP_496440.1	81	68.5514	43	35	hypothetical protein W02B12.1
Locus_8552_Transcript_1/1_Conf_1.000	327	0							
Locus_8553_Transcript_1/1_Conf_1.000	450	0							
Locus_8554_Transcript_1/1_Conf_1.000	224	13	1.78E-06	XP_002631239.1	69	55.8398	52	36	C. briggsae CBR-LACT-3 protein
Locus_8555_Transcript_1/1_Conf_1.000	1673	20	2.00E-139	NP_491674.2	73	500.745	415	307	hypothetical protein F56H1.5
Locus_8556_Transcript_1/2_Conf_1.000	1646	20	6.31E-122	XP_001893038.1	72	442.58	390	282	Thioredoxin family protein

Locus_8556_Transcript_2/2_Conf_1.000	1622	20	4.58E-125	XP_001893038.1	72	452.981	390	284	Thioredoxin family protein
Locus_8557_Transcript_1/1_Conf_1.000	324	4	3.53E-15	XP_002642484.1	73	84.7297	94	69	Hypothetical protein CBG06903
Locus_8558_Transcript_1/1_Conf_1.000	348	0							
Locus_8559_Transcript_1/2_Conf_1.000	1538	20	3.17E-128	NP_490867.3	82	463.381	413	342	hypothetical protein Y73E7A.3
Locus_8559_Transcript_2/2_Conf_1.000	307	0							
Locus_856_Transcript_1/1_Conf_1.000	1887	20	1.59E-71	NP_506151.1	53	275.404	643	346	hypothetical protein C14C10.4
Locus_8560_Transcript_1/1_Conf_1.000	966	0							
Locus_8561_Transcript_1/1_Conf_1.000	1850	20	0	NP_001040665.1	97	884.019	495	483	Transbilayer Amphipath Transporters (subfamily IV P-type ATPase) family member (tat-5)
Locus_8562_Transcript_1/1_Conf_1.000	514	0							
Locus_8563_Transcript_1/1_Conf_1.000	341	0							
Locus_8564_Transcript_1/1_Conf_1.000	323	20	6.40E-49	XP_001899339.1	94	196.823	107	101	protein unc-22
Locus_8565_Transcript_1/1_Conf_1.000	901	20	2.78E-140	NP_495863.1	91	502.286	293	267	PhenylAlanine Hydroxylase family member (pah-1)
Locus_8566_Transcript_1/1_Conf_1.000	1024	20	2.14E-57	XP_001902793.1	66	227.254	187	125	Laminin EGF-like
Locus_8567_Transcript_1/1_Conf_1.000	578	20	2.26E-61	EFO22680.1	81	238.81	192	157	hypothetical protein LOAG_05804
Locus_8568_Transcript_1/1_Conf_1.000	380	0							
Locus_8569_Transcript_1/1_Conf_1.000	701	20	1.52E-27	NP_499390.3	50	127.102	221	111	HEXosaminidase family member (hex-3)

Locus_857_Transcript_1/1_Conf_1.000	398	3	2.91E-17	NP_741656.2	69	91.6633	76	53	hypothetical protein Y39B6A.41
Locus_8570_Transcript_1/1_Conf_1.000	273	0							
Locus_8571_Transcript_1/1_Conf_1.000	222	0							
Locus_8572_Transcript_1/1_Conf_1.000	150	0							
Locus_8573_Transcript_1/2_Conf_1.000	323	0							
Locus_8573_Transcript_2/2_Conf_1.000	320	0							
Locus_8574_Transcript_1/1_Conf_1.000	894	4	6.13E-23	NP_506080.1	50	112.464	290	146	hypothetical protein F55C5.4
Locus_8575_Transcript_1/1_Conf_1.000	181	0							
Locus_8576_Transcript_1/1_Conf_1.000	534	3	1.48E-39	XP_002642777.1	67	166.007	173	117	Hypothetical protein CBG21170
Locus_8577_Transcript_1/1_Conf_1.000	136	0							
Locus_8578_Transcript_1/1_Conf_1.000	348	20	1.34E-38	NP_502856.1	81	162.54	115	94	Nuclear Hormone Receptor family member (nhr-5)
Locus_8579_Transcript_1/2_Conf_1.000	420	20	3.33E-05	XP_002128415.1	61	51.6026	62	38	PREDICTED: similar to Microspherule protein 1
Locus_8579_Transcript_2/2_Conf_1.000	387	20	3.27E-05	XP_002128415.1	61	51.6026	62	38	PREDICTED: similar to Microspherule protein 1
Locus_858_Transcript_1/1_Conf_1.000	352	20	2.52E-29	XP_001138809.1	98	131.724	115	113	PREDICTED: similar to Protein S100-A6 (S100 calcium-binding protein A6) (Calcyclin) (Prolactin receptor-associated protein) (PRA) (Growth factor-inducible protein 2A9) (MLN 4)

Locus_8580_Transcript_1/1_Conf_1.000	202	20	3.89E-14	NP_506236.1	73	81.2629	68	50	hypothetical protein T16G1.4
Locus_8581_Transcript_1/1_Conf_1.000	515	20	9.10E-09	ABP94090.1	53	63.5438	105	56	venom C-type lectin galactose binding isoform variant 1
Locus_8582_Transcript_1/1_Conf_1.000	369	0							
Locus_8583_Transcript_1/2_Conf_1.000	694	20	2.15E-26	BAB68205.1	75	123.25	115	87	keratin-like protein
Locus_8583_Transcript_2/2_Conf_1.000	764	20	2.86E-25	BAB68205.1	74	119.783	115	86	keratin-like protein
Locus_8584_Transcript_1/1_Conf_1.000	1053	20	7.99E-23	EFO23240.1	84	112.464	75	63	protein-tyrosine phosphatase

Locus_8585_Transcript_1/1_Conf_1.000	354	20	7.05E-32	NP_492254.1	79	140.198	105	83	protein KINase family member (kin-10)
Locus_8586_Transcript_1/1_Conf_1.000	256	0							
Locus_8587_Transcript_1/1_Conf_1.000	721	20	1.63E-88	NP_501686.2	81	329.717	217	177	hypothetical protein C33A12.3
Locus_8588_Transcript_1/1_Conf_1.000	425	1	1.64E-20	EFO27968.1	57	102.449	140	80	hypothetical protein LOAG_00508
Locus_8589_Transcript_1/1_Conf_1.000	488	6	2.63E-10	XP_002638485.1	67	68.5514	76	51	Hypothetical protein CBG12913
Locus_859_Transcript_1/2_Conf_1.000	817	20	1.76E-71	AAF13167.1	74	273.478	203	152	AF173174_1CLC chloride channel protein
Locus_859_Transcript_2/2_Conf_1.000	811	20	7.29E-70	AAF13167.1	73	268.085	203	150	AF173174_1CLC chloride channel protein
Locus_8590_Transcript_1/1_Conf_1.000	585	0							

Locus_8591_Transcript_1/1_Conf_1.000	888	20	1.07E-19	XP_001897316.1	57	101.679	205	117	hypothetical protein
Locus_8592_Transcript_1/2_Conf_1.000	273	20	5.96E-15	NP_501769.1	77	83.9593	58	45	hypothetical protein K07F5.12
Locus_8592_Transcript_2/2_Conf_1.000	225	5	5.51E-08	XP_002633781.1	76	60.8474	42	32	Hypothetical protein CBG03472
Locus_8593_Transcript_1/1_Conf_1.000	617	20	1.21E-29	XP_002642925.1	63	133.65	165	105	Hypothetical protein CBG15201
Locus_8594_Transcript_1/1_Conf_1.000	157	0							
Locus_8595_Transcript_1/1_Conf_1.000	443	9	7.61E-42	CAA86058.2	83	173.326	144	120	C. elegans protein B0393.5, partially confirmed by transcript evidence

Locus_8596_Transcript_1/1_Conf_1.000	797	20	1.60E-37	EFO16938.1	74	160.614	131	98	hypothetical protein LOAG_11565
Locus_8597_Transcript_1/1_Conf_1.000	264	0							
Locus_8598_Transcript_1/1_Conf_1.000	625	20	2.46E-86	NP_505879.1	89	322.013	200	178	hypothetical protein F47G9.1
Locus_8599_Transcript_1/1_Conf_1.000	352	0							
Locus_86_Transcript_1/1_Conf_1.000	394	0							
Locus_860_Transcript_1/1_Conf_1.000	736	20	2.19E-43	XP_002640130.1	60	179.874	235	142	C. briggsae CBR-NPP-12 protein
Locus_8600_Transcript_1/1_Conf_1.000	699	20	1.16E-51	NP_496729.2	75	207.223	194	146	Beta-Carotene 15,15'-MonoOxygenase family member (bcmo-1)
Locus_8601_Transcript_1/1_Conf_1.000	621	2	6.26E-42	XP_002631595.1	60	174.481	206	125	Hypothetical protein CBG20775
Locus_8602_Transcript_1/1_Conf_1.000	594	0							
Locus_8603_Transcript_1/1_Conf_1.000	249	20	3.58E-12	XP_001893353.1	69	74.7146	69	48	Protein-tyrosine phosphatase containing protein
Locus_8604_Transcript_1/1_Conf_1.000	1889	20	2.56E-154	NP_001021859.1	67	550.436	624	419	Variable ABnormal morphology family member (vab-10)
Locus_8605_Transcript_1/1_Conf_1.000	507	0							
Locus_8606_Transcript_1/1_Conf_1.000	1206	20	2.88E-107	NP_510713.1	74	393.275	362	271	Cyclase ASsociated protein Homolog family member (cas-1)
Locus_8607_Transcript_1/1_Conf_1.000	668	20	1.34E-67	XP_001510969.1	100	259.996	143	143	PREDICTED: similar to Mus musculus ribosomal protein L19
Locus_8608_Transcript_1/1_Conf_1.000	388	0							
Locus_8609_Transcript_1/1_Conf_1.000	674	20	7.29E-53	NP_497275.1	66	211.075	199	132	hypothetical protein K02F3.10

Locus_861_Transcript_1/1_Conf_1.000	1867	0							
Locus_8610_Transcript_1/1_Conf_1.000	409	20	1.20E-15	XP_002640083.1	58	86.2705	137	80	C. briggsae CBR-FRK-1 protein
Locus_8611_Transcript_1/1_Conf_1.000	324	0							
Locus_8612_Transcript_1/1_Conf_1.000	412	0							
Locus_8613_Transcript_1/1_Conf_1.000	547	5	6.12E-07	CAA10033.1	51	57.7658	164	85	DYS-1 protein
Locus_8614_Transcript_1/1_Conf_1.000	364	20	1.19E-23	NP_502448.1	72	112.849	100	72	hypothetical protein ZK896.9
Locus_8615_Transcript_1/1_Conf_1.000	358	20	4.72E-20	NP_001021401.1	79	100.908	62	49	hypothetical protein F21F3.7
Locus_8616_Transcript_1/1_Conf_1.000	257	20	1.60E-23	CAR63542.1	98	112.464	57	56	putative Pre-mRNA splicing protein
Locus_8617_Transcript_1/1_Conf_1.000	668	20	3.66E-49	EFO22579.1	74	198.749	171	127	hypothetical protein LOAG_05905
Locus_8618_Transcript_1/1_Conf_1.000	860	20	5.39E-122	XP_002637013.1	79	441.425	288	228	C. briggsae CBR-NID-1 protein
Locus_8619_Transcript_1/1_Conf_1.000	1814	20	1.61E-81	XP_001895729.1	55	308.531	507	282	Ubiquitin carboxyl-terminal hydrolase family protein
Locus_862_Transcript_1/2_Conf_1.000	2085	8	5.40E-68	NP_741334.3	68	263.848	253	173	hypothetical protein Y71G10AL.1
Locus_862_Transcript_2/2_Conf_1.000	2079	8	5.38E-68	NP_741334.3	68	263.848	253	173	hypothetical protein Y71G10AL.1

Locus_8620_Transcript_1/1_Conf_1.000	975	20	8.38E-16	EFO24312.1	50	88.9669	212	107	hypothetical protein LOAG_04179
Locus_8621_Transcript_1/1_Conf_1.000	480	0							
Locus_8622_Transcript_1/1_Conf_1.000	273	0							
Locus_8623_Transcript_1/1_Conf_1.000	358	0							
Locus_8624_Transcript_1/1_Conf_1.000	610	20	1.49E-40	EFO18652.1	64	169.859	204	131	hypothetical protein LOAG_09840
Locus_8625_Transcript_1/1_Conf_1.000	859	11	3.68E-54	NP_001023577.1	68	216.083	237	163	Prion-like-(Q/N-rich)-domain-bearing protein family member (pqn-89)
Locus_8626_Transcript_1/1_Conf_1.000	328	5	1.74E-30	AAL77521.1	77	135.576	109	84	L80003_1guanylyl cyclase
Locus_8627_Transcript_1/1_Conf_1.000	685	20	1.58E-66	NP_001022840.1	84	256.529	187	158	hypothetical protein Y39A1A.21
Locus_8628_Transcript_1/1_Conf_1.000	139	0							
Locus_8629_Transcript_1/1_Conf_1.000	1059	2	1.43E-11	XP_001898424.1	48	75.0998	254	124	DEAD/H
Locus_863_Transcript_1/2_Conf_1.000	709	20	1.34E-55	NP_001023947.1	62	220.32	236	148	Farnesylated-proteins Converting Enzyme (FACE) family member (fce-2)
Locus_863_Transcript_2/2_Conf_1.000	709	20	1.75E-55	NP_001023947.1	62	219.935	236	148	Farnesylated-proteins Converting Enzyme (FACE) family member (fce-2)
Locus_8630_Transcript_1/2_Conf_1.000	351	0							
Locus_8630_Transcript_2/2_Conf_1.000	357	0							
Locus_8631_Transcript_1/1_Conf_1.000	674	20	3.51E-39	NP_001041137.1	56	165.622	225	126	Alpha MANnosidase family member (aman-2)
Locus_8632_Transcript_1/1_Conf_1.000	915	20	1.38E-17	XP_001896161.1	63	94.7449	105	67	tRNA intron endonuclease family protein

Locus_8633_Transcript_1/1_Conf_1.000	331	20	3.50E-23	XP_002636475.1	64	111.309	110	71	Hypothetical protein CBG23146
Locus_8634_Transcript_1/1_Conf_1.000	277	20	7.46E-34	NP_500240.1	83	146.747	92	77	hypothetical protein Y69A2AR.31
Locus_8635_Transcript_1/1_Conf_1.000	922	7	9.02E-25	P34288.4	76	118.627	90	69	GTPase-activating protein pac-1
Locus_8636_Transcript_1/1_Conf_1.000	757	20	7.34E-58	XP_002634587.1	68	228.024	220	150	Hypothetical protein CBG08398
Locus_8637_Transcript_1/1_Conf_1.000	349	20	1.64E-28	XP_002642830.1	84	129.028	115	97	Hypothetical protein CBG21229
Locus_8638_Transcript_1/1_Conf_1.000	641	20	3.02E-58	ACI49192.1	71	228.794	211	151	hypothetical protein Csp3_JD03.001
Locus_8639_Transcript_1/1_Conf_1.000	985	9	9.44E-07	XP_394132.3	55	58.9214	93	52	PREDICTED: similar to CG31646-PA
Locus_864_Transcript_1/1_Conf_1.000	1251	20	2.56E-21	XP_002633442.1	47	107.842	227	107	Hypothetical protein CBG06210
Locus_8640_Transcript_1/1_Conf_1.000	149	2	7.73E-10	XP_002638375.1	79	67.0106	43	34	Hypothetical protein CBG18580
Locus_8641_Transcript_1/1_Conf_1.000	721	20	2.32E-26	NP_508196.1	71	123.25	139	100	STAUfen (dsRNA binding protein) homolog family member (stau-1)
Locus_8642_Transcript_1/1_Conf_1.000	225	20	3.80E-25	EAW84826.1	100	117.857	53	53	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13
Locus_8643_Transcript_1/1_Conf_1.000	631	20	4.09E-36	XP_001892146.1	68	155.221	165	113	coronin 2A

Locus_8644_Transcript_1/1_Conf_1.000	381	5	5.57E-37	ABS50363.1	88	157.147	101	89	LIM domain protein variant
Locus_8645_Transcript_1/1_Conf_1.000	1024	20	3.06E-88	NP_497510.2	66	329.717	356	236	hypothetical protein C39B5.6
Locus_8646_Transcript_1/2_Conf_1.000	281	0							
Locus_8646_Transcript_2/2_Conf_1.000	275	0							
Locus_8647_Transcript_1/1_Conf_1.000	157	0							
Locus_8648_Transcript_1/1_Conf_1.000	545	20	1.24E-52	XP_002639368.1	88	209.534	135	120	C. briggsae CBR-GNRR-1 protein
Locus_8649_Transcript_1/1_Conf_1.000	372	0							
Locus_865_Transcript_1/1_Conf_1.000	495	0							
Locus_8650_Transcript_1/1_Conf_1.000	242	7	1.52E-18	EFO27604.1	75	95.9005	77	58	hypothetical protein LOAG_00873
Locus_8651_Transcript_1/1_Conf_1.000	256	0							
Locus_8652_Transcript_1/1_Conf_1.000	392	20	2.84E-17	NP_494886.1	89	91.6633	66	59	hypothetical protein R05F9.6
Locus_8653_Transcript_1/1_Conf_1.000	654	14	1.24E-09	EFN66847.1	49	67.3958	111	55	hypothetical protein EAG_08499
Locus_8654_Transcript_1/1_Conf_1.000	1698	20	1.72E-45	NP_001024604.1	61	188.734	219	135	abnormal DAuer Formation family member (daf-3)
Locus_8655_Transcript_1/1_Conf_1.000	195	0							
Locus_8656_Transcript_1/1_Conf_1.000	545	0							

Locus_8657_Transcript_1/1_Conf_1.000	835	20	1.20E-46	NP_503446.1	62	191.045	200	124	Cell Division Cycle related family member (cdc-25.2)
Locus_8658_Transcript_1/1_Conf_1.000	130	3	1.48E-05	NP_499466.1	62	52.7582	59	37	Neuropeptide-Like Protein family member (nlp-21)
Locus_8659_Transcript_1/1_Conf_1.000	494	20	2.77E-20	XP_001894296.1	58	101.679	167	98	hypothetical protein
Locus_866_Transcript_1/1_Conf_1.000	380	5	1.69E-09	XP_001896009.1	59	65.855	93	55	hypothetical protein Bm1_22765
Locus_8660_Transcript_1/2_Conf_1.000	1112	7	7.87E-24	XP_001902037.1	46	115.931	317	146	hypothetical protein Bm1_52845
Locus_8660_Transcript_2/2_Conf_1.000	1112	7	1.59E-24	XP_001902037.1	47	118.242	317	151	hypothetical protein Bm1_52845
Locus_8661_Transcript_1/1_Conf_1.000	1542	20	3.41E-98	A8XU68.2	69	363.614	321	223	5'-tyrosyl-DNA phosphodiesterase
Locus_8662_Transcript_1/1_Conf_1.000	367	20	4.23E-13	NP_499492.1	56	77.7962	112	63	hypothetical protein Y66D12A.10
Locus_8663_Transcript_1/1_Conf_1.000	886	20	8.31E-57	NP_505919.3	67	224.942	246	167	hypothetical protein C55A6.3
Locus_8664_Transcript_1/2_Conf_1.000	1881	9	4.84E-12	EFO25616.1	41	77.7962	314	130	hypothetical protein LOAG_02872
Locus_8664_Transcript_2/2_Conf_1.000	1833	9	4.68E-12	EFO25616.1	41	77.7962	314	130	hypothetical protein LOAG_02872
Locus_8665_Transcript_1/1_Conf_1.000	661	20	2.55E-71	XP_002630825.1	85	272.322	219	187	Hypothetical protein CBG02527

Locus_8666_Transcript_1/1_Conf_1.000	713	20	3.70E-37	AAO39173.1	68	159.073	207	141	nuclear receptor NHR-32
Locus_8667_Transcript_1/4_Conf_0.667	1578	20	2.93E-161	XP_002641487.1	80	573.163	476	382	Hypothetical protein CBG09778
Locus_8667_Transcript_2/4_Conf_0.667	1673	20	4.13E-161	XP_002641487.1	80	572.778	476	381	Hypothetical protein CBG09778
Locus_8667_Transcript_3/4_Conf_0.556	1650	20	7.91E-165	XP_002641487.1	80	585.104	467	377	Hypothetical protein CBG09778
Locus_8667_Transcript_4/4_Conf_0.667	1673	20	3.16E-161	XP_002641487.1	80	573.163	476	382	Hypothetical protein CBG09778
Locus_8668_Transcript_1/1_Conf_1.000	568	4	6.51E-34	NP_490772.2	59	147.517	191	114	hypothetical protein Y18H1A.3
Locus_8669_Transcript_1/1_Conf_1.000	699	20	2.94E-63	XP_002639231.1	72	245.743	204	147	Hypothetical protein CBG03787
Locus_867_Transcript_1/1_Conf_1.000	915	20	3.68E-87	NP_496490.2	71	325.865	306	218	NEPrilysin metallopeptidase family member (nep-1)
Locus_8670_Transcript_1/1_Conf_1.000	347	4	1.88E-32	NP_503059.2	85	142.124	115	98	hypothetical protein ZK550.3
Locus_8671_Transcript_1/1_Conf_1.000	853	0							
Locus_8672_Transcript_1/1_Conf_1.000	699	4	4.86E-50	XP_002632215.1	90	201.83	128	116	Hypothetical protein CBG07083

Locus_8673_Transcript_1/3_Conf_0.286	342	20	1.95E-29	XP_002633708.1	77	132.109	102	79	C. briggsae CBR-TRAM-1 protein
Locus_8673_Transcript_2/3_Conf_0.714	1604	20	1.56E-101	XP_002633708.1	73	374.785	332	244	C. briggsae CBR-TRAM-1 protein
Locus_8673_Transcript_3/3_Conf_0.714	1607	20	1.56E-101	XP_002633708.1	73	374.785	332	244	C. briggsae CBR-TRAM-1 protein
Locus_8674_Transcript_1/2_Conf_1.000	181	0							
Locus_8674_Transcript_2/2_Conf_1.000	190	0							
Locus_8675_Transcript_1/1_Conf_1.000	436	0							
Locus_8676_Transcript_1/1_Conf_1.000	161	0							
Locus_8677_Transcript_1/1_Conf_1.000	748	0							
Locus_8678_Transcript_1/1_Conf_1.000	925	20	1.05E-105	XP_002631798.1	87	387.497	246	216	C. briggsae CBR-TPI-1 protein

Locus_8679_Transcript_1/1_Conf_1.000	1378	20	2.87E-77	XP_002631175.1	88	293.893	186	165	Hypothetical protein CBG02961
Locus_868_Transcript_1/1_Conf_1.000	550	8	3.53E-10	AAO63578.1	46	68.5514	166	78	secreted protein 6 precursor
Locus_8680_Transcript_1/1_Conf_1.000	1079	20	3.75E-108	NP_499084.1	72	395.971	320	233	hypothetical protein B0464.9
Locus_8681_Transcript_1/1_Conf_1.000	270	14	3.63E-12	CAC38987.1	94	74.7146	36	34	cooperia receptor-like protein
Locus_8682_Transcript_1/2_Conf_1.000	1246	0							
Locus_8682_Transcript_2/2_Conf_1.000	1198	0							
Locus_8683_Transcript_1/1_Conf_1.000	451	20	2.42E-32	EFO19871.1	98	141.739	74	73	hypothetical protein LOAG_08622
Locus_8684_Transcript_1/1_Conf_1.000	270	0							
Locus_8685_Transcript_1/1_Conf_1.000	1049	20	2.21E-41	NP_498335.1	55	174.096	275	153	NeuroFibroMatosis homolog family member (nfm-1)
Locus_8686_Transcript_1/1_Conf_1.000	836	17	8.28E-64	CAB59919.1	65	248.054	310	204	hypothetical protein
Locus_8687_Transcript_1/1_Conf_1.000	769	20	3.64E-60	XP_002631097.1	80	235.728	187	151	Hypothetical protein CBG02871

Locus_8688_Transcript_1/1_Conf_1.000	616	10	3.44E-08	AAO63578.1	42	62.3882	154	66	secreted protein 6 precursor
Locus_8689_Transcript_1/1_Conf_1.000	711	1	1.02E-10	NP_001122712.1	52	71.2478	149	78	hypothetical protein R10E9.3
Locus_869_Transcript_1/2_Conf_1.000	1978	20	0	NP_493464.1	80	711.835	539	436	DNaJ domain (prokaryotic heat shock protein) family member (dnj-29)
Locus_869_Transcript_2/2_Conf_1.000	1972	20	0	NP_493464.1	81	717.998	536	437	DNaJ domain (prokaryotic heat shock protein) family member (dnj-29)
Locus_8690_Transcript_1/1_Conf_1.000	296	0							
Locus_8691_Transcript_1/1_Conf_1.000	1008	0							
Locus_8692_Transcript_1/1_Conf_1.000	660	0							
Locus_8693_Transcript_1/1_Conf_1.000	195	0							
Locus_8694_Transcript_1/1_Conf_1.000	798	20	1.09E-118	NP_001024542.1	82	430.254	277	228	UNCoordinated family member (unc-115)
Locus_8695_Transcript_1/1_Conf_1.000	517	4	8.93E-36	XP_002630694.1	70	153.295	174	122	Hypothetical protein CBG02376
Locus_8696_Transcript_1/1_Conf_1.000	337	20	1.83E-32	XP_002639509.1	96	142.124	77	74	C. briggsae CBR-SNR-7 protein
Locus_8697_Transcript_1/1_Conf_1.000	1146	20	3.56E-144	NP_501372.1	81	515.768	387	315	PCTAIRE class cell cycle kinase family member (pct-1)
Locus_8698_Transcript_1/1_Conf_1.000	418	0							
Locus_8699_Transcript_1/2_Conf_1.000	1908	20	0	XP_002634993.1	85	664.07	469	401	Hypothetical protein CBG13533
Locus_8699_Transcript_2/2_Conf_1.000	1908	20	0	XP_002634993.1	85	664.07	469	401	Hypothetical protein CBG13533

Locus_87_Transcript_1/2_Conf_1.000	6171	20	0	XP_002639045.1	79	1720.29	1343	1065	C. briggsae CBR-TAG-192 protein
Locus_87_Transcript_2/2_Conf_1.000	6156	20	0	XP_002639045.1	79	1726.07	1338	1065	C. briggsae CBR-TAG-192 protein
Locus_870_Transcript_1/1_Conf_1.000	706	20	4.84E-82	EFO20586.1	79	308.145	235	187	anion exchange protein
Locus_8700_Transcript_1/1_Conf_1.000	620	0							
Locus_8701_Transcript_1/1_Conf_1.000	994	20	1.83E-74	XP_002640627.1	82	283.878	209	172	C. briggsae CBR-UNC-95 protein
Locus_8702_Transcript_1/1_Conf_1.000	141	4	2.66E-07	EFO20706.1	73	58.5362	45	33	hypothetical protein LOAG_07782
Locus_8703_Transcript_1/1_Conf_1.000	1785	0							
Locus_8704_Transcript_1/1_Conf_1.000	820	20	2.30E-95	NP_001021021.1	87	352.829	225	197	hypothetical protein C32F10.8
Locus_8705_Transcript_1/1_Conf_1.000	210	0							
Locus_8706_Transcript_1/1_Conf_1.000	155	2	3.02E-06	NP_498825.1	66	55.0694	48	32	hypothetical protein F10E9.4
Locus_8707_Transcript_1/1_Conf_1.000	1015	20	4.35E-95	NP_495019.1	76	352.443	321	247	Masculinisation Of Germline family member (mog-5)
Locus_8708_Transcript_1/2_Conf_1.000	2517	20	4.03E-105	XP_002634366.1	57	387.497	587	340	Hypothetical protein CBG17718

Locus_8708_Transcript_2/2_Conf_1.000	2517	20	4.03E-105	XP_002634366.1	57	387.497	587	340	Hypothetical protein CBG17718
Locus_8709_Transcript_1/1_Conf_1.000	271	6	4.44E-10	NP_497545.1	69	67.781	89	62	hypothetical protein H14E04.2
Locus_871_Transcript_1/1_Conf_1.000	1198	20	1.55E-137	XP_002641677.1	85	493.812	316	270	C. briggsae CBR-CDK-1 protein
Locus_8710_Transcript_1/1_Conf_1.000	281	0							
Locus_8711_Transcript_1/1_Conf_1.000	290	0							
Locus_8712_Transcript_1/1_Conf_1.000	488	20	2.43E-40	NP_496534.1	68	168.318	162	111	Nuclear Pore complex Protein family member (npp-3)
Locus_8713_Transcript_1/1_Conf_1.000	926	20	2.35E-81	XP_002647135.1	73	306.605	247	181	Hypothetical protein CBG16432
Locus_8714_Transcript_1/1_Conf_1.000	205	0							
Locus_8715_Transcript_1/1_Conf_1.000	582	0							
Locus_8716_Transcript_1/2_Conf_1.000	1741	20	4.19E-47	CAR97812.1	46	194.126	619	289	C. elegans protein C36A4.8a, partially confirmed by transcript evidence
Locus_8716_Transcript_2/2_Conf_1.000	1741	20	5.47E-47	CAR97812.1	47	193.741	619	291	C. elegans protein C36A4.8a, partially confirmed by transcript evidence
Locus_8717_Transcript_1/1_Conf_1.000	476	20	3.98E-27	NP_741529.1	82	124.405	84	69	hypothetical protein C37H5.6
Locus_8718_Transcript_1/1_Conf_1.000	329	2	5.98E-23	NP_498314.2	71	110.538	110	79	hypothetical protein ZK328.6

Locus_8719_Transcript_1/1_Conf_1.000	203	3	3.89E-14	XP_002634053.1	81	81.2629	65	53	Hypothetical protein CBG01593
Locus_872_Transcript_1/1_Conf_1.000	651	0							
Locus_8720_Transcript_1/2_Conf_1.000	1352	12	2.47E-41	XP_002633559.1	68	174.481	153	105	C. briggsae CBR-PQN-89 protein
Locus_8720_Transcript_2/2_Conf_1.000	1352	12	2.47E-41	XP_002633559.1	68	174.481	153	105	C. briggsae CBR-PQN-89 protein
Locus_8721_Transcript_1/1_Conf_1.000	354	12	2.98E-06	EEE23923.1	50	55.0694	108	55	hypothetical protein TGGT1_030040
Locus_8722_Transcript_1/1_Conf_1.000	669	0							
Locus_8723_Transcript_1/2_Conf_1.000	1364	20	4.43E-30	NP_740929.2	79	137.117	102	81	hypothetical protein Y105E8A.1
Locus_8723_Transcript_2/2_Conf_1.000	1326	20	4.26E-30	NP_740929.2	79	137.117	102	81	hypothetical protein Y105E8A.1
Locus_8724_Transcript_1/1_Conf_1.000	751	4	1.02E-51	NP_495268.1	80	207.608	145	117	GLoBin family member (glb-10)
Locus_8725_Transcript_1/1_Conf_1.000	858	20	9.41E-42	XP_002638524.1	59	174.866	260	154	C. briggsae CBR-AMX-3 protein
Locus_8726_Transcript_1/1_Conf_1.000	988	20	3.82E-40	EFO13398.1	56	169.859	228	128	hypothetical protein LOAG_15131
Locus_8727_Transcript_1/1_Conf_1.000	242	10	2.86E-17	XP_002643956.1	66	91.6633	75	50	Hypothetical protein CBG17315
Locus_8728_Transcript_1/1_Conf_1.000	1010	20	2.38E-61	ACN93882.1	96	240.35	126	121	putative glutamate-cysteine ligase catalytic subunit
Locus_8729_Transcript_1/1_Conf_1.000	603	0							
Locus_873_Transcript_1/1_Conf_1.000	1765	20	0	NP_510711.2	84	704.516	464	392	AMP-Activated Kinase family member (aak-2)
Locus_8730_Transcript_1/1_Conf_1.000	690	20	2.30E-113	XP_002798294.1	95	412.149	218	209	PREDICTED: hypothetical protein LOC100430699 isoform 1
Locus_8731_Transcript_1/3_Conf_0.667	990	20	3.29E-108	XP_002631117.1	73	395.971	325	240	Hypothetical protein CBG02892

Locus_8731_Transcript_2/3_Conf_0.667	991	20	3.29E-108	XP_002631117.1	73	395.971	325	240	Hypothetical protein CBG02892
Locus_8731_Transcript_3/3_Conf_0.667	990	20	3.29E-108	XP_002631117.1	73	395.971	325	240	Hypothetical protein CBG02892
Locus_8732_Transcript_1/1_Conf_1.000	147	0							
Locus_8733_Transcript_1/1_Conf_1.000	520	20	8.00E-32	XP_002646686.1	69	140.198	144	100	Hypothetical protein CBG13063
Locus_8734_Transcript_1/4_Conf_0.667	1290	0							
Locus_8734_Transcript_2/4_Conf_0.222	316	0							
Locus_8734_Transcript_3/4_Conf_0.667	1290	0							
Locus_8734_Transcript_4/4_Conf_0.667	1290	0							
Locus_8735_Transcript_1/1_Conf_1.000	404	20	2.79E-12	XP_001892288.1	59	75.0998	92	55	UPF0017 protein CG3488
Locus_8736_Transcript_1/1_Conf_1.000	660	20	1.08E-45	XP_001895971.1	63	187.193	219	139	hypothetical protein
Locus_8737_Transcript_1/1_Conf_1.000	470	7	2.62E-10	NP_491776.1	59	68.5514	81	48	hypothetical protein T09B4.7
Locus_8738_Transcript_1/1_Conf_1.000	270	4	5.07E-14	NP_497743.1	65	80.8777	93	61	hypothetical protein C46F11.4
Locus_8739_Transcript_1/1_Conf_1.000	983	20	3.81E-125	XP_002642323.1	89	452.21	265	237	C. briggsae CBR-RIB-2 protein
Locus_874_Transcript_1/1_Conf_1.000	1817	20	3.22E-106	XP_001900236.1	59	390.578	541	321	CUT domain containing protein

Locus_8740_Transcript_1/1_Conf_1.000	123	0							
Locus_8741_Transcript_1/1_Conf_1.000	186	0							
Locus_8742_Transcript_1/2_Conf_1.000	1173	20	2.09E-38	XP_395372.2	48	164.466	331	162	PREDICTED: similar to CG7565-PA
Locus_8742_Transcript_2/2_Conf_1.000	1173	20	7.93E-38	XP_395372.2	48	162.54	331	161	PREDICTED: similar to CG7565-PA
Locus_8743_Transcript_1/1_Conf_1.000	393	0							
Locus_8744_Transcript_1/1_Conf_1.000	1155	4	9.86E-09	NP_506662.1	40	65.855	225	92	hypothetical protein ZC412.3
Locus_8745_Transcript_1/1_Conf_1.000	549	20	1.19E-74	XP_002647384.1	85	282.722	187	160	Hypothetical protein CBG06449
Locus_8746_Transcript_1/1_Conf_1.000	487	20	2.96E-62	NP_508943.3	95	241.121	118	113	UNCoordinated family member (unc-97)
Locus_8747_Transcript_1/1_Conf_1.000	1005	20	4.26E-111	NP_507876.1	82	405.601	293	242	DeCapping Scavenger enzyme homolog family member (dcs-1)
Locus_8748_Transcript_1/1_Conf_1.000	1545	20	0	NP_492785.1	91	723.005	432	395	Eukaryotic Initiation Factor family member (eif-3.E)
Locus_8749_Transcript_1/1_Conf_1.000	299	0							
Locus_875_Transcript_1/1_Conf_1.000	233	0							
Locus_8750_Transcript_1/1_Conf_1.000	174	0							
Locus_8751_Transcript_1/1_Conf_1.000	1151	4	9.75E-17	NP_741942.1	47	92.4337	269	129	SUppressor of activated let-60 Ras family member (sur-7)
Locus_8752_Transcript_1/1_Conf_1.000	355	20	9.19E-40	XP_002632757.1	81	166.392	117	95	C. briggsae CBR-EOR-1 protein
Locus_8753_Transcript_1/1_Conf_1.000	446	20	1.68E-57	EFO14962.1	85	225.328	144	123	AQR protein
Locus_8754_Transcript_1/1_Conf_1.000	703	2	2.82E-05	AAY29120.1	44	53.1434	223	100	cement precursor protein 3B variant 1

Locus_8755_Transcript_1/1_Conf_1.000	1920	20	2.55E-08	XP_002194548.1	39	65.4698	470	185	PREDICTED: death inducer-obliterator 1
Locus_8756_Transcript_1/1_Conf_1.000	680	0							
Locus_8757_Transcript_1/1_Conf_1.000	425	20	3.16E-56	EFO19846.1	86	221.09	140	121	cleavage and polyadenylation specificity factor subunit 2
Locus_8758_Transcript_1/1_Conf_1.000	349	16	3.21E-16	CAA40299.1	86	88.1965	116	100	alpha1(IV) collagen
Locus_8759_Transcript_1/1_Conf_1.000	488	20	3.16E-56	XP_001902033.1	78	221.09	157	123	ring finger protein 1
Locus_876_Transcript_1/1_Conf_1.000	352	19	6.02E-15	AAD51334.1	81	83.9593	55	45	Kunitz type serine protease inhibitor
Locus_8760_Transcript_1/2_Conf_1.000	785	0							
Locus_8760_Transcript_2/2_Conf_1.000	693	1	8.80E-04	XP_001717004.1	40	48.1358	115	46	PREDICTED: hypothetical protein
Locus_8761_Transcript_1/2_Conf_1.000	707	20	7.98E-85	NP_871967.1	89	317.39	188	168	TBC (Tre-2/Bub2/Cdc16) domain family member (tbc-15)
Locus_8761_Transcript_2/2_Conf_1.000	780	20	2.19E-84	NP_871967.1	89	316.235	188	168	TBC (Tre-2/Bub2/Cdc16) domain family member (tbc-15)
Locus_8762_Transcript_1/1_Conf_1.000	704	20	3.60E-85	AAG29105.1	75	318.546	234	177	AF273705_1zinc metallopeptidase 2 MEP2
Locus_8763_Transcript_1/1_Conf_1.000	397	0							
Locus_8764_Transcript_1/1_Conf_1.000	533	4	3.28E-63	NP_501400.1	85	244.588	161	138	hypothetical protein F35H10.10
Locus_8765_Transcript_1/1_Conf_1.000	351	20	6.42E-25	NP_502129.1	93	117.087	66	62	hypothetical protein B0035.5

Locus_8766_Transcript_1/2_Conf_1.000	679	20	7.27E-24	EFO17488.1	62	114.775	140	87	hypothetical protein LOAG_11011
Locus_8766_Transcript_2/2_Conf_1.000	679	20	7.27E-24	EFO17488.1	62	114.775	140	87	hypothetical protein LOAG_11011
Locus_8767_Transcript_1/1_Conf_1.000	764	20	5.19E-43	EFO27634.1	83	178.718	112	94	hypothetical protein LOAG_00851
Locus_8768_Transcript_1/1_Conf_1.000	206	0							
Locus_8769_Transcript_1/1_Conf_1.000	353	0							
Locus_877_Transcript_1/2_Conf_1.000	330	0							
Locus_877_Transcript_2/2_Conf_1.000	344	0							
Locus_8770_Transcript_1/2_Conf_1.000	1171	4	2.83E-11	EFO22760.1	43	74.3294	191	84	hypothetical protein LOAG_05724
Locus_8770_Transcript_2/2_Conf_1.000	1162	4	1.81E-10	EFO22760.1	43	71.633	198	87	hypothetical protein LOAG_05724
Locus_8771_Transcript_1/2_Conf_1.000	1926	0							
Locus_8771_Transcript_2/2_Conf_1.000	356	3	1.64E-04	XP_001896320.1	75	49.2914	44	33	Bromodomain containing protein
Locus_8772_Transcript_1/1_Conf_1.000	593	20	1.51E-39	XP_002637033.1	69	166.392	143	100	C. briggsae CBR-AOS-1 protein
Locus_8773_Transcript_1/1_Conf_1.000	133	0							
Locus_8774_Transcript_1/3_Conf_0.600	362	0							
Locus_8774_Transcript_2/3_Conf_0.600	363	0							
Locus_8774_Transcript_3/3_Conf_0.600	362	0							
Locus_8775_Transcript_1/1_Conf_1.000	285	20	4.06E-35	CAA21622.4	90	150.984	94	85	C. elegans protein Y43F8C.12, partially confirmed by transcript evidence
Locus_8776_Transcript_1/2_Conf_1.000	519	0							
Locus_8776_Transcript_2/2_Conf_1.000	520	0							
Locus_8777_Transcript_1/1_Conf_1.000	578	20	1.56E-70	NP_500620.1	85	269.24	181	154	hypothetical protein K08F11.5
Locus_8778_Transcript_1/2_Conf_1.000	364	10	1.24E-04	XP_002043604.1	48	49.6766	103	50	GM16842
Locus_8778_Transcript_2/2_Conf_1.000	370	13	4.37E-05	XP_002043604.1	48	51.2174	107	52	GM16842

Locus_8779_Transcript_1/2_Conf_1.000	351	8	3.31E-11	XP_002633023.1	59	68.9366	71	42	Hypothetical protein CBG21797
Locus_8779_Transcript_2/2_Conf_1.000	1318	20	2.80E-58	NP_501604.2	66	230.72	261	173	hypothetical protein C46C2.2
Locus_878_Transcript_1/1_Conf_1.000	1422	7	3.85E-08	NP_492632.1	44	64.3142	139	62	hypothetical protein T24D1.5
Locus_8780_Transcript_1/1_Conf_1.000	952	20	1.65E-61	XP_002643891.1	58	240.736	310	180	Hypothetical protein CBG02143
Locus_8781_Transcript_1/1_Conf_1.000	285	20	4.23E-08	CAN88212.1	53	61.2326	71	38	notch homolog 1b
Locus_8782_Transcript_1/2_Conf_1.000	370	0							
Locus_8782_Transcript_2/2_Conf_1.000	375	0							
Locus_8783_Transcript_1/1_Conf_1.000	715	0							
Locus_8784_Transcript_1/1_Conf_1.000	503	20	3.18E-64	XP_002640833.1	85	247.669	167	142	C. briggsae CBR-KLP-20 protein
Locus_8785_Transcript_1/1_Conf_1.000	978	8	1.88E-15	EFO18438.1	47	87.8113	232	110	zinc finger protein
Locus_8786_Transcript_1/1_Conf_1.000	656	0							
Locus_8787_Transcript_1/1_Conf_1.000	236	20	3.64E-20	NP_499865.1	76	101.293	73	56	hypothetical protein F29C4.6
Locus_8788_Transcript_1/1_Conf_1.000	158	0							
Locus_8789_Transcript_1/1_Conf_1.000	394	20	3.09E-51	XP_002919231.1	100	204.527	126	126	PREDICTED: 60S ribosomal protein L31-like

Locus_879_Transcript_1/1_Conf_1.000	598	20	1.22E-60	XP_002640640.1	71	236.498	203	146	C. briggsae CBR-FRM-1 protein
Locus_8790_Transcript_1/1_Conf_1.000	254	0							
Locus_8791_Transcript_1/1_Conf_1.000	162	0							
Locus_8792_Transcript_1/1_Conf_1.000	887	20	1.19E-71	A8XFF4.2	67	274.248	297	201	Protein arginine N-methyltransferase 7
Locus_8793_Transcript_1/1_Conf_1.000	239	6	2.13E-20	AAT12422.1	78	102.064	79	62	hypothetical protein isoform a
Locus_8794_Transcript_1/1_Conf_1.000	583	20	2.26E-48	NP_507205.2	63	195.667	180	114	O-ACyltransferase homolog family member (oac-53)
Locus_8795_Transcript_1/1_Conf_1.000	294	0							
Locus_8796_Transcript_1/1_Conf_1.000	419	12	1.23E-07	XP_001161945.1	58	59.6918	68	40	PREDICTED: pleckstrin homology-like domain, family B, member 1 isoform 1
Locus_8797_Transcript_1/1_Conf_1.000	203	20	7.59E-10	EFO26165.1	63	67.0106	65	41	hypothetical protein LOAG_02323
Locus_8798_Transcript_1/1_Conf_1.000	552	20	1.43E-75	NP_492476.1	89	285.804	187	168	hypothetical protein F14B4.3
Locus_8799_Transcript_1/1_Conf_1.000	689	6	2.56E-48	NP_506082.2	63	196.052	233	148	hypothetical protein F55C5.7
Locus_88_Transcript_1/1_Conf_1.000	351	20	3.08E-27	ACI49235.1	83	124.79	103	86	hypothetical protein Csp3_JD06.001

Locus_880_Transcript_1/1_Conf_1.000	2673	20	0	NP_490744.1	83	980.704	718	603	fatty Acid CoA Synthetase family member (acs-13)
Locus_8800_Transcript_1/1_Conf_1.000	1147	19	9.34E-36	NP_001023856.1	48	155.606	360	174	hypothetical protein F26F12.3
Locus_8801_Transcript_1/1_Conf_1.000	782	5	1.65E-23	NP_001021410.2	59	114.005	149	89	LIM domain family member (lim-9)
Locus_8802_Transcript_1/1_Conf_1.000	378	0							
Locus_8803_Transcript_1/1_Conf_1.000	515	20	3.66E-42	XP_002640970.1	70	174.481	177	124	Hypothetical protein CBG11716
Locus_8804_Transcript_1/1_Conf_1.000	319	0							
Locus_8805_Transcript_1/2_Conf_1.000	2335	20	1.15E-106	ADE60683.1	72	392.504	339	247	Diacylglycerol kinase protein 4, isoform a, partially confirmed by transcript evidence

Locus_8805_Transcript_2/2_Conf_1.000	2323	20	1.14E-106	ADE60683.1	72	392.504	339	247	Diacylglycerol kinase protein 4, isoform a, partially confirmed by transcript evidence
Locus_8806_Transcript_1/2_Conf_1.000	461	0							
Locus_8806_Transcript_2/2_Conf_1.000	461	0							
Locus_8807_Transcript_1/1_Conf_1.000	606	20	1.84E-59	XP_002641254.1	78	232.646	185	145	C. briggsae CBR-DHS-9 protein
Locus_8808_Transcript_1/1_Conf_1.000	635	20	1.28E-61	NP_500216.1	76	239.965	211	162	hypothetical protein Y69A2AR.16
Locus_8809_Transcript_1/1_Conf_1.000	133	0							
Locus_881_Transcript_1/1_Conf_1.000	2797	20	4.17E-175	XP_002639624.1	62	620.157	820	516	C. briggsae CBR-LSS-4 protein
Locus_8810_Transcript_1/1_Conf_1.000	477	20	4.21E-53	XP_002641484.1	83	210.69	159	133	Hypothetical protein CBG09775
Locus_8811_Transcript_1/1_Conf_1.000	221	0							
Locus_8812_Transcript_1/1_Conf_1.000	148	2	5.01E-09	NP_498946.1	77	64.3142	45	35	hypothetical protein F54F2.7

Locus_8813_Transcript_1/1_Conf_1.000	692	20	9.12E-78	XP_001899166.1	80	293.893	208	167	GTP-ase activating protein for Arf containing protein
Locus_8814_Transcript_1/1_Conf_1.000	1128	20	1.66E-61	CAR63701.1	92	241.121	138	128	hypothetical protein
Locus_8815_Transcript_1/1_Conf_1.000	290	3	3.23E-08	ACI49149.1	69	61.6178	59	41	hypothetical protein Cbre_JD20.004
Locus_8816_Transcript_1/1_Conf_1.000	386	20	1.80E-11	EFO19656.1	57	72.4034	106	61	hypothetical protein LOAG_08835
Locus_8817_Transcript_1/1_Conf_1.000	435	20	2.75E-20	XP_002639937.1	88	101.679	71	63	Hypothetical protein CBG08274
Locus_8818_Transcript_1/1_Conf_1.000	623	0							
Locus_8819_Transcript_1/1_Conf_1.000	1006	20	1.89E-159	NP_498260.2	92	566.229	335	310	DEAD boX helicase homolog family member (ddx-23)
Locus_882_Transcript_1/1_Conf_1.000	445	20	1.65E-12	NP_491682.1	68	75.8702	93	64	MTK1/MEKK4 homolog family member (mtk-1)
Locus_8820_Transcript_1/1_Conf_1.000	696	0							
Locus_8821_Transcript_1/1_Conf_1.000	714	20	1.16E-46	NP_508439.2	63	190.66	235	149	hypothetical protein C43H6.1

Locus_8822_Transcript_1/1_Conf_1.000	1464	2	9.88E-07		72	59.6918	51	37	C02F5.1 protein
Locus_8823_Transcript_1/1_Conf_1.000	154	0							
Locus_8824_Transcript_1/3_Conf_0.714	1262	20	9.04E-71	XP_002631291.1	83	261.536	184	154	Hypothetical protein CBG03104
Locus_8824_Transcript_2/3_Conf_0.714	921	20	3.86E-76	NP_496245.1	81	289.271	212	173	hypothetical protein ZK673.2
Locus_8824_Transcript_3/3_Conf_0.714	1186	20	5.71E-76	NP_496245.1	81	289.271	212	173	hypothetical protein ZK673.2
Locus_8825_Transcript_1/1_Conf_1.000	139	0							
Locus_8826_Transcript_1/1_Conf_1.000	425	0							
Locus_8827_Transcript_1/2_Conf_1.000	773	20	3.10E-67	XP_002645151.1	91	259.225	157	143	C. briggsae CBR-TNT-3 protein
Locus_8827_Transcript_2/2_Conf_1.000	612	20	1.89E-67	XP_002645151.1	91	259.225	157	143	C. briggsae CBR-TNT-3 protein
Locus_8828_Transcript_1/1_Conf_1.000	159	0							
Locus_8829_Transcript_1/1_Conf_1.000	531	20	1.48E-39	XP_002643586.1	66	166.007	179	119	C. briggsae CBR-SYM-4 protein
Locus_883_Transcript_1/2_Conf_1.000	303	12	2.42E-24	NP_498341.1	72	115.161	94	68	hypothetical protein F42A10.7
Locus_883_Transcript_2/2_Conf_1.000	303	12	2.41E-24	NP_498341.1	72	115.161	94	68	hypothetical protein F42A10.7
Locus_8830_Transcript_1/1_Conf_1.000	411	20	1.01E-38	NP_503109.1	75	162.925	124	93	beta-LACTamase domain containing family member (lact-6)
Locus_8831_Transcript_1/1_Conf_1.000	589	20	8.09E-62	NP_508978.3	77	240.35	195	152	hypothetical protein F13D11.4
Locus_8832_Transcript_1/1_Conf_1.000	216	0							
Locus_8833_Transcript_1/2_Conf_1.000	648	20	6.45E-104	XP_002640347.1	94	380.563	216	205	C. briggsae CBR-HAF-9 protein

Locus_8833_Transcript_2/2_Conf_1.000	337	20	3.29E-53	CAP37340.2	95	211.075	112	107	CBR-HAF-9 protein
Locus_8834_Transcript_1/1_Conf_1.000	633	20	2.50E-57	NP_492322.1	88	225.713	133	118	associated with RAN (nuclear import/export) function family member (ran-4)
Locus_8835_Transcript_1/1_Conf_1.000	1411	20	3.52E-46	XP_002637954.1	55	190.66	391	218	Hypothetical protein CBG04771
Locus_8836_Transcript_1/2_Conf_1.000	677	2	2.32E-06	NP_001022338.1	67	56.6102	43	29	hypothetical protein T09F3.5
Locus_8836_Transcript_2/2_Conf_1.000	677	2	2.32E-06	NP_001022338.1	67	56.6102	43	29	hypothetical protein T09F3.5
Locus_8837_Transcript_1/1_Conf_1.000	409	20	8.85E-35	XP_002632524.1	78	149.828	118	93	Hypothetical protein CBG13772
Locus_8838_Transcript_1/2_Conf_1.000	1091	20	5.34E-102	NP_491765.2	68	375.555	344	236	hypothetical protein T27A3.2
Locus_8838_Transcript_2/2_Conf_1.000	1134	20	3.02E-103	NP_491765.2	68	379.793	348	239	hypothetical protein T27A3.2
Locus_8839_Transcript_1/1_Conf_1.000	838	2	2.21E-32	XP_001891951.1	53	143.665	277	149	hypothetical protein
Locus_884_Transcript_1/1_Conf_1.000	327	0							
Locus_8840_Transcript_1/1_Conf_1.000	1219	20	1.39E-32	XP_001899905.1	53	145.206	267	142	F-box domain containing protein
Locus_8841_Transcript_1/1_Conf_1.000	231	12	7.37E-13	XP_001897369.1	77	77.0258	61	47	Protein kinase domain containing protein

Locus_8842_Transcript_1/1_Conf_1.000	130	0							
Locus_8843_Transcript_1/1_Conf_1.000	318	0							
Locus_8844_Transcript_1/1_Conf_1.000	184	1	9.80E-05	ABI52743.1	53	50.0618	65	35	10 kDa putative secreted protein
Locus_8845_Transcript_1/1_Conf_1.000	619	9	1.46E-14	XP_002642159.1	51	83.5741	163	84	Hypothetical protein CBG18119
Locus_8846_Transcript_1/1_Conf_1.000	1078	20	5.91E-37	XP_002630854.1	66	159.458	206	138	C. briggsae CBR-RAN-5 protein
Locus_8847_Transcript_1/1_Conf_1.000	1521	20	7.92E-148	AAA18956.1	96	528.48	285	275	Sur-1 MAP kinase
Locus_8848_Transcript_1/1_Conf_1.000	1172	20	1.35E-29	XP_002644148.1	43	135.191	391	170	Hypothetical protein CBG04520
Locus_8849_Transcript_1/1_Conf_1.000	293	0							
Locus_885_Transcript_1/3_Conf_0.286	541	5	2.82E-09	NP_499247.2	57	65.4698	85	49	hypothetical protein ZK1128.2
Locus_885_Transcript_2/3_Conf_0.714	1766	20	2.50E-108	EFO26532.1	70	258.84	258	182	hypothetical protein LOAG_01952
Locus_885_Transcript_3/3_Conf_0.714	1750	20	1.52E-113	EFO26532.1	65	414.846	485	318	hypothetical protein LOAG_01952

Locus_8850_Transcript_1/1_Conf_1.000	1048	20	1.66E-105	NP_497416.4	79	387.111	294	235	Sodium:Neurotransmitter symporter Family family member (snf-6)
Locus_8851_Transcript_1/1_Conf_1.000	1212	16	6.84E-32	NP_001023856.1	46	142.895	370	172	hypothetical protein F26F12.3
Locus_8852_Transcript_1/1_Conf_1.000	242	0							
Locus_8853_Transcript_1/1_Conf_1.000	235	0							
Locus_8854_Transcript_1/1_Conf_1.000	302	2	8.66E-06	NP_494563.1	66	53.5286	60	40	hypothetical protein Y49F6B.2
Locus_8855_Transcript_1/1_Conf_1.000	1639	13	2.53E-30	EFO25015.1	46	138.272	380	177	hypothetical protein LOAG_03469
Locus_8856_Transcript_1/2_Conf_1.000	824	20	2.06E-51	NP_496985.1	85	206.838	129	110	hypothetical protein R06A4.9
Locus_8856_Transcript_2/2_Conf_1.000	1897	20	0	XP_001898532.1	81	770	528	430	wdc146
Locus_8857_Transcript_1/3_Conf_0.222	180	0							
Locus_8857_Transcript_2/3_Conf_0.556	677	20	9.43E-08	CAK12529.1	50	61.2326	155	78	putative group 3 late embryogenesis abundant protein
Locus_8857_Transcript_3/3_Conf_0.667	587	20	2.75E-09	NP_001024044.1	46	65.855	158	73	hypothetical protein K08H10.2
Locus_8858_Transcript_1/2_Conf_1.000	1264	20	1.68E-105	XP_002631048.1	81	387.497	310	253	Hypothetical protein CBG02810
Locus_8858_Transcript_2/2_Conf_1.000	381	2	3.63E-12	NP_496794.1	73	74.7146	90	66	hypothetical protein F32A11.1

Locus_8859_Transcript_1/1_Conf_1.000	589	14	1.65E-14	XP_002646138.1	48	83.1889	189	91	Hypothetical protein CBG08018
Locus_886_Transcript_1/3_Conf_0.714	3456	20	3.34E-161	NP_494929.3	60	574.318	892	536	hypothetical protein F33G12.5
Locus_886_Transcript_2/3_Conf_0.714	3501	20	5.39E-167	NP_494929.3	60	593.578	897	546	hypothetical protein F33G12.5
Locus_886_Transcript_3/3_Conf_0.714	3486	20	7.49E-169	NP_494929.3	61	599.742	892	546	hypothetical protein F33G12.5
Locus_8860_Transcript_1/1_Conf_1.000	563	20	7.62E-64	XP_973257.1	76	246.899	180	138	PREDICTED: similar to adp,atp carrier protein
Locus_8861_Transcript_1/1_Conf_1.000	372	20	1.89E-08	XP_001629102.1	91	62.3882	35	32	predicted protein
Locus_8862_Transcript_1/1_Conf_1.000	329	4	1.43E-08	EFO17660.1	51	62.7734	97	50	zinc finger protein
Locus_8863_Transcript_1/1_Conf_1.000	643	20	1.62E-67	NP_502295.1	78	259.61	199	156	yeast MON (monensin-resistant) homolog family member (mon-2)
Locus_8864_Transcript_1/1_Conf_1.000	262	20	1.02E-38	XP_002635291.1	91	162.925	87	80	Hypothetical protein CBG11538
Locus_8865_Transcript_1/1_Conf_1.000	458	20	7.16E-61	XP_002745056.1	95	236.498	143	137	PREDICTED: 40S ribosomal protein S24-like
Locus_8866_Transcript_1/1_Conf_1.000	633	20	3.85E-58	EFO15888.1	71	228.409	196	141	mediator protein 20

Locus_8867_Transcript_1/1_Conf_1.000	470	20	3.26E-61	NP_001021979.1	90	237.654	156	141	Serine Palmitoyl Transferase famiLy family member (sptl-1)
Locus_8868_Transcript_1/1_Conf_1.000	200	20	3.64E-28	EDL24575.1	95	127.872	66	63	mCG140959, isoform CRA_e
Locus_8869_Transcript_1/1_Conf_1.000	879	20	7.61E-87	AAC39119.1	78	324.709	239	187	low-affinity peptide transporter
Locus_887_Transcript_1/2_Conf_1.000	1113	0							
Locus_887_Transcript_2/2_Conf_1.000	894	0							
Locus_8870_Transcript_1/2_Conf_1.000	494	20	9.17E-40	XP_002640765.1	94	166.392	85	80	C. briggsae CBR-CKS-1 protein
Locus_8870_Transcript_2/2_Conf_1.000	485	20	9.29E-40	XP_002640765.1	94	166.392	85	80	C. briggsae CBR-CKS-1 protein
Locus_8871_Transcript_1/1_Conf_1.000	368	20	1.82E-40	ACJ01664.1	79	168.703	122	97	DAF-12 C4

Locus_8872_Transcript_1/1_Conf_1.000	330	20	2.66E-39	AAF82410.1	88	164.851	109	96	AF221132_1diacylglycerol acyltransferase
Locus_8873_Transcript_1/1_Conf_1.000	472	17	1.13E-05	ZP_05118388.1	47	53.1434	143	68	peptidase S1 and S6, chymotrypsin/Hap
Locus_8874_Transcript_1/1_Conf_1.000	319	20	1.74E-54	ADK47995.1	100	215.312	106	106	c-myc promoter-binding protein 1
Locus_8875_Transcript_1/1_Conf_1.000	549	20	1.38E-30	XP_001894778.1	55	136.346	200	111	Pyridine nucleotide-disulphide oxidoreductase family protein
Locus_8876_Transcript_1/1_Conf_1.000	247	20	7.25E-13	NP_508461.1	85	77.0258	71	61	Amino Acid Transporter family member (aat-3)
Locus_8877_Transcript_1/1_Conf_1.000	327	20	7.32E-21	NP_741234.1	72	103.605	91	66	hypothetical protein C29E4.12
Locus_8878_Transcript_1/1_Conf_1.000	1203	20	4.44E-100	NP_490725.2	70	369.392	351	249	hypothetical protein R119.2
Locus_8879_Transcript_1/1_Conf_1.000	147	2	1.08E-19	XP_002824585.1	100	99.7525	48	48	PREDICTED: hypothetical protein LOC100433574
Locus_888_Transcript_1/1_Conf_1.000	501	20	3.51E-63	NP_501223.1	88	244.202	141	125	DIFferentiation abnormal family member (dif-1)
Locus_8880_Transcript_1/1_Conf_1.000	167	0							
Locus_8881_Transcript_1/1_Conf_1.000	273	0							
Locus_8882_Transcript_1/1_Conf_1.000	671	20	4.39E-42	XP_002630027.1	80	175.252	171	138	Hypothetical protein CBG13394
Locus_8883_Transcript_1/1_Conf_1.000	425	0							

Locus_8884_Transcript_1/1_Conf_1.000	1229	20	0	NP_001023451.1	93	649.432	382	357	Vacuolar H ATPase family member (vha-11)
Locus_8885_Transcript_1/1_Conf_1.000	1620	20	9.71E-176	NP_502354.2	80	621.313	475	382	yeast SEC homolog family member (sec-24.2)
Locus_8886_Transcript_1/1_Conf_1.000	1301	0							
Locus_8887_Transcript_1/1_Conf_1.000	876	20	2.03E-132	AAX42917.1	99	476.093	252	251	serine protease inhibitor Kunitz type 2
Locus_8888_Transcript_1/1_Conf_1.000	439	20	3.68E-33	CBK19483.1	66	144.436	136	90	C. elegans protein Y116A8C.27b, confirmed by transcript evidence
Locus_8889_Transcript_1/1_Conf_1.000	1564	20	6.03E-42	NP_504247.2	52	176.792	443	233	hypothetical protein F54D11.2
Locus_889_Transcript_1/1_Conf_1.000	1883	20	4.24E-125	NP_740883.1	66	453.366	511	338	hypothetical protein F15C11.2

Locus_8890_Transcript_1/1_Conf_1.000	923	20	8.86E-89	XP_002630114.1	70	331.257	312	220	C. briggsae CBR-PYR-1 protein
Locus_8891_Transcript_1/1_Conf_1.000	606	20	1.40E-91	NP_492587.1	86	339.347	201	174	GEI-4(Four) Interacting protein family member (gfi-2)
Locus_8892_Transcript_1/1_Conf_1.000	347	1	2.83E-04	XP_002643135.1	56	48.521	85	48	Hypothetical protein CBG15312
Locus_8893_Transcript_1/1_Conf_1.000	889	20	7.22E-101	XP_002629959.1	75	371.318	295	224	Hypothetical protein CBG03683
Locus_8894_Transcript_1/1_Conf_1.000	1053	20	6.62E-94	NP_509282.2	76	348.591	297	227	Temporarily Assigned Gene name family member (tag-197)
Locus_8895_Transcript_1/1_Conf_1.000	250	20	3.81E-30	ADF56001.1	98	134.42	82	81	nicotinic acetylcholine receptor alpha subunit 38
Locus_8896_Transcript_1/1_Conf_1.000	352	0							
Locus_8897_Transcript_1/2_Conf_1.000	904	20	3.19E-35	NP_499252.2	81	153.295	109	89	hypothetical protein ZK1128.7

Locus_8897_Transcript_2/2_Conf_1.000	948	20	3.48E-35	NP_499252.2	81	153.295	109	89	hypothetical protein ZK1128.7
Locus_8898_Transcript_1/1_Conf_1.000	585	20	5.84E-52	NP_001123151.1	77	207.608	172	133	hypothetical protein F55A4.8
Locus_8899_Transcript_1/1_Conf_1.000	153	20	1.76E-22	XP_002917905.1	100	108.997	50	50	PREDICTED: nucleobindin-1-like
Locus_89_Transcript_2/3_Conf_0.333	2094	20	0	NP_001021542.1	86	1013.83	660	573	BLIstered cuticle family member (bli-4)
Locus_89_Transcript_3/3_Conf_0.500	3188	20	0	NP_001021543.1	82	1325.46	917	752	BLIstered cuticle family member (bli-4)
Locus_890_Transcript_1/1_Conf_1.000	703	0							
Locus_8900_Transcript_1/1_Conf_1.000	529	20	1.46E-31	NP_504540.2	64	139.428	171	111	hypothetical protein C04E6.11
Locus_8901_Transcript_1/3_Conf_0.571	1935	20	1.46E-112	XP_002630472.1	68	411.764	385	264	Hypothetical protein CBG11206
Locus_8901_Transcript_2/3_Conf_0.714	2273	20	8.21E-118	XP_002630472.1	61	429.483	477	295	Hypothetical protein CBG11206
Locus_8901_Transcript_3/3_Conf_0.571	1941	20	1.46E-112	XP_002630472.1	68	411.764	385	264	Hypothetical protein CBG11206

Locus_8902_Transcript_1/1_Conf_1.000	610	20	5.66E-40	XP_002630921.1	61	167.933	193	118	Hypothetical protein CBG02647
Locus_8903_Transcript_1/1_Conf_1.000	312	20	3.56E-39	XP_002633437.1	85	164.466	103	88	C. briggsae CBR-UNC-22 protein
Locus_8904_Transcript_1/1_Conf_1.000	593	20	8.58E-27	NP_494807.1	61	124.02	152	93	Variable ABnormal morphology family member (vab-1)
Locus_8905_Transcript_1/1_Conf_1.000	218	0							
Locus_8906_Transcript_1/2_Conf_1.000	363	6	1.91E-13	EFO27506.1	95	78.9518	43	41	hypothetical protein LOAG_00970
Locus_8906_Transcript_2/2_Conf_1.000	407	0							
Locus_8907_Transcript_1/1_Conf_1.000	224	20	1.11E-16	XP_002639771.1	81	89.7373	71	58	Hypothetical protein CBG02217
Locus_8908_Transcript_1/3_Conf_0.750	2029	20	2.87E-167	XP_002631785.1	71	593.578	571	408	Hypothetical protein CBG20998
Locus_8908_Transcript_2/3_Conf_0.750	2029	20	2.87E-167	XP_002631785.1	71	593.578	571	408	Hypothetical protein CBG20998
Locus_8908_Transcript_3/3_Conf_0.750	2029	20	2.87E-167	XP_002631785.1	71	593.578	571	408	Hypothetical protein CBG20998
Locus_8909_Transcript_1/1_Conf_1.000	247	1	5.94E-07	CAG28316.1	72	57.3806	43	31	spindle assembly abnormal protein 5, SAS-5
Locus_891_Transcript_1/1_Conf_1.000	760	0							
Locus_8910_Transcript_1/1_Conf_1.000	259	1	6.30E-04	AAO12213.1	61	47.3654	39	24	serine protease 1
Locus_8911_Transcript_1/1_Conf_1.000	884	20	8.66E-123	XP_002645904.1	86	444.121	294	254	C. briggsae CBR-MRP-5 protein
Locus_8912_Transcript_1/2_Conf_1.000	1881	20	0	NP_495537.1	73	696.427	608	449	HAIF transporter (PGP related) family member (haf-2)

Locus_8912_Transcript_2/2_Conf_1.000	1881	20	0	NP_495537.1	73	696.427	608	449	HAlF transporter (PGP related) family member (haf-2)
Locus_8913_Transcript_1/2_Conf_1.000	795	20	1.18E-48	XP_002630890.1	80	197.593	172	139	Hypothetical protein CBG02611
Locus_8913_Transcript_2/2_Conf_1.000	594	20	3.31E-26	XP_002630890.1	78	122.094	117	92	Hypothetical protein CBG02611
Locus_8914_Transcript_1/1_Conf_1.000	372	4	9.99E-18	NP_505689.1	63	93.2041	126	80	hypothetical protein Y32F6B.1
Locus_8915_Transcript_1/1_Conf_1.000	1023	20	2.52E-74	CBI63220.1	83	283.493	191	159	C. elegans protein F53A2.6a, confirmed by transcript evidence
Locus_8916_Transcript_1/1_Conf_1.000	641	20	7.51E-25	NP_499644.1	79	117.857	92	73	hypothetical protein Y111B2A.13
Locus_8917_Transcript_1/1_Conf_1.000	636	0							
Locus_8918_Transcript_1/1_Conf_1.000	863	20	7.91E-89	NP_506413.1	79	331.257	283	224	hypothetical protein F53C11.3
Locus_8919_Transcript_1/1_Conf_1.000	324	4	1.81E-11	XP_002639110.1	74	72.4034	62	46	C. briggsae CBR-ELO-8 protein
Locus_892_Transcript_1/1_Conf_1.000	1677	20	4.05E-132	EFO19476.1	94	476.478	286	269	hypothetical protein LOAG_09017

Locus_8920_Transcript_1/1_Conf_1.000	876	20	6.52E-22	BAH83642.1	63	108.997	128	81	AP-2
Locus_8921_Transcript_1/1_Conf_1.000	502	0							
Locus_8922_Transcript_1/1_Conf_1.000	130	20	5.78E-18	XP_002825166.1	100	93.9745	43	43	PREDICTED: cytoplasmic dynein 1 heavy chain 1-like, partial
Locus_8923_Transcript_1/1_Conf_1.000	365	20	4.85E-17	XP_002636354.1	57	90.8929	114	65	Hypothetical protein CBG08651
Locus_8924_Transcript_1/1_Conf_1.000	943	20	1.91E-110	XP_001894879.1	85	403.29	280	239	Dedicator of cytokinesis family protein
Locus_8925_Transcript_1/1_Conf_1.000	158	0							
Locus_8926_Transcript_1/3_Conf_0.600	861	10	8.37E-06	XP_795905.1	45	55.4546	171	78	PREDICTED: similar to cyclin B3
Locus_8926_Transcript_2/3_Conf_0.400	685	14	5.35E-06	XP_795905.1	45	55.4546	171	78	PREDICTED: similar to cyclin B3
Locus_8926_Transcript_3/3_Conf_0.600	978	10	1.03E-05	XP_795905.1	45	55.4546	171	78	PREDICTED: similar to cyclin B3

Locus_8927_Transcript_1/1_Conf_1.000	2101	20	0	ACY39994.1	79	845.114	681	540	C. elegans FLN-2 protein, isoform d
Locus_8928_Transcript_1/1_Conf_1.000	298	0							
Locus_8929_Transcript_1/1_Conf_1.000	636	0							
Locus_893_Transcript_1/1_Conf_1.000	1742	20	1.01E-125	NP_502036.1	78	455.292	390	306	hypothetical protein ZK593.8
Locus_8930_Transcript_1/1_Conf_1.000	953	20	4.88E-122	XP_002630884.1	94	441.81	294	278	C. briggsae CBR-PHB-2 protein
Locus_8931_Transcript_1/1_Conf_1.000	1004	20	7.73E-113	XP_002649082.1	89	411.379	266	237	C. briggsae CBR-HAF-4 protein
Locus_8932_Transcript_1/1_Conf_1.000	475	0							
Locus_8933_Transcript_1/1_Conf_1.000	516	0							
Locus_8934_Transcript_1/1_Conf_1.000	350	20	4.16E-40	XP_002642654.1	83	167.548	104	87	C. briggsae CBR-PCP-1.1 protein
Locus_8935_Transcript_1/1_Conf_1.000	443	2	3.92E-30	XP_002638582.1	66	134.42	148	99	Hypothetical protein CBG05629
Locus_8936_Transcript_1/1_Conf_1.000	282	0							
Locus_8937_Transcript_1/1_Conf_1.000	162	0							
Locus_8938_Transcript_1/1_Conf_1.000	462	13	3.42E-34	NP_001021706.1	80	147.902	101	81	hypothetical protein Y106G6D.8
Locus_8939_Transcript_1/1_Conf_1.000	484	20	4.92E-49	NP_499001.1	74	197.208	162	121	hypothetical protein R107.2
Locus_894_Transcript_1/1_Conf_1.000	348	0							
Locus_8940_Transcript_1/1_Conf_1.000	701	20	1.73E-39	NP_492382.2	80	166.777	116	93	hypothetical protein F36A2.8
Locus_8941_Transcript_1/1_Conf_1.000	1519	0							

Locus_8942_Transcript_1/1_Conf_1.000	888	20	2.81E-129	XP_002646930.1	93	465.692	290	270	Hypothetical protein CBG19635
Locus_8943_Transcript_1/1_Conf_1.000	773	20	2.71E-71	NP_498544.1	76	272.707	224	172	hypothetical protein ZK418.5
Locus_8944_Transcript_1/2_Conf_1.000	1496	20	1.62E-121	CAB05598.2	69	441.039	496	347	C. elegans protein R11A5.1a, partially confirmed by transcript evidence
Locus_8944_Transcript_2/2_Conf_1.000	922	20	1.75E-44	CAB05601.2	60	184.111	305	184	C. elegans protein R11A5.1b, partially confirmed by transcript evidence
Locus_8945_Transcript_1/2_Conf_1.000	604	0							
Locus_8945_Transcript_2/2_Conf_1.000	601	0							
Locus_8946_Transcript_1/1_Conf_1.000	564	11	1.81E-20	NP_504170.1	68	102.834	115	79	Neuropeptide-Like Protein family member (nlp-13)
Locus_8947_Transcript_1/1_Conf_1.000	515	0							
Locus_8948_Transcript_1/1_Conf_1.000	369	0							
Locus_8949_Transcript_1/1_Conf_1.000	139	0							
Locus_895_Transcript_1/1_Conf_1.000	1000	20	3.05E-77	NP_491855.1	70	293.123	333	235	Nuclear Pore complex Protein family member (npp-12)
Locus_8950_Transcript_1/1_Conf_1.000	644	4	1.17E-25	XP_002638473.1	53	120.553	214	115	Hypothetical protein CBG12901
Locus_8951_Transcript_1/1_Conf_1.000	412	20	1.31E-38	AAQ75756.1	81	162.54	103	84	zinc metallopeptidase 6
Locus_8952_Transcript_1/1_Conf_1.000	634	20	1.06E-31	EFO22999.1	74	140.584	174	129	hypothetical protein LOAG_05485
Locus_8953_Transcript_1/1_Conf_1.000	1077	20	1.42E-123	NP_001021728.1	85	447.203	362	309	Na/H eXchanger family member (nhx-8)

Locus_8954_Transcript_1/1_Conf_1.000	815	20	2.26E-103	NP_495800.1	85	379.407	237	202	hypothetical protein T13H5.5
Locus_8955_Transcript_1/1_Conf_1.000	158	0							
Locus_8956_Transcript_1/1_Conf_1.000	978	3	1.82E-10	XP_002642436.1	43	71.2478	318	137	Hypothetical protein CBG06840
Locus_8957_Transcript_1/1_Conf_1.000	619	0							
Locus_8958_Transcript_1/1_Conf_1.000	276	0							
Locus_8959_Transcript_1/1_Conf_1.000	761	20	5.69E-42	NP_498935.1	74	175.252	167	124	MiTochondrial Single Stranded DNA binding protein family member (mtss-1)
Locus_896_Transcript_1/6_Conf_0.667	2520	20	0	XP_002641666.1	85	1089.72	764	654	C. briggsae CBR-MCM-6 protein
Locus_896_Transcript_2/6_Conf_0.667	2516	20	0	XP_002641666.1	85	1089.72	764	654	C. briggsae CBR-MCM-6 protein

Locus_896_Transcript_3/6_Conf_0.667	2516	20	0	XP_002641666.1	85	1089.72	764	654	C. briggsae CBR-MCM-6 protein
Locus_896_Transcript_4/6_Conf_0.667	2516	20	0	XP_002641666.1	85	1089.72	764	654	C. briggsae CBR-MCM-6 protein
Locus_896_Transcript_5/6_Conf_0.667	2516	20	0	XP_002641666.1	85	1089.72	764	654	C. briggsae CBR-MCM-6 protein

Locus_896_Transcript_6/6_Conf_0.667	2516	20	0	XP_002641666.1	85	1089.72	764	654	C. briggsae CBR-MCM-6 protein
Locus_8960_Transcript_1/1_Conf_1.000	178	0							
Locus_8961_Transcript_1/1_Conf_1.000	310	0							
Locus_8962_Transcript_1/1_Conf_1.000	1315	20	1.07E-142	XP_002632302.1	72	511.146	411	300	Hypothetical protein CBG07203
Locus_8963_Transcript_1/1_Conf_1.000	198	20	9.59E-21	NP_001020988.1	85	103.219	63	54	UNCoordinated family member (unc-89)

Locus_8964_Transcript_1/1_Conf_1.000	506	20	3.38E-53	NP_509229.1	76	211.075	169	130	SUppressor of activated let-60 Ras family member (sur-5)
Locus_8965_Transcript_1/1_Conf_1.000	614	20	7.20E-59	NP_506513.1	75	230.72	184	139	TRNA Methylase family member (trm-1)
Locus_8966_Transcript_1/1_Conf_1.000	272	0							
Locus_8967_Transcript_1/1_Conf_1.000	189	0							
Locus_8968_Transcript_1/1_Conf_1.000	249	20	5.33E-24	NP_491246.4	82	114.005	82	68	COenzyme Q (ubiquinone) biosynthesis family member (coq-4)
Locus_8969_Transcript_1/1_Conf_1.000	372	0							
Locus_897_Transcript_1/3_Conf_0.294	364	0							
Locus_897_Transcript_2/3_Conf_0.412	401	2	2.22E-09	ABB53347.1	56	65.4698	72	41	secreted protein 5 precursor
Locus_897_Transcript_3/3_Conf_0.824	453	1	3.63E-04	ABB53347.1	55	48.1358	76	42	secreted protein 5 precursor
Locus_8970_Transcript_1/1_Conf_1.000	551	0							
Locus_8971_Transcript_1/1_Conf_1.000	556	20	1.42E-62	AAC78238.2	79	242.662	191	151	Guanylyl cyclase protein 28, isoform d
Locus_8972_Transcript_1/1_Conf_1.000	433	20	9.49E-21	XP_001893053.1	70	103.219	109	77	hypothetical protein
Locus_8973_Transcript_1/1_Conf_1.000	830	4	1.45E-36	NP_001022299.1	65	157.532	147	97	hypothetical protein T01E8.8
Locus_8974_Transcript_1/1_Conf_1.000	1085	20	4.32E-112	NP_502898.1	82	409.068	281	231	hypothetical protein Y105C5B.9
Locus_8975_Transcript_1/1_Conf_1.000	671	20	2.47E-61	NP_497657.1	78	239.195	195	154	SurFeit homolog family member (sft-1)
Locus_8976_Transcript_1/2_Conf_1.000	394	1	1.66E-04	ZP_01156726.1	51	49.2914	62	32	helicase, putative
Locus_8976_Transcript_2/2_Conf_1.000	312	1	1.67E-04	ZP_01156726.1	51	49.2914	62	32	helicase, putative
Locus_8977_Transcript_1/1_Conf_1.000	136	0							
Locus_8978_Transcript_1/1_Conf_1.000	167	0							
Locus_8979_Transcript_1/1_Conf_1.000	238	0							

Locus_898_Transcript_1/2_Conf_1.000	308	20	2.95E-14	NP_501241.1	85	81.6481	62	53	Pur alpha Like Protein family member (plp-1)
Locus_898_Transcript_2/2_Conf_1.000	829	20	3.21E-60	EFO17451.1	73	236.113	241	176	PurA ssDNA and RNA-binding protein
Locus_8980_Transcript_1/1_Conf_1.000	1046	4	2.38E-11	NP_502521.2	52	74.3294	218	114	hypothetical protein B0564.7
Locus_8981_Transcript_1/1_Conf_1.000	404	20	9.17E-56	XP_002629896.1	85	219.55	134	114	Hypothetical protein CBG21934
Locus_8982_Transcript_1/1_Conf_1.000	291	0							
Locus_8983_Transcript_1/1_Conf_1.000	512	0							
Locus_8984_Transcript_1/1_Conf_1.000	1129	20	2.15E-101	NP_497943.2	75	373.629	377	285	hypothetical protein F10F2.4
Locus_8985_Transcript_1/1_Conf_1.000	433	5	2.39E-56	A8XP97.2	83	221.476	144	120	Voltage-dependent calcium channel unc-36
Locus_8986_Transcript_1/2_Conf_1.000	202	0							

Locus_8986_Transcript_2/2_Conf_1.000	652	20	4.16E-42	CAR63706.1	89	175.252	115	103	putative FOS (B-Zip transcription factor) homolog family member
Locus_8987_Transcript_1/1_Conf_1.000	1371	5	3.62E-64	XP_002642202.1	54	250.366	410	222	Hypothetical protein CBG18175
Locus_8988_Transcript_1/1_Conf_1.000	509								
Locus_8989_Transcript_1/1_Conf_1.000	1550	20	9.67E-93	NP_492602.1	59	345.51	519	307	HRD-Like (E3 ubiquitin ligase related) family member (hrdl-1)
Locus_899_Transcript_1/3_Conf_0.667	615	6	1.76E-12	XP_002632465.1	57	76.6406	97	56	C. briggsae CBR-JAC-1 protein
Locus_899_Transcript_2/3_Conf_0.667	619	6	1.79E-12	XP_002632465.1	57	76.6406	97	56	C. briggsae CBR-JAC-1 protein
Locus_899_Transcript_3/3_Conf_0.667	615	6	1.76E-12	XP_002632465.1	57	76.6406	97	56	C. briggsae CBR-JAC-1 protein
Locus_8990_Transcript_1/1_Conf_1.000	1258	20	4.21E-141	XP_002647075.1	94	505.753	272	256	C. briggsae CBR-PAT-3 protein
Locus_8991_Transcript_1/1_Conf_1.000	262	3	1.44E-08	NP_498871.2	58	62.7734	87	51	hypothetical protein F42H10.5
Locus_8992_Transcript_1/2_Conf_1.000	224	0							
Locus_8992_Transcript_2/2_Conf_1.000	681	2	9.02E-06	NP_001041088.1	41	54.6842	230	95	hypothetical protein C27A7.3

Locus_8993_Transcript_1/1_Conf_1.000	664	20	4.71E-65	NP_499755.1	87	251.521	173	152	LIS-1 (human lissencephaly gene) related family member (lis-1)
Locus_8994_Transcript_1/1_Conf_1.000	1562	20	1.79E-70	XP_002639296.1	55	271.552	495	274	Hypothetical protein CBG03866
Locus_8995_Transcript_1/1_Conf_1.000	866	20	1.78E-80	NP_741661.1	75	303.523	260	195	hypothetical protein Y39B6A.36
Locus_8996_Transcript_1/1_Conf_1.000	1042	20	2.54E-106	NP_001122738.1	72	389.808	332	242	hypothetical protein Y67D2.4
Locus_8997_Transcript_1/1_Conf_1.000	548	20	1.82E-51	NP_499777.1	90	205.682	123	111	hypothetical protein F45G2.10
Locus_8998_Transcript_1/1_Conf_1.000	2417	20	5.85E-53	EFO26605.1	50	214.157	484	242	hypothetical protein LOAG_01878
Locus_8999_Transcript_1/1_Conf_1.000	179	0							

Locus_9_Transcript_1/5_Conf_0.750	2646	20	0	XP_002646785.1	88	1246.11	832	733	C. briggsae CBR-MCM-2 protein
Locus_9_Transcript_2/5_Conf_0.750	2646	20	0	XP_002646785.1	88	1246.11	832	733	C. briggsae CBR-MCM-2 protein
Locus_9_Transcript_3/5_Conf_0.750	2646	20	0	XP_002646785.1	88	1246.11	832	733	C. briggsae CBR-MCM-2 protein

Locus_9_Transcript_4/5_Conf_0.750	2646	20	0	XP_002646785.1	88	1246.11	832	733	C. briggsae CBR-MCM-2 protein
Locus_9_Transcript_5/5_Conf_0.750	2646	20	0	XP_002646785.1	88	1246.11	832	733	C. briggsae CBR-MCM-2 protein
Locus_90_Transcript_1/1_Conf_1.000	221	2	4.69E-07	P27613.1	85	57.7658	35	30	Globin-like host-protective antigen
Locus_900_Transcript_1/1_Conf_1.000	1374	20	0	XP_002636570.1	94	756.133	457	430	C. briggsae CBR-PYC-1 protein
Locus_9000_Transcript_1/1_Conf_1.000	1218	20	1.15E-119	AAK31453.4	71	434.491	421	300	Hypothetical protein C25H3.8

Locus_9001_Transcript_1/1_Conf_1.000	214	20	2.32E-19	Q5RE15.2	100	98.5969	47	47	26S proteasome non-ATPase regulatory subunit 8
Locus_9002_Transcript_1/1_Conf_1.000	1149	20	3.37E-118	EFO26333.1	78	429.483	325	254	hypothetical protein LOAG_02157
Locus_9003_Transcript_1/1_Conf_1.000	567	20	2.93E-26	EFO27926.1	70	122.094	132	93	hypothetical protein LOAG_00563
Locus_9004_Transcript_1/1_Conf_1.000	638	20	6.17E-88	XP_002634875.1	89	327.405	211	188	Hypothetical protein CBG10541
Locus_9005_Transcript_1/1_Conf_1.000	1537	5	1.20E-18	XP_001899377.1	62	99.3673	141	88	hypothetical protein Bm1_39610
Locus_9006_Transcript_1/1_Conf_1.000	489	20	1.63E-36	NP_505849.2	66	155.606	160	107	hypothetical protein T19B10.3
Locus_9007_Transcript_1/1_Conf_1.000	273	20	3.72E-33	AAK29933.3	90	144.436	91	82	Rab connectin related protein 2, partially confirmed by transcript evidence
Locus_9008_Transcript_1/1_Conf_1.000	1785	20	6.90E-53	XP_001900516.1	52	213.386	455	241	hypothetical protein Bm1_45270
Locus_9009_Transcript_1/1_Conf_1.000	128	0							
Locus_901_Transcript_1/1_Conf_1.000	431	0							
Locus_9010_Transcript_1/1_Conf_1.000	1025	20	4.06E-40	XP_001896056.1	55	169.859	346	192	hypothetical protein
Locus_9011_Transcript_1/1_Conf_1.000	773	20	6.29E-44	EFO25106.1	57	181.8	258	149	hypothetical protein LOAG_03373
Locus_9012_Transcript_1/1_Conf_1.000	1015	20	5.17E-72	XP_002631797.1	73	275.789	334	247	C. briggsae CBR-CYN-16 protein
Locus_9013_Transcript_1/1_Conf_1.000	504	20	6.17E-47	XP_001896343.1	69	190.274	163	114	Arginine-tRNA-protein transferase, C terminus containing protein
Locus_9014_Transcript_1/1_Conf_1.000	1103	20	2.84E-159	XP_002639536.1	91	565.844	338	308	C. briggsae CBR-FBP-1 protein
Locus_9015_Transcript_1/1_Conf_1.000	577	11	1.34E-13	XP_002643226.1	52	80.1073	140	74	Hypothetical protein CBG08091
Locus_9016_Transcript_1/3_Conf_0.714	1450	20	1.15E-124	EFO15931.1	69	451.44	399	279	hypothetical protein LOAG_12577

Locus_9016_Transcript_2/3_Conf_0.714	1450	20	1.96E-124	EFO15931.1	69	450.669	399	279	hypothetical protein LOAG_12577
Locus_9016_Transcript_3/3_Conf_0.714	1450	20	1.15E-124	EFO15931.1	69	451.44	399	279	hypothetical protein LOAG_12577
Locus_9017_Transcript_1/1_Conf_1.000	216	0							
Locus_9018_Transcript_1/10_Conf_0.077	246	20	1.27E-41	ABU86835.1	97	172.555	81	79	MHC class I antigen
Locus_9018_Transcript_10/10_Conf_0.500	616	20	6.28E-119	AAA03661.1	98	430.254	205	202	lymphocyte antigen
Locus_9018_Transcript_2/10_Conf_0.385	689	20	3.49E-130	CBW44114.1	97	468.003	229	223	MHC class I antigen
Locus_9018_Transcript_3/10_Conf_0.192	277	20	7.43E-50	CBX19818.1	100	199.904	92	92	MHC class I antigen
Locus_9018_Transcript_4/10_Conf_0.115	345	20	4.14E-64	ADN92657.1	100	247.284	115	115	MHC class I antigen
Locus_9018_Transcript_5/10_Conf_0.115	286	20	1.26E-52	ADN92581.1	100	209.149	95	95	MHC class I antigen

Locus_9018_Transcript_6/10_Conf_0.115	265	20	2.68E-47	BAI50007.1	100	191.43	88	88	MHC class I antigen
Locus_9018_Transcript_7/10_Conf_0.423	616	20	3.94E-113	CBV36823.1	99	410.994	205	203	MHC class I antigen
Locus_9018_Transcript_8/10_Conf_0.385	538	20	3.41E-100	ABS29696.1	96	367.466	179	173	MHC class I antigen
Locus_9018_Transcript_9/10_Conf_0.115	418	20	1.25E-76	CAD62286.1	97	288.886	139	136	MHC class I antigen
Locus_9019_Transcript_1/1_Conf_1.000	683	20	1.61E-71	XP_002633890.1	84	273.092	174	147	Hypothetical protein CBG19952
Locus_902_Transcript_1/1_Conf_1.000	520	20	3.82E-50	AAN11401.1	71	201.06	156	112	metalloprotease 1 precursor
Locus_9020_Transcript_1/2_Conf_1.000	879	20	7.85E-92	NP_506824.1	76	341.273	262	201	hypothetical protein T06E6.1
Locus_9020_Transcript_2/2_Conf_1.000	879	20	7.85E-92	NP_506824.1	76	341.273	262	201	hypothetical protein T06E6.1
Locus_9021_Transcript_1/1_Conf_1.000	150	1	2.84E-04	ACY03364.1	71	48.521	35	25	facilitative hexose transporter
Locus_9022_Transcript_1/1_Conf_1.000	131	0							

Locus_9023_Transcript_1/3_Conf_0.333	255	20	3.12E-19	EFO19966.1	72	98.2117	83	60	hypothetical protein LOAG_08525
Locus_9023_Transcript_2/3_Conf_0.667	1119	20	7.44E-147	EFO19966.1	82	524.628	371	307	hypothetical protein LOAG_08525
Locus_9023_Transcript_3/3_Conf_0.667	1119	20	6.30E-146	EFO19966.1	82	521.546	371	306	hypothetical protein LOAG_08525
Locus_9024_Transcript_1/1_Conf_1.000	476	0							
Locus_9025_Transcript_1/1_Conf_1.000	452	0							
Locus_9026_Transcript_1/1_Conf_1.000	1635	20	4.86E-74	EFO26882.1	55	283.493	565	316	synembryn
Locus_9027_Transcript_1/1_Conf_1.000	137	0							
Locus_9028_Transcript_1/1_Conf_1.000	438	6	1.84E-16	XP_002631371.1	58	88.9669	140	82	Hypothetical protein CBG03213
Locus_9029_Transcript_1/1_Conf_1.000	546	20	9.38E-32	NP_501279.1	79	140.198	103	82	human HCF1 related family member (hcf-1)
Locus_903_Transcript_1/3_Conf_0.667	398	4	4.80E-12	XP_002640867.1	70	74.3294	60	42	Hypothetical protein CBG15758
Locus_903_Transcript_2/3_Conf_0.500	455	4	1.16E-10	XP_002640867.1	65	69.707	61	40	Hypothetical protein CBG15758
Locus_903_Transcript_3/3_Conf_0.667	416	4	4.68E-12	XP_002640867.1	70	74.3294	60	42	Hypothetical protein CBG15758
Locus_9030_Transcript_1/1_Conf_1.000	689	6	1.47E-11	NP_502195.3	58	73.9442	129	75	hypothetical protein F58B3.4
Locus_9031_Transcript_1/1_Conf_1.000	1014	20	9.02E-109	XP_002638606.1	75	397.897	337	253	Hypothetical protein CBG05657
Locus_9032_Transcript_1/1_Conf_1.000	245	0							
Locus_9033_Transcript_1/2_Conf_1.000	323	2	2.54E-05	CAT01093.1	50	51.9878	59	30	C. elegans protein Y53C12A.10, confirmed by transcript evidence
Locus_9033_Transcript_2/2_Conf_1.000	822	20	8.85E-79	CAT01093.1	82	297.745	197	163	C. elegans protein Y53C12A.10, confirmed by transcript evidence
Locus_9034_Transcript_1/1_Conf_1.000	441	0							

Locus_9035_Transcript_1/1_Conf_1.000	1160	20	0	NP_501998.1	92	645.195	375	345	hypothetical protein T25B9.9
Locus_9036_Transcript_1/1_Conf_1.000	628	20	1.57E-64	NP_496100.1	76	249.595	216	166	hypothetical protein Y53C12B.1
Locus_9037_Transcript_1/1_Conf_1.000	1208	20	6.19E-118	XP_002645068.1	73	428.713	395	291	C. briggsae CBR-TAG-197 protein

Locus_9038_Transcript_1/1_Conf_1.000	925	20	9.92E-64	XP_002639900.1	66	248.054	308	204	C. briggsae CBR-APR-1 protein
Locus_9039_Transcript_1/2_Conf_1.000	273	4	4.55E-31	XP_002637828.1	82	137.502	90	74	Hypothetical protein CBG04618
Locus_9039_Transcript_2/2_Conf_1.000	273	4	4.55E-31	XP_002637828.1	82	137.502	90	74	Hypothetical protein CBG04618
Locus_904_Transcript_1/1_Conf_1.000	713	12	1.08E-36	XP_002646571.1	64	157.532	162	105	Hypothetical protein CBG20429

Locus_9040_Transcript_1/1_Conf_1.000	639	20	1.08E-47	NP_501093.1	66	193.741	209	139	Kinesin-Like Protein family member (klp-18)
Locus_9041_Transcript_1/1_Conf_1.000	227	0							
Locus_9042_Transcript_1/1_Conf_1.000	169	0							
Locus_9043_Transcript_1/1_Conf_1.000	144	0							
Locus_9044_Transcript_1/1_Conf_1.000	363	0							
Locus_9045_Transcript_1/1_Conf_1.000	375	0							
Locus_9046_Transcript_1/1_Conf_1.000	1376	6	8.11E-56	XP_002646592.1	49	222.631	469	232	C. briggsae CBR-EKL-1 protein
Locus_9047_Transcript_1/1_Conf_1.000	552	20	6.25E-63	NP_504274.2	79	243.817	185	147	UDP-GlucuronosylTransferase family member (ugt-61)
Locus_9048_Transcript_1/1_Conf_1.000	1751	20	0	XP_002630326.1	85	814.683	575	489	Hypothetical protein CBG04253
Locus_9049_Transcript_1/1_Conf_1.000	975	20	2.92E-85	NP_497835.1	75	319.701	262	199	hypothetical protein C16C10.2
Locus_905_Transcript_1/1_Conf_1.000	778								
Locus_9050_Transcript_1/1_Conf_1.000	278	20	2.33E-27	XP_002631614.1	85	125.176	90	77	C. briggsae CBR-MAC-1 protein
Locus_9051_Transcript_1/2_Conf_1.000	938	20	3.50E-56	NP_497422.3	61	223.016	274	169	hypothetical protein Y67D2.2
Locus_9051_Transcript_2/2_Conf_1.000	1647	20	1.46E-110	NP_497422.3	65	404.831	470	307	hypothetical protein Y67D2.2

Locus_9052_Transcript_1/1_Conf_1.000	330	20	4.13E-24	NP_498815.1	79	114.39	97	77	hypothetical protein F09G8.3
Locus_9053_Transcript_1/1_Conf_1.000	174	0							
Locus_9054_Transcript_1/1_Conf_1.000	597	20	7.01E-24	EFO25241.1	76	114.39	93	71	CMGC/CDK protein kinase
Locus_9055_Transcript_1/1_Conf_1.000	362	20	5.56E-21	XP_001895126.1	87	103.99	66	58	hypothetical protein
Locus_9056_Transcript_1/5_Conf_0.714	2663	20	8.79E-66	NP_499624.2	43	256.914	850	366	ANIllin (actin binding protein) family member (ani-1)
Locus_9056_Transcript_2/5_Conf_0.714	2729	20	2.15E-67	NP_499624.2	42	262.307	873	375	ANIllin (actin binding protein) family member (ani-1)
Locus_9056_Transcript_3/5_Conf_0.643	2720	20	9.63E-68	NP_499624.2	42	263.462	868	372	ANIllin (actin binding protein) family member (ani-1)
Locus_9056_Transcript_4/5_Conf_0.714	2717	20	1.06E-66	NP_499624.2	43	259.996	869	375	ANIllin (actin binding protein) family member (ani-1)
Locus_9056_Transcript_5/5_Conf_0.714	2717	20	1.81E-66	NP_499624.2	42	259.225	868	372	ANIllin (actin binding protein) family member (ani-1)
Locus_9057_Transcript_1/1_Conf_1.000	373	20	4.80E-12	NP_497657.1	64	74.3294	84	54	SurFeit homolog family member (sft-1)
Locus_9058_Transcript_1/1_Conf_1.000	920	3	7.52E-56	XP_002629981.1	82	221.861	155	128	Hypothetical protein CBG13343
Locus_9059_Transcript_1/1_Conf_1.000	381	0							
Locus_906_Transcript_1/1_Conf_1.000	1936	20	1.54E-154	A8XXC0.2	66	551.206	560	375	Tubulin--tyrosine ligase-like protein 12
Locus_9060_Transcript_1/1_Conf_1.000	620	20	2.00E-80	CAR97821.1	82	302.368	207	170	C. elegans protein F11C1.5d, partially confirmed by transcript evidence
Locus_9061_Transcript_1/1_Conf_1.000	289	0							
Locus_9062_Transcript_1/1_Conf_1.000	457	20	2.03E-39	XP_002646729.1	89	165.236	113	101	C. briggsae CBR-PRX-13 protein
Locus_9063_Transcript_1/1_Conf_1.000	251	6	3.23E-29	XP_002641621.1	86	131.339	83	72	Hypothetical protein CBG09941
Locus_9064_Transcript_1/1_Conf_1.000	419	20	3.77E-57	ACD88894.1	92	224.172	128	118	transthyretin-like protein
Locus_9065_Transcript_1/1_Conf_1.000	315	0							

Locus_9066_Transcript_1/1_Conf_1.000	416	20	3.43E-55	EFO20551.1	90	217.624	129	117	hypothetical protein LOAG_07939
Locus_9067_Transcript_1/2_Conf_1.000	471	20	1.13E-21	NP_492409.2	56	106.301	146	83	hypothetical protein F53B6.7
Locus_9067_Transcript_2/2_Conf_1.000	527	20	5.43E-23	XP_002639679.1	58	110.923	163	96	Hypothetical protein CBG12398
Locus_9068_Transcript_1/2_Conf_1.000	1213	20	4.43E-105	XP_002646593.1	69	227.639	218	151	C. briggsae CBR-PRPF-4 protein
Locus_9068_Transcript_2/2_Conf_1.000	1107	20	6.47E-111	XP_002646593.1	76	405.216	320	245	C. briggsae CBR-PRPF-4 protein
Locus_9069_Transcript_1/1_Conf_1.000	206	0							
Locus_907_Transcript_1/1_Conf_1.000	1870	20	0	XP_002649013.1	91	887.486	538	492	Hypothetical protein CBG21460
Locus_9070_Transcript_1/1_Conf_1.000	800	20	2.40E-49	XP_001950093.1	61	199.904	255	156	PREDICTED: similar to cullin

Locus_9071_Transcript_1/1_Conf_1.000	434	20	1.19E-39	XP_001899873.1	77	166.007	111	86	protein kinase C substrate 80K-H
Locus_9072_Transcript_1/1_Conf_1.000	870	20	1.57E-84	Q03566.2	77	317.005	280	218	Probable G-protein coupled receptor tkr-1
Locus_9073_Transcript_1/2_Conf_1.000	1391	20	0	XP_002630467.1	91	721.85	465	425	C. briggsae CBR-UNC-104 protein
Locus_9073_Transcript_2/2_Conf_1.000	1397	20	0	XP_002630467.1	91	721.85	466	425	C. briggsae CBR-UNC-104 protein
Locus_9074_Transcript_1/1_Conf_1.000	1271	0							
Locus_9075_Transcript_1/1_Conf_1.000	385	0							
Locus_9076_Transcript_1/1_Conf_1.000	348	20	8.36E-49	NP_491993.1	95	196.438	115	110	CRAL/TRIO and GOLD domain containing family member (ctg-1)
Locus_9077_Transcript_1/1_Conf_1.000	227	19	9.08E-11	XP_001901053.1	65	70.0922	75	49	Frizzled/Smoothened family membrane region containing protein

Locus_9078_Transcript_1/1_Conf_1.000	432	4	5.21E-19	XP_002634885.1	55	97.4413	134	74	Hypothetical protein CBG10553
Locus_9079_Transcript_1/1_Conf_1.000	622	20	6.05E-45	XP_002644547.1	69	184.496	156	109	C. briggsae CBR-DGK-2 protein
Locus_908_Transcript_1/1_Conf_1.000	172	20	2.50E-13	1TOV	88	78.5666	43	38	Cap-Gly Domain Of F53f4.3
Locus_9080_Transcript_1/3_Conf_0.714	2649	7	4.12E-15	XP_001896575.1	42	88.5817	416	178	hypothetical protein Bm1_25580
Locus_9080_Transcript_2/3_Conf_0.714	2649	12	4.12E-15	XP_001896575.1	42	88.5817	416	178	hypothetical protein Bm1_25580
Locus_9080_Transcript_3/3_Conf_0.714	2649	10	4.12E-15	XP_001896575.1	42	88.5817	416	178	hypothetical protein Bm1_25580
Locus_9081_Transcript_1/1_Conf_1.000	222	20	6.29E-20	EFN80829.1	81	100.523	74	60	Dephospho-CoA kinase domain-containing protein
Locus_9082_Transcript_1/1_Conf_1.000	1805	14	3.44E-84	EFO26517.1	72	317.39	280	204	hypothetical protein LOAG_01973
Locus_9083_Transcript_1/1_Conf_1.000	559	0							
Locus_9084_Transcript_1/1_Conf_1.000	950	20	3.20E-97	XP_002647026.1	73	359.377	306	225	C. briggsae CBR-PUP-2 protein
Locus_9085_Transcript_1/1_Conf_1.000	653	20	3.71E-91	XP_002637616.1	85	338.191	218	187	Hypothetical protein CBG19359
Locus_9086_Transcript_1/1_Conf_1.000	1035	20	2.35E-27	CAG02388.1	60	127.487	140	84	unnamed protein product

Locus_9087_Transcript_1/1_Conf_1.000	2072	20	0	ADC52457.1	98	835.484	512	502	NADH dehydrogenase subunit 5
Locus_9088_Transcript_1/1_Conf_1.000	458	0							
Locus_9089_Transcript_1/1_Conf_1.000	216	20	1.60E-28	CAR63545.1	91	129.028	72	66	putative Hsp90 protein
Locus_909_Transcript_1/1_Conf_1.000	390	4	2.03E-15	EFO23348.1	60	85.5001	129	78	hypothetical protein LOAG_05138
Locus_9090_Transcript_1/1_Conf_1.000	1151	0							
Locus_9091_Transcript_1/2_Conf_1.000	775	20	2.75E-47	NP_498576.1	80	192.971	148	119	hypothetical protein F37C12.1
Locus_9091_Transcript_2/2_Conf_1.000	773	20	2.73E-47	NP_498576.1	80	192.971	148	119	hypothetical protein F37C12.1
Locus_9092_Transcript_1/1_Conf_1.000	488	0							
Locus_9093_Transcript_1/2_Conf_1.000	1244	20	1.66E-97	NP_492092.1	69	360.918	368	256	hypothetical protein C15A11.7
Locus_9093_Transcript_2/2_Conf_1.000	1146	20	2.67E-99	XP_002646241.1	72	366.696	330	238	Hypothetical protein CBG11935
Locus_9094_Transcript_1/1_Conf_1.000	302	11	3.39E-18	XP_002639148.1	71	94.7449	100	71	C. briggsae CBR-SULP-6 protein
Locus_9095_Transcript_1/1_Conf_1.000	830	20	1.43E-92	NP_001040789.1	84	343.584	276	233	hypothetical protein H20J04.4
Locus_9096_Transcript_1/1_Conf_1.000	592	3	1.86E-13	NP_871669.1	49	79.7221	175	86	SET (trithorax/polycomb) domain containing family member (set-3)
Locus_9097_Transcript_1/1_Conf_1.000	562	4	3.05E-04	CAZ65476.1	58	48.9062	58	34	C. elegans protein C36B1.8c, confirmed by transcript evidence
Locus_9098_Transcript_1/1_Conf_1.000	156	0							
Locus_9099_Transcript_1/1_Conf_1.000	868	20	1.75E-43	NP_001122880.1	52	180.644	293	154	Temporarily Assigned Gene name family member (tag-333)

Locus_91_Transcript_1/2_Conf_1.000	1814	20	5.06E-35	XP_783989.2	43	154.066	591	256	PREDICTED: similar to Rad50-interacting protein 1
Locus_91_Transcript_2/2_Conf_1.000	1814	20	5.06E-35	XP_783989.2	43	154.066	591	256	PREDICTED: similar to Rad50-interacting protein 1
Locus_910_Transcript_1/1_Conf_1.000	3597	20	5.27E-101	XP_001900253.1	46	374.4	1179	549	hypothetical protein Bm1_43955
Locus_9100_Transcript_1/1_Conf_1.000	553	20	1.89E-51	XP_002637738.1	86	205.682	129	112	Hypothetical protein CBG11604
Locus_9101_Transcript_1/1_Conf_1.000	1046	20	6.56E-78	XP_002629707.1	68	295.434	309	211	Hypothetical protein CBG00934
Locus_9102_Transcript_1/1_Conf_1.000	135	20	2.05E-07	P30616.1	68	58.9214	45	31	Pyruvate kinase 2
Locus_9103_Transcript_1/1_Conf_1.000	143	0							
Locus_9104_Transcript_1/1_Conf_1.000	326	20	2.52E-29	XP_002642780.1	74	131.724	106	79	Hypothetical protein CBG21174
Locus_9105_Transcript_1/1_Conf_1.000	478	20	1.65E-49	XP_001901593.1	80	198.749	157	126	Elongation factor G C-terminus family protein
Locus_9106_Transcript_1/1_Conf_1.000	701	20	9.97E-104	NP_500145.2	88	380.178	234	206	hypothetical protein F52C12.4
Locus_9107_Transcript_1/1_Conf_1.000	408	20	1.72E-54	XP_002642177.1	86	215.312	132	114	Hypothetical protein CBG18144
Locus_9108_Transcript_1/2_Conf_1.000	682	20	4.12E-59	CAM84574.1	67	231.876	209	141	intestinal prolyl carboxypeptidase 2
Locus_9108_Transcript_2/2_Conf_1.000	789	20	2.18E-63	CAM84574.1	62	246.514	261	163	intestinal prolyl carboxypeptidase 2

Locus_9109_Transcript_1/2_Conf_1.000	977	20	1.19E-70	NP_507245.1	62	271.166	316	197	hypothetical protein T20B3.1
Locus_9109_Transcript_2/2_Conf_1.000	977	20	1.41E-71	NP_507245.1	62	274.248	316	198	hypothetical protein T20B3.1
Locus_911_Transcript_1/1_Conf_1.000	1600	20	5.52E-107	NP_741223.1	67	392.889	458	307	hypothetical protein F56C9.10
Locus_9110_Transcript_1/1_Conf_1.000	209	0							
Locus_9111_Transcript_1/1_Conf_1.000	472	20	2.26E-38	NP_497853.1	73	161.77	160	117	hypothetical protein T08A11.2
Locus_9112_Transcript_1/1_Conf_1.000	422	20	2.89E-33	NP_499585.1	75	144.821	140	106	OSMotic avoidance abnormal family member (osm-12)
Locus_9113_Transcript_1/1_Conf_1.000	437	2	2.04E-07	NP_001024812.1	46	58.9214	99	46	hypothetical protein M163.8
Locus_9114_Transcript_1/1_Conf_1.000	348	2	2.30E-06	NP_497103.1	54	55.4546	93	51	hypothetical protein Y53F4B.18
Locus_9115_Transcript_1/2_Conf_1.000	1651	0							
Locus_9115_Transcript_2/2_Conf_1.000	1501	0							
Locus_9116_Transcript_1/1_Conf_1.000	591	0							
Locus_9117_Transcript_1/1_Conf_1.000	382	20	1.09E-32	XP_002641709.1	73	142.895	125	92	C. briggsae CBR-CED-7 protein
Locus_9118_Transcript_1/1_Conf_1.000	441	20	1.29E-49	XP_002636806.1	80	199.134	147	118	Hypothetical protein CBG09248
Locus_9119_Transcript_1/1_Conf_1.000	375	20	7.11E-24	NP_491986.1	57	113.62	128	74	hypothetical protein C30F12.2

Locus_912_Transcript_1/1_Conf_1.000	774	20	6.31E-60	NP_508674.1	92	234.958	138	127	SUPpressor family member (sup-12)
Locus_9120_Transcript_1/2_Conf_1.000	728	20	5.95E-62	XP_002631267.1	75	241.506	242	183	C. briggsae CBR-PRO-1 protein
Locus_9120_Transcript_2/2_Conf_1.000	728	20	7.77E-62	XP_002631267.1	75	241.121	242	183	C. briggsae CBR-PRO-1 protein
Locus_9121_Transcript_1/1_Conf_1.000	991	2	1.17E-04	XP_002021005.1	37	51.9878	176	66	GL25064
Locus_9122_Transcript_1/1_Conf_1.000	659	5	2.18E-46	XP_002644341.1	60	189.504	220	133	Hypothetical protein CBG14163
Locus_9123_Transcript_1/1_Conf_1.000	253	1	1.32E-17	NP_001023480.2	77	92.8189	74	57	hypothetical protein Y4C6B.7
Locus_9124_Transcript_1/1_Conf_1.000	302	1	1.25E-04	NP_001022284.1	52	49.6766	70	37	hypothetical protein R12C12.10
Locus_9125_Transcript_1/1_Conf_1.000	507	0							
Locus_9126_Transcript_1/1_Conf_1.000	283	0							
Locus_9127_Transcript_1/1_Conf_1.000	468	20	7.84E-23	CAB03414.3	55	110.153	158	87	Hypothetical protein T23G11.5a
Locus_9128_Transcript_1/2_Conf_1.000	487	20	9.77E-82	EFO23081.1	98	305.834	160	157	adaptor protein complex AP-2
Locus_9128_Transcript_2/2_Conf_1.000	543	20	9.35E-93	EFO23081.1	97	342.813	180	176	adaptor protein complex AP-2
Locus_9129_Transcript_1/1_Conf_1.000	427	20	1.28E-49	XP_002640436.1	78	199.134	141	110	Hypothetical protein CBG08488
Locus_913_Transcript_1/1_Conf_1.000	436	0							

Locus_9130_Transcript_1/1_Conf_1.000	341	20	3.12E-32	XP_002630855.1	84	141.354	90	76	Hypothetical protein CBG02570
Locus_9131_Transcript_1/1_Conf_1.000	1244	20	2.17E-89	NP_490849.4	62	333.954	399	251	SET (trithorax/polycomb) domain containing family member (set-29)
Locus_9132_Transcript_1/1_Conf_1.000	1183	20	6.18E-131	NP_496280.1	79	471.855	346	276	mammalian cell Death Associated Protein related family member (dap-3)
Locus_9133_Transcript_1/2_Conf_1.000	903	20	1.07E-56	XP_002634163.1	69	175.252	168	116	Hypothetical protein CBG01728
Locus_9133_Transcript_2/2_Conf_1.000	847	20	7.97E-62	XP_002634163.1	70	241.506	226	159	Hypothetical protein CBG01728
Locus_9134_Transcript_1/1_Conf_1.000	726	20	3.36E-73	NP_499802.2	80	278.87	210	170	hypothetical protein Y76A2B.6
Locus_9135_Transcript_1/1_Conf_1.000	829	20	3.94E-42	EFO26950.1	60	176.022	249	151	eukaryotic translation initiation factor 3 subunit 8
Locus_9136_Transcript_1/1_Conf_1.000	297	0							
Locus_9137_Transcript_1/1_Conf_1.000	224	0							
Locus_9138_Transcript_1/2_Conf_1.000	1362	20	1.10E-75	NP_001033372.1	88	238.81	153	135	hypothetical protein T15B12.1
Locus_9138_Transcript_2/2_Conf_1.000	1319	20	3.76E-79	NP_001033372.1	78	300.056	242	189	hypothetical protein T15B12.1
Locus_9139_Transcript_1/1_Conf_1.000	418	0							
Locus_914_Transcript_1/3_Conf_0.714	2649	20	0	NP_741748.2	72	744.191	704	511	Sensory AXon guidance family member (sax-3)
Locus_914_Transcript_2/3_Conf_0.714	2667	20	0	NP_741748.2	75	784.252	694	522	Sensory AXon guidance family member (sax-3)
Locus_914_Transcript_3/3_Conf_0.714	2700	20	0	NP_741748.2	74	777.704	704	524	Sensory AXon guidance family member (sax-3)

Locus_9140_Transcript_1/1_Conf_1.000	354	20	3.62E-28	XP_001897467.1	79	127.872	89	71	CAP-Gly domain containing protein
Locus_9141_Transcript_1/1_Conf_1.000	199	20	4.59E-31	XP_002917824.1	100	137.502	65	65	PREDICTED: LOW QUALITY PROTEIN: ubiquitin-like modifier-activating enzyme 1-like
Locus_9142_Transcript_1/1_Conf_1.000	835	20	1.04E-74	XP_002640365.1	82	284.263	182	150	Hypothetical protein CBG20269
Locus_9143_Transcript_1/1_Conf_1.000	501	20	1.14E-29	CAR63556.1	74	132.88	167	124	putative Lin-5 (Five) Interacting protein
Locus_9144_Transcript_1/1_Conf_1.000	1046	20	8.39E-150	AAR07614.1	94	534.258	294	278	UNC-18
Locus_9145_Transcript_1/1_Conf_1.000	860	0							
Locus_9146_Transcript_1/1_Conf_1.000	860	0							
Locus_9147_Transcript_1/6_Conf_0.154	249	1	2.49E-05	NP_490891.1	59	51.9878	64	38	hypothetical protein Y71G12B.8

Locus_9147_Transcript_2/6_Conf_0.462	1633	20	3.71E-74	EFO21790.1	68	283.878	301	205	hypothetical protein LOAG_06696
Locus_9147_Transcript_3/6_Conf_0.615	2057	20	4.95E-74	EFO21790.1	68	283.878	301	205	hypothetical protein LOAG_06696
Locus_9147_Transcript_4/6_Conf_0.462	1633	20	3.71E-74	EFO21790.1	68	283.878	301	205	hypothetical protein LOAG_06696
Locus_9147_Transcript_5/6_Conf_0.231	548	2	1.90E-16	NP_490891.1	59	89.3521	121	72	hypothetical protein Y71G12B.8
Locus_9147_Transcript_6/6_Conf_0.462	1633	20	3.71E-74	EFO21790.1	68	283.878	301	205	hypothetical protein LOAG_06696
Locus_9148_Transcript_1/1_Conf_1.000	231	0							
Locus_9149_Transcript_1/1_Conf_1.000	479	4	4.38E-26	XP_002632865.1	88	120.939	70	62	Hypothetical protein CBG15064
Locus_915_Transcript_1/1_Conf_1.000	635	20	7.02E-60	NP_499173.1	75	234.187	212	160	hypothetical protein ZK632.3
Locus_9150_Transcript_1/1_Conf_1.000	470	2	2.60E-26	NP_497272.1	83	121.709	93	78	hypothetical protein K02F3.9
Locus_9151_Transcript_1/1_Conf_1.000	558	5	1.29E-15	XP_002644427.1	100	86.6557	58	58	Hypothetical protein CBG14284
Locus_9152_Transcript_1/1_Conf_1.000	344	20	5.62E-61	2QUJ	100	236.884	114	114	CrystalStructures Of Human Tryptophanyl-Trna Synthetase In Complex With Trpamp
Locus_9153_Transcript_1/1_Conf_1.000	128	8	8.68E-06	XP_002633175.1	73	53.5286	42	31	Hypothetical protein CBG05887
Locus_9154_Transcript_1/1_Conf_1.000	809	0							
Locus_9155_Transcript_1/1_Conf_1.000	317	6	4.82E-12	NP_504235.2	55	74.3294	104	58	Drosophila SOS homolog family member (sos-1)
Locus_9156_Transcript_1/4_Conf_0.538	1317	20	1.43E-70	NP_493353.3	63	271.552	266	168	Specificity Protein) Transcription Factor family member (sptf-3)
Locus_9156_Transcript_2/4_Conf_0.308	454	3	1.42E-08	XP_001902916.1	50	62.7734	115	58	Zinc finger, C2H2 type family protein
Locus_9156_Transcript_3/4_Conf_0.308	347	0							

Locus_9156_Transcript_4/4_Conf_0.538	1311	20	1.68E-71	NP_493353.3	62	274.633	266	167	Specificity Protein) Transcription Factor family member (sptf-3)
Locus_9157_Transcript_1/1_Conf_1.000	373	0							
Locus_9158_Transcript_1/1_Conf_1.000	328	20	1.80E-19	XP_001898245.1	71	98.9821	97	69	Protein kinase domain containing protein
Locus_9159_Transcript_1/1_Conf_1.000	196	0							
Locus_916_Transcript_1/1_Conf_1.000	239	0							
Locus_9160_Transcript_1/1_Conf_1.000	1069	20	1.07E-131	NP_501169.1	87	474.167	333	293	hypothetical protein F42C5.9
Locus_9161_Transcript_1/1_Conf_1.000	920	20	2.85E-71	NP_500157.2	76	273.092	263	202	Cleavage and Polyadenylation Specificity Factor family member (cpsf-1)
Locus_9162_Transcript_1/1_Conf_1.000	255	20	2.47E-16	XP_002637827.1	94	88.5817	85	80	Hypothetical protein CBG04617
Locus_9163_Transcript_1/1_Conf_1.000	659	2	1.43E-05	EFO18975.1	89	53.9138	37	33	hypothetical protein LOAG_09519
Locus_9164_Transcript_1/1_Conf_1.000	1249	20	3.40E-58	XP_001891849.1	55	230.335	415	232	Retinoblastoma-associated protein A domain containing protein
Locus_9165_Transcript_1/1_Conf_1.000	747	0							
Locus_9166_Transcript_1/1_Conf_1.000	520	20	2.68E-11	EFO23036.1	42	72.0182	145	62	CBP-B
Locus_9167_Transcript_1/1_Conf_1.000	189	0							
Locus_9168_Transcript_1/1_Conf_1.000	330	0							
Locus_9169_Transcript_1/1_Conf_1.000	398	2	7.31E-07	XP_002633405.1	65	41.2022	38	25	C. briggsae CBR-LPR-2 protein
Locus_917_Transcript_1/8_Conf_0.632	2750	20	1.37E-29	XP_002670743.1	37	136.732	616	229	predicted protein
Locus_917_Transcript_2/8_Conf_0.632	2725	20	3.59E-30	XP_002670743.1	36	138.658	612	225	predicted protein

Locus_917_Transcript_3/8_Conf_0.526	2359	20	3.03E-30	XP_002670743.1	36	138.658	612	225	predicted protein
Locus_917_Transcript_4/8_Conf_0.526	2393	20	3.08E-30	XP_002670743.1	36	138.658	612	225	predicted protein
Locus_917_Transcript_5/8_Conf_0.368	1715	20	6.00E-22	XP_003045704.1	36	110.538	393	143	hypothetical protein NECHADRAFT_34117
Locus_917_Transcript_6/8_Conf_0.316	1027	20	3.70E-25	AAO63577.1	52	120.168	189	99	secreted protein 5 precursor
Locus_917_Transcript_7/8_Conf_0.105	305	20	2.51E-13	AAO63577.1	57	78.5666	90	52	secreted protein 5 precursor
Locus_917_Transcript_8/8_Conf_0.632	2750	20	3.60E-30	XP_002670743.1	36	138.658	612	225	predicted protein
Locus_9170_Transcript_1/1_Conf_1.000	398	20	1.18E-34	NP_497604.2	78	149.443	126	99	SET (trithorax/polycomb) domain containing family member (set-27)
Locus_9171_Transcript_1/1_Conf_1.000	409	20	4.38E-42	NP_502295.1	90	174.096	121	109	yeast MON (monensin-resistant) homolog family member (mon-2)
Locus_9172_Transcript_1/1_Conf_1.000	366	20	2.17E-17	ACI49172.1	67	92.0485	113	76	hypothetical protein Csp3_JD01.004
Locus_9173_Transcript_1/1_Conf_1.000	637	20	9.65E-41	XP_001895169.1	72	170.629	161	117	TM2 domain containing protein
Locus_9174_Transcript_1/1_Conf_1.000	962	20	1.70E-13	NP_496141.1	43	81.2629	229	100	hypothetical protein C05C10.2
Locus_9175_Transcript_1/1_Conf_1.000	341	2	6.07E-36	NP_500987.3	75	153.68	112	84	hypothetical protein Y73B6BL.1
Locus_9176_Transcript_1/1_Conf_1.000	358	0							
Locus_9177_Transcript_1/1_Conf_1.000	715	20	5.21E-47	XP_002648157.1	79	191.815	150	119	Hypothetical protein CBG24238
Locus_9178_Transcript_1/1_Conf_1.000	227	0							
Locus_9179_Transcript_1/1_Conf_1.000	306	20	2.10E-28	NP_498391.1	74	128.642	100	74	hypothetical protein C56G2.15
Locus_918_Transcript_1/3_Conf_0.600	669	0							
Locus_918_Transcript_2/3_Conf_0.400	2103	20	0	CAD44515.1	78	680.633	547	431	VAB-10A protein
Locus_918_Transcript_3/3_Conf_0.400	2324	20	0	NP_509293.1	88	1055.43	709	626	Propionyl Coenzyme A Carboxylase Alpha subunit family member (pcca-1)

Locus_9180_Transcript_1/1_Conf_1.000	451								
Locus_9181_Transcript_1/1_Conf_1.000	675	20	1.05E-99	NP_502268.1	88	366.696	218	194	TRNA Guanine Transglycosylase family member (tgt-1)
Locus_9182_Transcript_1/1_Conf_1.000	199	0							
Locus_9183_Transcript_1/1_Conf_1.000	172	0							
Locus_9184_Transcript_1/1_Conf_1.000	903	20	2.20E-52	NP_505927.2	57	210.305	307	175	CCCH-type zinc finger transcription factor family member (ccch-1)
Locus_9185_Transcript_1/1_Conf_1.000	329	0							
Locus_9186_Transcript_1/1_Conf_1.000	502	0							
Locus_9187_Transcript_1/1_Conf_1.000	982	20	5.15E-122	NP_001024981.1	82	441.81	327	270	Lin-5 (Five) Interacting protein family member (lfi-1)
Locus_9188_Transcript_1/1_Conf_1.000	436	0							
Locus_9189_Transcript_1/1_Conf_1.000	268	0							
Locus_919_Transcript_1/1_Conf_1.000	2103	20	0	XP_002643773.1	91	1176.39	700	641	Hypothetical protein CBG01975
Locus_9190_Transcript_1/1_Conf_1.000	1246	20	0	AAP36549.1	100	674.085	335	335	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase
Locus_9191_Transcript_1/2_Conf_1.000	1974	20	0	NP_502558.2	70	660.603	655	465	hypothetical protein Y67H2A.7
Locus_9191_Transcript_2/2_Conf_1.000	1974	20	0	NP_502558.2	70	659.062	655	465	hypothetical protein Y67H2A.7
Locus_9192_Transcript_1/1_Conf_1.000	398	9	1.94E-29	ACS72232.1	71	132.109	129	92	hypothetical protein
Locus_9193_Transcript_1/1_Conf_1.000	263	4	6.67E-22	NP_001040644.1	95	107.071	71	68	hypothetical protein C53H9.3
Locus_9194_Transcript_1/1_Conf_1.000	324	2	1.94E-05	NP_510576.2	65	52.373	52	34	hypothetical protein K09E9.1

Locus_9195_Transcript_1/1_Conf_1.000	3664	20	0	XP_001898232.1	67	945.651	1095	743	kap beta 3 protein
Locus_9196_Transcript_1/1_Conf_1.000	262	3	5.86E-10	NP_001122554.1	62	67.3958	78	49	hypothetical protein Y71G12A.2
Locus_9197_Transcript_1/1_Conf_1.000	390	20	3.35E-18	NP_491679.1	62	94.7449	114	71	RuNT related family member (rnt-1)
Locus_9198_Transcript_1/1_Conf_1.000	798	20	2.68E-08	EFO27106.1	71	63.5438	83	59	D10Ertd718e protein
Locus_9199_Transcript_1/1_Conf_1.000	294	20	1.24E-52	AAH03896.2	100	209.149	98	98	Rpl17 protein
Locus_92_Transcript_1/1_Conf_1.000	1778	20	0	NP_740994.1	89	823.157	519	466	hypothetical protein C17G10.9
Locus_920_Transcript_1/1_Conf_1.000	217	0							
Locus_9200_Transcript_1/3_Conf_0.600	505	20	1.25E-39	NP_001032988.1	74	166.007	162	120	hypothetical protein Y51F10.4
Locus_9200_Transcript_2/3_Conf_0.600	710	20	4.18E-49	NP_001032988.1	68	198.749	251	173	hypothetical protein Y51F10.4
Locus_9200_Transcript_3/3_Conf_0.600	505	20	1.25E-39	NP_001032988.1	74	166.007	162	120	hypothetical protein Y51F10.4
Locus_9201_Transcript_1/1_Conf_1.000	1018	5	3.41E-31	XP_002636261.1	51	140.198	239	124	C. briggsae CBR-LIN-25 protein
Locus_9202_Transcript_1/1_Conf_1.000	766	2	2.45E-16	NP_500786.1	52	90.1225	231	121	hypothetical protein Y4C6B.1

Locus_9203_Transcript_1/1_Conf_1.000	675	20	1.10E-56	EFO23663.1	73	223.787	208	153	myosin xviiia
Locus_9204_Transcript_1/1_Conf_1.000	374	0							
Locus_9205_Transcript_1/1_Conf_1.000	1418	3	1.82E-34	NP_498724.3	46	151.754	466	218	Nuclear Pore complex Protein family member (npp-15)
Locus_9206_Transcript_1/1_Conf_1.000	263	20	1.63E-44	CBW39478.1	100	182.185	87	87	MHC class II antigen
Locus_9207_Transcript_1/1_Conf_1.000	131	0							
Locus_9208_Transcript_1/1_Conf_1.000	509	2	1.80E-09	NP_491390.2	51	65.855	167	86	hypothetical protein D1007.15
Locus_9209_Transcript_1/2_Conf_1.000	594	20	1.92E-58	NP_497750.1	84	229.18	152	128	hypothetical protein C14B1.5
Locus_9209_Transcript_2/2_Conf_1.000	779	20	3.49E-58	NP_497750.1	84	229.18	152	128	hypothetical protein C14B1.5
Locus_921_Transcript_1/1_Conf_1.000	284	0							
Locus_9210_Transcript_1/1_Conf_1.000	256	0							
Locus_9211_Transcript_1/1_Conf_1.000	332	0							
Locus_9212_Transcript_1/1_Conf_1.000	157	0							
Locus_9213_Transcript_1/2_Conf_1.000	1129	20	1.07E-92	XP_002633395.1	63	344.739	422	267	C. briggsae CBR-KIN-4 protein

Locus_9213_Transcript_2/2_Conf_1.000	1114	20	5.19E-92	NP_502161.2	63	342.428	420	268	protein KINase family member (kin-4)
Locus_9214_Transcript_1/1_Conf_1.000	618	20	1.42E-09	XP_001898759.1	67	67.0106	120	81	collagen col-34
Locus_9215_Transcript_1/1_Conf_1.000	311	0							
Locus_9216_Transcript_1/2_Conf_1.000	546	20	1.03E-46	XP_002631580.1	71	189.889	171	123	Hypothetical protein CBG20758
Locus_9216_Transcript_2/2_Conf_1.000	651	20	3.51E-57	XP_002631580.1	72	225.328	200	145	Hypothetical protein CBG20758
Locus_9217_Transcript_1/1_Conf_1.000	593	20	2.47E-66	NP_495019.1	96	255.373	131	126	Masculinisation Of Germline family member (mog-5)
Locus_9218_Transcript_1/1_Conf_1.000	594	0							
Locus_9219_Transcript_1/1_Conf_1.000	574	0							
Locus_922_Transcript_1/1_Conf_1.000	624	20	4.26E-38	EFO26612.1	61	161.77	203	125	hypothetical protein LOAG_01868
Locus_9220_Transcript_1/1_Conf_1.000	1076	20	1.32E-12	NP_001021459.2	40	78.5666	262	107	hypothetical protein F36H2.3
Locus_9221_Transcript_1/1_Conf_1.000	149	0							
Locus_9222_Transcript_1/1_Conf_1.000	267	0							
Locus_9223_Transcript_1/1_Conf_1.000	1731	0							
Locus_9224_Transcript_1/1_Conf_1.000	202	0							

Locus_9225_Transcript_1/1_Conf_1.000	436	20	1.36E-35	XP_002631793.1	75	152.525	132	100	C. briggsae CBR-CNT-1 protein
Locus_9226_Transcript_1/1_Conf_1.000	1386	20	4.23E-161	NP_498311.2	74	572.392	482	361	CYtoKinesis defect family member (cyk-3)
Locus_9227_Transcript_1/1_Conf_1.000	812	20	1.78E-108	NP_499799.1	86	396.356	256	221	fatty Acid CoA Synthetase family member (acs-14)
Locus_9228_Transcript_1/2_Conf_1.000	677	0							
Locus_9228_Transcript_2/2_Conf_1.000	675	0							
Locus_9229_Transcript_1/1_Conf_1.000	489	5	7.85E-15	XP_002642876.1	74	83.5741	87	65	Hypothetical protein CBG15146
Locus_923_Transcript_1/1_Conf_1.000	2530	20	0	XP_002631365.1	77	834.713	720	558	C. briggsae CBR-RHA-1 protein
Locus_9230_Transcript_1/1_Conf_1.000	591	20	8.45E-83	NP_498936.1	89	310.071	186	167	hypothetical protein K02D10.1
Locus_9231_Transcript_1/1_Conf_1.000	208	5	1.05E-11		70	73.1738	67	47	hypothetical protein T26A5.5 - Caenorhabditis elegans
Locus_9232_Transcript_1/1_Conf_1.000	342	20	4.21E-24	XP_002640824.1	77	114.39	92	71	Hypothetical protein CBG15711

Locus_9233_Transcript_1/1_Conf_1.000	928	3	8.04E-05	XP_001992050.1	49	52.373	171	85	GH24427
Locus_9234_Transcript_1/1_Conf_1.000	179	0							
Locus_9235_Transcript_1/2_Conf_1.000	2397	20	0	XP_002642710.1	88	1163.67	763	675	C. briggsae CBR-MCM-5 protein
Locus_9235_Transcript_2/2_Conf_1.000	2609	20	0	XP_002642710.1	88	1161.75	762	674	C. briggsae CBR-MCM-5 protein
Locus_9236_Transcript_1/2_Conf_1.000	131	0							
Locus_9237_Transcript_1/1_Conf_1.000	342	20	1.10E-56	XP_002637464.1	97	222.631	113	110	Hypothetical protein CBG19177
Locus_9238_Transcript_1/1_Conf_1.000	291	2	1.11E-08	NP_505680.2	68	63.1586	54	37	hypothetical protein Y32F6A.4
Locus_9239_Transcript_1/1_Conf_1.000	884	20	5.53E-61	NP_001022960.1	84	238.81	166	140	hypothetical protein Y82E9BR.16
Locus_924_Transcript_1/2_Conf_1.000	478	8	5.57E-05	XP_002644234.1	66	50.8322	84	56	C. briggsae CBR-MIG-15 protein
Locus_924_Transcript_2/2_Conf_1.000	238	0							
Locus_9240_Transcript_1/1_Conf_1.000	1877	20	0	NP_740814.1	90	836.254	542	490	alpha-CaTuliN (catenin/vinculin related) family member (ctn-1)

Locus_9241_Transcript_1/1_Conf_1.000	455	20	1.61E-44		88	182.185	109	96	hypothetical protein T26E3.3
Locus_9242_Transcript_1/1_Conf_1.000	319	0							
Locus_9243_Transcript_1/1_Conf_1.000	565	20	6.62E-31	XP_001900298.1	61	137.502	180	111	putative WD-40 repeat protein
Locus_9244_Transcript_1/2_Conf_1.000	826	20	2.82E-141	NP_741181.1	95	505.368	275	263	hypothetical protein T12A2.15
Locus_9244_Transcript_2/2_Conf_1.000	826	20	2.82E-141	NP_741181.1	95	505.368	275	263	hypothetical protein T12A2.15
Locus_9245_Transcript_1/1_Conf_1.000	142	3	4.23E-13	NP_492772.1	85	77.7962	47	40	SET (trithorax/polycomb) domain containing family member (set-18)
Locus_9246_Transcript_1/1_Conf_1.000	173	0							
Locus_9247_Transcript_1/1_Conf_1.000	605	1	6.14E-07	EFO26102.1	48	58.151	130	63	hypothetical protein LOAG_02385
Locus_9248_Transcript_1/1_Conf_1.000	292	2	6.71E-06	NP_506151.1	58	53.9138	67	39	hypothetical protein C14C10.4
Locus_9249_Transcript_1/1_Conf_1.000	195	4	2.22E-09	NP_001022814.1	70	65.4698	57	40	ODoRant response abnormal family member (odr-4)
Locus_925_Transcript_1/5_Conf_0.692	1879	20	2.15E-36	XP_002630499.1	56	158.688	302	170	Hypothetical protein CBG11240
Locus_925_Transcript_2/5_Conf_0.692	1879	20	3.11E-35	XP_002630499.1	56	154.836	288	164	Hypothetical protein CBG11240
Locus_925_Transcript_3/5_Conf_0.692	1879	20	2.15E-36	XP_002630499.1	56	158.688	302	170	Hypothetical protein CBG11240
Locus_925_Transcript_4/5_Conf_0.692	1879	20	2.38E-35	XP_002630499.1	55	155.221	302	169	Hypothetical protein CBG11240
Locus_925_Transcript_5/5_Conf_0.692	1879	20	2.15E-36	XP_002630499.1	56	158.688	302	170	Hypothetical protein CBG11240
Locus_9250_Transcript_1/1_Conf_1.000	559	20	8.26E-71	NP_494991.1	78	270.011	187	147	Phosphoethanolamine MethyTransferase family member (pmt-1)
Locus_9251_Transcript_1/1_Conf_1.000	236	0							

Locus_9252_Transcript_1/1_Conf_1.000	683	20	4.75E-31	NP_001023271.1	66	138.658	145	96	hypothetical protein K07F5.16
Locus_9253_Transcript_1/1_Conf_1.000	234	3	5.44E-16	XP_002646617.1	87	87.4261	58	51	Hypothetical protein CBG20503
Locus_9254_Transcript_1/1_Conf_1.000	539	20	2.25E-43	NP_001123184.1	77	178.718	136	106	O-GlcNAc selective N-Acetyl-beta-D-glucosaminidase (O-GlcNAcase) family member (oga-1)
Locus_9255_Transcript_1/1_Conf_1.000	490	20	2.32E-75	AAP36586.1	100	284.648	135	135	Homo sapiens lectin, galactoside-binding, soluble, 1 (galectin 1)
Locus_9256_Transcript_1/1_Conf_1.000	349	0							
Locus_9257_Transcript_1/1_Conf_1.000	230	20	1.64E-20	XP_001895480.1	81	102.449	75	61	Immunoglobulin I-set domain containing protein
Locus_9258_Transcript_1/1_Conf_1.000	592	20	1.08E-45	NP_741659.2	73	186.808	158	116	REPS (RalBP1-associated Eps domain-containing protein) homolog family member (reps-1)
Locus_9259_Transcript_1/1_Conf_1.000	531	3	9.33E-26	NP_490738.1	81	120.168	82	67	hypothetical protein W04C9.2
Locus_926_Transcript_1/1_Conf_1.000	692	0							
Locus_9260_Transcript_1/1_Conf_1.000	1210	20	2.64E-76	EFO22906.1	70	290.426	277	196	hypothetical protein LOAG_05578
Locus_9261_Transcript_1/1_Conf_1.000	422	20	2.38E-19	XP_002735650.1	52	98.5969	128	67	PREDICTED: low density lipoprotein receptor-related protein 1-like, partial

Locus_9262_Transcript_1/1_Conf_1.000	175	20	9.82E-10	NP_501480.2	68	66.6254	57	39	CYtochrome P450 family member (cyp-33E1)
Locus_9263_Transcript_1/2_Conf_1.000	1058	20	3.36E-37	EFO19657.1	51	160.229	316	162	hypothetical protein LOAG_08836
Locus_9263_Transcript_2/2_Conf_1.000	1070	20	3.42E-37	EFO19657.1	51	160.229	316	162	hypothetical protein LOAG_08836
Locus_9264_Transcript_1/1_Conf_1.000	521	0							
Locus_9265_Transcript_1/1_Conf_1.000	607	0							
Locus_9266_Transcript_1/1_Conf_1.000	797	20	8.14E-66	XP_002633365.1	79	254.603	226	179	Hypothetical protein CBG06109
Locus_9267_Transcript_1/1_Conf_1.000	1495	20	3.03E-152	XP_002630028.1	77	543.117	456	352	Hypothetical protein CBG13395
Locus_9268_Transcript_1/1_Conf_1.000	1212	20	7.68E-92	XP_001902417.1	66	342.043	387	256	BTB/POZ domain containing protein
Locus_9269_Transcript_1/1_Conf_1.000	1107	20	3.52E-133	XP_002645119.1	79	479.174	363	288	Hypothetical protein CBG16813
Locus_927_Transcript_1/2_Conf_1.000	266	0							
Locus_927_Transcript_2/2_Conf_1.000	168	0							
Locus_9270_Transcript_1/1_Conf_1.000	343	20	4.34E-37	XP_002642871.1	85	157.532	98	84	Hypothetical protein CBG15141
Locus_9271_Transcript_1/2_Conf_1.000	1009	20	3.97E-32	XP_002631067.1	46	143.28	330	154	C. briggsae CBR-TRR-1 protein
Locus_9271_Transcript_2/2_Conf_1.000	1114	20	4.62E-32	XP_002631067.1	46	143.28	330	154	C. briggsae CBR-TRR-1 protein
Locus_9272_Transcript_1/1_Conf_1.000	634	0							
Locus_9273_Transcript_1/1_Conf_1.000	543	5	3.86E-38	NP_494991.1	71	161.384	138	98	Phosphoethanolamine MethyTransferase family member (pmt-1)
Locus_9274_Transcript_1/1_Conf_1.000	634	20	1.63E-40	XP_002640675.1	89	169.859	111	99	Hypothetical protein CBG19737
Locus_9275_Transcript_1/1_Conf_1.000	609	20	8.41E-52	XP_002648175.1	84	207.223	139	118	Hypothetical protein CBG24261

Locus_9276_Transcript_1/1_Conf_1.000	167	0							
Locus_9277_Transcript_1/1_Conf_1.000	415	4	1.46E-13	XP_002635293.1	90	79.337	41	37	C. briggsae CBR-GRL-17 protein
Locus_9278_Transcript_1/2_Conf_1.000	496	2	6.18E-04	ACF82543.1	38	47.3654	151	58	unknown
Locus_9278_Transcript_2/2_Conf_1.000	529	2	4.42E-04	ACF82543.1	38	48.1358	144	55	unknown
Locus_9279_Transcript_1/2_Conf_1.000	237	0							
Locus_9279_Transcript_2/2_Conf_1.000	276	0							
Locus_928_Transcript_1/1_Conf_1.000	1287	20	1.84E-131	NP_741009.1	82	473.781	341	283	hypothetical protein C56C10.7
Locus_9280_Transcript_1/2_Conf_1.000	881	20	8.22E-49	NP_494448.1	73	198.364	172	127	hypothetical protein Y25C1A.13
Locus_9280_Transcript_2/2_Conf_1.000	1209	20	1.37E-48	NP_494448.1	73	198.364	172	127	hypothetical protein Y25C1A.13
Locus_9281_Transcript_1/1_Conf_1.000	282	20	1.55E-42	XP_002646472.1	98	175.637	94	93	C. briggsae CBR-NSF-1 protein
Locus_9282_Transcript_1/1_Conf_1.000	831	20	7.20E-60	NP_510484.1	86	234.958	165	142	hypothetical protein F20D1.1
Locus_9283_Transcript_1/1_Conf_1.000	287	20	4.20E-32	NP_495697.2	92	140.969	94	87	Lim and Transglutaminase Domain family member (ltd-1)
Locus_9284_Transcript_1/1_Conf_1.000	845	6	5.37E-18	ACI49218.1	49	95.9005	210	103	hypothetical protein Csp3_JD05.003
Locus_9285_Transcript_1/1_Conf_1.000	312	0							
Locus_9286_Transcript_1/2_Conf_1.000	1505	20	2.06E-15	EFA81073.1	56	88.5817	126	71	hypothetical protein PPL_05909
Locus_9286_Transcript_2/2_Conf_1.000	1475	20	2.00E-15	EFA81073.1	56	88.5817	126	71	hypothetical protein PPL_05909
Locus_9287_Transcript_1/1_Conf_1.000	173	0							
Locus_9288_Transcript_1/1_Conf_1.000	547	0							
Locus_9289_Transcript_1/1_Conf_1.000	1987	6	2.99E-52	EFO23863.1	50	211.46	441	222	hypothetical protein LOAG_04618

Locus_929_Transcript_1/9_Conf_0.545	2096	20	0	XP_002641367.1	80	944.88	694	560	C. briggsae CBR-GBF-1 protein
Locus_929_Transcript_2/9_Conf_0.545	2096	20	0	XP_002641367.1	80	945.266	694	560	C. briggsae CBR-GBF-1 protein
Locus_929_Transcript_3/9_Conf_0.500	2096	20	0	XP_002641367.1	80	944.88	694	560	C. briggsae CBR-GBF-1 protein
Locus_929_Transcript_4/9_Conf_0.545	2096	20	0	XP_002641367.1	80	944.88	694	560	C. briggsae CBR-GBF-1 protein
Locus_929_Transcript_5/9_Conf_0.136	369	20	4.80E-28	NP_499522.2	83	127.487	116	97	GBF1(Golgi-specific Brefeldin-A-resistant Factor 1) homolog family member (gbf-1)
Locus_929_Transcript_6/9_Conf_0.545	2096	20	0	XP_002641367.1	80	946.036	694	560	C. briggsae CBR-GBF-1 protein

Locus_929_Transcript_7/9_Conf_0.136	369	20	4.80E-28	NP_499522.2	83	127.487	116	97	GBF1(Golgi-specific Brefeldin-A-resistant Factor 1) homolog family member (gbf-1)
Locus_929_Transcript_8/9_Conf_0.318	1130	20	1.18E-83	XP_002641367.1	83	314.694	219	182	C. briggsae CBR-GBF-1 protein
Locus_929_Transcript_9/9_Conf_0.545	2096	20	0	XP_002641367.1	80	944.88	694	560	C. briggsae CBR-GBF-1 protein
Locus_9290_Transcript_1/1_Conf_1.000	1055	20	8.32E-113	NP_494721.1	82	411.379	304	250	hypothetical protein R11F4.1
Locus_9291_Transcript_1/2_Conf_1.000	329	0							
Locus_9291_Transcript_2/2_Conf_1.000	329	0							

Locus_9292_Transcript_1/1_Conf_1.000	569	20	1.22E-64	EFO26328.1	81	249.595	183	150	hypothetical protein LOAG_02152
Locus_9293_Transcript_1/1_Conf_1.000	644	0							
Locus_9294_Transcript_1/1_Conf_1.000	224	0							
Locus_9295_Transcript_1/2_Conf_1.000	665	0							
Locus_9295_Transcript_2/2_Conf_1.000	668	0							
Locus_9296_Transcript_1/1_Conf_1.000	279	1	2.66E-15	NP_001076673.1	73	85.1149	67	49	hypothetical protein F01G4.6
Locus_9297_Transcript_1/1_Conf_1.000	1451	20	4.77E-163	NP_001022412.1	73	578.941	521	381	CeNTaurin family member (cnt-1)
Locus_9298_Transcript_1/1_Conf_1.000	177	0							
Locus_9299_Transcript_1/1_Conf_1.000	412	20	2.04E-23	EFO20527.1	70	112.079	95	67	hypothetical protein LOAG_07962
Locus_93_Transcript_1/6_Conf_0.444	916	20	4.56E-37	NP_001123117.1	67	159.458	182	122	VITellogenin structural genes (yolk protein genes) family member (vit-2)
Locus_93_Transcript_2/6_Conf_0.444	916	20	3.99E-33	NP_001123117.1	66	146.362	168	112	VITellogenin structural genes (yolk protein genes) family member (vit-2)
Locus_93_Transcript_3/6_Conf_0.361	521	20	7.24E-33	Q94637.1	71	143.665	151	108	Vitellogenin-6
Locus_93_Transcript_4/6_Conf_0.361	563	20	2.16E-34	NP_001123117.1	63	149.058	185	118	VITellogenin structural genes (yolk protein genes) family member (vit-2)
Locus_93_Transcript_5/6_Conf_0.444	816	20	3.69E-53	NP_001123117.1	63	212.616	277	177	VITellogenin structural genes (yolk protein genes) family member (vit-2)
Locus_93_Transcript_6/6_Conf_0.444	774	20	2.94E-49	NP_001123117.1	63	199.519	263	167	VITellogenin structural genes (yolk protein genes) family member (vit-2)

Locus_930_Transcript_1/1_Conf_1.000	685	20	1.34E-49	CAR63550.1	92	200.29	135	125	putative Mediator of RNA polymerase II transcription subunit 6
Locus_9300_Transcript_1/1_Conf_1.000	496	17	1.13E-05	XP_002869793.1	56	53.1434	73	41	predicted protein

Locus_9301_Transcript_1/1_Conf_1.000	166	1	4.44E-18	AAG39288.1	100	94.3597	55	55	AF113217_1MSTP037
Locus_9302_Transcript_1/2_Conf_1.000	1411	16	8.74E-13	XP_002639571.1	42	79.7221	325	138	Hypothetical protein CBG04202
Locus_9302_Transcript_2/2_Conf_1.000	1405	7	8.69E-13	XP_002639571.1	42	79.7221	325	138	Hypothetical protein CBG04202
Locus_9303_Transcript_1/1_Conf_1.000	328	20	4.01E-19	XP_002640962.1	83	97.8265	65	54	Hypothetical protein CBG11705
Locus_9304_Transcript_1/1_Conf_1.000	370	20	2.31E-14	EFO23176.1	60	82.0333	86	52	hypothetical protein LOAG_05303
Locus_9305_Transcript_1/1_Conf_1.000	675	19	1.78E-14	XP_001504747.2	48	83.5741	185	90	PREDICTED: similar to survival of motor neuron 1, telomeric
Locus_9306_Transcript_1/1_Conf_1.000	182	20	1.56E-18	XP_002637557.1	91	95.9005	56	51	Hypothetical protein CBG19289
Locus_9307_Transcript_1/1_Conf_1.000	234	0							
Locus_9308_Transcript_1/1_Conf_1.000	155	0							
Locus_9309_Transcript_1/1_Conf_1.000	834	0							
Locus_931_Transcript_1/1_Conf_1.000	355	20	1.58E-15	XP_002643787.1	57	85.8853	124	71	Hypothetical protein CBG01998
Locus_9310_Transcript_1/1_Conf_1.000	157	0							

Locus_9311_Transcript_1/1_Conf_1.000	494	20	1.78E-51	ABV23486.2	77	205.297	157	121	Hypothetical protein Y94H6A.7
Locus_9312_Transcript_1/3_Conf_0.400	401	3	1.03E-06	NP_502349.1	68	56.6102	58	40	Ubiquitin Fusion Degradation (yeast UFD homolog) family member (ufd-1)
Locus_9312_Transcript_2/3_Conf_0.600	1018	20	1.62E-73	NP_502349.1	68	280.796	288	198	Ubiquitin Fusion Degradation (yeast UFD homolog) family member (ufd-1)
Locus_9312_Transcript_3/3_Conf_0.600	1000	20	1.12E-71	NP_502349.1	68	274.633	281	193	Ubiquitin Fusion Degradation (yeast UFD homolog) family member (ufd-1)
Locus_9313_Transcript_1/1_Conf_1.000	165	0							
Locus_9314_Transcript_1/1_Conf_1.000	485	20	4.95E-25	XP_001898906.1	71	117.472	113	81	Male sterility protein
Locus_9315_Transcript_1/1_Conf_1.000	149	1	7.49E-05	XP_001520666.1	85	50.447	34	29	PREDICTED: similar to snRNP core protein SMX5d
Locus_9316_Transcript_1/2_Conf_1.000	528	1	4.42E-04	XP_001975649.1	47	48.1358	131	62	GG20442
Locus_9316_Transcript_2/2_Conf_1.000	528	1	4.42E-04	XP_001975649.1	47	48.1358	131	62	GG20442
Locus_9317_Transcript_1/1_Conf_1.000	674	20	9.25E-40	XP_002634958.1	79	167.548	148	117	Hypothetical protein CBG13493
Locus_9318_Transcript_1/1_Conf_1.000	293	0							
Locus_9319_Transcript_1/1_Conf_1.000	303	20	1.05E-27	XP_002637403.1	78	126.331	91	71	Hypothetical protein CBG19110
Locus_932_Transcript_1/2_Conf_1.000	2353	20	2.29E-70	XP_001894300.1	73	271.937	244	179	DnaJ domain containing protein
Locus_932_Transcript_2/2_Conf_1.000	1053	20	2.00E-74	XP_001894300.1	67	283.878	302	204	DnaJ domain containing protein
Locus_9320_Transcript_1/1_Conf_1.000	449	0							

Locus_9321_Transcript_1/1_Conf_1.000	510	20	2.23E-52	NP_496492.1	87	208.379	132	115	hypothetical protein C47D12.2
Locus_9322_Transcript_1/1_Conf_1.000	327	20	5.05E-30	XP_001148215.1	100	134.035	81	81	PREDICTED: guanylate binding protein 2, interferon-inducible isoform 1
Locus_9323_Transcript_1/1_Conf_1.000	176	4	3.73E-09	XP_002638565.1	86	64.6994	38	33	Hypothetical protein CBG05606
Locus_9324_Transcript_1/1_Conf_1.000	161	0							
Locus_9325_Transcript_1/1_Conf_1.000	147	0							
Locus_9326_Transcript_1/1_Conf_1.000	475	0							
Locus_9327_Transcript_1/1_Conf_1.000	410	0							
Locus_9328_Transcript_1/3_Conf_0.778	1493	20	8.29E-09	XP_002166796.1	40	66.6254	422	170	PREDICTED: similar to U1 small nuclear ribonucleoprotein A, partial
Locus_9328_Transcript_2/3_Conf_0.778	1322	6	5.94E-08	XP_002166796.1	40	63.5438	430	173	PREDICTED: similar to U1 small nuclear ribonucleoprotein A, partial
Locus_9328_Transcript_3/3_Conf_0.778	1550	19	8.67E-09	XP_002166796.1	40	66.6254	422	170	PREDICTED: similar to U1 small nuclear ribonucleoprotein A, partial
Locus_9329_Transcript_1/1_Conf_1.000	171	0							
Locus_933_Transcript_1/1_Conf_1.000	212	0							
Locus_9330_Transcript_1/1_Conf_1.000	1742	20	3.25E-90	ACI49036.1	77	309.686	231	179	hypothetical protein Cbre_JD07.003
Locus_9331_Transcript_1/1_Conf_1.000	1136	20	2.85E-77	NP_491454.2	72	293.508	257	187	hypothetical protein F54D7.2
Locus_9332_Transcript_1/1_Conf_1.000	916	20	4.34E-88	XP_001898477.1	73	328.946	286	211	E1-E2 ATPase family protein
Locus_9333_Transcript_1/1_Conf_1.000	757	20	4.07E-24	XP_002638619.1	51	115.931	229	118	Hypothetical protein CBG05671
Locus_9334_Transcript_1/1_Conf_1.000	1317	20	8.49E-148	NP_502604.1	83	528.094	376	313	SELD (SelD homolog) involved in selenophosphate synthesis family member (seld-1)
Locus_9335_Transcript_1/1_Conf_1.000	934	20	5.01E-63	XP_001898033.1	66	245.743	301	199	UDP-glucose:Glycoprotein Glucosyltransferase containing protein

Locus_9336_Transcript_1/1_Conf_1.000	303	0							
Locus_9337_Transcript_1/1_Conf_1.000	245	0							
Locus_9338_Transcript_1/1_Conf_1.000	568	0							
Locus_9339_Transcript_1/1_Conf_1.000	751	20	2.80E-33	NP_496325.1	54	146.362	230	126	Nuclear Pore complex Protein family member (npp-19)
Locus_934_Transcript_1/2_Conf_1.000	411	20	8.55E-22	XP_002132837.1	57	106.686	130	75	GA26044
Locus_934_Transcript_2/2_Conf_1.000	1482	20	1.82E-32	EFN76280.1	52	145.206	280	148	Serine/threonine-protein kinase grp
Locus_9340_Transcript_1/1_Conf_1.000	439	0							
Locus_9341_Transcript_1/1_Conf_1.000	312	0							
Locus_9342_Transcript_1/3_Conf_0.400	1173	20	4.51E-142	XP_002647050.1	97	508.834	269	263	C. briggsae CBR-UNC-64 protein

Locus_9342_Transcript_2/3_Conf_0.600	1178	20	2.48E-148	NP_001022615.1	96	529.635	291	281	UNCoordinated family member (unc-64)
Locus_9342_Transcript_3/3_Conf_0.600	1113	20	8.44E-143	XP_002647050.1	95	511.146	293	281	C. briggsae CBR-UNC-64 protein
Locus_9343_Transcript_1/1_Conf_1.000	737	20	2.21E-112	NP_001122565.1	96	409.068	245	236	Variable ABnormal morphology family member (vab-10)
Locus_9344_Transcript_1/1_Conf_1.000	681	20	2.15E-07	XP_001898127.1	43	60.077	192	84	CG32584-PB
Locus_9345_Transcript_1/1_Conf_1.000	550	20	6.83E-38	XP_001902677.1	66	160.614	154	103	5'-nucleotidase, cytosolic III
Locus_9346_Transcript_1/1_Conf_1.000	198	0							

Locus_9347_Transcript_1/1_Conf_1.000	143	20	9.11E-16	XP_791039.2	91	86.6557	47	43	PREDICTED: similar to HCF
Locus_9348_Transcript_1/1_Conf_1.000	343	0							
Locus_9349_Transcript_1/2_Conf_1.000	1027	20	2.13E-119	XP_002631088.1	92	423.705	247	229	Hypothetical protein CBG02861
Locus_9349_Transcript_2/2_Conf_1.000	1448	20	0	NP_496469.1	91	668.692	396	363	hypothetical protein F54D5.7
Locus_935_Transcript_1/1_Conf_1.000	922	20	1.96E-104	NP_498671.2	82	383.259	256	212	Uridine PhosPhorylase family member (upp-1)
Locus_9350_Transcript_1/1_Conf_1.000	939	20	4.29E-62	NP_741714.1	75	242.662	237	179	related to yeast Vacuolar Protein Sorting factor family member (vps-45)
Locus_9351_Transcript_1/1_Conf_1.000	794	20	9.22E-70	NP_495662.2	86	267.7	236	205	PaTChed family member (ptc-1)
Locus_9352_Transcript_1/1_Conf_1.000	770	4	2.09E-23	XP_002640753.1	56	113.62	195	110	Hypothetical protein CBG24190
Locus_9353_Transcript_1/1_Conf_1.000	775	20	2.43E-19	CAA21536.2	64	100.138	115	74	C. elegans protein Y37D8A.21, confirmed by transcript evidence
Locus_9354_Transcript_1/1_Conf_1.000	414	20	2.66E-15	EFO19751.1	76	85.1149	71	54	prefoldin subunit 4
Locus_9355_Transcript_1/1_Conf_1.000	287	0							

Locus_9356_Transcript_1/1_Conf_1.000	384	20	2.58E-26	XP_002631057.1	86	121.709	73	63	Hypothetical protein CBG02821
Locus_9357_Transcript_1/1_Conf_1.000	1197	20	9.17E-106	XP_001900080.1	71	388.267	369	263	Protein-tyrosine phosphatase containing protein
Locus_9358_Transcript_1/1_Conf_1.000	616	20	3.41E-40	EFO26237.1	66	168.703	170	113	hypothetical protein LOAG_02249
Locus_9359_Transcript_1/1_Conf_1.000	200	0							
Locus_936_Transcript_1/1_Conf_1.000	1563	20	0	XP_002631703.1	83	704.516	502	420	Hypothetical protein CBG20902
Locus_9360_Transcript_1/1_Conf_1.000	553	20	3.79E-60	NP_500728.1	80	234.572	161	130	hypothetical protein C24D10.6
Locus_9361_Transcript_1/1_Conf_1.000	388	20	4.36E-42	XP_001891800.1	86	174.096	129	112	hypothetical protein
Locus_9362_Transcript_1/1_Conf_1.000	1257	20	0	ACJ65067.1	96	726.087	378	363	Lgc-53
Locus_9363_Transcript_1/1_Conf_1.000	142	6	1.01E-06	XP_002639297.1	70	56.6102	41	29	Hypothetical protein CBG03867

Locus_9364_Transcript_1/1_Conf_1.000	1265	20	2.58E-122	XP_002640436.1	77	443.351	351	271	Hypothetical protein CBG08488
Locus_9365_Transcript_1/1_Conf_1.000	652	20	3.89E-48	NP_001023390.1	82	195.282	125	103	PDZ eXchange Factor family member (pxf-1)
Locus_9366_Transcript_1/1_Conf_1.000	525	0							
Locus_9367_Transcript_1/1_Conf_1.000	289	2	1.94E-29	EAW99534.1	90	132.109	73	66	hCG1989828
Locus_9368_Transcript_1/1_Conf_1.000	188	0							
Locus_9369_Transcript_1/1_Conf_1.000	1251	20	7.73E-119	NP_500157.2	68	431.795	430	295	Cleavage and Polyadenylation Specificity Factor family member (cpsf-1)
Locus_937_Transcript_1/1_Conf_1.000	1615	0							
Locus_9370_Transcript_1/1_Conf_1.000	131	0							
Locus_9371_Transcript_1/1_Conf_1.000	407	20	2.85E-41	NP_505349.1	90	171.4	94	85	hypothetical protein C25E10.12
Locus_9372_Transcript_1/1_Conf_1.000	339	20	5.00E-14	Q16937.1	62	80.8777	72	45	Ancylostoma secreted protein
Locus_9373_Transcript_1/1_Conf_1.000	540	2	2.74E-04	XP_001893013.1	44	48.9062	169	75	hypothetical protein Bm1_07715
Locus_9374_Transcript_1/1_Conf_1.000	318	0							
Locus_9375_Transcript_1/1_Conf_1.000	898	20	4.25E-40	EFO27819.1	76	169.474	172	131	hypothetical protein LOAG_00655
Locus_9376_Transcript_1/1_Conf_1.000	977	20	7.41E-97	NP_492351.1	78	358.221	283	221	hypothetical protein K07A12.7
Locus_9377_Transcript_1/1_Conf_1.000	437	20	3.22E-45	XP_001902787.1	83	184.496	132	110	SD24044p
Locus_9378_Transcript_1/1_Conf_1.000	268	20	1.99E-26	XP_001896269.1	90	122.094	88	80	BTB/POZ domain containing protein
Locus_9379_Transcript_1/1_Conf_1.000	1073	5	1.72E-12	A8X9H4.2	61	78.1814	83	51	Chondroitin proteoglycan 4
Locus_938_Transcript_1/1_Conf_1.000	1667	20	9.74E-179	NP_495768.1	74	631.328	496	371	hypothetical protein F49E12.1
Locus_9380_Transcript_1/1_Conf_1.000	315	0							
Locus_9381_Transcript_1/2_Conf_1.000	673	5	3.78E-17	NP_495424.2	51	92.4337	158	82	hypothetical protein F22D3.6
Locus_9381_Transcript_2/2_Conf_1.000	468	5	2.21E-17	NP_495424.2	51	92.0485	157	81	hypothetical protein F22D3.6
Locus_9382_Transcript_1/1_Conf_1.000	517	3	7.38E-06	XP_002932706.1	39	53.9138	158	63	PREDICTED: hypothetical protein LOC779458

Locus_9383_Transcript_1/1_Conf_1.000	731	3	3.81E-16	XP_002631172.1	79	89.3521	63	50	Hypothetical protein CBG02958
Locus_9384_Transcript_1/2_Conf_1.000	1497	3	8.51E-54	NP_001041132.1	51	216.083	523	268	hypothetical protein F58E10.1
Locus_9384_Transcript_2/2_Conf_1.000	1539	3	1.66E-68	NP_001041133.1	53	265.003	562	302	hypothetical protein F58E10.1
Locus_9385_Transcript_1/2_Conf_1.000	705	0							
Locus_9385_Transcript_2/2_Conf_1.000	320	0							
Locus_9386_Transcript_1/1_Conf_1.000	468	7	1.06E-11	XP_001893483.1	54	73.1738	146	79	hypothetical protein Bm1_10050
Locus_9387_Transcript_1/1_Conf_1.000	525	3	2.62E-09	NP_491108.2	63	65.4698	102	65	LiPid Depleted family member (lpd-6)
Locus_9388_Transcript_1/1_Conf_1.000	863	4	4.12E-37	XP_001893140.1	64	159.458	172	111	hypothetical protein Bm1_08345
Locus_9389_Transcript_1/1_Conf_1.000	238	0							
Locus_939_Transcript_1/2_Conf_1.000	449	20	4.59E-31	EFO16907.1	82	137.502	106	87	sarcoma antigen NY-SAR-91
Locus_939_Transcript_2/2_Conf_1.000	449	20	4.58E-31	EFO16907.1	82	137.502	106	87	sarcoma antigen NY-SAR-91
Locus_9390_Transcript_1/3_Conf_0.500	748	20	1.34E-120	NP_510442.2	93	436.417	240	225	hypothetical protein F40E10.6
Locus_9390_Transcript_2/3_Conf_0.500	766	20	5.66E-122	NP_510442.2	90	441.039	253	230	hypothetical protein F40E10.6
Locus_9390_Transcript_3/3_Conf_0.500	765	20	8.73E-123	NP_510442.2	91	443.736	255	233	hypothetical protein F40E10.6
Locus_9391_Transcript_1/1_Conf_1.000	424	12	4.14E-48	CBK19481.1	92	194.126	108	100	C. elegans protein Y105C5A.15a, partially confirmed by transcript evidence
Locus_9392_Transcript_1/1_Conf_1.000	406	20	1.74E-22	NP_001021008.1	59	108.997	132	78	PolyBRoMo domain containing family member (pbrm-1)
Locus_9393_Transcript_1/1_Conf_1.000	1502	20	8.63E-14	EFO20919.1	54	83.1889	122	66	hypothetical protein LOAG_07571
Locus_9394_Transcript_1/1_Conf_1.000	277	20	2.18E-17	CBL43463.1	83	92.0485	59	49	C. elegans protein Y52B11C.1, partially confirmed by transcript evidence
Locus_9395_Transcript_1/1_Conf_1.000	777	20	1.77E-94	CAZ65484.1	78	349.747	257	203	C. elegans protein F02H6.5c, confirmed by transcript evidence
Locus_9396_Transcript_1/1_Conf_1.000	567	20	3.44E-43	EFO23880.1	80	178.333	172	139	transportin-SR

Locus_9397_Transcript_1/1_Conf_1.000	655	20	2.69E-89	NP_504166.2	86	332.028	218	188	hypothetical protein H43I07.2
Locus_9398_Transcript_1/1_Conf_1.000	220	20	5.91E-18	EFO24415.1	80	93.9745	72	58	hypothetical protein LOAG_04067
Locus_9399_Transcript_1/1_Conf_1.000	1394	20	9.08E-164	NP_001022390.1	85	581.252	428	365	Rho GTPase Activating protein family member (rga-1)
Locus_94_Transcript_1/4_Conf_0.214	461	9	2.25E-06	NP_495083.1	45	55.4546	97	44	LYSozyme family member (lys-8)
Locus_94_Transcript_2/4_Conf_0.214	419	9	3.02E-06	NP_495083.1	45	55.0694	95	43	LYSozyme family member (lys-8)
Locus_94_Transcript_3/4_Conf_0.429	840	20	4.65E-30	NP_495083.1	52	135.961	216	113	LYSozyme family member (lys-8)
Locus_94_Transcript_4/4_Conf_0.429	840	20	4.65E-30	NP_495083.1	52	135.961	216	113	LYSozyme family member (lys-8)
Locus_940_Transcript_1/2_Conf_1.000	2766	4	2.13E-30	NP_495686.2	45	139.428	514	233	hypothetical protein T05H10.1
Locus_940_Transcript_2/2_Conf_1.000	2766	4	6.19E-30	NP_495686.2	45	137.887	514	233	hypothetical protein T05H10.1
Locus_9400_Transcript_1/1_Conf_1.000	145	0							
Locus_9401_Transcript_1/1_Conf_1.000	446	0							

Locus_9402_Transcript_1/1_Conf_1.000	1124	20	6.11E-149	NP_508927.2	86	531.561	356	307	DihydroPYrimidine Dehydrogenase family member (dpyd-1)
Locus_9403_Transcript_1/1_Conf_1.000	1236	20	0	EFO21881.1	96	673.7	378	364	DNA-directed RNA polymerase II second largest subunit
Locus_9404_Transcript_1/1_Conf_1.000	166	20	4.44E-18	NP_509932.2	92	94.3597	54	50	LEVamisole resistant family member (lev-8)
Locus_9405_Transcript_1/1_Conf_1.000	244	0							
Locus_9406_Transcript_1/2_Conf_1.000	780	0							
Locus_9406_Transcript_2/2_Conf_1.000	1175	1	2.57E-04	CAR63591.1	69	51.2174	52	36	putative myelin transcription factor 1-like
Locus_9407_Transcript_1/1_Conf_1.000	360	0							
Locus_9408_Transcript_1/1_Conf_1.000	184	0							
Locus_9409_Transcript_1/1_Conf_1.000	789	20	6.54E-76	NP_509268.1	86	288.115	186	160	hypothetical protein F48E3.3
Locus_941_Transcript_1/1_Conf_1.000	523	4	4.62E-43	XP_002642171.1	73	177.563	148	109	Hypothetical protein CBG18136
Locus_9410_Transcript_1/2_Conf_1.000	1711	20	0		76	644.425	535	409	protein C16A3.1

Locus_9410_Transcript_2/2_Conf_1.000	1887	20	0		76	641.343	534	408	protein C16A3.1
Locus_9411_Transcript_1/3_Conf_0.400	542	20	1.52E-71	A8WPF0.2	82	272.322	186	154	Succinate dehydrogenase ubiquinone iron-sulfur subunit, mitochondria
Locus_9411_Transcript_2/3_Conf_0.600	943	20	3.25E-118	A8WPF0.2	91	429.098	240	220	Succinate dehydrogenase ubiquinone iron-sulfur subunit, mitochondrial
Locus_9411_Transcript_3/3_Conf_0.400	638	20	1.09E-68	A8WPF0.2	92	263.462	139	129	Succinate dehydrogenase ubiquinone iron-sulfur subunit, mitochondria

Locus_9412_Transcript_1/1_Conf_1.000	524	10	1.49E-25	XP_002645282.1	80	119.398	110	89	C. briggsae CBR-AJM-1 protein
Locus_9413_Transcript_1/1_Conf_1.000	316	5	1.27E-04	NP_001123111.1	66	49.6766	50	33	PeRoXisome assembly factor family member (prx-3)
Locus_9414_Transcript_1/1_Conf_1.000	340	5	4.66E-28	XP_002646741.1	76	127.487	109	83	Hypothetical protein CBG13135
Locus_9415_Transcript_1/1_Conf_1.000	247	0							
Locus_9416_Transcript_1/2_Conf_1.000	1244	20	2.67E-71	EFO20351.1	58	273.863	402	237	phosphatidylinositol 3
Locus_9416_Transcript_2/2_Conf_1.000	1244	20	8.03E-68	EFO20351.1	58	262.307	402	237	phosphatidylinositol 3
Locus_9417_Transcript_1/2_Conf_1.000	1077	20	3.55E-74	EFO28087.1	66	283.108	291	194	coronin 2A
Locus_9417_Transcript_2/2_Conf_1.000	1078	20	3.55E-74	EFO28087.1	66	283.108	291	194	coronin 2A
Locus_9418_Transcript_1/1_Conf_1.000	431	20	5.19E-43	NP_491270.2	72	177.178	143	104	Low-density lipoprotein Receptor Related family member (lrp-2)
Locus_9419_Transcript_1/1_Conf_1.000	271	1	8.11E-04	CAB40818.1	54	46.9802	92	50	intermediate filament
Locus_942_Transcript_1/1_Conf_1.000	2062	20	7.70E-176	XP_002633023.1	85	622.083	424	363	Hypothetical protein CBG21797
Locus_9420_Transcript_1/1_Conf_1.000	929	4	1.42E-09	NP_001022632.1	50	68.1662	159	80	Gamma-tubulin Interacting Protein family member (gip-1)
Locus_9421_Transcript_1/1_Conf_1.000	453	1	1.63E-04	XP_002648823.1	42	49.2914	87	37	Hypothetical protein CBG16936
Locus_9422_Transcript_1/1_Conf_1.000	397	9	1.02E-46	XP_002633446.1	89	189.504	118	106	Hypothetical protein CBG06214

Locus_9423_Transcript_1/1_Conf_1.000	1115	20	2.80E-37	EFO18643.1	70	160.614	167	117	dual specificity phosphatase
Locus_9424_Transcript_1/1_Conf_1.000	1295	8	3.43E-69	CBW44396.1	64	266.929	332	214	C. elegans protein Y43F8B.1e, partially confirmed by transcript evidence
Locus_9425_Transcript_1/1_Conf_1.000	1564	20	3.27E-80	NP_496542.1	55	303.908	478	265	hypothetical protein ZK930.1
Locus_9426_Transcript_1/1_Conf_1.000	138	0							
Locus_9427_Transcript_1/1_Conf_1.000	359	2	9.20E-24	XP_002643597.1	71	113.235	92	66	Hypothetical protein CBG16326
Locus_9428_Transcript_1/1_Conf_1.000	1016	0							
Locus_9429_Transcript_1/3_Conf_0.846	1357	1	7.07E-04	XP_001369383.1	38	50.0618	451	175	PREDICTED: similar to cellulosomal scaffoldin anchoring protein, putative
Locus_9429_Transcript_2/3_Conf_0.846	1357	2	1.86E-04	XP_001369383.1	39	51.9878	451	176	PREDICTED: similar to cellulosomal scaffoldin anchoring protein, putative
Locus_9429_Transcript_3/3_Conf_0.846	1357	0							
Locus_943_Transcript_1/1_Conf_1.000	201	16	8.64E-22	XP_001624697.1	81	106.686	66	54	predicted protein
Locus_9430_Transcript_1/1_Conf_1.000	378	0							
Locus_9431_Transcript_1/1_Conf_1.000	794	0							
Locus_9432_Transcript_1/1_Conf_1.000	565	20	3.58E-85	XP_002645087.1	93	317.775	188	176	Hypothetical protein CBG16761
Locus_9433_Transcript_1/1_Conf_1.000	378	20	5.19E-59	BAG57116.1	100	230.335	105	105	unnamed protein product
Locus_9434_Transcript_1/1_Conf_1.000	1285	20	3.99E-86	NP_495323.1	61	323.168	426	261	Temporarily Assigned Gene name family member (tag-184)
Locus_9435_Transcript_1/3_Conf_0.400	299	0							
Locus_9435_Transcript_2/3_Conf_0.600	1064	20	4.57E-42	XP_002640153.1	76	176.407	209	159	Hypothetical protein CBG12652
Locus_9435_Transcript_3/3_Conf_0.600	1166	20	5.60E-44	XP_002640153.1	72	182.956	228	166	Hypothetical protein CBG12652
Locus_9436_Transcript_1/1_Conf_1.000	137	20	3.73E-09	NP_001123161.1	69	64.6994	42	29	hypothetical protein K03A11.6
Locus_9437_Transcript_1/1_Conf_1.000	226	20	1.27E-12	XP_002742121.1	68	76.2554	74	51	PREDICTED: endonuclease-reverse transcriptase HmRTE-e01-like, partial
Locus_9438_Transcript_1/1_Conf_1.000	588	20	2.63E-20	CAD21647.3	60	102.449	157	95	C. elegans protein T03F6.6, confirmed by transcript evidence

Locus_9439_Transcript_1/1_Conf_1.000	1146	0							
Locus_944_Transcript_1/2_Conf_1.000	1498	20	2.32E-51	XP_001894111.1	83	207.994	179	149	IWS1 C-terminus family protein
Locus_944_Transcript_2/2_Conf_1.000	1492	20	2.30E-51	XP_001894111.1	83	207.994	179	149	IWS1 C-terminus family protein
Locus_9440_Transcript_1/2_Conf_1.000	364	20	7.71E-31	NP_001021422.1	73	136.732	120	88	hypothetical protein F27D4.7
Locus_9440_Transcript_2/2_Conf_1.000	364	20	7.71E-31	NP_001021422.1	73	136.732	120	88	hypothetical protein F27D4.7
Locus_9441_Transcript_1/1_Conf_1.000	705	20	8.55E-79	NP_503409.1	86	297.36	189	164	SyNapTotagmin family member (snt-5)
Locus_9442_Transcript_1/2_Conf_1.000	350	0							
Locus_9442_Transcript_2/2_Conf_1.000	348	0							
Locus_9443_Transcript_1/1_Conf_1.000	905	20	4.25E-80	XP_002633330.1	79	302.368	263	209	C. briggsae CBR-DNJ-2 protein
Locus_9444_Transcript_1/1_Conf_1.000	593	20	6.02E-97	CAR63664.1	94	357.066	197	186	putative Dynein Heavy Chain family member
Locus_9445_Transcript_1/1_Conf_1.000	142	0							
Locus_9446_Transcript_1/1_Conf_1.000	351	20	7.60E-18	NP_507806.2	72	93.5893	84	61	hypothetical protein Y43F8C.6
Locus_9447_Transcript_1/1_Conf_1.000	395	0							
Locus_9448_Transcript_1/1_Conf_1.000	308	4	3.49E-07	CBM41222.1	53	58.151	82	44	C. elegans protein T10G3.3b, partially confirmed by transcript evidence
Locus_9449_Transcript_1/1_Conf_1.000	1028	20	5.64E-74	XP_002639957.1	76	282.337	230	176	C. briggsae CBR-SNF-1 protein
Locus_945_Transcript_1/3_Conf_0.750	391	0							
Locus_945_Transcript_2/3_Conf_0.625	392	0							
Locus_945_Transcript_3/3_Conf_0.750	391	0							
Locus_9450_Transcript_1/1_Conf_1.000	426	6	9.86E-34	NP_499474.1	82	146.362	103	85	BED-type zinc finger transcription factor family member (bed-2)
Locus_9451_Transcript_1/2_Conf_1.000	839	20	3.23E-116	NP_503114.1	86	422.165	267	230	fatty acid ELOngation family member (elo-2)
Locus_9451_Transcript_2/2_Conf_1.000	839	20	9.39E-116	NP_503114.1	85	420.624	267	229	fatty acid ELOngation family member (elo-2)
Locus_9452_Transcript_1/1_Conf_1.000	414	20	3.23E-29	NP_507813.1	65	131.339	135	89	hypothetical protein Y43F8C.13
Locus_9453_Transcript_1/1_Conf_1.000	732	20	9.10E-42	XP_002641174.1	76	174.481	135	103	Hypothetical protein CBG09035
Locus_9454_Transcript_1/1_Conf_1.000	1583	20	2.18E-156	CAA84656.2	71	556.984	538	383	C. elegans protein F10F2.2, confirmed by transcript evidence
Locus_9455_Transcript_1/1_Conf_1.000	364	20	6.52E-30	XP_002645988.1	75	133.65	111	84	Hypothetical protein CBG07773

Locus_9456_Transcript_1/1_Conf_1.000	336	0							
Locus_9457_Transcript_1/1_Conf_1.000	571	0							
Locus_9458_Transcript_1/1_Conf_1.000	210	0							
Locus_9459_Transcript_1/1_Conf_1.000	814	20	2.90E-50	XP_002634501.1	61	202.986	286	177	C. briggsae CBR-SMGL-2 protein
Locus_946_Transcript_1/1_Conf_1.000	1283	1	1.00E-04	NP_493046.2	50	52.7582	124	62	hypothetical protein F58D5.5
Locus_9460_Transcript_1/1_Conf_1.000	261	0							
Locus_9461_Transcript_1/1_Conf_1.000	303	0							
Locus_9462_Transcript_1/1_Conf_1.000	274	0							
Locus_9463_Transcript_1/1_Conf_1.000	177	0							
Locus_9464_Transcript_1/1_Conf_1.000	203	0							
Locus_9465_Transcript_1/1_Conf_1.000	353	20	5.23E-43	XP_002642228.1	90	177.178	93	84	Hypothetical protein CBG18204
Locus_9466_Transcript_1/1_Conf_1.000	522	3	4.21E-20	XP_002633326.1	68	101.293	116	79	Hypothetical protein CBG06063
Locus_9467_Transcript_1/1_Conf_1.000	290	0							
Locus_9468_Transcript_1/1_Conf_1.000	442	3	1.14E-21	XP_002637243.1	72	106.301	142	103	Hypothetical protein CBG18919
Locus_9469_Transcript_1/1_Conf_1.000	1274	20	8.42E-113	XP_001899184.1	63	411.764	466	298	SWIM zinc finger family protein
Locus_947_Transcript_1/2_Conf_1.000	804	5	6.92E-12	XP_002634825.1	59	75.485	137	81	Hypothetical protein CBG13933
Locus_947_Transcript_2/2_Conf_1.000	804	5	6.92E-12	XP_002634825.1	59	75.485	137	81	Hypothetical protein CBG13933
Locus_9470_Transcript_1/1_Conf_1.000	650	20	5.18E-53	XP_002645123.1	76	211.46	177	136	Hypothetical protein CBG16817
Locus_9471_Transcript_1/1_Conf_1.000	553	0							
Locus_9472_Transcript_1/1_Conf_1.000	301	0							
Locus_9473_Transcript_1/2_Conf_1.000	919	0							
Locus_9473_Transcript_2/2_Conf_1.000	444	0							
Locus_9474_Transcript_1/1_Conf_1.000	496	0							

Locus_9475_Transcript_1/1_Conf_1.000	177	20	3.13E-24	NP_506269.1	98	114.775	58	57	EATing: abnormal pharyngeal pumping family member (eat-6)
Locus_9476_Transcript_1/1_Conf_1.000	260	5	7.40E-21	XP_001897819.1	89	103.605	66	59	Surfeit locus protein 5 containing protein
Locus_9477_Transcript_1/1_Conf_1.000	952	20	8.85E-140	XP_002642201.1	86	500.745	297	256	C. briggsae CBR-ARX-3 protein
Locus_9478_Transcript_1/1_Conf_1.000	1230	20	3.16E-125	XP_002642224.1	86	452.981	292	253	Hypothetical protein CBG18198
Locus_9479_Transcript_1/1_Conf_1.000	1011	5	5.83E-100	NP_001022726.1	79	368.622	321	256	hypothetical protein R144.12
Locus_948_Transcript_1/2_Conf_1.000	362	0							
Locus_948_Transcript_2/2_Conf_1.000	362	0							

Locus_9480_Transcript_1/1_Conf_1.000	515	20	8.97E-57	EFO25632.1	84	223.016	167	141	zinc finger protein
Locus_9481_Transcript_1/1_Conf_1.000	281	0							
Locus_9482_Transcript_1/1_Conf_1.000	297	2	2.36E-19	NP_506377.2	71	98.5969	91	65	hypothetical protein F53F4.12
Locus_9483_Transcript_1/1_Conf_1.000	159	0							
Locus_9484_Transcript_1/1_Conf_1.000	1050	0							
Locus_9485_Transcript_1/1_Conf_1.000	178	0							
Locus_9486_Transcript_1/1_Conf_1.000	335	0							
Locus_9487_Transcript_1/1_Conf_1.000	749	20	1.23E-65	XP_002641974.1	85	253.832	163	140	Hypothetical protein CBG16681
Locus_9488_Transcript_1/1_Conf_1.000	618	20	1.18E-48	XP_001892599.1	81	196.823	156	127	oxidoreductase, zinc-binding dehydrogenase family protein
Locus_9489_Transcript_1/1_Conf_1.000	887	20	3.70E-81	XP_002642305.1	78	305.834	254	199	Hypothetical protein CBG18297
Locus_949_Transcript_1/1_Conf_1.000	1470	20	5.23E-32	AAO63576.1	60	143.665	175	105	secreted protein 4 precursor
Locus_9490_Transcript_1/1_Conf_1.000	302	0							
Locus_9491_Transcript_1/1_Conf_1.000	148	0							
Locus_9492_Transcript_1/2_Conf_1.000	1226	20	7.66E-39	NP_001122711.1	61	166.007	186	114	CBP/p300 homolog family member (cbp-1)

Locus_9492_Transcript_2/2_Conf_1.000	1217	20	2.88E-38	NP_001122711.1	61	164.081	183	113	CBP/p300 homolog family member (cbp-1)
Locus_9493_Transcript_1/1_Conf_1.000	366	1	3.25E-05	NP_490742.1	56	51.6026	75	42	DEfective P granules and Sterile family member (deps-1)
Locus_9494_Transcript_1/1_Conf_1.000	1787	20	0	EFO27339.1	78	737.643	601	474	dynein heavy chain protein 1
Locus_9495_Transcript_1/1_Conf_1.000	613	10	6.13E-42	ADI24664.1	81	174.481	132	107	Hypothetical protein Y38C1AA.14
Locus_9496_Transcript_1/1_Conf_1.000	562	0							
Locus_9497_Transcript_1/1_Conf_1.000	596	4	4.78E-25	XP_002644764.1	85	118.242	77	66	Hypothetical protein CBG14775
Locus_9498_Transcript_1/1_Conf_1.000	131	0							
Locus_9499_Transcript_1/1_Conf_1.000	762	20	1.77E-75	EFO21942.1	77	286.574	225	175	kynurenine-oxoglutarate transaminase
Locus_95_Transcript_1/1_Conf_1.000	1105	20	1.61E-53	XP_002636220.1	56	214.542	315	177	Hypothetical protein CBG12141
Locus_950_Transcript_1/1_Conf_1.000	1825	20	7.87E-09	ACD88885.1	67	65.855	76	51	propionyl-coenzyme A carboxylase beta subunit
Locus_9500_Transcript_1/1_Conf_1.000	320	20	1.87E-40	NP_498418.2	80	168.703	108	87	hypothetical protein T26A5.5
Locus_9501_Transcript_1/1_Conf_1.000	1076	20	1.62E-119	NP_504433.2	89	433.721	258	232	hypothetical protein F08F3.4
Locus_9502_Transcript_1/1_Conf_1.000	163	0							
Locus_9503_Transcript_1/1_Conf_1.000	598	0							
Locus_9504_Transcript_1/1_Conf_1.000	369	3	1.71E-09	NP_492202.2	55	65.855	121	67	hypothetical protein C54G4.3
Locus_9505_Transcript_1/1_Conf_1.000	335	4	3.27E-13	XP_002638288.1	61	78.1814	103	63	Hypothetical protein CBG22835

Locus_9506_Transcript_1/1_Conf_1.000	267	5	2.89E-09	XP_002639084.1	63	65.0846	85	54	Hypothetical protein CBG14902
Locus_9507_Transcript_1/1_Conf_1.000	407	0							
Locus_9508_Transcript_1/2_Conf_1.000	1293	20	1.99E-109	NP_501598.2	74	400.593	315	235	Prolyl Carboxy Peptidase like family member (pcp-3)
Locus_9508_Transcript_2/2_Conf_1.000	443	20	5.44E-48	XP_002633021.1	76	193.741	147	112	Hypothetical protein CBG21793
Locus_9509_Transcript_1/1_Conf_1.000	694	20	7.30E-75	XP_002640668.1	95	284.263	231	220	C. briggsae CBR-UNC-54 protein
Locus_951_Transcript_1/1_Conf_1.000	816	0							
Locus_9510_Transcript_1/1_Conf_1.000	230	0							
Locus_9511_Transcript_1/1_Conf_1.000	364	20	3.59E-20	XP_002630503.1	76	101.293	101	77	Hypothetical protein CBG24740
Locus_9512_Transcript_1/1_Conf_1.000	253	0							
Locus_9513_Transcript_1/1_Conf_1.000	925	20	4.00E-89	XP_002643773.1	92	332.413	188	173	Hypothetical protein CBG01975
Locus_9514_Transcript_1/1_Conf_1.000	905	1	4.97E-04	NP_501638.1	39	49.6766	237	94	hypothetical protein F49C12.15
Locus_9515_Transcript_1/1_Conf_1.000	834	20	7.34E-20	XP_001897972.1	53	102.064	186	99	YY1-associated factor 2
Locus_9516_Transcript_1/1_Conf_1.000	481	5	9.10E-24	XP_002633740.1	65	113.235	135	89	Hypothetical protein CBG03425
Locus_9517_Transcript_1/1_Conf_1.000	587	20	4.65E-33	NP_506445.2	72	144.821	122	88	Serine Palmitoyl Transferase famiLy family member (sptl-3)
Locus_9518_Transcript_1/1_Conf_1.000	210	0							
Locus_9519_Transcript_1/1_Conf_1.000	358	0							
Locus_952_Transcript_1/1_Conf_1.000	834	0							
Locus_9520_Transcript_1/1_Conf_1.000	169	0							
Locus_9521_Transcript_1/1_Conf_1.000	260	0							
Locus_9522_Transcript_1/1_Conf_1.000	879	20	4.08E-48	XP_002636541.1	55	196.052	299	165	Hypothetical protein CBG23228
Locus_9523_Transcript_1/1_Conf_1.000	328	0							

Locus_9524_Transcript_1/1_Conf_1.000	1351	20	1.32E-26	XP_002725019.1	43	125.561	309	135	PREDICTED: aminoadipate-semialdehyde dehydrogenase-like
Locus_9525_Transcript_1/1_Conf_1.000	370	0							
Locus_9526_Transcript_1/1_Conf_1.000	372	20	9.63E-29	XP_002643980.1	89	129.798	82	73	C. briggsae CBR-OCT-2 protein
Locus_9527_Transcript_1/1_Conf_1.000	1401	20	4.99E-77	XP_001895135.1	55	293.123	456	254	replication factor A 73 kDa subunit
Locus_9528_Transcript_1/1_Conf_1.000	506	20	9.61E-16	XP_001948496.1	48	86.6557	129	62	PREDICTED: hypothetical protein
Locus_9529_Transcript_1/1_Conf_1.000	576	20	2.34E-50	NP_490774.2	73	202.216	194	142	PIF1p DNA helicase (yeast) homolog family member (pif-1)
Locus_953_Transcript_1/3_Conf_0.714	826	20	8.72E-42	NP_741664.1	56	174.866	268	152	hypothetical protein Y39B6A.33
Locus_953_Transcript_2/3_Conf_0.714	826	20	1.49E-41	NP_741664.1	56	174.096	268	152	hypothetical protein Y39B6A.33
Locus_953_Transcript_3/3_Conf_0.714	826	20	1.49E-41	NP_741664.1	56	174.096	268	152	hypothetical protein Y39B6A.33
Locus_9530_Transcript_1/1_Conf_1.000	568	0							
Locus_9531_Transcript_1/1_Conf_1.000	535	20	1.21E-41	XP_002642389.1	69	172.94	155	108	C. briggsae CBR-TAG-235 protein
Locus_9532_Transcript_1/1_Conf_1.000	1646	20	1.83E-129	ACI49172.1	68	467.618	550	374	hypothetical protein Csp3_JD01.004
Locus_9533_Transcript_1/1_Conf_1.000	1097	20	3.82E-23	XP_002129449.1	48	113.62	245	118	PREDICTED: hypothetical protein

Locus_9534_Transcript_1/1_Conf_1.000	304	20	3.59E-36	XP_002642379.1	83	154.451	99	83	Hypothetical protein CBG18383
Locus_9535_Transcript_1/1_Conf_1.000	2596	20	0	NP_493625.4	70	887.871	890	625	hypothetical protein F31C3.3
Locus_9536_Transcript_1/1_Conf_1.000	320	20	1.48E-53	AAB99830.2	93	212.231	106	99	thrombospondin
Locus_9537_Transcript_1/1_Conf_1.000	1135	20	8.82E-95	EFO23011.1	71	351.673	327	233	zinc finger protein 395
Locus_9538_Transcript_1/1_Conf_1.000	706	20	2.63E-120	NP_492020.1	98	435.261	201	198	hypothetical protein K10D3.4
Locus_9539_Transcript_1/1_Conf_1.000	810	0							
Locus_954_Transcript_1/4_Conf_0.333	1764	20	1.11E-87	NP_500618.1	83	328.946	233	195	COP9/Signalosome and eIF3 complex shared subunit family member (cif-1)
Locus_954_Transcript_2/4_Conf_0.333	1764	20	1.11E-87	NP_500618.1	83	328.946	233	195	COP9/Signalosome and eIF3 complex shared subunit family member (cif-1)
Locus_954_Transcript_3/4_Conf_0.417	1648	20	8.51E-135	NP_500618.1	78	485.337	390	308	COP9/Signalosome and eIF3 complex shared subunit family member (cif-1)
Locus_954_Transcript_4/4_Conf_0.417	1648	20	8.51E-135	NP_500618.1	78	485.337	390	308	COP9/Signalosome and eIF3 complex shared subunit family member (cif-1)

Locus_9540_Transcript_1/1_Conf_1.000	349	20	7.06E-56	XP_002804745.1	96	219.935	112	108	PREDICTED: hypothetical protein LOC100430062
Locus_9541_Transcript_1/2_Conf_1.000	848	4	1.33E-24	XP_002631646.1	43	117.857	333	145	C. briggsae CBR-LEM-2 protein
Locus_9541_Transcript_2/2_Conf_1.000	830	17	2.57E-25	XP_002631646.1	43	120.168	333	145	C. briggsae CBR-LEM-2 protein
Locus_9542_Transcript_1/1_Conf_1.000	222	0							
Locus_9543_Transcript_1/1_Conf_1.000	331	4	2.43E-08	XP_310525.4	88	62.003	35	31	AGAP000558-PA
Locus_9544_Transcript_1/1_Conf_1.000	918	5	1.09E-30	XP_002636795.1	58	138.272	244	143	Hypothetical protein CBG23538
Locus_9545_Transcript_1/1_Conf_1.000	414	0							
Locus_9546_Transcript_1/1_Conf_1.000	818	20	3.45E-59	XP_002636774.1	80	232.646	205	164	Hypothetical protein CBG23508
Locus_9547_Transcript_1/1_Conf_1.000	873	20	5.06E-107	XP_002633377.1	80	391.734	308	249	C. briggsae CBR-TAG-13 protein
Locus_9548_Transcript_1/1_Conf_1.000	519	3	5.21E-15	NP_001041224.1	72	84.3445	79	57	hypothetical protein C35B8.4
Locus_9549_Transcript_1/2_Conf_1.000	466	0							
Locus_9549_Transcript_2/2_Conf_1.000	1968	20	2.55E-96	XP_001898467.1	63	357.836	475	303	FYVE zinc finger family protein

Locus_955_Transcript_1/1_Conf_1.000	622	20	8.70E-60	XP_002632116.1	82	233.802	159	131	Hypothetical protein CBG06970
Locus_9550_Transcript_1/1_Conf_1.000	455	20	1.73E-22	NP_001022488.1	65	108.997	149	97	UNCoordinated family member (unc-52)
Locus_9551_Transcript_1/1_Conf_1.000	946	20	3.55E-64	XP_002638764.1	65	249.595	297	196	C. briggsae CBR-PTR-11 protein
Locus_9552_Transcript_1/1_Conf_1.000	325	20	5.05E-46	XP_002642541.1	92	187.193	108	100	C. briggsae CBR-DNJ-16 protein
Locus_9553_Transcript_1/1_Conf_1.000	137	0							
Locus_9554_Transcript_1/1_Conf_1.000	185	0							
Locus_9555_Transcript_1/1_Conf_1.000	399	20	5.27E-27	XP_002639434.1	80	124.02	96	77	Hypothetical protein CBG04027
Locus_9556_Transcript_1/1_Conf_1.000	354	20	1.58E-15	XP_001893896.1	100	85.8853	39	39	ubiquitin
Locus_9557_Transcript_1/1_Conf_1.000	818	20	1.62E-16	NP_507534.1	63	90.8929	119	75	hypothetical protein Y37H2A.1
Locus_9558_Transcript_1/1_Conf_1.000	429	0							
Locus_9559_Transcript_1/2_Conf_1.000	585	20	3.21E-42	NP_496711.1	81	175.252	122	100	PhosphatidylInositol SYnthase family member (pisy-1)
Locus_9559_Transcript_2/2_Conf_1.000	447	20	1.16E-42	NP_496711.1	80	176.022	125	101	PhosphatidylInositol SYnthase family member (pisy-1)
Locus_956_Transcript_1/1_Conf_1.000	299	20	3.07E-27	XP_001898464.1	75	124.79	98	74	Innexin inx-3
Locus_9560_Transcript_1/1_Conf_1.000	447	20	1.81E-19	NP_741285.1	75	98.9821	87	66	hypothetical protein Y38C1AA.1
Locus_9561_Transcript_1/1_Conf_1.000	188	0							
Locus_9562_Transcript_1/1_Conf_1.000	212	0							
Locus_9563_Transcript_1/1_Conf_1.000	459	0							
Locus_9564_Transcript_1/4_Conf_0.375	347	20	1.94E-29	XP_002646542.1	86	132.109	86	74	Hypothetical protein CBG20397

Locus_9564_Transcript_2/4_Conf_0.375	305	20	5.94E-31	XP_002646542.1	86	137.117	90	78	Hypothetical protein CBG20397
Locus_9564_Transcript_3/4_Conf_0.375	1171	20	5.62E-60	XP_002646542.1	81	236.113	162	132	Hypothetical protein CBG20397
Locus_9564_Transcript_4/4_Conf_0.375	1171	20	9.59E-60	XP_002646542.1	81	235.343	161	131	Hypothetical protein CBG20397
Locus_9565_Transcript_1/1_Conf_1.000	129	0							
Locus_9566_Transcript_1/1_Conf_1.000	259	3	1.89E-08	NP_509643.1	58	62.3882	90	53	hypothetical protein F36G3.2
Locus_9567_Transcript_1/1_Conf_1.000	390	0							
Locus_9568_Transcript_1/1_Conf_1.000	130	0							
Locus_9569_Transcript_1/1_Conf_1.000	1051	20	1.66E-137	XP_002640755.1	90	493.426	299	272	C. briggsae CBR-ARX-4 protein
Locus_957_Transcript_1/1_Conf_1.000	1916	20	9.86E-53	NP_501987.1	61	213.001	273	169	CYclin B family member (cyb-1)
Locus_9570_Transcript_1/1_Conf_1.000	591	2	4.24E-42	NP_498567.1	64	174.866	194	125	hypothetical protein K04G7.1
Locus_9571_Transcript_1/1_Conf_1.000	162	20	2.70E-15	XP_002633256.1	91	85.1149	46	42	Hypothetical protein CBG05981
Locus_9572_Transcript_1/1_Conf_1.000	1007	10	1.08E-13	EFO15513.1	50	82.0333	221	112	hypothetical protein LOAG_12997
Locus_9573_Transcript_1/3_Conf_0.500	454	20	1.42E-08	XP_002639129.1	44	62.7734	152	68	Hypothetical protein CBG14949

Locus_9573_Transcript_2/3_Conf_0.333	638	20	2.40E-07	XP_001373707.1	42	59.6918	157	66	PREDICTED: similar to epithin
Locus_9573_Transcript_3/3_Conf_0.500	454	20	1.42E-08	XP_002639129.1	44	62.7734	152	68	Hypothetical protein CBG14949
Locus_9574_Transcript_1/1_Conf_1.000	173	5	2.77E-12	XP_002638900.1	78	75.0998	57	45	Hypothetical protein CBG22126
Locus_9575_Transcript_1/1_Conf_1.000	305	0							
Locus_9576_Transcript_1/1_Conf_1.000	239	4	1.02E-22	CBA10135.1	93	109.768	79	74	DAF-16B transcription factor
Locus_9577_Transcript_1/1_Conf_1.000	730	0							
Locus_9578_Transcript_1/1_Conf_1.000	1352	20	6.22E-77	NP_001024778.2	64	292.738	342	222	neuRonal IGCAM family member (rig-1)
Locus_9579_Transcript_1/1_Conf_1.000	299	5	1.14E-05	EFO27165.1	57	53.1434	64	37	hypothetical protein LOAG_01310
Locus_958_Transcript_1/1_Conf_1.000	614	0							
Locus_9580_Transcript_1/1_Conf_1.000	226	20	1.65E-12	XP_001648264.1	76	75.8702	60	46	aromatic amino acid decarboxylase
Locus_9581_Transcript_1/1_Conf_1.000	152	0							
Locus_9582_Transcript_1/1_Conf_1.000	1924	5	4.72E-63	XP_002640718.1	46	247.284	650	305	Hypothetical protein CBG19785
Locus_9583_Transcript_1/1_Conf_1.000	342	0							
Locus_9584_Transcript_1/1_Conf_1.000	484	1	1.96E-05	EFO23192.1	66	52.373	39	26	Mob1/phocein family protein
Locus_9585_Transcript_1/1_Conf_1.000	748	20	3.14E-61	XP_001898476.1	88	239.195	164	145	Amino acid permease family protein
Locus_9586_Transcript_1/1_Conf_1.000	583	20	9.81E-52	NP_493553.1	80	206.838	152	122	hypothetical protein Y54E5A.5
Locus_9587_Transcript_1/1_Conf_1.000	180	0							
Locus_9588_Transcript_1/1_Conf_1.000	359	20	2.68E-23	NP_505849.2	59	111.694	123	73	hypothetical protein T19B10.3
Locus_9589_Transcript_1/1_Conf_1.000	771	20	1.51E-21	AAK60209.1	52	107.457	185	98	vap-1
Locus_959_Transcript_1/1_Conf_1.000	203	0							

Locus_9590_Transcript_1/1_Conf_1.000	1053	20	9.41E-32	AAO63577.1	50	142.124	256	129	secreted protein 5 precursor
Locus_9591_Transcript_1/1_Conf_1.000	897	5	2.05E-18	NP_001022759.1	45	97.4413	238	108	hypothetical protein T12D8.9
Locus_9592_Transcript_1/1_Conf_1.000	302	0							
Locus_9593_Transcript_1/1_Conf_1.000	166	20	8.94E-19	EFO18176.1	94	96.6709	54	51	hypothetical protein LOAG_10319
Locus_9594_Transcript_1/1_Conf_1.000	1510	20	3.98E-67	XP_002637568.1	56	260.381	457	257	Hypothetical protein CBG19301
Locus_9595_Transcript_1/1_Conf_1.000	337	20	3.94E-43	NP_502964.2	85	177.563	112	96	hypothetical protein Y51H4A.7
Locus_9596_Transcript_1/1_Conf_1.000	711	20	1.30E-74	XP_001899675.1	84	283.493	205	174	Zinc finger DHHC domain containing protein 5
Locus_9597_Transcript_1/1_Conf_1.000	128	0							
Locus_9598_Transcript_1/1_Conf_1.000	682	20	6.57E-65	NP_499895.2	73	251.136	229	168	hypothetical protein T21D12.9
Locus_9599_Transcript_1/1_Conf_1.000	172	4	8.06E-12	NP_495784.1	81	73.559	55	45	ZYGote defective: embryonic lethal family member (zyg-9)
Locus_96_Transcript_1/1_Conf_1.000	629	20	1.70E-26	NP_493023.1	85	123.25	78	67	hypothetical protein R09B3.3
Locus_960_Transcript_1/1_Conf_1.000	1329	20	1.37E-153	O44126.1	97	547.354	279	272	32 kDa beta-galactoside-binding lectin
Locus_9600_Transcript_1/2_Conf_1.000	498	0							
Locus_9600_Transcript_2/2_Conf_1.000	494	0							
Locus_9601_Transcript_1/2_Conf_1.000	753	20	6.66E-19	NP_497810.1	54	98.5969	214	116	ReCQ DNA helicase family member (rcq-5)
Locus_9601_Transcript_2/2_Conf_1.000	756	20	6.72E-19	NP_497810.1	54	98.5969	214	116	ReCQ DNA helicase family member (rcq-5)
Locus_9602_Transcript_1/1_Conf_1.000	734	13	3.02E-45	NP_509422.1	67	186.037	173	116	hypothetical protein F41D9.2
Locus_9603_Transcript_1/1_Conf_1.000	959	1	4.18E-04	NP_648504.2	39	50.0618	259	102	mucin 68D
Locus_9604_Transcript_1/1_Conf_1.000	902	20	2.36E-22	XP_002639720.1	47	110.538	280	133	Hypothetical protein CBG12446
Locus_9605_Transcript_1/1_Conf_1.000	261	0							
Locus_9606_Transcript_1/1_Conf_1.000	856	20	8.21E-30	NP_495102.1	65	135.191	141	92	hypothetical protein F59E12.11
Locus_9607_Transcript_1/1_Conf_1.000	242	3	1.29E-09	XP_001902362.1	65	66.2402	76	50	hypothetical protein Bm1_54520

Locus_9608_Transcript_1/1_Conf_1.000	399	20	1.92E-61	NP_001018146.1	100	238.424	116	116	nucleoside diphosphate kinase B
Locus_9609_Transcript_1/1_Conf_1.000	417	20	4.79E-36	CAZ39159.1	78	154.066	116	91	C. elegans protein C01C7.1b, partially confirmed by transcript evidence
Locus_961_Transcript_1/1_Conf_1.000	204	0							
Locus_9610_Transcript_1/1_Conf_1.000	565	20	1.09E-49	XP_001898209.1	80	199.904	150	120	Variant SH3 domain containing protein
Locus_9611_Transcript_1/4_Conf_0.286	333	0							
Locus_9611_Transcript_2/4_Conf_0.429	684	0							
Locus_9611_Transcript_3/4_Conf_0.571	973	0							
Locus_9611_Transcript_4/4_Conf_0.429	675	0							
Locus_9612_Transcript_1/1_Conf_1.000	806	20	1.73E-79	NP_490770.1	79	300.056	204	163	hypothetical protein Y18H1A.4
Locus_9613_Transcript_1/1_Conf_1.000	294	0							
Locus_9614_Transcript_1/1_Conf_1.000	1878	20	0	NP_741684.2	81	704.901	628	513	PROximal proliferation in germline family member (pro-3)

Locus_9615_Transcript_1/1_Conf_1.000	1154	20	4.55E-14	XP_001899498.1	66	83.5741	117	78	Core histone H2A/H2B/H3/H4 family protein
Locus_9616_Transcript_1/1_Conf_1.000	580	0							
Locus_9617_Transcript_1/1_Conf_1.000	617	0							
Locus_9618_Transcript_1/1_Conf_1.000	455	20	1.76E-75	NP_001024407.1	98	285.034	151	149	INneXin family member (inx-1)
Locus_9619_Transcript_1/1_Conf_1.000	646	20	2.25E-16	NP_501363.1	69	89.7373	82	57	P38 Map Kinase family member (pmk-3)
Locus_962_Transcript_1/1_Conf_1.000	230	2	3.78E-25	XP_002642486.1	86	117.857	76	66	Hypothetical protein CBG06905
Locus_9620_Transcript_1/1_Conf_1.000	263	4	1.88E-08	EFO24584.1	73	62.3882	56	41	hypothetical protein LOAG_03906
Locus_9621_Transcript_1/1_Conf_1.000	1156	20	1.42E-15	EFO26150.1	68	88.5817	89	61	RNase3 domain-containing protein
Locus_9622_Transcript_1/1_Conf_1.000	836	20	2.30E-106	NP_492651.1	100	389.423	190	190	Neuronal Calcium Sensor family member (ncs-2)
Locus_9623_Transcript_1/1_Conf_1.000	375	6	1.49E-13	Q94125.6	56	79.337	134	76	Phosphatidylinositol 3-kinase age-1
Locus_9624_Transcript_1/1_Conf_1.000	299	20	3.28E-29	XP_002642057.1	90	131.339	99	90	C. briggsae CBR-COL-89 protein
Locus_9625_Transcript_1/1_Conf_1.000	221	0							
Locus_9626_Transcript_1/1_Conf_1.000	361	2	7.77E-15	NP_001021401.1	55	83.5741	102	57	hypothetical protein F21F3.7
Locus_9627_Transcript_1/1_Conf_1.000	287	0							
Locus_9628_Transcript_1/1_Conf_1.000	357	20	1.91E-29	NP_496328.2	72	132.109	111	81	hypothetical protein R06F6.8
Locus_9629_Transcript_1/1_Conf_1.000	523	20	5.89E-14	XP_001991589.1	51	80.8777	131	68	GH11980

Locus_963_Transcript_1/1_Conf_1.000	1776	20	0	XP_002637342.1	89	842.803	527	473	C. briggsae CBR-UNC-70 protein
Locus_9630_Transcript_1/1_Conf_1.000	405	20	1.68E-25	NP_494789.1	64	119.013	128	83	hypothetical protein W06B4.2
Locus_9631_Transcript_1/1_Conf_1.000	693	20	1.78E-113	XP_002634804.1	94	412.535	230	217	Hypothetical protein CBG13909
Locus_9632_Transcript_1/1_Conf_1.000	245	0							
Locus_9633_Transcript_1/1_Conf_1.000	457	20	2.33E-19	NP_497591.1	68	98.5969	86	59	Protein Phosphatase Four Regulatory subunit family member (ppfr-4)

Locus_9634_Transcript_1/1_Conf_1.000	290	5	4.98E-09	XP_002638740.1	62	64.3142	100	62	Hypothetical protein CBG18542
Locus_9635_Transcript_1/1_Conf_1.000	232	0							
Locus_9636_Transcript_1/3_Conf_0.750	1378	20	2.24E-21	EFO24656.1	42	108.227	456	193	hypothetical protein LOAG_03825
Locus_9636_Transcript_2/3_Conf_0.750	1369	20	6.45E-21	EFO24656.1	40	106.686	451	183	hypothetical protein LOAG_03825
Locus_9636_Transcript_3/3_Conf_0.750	1378	20	2.92E-21	EFO24656.1	42	107.842	456	193	hypothetical protein LOAG_03825
Locus_9637_Transcript_1/1_Conf_1.000	204	20	5.39E-32	XP_001162433.1	100	140.584	68	68	PREDICTED: hypothetical protein isoform 1

Locus_9638_Transcript_1/1_Conf_1.000	1587	20	1.29E-140	XP_002636698.1	91	504.597	398	364	C. briggsae CBR-MYO-3 protein
Locus_9639_Transcript_1/1_Conf_1.000	413	20	3.01E-59	XP_001103861.2	99	231.106	124	123	PREDICTED: 60S ribosomal protein L35a-like isoform 2
Locus_964_Transcript_1/2_Conf_1.000	852	20	3.42E-36	XP_001897844.1	74	156.377	151	113	Glucosamine 6-phosphate N-acetyltransferase
Locus_964_Transcript_2/2_Conf_1.000	972	20	4.25E-36	XP_001897844.1	74	156.377	151	113	Glucosamine 6-phosphate N-acetyltransferase
Locus_9640_Transcript_1/1_Conf_1.000	250	0							
Locus_9641_Transcript_1/1_Conf_1.000	841	20	1.80E-82	XP_002634238.1	76	310.071	289	221	Hypothetical protein CBG01808
Locus_9642_Transcript_1/1_Conf_1.000	176	1	1.62E-04	EFO21687.1	66	49.2914	48	32	hypothetical protein LOAG_06803
Locus_9643_Transcript_1/2_Conf_1.000	245	0							
Locus_9643_Transcript_2/2_Conf_1.000	444	0							
Locus_9644_Transcript_1/1_Conf_1.000	589	20	3.42E-36	XP_002635180.1	69	155.221	178	124	Hypothetical protein CBG11418

Locus_9645_Transcript_1/1_Conf_1.000	316	8	1.40E-11	XP_002633387.1	51	72.7886	123	63	C. briggsae CBR-TWK-25 protein
Locus_9646_Transcript_1/2_Conf_1.000	679	0							
Locus_9646_Transcript_2/2_Conf_1.000	859	0							
Locus_9647_Transcript_1/1_Conf_1.000	368	2	5.92E-07	NP_741438.1	63	57.3806	52	33	hypothetical protein D2024.5
Locus_9648_Transcript_1/4_Conf_0.600	1629	20	9.86E-152	EFO20351.1	69	541.576	553	384	phosphatidylinositol 3
Locus_9648_Transcript_2/4_Conf_0.700	2415	20	0	EFO20351.1	64	692.575	803	518	phosphatidylinositol 3
Locus_9648_Transcript_3/4_Conf_0.700	2415	20	0	EFO20351.1	64	693.73	803	518	phosphatidylinositol 3

Locus_9648_Transcript_4/4_Conf_0.700	2415	20	0	EFO20351.1	64	692.189	803	518	phosphatidylinositol 3
Locus_9649_Transcript_1/1_Conf_1.000	246	4	2.10E-20	XP_002644999.1	75	102.064	83	63	C. briggsae CBR-PGP-10 protein
Locus_965_Transcript_1/1_Conf_1.000	1000	20	4.24E-95	ACS48688.1	96	352.443	314	304	NADH dehydrogenase subunit 1
Locus_9650_Transcript_1/2_Conf_1.000	1676	17	4.11E-76	NP_497189.2	76	290.426	302	230	GEX Interacting protein family member (gei-4)
Locus_9650_Transcript_2/2_Conf_1.000	1649	17	4.02E-76	NP_497189.2	76	290.426	302	230	GEX Interacting protein family member (gei-4)
Locus_9651_Transcript_1/1_Conf_1.000	1374	20	7.73E-107	XP_002037129.1	71	392.119	363	261	GM12747
Locus_9652_Transcript_1/1_Conf_1.000	221	0							
Locus_9653_Transcript_1/1_Conf_1.000	520	3	4.87E-21	NP_001023671.1	67	104.375	159	108	hypothetical protein C24B9.3
Locus_9654_Transcript_1/1_Conf_1.000	830	20	9.21E-108	XP_001896104.1	82	394.045	280	232	RNA lariat debranching enzyme
Locus_9655_Transcript_1/1_Conf_1.000	489	4	2.61E-18	NP_001021055.1	57	95.1301	172	99	EYA (Drosophila eyes absent) homolog family member (eya-1)
Locus_9656_Transcript_1/1_Conf_1.000	163	0							
Locus_9657_Transcript_1/1_Conf_1.000	202	0							

Locus_9658_Transcript_1/1_Conf_1.000	265	0							
Locus_9659_Transcript_1/2_Conf_1.000	332	0							
Locus_9659_Transcript_2/2_Conf_1.000	346	0							
Locus_966_Transcript_1/2_Conf_1.000	755	20	8.33E-54	NP_496228.1	77	214.542	133	103	hypothetical protein C07E3.9
Locus_966_Transcript_2/2_Conf_1.000	759	20	8.47E-54	NP_496228.1	77	214.542	133	103	hypothetical protein C07E3.9
Locus_9660_Transcript_1/1_Conf_1.000	1187	20	0	XP_003108860.1	90	659.448	395	358	hypothetical protein CRE_11716
Locus_9661_Transcript_1/1_Conf_1.000	1056	5	2.05E-18	NP_495603.1	62	97.8265	166	103	hypothetical protein F18A1.6

Locus_9662_Transcript_1/1_Conf_1.000	1439	20	4.75E-139	NP_497918.1	70	499.204	455	321	UDP-GlucuronosylTransferase family member (ugt-62)
Locus_9663_Transcript_1/1_Conf_1.000	425	0							
Locus_9664_Transcript_1/1_Conf_1.000	218	0							
Locus_9665_Transcript_1/1_Conf_1.000	390	4	4.52E-23	NP_510548.2	68	110.923	133	91	hypothetical protein F39D8.3
Locus_9666_Transcript_1/1_Conf_1.000	1179	20	1.29E-112	NP_491479.2	72	410.994	370	268	ACyLtransferase-like family member (acl-11)
Locus_9667_Transcript_1/1_Conf_1.000	707	4	1.10E-17	XP_002637263.1	51	94.3597	248	128	Hypothetical protein CBG18943
Locus_9668_Transcript_1/1_Conf_1.000	1196	20	4.51E-121	EFO25561.1	86	439.113	307	265	RhoGAP domain-containing protein
Locus_9669_Transcript_1/1_Conf_1.000	1413	6	1.82E-18		42	98.5969	380	161	hypothetical protein EEED8.1
Locus_967_Transcript_1/1_Conf_1.000	850	20	1.38E-138	XP_002636769.1	95	496.508	263	251	C. briggsae CBR-EGL-10 protein
Locus_9670_Transcript_1/1_Conf_1.000	935	20	1.92E-38	XP_002641105.1	56	164.081	238	135	Hypothetical protein CBG17486
Locus_9671_Transcript_1/2_Conf_1.000	576	20	1.28E-64	XP_002639248.1	83	249.595	173	144	C. briggsae CBR-SUR-6 protein
Locus_9671_Transcript_2/2_Conf_1.000	582	20	1.32E-64	XP_002639248.1	83	249.595	173	144	C. briggsae CBR-SUR-6 protein

Locus_9672_Transcript_1/1_Conf_1.000	353	20	1.47E-45	NP_001024761.1	83	185.652	118	98	ForKHead transcription factor family member (fkh-9)
Locus_9673_Transcript_1/1_Conf_1.000	394	20	2.28E-62	XP_002629875.1	95	241.506	131	125	C. briggsae CBR-LET-75 protein
Locus_9674_Transcript_1/2_Conf_1.000	658	16	6.83E-24	NP_493670.2	86	114.775	80	69	hypothetical protein T25D3.4
Locus_9674_Transcript_2/2_Conf_1.000	254	16	3.23E-24	NP_493670.2	86	114.775	80	69	hypothetical protein T25D3.4
Locus_9675_Transcript_1/1_Conf_1.000	252	20	2.65E-26	NP_741109.1	79	121.709	83	66	FERM domain (protein4.1-ezrin-radixin-moesin) family member (frm-8)
Locus_9676_Transcript_1/1_Conf_1.000	248	20	5.90E-31	XP_002923900.1	100	137.117	67	67	PREDICTED: 60S ribosomal protein L22-like
Locus_9677_Transcript_1/1_Conf_1.000	853	5	4.96E-19	NP_001022203.1	48	99.3673	326	157	hypothetical protein F54D5.5
Locus_9678_Transcript_1/1_Conf_1.000	1273	20	3.73E-161	NP_494737.1	81	572.392	438	355	Temporarily Assigned Gene name family member (tag-149)

Locus_9679_Transcript_1/1_Conf_1.000	630	0							
Locus_968_Transcript_1/1_Conf_1.000	243	0							
Locus_9680_Transcript_1/1_Conf_1.000	872	0							
Locus_9681_Transcript_1/2_Conf_1.000	431	0							
Locus_9681_Transcript_2/2_Conf_1.000	431	0							
Locus_9682_Transcript_1/1_Conf_1.000	652	0							
Locus_9683_Transcript_1/1_Conf_1.000	747	2	2.28E-19	XP_002636542.1	72	100.138	97	70	C. briggsae CBR-TTLL-5 protein
Locus_9684_Transcript_1/1_Conf_1.000	997	20	4.46E-20	EFO17367.1	81	103.219	70	57	hypothetical protein LOAG_11131
Locus_9685_Transcript_1/1_Conf_1.000	1352	20	3.27E-110	EFO20721.1	69	403.29	444	310	hypothetical protein LOAG_07768
Locus_9686_Transcript_1/1_Conf_1.000	288	20	1.04E-14	XP_002642404.1	68	83.1889	86	59	Hypothetical protein CBG06798
Locus_9687_Transcript_1/1_Conf_1.000	544	0							
Locus_9688_Transcript_1/2_Conf_1.000	908	20	1.52E-85	NP_001023017.1	73	320.472	300	221	UNCoordinated family member (unc-32)
Locus_9688_Transcript_2/2_Conf_1.000	902	20	6.70E-102	NP_001023018.1	76	374.785	294	224	UNCoordinated family member (unc-32)
Locus_9689_Transcript_1/1_Conf_1.000	373	20	3.06E-67	XP_002833943.1	100	257.684	124	124	PREDICTED: 60S ribosomal protein L5-like isoform 2
Locus_969_Transcript_1/1_Conf_1.000	473	0							
Locus_9690_Transcript_1/2_Conf_1.000	455	0							
Locus_9690_Transcript_2/2_Conf_1.000	407	0							
Locus_9691_Transcript_1/1_Conf_1.000	559	20	4.26E-51	ACZ13335.1	78	204.527	157	124	60S ribosomal protein L5

Locus_9692_Transcript_1/1_Conf_1.000	1401	20	7.57E-134	NP_491994.2	75	481.871	470	355	hypothetical protein H06O01.2
Locus_9693_Transcript_1/1_Conf_1.000	486	0							
Locus_9694_Transcript_1/1_Conf_1.000	190	0							
Locus_9695_Transcript_1/1_Conf_1.000	422	3	3.10E-19	NP_741539.2	71	98.2117	110	79	hypothetical protein C18C4.5
Locus_9696_Transcript_1/1_Conf_1.000	212	0							
Locus_9697_Transcript_1/1_Conf_1.000	238	0							
Locus_9698_Transcript_1/1_Conf_1.000	522	20	4.62E-43	XP_002642541.1	73	177.563	173	127	C. briggsae CBR-DNJ-16 protein
Locus_9699_Transcript_1/1_Conf_1.000	610	20	2.36E-62	NP_001024672.1	72	242.276	204	147	yeast SIR related family member (sir-2.2)
Locus_97_Transcript_10/17_Conf_0.302	1213	20	3.19E-16	ABB53347.1	40	68.9366	197	79	secreted protein 5 precursor
Locus_97_Transcript_12/17_Conf_0.283	991	20	8.35E-12	ABB53347.1	40	68.9366	197	79	secreted protein 5 precursor
Locus_97_Transcript_13/17_Conf_0.302	943	20	4.52E-11	AAN11402.1	42	73.1738	226	95	secreted-protein 1 precursor
Locus_97_Transcript_14/17_Conf_0.321	1228	20	9.28E-16	ABB53347.1	40	68.9366	197	79	secreted protein 5 precursor
Locus_97_Transcript_15/17_Conf_0.377	1228	20	1.35E-13	ABB53347.1	41	67.0106	153	63	secreted protein 5 precursor
Locus_97_Transcript_16/17_Conf_0.170	678	20	1.57E-10	AAO63577.1	40	70.4774	230	93	secreted protein 5 precursor
Locus_97_Transcript_17/17_Conf_0.321	1228	20	3.64E-14	ABB53347.1	40	68.9366	197	79	secreted protein 5 precursor
Locus_97_Transcript_4/17_Conf_1.000	177	0							
Locus_97_Transcript_5/17_Conf_1.000	130	0							
Locus_97_Transcript_6/17_Conf_1.000	256	0							
Locus_97_Transcript_7/17_Conf_1.000	207	0							
Locus_97_Transcript_8/17_Conf_0.264	1212	20	3.58E-14	ABB53347.1	40	68.9366	197	79	secreted protein 5 precursor
Locus_97_Transcript_9/17_Conf_0.038	532	3	2.82E-06	NP_491269.1	50	55.4546	114	57	EGG sterile (unfertilizable) family member (egg-4)
Locus_970_Transcript_1/4_Conf_0.500	427	0							
Locus_970_Transcript_2/4_Conf_0.667	527	0							
Locus_970_Transcript_3/4_Conf_0.750	1161	20	5.24E-26	XP_002633697.1	85	123.25	76	65	Hypothetical protein CBG03380
Locus_970_Transcript_4/4_Conf_0.750	536	0							
Locus_9700_Transcript_1/1_Conf_1.000	135	5	5.21E-11	XP_002644341.1	76	70.8626	42	32	Hypothetical protein CBG14163

Locus_9701_Transcript_1/1_Conf_1.000	146	20	1.12E-16	XP_002639062.1	93	89.7373	48	45	Hypothetical protein CBG14873
Locus_9702_Transcript_1/1_Conf_1.000	414	4	5.00E-22	XP_002632204.1	78	107.457	80	63	Hypothetical protein CBG07071
Locus_9703_Transcript_1/1_Conf_1.000	490	20	6.77E-67	CAX65056.1	85	256.529	163	140	C. elegans protein F25C8.3d, partially confirmed by transcript evidence
Locus_9704_Transcript_1/1_Conf_1.000	988	20	2.82E-43	NP_493626.1	80	180.259	138	111	hypothetical protein F31C3.4
Locus_9705_Transcript_1/1_Conf_1.000	1002	1	9.11E-05	XP_001900983.1	45	52.373	115	52	La domain containing protein
Locus_9706_Transcript_1/2_Conf_1.000	1525	14	3.84E-09	NP_496398.2	41	67.781	376	156	hypothetical protein T06D8.1
Locus_9706_Transcript_2/2_Conf_1.000	1525	12	4.69E-07	NP_496398.2	49	60.8474	212	105	hypothetical protein T06D8.1
Locus_9707_Transcript_1/1_Conf_1.000	729	20	3.27E-84	NP_510603.1	77	315.464	241	186	hypothetical protein F59F4.1
Locus_9708_Transcript_1/1_Conf_1.000	758	20	2.02E-15	XP_002129449.1	46	87.0409	235	110	PREDICTED: hypothetical protein
Locus_9709_Transcript_1/1_Conf_1.000	408	0							
Locus_971_Transcript_1/1_Conf_1.000	303	0							
Locus_9710_Transcript_1/1_Conf_1.000	661	20	2.13E-118	XP_002748370.1	100	428.713	213	213	PREDICTED: 40S ribosomal protein S3a-like

Locus_9711_Transcript_1/1_Conf_1.000	311	6	7.70E-31	AAT07449.1	90	136.732	82	74	putative protein
Locus_9712_Transcript_1/1_Conf_1.000	269	20	2.35E-35	NP_494721.1	92	151.754	89	82	hypothetical protein R11F4.1
Locus_9713_Transcript_1/1_Conf_1.000	2331	20	3.65E-36	CAN99691.2	47	158.303	416	196	C. elegans protein F54B3.1b, partially confirmed by transcript evidence
Locus_9714_Transcript_1/1_Conf_1.000	380	20	2.89E-09	XP_002739063.1	51	65.0846	119	61	PREDICTED: Rho-GTPase-activating protein, putative-like
Locus_9715_Transcript_1/1_Conf_1.000	406								
Locus_9716_Transcript_1/2_Conf_1.000	1271	20	1.07E-91	XP_002637127.1	83	341.658	255	212	Hypothetical protein CBG09629
Locus_9716_Transcript_2/2_Conf_1.000	902	20	6.28E-92	XP_002637127.1	83	341.658	255	212	Hypothetical protein CBG09629
Locus_9717_Transcript_1/1_Conf_1.000	629	20	1.60E-16	EFO25022.1	80	90.1225	65	52	hypothetical protein LOAG_03465
Locus_9718_Transcript_1/1_Conf_1.000	166	20	1.80E-19	NP_504235.2	94	98.9821	55	52	Drosophila SOS homolog family member (sos-1)
Locus_9719_Transcript_1/1_Conf_1.000	310	0							
Locus_972_Transcript_1/1_Conf_1.000	592	0							
Locus_9720_Transcript_1/1_Conf_1.000	267	18	9.29E-08	YP_001531603.1	65	60.077	60	39	putative Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II
Locus_9721_Transcript_1/1_Conf_1.000	235	20	4.17E-08	XP_001896983.1	65	61.2326	58	38	small nuclear ribonucleoprotein

Locus_9722_Transcript_1/2_Conf_1.000	1227	2	7.02E-08	NP_500719.1	42	63.1586	251	106	hypothetical protein C02B10.5
Locus_9722_Transcript_2/2_Conf_1.000	632	2	8.04E-08	XP_002633911.1	57	61.2326	109	63	Hypothetical protein CBG19977
Locus_9723_Transcript_1/1_Conf_1.000	478	20	4.55E-15	EFO25858.1	46	84.3445	167	77	low-density lipoprotein receptor repeat class B containing protein
Locus_9724_Transcript_1/2_Conf_1.000	1091	3	9.63E-27	NP_491750.3	47	125.561	380	180	hypothetical protein C27A12.9
Locus_9724_Transcript_2/2_Conf_1.000	1038	3	2.02E-15	EFO24581.1	44	63.5438	205	92	hypothetical protein LOAG_03903
Locus_9725_Transcript_1/1_Conf_1.000	418	9	2.07E-55	NP_493641.2	88	218.394	138	122	hypothetical protein F23F1.2
Locus_9726_Transcript_1/1_Conf_1.000	342	20	9.40E-16	XP_001892364.1	62	86.6557	114	71	Helix-hairpin-helix motif family protein
Locus_9727_Transcript_1/1_Conf_1.000	863	0							
Locus_9728_Transcript_1/1_Conf_1.000	744	20	3.44E-68	NP_508994.1	69	262.307	253	176	abnormal cell MIGration family member (mig-23)
Locus_9729_Transcript_1/2_Conf_1.000	770	4	9.03E-35	XP_002631099.1	55	151.369	256	141	C. briggsae CBR-OOC-3 protein
Locus_9729_Transcript_2/2_Conf_1.000	731	4	3.55E-30	XP_002631099.1	53	135.961	242	130	C. briggsae CBR-OOC-3 protein

Locus_973_Transcript_1/1_Conf_1.000	1097	20	1.99E-80	NP_505829.1	92	303.908	175	161	ATP synthase subunit family member (atp-5)
Locus_9730_Transcript_1/4_Conf_0.700	1245	20	6.94E-120	XP_001896847.1	77	435.261	352	273	Activator 1 38 kDa subunit (Replication factor C 38 kDa subunit)
Locus_9730_Transcript_2/4_Conf_0.700	1245	20	6.94E-120	XP_001896847.1	77	435.261	352	273	Activator 1 38 kDa subunit (Replication factor C 38 kDa subunit)
Locus_9730_Transcript_3/4_Conf_0.700	1245	20	6.94E-120	XP_001896847.1	77	435.261	352	273	Activator 1 38 kDa subunit (Replication factor C 38 kDa subunit)

Locus_9730_Transcript_4/4_Conf_0.700	1245	20	6.94E-120	XP_001896847.1	77	435.261	352	273	Activator 1 38 kDa subunit (Replication factor C 38 kDa subunit)
Locus_9731_Transcript_1/1_Conf_1.000	1189	20	5.34E-90	NP_001022020.1	68	335.88	398	274	PeRoXisome assembly factor family member (prx-5)
Locus_9732_Transcript_1/1_Conf_1.000	326	6	6.67E-06	EFO27165.1	48	53.9138	95	46	hypothetical protein LOAG_01310
Locus_9733_Transcript_1/2_Conf_1.000	1078	20	1.19E-29	EFO18262.1	68	135.191	122	83	hypothetical protein LOAG_10233
Locus_9733_Transcript_2/2_Conf_1.000	1021	20	1.10E-29	EFO18262.1	68	135.191	122	83	hypothetical protein LOAG_10233
Locus_9734_Transcript_1/1_Conf_1.000	306	20	4.53E-31	NP_505629.2	83	137.502	101	84	abnormal DAuer Formation family member (daf-36)
Locus_9735_Transcript_1/1_Conf_1.000	1057	20	3.80E-73	XP_001893036.1	78	279.641	232	181	SMC family, C-terminal domain containing protein
Locus_9736_Transcript_1/1_Conf_1.000	1040	2	1.38E-11	XP_002632825.1	41	75.0998	278	115	Hypothetical protein CBG15012
Locus_9737_Transcript_1/2_Conf_1.000	1587	1	3.90E-04	CBK22679.2	40	51.2174	362	146	unnamed protein product
Locus_9737_Transcript_2/2_Conf_1.000	720	0							
Locus_9738_Transcript_1/1_Conf_1.000	511	3	2.59E-08	XP_002636261.1	54	62.003	124	67	C. briggsae CBR-LIN-25 protein
Locus_9739_Transcript_1/1_Conf_1.000	501	0							
Locus_974_Transcript_1/1_Conf_1.000	1069	4	3.08E-46	XP_001901375.1	66	190.274	215	143	hypothetical protein Bm1_49545

Locus_9740_Transcript_1/1_Conf_1.000	762	20	1.12E-37	Q94125.6	78	160.999	122	96	Phosphatidylinositol 3-kinase age-1
Locus_9741_Transcript_1/1_Conf_1.000	253	0							
Locus_9742_Transcript_1/1_Conf_1.000	680	20	6.94E-67	NP_509174.1	77	257.684	188	146	hypothetical protein C16E9.2
Locus_9743_Transcript_1/1_Conf_1.000	743	0							
Locus_9744_Transcript_1/1_Conf_1.000	613	20	8.32E-23	XP_001641064.1	64	110.923	117	75	predicted protein
Locus_9745_Transcript_1/1_Conf_1.000	299	20	2.42E-48	A8XQD5.2	96	194.897	99	96	Serine/threonine-protein kinase dkf-2
Locus_9746_Transcript_1/1_Conf_1.000	428	0							
Locus_9747_Transcript_1/1_Conf_1.000	423	20	2.35E-51	XP_396773.2	80	204.912	140	113	PREDICTED: similar to Probable phospholipid-transporting ATPase ID (ATPase class I type 8B member 2) isoform 1
Locus_9748_Transcript_1/1_Conf_1.000	486	20	2.80E-20	EFO28285.1	75	101.679	80	60	hypothetical protein LOAG_00209
Locus_9749_Transcript_1/2_Conf_1.000	376	2	7.13E-16	EFO20991.1	61	87.0409	109	67	hypothetical protein LOAG_07497
Locus_9749_Transcript_2/2_Conf_1.000	848	2	4.14E-18	EFO20991.1	51	96.2857	252	129	hypothetical protein LOAG_07497
Locus_975_Transcript_1/1_Conf_1.000	212	13	9.49E-13	CAA26849.1	76	76.6406	64	49	put. vitellogenin

Locus_9750_Transcript_1/3_Conf_0.667	769	20	3.73E-89	NP_491654.1	80	332.028	248	199	CIR (transcription factor CBF1 Interacting coRepressor) homolog family member (cir-1)
Locus_9750_Transcript_2/3_Conf_0.667	769	20	2.41E-96	NP_491654.1	80	355.91	248	199	CIR (transcription factor CBF1 Interacting coRepressor) homolog family member (cir-1)
Locus_9750_Transcript_3/3_Conf_0.667	769	20	3.73E-89	NP_491654.1	80	332.028	248	199	CIR (transcription factor CBF1 Interacting coRepressor) homolog family member (cir-1)
Locus_9751_Transcript_1/1_Conf_1.000	497	20	2.72E-76	XP_002629829.1	90	287.73	164	149	C. briggsae CBR-PLC-3 protein
Locus_9752_Transcript_1/1_Conf_1.000	638	20	1.94E-49	EFO26908.1	76	199.519	181	138	hypothetical protein LOAG_01583
Locus_9753_Transcript_1/1_Conf_1.000	398	0							
Locus_9754_Transcript_1/1_Conf_1.000	282	0							
Locus_9755_Transcript_1/1_Conf_1.000	584	20	1.24E-62	XP_002636962.1	78	243.047	195	153	C. briggsae CBR-MAX-1 protein
Locus_9756_Transcript_1/1_Conf_1.000	299	1	8.70E-06	AAF59456.4	58	53.5286	73	43	Smg-associated and lethal protein 2, partially confirmed by transcript evidence

Locus_9757_Transcript_1/1_Conf_1.000	288	20	1.50E-13	XP_002761974.1	100	79.337	37	37	PREDICTED: coatomer subunit epsilon-like
Locus_9758_Transcript_1/1_Conf_1.000	446	20	4.05E-11	NP_001040712.1	90	71.2478	60	54	hypothetical protein Y73E7A.1
Locus_9759_Transcript_1/1_Conf_1.000	245	0							
Locus_976_Transcript_1/3_Conf_0.667	1552	20	0	ACS29571.1	99	796.579	427	426	beta-tubulin isotype 2
Locus_976_Transcript_2/3_Conf_0.667	1656	20	0	AAP20435.1	97	820.461	455	444	beta-tubulin isotype 2
Locus_976_Transcript_3/3_Conf_0.667	1638	20	0	AAP20435.1	98	827.009	449	444	beta-tubulin isotype 2
Locus_9760_Transcript_1/2_Conf_1.000	839	20	5.62E-44	CBW48423.1	82	182.185	134	111	Hypothetical protein M04G12.1d
Locus_9760_Transcript_2/2_Conf_1.000	742	20	4.48E-44	CBW48423.1	82	182.185	134	111	Hypothetical protein M04G12.1d
Locus_9761_Transcript_1/1_Conf_1.000	213	3	4.54E-15	NP_504167.1	95	84.3445	48	46	hypothetical protein H43I07.1
Locus_9762_Transcript_1/1_Conf_1.000	724	20	1.88E-92	NP_502613.2	81	342.813	241	196	QUInine non-avoider family member (qui-1)
Locus_9763_Transcript_1/1_Conf_1.000	478	5	4.53E-31	CAR97841.1	77	137.502	130	101	C. elegans protein F59A2.2b, partially confirmed by transcript evidence
Locus_9764_Transcript_1/1_Conf_1.000	856	20	1.72E-128	CAE11873.1	100	462.996	239	239	hypothetical protein

Locus_9765_Transcript_1/1_Conf_1.000	799	20	1.46E-30	XP_001898119.1	55	137.502	277	153	Surp module family protein
Locus_9766_Transcript_1/1_Conf_1.000	407	0							
Locus_9767_Transcript_1/1_Conf_1.000	157	20	3.79E-17	ACI48997.1	90	91.2781	52	47	hypothetical protein Cbre_JD01.004
Locus_9768_Transcript_1/1_Conf_1.000	1087								
Locus_9769_Transcript_1/1_Conf_1.000	284	0							
Locus_977_Transcript_1/1_Conf_1.000	2402	20	0	XP_002643773.1	89	1281.93	802	715	Hypothetical protein CBG01975
Locus_9770_Transcript_1/1_Conf_1.000	154	0							
Locus_9771_Transcript_1/1_Conf_1.000	916	20	1.83E-70	NP_496339.1	67	270.396	308	209	ORC family member (orc-2)
Locus_9772_Transcript_1/2_Conf_1.000	496	20	5.90E-47	CBA11613.1	73	190.274	136	100	C. elegans protein F54F3.1c, partially confirmed by transcript evidence
Locus_9772_Transcript_2/2_Conf_1.000	481	20	3.43E-47	CBA11613.1	74	191.045	132	98	C. elegans protein F54F3.1c, partially confirmed by transcript evidence
Locus_9773_Transcript_1/1_Conf_1.000	187	0							
Locus_9774_Transcript_1/1_Conf_1.000	361	20	4.54E-31	XP_002639522.1	86	137.502	82	71	Hypothetical protein CBG04128
Locus_9775_Transcript_1/1_Conf_1.000	988	20	1.72E-16	XP_002645247.1	55	91.2781	204	113	Hypothetical protein CBG00124
Locus_9776_Transcript_1/1_Conf_1.000	344	0							
Locus_9777_Transcript_1/1_Conf_1.000	195	4	1.88E-08	Q22141.2	78	62.3882	47	37	Post-GPI attachment to proteins factor 2

Locus_9778_Transcript_1/1_Conf_1.000	325	20	3.88E-38	NP_504553.1	86	160.999	106	92	Adenylyl CYclase family member (acy-2)
Locus_9779_Transcript_1/1_Conf_1.000	403	0							
Locus_978_Transcript_1/4_Conf_0.333	1108	20	3.00E-116	NP_491824.1	80	422.935	343	277	IMportin Alpha family member (ima-2)
Locus_978_Transcript_2/4_Conf_0.667	1725	20	2.34E-175	NP_491824.1	79	620.157	514	411	IMportin Alpha family member (ima-2)
Locus_978_Transcript_3/4_Conf_0.667	1716	20	3.05E-175	NP_491824.1	79	619.772	514	410	IMportin Alpha family member (ima-2)
Locus_978_Transcript_4/4_Conf_0.667	1725	20	2.34E-175	NP_491824.1	79	620.157	514	411	IMportin Alpha family member (ima-2)
Locus_9780_Transcript_1/1_Conf_1.000	347	20	2.81E-28	XP_002633391.1	68	128.257	111	76	Hypothetical protein CBG06150
Locus_9781_Transcript_1/1_Conf_1.000	366	4	2.03E-15	NP_493592.1	74	85.5001	78	58	hypothetical protein F32A7.4
Locus_9782_Transcript_1/1_Conf_1.000	273	0							
Locus_9783_Transcript_1/1_Conf_1.000	195	0							
Locus_9784_Transcript_1/1_Conf_1.000	487	20	6.19E-44	EFO16233.1	70	180.259	162	114	variant SH3 domain-containing protein
Locus_9785_Transcript_1/1_Conf_1.000	320	8	1.18E-18	EFO18114.1	59	96.2857	116	69	hypothetical protein LOAG_10384
Locus_9786_Transcript_1/1_Conf_1.000	487	19	3.37E-66	XP_002633478.1	84	254.218	164	139	Hypothetical protein CBG06249

Locus_9787_Transcript_1/2_Conf_1.000	439	2	2.94E-06	XP_001917324.1	50	55.0694	102	52	PREDICTED: similar to proteoglycan 3
Locus_9787_Transcript_2/2_Conf_1.000	506	20	2.15E-07	P83514.1	52	58.9214	105	55	Struthiocalcin-1
Locus_9788_Transcript_1/1_Conf_1.000	886	20	2.65E-87	XP_002634120.1	86	326.25	205	178	Hypothetical protein CBG01674
Locus_9789_Transcript_1/1_Conf_1.000	798	20	5.04E-15	NP_001033343.1	45	85.8853	210	96	hypothetical protein B0336.5
Locus_979_Transcript_1/1_Conf_1.000	2563	20	2.92E-26	XP_002639167.1	54	125.561	207	112	C. briggsae CBR-HSR-9 protein
Locus_9790_Transcript_1/1_Conf_1.000	775	0							
Locus_9791_Transcript_1/1_Conf_1.000	959	20	1.66E-69	NP_492749.2	74	267.314	316	234	abnormal CHEmotaxis family member (che-13)
Locus_9792_Transcript_1/1_Conf_1.000	1139	0							
Locus_9793_Transcript_1/1_Conf_1.000	308	5	4.41E-10	XP_002641150.1	62	67.781	90	56	Hypothetical protein CBG09002
Locus_9794_Transcript_1/1_Conf_1.000	486	0							
Locus_9795_Transcript_1/1_Conf_1.000	314	20	3.01E-38	XP_002646356.1	84	161.384	103	87	Hypothetical protein CBG12070
Locus_9796_Transcript_1/1_Conf_1.000	162	20	5.63E-13	NP_492483.1	82	77.411	50	41	hypothetical protein F26H9.5
Locus_9797_Transcript_1/2_Conf_1.000	991	0							
Locus_9797_Transcript_2/2_Conf_1.000	976	0							
Locus_9798_Transcript_1/1_Conf_1.000	488	20	6.61E-46	NP_504486.4	82	186.808	139	115	Adenylyl CYclase family member (acy-4)

Locus_9799_Transcript_1/1_Conf_1.000	474	20	4.98E-62	XP_002644184.1	95	240.35	141	134	C. briggsae CBR-ERD-2 protein
Locus_98_Transcript_1/2_Conf_1.000	251	0							
Locus_98_Transcript_2/2_Conf_1.000	251	0							
Locus_980_Transcript_1/1_Conf_1.000	3160	20	4.48E-56	XP_001896046.1	61	224.942	247	152	mbt repeat family protein
Locus_9800_Transcript_1/1_Conf_1.000	333	6	1.73E-22	EFO27944.1	72	108.997	83	60	PWWP domain-containing protein
Locus_9801_Transcript_1/1_Conf_1.000	515	20	2.59E-88	XP_002644330.1	98	327.791	171	169	C. briggsae CBR-SPC-1 protein
Locus_9802_Transcript_1/1_Conf_1.000	149	0							
Locus_9803_Transcript_1/1_Conf_1.000	320	6	7.67E-10	NP_501124.1	58	67.0106	85	50	hypothetical protein C34D4.3
Locus_9804_Transcript_1/1_Conf_1.000	479	3	1.16E-10	NP_491340.2	52	69.707	119	62	histone METhyltransferase-like family member (met-1)
Locus_9805_Transcript_1/1_Conf_1.000	1547	20	9.40E-64	NP_493980.1	51	249.21	517	268	hypothetical protein H17B01.4
Locus_9806_Transcript_1/1_Conf_1.000	693	20	5.45E-46	XP_002640726.1	99	188.348	146	145	C. briggsae CBR-LEV-11 protein, isoform a
Locus_9807_Transcript_1/1_Conf_1.000	131	0							

Locus_9808_Transcript_1/1_Conf_1.000	198	2	1.34E-06	BAA09730.1	60	56.225	65	39	receptor tyrosine kinase
Locus_9809_Transcript_1/1_Conf_1.000	356	2	9.60E-05	A8WL06.2	61	50.0618	57	35	Homeobox protein unc-62
Locus_981_Transcript_1/1_Conf_1.000	1114	2	2.01E-27	XP_002636560.1	85	127.872	74	63	Hypothetical protein CBG23251
Locus_9810_Transcript_1/1_Conf_1.000	625	11	1.65E-74	NP_498645.1	79	282.722	206	163	MUscle Positioning family member (mup-4)
Locus_9811_Transcript_1/1_Conf_1.000	357	20	1.68E-25	XP_002644857.1	61	119.013	118	72	Hypothetical protein CBG05030
Locus_9812_Transcript_1/2_Conf_1.000	2153	20	7.13E-164	XP_001900316.1	60	582.408	738	443	GATA zinc finger family protein
Locus_9812_Transcript_2/2_Conf_1.000	2153	20	7.13E-164	XP_001900316.1	60	582.408	738	443	GATA zinc finger family protein
Locus_9813_Transcript_1/1_Conf_1.000	677	20	9.94E-58	NP_496281.1	77	227.254	177	138	hypothetical protein C14A4.14
Locus_9814_Transcript_1/1_Conf_1.000	321	2	2.53E-29	NP_500597.1	69	131.724	105	73	hypothetical protein F19C7.1
Locus_9815_Transcript_1/1_Conf_1.000	195	0							
Locus_9816_Transcript_1/1_Conf_1.000	932	0							
Locus_9817_Transcript_1/1_Conf_1.000	292	0							
Locus_9818_Transcript_1/1_Conf_1.000	657	20	1.02E-11	XP_001901150.1	48	74.3294	178	87	topoisomerase
Locus_9819_Transcript_1/1_Conf_1.000	247	0							

Locus_982_Transcript_1/1_Conf_1.000	1067	20	3.61E-180	XP_002636834.1	92	635.18	355	328	Hypothetical protein CBG09283
Locus_9820_Transcript_1/1_Conf_1.000	1609	20	3.54E-53	XP_001979947.1	49	214.157	452	225	GG21187
Locus_9821_Transcript_1/1_Conf_1.000	583	10	1.74E-24	NP_500399.2	54	116.316	181	98	hypothetical protein Y37E11AL.2
Locus_9822_Transcript_1/1_Conf_1.000	463	0							
Locus_9823_Transcript_1/1_Conf_1.000	151	0							
Locus_9824_Transcript_1/1_Conf_1.000	783	20	5.83E-69	XP_001899165.1	70	265.003	232	164	hypothetical protein
Locus_9825_Transcript_1/1_Conf_1.000	380	0							
Locus_9826_Transcript_1/1_Conf_1.000	471	0							
Locus_9827_Transcript_1/1_Conf_1.000	248	20	2.83E-33	XP_002630581.1	89	144.821	82	73	Hypothetical protein CBG13037
Locus_9828_Transcript_1/1_Conf_1.000	779	4	7.38E-08	EFO27630.1	43	62.003	208	90	hypothetical protein LOAG_00847
Locus_9829_Transcript_1/1_Conf_1.000	132	0							
Locus_983_Transcript_1/1_Conf_1.000	2125	20	1.81E-127	NP_001023842.1	70	461.455	449	318	Temporarily Assigned Gene name family member (tag-93)
Locus_9830_Transcript_1/1_Conf_1.000	133	0							
Locus_9831_Transcript_1/1_Conf_1.000	470	2	1.81E-11	EFO19956.1	53	72.4034	146	78	hypothetical protein LOAG_08535
Locus_9832_Transcript_1/1_Conf_1.000	201	20	4.90E-25	AAA03517.1	88	117.472	67	59	kinesin-related protein
Locus_9833_Transcript_1/1_Conf_1.000	364	0							

Locus_9834_Transcript_1/1_Conf_1.000	408	20	6.30E-57	XP_002642615.1	80	223.402	136	109	C. briggsae CBR-MUP-4 protein
Locus_9835_Transcript_1/3_Conf_0.667	1371	20	1.21E-51	NP_499624.2	56	208.764	281	160	ANIllin (actin binding protein) family member (ani-1)
Locus_9835_Transcript_2/3_Conf_0.667	1421	20	1.26E-51	NP_499624.2	56	208.764	281	160	ANIllin (actin binding protein) family member (ani-1)
Locus_9835_Transcript_3/3_Conf_0.667	1366	20	1.20E-51	NP_499624.2	56	208.764	281	160	ANIllin (actin binding protein) family member (ani-1)
Locus_9837_Transcript_1/1_Conf_1.000	323	3	2.81E-04	EFO17760.1	62	48.521	77	48	hypothetical protein LOAG_10739
Locus_9838_Transcript_1/1_Conf_1.000	185	0							
Locus_9839_Transcript_1/1_Conf_1.000	177	20	9.14E-16	CAC10528.1	79	86.6557	59	47	putative inositol 1,4,5-trisphosphate receptor
Locus_984_Transcript_1/1_Conf_1.000	1797	20	2.02E-60	XP_002647233.1	45	238.424	653	296	Hypothetical protein CBG24575
Locus_9840_Transcript_1/1_Conf_1.000	457	0							
Locus_9841_Transcript_1/1_Conf_1.000	799	0							
Locus_9842_Transcript_1/3_Conf_0.600	590	0							
Locus_9842_Transcript_2/3_Conf_0.400	763	0							
Locus_9842_Transcript_3/3_Conf_0.600	590	0							

Locus_9843_Transcript_1/1_Conf_1.000	716	20	8.27E-61	ACI49081.1	69	237.654	215	150	hypothetical protein Cbre_JD11.005
Locus_9844_Transcript_1/1_Conf_1.000	632	20	7.93E-56	EFO18183.1	76	220.705	150	115	hypothetical protein LOAG_10311
Locus_9845_Transcript_1/2_Conf_1.000	289	20	1.07E-11	EFO22450.1	67	73.1738	52	35	cold-shock DNA-binding domain-containing protein
Locus_9845_Transcript_2/2_Conf_1.000	606	14	1.87E-11	EFO22450.1	67	73.1738	52	35	cold-shock DNA-binding domain-containing protein
Locus_9846_Transcript_1/1_Conf_1.000	216	7	1.01E-06	XP_002633498.1	65	56.6102	64	42	Hypothetical protein CBG06270
Locus_9847_Transcript_1/1_Conf_1.000	167	0							
Locus_9848_Transcript_1/1_Conf_1.000	191	5	1.90E-08	NP_505419.3	82	62.3882	56	46	hypothetical protein K07B1.7
Locus_9849_Transcript_1/2_Conf_1.000	1030	20	4.11E-141	NP_491574.1	86	505.368	343	297	hypothetical protein F55A12.8
Locus_9849_Transcript_2/2_Conf_1.000	736	20	5.48E-95	XP_002639614.1	87	351.288	246	215	Hypothetical protein CBG12327
Locus_985_Transcript_1/1_Conf_1.000	464	20	1.98E-74	XP_001900952.1	93	281.567	147	137	G10 protein homolog
Locus_9850_Transcript_1/1_Conf_1.000	335	0							

Locus_9851_Transcript_1/1_Conf_1.000	248	20	8.00E-20	ABR87581.1	98	100.138	52	51	small subunit ribosomal protein 28
Locus_9852_Transcript_1/2_Conf_1.000	607	20	4.75E-15	XP_002636626.1	69	85.1149	104	72	C. briggsae CBR-AMAN-2 protein
Locus_9852_Transcript_2/2_Conf_1.000	601	20	4.62E-15	XP_002636626.1	69	85.1149	104	72	C. briggsae CBR-AMAN-2 protein
Locus_9853_Transcript_1/2_Conf_1.000	1147	20	6.46E-45	XP_002640501.1	53	186.037	311	166	Hypothetical protein CBG13640
Locus_9853_Transcript_2/2_Conf_1.000	1096	20	1.03E-44	XP_002640501.1	53	185.267	308	164	Hypothetical protein CBG13640
Locus_9854_Transcript_1/1_Conf_1.000	1030	20	2.19E-134	NP_493036.1	82	483.026	307	253	hypothetical protein Y53C10A.5
Locus_9855_Transcript_1/3_Conf_0.667	514	10	2.08E-37	XP_002634376.1	72	158.688	154	111	C. briggsae CBR-ORA-1 protein
Locus_9855_Transcript_2/3_Conf_0.667	514	10	2.08E-37	XP_002634376.1	72	158.688	154	111	C. briggsae CBR-ORA-1 protein
Locus_9855_Transcript_3/3_Conf_0.667	514	10	2.08E-37	XP_002634376.1	72	158.688	154	111	C. briggsae CBR-ORA-1 protein
Locus_9856_Transcript_1/1_Conf_1.000	368	20	2.39E-32	XP_002646356.1	76	141.739	121	92	Hypothetical protein CBG12070
Locus_9857_Transcript_1/2_Conf_1.000	472	0							
Locus_9857_Transcript_2/2_Conf_1.000	416	0							
Locus_9858_Transcript_1/1_Conf_1.000	466	20	1.48E-29	XP_001898226.1	65	132.494	152	99	exosome component 2
Locus_9859_Transcript_1/1_Conf_1.000	453	5	6.31E-49	NP_500240.1	75	196.823	154	116	hypothetical protein Y69A2AR.31
Locus_986_Transcript_1/1_Conf_1.000	2063	20	1.75E-95	XP_002641590.1	63	355.14	438	280	Hypothetical protein CBG09894
Locus_9860_Transcript_1/1_Conf_1.000	543	20	1.43E-08	XP_001101104.1	55	63.1586	97	54	PREDICTED: hepatitis B virus X-interacting protein isoform 4
Locus_9861_Transcript_1/1_Conf_1.000	323	20	3.51E-47	XP_002640613.1	96	191.045	100	96	Hypothetical protein CBG08724
Locus_9862_Transcript_1/1_Conf_1.000	595	2	1.45E-05	XP_001893945.1	54	53.5286	91	50	hypothetical protein Bm1_12375
Locus_9863_Transcript_1/1_Conf_1.000	1184	20	8.81E-61	NP_493014.1	63	238.81	338	214	hypothetical protein Y47H9C.7
Locus_9864_Transcript_1/1_Conf_1.000	909	20	1.10E-75	CBA11613.1	69	287.73	286	198	C. elegans protein F54F3.1c, partially confirmed by transcript evidence
Locus_9865_Transcript_1/1_Conf_1.000	323	0							
Locus_9866_Transcript_1/1_Conf_1.000	508	20	2.27E-20	NP_491200.1	80	102.064	87	70	hypothetical protein D1037.1
Locus_9867_Transcript_1/3_Conf_0.600	805	0							
Locus_9867_Transcript_2/3_Conf_0.400	790	0							

Locus_9867_Transcript_3/3_Conf_0.600	801	0							
Locus_9868_Transcript_1/1_Conf_1.000	495	1	2.96E-06	NP_501238.1	45	55.0694	161	73	hypothetical protein F45E4.3
Locus_9869_Transcript_1/1_Conf_1.000	856	2	1.08E-13	EFO20450.1	48	81.6481	183	88	hypothetical protein LOAG_08039
Locus_987_Transcript_1/2_Conf_1.000	1046	20	2.03E-87	XP_002642883.1	90	327.02	192	174	C. briggsae CBR-RAB-18 protein
Locus_987_Transcript_2/2_Conf_1.000	1019	20	1.97E-87	XP_002642883.1	90	327.02	192	174	C. briggsae CBR-RAB-18 protein
Locus_9870_Transcript_1/1_Conf_1.000	439	0							
Locus_9871_Transcript_1/1_Conf_1.000	1071	5	7.53E-93	XP_002636984.1	84	345.125	233	196	Hypothetical protein CBG09472
Locus_9872_Transcript_1/1_Conf_1.000	328	2	1.69E-17	XP_002641529.1	61	92.4337	85	52	Hypothetical protein CBG09826
Locus_9873_Transcript_1/1_Conf_1.000	613	3	1.67E-31	XP_002643749.1	62	139.813	204	128	Hypothetical protein CBG01946
Locus_9874_Transcript_1/1_Conf_1.000	1049	20	1.83E-120	NP_492839.4	79	436.802	347	277	Leucine-rich repeats, Ras-like domain, Kinase family member (lrk-1)
Locus_9875_Transcript_1/1_Conf_1.000	271	1	1.02E-14	CAR63536.1	71	83.1889	71	51	hypothetical protein
Locus_9876_Transcript_1/1_Conf_1.000	357	4	1.02E-06	NP_491791.1	65	56.6102	61	40	hypothetical protein T08B2.8
Locus_9877_Transcript_1/1_Conf_1.000	794	20	1.23E-98	XP_002633097.1	86	363.614	255	220	C. briggsae CBR-RPC-1 protein
Locus_9878_Transcript_1/1_Conf_1.000	235	0							
Locus_9879_Transcript_1/1_Conf_1.000	471	0							

Locus_988_Transcript_1/1_Conf_1.000	753	20	7.19E-98	NP_502077.1	93	360.918	202	188	Ribosomal Protein, Small subunit family member (rps-5)
Locus_9880_Transcript_1/1_Conf_1.000	170	20	5.78E-18	XP_002646171.1	87	93.9745	56	49	C. briggsae CBR-APB-3 protein
Locus_9881_Transcript_1/1_Conf_1.000	1464	20	8.42E-99	NP_497659.1	74	365.54	289	214	hypothetical protein Y53G8B.2
Locus_9882_Transcript_1/1_Conf_1.000	299	4	1.30E-09	XP_002629686.1	64	66.2402	90	58	Hypothetical protein CBG00906
Locus_9883_Transcript_1/1_Conf_1.000	467	2	1.14E-13	NP_502446.2	69	79.7221	79	55	hypothetical protein M02B1.2
Locus_9884_Transcript_1/1_Conf_1.000	391	1	9.47E-05	EFO16804.1	47	50.0618	111	53	hypothetical protein LOAG_11699
Locus_9885_Transcript_1/2_Conf_1.000	1636	20	7.81E-165	BAB61756.1	74	585.104	456	341	N-deactylase/N-sulfotransferase
Locus_9885_Transcript_2/2_Conf_1.000	1636	20	5.06E-164	BAB61756.1	74	582.408	456	340	N-deactylase/N-sulfotransferase
Locus_9886_Transcript_1/1_Conf_1.000	316	0							

Locus_9887_Transcript_1/1_Conf_1.000	667	20	1.10E-53	NP_509947.1	69	213.772	222	154	hypothetical protein T04F8.2
Locus_9888_Transcript_1/1_Conf_1.000	620	12	1.28E-18	XP_002646180.1	57	97.0561	145	84	Hypothetical protein CBG23746
Locus_9889_Transcript_1/1_Conf_1.000	424	2	5.66E-05	NP_001023316.1	73	50.8322	34	25	hypothetical protein M04B2.6
Locus_989_Transcript_1/1_Conf_1.000	1481	20	2.28E-168	XP_001891856.1	88	596.66	393	348	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase
Locus_9890_Transcript_1/1_Conf_1.000	141	4	8.83E-11	EFO27903.1	83	70.0922	43	36	mediator complex subunit rgr-1
Locus_9891_Transcript_1/1_Conf_1.000	399	0							
Locus_9892_Transcript_1/1_Conf_1.000	297	0							
Locus_9893_Transcript_1/1_Conf_1.000	577	20	1.80E-34	XP_001894647.1	60	149.443	187	114	CG33108-PA
Locus_9894_Transcript_1/1_Conf_1.000	518	12	2.29E-07	XP_002634855.1	64	58.9214	78	50	C. briggsae CBR-DNJ-15 protein
Locus_9895_Transcript_1/3_Conf_0.667	989	20	8.40E-80	AAA21167.2	81	301.597	226	184	Hypothetical protein F57B9.1
Locus_9895_Transcript_2/3_Conf_0.333	486	20	2.14E-28	AAA21167.2	79	128.642	97	77	Hypothetical protein F57B9.1
Locus_9895_Transcript_3/3_Conf_0.667	989	20	8.40E-80	AAA21167.2	81	301.597	226	184	Hypothetical protein F57B9.1
Locus_9896_Transcript_1/1_Conf_1.000	378	3	7.12E-08	XP_002646489.1	91	60.4622	36	33	Hypothetical protein CBG19471
Locus_9897_Transcript_1/1_Conf_1.000	1204	20	4.35E-55	NP_501435.1	56	219.935	276	155	hypothetical protein T26A8.4
Locus_9898_Transcript_1/1_Conf_1.000	324	0							
Locus_9899_Transcript_1/1_Conf_1.000	1140	20	7.56E-46	XP_001893150.1	56	189.119	347	197	hypothetical protein Bm1_08395
Locus_99_Transcript_1/3_Conf_0.727	236	19	4.76E-12	XP_001891902.1	77	74.3294	49	38	rRNA promoter binding protein
Locus_99_Transcript_2/3_Conf_0.545	251	20	1.19E-15	XP_001893546.1	78	86.2705	57	45	unspecific monooxygenase

Locus_99_Transcript_3/3_Conf_0.818	255	20	1.23E-15	XP_001893546.1	78	86.2705	57	45	unspecific monooxygenase
Locus_990_Transcript_1/1_Conf_1.000	1550	20	6.36E-153	NP_740966.1	75	545.428	484	365	hypothetical protein C24H12.4
Locus_9900_Transcript_1/1_Conf_1.000	628	20	5.61E-54	XP_002631704.1	71	214.542	202	144	Hypothetical protein CBG20903
Locus_9901_Transcript_1/1_Conf_1.000	486	4	1.58E-31	NP_501219.1	74	139.043	124	92	hypothetical protein R05G6.1
Locus_9902_Transcript_1/1_Conf_1.000	348	20	3.63E-44	XP_002643480.1	86	181.03	113	98	Hypothetical protein CBG16145
Locus_9903_Transcript_1/1_Conf_1.000	938	20	4.17E-25	EFN66773.1	57	119.783	191	109	Cullin-4B
Locus_9904_Transcript_1/1_Conf_1.000	1163	20	1.21E-22	XP_001896275.1	45	112.079	386	175	Ubiquitin carboxyl-terminal hydrolase family protein
Locus_9905_Transcript_1/1_Conf_1.000	659	20	1.05E-40	EFO24231.1	88	170.629	114	101	transcription elongation factor SPT4
Locus_9906_Transcript_1/1_Conf_1.000	475	20	6.37E-17	XP_002631797.1	78	90.5077	66	52	C. briggsae CBR-CYN-16 protein
Locus_9907_Transcript_1/1_Conf_1.000	364	4	8.56E-14	XP_001895599.1	61	80.1073	83	51	hypothetical protein Bm1_20725
Locus_9908_Transcript_1/1_Conf_1.000	706	20	1.05E-44	XP_002637085.1	59	184.111	242	144	Hypothetical protein CBG09584
Locus_9909_Transcript_1/1_Conf_1.000	132	0							
Locus_991_Transcript_1/1_Conf_1.000	622	20	3.00E-44	NP_491456.2	70	182.185	183	129	hypothetical protein F57C9.6
Locus_9910_Transcript_1/1_Conf_1.000	288	20	5.11E-38	NP_783313.1	100	160.614	91	91	NADH dehydrogenase ubiquinone 1 alpha subcomplex subunit 11 isoform 1
Locus_9911_Transcript_1/1_Conf_1.000	1154	20	1.85E-124	XP_002641545.1	91	450.284	268	246	Hypothetical protein CBG09844

Locus_9912_Transcript_1/1_Conf_1.000	1172	20	4.19E-39	NP_502675.4	62	166.777	213	134	hypothetical protein Y37A1A.3
Locus_9913_Transcript_1/1_Conf_1.000	724	20	2.26E-29	XP_001891854.1	73	133.265	150	110	Conserved oligomeric Golgi complex component 4
Locus_9914_Transcript_1/1_Conf_1.000	503	0							
Locus_9915_Transcript_1/1_Conf_1.000	1034	20	8.24E-65	XP_002637680.1	74	251.906	199	148	C. briggsae CBR-UDA-1 protein
Locus_9916_Transcript_1/1_Conf_1.000	680	20	3.57E-55	XP_002636583.1	63	218.779	229	146	Hypothetical protein CBG23277
Locus_9917_Transcript_1/1_Conf_1.000	219	0							
Locus_9918_Transcript_1/1_Conf_1.000	1384	20	7.44E-158	AAQ06435.1	83	561.607	391	327	ABC6 protein
Locus_9919_Transcript_1/1_Conf_1.000	382	0							
Locus_992_Transcript_1/2_Conf_1.000	1138	20	2.20E-69	XP_002637173.1	71	267.314	267	190	Hypothetical protein CBG09691
Locus_992_Transcript_2/2_Conf_1.000	1138	20	2.20E-69	XP_002637173.1	71	267.314	267	190	Hypothetical protein CBG09691
Locus_9920_Transcript_1/1_Conf_1.000	191	0							
Locus_9921_Transcript_1/1_Conf_1.000	202	0							
Locus_9922_Transcript_1/1_Conf_1.000	395	8	2.30E-30	XP_002639325.1	67	135.191	134	91	Hypothetical protein CBG03903
Locus_9923_Transcript_1/1_Conf_1.000	321	6	1.14E-21	XP_002644355.1	63	106.301	107	68	C. briggsae CBR-DDR-2 protein
Locus_9924_Transcript_1/2_Conf_1.000	361	20	1.20E-15	XP_002196552.1	57	86.2705	106	61	PREDICTED: similar to ubiquitin specific protease 5 (isopeptidase T) isoform 1
Locus_9924_Transcript_2/2_Conf_1.000	361	20	1.20E-15	XP_002196552.1	57	86.2705	106	61	PREDICTED: similar to ubiquitin specific protease 5 (isopeptidase T) isoform 1
Locus_9925_Transcript_1/1_Conf_1.000	725	20	5.21E-26	XP_001626797.1	61	122.094	190	116	predicted protein

Locus_9926_Transcript_1/2_Conf_1.000	1288	20	1.00E-153	NP_501087.1	81	547.74	383	314	hypothetical protein C06G3.5
Locus_9926_Transcript_2/2_Conf_1.000	1288	20	1.00E-153	NP_501087.1	81	547.74	383	314	hypothetical protein C06G3.5
Locus_9927_Transcript_1/1_Conf_1.000	902	20	3.38E-45	XP_002629727.1	59	186.422	256	153	Hypothetical protein CBG00958
Locus_9928_Transcript_1/1_Conf_1.000	208	17	1.68E-17	XP_002643097.1	82	92.4337	57	47	Hypothetical protein CBG23021
Locus_9929_Transcript_1/1_Conf_1.000	501	20	4.32E-45	XP_002642024.1	70	184.111	166	117	Hypothetical protein CBG17960
Locus_993_Transcript_1/1_Conf_1.000	1526	20	0	XP_002641126.1	83	671.774	473	393	C. briggsae CBR-UCR-1 protein

Locus_9930_Transcript_1/1_Conf_1.000	874	20	8.34E-110	XP_002636865.1	92	400.979	227	209	Hypothetical protein CBG09322
Locus_9931_Transcript_1/2_Conf_1.000	430	20	8.88E-35	XP_001893025.1	82	149.828	97	80	enhancer of rudimentary homolog
Locus_9931_Transcript_2/2_Conf_1.000	460	20	8.77E-35	XP_001893025.1	82	149.828	97	80	enhancer of rudimentary homolog
Locus_9932_Transcript_1/1_Conf_1.000	227	18	4.49E-18	NP_001023620.1	74	94.3597	75	56	hypothetical protein ZK792.4
Locus_9933_Transcript_1/1_Conf_1.000	250	20	1.72E-06	ADD18404.1	63	55.8398	58	37	clip-domain serine protease
Locus_9934_Transcript_1/1_Conf_1.000	171	0							
Locus_9935_Transcript_1/1_Conf_1.000	210	20	7.73E-31	XP_002819977.1	97	136.732	70	68	PREDICTED: hypothetical protein LOC100458687
Locus_9936_Transcript_1/1_Conf_1.000	1016	0							
Locus_9937_Transcript_1/1_Conf_1.000	219	0							
Locus_9938_Transcript_1/1_Conf_1.000	156	20	1.82E-19	ABC40752.1	100	98.9821	51	51	myosin heavy chain
Locus_9939_Transcript_1/1_Conf_1.000	312	6	1.45E-16	XP_001891702.1	77	89.3521	62	48	Hypothetical 30.5 kDa protein ZK1321.3 in chromosome II, putative
Locus_994_Transcript_1/2_Conf_1.000	2096	1	4.23E-04	NP_001166287.1	37	51.6026	421	157	sericin 2 isoform 1 precursor
Locus_994_Transcript_2/2_Conf_1.000	573	0							
Locus_9940_Transcript_1/1_Conf_1.000	633	0							

Locus_9941_Transcript_1/1_Conf_1.000	471	4	8.04E-36	XP_002646088.1	69	153.295	155	108	Hypothetical protein CBG07955
Locus_9942_Transcript_1/1_Conf_1.000	1132	0							
Locus_9943_Transcript_1/1_Conf_1.000	404	4	3.78E-09	XP_001899104.1	55	64.6994	99	55	hypothetical protein Bm1_38255
Locus_9944_Transcript_1/2_Conf_1.000	365	20	3.96E-27	NP_492616.1	67	124.405	115	78	Nematode AStacin protease family member (nas-5)
Locus_9944_Transcript_2/2_Conf_1.000	494	20	2.12E-28	NP_492616.1	58	128.642	162	95	Nematode AStacin protease family member (nas-5)
Locus_9945_Transcript_1/1_Conf_1.000	562	20	8.74E-52	NP_495017.1	75	206.838	187	142	PINK (PTEN-induced kinase) homolog family member (pink-1)
Locus_9946_Transcript_1/1_Conf_1.000	589	20	1.07E-05	XP_001318162.1	48	53.9138	135	65	viral A-type inclusion protein

Locus_9947_Transcript_1/1_Conf_1.000	300	20	7.01E-48	NP_504661.1	95	193.356	99	95	Daf-12, REdundant with family member (dre-1)
Locus_9948_Transcript_1/1_Conf_1.000	133	0							
Locus_9949_Transcript_1/1_Conf_1.000	728	20	6.55E-77	NP_001122460.1	76	291.197	241	184	Ortholog of Drosophila DRoSHa gene family member (drsh-1)
Locus_995_Transcript_1/2_Conf_1.000	1145	20	7.96E-112	NP_741085.1	71	408.297	383	275	hypothetical protein F42G9.6
Locus_995_Transcript_2/2_Conf_1.000	1055	20	4.13E-112	NP_741084.1	74	409.068	354	265	hypothetical protein F42G9.6
Locus_9950_Transcript_1/1_Conf_1.000	166	0							
Locus_9951_Transcript_1/1_Conf_1.000	1379								
Locus_9952_Transcript_1/1_Conf_1.000	499	0							
Locus_9953_Transcript_1/1_Conf_1.000	172	0							
Locus_9954_Transcript_1/1_Conf_1.000	131	20	2.51E-13	NP_495706.2	95	78.5666	43	41	hypothetical protein F10B5.8
Locus_9955_Transcript_1/1_Conf_1.000	227	20	2.72E-23	EFO26146.1	83	111.694	74	62	hypothetical protein LOAG_02340
Locus_9956_Transcript_1/1_Conf_1.000	677	20	2.05E-87	XP_002633788.1	83	325.865	219	183	C. briggsae CBR-FAT-4 protein
Locus_9957_Transcript_1/1_Conf_1.000	404	0							
Locus_9958_Transcript_1/1_Conf_1.000	459	0							
Locus_9959_Transcript_1/1_Conf_1.000	230	20	5.49E-08	XP_001896251.1	71	60.8474	45	32	GRF zinc finger family protein
Locus_996_Transcript_1/1_Conf_1.000	1227	20	5.03E-115	CAR63667.1	82	419.083	278	228	putative WD-repeat protein
Locus_9960_Transcript_1/1_Conf_1.000	374	0							

Locus_9961_Transcript_1/1_Conf_1.000	565	20	5.89E-88	NP_001122711.1	89	327.02	188	168	CBP/p300 homolog family member (cbp-1)
Locus_9962_Transcript_1/1_Conf_1.000	220	0							
Locus_9963_Transcript_1/1_Conf_1.000	299	20	6.87E-11	XP_002923775.1	100	70.4774	60	60	PREDICTED: hypothetical protein LOC100476237
Locus_9964_Transcript_1/1_Conf_1.000	145	0							
Locus_9965_Transcript_1/1_Conf_1.000	894	20	1.42E-104	NP_496177.2	90	383.645	250	227	Proteasome Alpha Subunit family member (pas-7)
Locus_9966_Transcript_1/1_Conf_1.000	189	20	1.54E-26	EAW55604.1	100	122.479	62	62	hypothetical protein FLJ14346, isoform CRA_c

Locus_9967_Transcript_1/1_Conf_1.000	326	20	5.42E-32	XP_002640962.1	79	140.584	108	86	Hypothetical protein CBG11705
Locus_9968_Transcript_1/1_Conf_1.000	398	20	5.10E-38	NP_001022450.1	77	160.614	132	102	hypothetical protein Y48E1A.1
Locus_9969_Transcript_1/1_Conf_1.000	219	20	1.36E-14	EFO25702.1	73	82.8037	72	53	hypothetical protein LOAG_02781
Locus_997_Transcript_1/1_Conf_1.000	376	20	4.58E-47	ABX75173.1	86	190.66	108	93	RNA polymerase III 12.5 kDa polypeptide
Locus_9970_Transcript_1/2_Conf_1.000	333	20	8.57E-22	EFO25910.1	81	106.686	69	56	hypothetical protein LOAG_02581
Locus_9970_Transcript_2/2_Conf_1.000	333	20	8.58E-22	EFO25910.1	81	106.686	69	56	hypothetical protein LOAG_02581
Locus_9971_Transcript_1/1_Conf_1.000	716	20	1.46E-65	XP_002646453.1	87	253.447	154	135	C. briggsae CBR-SMD-1 protein
Locus_9972_Transcript_1/1_Conf_1.000	1107	20	1.07E-89	XP_001893326.1	72	334.724	304	219	Dehydrogenases, short chain protein 30

Locus_9973_Transcript_1/1_Conf_1.000	363	0							
Locus_9974_Transcript_1/1_Conf_1.000	347	0							
Locus_9975_Transcript_1/1_Conf_1.000	629	19	5.26E-44	NP_510787.2	77	181.415	134	104	hypothetical protein T08G2.2
Locus_9976_Transcript_1/1_Conf_1.000	597	20	8.00E-28	NP_499817.2	53	127.487	188	101	Acyl-Coenzyme A Binding Protein family member (acbp-5)
Locus_9977_Transcript_1/1_Conf_1.000	233	20	4.91E-33	XP_002647642.1	90	144.05	77	70	Hypothetical protein CBG06741
Locus_9978_Transcript_1/1_Conf_1.000	440	20	2.15E-49	XP_002642413.1	93	198.364	113	106	Hypothetical protein CBG06810
Locus_9979_Transcript_1/1_Conf_1.000	979	20	3.77E-24	XP_001893256.1	87	116.701	64	56	Hypothetical zinc finger protein B0310.2 in chromosome X, putative
Locus_998_Transcript_1/1_Conf_1.000	285	20	4.33E-45	EFO21508.1	100	184.111	94	94	ubiquitin C II
Locus_9980_Transcript_1/1_Conf_1.000	490	20	1.12E-53	XP_002641555.1	86	212.616	143	123	Hypothetical protein CBG09854
Locus_9981_Transcript_1/1_Conf_1.000	251	0							
Locus_9982_Transcript_1/1_Conf_1.000	593	20	1.24E-17	XP_787754.1	62	93.5893	100	62	PREDICTED: similar to Autophagy-specific protein, putative
Locus_9983_Transcript_1/1_Conf_1.000	410	0							
Locus_9984_Transcript_1/1_Conf_1.000	914	20	3.64E-103	XP_002643347.1	96	379.022	205	197	C. briggsae CBR-RAB-6.2 protein
Locus_9985_Transcript_1/1_Conf_1.000	475	4	7.01E-32	XP_002634331.1	75	140.198	132	99	C. briggsae CBR-IMP-3 protein
Locus_9986_Transcript_1/1_Conf_1.000	464	5	1.35E-22	XP_001892273.1	57	109.383	157	91	hypothetical protein
Locus_9987_Transcript_1/1_Conf_1.000	978	6	4.01E-42	XP_002639130.1	74	176.407	166	123	Hypothetical protein CBG14950
Locus_9988_Transcript_1/1_Conf_1.000	251	0							

Locus_9989_Transcript_1/1_Conf_1.000	302	20	1.93E-13	XP_001902812.1	97	78.9518	37	36	40S ribosomal protein S29
Locus_999_Transcript_1/3_Conf_0.400	3371	20	0	ABC40752.1	97	1927.91	1113	1088	myosin heavy chain
Locus_999_Transcript_2/3_Conf_0.400	3622	20	0	ABC40752.1	97	2083.92	1194	1168	myosin heavy chain
Locus_999_Transcript_3/3_Conf_0.400	776	20	5.19E-46	XP_002646204.1	84	188.734	132	111	C. briggsae CBR-PFN-1 protein
Locus_9990_Transcript_1/1_Conf_1.000	480	20	6.09E-28	NP_001022027.1	63	127.102	160	102	hypothetical protein C44B7.6
Locus_9991_Transcript_1/1_Conf_1.000	363	0							
Locus_9992_Transcript_1/2_Conf_1.000	581	20	2.37E-58	XP_002631391.1	79	228.794	154	123	Hypothetical protein CBG03233

Locus_9992_Transcript_2/2_Conf_1.000	701	20	3.71E-58	XP_002631391.1	79	228.794	154	123	Hypothetical protein CBG03233
Locus_9993_Transcript_1/1_Conf_1.000	1399	20	1.14E-105	XP_002646302.1	72	388.267	321	234	Hypothetical protein CBG12009
Locus_9994_Transcript_1/1_Conf_1.000	180	20	2.11E-15	XP_001895773.1	81	85.5001	54	44	CG30390-PA
Locus_9995_Transcript_1/1_Conf_1.000	930	20	2.29E-100	NP_498815.1	76	369.777	298	229	hypothetical protein F09G8.3
Locus_9996_Transcript_1/1_Conf_1.000	215	2	7.01E-08	XP_002638798.1	80	60.4622	46	37	C. briggsae CBR-PIF-1 protein
Locus_9997_Transcript_1/1_Conf_1.000	969	20	8.58E-130	XP_002633709.1	86	467.618	299	259	Hypothetical protein CBG03392
Locus_9998_Transcript_1/1_Conf_1.000	537	0							
Locus_9999_Transcript_1/1_Conf_1.000	273	0							

	BLAST2GO					
Specie	**Blast2GO Seq. Description**	**#GOs (Annotated)**	**GOs (Annotated)**	**GOs Mapped but not annotated**	**Enzyme Codes**	**InterProScan**
	-	0				SignalP (SIGNALP)
	-	0				IPR017956
	-	0				IPR017956
	-	0				IPR017956
Nippostrongylus brasiliensis	globin	6	F:GO:0020037; C:GO:0005615; C:GO:0005737; F:GO:0005344; P:GO:0015671; F:GO:0019825	-		IPR009050; IPR012292
Caenorhabditis briggsae	tricarboxylate transport mitochondrial	8	F:GO:0005371; F:GO:0005488; C:GO:0005743; C:GO:0016006; C:GO:0005811; P:GO:0006843; P:GO:0055085; C:GO:0016021	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF62 (PANTHER)
Brugia malayi	hypothetical protein Bm1_08910 [Brugia malayi]	0				-
Loa loa	protein suppressor of forked	2	P:GO:0009792; P:GO:0000003	-		IPR008847; PTHR19980 (PANTHER)
Caenorhabditis elegans	dopey family member 1	2	P:GO:0015031; P:GO:0007275	-		IPR007249; PTHR14042 (PANTHER)
Caenorhabditis briggsae	gamma-glutamyl cyclotransferase	4	F:GO:0003839; P:GO:0001836; C:GO:0005829; F:GO:0042803	-	EC:2.3.2.4	SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Homo sapiens	immunoglobulin heavy chain	4	P:GO:0018298; P:GO:0006955; F:GO:0003823; F:GO:0005515	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	carnitine acetyltransferase	3	F:GO:0008415; P:GO:0040011; C:GO:0005739	-		-

Brugia malayi	vinculin family protein	15	P:GO:0016337; C:GO:0030424; P:GO:0021942; C:GO:0005913; P:GO:0048854; P:GO:0051823; P:GO:0060134; F:GO:0045296; C:GO:0015629; P:GO:0007409; F:GO:0005200; C:GO:0016323; C:GO:0030027; C:GO:0005737; P:GO:0048813	-		-
	-	0				-
	-	0				-
Brachyspira hyodysenteriae WA1	cop1-interacting protein 4	0				-
Caenorhabditis elegans	solute carrier family 12 (potassium chloride transporters) member 6 isoform 2	3	P:GO:0055085; P:GO:0006811; C:GO:0016020	-		PTHR11827 (PANTHER), PTHR11827:SF5 (PANTHER)
Loa loa	alpha beta hydrolase2	2	F:GO:0016298; P:GO:0006629	-		G3DSA:3.40.50.1820 (GENE3D), PTHR10794 (PANTHER), PTHR10794:SF9 (PANTHER), SSF53474 (SUPERFAMILY)
	-	0				IPR013083; SSF57850 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-emb-9 protein	4	F:GO:0005515; P:GO:0009987; P:GO:0016043; C:GO:0005581	-		IPR008160; PTHR10499 (PANTHER), PTHR10499:SF114 (PANTHER)
Caenorhabditis briggsae	ras-like protein 2	9	F:GO:0005525; C:GO:0005622; F:GO:0005515; P:GO:0006913; P:GO:0030335; P:GO:0006886; C:GO:0016020; P:GO:0007265; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001806; IPR003577; IPR005225; IPR013753; IPR015592; IPR020849; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
Ancylostoma caninum	secreted protein 6 precursor	0		C:GO:0005576		-
Caenorhabditis elegans	hypothetical protein F10G8.8 [Caenorhabditis elegans]	0		F:GO:0005515		IPR001849
Ailuropoda melanoleuca	daz associated protein 1	8	C:GO:0005730; P:GO:0007283; P:GO:0030154; C:GO:0005844; F:GO:0003723; P:GO:0007275; C:GO:0005739; F:GO:0000166	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF10 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-tnt-3 protein	0		P:GO:0006952; P:GO:0043050		-

Caenorhabditis sp. PS1010	galactoki-se 2	3	P:GO:0005975; P:GO:0044237; F:GO:0004335	-	EC:2.7.1.6	IPR000705; IPR006203; IPR006204; IPR006206; IPR013750; IPR014721; IPR020568; G3DSA:3.30.70.890 (GENE3D), PTHR10457 (PANTHER), PTHR10457:SF7 (PANTHER), SSF55060 (SUPERFAMILY)
Caenorhabditis elegans	small nucleolar ribonucleoprotein complex subunit	1	P:GO:0006898	-		IPR001680; IPR015943; IPR017986; IPR019781; IPR019782; PTHR19853 (PANTHER)
	-	0				-
Loa loa	r- polymerase-associated protein rtf1 homolog	10	P:GO:0035121; C:GO:0005730; P:GO:0043473; P:GO:0007507; P:GO:0014032; F:GO:0005515; P:GO:0016043; P:GO:0001756; C:GO:0005737; P:GO:0006350	-		IPR004343; PTHR13115 (PANTHER)
	-	0				-
Caenorhabditis briggsae	heat shock protein 75	6	P:GO:0006457; C:GO:0005811; P:GO:0006950; P:GO:0040010; F:GO:0005524; F:GO:0051082	-		IPR001404; IPR003594; IPR020575; PTHR11528:SF24 (PANTHER)
Caenorhabditis elegans	sphingomyelin phosphodiesterase neutral membrane (neutral sphingomyeli-se)	3	P:GO:0050794; F:GO:0016787; C:GO:0016020	-		IPR005135; G3DSA:3.60.10.10 (GENE3D), PTHR12393 (PANTHER)
	-	0				-
Caenorhabditis briggsae	u2 snrnp auxiliary factor small subunit	13	F:GO:0003723; C:GO:0015030; C:GO:0005681; F:GO:0008270; P:GO:0040007; F:GO:0050733; P:GO:0040035; P:GO:0018996; P:GO:0002119; F:GO:0000166; P:GO:0040011; P:GO:0000398; P:GO:0009792	-		IPR000504; IPR000571; IPR009145; IPR012677; SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	u2 snrnp auxiliary factor small subunit	13	F:GO:0003723; C:GO:0015030; C:GO:0005681; F:GO:0008270; P:GO:0040007; F:GO:0050733; P:GO:0040035; P:GO:0018996; P:GO:0002119; F:GO:0000166; P:GO:0040011; P:GO:0000398; P:GO:0009792	-		IPR000504; IPR000571; IPR009145; IPR012677; SSF54928 (SUPERFAMILY)

Caenorhabditis elegans	hypothetical protein T07C12.12 [Caenorhabditis elegans]	0				PTHR14790 (PANTHER), PTHR14790:SF2 (PANTHER)
Loa loa	upf3 regulator of nonsense transcripts homolog a	1	F:GO:0005488	-		IPR005120; IPR012677; IPR018247; PTHR13112 (PANTHER), SSF54928 (SUPERFAMILY)
Loa loa	protein ki-se n2	5	P:GO:0006468; C:GO:0005622; F:GO:0005524; P:GO:0007165; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR000961; IPR008271; IPR011009; IPR017442; IPR017892; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22985 (PANTHER), PTHR22985:SF54 (PANTHER)
Caenorhabditis elegans	regulator of g-protein sig-ling 7	2	F:GO:0004871; P:GO:0023052	-		IPR000342; IPR016137; G3DSA:1.10.167.10 (GENE3D), G3DSA:1.10.196.10 (GENE3D), PTHR10845 (PANTHER), PTHR10845:SF29 (PANTHER)
Brugia malayi	transcription elongation factor b polypeptide 1	1	F:GO:0005515	-		IPR011333; IPR016073; PTHR20648 (PANTHER)
Caenorhabditis sp. PS1010	mr- cap guanine-n7 methyltransferase	4	F:GO:0004482; P:GO:0006370; F:GO:0003723; C:GO:0005634	-	EC:2.1.1.56	IPR004971; G3DSA:3.40.50.150 (GENE3D), PTHR12189 (PANTHER), SSF53335 (SUPERFAMILY)
	-	0				-
	-	0				-
Pongo abelii	cd68 molecule	5	C:GO:0005624; C:GO:0016021; C:GO:0005765; C:GO:0010008; C:GO:0005886	-		IPR002000; PTHR11506:SF2 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0004385; C:GO:0016020; F:GO:0005515		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR10316 (PANTHER), PTHR10316:SF7 (PANTHER)
Ancylostoma caninum	metalloprotease 1 precursor	3	F:GO:0046872; P:GO:0000003; F:GO:0008237	-		IPR001506; IPR013032; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
Ancylostoma caninum	metalloprotease 1 precursor	3	F:GO:0046872; P:GO:0000003; F:GO:0008237	-		IPR001506; IPR013032; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	hepatocellular carcinoma-associated antigen 59 family protein	0		F:GO:0005509		IPR010756; PTHR13486:SF1 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	tyrosyl-tr- synthetase	6	P:GO:0000003; F:GO:0000166; P:GO:0006418; F:GO:0004831; P:GO:0009792; P:GO:0007040	-	EC:6.1.1.1	IPR002305; IPR015624; G3DSA:1.10.240.10 (GENE3D), PTHR11946 (PANTHER), SignalP (SIGNALP), SSF52374 (SUPERFAMILY)

Caenorhabditis elegans	zipper cg15792-pd	32	P:GO:0045200; C:GO:0016461; P:GO:0035159; P:GO:0031036; C:GO:0016460; P:GO:0007409; P:GO:0035072; P:GO:0007443; P:GO:0007395; P:GO:0045214; P:GO:0035017; C:GO:0016021; P:GO:0006936; P:GO:0007297; P:GO:0046663; F:GO:0003779; P:GO:0001736; F:GO:0032027; P:GO:0008258; P:GO:0051259; P:GO:0016203; C:GO:0032154; C:GO:0045179; F:GO:0003774; P:GO:0045184; P:GO:0035317; C:GO:0030018;	-		IPR001609; PTHR13140 (PANTHER), PTHR13140:SF23 (PANTHER), SSF52540 (SUPERFAMILY)
Loa loa	hypothetical protein LOAG_00061 [Loa loa]	0		F:GO:0030246		-
Brugia malayi	sec63 domain containing protein	1	F:GO:0005515	-		G3DSA:2.60.40.150 (GENE3D), PTHR11752 (PANTHER), PTHR11752:SF7 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		C:GO:0016021; P:GO:0055085		IPR011701; IPR016196; G3DSA:1.20.1250.20 (GENE3D), PTHR11662 (PANTHER), PTHR11662:SF17 (PANTHER)
	-	0				-
Caenorhabditis elegans	loc443620 protein	0		F:GO:0003674; C:GO:0005737; F:GO:0004872; F:GO:0004871; F:GO:0004930; C:GO:0016021; P:GO:0007165; P:GO:0007186		IPR019167; PTHR21551 (PANTHER)
	-	0				-
Caenorhabditis briggsae	chromosome 9 open reading frame 5	1	F:GO:0005515	-		IPR000215; SignalP (SIGNALP)
Caenorhabditis briggsae	chromosome 9 open reading frame 5	1	F:GO:0005515	-		IPR000215; SignalP (SIGNALP)
Pan troglodytes	ribonuclease pancreatic precursor	3	C:GO:0005576; F:GO:0003676; F:GO:0004522	-	EC:3.1.27.5	SignalP (SIGNALP)
Caenorhabditis elegans	zinc c2h2 type family protein	0		F:GO:0003676; P:GO:0045944; F:GO:0008270; C:GO:0005634; P:GO:0006917; C:GO:0005622		IPR007087; IPR015880; PTHR14738 (PANTHER), PTHR14738:SF6 (PANTHER)

Loa loa	zinc c2h2 type family protein	6	P:GO:0009987; F:GO:0008270; F:GO:0003676; C:GO:0005622; F:GO:0005515; P:GO:0040015	-		IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis briggsae	mitochondrial ribosomal protein l1	10	P:GO:0006412; P:GO:0040010; F:GO:0003723; P:GO:0006396; C:GO:0005840; P:GO:0008340; F:GO:0003735; P:GO:0002119; P:GO:0006898; P:GO:0009792	-	EC:3.6.5.3	IPR002143; PTHR23105 (PANTHER), PTHR23105:SF8 (PANTHER)
Caenorhabditis elegans	par-6 at contacts (abnormal early localization of par-6) family member (pac-1)	2	F:GO:0005100; P:GO:0007266	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	ubiquinol-cytochrome c chaperone family protein	1	P:GO:0009792	-		-
Loa loa	taf2 r- polymerase tata box binding protein -associated 150kda	7	P:GO:0010552; P:GO:0006367; F:GO:0010843; P:GO:0000086; C:GO:0033276; F:GO:0005515; C:GO:0005669	-		IPR014782; PTHR15137 (PANTHER), PTHR15137:SF7 (PANTHER), SSF55486 (SUPERFAMILY), SSF63737 (SUPERFAMILY)
Brugia malayi	c2h2 transcription factor	0		P:GO:0006355; F:GO:0046872; F:GO:0003676; P:GO:0008150; F:GO:0008270; C:GO:0005634; C:GO:0005622		IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)

Caenorhabditis briggsae	protein transport protein sec23	28	P:GO:0071711; P:GO:0008360; F:GO:0005515; F:GO:0008270; P:GO:0035293; P:GO:0040010; P:GO:0006898; P:GO:0034394; C:GO:0030127; P:GO:0048081; P:GO:0007029; P:GO:0018996; P:GO:0006886; P:GO:0050774; P:GO:0007030; P:GO:0009792; P:GO:0035149; F:GO:0005096; P:GO:0016203; P:GO:0022409; C:GO:0005795; P:GO:0002119; P:GO:0006888; P:GO:0030011; P:GO:0048477; P:GO:0030421; C:GO:0005783; P:GO:0003331	-		IPR006895; IPR006896; PTHR11141 (PANTHER), SSF53300 (SUPERFAMILY), SSF81995 (SUPERFAMILY)
Loa loa	mitochondrial import inner membrane translocase subunit	9	F:GO:0015450; C:GO:0005743; F:GO:0046872; P:GO:0045039; P:GO:0040035; C:GO:0042719; P:GO:0040011; P:GO:0009792; P:GO:0040018	-		IPR004217; PTHR10898 (PANTHER), PTHR10898:SF9 (PANTHER), SSF144122 (SUPERFAMILY)
Loa loa	egl-1 suppressor uptake defective raf enhancer family member (eor-2)	0				-
Caenorhabditis briggsae	atp synthase subunit mitochondrial	4	P:GO:0006412; P:GO:0006139; P:GO:0044281; C:GO:0005737	-	EC:3.6.5.3	G3DSA:3.80.10.10 (GENE3D), PTHR13382 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	iron-sulfur cluster scaffold variant 2	9	P:GO:0009792; P:GO:0002119; P:GO:0016226; F:GO:0051536; F:GO:0005506; F:GO:0032947; P:GO:0040007; C:GO:0005829; C:GO:0005739	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Loa loa	briggsae cbr-mec-17 protein	0				IPR007965

Loa loa	kh domain containing protein	0		F:GO:0003723		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF281 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		C:GO:0033162; C:GO:0005634; C:GO:0019717; C:GO:0014069; C:GO:0005789; C:GO:0005783; C:GO:0045202; C:GO:0033267; P:GO:0048812; C:GO:0043197; C:GO:0010008; C:GO:0030054; C:GO:0005737; C:GO:0005768; C:GO:0030672; C:GO:0031410; C:GO:0030426; C:GO:0045211; P:GO:0031532; C:GO:0005886; P:GO:0060159; C:GO:0043005; P:GO:0031175		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	riken cd- isoform cra_a	0		F:GO:0003676; F:GO:0003674; F:GO:0000166; P:GO:0008150; C:GO:0005575		-
Caenorhabditis elegans	hypothetical protein Y47A7.1 [Caenorhabditis elegans]	0		F:GO:0005488		-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein C46H3.2 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	elongation factor tu gtp binding domain containing 2	15	F:GO:0003746; C:GO:0015030; P:GO:0000910; P:GO:0040007; C:GO:0016607; P:GO:0000003; P:GO:0008380; P:GO:0018996; P:GO:0002119; F:GO:0005515; P:GO:0040011; F:GO:0003924; C:GO:0030529; P:GO:0009792; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000795; IPR005225; G3DSA:3.40.50.300 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF15 (PANTHER), SSF52540 (SUPERFAMILY)

Homo sapiens	peptide transporter	19	F:GO:0046979; C:GO:0042825; P:GO:0019060; F:GO:0015197; C:GO:0005792; P:GO:0042270; F:GO:0043531; C:GO:0005829; F:GO:0046982; F:GO:0046978; P:GO:0046967; P:GO:0015833; F:GO:0042626; P:GO:0019885; P:GO:0055085; F:GO:0042605; F:GO:0042803; F:GO:0005524; C:GO:0005739	-		IPR011527; IPR017940; G3DSA:1.20.1560.10 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF79 (PANTHER), SignalP (SIGNALP)
Loa loa	organic solute transporter alpha	0		C:GO:0016021; P:GO:0009792; F:GO:0005215; P:GO:0006810		-
Caenorhabditis elegans	g-protein coupled receptor	5	F:GO:0004872; P:GO:0035075; P:GO:0040017; P:GO:0007186; C:GO:0016021	-		IPR000276; IPR017452; G3DSA:1.20.1070.10 (GENE3D), PTHR19266 (PANTHER), PTHR19266:SF68 (PANTHER), SignalP (SIGNALP), SSF81321 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		IPR000866; IPR012335; IPR012336; IPR017936; PTHR13871 (PANTHER), PTHR13871:SF4 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		IPR000866; IPR012335; IPR012336; IPR017936; PTHR13871 (PANTHER), PTHR13871:SF4 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-hum-7 protein	5	F:GO:0046872; C:GO:0016459; F:GO:0005524; P:GO:0007165; F:GO:0003774	-		-
Caenorhabditis briggsae	briggsae cbr-nol-6 protein	0				-
Brugia malayi	asparagi-se family protein	0		F:GO:0005488; F:GO:0016787		-
Caenorhabditis elegans	briggsae cbr-pvf-1 protein	1	F:GO:0016301	-		IPR000072; IPR004153; IPR017948; G3DSA:2.10.90.10 (GENE3D), PTHR11633 (PANTHER), PTHR11633:SF1 (PANTHER), SSF57501 (SUPERFAMILY)
Brugia malayi	protein mitochondrial precursor	1	F:GO:0005488	-		IPR000740; PTHR21237:SF8 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	zinc finger ccch-type containing 15	3	F:GO:0046872; C:GO:0044424; P:GO:0019221	-		IPR000571; G3DSA:4.10.1000.10 (GENE3D), PTHR12681 (PANTHER), SSF90229 (SUPERFAMILY)

Caenorhabditis elegans	zinc finger ccch-type containing 15	3	F:GO:0046872; C:GO:0044424; P:GO:0019221	-		IPR000571; G3DSA:4.10.1000.10 (GENE3D), PTHR12681 (PANTHER), SSF90229 (SUPERFAMILY)
Caenorhabditis elegans	mlx interacting protein	9	F:GO:0030528; P:GO:0040010; F:GO:0005488; P:GO:0045449; P:GO:0002119; P:GO:0006898; P:GO:0009792; C:GO:0005737; C:GO:0005634	-		PTHR15741 (PANTHER), PTHR15741:SF1 (PANTHER)
Brugia malayi	endoribonuclease dicer	10	F:GO:0004525; P:GO:0006396; C:GO:0005622; F:GO:0003677; F:GO:0003725; F:GO:0003993; F:GO:0005524; F:GO:0005515; P:GO:0035194; F:GO:0004386	-	EC:3.1.26.3; EC:3.1.3.2	IPR006935; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR14950 (PANTHER), PTHR14950:SF3 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-cka-1 protein	6	C:GO:0005887; F:GO:0019904; C:GO:0005938; F:GO:0005069; F:GO:0005080; P:GO:0006612	-		-
Caenorhabditis elegans	4-hydroxyphenylpyruvate dioxyge-se	9	C:GO:0005829; P:GO:0040010; F:GO:0003868; C:GO:0000139; F:GO:0046872; P:GO:0055114; P:GO:0006559; P:GO:0006572; C:GO:0005789	-	EC:1.13.11.27	IPR004360; IPR005956; G3DSA:3.10.180.10 (GENE3D), SSF54593 (SUPERFAMILY)
Caenorhabditis elegans	4-hydroxyphenylpyruvate dioxyge-se	9	C:GO:0005829; P:GO:0040010; F:GO:0003868; C:GO:0000139; F:GO:0046872; P:GO:0055114; P:GO:0006559; P:GO:0006572; C:GO:0005789	-	EC:1.13.11.27	IPR004360; IPR005956; G3DSA:3.10.180.10 (GENE3D), SSF54593 (SUPERFAMILY)
Caenorhabditis elegans	4-hydroxyphenylpyruvate dioxyge-se	9	C:GO:0005829; P:GO:0040010; F:GO:0003868; C:GO:0000139; F:GO:0046872; P:GO:0055114; P:GO:0006559; P:GO:0006572; C:GO:0005789	-	EC:1.13.11.27	IPR004360; IPR005956; G3DSA:3.10.180.10 (GENE3D), SSF54593 (SUPERFAMILY)
Loa loa	retinoblastoma-associated protein a domain containing protein	0				IPR013763

	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG14951 [Caenorhabditis briggsae]	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	vacuolar protein sorting-associated protein	1	P:GO:0008104	-		-
Loa loa	cap-gly domain containing protein	0				IPR022157; PTHR18916 (PANTHER), PTHR18916:SF2 (PANTHER)
Caenorhabditis briggsae	ke (drosophila actin-binding) homolog family member (ketn-1)	1	P:GO:0000003	-		-
Caenorhabditis briggsae	adenosylmethionine decarboxylase 1	6	P:GO:0006597; F:GO:0004014; P:GO:0008295; P:GO:0040011; C:GO:0005829; P:GO:0007413	-	EC:4.1.1.50	IPR001985; IPR016067; IPR018166
	-	0				-
Caenorhabditis briggsae	aliphatic nitrilase	3	F:GO:0016810; P:GO:0000003; P:GO:0006807	-		IPR003010; PTHR23088 (PANTHER)
Caenorhabditis elegans	msp domain containing protein	0		C:GO:0005856; F:GO:0005198		IPR000535; IPR008962; PTHR21513 (PANTHER), PTHR21513:SF2 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-aph-2 protein	8	P:GO:0009792; P:GO:0048598; P:GO:0007219; C:GO:0005886; P:GO:0060465; P:GO:0018991; P:GO:0040010; P:GO:0060581	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	gamma-glutamyltranspeptidase family protein	1	F:GO:0003840	-	EC:2.3.2.2	IPR000101; SignalP (SIGNALP), SSF56235 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-met-2 protein	0		F:GO:0008168; F:GO:0016740; F:GO:0008270; F:GO:0018024; P:GO:0016568; C:GO:0005634; F:GO:0003677		PTHR22884 (PANTHER), PTHR22884:SF24 (PANTHER)
	-	0				-
	-	0				-

Candida dubliniensis CD36	viral a-type inclusion protein	0		F:GO:0008565; P:GO:0006886; F:GO:0003674; F:GO:0005524; C:GO:0016020; C:GO:0016459; C:GO:0000139; P:GO:0008150; F:GO:0000166; P:GO:0048280; C:GO:0005737; F:GO:0005488; F:GO:0003779; F:GO:0003774; P:GO:0055114; C:GO:0005622; F:GO:0032440; F:GO:0016491		-
Candida dubliniensis CD36	viral a-type inclusion protein	12	P:GO:0009653; P:GO:0006810; F:GO:0005515; F:GO:0017111; C:GO:0044430; C:GO:0015629; P:GO:0051649; P:GO:0006996; P:GO:0030154; P:GO:0002376; C:GO:0005886; C:GO:0044444	-	EC:3.6.1.15	-
Ostertagia ostertagi	calcium-dependent apyrase	1	F:GO:0016787	-		-
	-	0				-
Loa loa	hypothetical protein LOAG_14552 [Loa loa]	0				SignalP (SIGNALP)
Oryza sativa Indica Group	histone deacetylase hd2	0				-
Caenorhabditis briggsae	plexin a	3	F:GO:0004872; P:GO:0007411; C:GO:0016020	-		IPR002165; IPR003659; IPR015943; IPR016201; G3DSA:3.30.1680.10 (GENE3D), PTHR22625 (PANTHER), PTHR22625:SF11 (PANTHER)
Caenorhabditis briggsae	plexin a	3	F:GO:0004872; P:GO:0007411; C:GO:0016020	-		IPR002165; IPR003659; IPR015943; IPR016201; G3DSA:3.30.1680.10 (GENE3D), PTHR22625 (PANTHER), PTHR22625:SF11 (PANTHER)
Caenorhabditis briggsae	plexin a	3	F:GO:0004872; P:GO:0007411; C:GO:0016020	-		IPR002165; IPR003659; IPR015943; IPR016201; G3DSA:3.30.1680.10 (GENE3D), PTHR22625 (PANTHER), PTHR22625:SF11 (PANTHER)
Caenorhabditis elegans	ornithine aminotransferase precursor	4	P:GO:0006591; F:GO:0030170; C:GO:0005759; F:GO:0004587	-	EC:2.6.1.13	-
	-	0				-

Loa loa	mitochondrial phosphate carrier protein	13	P:GO:0055085; P:GO:0040010; P:GO:0006310; C:GO:0005743; F:GO:0015293; P:GO:0006091; P:GO:0040035; F:GO:0003677; P:GO:0002119; F:GO:0015320; P:GO:0009792; P:GO:0015074; C:GO:0005887	-		-
Loa loa	glycosyl hydrolase family 85 protein	2	F:GO:0016798; C:GO:0005622	-		IPR005201
Caenorhabditis elegans	briggsae cbr-nmy-2 protein	26	P:GO:0046664; F:GO:0017111; P:GO:0045200; F:GO:0000166; P:GO:0035159; P:GO:0031036; C:GO:0016460; P:GO:0007443; P:GO:0007395; P:GO:0045214; P:GO:0035017; P:GO:0006936; P:GO:0007297; P:GO:0046663; F:GO:0032027; P:GO:0008258; P:GO:0051259; P:GO:0016203; C:GO:0032154; C:GO:0045179; P:GO:0045184; P:GO:0035317; C:GO:0030018; C:GO:0005886; P:GO:0007435; P:GO:0000910	-	EC:3.6.1.15	IPR002928; PTHR13140 (PANTHER), PTHR13140:SF23 (PANTHER)
Loa loa	structural mainte-nce of chromosomes smc2	4	F:GO:0005524; P:GO:0051276; C:GO:0005694; F:GO:0005515	-		IPR003395; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR18937 (PANTHER), PTHR18937:SF9 (PANTHER), SSF52540 (SUPERFAMILY)

Caenorhabditis elegans	udp-glucose pyrophosphorylase 2	14	F:GO:0003983; F:GO:0032557; P:GO:0040010; P:GO:0008340; C:GO:0005625; F:GO:0046872; F:GO:0042802; P:GO:0019255; F:GO:0005536; P:GO:0006011; P:GO:0002119; P:GO:0009792; P:GO:0006065; C:GO:0005737	-	EC:2.7.7.9	-
	-	0				IPR000436; IPR016060
Homo sapiens	ubiquitin-conjugating enzyme e2l 6	8	P:GO:0032020; P:GO:0019941; F:GO:0005515; P:GO:0016567; F:GO:0005524; F:GO:0004842; P:GO:0051246; F:GO:0042296	-	EC:6.3.2.19	-
	-	0				-
	-	0				-
Homo sapiens	immunoglobulin heavy chain	4	P:GO:0018298; P:GO:0006955; F:GO:0003823; F:GO:0005515	-		-
Caenorhabditis elegans	hypoxia associated factor	5	P:GO:0040007; P:GO:0040035; P:GO:0018996; P:GO:0002119; P:GO:0040011	-		IPR005011
Caenorhabditis elegans	phosphoribosylformylglyci-midine synthase	4	P:GO:0040010; P:GO:0009168; F:GO:0005515; F:GO:0004642	-	EC:6.3.5.3	IPR000728; IPR010918; IPR016188; PTHR10099 (PANTHER), SSF109736 (SUPERFAMILY), SSF82697 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	zinc finger protein 587-like	8	P:GO:0040010; F:GO:0008270; F:GO:0003676; C:GO:0005622; P:GO:0040035; P:GO:0002119; P:GO:0040011; P:GO:0009792	-		IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis elegans	yr51_caeel ame: full=uncharacterized protein	4	P:GO:0010171; P:GO:0002119; P:GO:0018996; P:GO:0040010	-		-

Caenorhabditis briggsae	trehalase family protein	7	F:GO:0004135; P:GO:0009792; P:GO:0002119; P:GO:0005978; P:GO:0005991; P:GO:0040007; F:GO:0004555	-	EC:3.2.1.33; EC:3.2.1.28	IPR001661; IPR008928; PTHR23403:SF1 (PANTHER)
Caenorhabditis elegans	ras-related protein rab-	5	F:GO:0005525; C:GO:0005886; P:GO:0007264; F:GO:0003924; P:GO:0015031	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001806; IPR002078; IPR003579; IPR005225; IPR013753; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF230 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	uncoordi-ted family member (unc-82)	0		F:GO:0004672; F:GO:0005524; F:GO:0000166; P:GO:0006468; F:GO:0004674		-
Caenorhabditis elegans	flavin monooxyge-se	7	F:GO:0004499; F:GO:0050661; P:GO:0055114; P:GO:0000003; C:GO:0031227; C:GO:0016021; F:GO:0050660	-	EC:1.14.13.8	IPR000960; IPR020946; G3DSA:3.50.50.60 (GENE3D), PTHR23023 (PANTHER), PTHR23023:SF4 (PANTHER), SSF51905 (SUPERFAMILY)
Caenorhabditis elegans	mitogen-activated protein ki-se associated protein 1	1	C:GO:0044464	-		IPR008828
Angiostrongylus cantonensis	elegans protein confirmed by transcript evidence	3	P:GO:0009792; F:GO:0005488; P:GO:0000003	-		IPR011990; IPR013026; IPR013105; IPR019734; PTHR16056 (PANTHER), SSF48452 (SUPERFAMILY)
Angiostrongylus cantonensis	elegans protein confirmed by transcript evidence	3	P:GO:0009792; F:GO:0005488; P:GO:0000003	-		IPR011990; IPR013026; IPR013105; IPR019734; PTHR16056 (PANTHER), SSF48452 (SUPERFAMILY)
Loa loa	hook homolog 1	7	C:GO:0070695; C:GO:0030897; P:GO:0008333; F:GO:0042802; P:GO:0045022; P:GO:0007032; P:GO:0007040	-		IPR008636; PTHR18947 (PANTHER), PTHR18947:SF8 (PANTHER), SSF116907 (SUPERFAMILY)
	-	0				IPR008191; G3DSA:2.30.30.140 (GENE3D), SSF63748 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				IPR008191; G3DSA:2.30.30.140 (GENE3D), SSF63748 (SUPERFAMILY)
	-	0				-

Pongo abelii	type alpha 1	31	P:GO:0060351; P:GO:0001957; P:GO:0071363; P:GO:0007605; P:GO:0034505; P:GO:0042542; P:GO:0001649; P:GO:0009612; P:GO:0001568; P:GO:0060325; F:GO:0005201; C:GO:0005615; P:GO:0048706; P:GO:0015031; F:GO:0048407; C:GO:0005737; P:GO:0043434; P:GO:0071300; P:GO:0007601; P:GO:0010812; C:GO:0005584; F:GO:0042802; P:GO:0060346; P:GO:0032964; P:GO:0030199; P:GO:0051591; P:GO:0031960;	-		IPR000885; PTHR10499 (PANTHER), PTHR10499:SF71 (PANTHER), PS51461 (PROFILE)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0008270; C:GO:0005622		-
Caenorhabditis briggsae	rho-associated protein ki-se 1	19	P:GO:0050901; P:GO:0032060; P:GO:0006468; P:GO:0007266; C:GO:0000139; P:GO:0007275; C:GO:0005814; P:GO:0022614; C:GO:0005829; P:GO:0043524; F:GO:0017049; F:GO:0046872; P:GO:0030036; F:GO:0004674; F:GO:0042802; P:GO:0030154; P:GO:0048477; F:GO:0005524; P:GO:0000910	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017441; IPR017442; IPR020684; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22988 (PANTHER)
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis briggsae	ubiquitin carboxyl-termi-l hydrolase 8	0		F:GO:0004221; C:GO:0005769; F:GO:0016787; C:GO:0019897; P:GO:0071108; P:GO:0007032; P:GO:0006511; F:GO:0008234; P:GO:0070536; F:GO:0004843; F:GO:0008233; C:GO:0005622; F:GO:0005515; P:GO:0007265; C:GO:0005829		IPR001763
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	hmg box family protein	9	C:GO:0005737; F:GO:0016566; P:GO:0016055; F:GO:0003677; P:GO:0008356; F:GO:0008134; F:GO:0019901; C:GO:0005634; F:GO:0042826	-		IPR000910; IPR009071; PTHR10373 (PANTHER), PTHR10373:SF1 (PANTHER)
Brugia malayi	hmg box family protein	9	C:GO:0005737; F:GO:0016566; P:GO:0016055; F:GO:0003677; P:GO:0008356; F:GO:0008134; F:GO:0019901; C:GO:0005634; F:GO:0042826	-		-
Loa loa	methylosome subunit picln	7	P:GO:0065008; P:GO:0040010; P:GO:0000003; P:GO:0002119; P:GO:0040011; P:GO:0006898; P:GO:0009792	-		IPR003521; PTHR21399 (PANTHER), PF03517 (PFAM)
Caenorhabditis briggsae	methylosome subunit picln	7	P:GO:0040010; P:GO:0048676; P:GO:0000003; P:GO:0002119; P:GO:0040011; P:GO:0006898; P:GO:0009792	-		IPR003521; PTHR21399 (PANTHER), PF03517 (PFAM)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	F:GO:0004672	-		IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF112 (PANTHER)

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	F:GO:0004672	-		IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF112 (PANTHER)
Caenorhabditis elegans	metabotropic glutamate receptor	4	P:GO:0007186; C:GO:0016021; P:GO:0007165; F:GO:0004930	-		G3DSA:3.40.50.2300 (GENE3D), PTHR11336 (PANTHER), PTHR11336:SF8 (PANTHER), SSF53822 (SUPERFAMILY)
Caenorhabditis elegans	cg16791 cg16791-pa	0				-
	-	0				-
Caenorhabditis elegans	uncoordi-ted family member (unc-79)	0		F:GO:0005488		PTHR21696 (PANTHER)
Caenorhabditis elegans	vesicle transport protein got1b	6	F:GO:0004871; C:GO:0005794; P:GO:0043123; P:GO:0006810; C:GO:0016020; C:GO:0005783	-		-
	-	0				-
Brugia malayi	ser thr protein phosphatase	0		F:GO:0016787; F:GO:0005506; F:GO:0005515; F:GO:0030145; F:GO:0004721		IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF2 (PANTHER), SSF56300 (SUPERFAMILY)
Brugia malayi	transcription initiation factor tfiid subunit 13	4	F:GO:0003702; F:GO:0003677; F:GO:0003743; P:GO:0006366	-		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-gpc-2 protein	9	C:GO:0016028; F:GO:0004871; P:GO:0007186; P:GO:0007602; P:GO:0035046; C:GO:0005834; F:GO:0003924; P:GO:0009792; C:GO:0005737	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Angiostrongylus cantonensis	pq loop repeat protein	0		F:GO:0003674; F:GO:0016853; F:GO:0047750; C:GO:0005575		IPR006603; PF04193 (PFAM), SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	zinc zz type family protein	0		F:GO:0000166; F:GO:0003779; F:GO:0005524; P:GO:0015870; F:GO:0008270; P:GO:0046716; C:GO:0016010; P:GO:0040017; C:GO:0016459; F:GO:0003774; P:GO:0007271; F:GO:0005515; F:GO:0005277		IPR018159; G3DSA:1.20.58.60 (GENE3D), SSF46966 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		-
Caenorhabditis briggsae	serine--pyruvate aminotransferase	7	P:GO:0046487; C:GO:0005777; P:GO:0009058; P:GO:0006625; F:GO:0008453; F:GO:0042803; F:GO:0030170	-	EC:2.6.1.44	IPR015421; IPR015424; PTHR21152 (PANTHER), PTHR21152:SF5 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	ccr4 associated	9	P:GO:0040035; P:GO:0009792; P:GO:0010171; P:GO:0002119; F:GO:0003676; C:GO:0043186; C:GO:0000932; C:GO:0005634; P:GO:0051729	-		IPR006941; IPR012337; G3DSA:3.30.420.10 (GENE3D), PTHR10797 (PANTHER)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG01673 [Caenorhabditis briggsae]	6	P:GO:0043254; P:GO:0006355; F:GO:0005524; F:GO:0016887; F:GO:0008134; C:GO:0005634	-		PTHR22908 (PANTHER), PTHR22908:SF13 (PANTHER)
Caenorhabditis briggsae	carbamoyl-phosphate synthase	7	P:GO:0006541; F:GO:0016812; F:GO:0016597; F:GO:0004086; F:GO:0005524; P:GO:0006207; F:GO:0004070	-	EC:3.5.2.0; EC:2.1.3.2	IPR005479; IPR005483; IPR011761; IPR013815; IPR013816; PTHR11405 (PANTHER), PTHR11405:SF3 (PANTHER), SSF56059 (SUPERFAMILY)
Loa loa	ifa-1	3	C:GO:0005882; F:GO:0005198; F:GO:0005515	-		SignalP (SIGNALP)
Brugia malayi	trehalose 6-phosphate synthase	3	F:GO:0003825; P:GO:0034608; P:GO:0005992	-	EC:2.4.1.15	IPR001830; G3DSA:3.40.50.2000 (GENE3D), PTHR10788 (PANTHER), SSF53756 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	scavenger receptor class a- c-type lectin (agap009143-pa)	3	F:GO:0005044; F:GO:0005488; C:GO:0016020	-		IPR001190; IPR017448; G3DSA:3.10.250.10 (GENE3D), PTHR19331 (PANTHER), PTHR19331:SF7 (PANTHER)

Caenorhabditis briggsae	annexin a7	3	P:GO:0065008; F:GO:0005515; C:GO:0044464	-		IPR001464; IPR018252; IPR018502; PTHR10502:SF30 (PANTHER)
	-	0				IPR017997
	-	0				IPR003071
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	3	F:GO:0004872; F:GO:0005515; P:GO:0006350	-		IPR000536; IPR008946; PTHR11865 (PANTHER), PTHR11865:SF236 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	F:GO:0005488; P:GO:0044237; P:GO:0043170; P:GO:0044238	-		IPR000152; IPR000742; IPR001881; IPR006210; IPR013032; IPR013091; IPR018097; G3DSA:2.10.25.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF87 (PANTHER), SSF57196 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG14899 [Caenorhabditis briggsae]	0				IPR007356; PTHR13563:SF3 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	5	P:GO:0018996; P:GO:0009792; P:GO:0040017; P:GO:0040010; P:GO:0040035	-		-
Loa loa	briggsae cbr-apb-1 protein	12	C:GO:0005829; P:GO:0040007; F:GO:0030276; P:GO:0000003; C:GO:0030666; P:GO:0002119; P:GO:0050690; C:GO:0030117; P:GO:0006898; P:GO:0009792; P:GO:0015031; C:GO:0005886	-		IPR008152; IPR009028; IPR012295; IPR013037; IPR013041; IPR015151; PTHR11134 (PANTHER), PTHR11134:SF3 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis elegans	chromosome 19 open reading frame 52	0		F:GO:0003674; P:GO:0008150; C:GO:0005575		IPR019322; PTHR21435 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG06447 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	kinesin-associated protein 3	11	P:GO:0006810; F:GO:0019894; F:GO:0032266; P:GO:0008285; P:GO:0006461; C:GO:0016939; P:GO:0007017; P:GO:0007165; P:GO:0046587; P:GO:0008104; C:GO:0005783	-		IPR008658; PTHR15605:SF1 (PANTHER), PF05804 (PFAM), SignalP (SIGNALP)
	-	0				-

Caenorhabditis briggsae	-related lipid transfer domain containing 7	0		C:GO:0005739		IPR002913; G3DSA:3.30.530.20 (GENE3D), PTHR19308 (PANTHER), SSF55961 (SUPERFAMILY)
Caenorhabditis briggsae	leptin receptor overlapping transcript-like 1	0		F:GO:0003674; F:GO:0004872; C:GO:0016021; C:GO:0016020; P:GO:0008150; C:GO:0005575		IPR007262; PS51257 (PROFILE), SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-nrf-5 protein	0		F:GO:0008289		IPR001124; IPR017943; G3DSA:3.15.20.10 (GENE3D)
Caenorhabditis briggsae	cytochrome family subfamily polypeptide 12	5	F:GO:0004497; F:GO:0005506; F:GO:0005515; P:GO:0008152; C:GO:0016020	-		IPR001128; IPR002401; IPR017972; PTHR19383:SF66 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0005515		-
Caenorhabditis briggsae	-+ k+ atpase alpha subunit	20	P:GO:0008340; P:GO:0015672; P:GO:0035158; P:GO:0008360; P:GO:0051124; P:GO:0035159; P:GO:0019991; P:GO:0009612; P:GO:0006754; F:GO:0005391; P:GO:0001700; C:GO:0005918; P:GO:0007268; C:GO:0005890; P:GO:0009266; C:GO:0005634; F:GO:0005524; P:GO:0050905; P:GO:0001894; P:GO:0008344	-	EC:3.6.3.9	IPR001757; IPR005775; IPR005834; IPR006068; IPR006069; IPR008250; IPR018303; G3DSA:1.20.1110.10 (GENE3D), G3DSA:2.70.150.10 (GENE3D), G3DSA:3.40.1110.10 (GENE3D), PTHR11939:SF100 (PANTHER), SSF56784 (SUPERFAMILY), SSF81653 (SUPERFAMILY), SSF81660 (SUPERFAMILY), SSF81665 (SUPERFAMILY)
Caenorhabditis elegans	-+ k+-atpase alpha subunit	20	P:GO:0008340; P:GO:0015672; P:GO:0035158; P:GO:0008360; P:GO:0051124; P:GO:0035159; P:GO:0019991; P:GO:0009612; P:GO:0006754; F:GO:0005391; P:GO:0001700; C:GO:0005918; P:GO:0007268; C:GO:0005890; P:GO:0009266; C:GO:0005634; F:GO:0005524; P:GO:0050905; P:GO:0001894; P:GO:0008344	-	EC:3.6.3.9	IPR001757; IPR005834; IPR006068; IPR006069; G3DSA:1.20.1110.10 (GENE3D), G3DSA:3.40.1110.10 (GENE3D), PTHR11939:SF100 (PANTHER), SSF56784 (SUPERFAMILY), SSF81660 (SUPERFAMILY), SSF81665 (SUPERFAMILY)

Caenorhabditis briggsae	aminomethyltransferase (glycine cleavage system protein t)	4	P:GO:0006546; F:GO:0004047; F:GO:0008483; C:GO:0005739	-	EC:2.1.2.10; EC:2.6.1.0	IPR013977; PTHR13847 (PANTHER), PTHR13847:SF5 (PANTHER), SSF101790 (SUPERFAMILY)
Caenorhabditis elegans	atp-binding sub-family b (mdr tap) member 9 isoform 1	5	F:GO:0016887; P:GO:0006810; C:GO:0016020; F:GO:0000166; F:GO:0005215	-		SignalP (SIGNALP)
Caenorhabditis elegans	abc transporter family protein	0		F:GO:0005524; F:GO:0016887; F:GO:0000166; C:GO:0016021; F:GO:0042626; F:GO:0017111; P:GO:0055085; P:GO:0006810		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein ZK418.2 [Caenorhabditis elegans]	0		F:GO:0005515		IPR000210; IPR011333; IPR013069
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	probable -dh dehydroge-se 1 alpha subcomplex subunit 12	3	F:GO:0009055; F:GO:0008137; C:GO:0016020	-	EC:1.6.5.3	IPR007763
Caenorhabditis elegans	d- polymerase epsilon	8	F:GO:0016779; F:GO:0003676; P:GO:0040035; P:GO:0040011; P:GO:0006139; P:GO:0006997; P:GO:0002009; P:GO:0009792	-	EC:2.7.7.0	IPR013697; PTHR10670 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-unc-45 protein	1	F:GO:0005488	-		PTHR22904 (PANTHER), PTHR22904:SF28 (PANTHER)
Caenorhabditis briggsae	lin-5 interacting protein family member (lfi-1)	6	C:GO:0005737; C:GO:0000776; F:GO:0005515; C:GO:0044430; P:GO:0000279; C:GO:0015630	-		-
Caenorhabditis elegans	lin-5 interacting protein family member (lfi-1)	4	F:GO:0005515; C:GO:0005694; P:GO:0009987; C:GO:0044446	-		PD968187 (PRODOM)
Caenorhabditis elegans	atm interactor	0		F:GO:0003676; F:GO:0046872; F:GO:0003674; P:GO:0008150; F:GO:0008270; C:GO:0005634; C:GO:0005575; C:GO:0005622		IPR007087; IPR015880; PTHR10593 (PANTHER), PTHR10593:SF10 (PANTHER)
Caenorhabditis elegans	glycosylphosphatidylinositol anchor attachment 1 -like	0		C:GO:0042765; C:GO:0016021; P:GO:0016255		IPR007246; SignalP (SIGNALP)

Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	5	P:GO:0009792; F:GO:0004356; F:GO:0005515; F:GO:0005524; P:GO:0006542	-	EC:6.3.1.2	IPR008146; IPR008147; IPR014746; G3DSA:3.10.20.70 (GENE3D), PTHR20852 (PANTHER), PTHR20852:SF14 (PANTHER), SignalP (SIGNALP), SSF55931 (SUPERFAMILY)
Loa loa	n terminus of rad21 rec8 like protein	0		C:GO:0000228		-
Caenorhabditis briggsae	briggsae cbr-rlbp-1 protein	0		P:GO:0007165; C:GO:0005622		PTHR12783 (PANTHER), PTHR12783:SF1 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-rlbp-1 protein	0		P:GO:0007165; C:GO:0005622		PTHR12783 (PANTHER), PTHR12783:SF1 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-rlbp-1 protein	0		P:GO:0007165; C:GO:0005622		PTHR12783 (PANTHER), PTHR12783:SF1 (PANTHER)
Callithrix jacchus	solute carrier family 25 (mitochondrial carrier adenine nucleotide translocator) member 6	7	P:GO:0006915; F:GO:0005515; P:GO:0055085; F:GO:0005471; C:GO:0005744; C:GO:0016021; P:GO:0044419	-		-
	-	0				IPR000436; SignalP (SIGNALP)
Caenorhabditis elegans	diazepam binding	2	F:GO:0000062; P:GO:0019915	-		IPR000582; IPR014352; IPR022408; PTHR23310:SF12 (PANTHER)
Caenorhabditis briggsae	mitochondrial folate transporter carrier	6	F:GO:0005488; P:GO:0055085; P:GO:0040010; P:GO:0008340; C:GO:0016021; C:GO:0005739	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF73 (PANTHER)
Caenorhabditis elegans	fip1 motif family protein	1	P:GO:0009792	-		IPR007854; PTHR13484 (PANTHER)
Caenorhabditis elegans	fip1 motif family protein	1	P:GO:0009792	-		IPR007854; PTHR13484 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	nuclear hormone receptor family member (nhr-25)	1	F:GO:0070016	-		IPR001723; IPR008946; PTHR11865 (PANTHER), PTHR11865:SF205 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Haemonchus contortus	cysteine protei-se	2	P:GO:0008152; F:GO:0008234	-		IPR000169; IPR000668; IPR013128; IPR015643; G3DSA:3.90.70.10 (GENE3D), SignalP (SIGNALP), SSF54001 (SUPERFAMILY)
	-	0				-
Loa loa	s1 r- binding domain containing protein	0		F:GO:0003723; F:GO:0005488; P:GO:0006397; P:GO:0006396; C:GO:0005622; C:GO:0005634		IPR003029; IPR012340; IPR016027; IPR022967; PTHR23270 (PANTHER)
Caenorhabditis briggsae	hatching enzyme	3	F:GO:0004222; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	IPR001506; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF80 (PANTHER)
Brugia malayi	lateral sig-ling target protein 2 homolog	5	C:GO:0005829; C:GO:0031901; P:GO:0007175; F:GO:0046872; F:GO:0032266	-		SignalP (SIGNALP)

Caenorhabditis elegans	uncoordi-ted family member (unc-13)	1	F:GO:0046872	-		IPR000008; IPR008973; IPR018029; IPR020477; G3DSA:2.60.40.150 (GENE3D), PTHR10480 (PANTHER)
Caenorhabditis briggsae	uncharacterized transposase-like protein	0		F:GO:0046872; P:GO:0055114; F:GO:0009055; F:GO:0016491; F:GO:0020037; F:GO:0005506; F:GO:0004497		-
Caenorhabditis elegans	g protein-coupled receptor isoform cra_a	1	C:GO:0016020	-		-
Caenorhabditis elegans	cysteine dioxyge-se	12	F:GO:0017172; C:GO:0005829; F:GO:0008198; P:GO:0007595; P:GO:0045471; P:GO:0055114; P:GO:0033762; P:GO:0019452; P:GO:0051384; P:GO:0051591; P:GO:0043200; C:GO:0005886	-	EC:1.13.11.20	-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	arginyltransferase 1	4	C:GO:0005737; F:GO:0004057; P:GO:0016598; C:GO:0005634	-	EC:2.3.2.8	IPR007471; PTHR21367 (PANTHER)
Caenorhabditis briggsae	cg15738 cg15738-pa	0		P:GO:0009058; C:GO:0005739; F:GO:0003674; F:GO:0016740; P:GO:0008150		-
	-	0				-
	-	0				-
Brugia malayi	tripeptidylpeptidase ii	5	P:GO:0019915; F:GO:0042277; P:GO:0006508; C:GO:0005625; F:GO:0008240	-		IPR000209; IPR015500; PTHR10795:SF33 (PANTHER)

Caenorhabditis briggsae	myosin heavy chain	36	P:GO:0006941; P:GO:0046664; P:GO:0045200; C:GO:0016461; P:GO:0035159; P:GO:0031036; P:GO:0035072; P:GO:0007443; P:GO:0007395; P:GO:0045214; P:GO:0035017; P:GO:0007297; C:GO:0031672; P:GO:0046663; F:GO:0003779; F:GO:0000146; P:GO:0001736; F:GO:0008307; F:GO:0032027; P:GO:0008258; P:GO:0051259; P:GO:0016203; C:GO:0032154; C:GO:0045179; F:GO:0032440; P:GO:0045184; C:GO:0005863; P:GO:0035317;	-	EC:1.3.1.74	SignalP (SIGNALP)
Caenorhabditis briggsae	ceramide ki-se	1	F:GO:0016301	-		IPR001206; PTHR12358 (PANTHER), PTHR12358:SF6 (PANTHER)
Ancylostoma caninum	venom allergen-like protein	1	P:GO:0009987	-		IPR001283; IPR014044; PTHR10334:SF11 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-cap-1 protein	14	P:GO:0035220; P:GO:0040010; C:GO:0071203; P:GO:0006911; F:GO:0003779; P:GO:0009792; P:GO:0010591; P:GO:0002119; C:GO:0008290; C:GO:0005869; P:GO:0007018; P:GO:0007294; P:GO:0051016; C:GO:0016324	-		IPR002189; IPR017865; SSF90096 (SUPERFAMILY)

Caenorhabditis briggsae	sig-l recognition particle 54 kda protein	16	F:GO:0008144; C:GO:0005786; F:GO:0030942; F:GO:0043021; C:GO:0005730; F:GO:0008312; C:GO:0016607; P:GO:0000003; P:GO:0006617; F:GO:0019003; P:GO:0002119; F:GO:0005515; F:GO:0003924; P:GO:0042493; P:GO:0006616; F:GO:0005525	-	EC:3.6.5.4; EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3	IPR004125; PTHR11564 (PANTHER), PTHR11564:SF5 (PANTHER)
	-	0				-
	-	0				IPR017956
Caenorhabditis elegans	monofunctio-l c1-tetrahydrofolate mitochondrial precursor	8	C:GO:0005739; F:GO:0004488; F:GO:0004477; P:GO:0009257; P:GO:0006730; F:GO:0005524; F:GO:0005515; F:GO:0004329	-	EC:1.5.1.5; EC:3.5.4.9; EC:6.3.4.3	IPR000559; G3DSA:3.10.410.10 (GENE3D), PTHR10025 (PANTHER), PTHR10025:SF4 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	nol6 protein	0		C:GO:0005694; F:GO:0003723; C:GO:0000794; P:GO:0006364; C:GO:0005634; C:GO:0005730		IPR005554
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	mitochondrial ribosomal protein l40	4	P:GO:0009792; P:GO:0002119; P:GO:0000003; P:GO:0040007	-		IPR019192; PTHR13359 (PANTHER), SignalP (SIGNALP)
	-	0				-
Brugia malayi	elegans protein confirmed by transcript evidence	4	P:GO:0000003; P:GO:0040010; P:GO:0006898; P:GO:0002119	-		IPR004296; PTHR21592 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein C01B10.3 [Caenorhabditis elegans]	1	F:GO:0005515	-		IPR005135; PTHR12997 (PANTHER), PTHR12997:SF3 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	C:GO:0044425	-		IPR002490; PTHR11629:SF23 (PANTHER)
Caenorhabditis elegans	glycerophosphoryl diester phosphodiesterase	3	P:GO:0006071; F:GO:0008889; P:GO:0006629	-	EC:3.1.4.46	-
Dictyostelium discoideum AX4	nudix hydrolase 8	0		F:GO:0016787; F:GO:0000210		IPR000086; IPR003293; IPR015797; IPR020084; IPR020476; PTHR13994 (PANTHER), PS51462 (PROFILE)
	-	0				-
	-	0				-

Caenorhabditis briggsae	polymerase (d- directed) epsilon	11	P:GO:0040035; P:GO:0009792; F:GO:0003887; P:GO:0006260; F:GO:0003677; P:GO:0006997; P:GO:0040011; C:GO:0005634; F:GO:0008270; F:GO:0000166; P:GO:0002009	-	EC:2.7.7.7	IPR006133; IPR012337; G3DSA:3.30.420.10 (GENE3D), PTHR10670 (PANTHER)
	-	0				-
Caenorhabditis briggsae	cg16865 cg16865-pa	1	F:GO:0005515	-		PTHR13420 (PANTHER)
Haemonchus contortus	astacin metalloprotease b	1	F:GO:0008233	-		SignalP (SIGNALP)
Caenorhabditis briggsae	d-2-like helicase	3	C:GO:0043231; P:GO:0006260; F:GO:0016787	-		IPR007807; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10887 (PANTHER), PTHR10887:SF14 (PANTHER), SSF52540 (SUPERFAMILY)
Homo sapiens	immunoglobulin kappa light chain variable region vk1	4	C:GO:0005576; F:GO:0005515; F:GO:0003823; P:GO:0006955	-		IPR003596; IPR013106; IPR013783; PTHR23267 (PANTHER), PTHR23267:SF33 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis briggsae	amp-dependent synthetase and ligase	0		F:GO:0003987; P:GO:0006629; F:GO:0004467; F:GO:0016874; C:GO:0016021; P:GO:0008152; F:GO:0003824; P:GO:0019915		IPR000873; G3DSA:3.40.50.980 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF43 (PANTHER), SSF56801 (SUPERFAMILY)
	-	0				-
Homo sapiens	complement component q alpha polypeptide	5	C:GO:0005602; P:GO:0045087; C:GO:0005794; P:GO:0006958; P:GO:0007267	-		-
Loa loa	peptidyl-prolyl cis-trans isomerase g	5	P:GO:0006457; C:GO:0071011; P:GO:0000398; F:GO:0003755; C:GO:0071013	-	EC:5.2.1.8	IPR002130; IPR015891; PTHR11071 (PANTHER), PTHR11071:SF56 (PANTHER)
Caenorhabditis elegans	ubiquitin carboxyl-termi-l hydrolase 28	9	F:GO:0004221; P:GO:0010212; P:GO:0042771; F:GO:0004843; F:GO:0005515; P:GO:0000077; P:GO:0016579; C:GO:0005654; P:GO:0008283	-	EC:3.1.2.15	IPR001394; IPR018200; PTHR10420 (PANTHER), PTHR10420:SF2 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis briggsae	glycine dehydroge-se	5	F:GO:0004375; F:GO:0030170; P:GO:0055114; F:GO:0016829; P:GO:0019464	-	EC:1.4.4.2	IPR015421; IPR015424; IPR020581

Caenorhabditis elegans	tyrosyl-tr- synthetase	3	P:GO:0009792; P:GO:0000003; P:GO:0006412	-	EC:3.6.5.3	-
Caenorhabditis elegans	28s ribosomal protein mitochondrial	6	P:GO:0006412; P:GO:0040010; C:GO:0005840; F:GO:0003735; P:GO:0006898; P:GO:0009792	-	EC:3.6.5.3	IPR000307; PTHR12919:SF1 (PANTHER)
Caenorhabditis elegans	adipocyte plasma membrane-associated protein	2	C:GO:0044464; F:GO:0003824	-		IPR004141; IPR011042; IPR018119; PTHR10426:SF6 (PANTHER), SignalP (SIGNALP), SSF63829 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Brugia malayi	novel rho gtpase activation protein	0		P:GO:0050790; F:GO:0003674; C:GO:0005737; P:GO:0008150; P:GO:0007165; F:GO:0005515; C:GO:0005575; C:GO:0005622		IPR000198; IPR004148; IPR008936; PTHR14130 (PANTHER), SSF103657 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	olfactomedin 1	0				IPR003112; PTHR23192 (PANTHER), PTHR23192:SF6 (PANTHER)
Ascaris suum	spliced leader 30 kda protein	0				-
	-	0				-
Loa loa	lethal family member (let-805)	8	P:GO:0018996; P:GO:0009792; P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		IPR003961; IPR008957; IPR013783; PR00014 (PRINTS), PTHR10489 (PANTHER), PTHR10489:SF17 (PANTHER)
Brugia malayi	btb poz domain containing protein	1	F:GO:0005515	-		IPR002083; IPR008974; IPR013322
Loa loa	elegans protein partially confirmed by transcript evidence	1	C:GO:0005811	-		IPR000120; PTHR11895:SF5 (PANTHER)
Caenorhabditis briggsae	deah (asp-glu-ala-his) box polypeptide 16	5	F:GO:0003724; F:GO:0008026; F:GO:0003676; F:GO:0005515; F:GO:0005524	-		IPR001482; G3DSA:3.40.50.300 (GENE3D), PTHR18934 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	probable tr- pseudouridine synthase 2	2	P:GO:0016070; F:GO:0005515	-		IPR002501; IPR020103; PTHR13195 (PANTHER)
	-	0				-
Loa loa	suppressor of ty 16 homolog	5	P:GO:0018996; C:GO:0005654; P:GO:0009792; P:GO:0001703; P:GO:0006350	-		IPR000994; G3DSA:3.40.350.10 (GENE3D), PTHR13980 (PANTHER), PTHR13980:SF6 (PANTHER)
Leishmania major strain Friedlin	proteophosphoglycan ppg4	0		F:GO:0005524; F:GO:0004479; P:GO:0006412; F:GO:0003774; C:GO:0016459		-

Caenorhabditis elegans	hus1-like protein	2	P:GO:0006259; P:GO:0006974	-		IPR007150
Caenorhabditis briggsae	acid phosphatase-like 2	1	F:GO:0016787	-		IPR000560; G3DSA:3.40.50.1240 (GENE3D), PTHR11567 (PANTHER), PTHR11567:SF6 (PANTHER), SSF53254 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	mitogen-activated protein ki-se ki-se ki-se 15	4	P:GO:0006468; F:GO:0005515; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	-
Caenorhabditis briggsae	isocitrate dehydroge-se	10	C:GO:0005962; P:GO:0006103; P:GO:0006734; P:GO:0055114; F:GO:0004449; P:GO:0006099; F:GO:0051287; F:GO:0005515; F:GO:0000287; P:GO:0006102	-	EC:1.1.1.41	IPR001804; PTHR11835:SF5 (PANTHER), SSF53659 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis elegans	short chain dehydroge-se reductase family protein	14	F:GO:0001968; P:GO:0008340; P:GO:0042303; P:GO:0032350; P:GO:0008610; F:GO:0016491; P:GO:0010811; P:GO:0030540; F:GO:0005518; C:GO:0031012; F:GO:0008201; P:GO:0030198; C:GO:0016020; P:GO:0009790	-		IPR002198; IPR002347; IPR016040; IPR020904; PTHR19410:SF38 (PANTHER), SignalP (SIGNALP), SSF51735 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	abnormal dye filling protein isoform partially confirmed by transcript evidence	6	C:GO:0005737; C:GO:0000776; F:GO:0005515; C:GO:0044430; P:GO:0000279; C:GO:0015630	-		PTHR23159 (PANTHER), PTHR23159:SF6 (PANTHER)
Caenorhabditis elegans	ccr (yeast ccr4 not complex component) homolog family member (ccr-4)	12	F:GO:0030528; P:GO:0008340; P:GO:0000289; P:GO:0040002; C:GO:0030014; F:GO:0005515; P:GO:0040011; P:GO:0048477; P:GO:0009792; C:GO:0005737; F:GO:0016787; P:GO:0040018	-		IPR001611; IPR003591; IPR005135; PR00019 (PRINTS), G3DSA:3.60.10.10 (GENE3D), G3DSA:3.80.10.10 (GENE3D), PTHR12121 (PANTHER), PTHR12121:SF13 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)

Caenorhabditis elegans	ccr (yeast ccr4 not complex component) homolog family member (ccr-4)	12	F:GO:0030528; P:GO:0008340; P:GO:0000289; P:GO:0040002; C:GO:0030014; F:GO:0005515; P:GO:0040011; P:GO:0048477; P:GO:0009792; C:GO:0005737; F:GO:0016787; P:GO:0040018	-		IPR001611; IPR003591; IPR005135; PR00019 (PRINTS), G3DSA:3.60.10.10 (GENE3D), G3DSA:3.80.10.10 (GENE3D), PTHR12121 (PANTHER), PTHR12121:SF13 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)
Drosophila simulans	isoform b	0		F:GO:0003677; F:GO:0005215; P:GO:0006810		-
Caenorhabditis elegans	gamma-soluble nsf attachment protein	4	F:GO:0005488; C:GO:0043231; C:GO:0044444; P:GO:0009987	-		IPR000744; IPR011990; PTHR13768:SF2 (PANTHER), SSF48452 (SUPERFAMILY)
Caenorhabditis elegans	heparan sulfate proteoglycan 2	13	P:GO:0048704; P:GO:0030155; P:GO:0002062; P:GO:0007420; P:GO:0045995; C:GO:0005606; P:GO:0030334; F:GO:0005102; P:GO:0001958; P:GO:0048738; P:GO:0008104; P:GO:0030198; P:GO:0060351	-		IPR002049; G3DSA:2.10.25.10 (GENE3D), PTHR10574 (PANTHER), PTHR10574:SF25 (PANTHER), SSF57196 (SUPERFAMILY)
	-	0				-
Drosophila sechellia	isoform c	0		F:GO:0003779; P:GO:0030036		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		-
	-	0				-
Brugia malayi	chromobox protein	7	P:GO:0006333; C:GO:0043234; C:GO:0000785; C:GO:0005634; C:GO:0005705; F:GO:0005515; F:GO:0003682	-		IPR000953; IPR008251; IPR016197; IPR017984; IPR018125; G3DSA:2.40.50.40 (GENE3D), PTHR22812 (PANTHER), PTHR22812:SF4 (PANTHER)
Brugia malayi	chromobox protein	7	P:GO:0006333; C:GO:0043234; C:GO:0000785; C:GO:0005634; C:GO:0005705; F:GO:0005515; F:GO:0003682	-		IPR000953; IPR008251; IPR016197; IPR017984; IPR018125; G3DSA:2.40.50.40 (GENE3D), PTHR22812 (PANTHER), PTHR22812:SF4 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F57C9.6 [Caenorhabditis elegans]	0		C:GO:0016021; P:GO:0007186		-
Caenorhabditis elegans	hypothetical protein Y67D8B.4 [Caenorhabditis elegans]	0				-
	-	0				-

	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein B0222.9 [Caenorhabditis elegans]	0		F:GO:0005506; F:GO:0009055; F:GO:0050660; P:GO:0055114; F:GO:0051537; F:GO:0016491; F:GO:0051536; F:GO:0003824; F:GO:0046872		PTHR11908 (PANTHER), PTHR11908:SF6 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	ph domain containing protein	0		F:GO:0046872; F:GO:0005089; F:GO:0008270; P:GO:0035023; C:GO:0005622		-
Caenorhabditis elegans	d- polymerase alpha catalytic subunit	25	P:GO:0045596; C:GO:0016363; P:GO:0000084; F:GO:0019103; F:GO:0003690; P:GO:0046677; C:GO:0005730; F:GO:0003887; F:GO:0030337; F:GO:0032403; P:GO:0006303; F:GO:0003896; P:GO:0006272; P:GO:0000731; P:GO:0006298; C:GO:0000785; F:GO:0017076; P:GO:0006270; C:GO:0005635; P:GO:0006273; C:GO:0005658; C:GO:0005654; P:GO:0008283; C:GO:0005737; F:GO:0003682	-	EC:2.7.7.7	IPR000276; IPR015088; PTHR10322 (PANTHER), PTHR10322:SF3 (PANTHER)
Loa loa	ring finger protein 170	1	F:GO:0005488	-		IPR001841; IPR010652; IPR013083; IPR017907; IPR018957; PTHR22894 (PANTHER), SignalP (SIGNALP), SSF57850 (SUPERFAMILY)
	-	0				-
Loa loa	elegans protein partially confirmed by transcript evidence	1	F:GO:0016787	-		IPR006186; G3DSA:3.60.21.10 (GENE3D), SSF56300 (SUPERFAMILY)
Angiostrongylus cantonensis	proline-rich protein prcc	2	F:GO:0005515; P:GO:0040011	-		IPR018800
Bombyx mori	endonuclease-reverse transcriptase	3	F:GO:0003676; F:GO:0016740; F:GO:0000166	-		-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG18490 [Caenorhabditis briggsae]	0				-
	-	0				-

Caenorhabditis elegans	hypothetical protein T04C4.1 [Caenorhabditis elegans]	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	zinc transporter zip9	3	P:GO:0030001; C:GO:0016020; F:GO:0046873	-		IPR003689; PTHR16133 (PANTHER)
Caenorhabditis briggsae	pyruvate muscle	14	P:GO:0012501; C:GO:0005829; F:GO:0030955; F:GO:0016830; C:GO:0005739; F:GO:0005524; F:GO:0004743; F:GO:0005515; F:GO:0000287; P:GO:0006096; C:GO:0019861; P:GO:0006725; P:GO:0009792; C:GO:0005634	-	EC:2.7.1.40	IPR001697; IPR015793; IPR015813; IPR018209
Necator americanus	elegans protein confirmed by transcript evidence	2	F:GO:0005515; P:GO:0008340	-		IPR004045; IPR004046; IPR010987; IPR012335; IPR012336; IPR017933; PTHR11571 (PANTHER), PTHR11571:SF6 (PANTHER)
	-	0				-
Caenorhabditis briggsae	ribosome production factor 1	10	P:GO:0006412; C:GO:0005730; P:GO:0006364; F:GO:0019843; P:GO:0040007; F:GO:0005524; P:GO:0002119; F:GO:0004812; C:GO:0030529; P:GO:0006898	-	EC:3.6.5.3	IPR007109; PTHR22734 (PANTHER)
	-	0				-
Caenorhabditis elegans	diacylglycerol ki-se epsilon	0		F:GO:0016301; P:GO:0007205; F:GO:0004143; F:GO:0016740; C:GO:0016021; P:GO:0023034		IPR000756; IPR001206; PTHR11255 (PANTHER), PTHR11255:SF7 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	8	P:GO:0009792; F:GO:0004743; F:GO:0016830; P:GO:0006725; F:GO:0005515; F:GO:0030955; F:GO:0000287; P:GO:0006096	-	EC:2.7.1.40	IPR001697; IPR015793; IPR015794; IPR015795; IPR015813
Caenorhabditis elegans	placental protein 11	3	F:GO:0004521; F:GO:0003723; P:GO:0008152	-		PTHR12439 (PANTHER), SSF142877 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-gob-1 protein	0		F:GO:0016787; F:GO:0004805		-

Caenorhabditis elegans	briggsae cbr-sep-1 protein	7	F:GO:0008233; C:GO:0043229; P:GO:0006996; P:GO:0007059; P:GO:0019538; P:GO:0007127; F:GO:0005515	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	slowpoke potassium channel family member (slo-2)	0		F:GO:0015269; F:GO:0005488; P:GO:0008152; C:GO:0016020; F:GO:0003824; P:GO:0006813; F:GO:0005216		-
	-	0				-
Danio rerio	kiaa1033 protein	0		P:GO:0016197; C:GO:0071203		-
Danio rerio	kiaa1033 protein	0		P:GO:0016197; C:GO:0071203		-
Danio rerio	kiaa1033 protein	0		P:GO:0016197; C:GO:0071203		-
	-	0				-
						IPR000152; IPR000742; IPR001881; IPR006209; IPR006210; IPR013032; IPR018097; PR00010 (PRINTS), G3DSA:2.10.25.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF226 (PANTHER), SSF57196 (SUPERFAMILY)
Caenorhabditis briggsae	isoform b	3	F:GO:0004591; F:GO:0030976; P:GO:0006096	-	EC:1.2.4.2	IPR011603
	-	0				-
Caenorhabditis sp. PS1010	hypothetical protein Csp3_JD07.006 [Caenorhabditis sp. PS1010]	0				-
Loa loa	prion-like-(q n-rich)-domain-bearing protein family member (pqn-42)	0		F:GO:0008430		IPR007671; PTHR10105 (PANTHER), SignalP (SIGNALP)
Haemonchus contortus	aspartyl protease family member (asp-2)	4	P:GO:0008219; F:GO:0016787; F:GO:0005515; P:GO:0040011	-		IPR001461; IPR001969; IPR009007; IPR021109; PTHR13683:SF53 (PANTHER), SignalP (SIGNALP)
Pongo abelii	histone-lysine n-methyltransferase setmar	0		F:GO:0016740; F:GO:0004803; P:GO:0006313; F:GO:0008168; C:GO:0005634; F:GO:0003677; F:GO:0016787; F:GO:0008270; F:GO:0018024; P:GO:0016568; P:GO:0015074; P:GO:0006281; C:GO:0005575; F:GO:0046872; F:GO:0004519		-

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	C:GO:0044464	-		IPR000904; IPR001605; IPR001849; IPR011993; G3DSA:1.10.1000.11 (GENE3D), PTHR10663 (PANTHER), PTHR10663:SF3 (PANTHER), SSF50729 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	C:GO:0044464	-		IPR000904; IPR001605; IPR001849; IPR011993; G3DSA:1.10.1000.11 (GENE3D), PTHR10663 (PANTHER), PTHR10663:SF3 (PANTHER), SSF50729 (SUPERFAMILY)
Strongylocentrotus purpuratus	replication factor c p37 subunit	0		F:GO:0016740; F:GO:0003677; C:GO:0005663; P:GO:0006260; F:GO:0003887; F:GO:0000166; F:GO:0017111; F:GO:0005524; F:GO:0016779; F:GO:0003689		IPR008921; IPR013748; G3DSA:1.20.272.10 (GENE3D), SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-gbf-1 protein	13	C:GO:0005829; P:GO:0008610; C:GO:0005739; P:GO:0046903; F:GO:0005086; P:GO:0045449; P:GO:0032012; F:GO:0003677; F:GO:0016563; F:GO:0005515; C:GO:0044431; F:GO:0003824; C:GO:0005634	-		-
Caenorhabditis briggsae	briggsae cbr-gbf-1 protein	16	C:GO:0005829; C:GO:0005777; P:GO:0008610; C:GO:0005739; P:GO:0046903; F:GO:0005086; P:GO:0045449; C:GO:0005795; P:GO:0032012; F:GO:0003677; C:GO:0005788; F:GO:0016563; F:GO:0005515; C:GO:0005801; F:GO:0003824; C:GO:0005634	-		-
Equus caballus	c-type lectin domain family member a	2	C:GO:0044464; F:GO:0005488	-		IPR001304; IPR016186; IPR016187; PTHR22800 (PANTHER), SignalP (SIGNALP)

						IPR000152; IPR000742; IPR001881; IPR006209; IPR006210; IPR013032; IPR018097; PR00010 (PRINTS), G3DSA:2.10.25.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF245 (PANTHER), SignalP (SIGNALP), SSF57196 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Danio rerio	novel protein containing multiple sushi domains (scr repeat)	0				IPR000436; IPR016060; SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	6	P:GO:0006633; F:GO:0004768; F:GO:0005506; P:GO:0055114; C:GO:0016021; C:GO:0005783	-	EC:1.14.19.1	-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	6	P:GO:0006633; F:GO:0004768; F:GO:0005506; P:GO:0055114; C:GO:0016021; C:GO:0005783	-	EC:1.14.19.1	IPR015876; PTHR11351 (PANTHER), PTHR11351:SF14 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	P:GO:0006633; F:GO:0004768; P:GO:0055114; C:GO:0016021	-	EC:1.14.19.1	IPR005804; IPR015876; PTHR11351 (PANTHER), PTHR11351:SF14 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	P:GO:0006633; F:GO:0004768; P:GO:0055114; C:GO:0016021	-	EC:1.14.19.1	IPR005804; IPR015876; PTHR11351 (PANTHER), PTHR11351:SF14 (PANTHER)
Caenorhabditis elegans	protein vprbp-like	2	C:GO:0044424; F:GO:0005488	-		PTHR13129 (PANTHER)
Caenorhabditis elegans	d-2-hydroxyglutarate mitochondrial	4	F:GO:0016614; P:GO:0008152; F:GO:0050660; P:GO:0010038	-		IPR004113; IPR016164; PTHR11748 (PANTHER), PTHR11748:SF7 (PANTHER)
	-	0				-
Caenorhabditis briggsae	death-associated protein ki-se 1	10	P:GO:0009103; F:GO:0005516; P:GO:0007243; F:GO:0004674; F:GO:0005524; C:GO:0015629; P:GO:0008624; C:GO:0005737; C:GO:0016020; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017441; IPR017442; IPR020675; IPR020676; G3DSA:3.30.200.20 (GENE3D)
Brugia malayi	prpf39 protein	2	C:GO:0005730; P:GO:0006396	-		IPR003107; IPR011990; PTHR17204 (PANTHER), PTHR17204:SF5 (PANTHER), SSF48452 (SUPERFAMILY)

Caenorhabditis elegans	beta-adrenergic receptor ki-se 2	13	F:GO:0047696; P:GO:0002029; C:GO:0030424; C:GO:0045202; C:GO:0043197; F:GO:0004872; F:GO:0004703; F:GO:0005524; C:GO:0043198; F:GO:0031698; P:GO:0007165; C:GO:0005634; P:GO:0006468	-	EC:2.7.11.15 ; EC:2.7.11.16	SignalP (SIGNALP)
	-	0				-
	-	0				-
Ostertagia ostertagi	ribosomal protein l38	7	P:GO:0009790; P:GO:0040035; P:GO:0002119; C:GO:0005840; F:GO:0003735; P:GO:0040010; P:GO:0006412	-	EC:3.6.5.3	-
Caenorhabditis elegans	low-density lipoprotein receptor repeat class b containing protein	8	P:GO:0006810; C:GO:0016021; P:GO:0050789; F:GO:0032403; P:GO:0009987; C:GO:0005886; P:GO:0008152; F:GO:0034185	-		-
Caenorhabditis briggsae	ww domain-binding protein 4	5	P:GO:0008380; P:GO:0032501; F:GO:0005515; C:GO:0044428; P:GO:0006397	-		IPR000690; IPR001202; IPR003604; IPR013085; G3DSA:2.20.70.10 (GENE3D), PTHR13173 (PANTHER), PTHR13173:SF10 (PANTHER), SSF57667 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	fra10ac1 protein isoform 2	1	F:GO:0005515	-		IPR019129; PTHR11567 (PANTHER), PTHR11567:SF25 (PANTHER)
Caenorhabditis briggsae	prp31 pre-mr- processing factor 31 homolog	11	C:GO:0071339; C:GO:0015030; F:GO:0003676; C:GO:0016607; P:GO:0040035; P:GO:0018996; P:GO:0040011; C:GO:0046540; P:GO:0002009; P:GO:0001703; P:GO:0000244	-		-
Loa loa	component of oligomeric golgi complex 6	1	C:GO:0005794	-		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		PTHR22746 (PANTHER), PTHR22746:SF6 (PANTHER)
	-	0				-

Homo sapiens	mhc class ii antigen	9	C:GO:0005789; C:GO:0005887; C:GO:0042613; C:GO:0005794; P:GO:0002504; C:GO:0031902; C:GO:0005765; F:GO:0032395; P:GO:0006955	-		-
	-	0				-
Brugia malayi	yrmc_caeel ame: full=uncharacterized protein	0				-
Loa loa	hypothetical protein LOAG_10600 [Loa loa]	0				-
Loa loa	yrmc_caeel ame: full=uncharacterized protein	0				-
Drosophila simulans	surfeit 6	4	P:GO:0002119; P:GO:0040007; P:GO:0006898; P:GO:0044085	-		IPR007019
Loa loa	elegans protein partially confirmed by transcript evidence	0		F:GO:0004500; C:GO:0016021; P:GO:0006548		IPR004877; IPR005018; IPR006593; PTHR23130 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	polyprenyl synthetase family protein	4	P:GO:0009792; P:GO:0002119; F:GO:0016740; P:GO:0040007	-		IPR000092; IPR008949; PTHR11525 (PANTHER)
Caenorhabditis elegans	hypothetical protein K06A4.7 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	cytidine deami-se	10	P:GO:0009790; P:GO:0046087; C:GO:0005622; F:GO:0047844; F:GO:0003723; F:GO:0005515; P:GO:0006217; F:GO:0004126; F:GO:0008270; P:GO:0009451	-	EC:3.5.4.14; EC:3.5.4.5	IPR002125; IPR006262; IPR016193; G3DSA:3.40.140.10 (GENE3D), PTHR11644 (PANTHER)
Caenorhabditis elegans	xpg i-region family protein	1	F:GO:0004518	-		IPR006084; IPR006085; IPR006086; IPR008918; IPR020045; G3DSA:1.10.150.20 (GENE3D), G3DSA:3.40.50.1010 (GENE3D), PTHR11081:SF8 (PANTHER), SSF88723 (SUPERFAMILY)
Caenorhabditis elegans	xpg i-region family protein	1	F:GO:0004518	-		IPR006084; IPR006085; IPR006086; IPR008918; IPR020045; G3DSA:1.10.150.20 (GENE3D), G3DSA:3.40.50.1010 (GENE3D), PTHR11081:SF8 (PANTHER), SSF88723 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	amplified in osteosarcoma	1	P:GO:0009987	-		IPR009011; IPR012913; PTHR15414 (PANTHER)
Loa loa	protein-tyrosine phosphatase containing protein	2	F:GO:0016791; P:GO:0006796	-	EC:3.1.3.0	-
Caenorhabditis elegans	polypeptide n-acetylgalactosaminyltransferase 10	5	C:GO:0000139; F:GO:0004653; F:GO:0005529; F:GO:0046872; C:GO:0016021	-	EC:2.4.1.41	IPR000772; IPR008997; G3DSA:2.80.10.50 (GENE3D), PTHR11675 (PANTHER), SSF53448 (SUPERFAMILY)

Caenorhabditis elegans	polypeptide n-acetylgalactosaminyltransferase 10	5	C:GO:0000139; F:GO:0004653; F:GO:0005529; F:GO:0046872; C:GO:0016021	-	EC:2.4.1.41	IPR000772; IPR008997; G3DSA:2.80.10.50 (GENE3D), PTHR11675 (PANTHER), SSF53448 (SUPERFAMILY)
Caenorhabditis elegans	polypeptide n-acetylgalactosaminyltransferase 10	5	C:GO:0000139; F:GO:0004653; F:GO:0005529; F:GO:0046872; C:GO:0016021	-	EC:2.4.1.41	IPR000772; IPR008997; G3DSA:2.80.10.50 (GENE3D), PTHR11675 (PANTHER), SSF53448 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-tat-3 protein	7	C:GO:0016021; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0015914; F:GO:0000287; F:GO:0004012	-	EC:3.6.3.1	IPR001757; IPR008250; G3DSA:2.70.150.10 (GENE3D), PTHR11939:SF14 (PANTHER), SSF81653 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-tat-3 protein	7	C:GO:0016021; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0015914; F:GO:0000287; F:GO:0004012	-	EC:3.6.3.1	IPR001757; IPR008250; G3DSA:2.70.150.10 (GENE3D), PTHR11939:SF14 (PANTHER), SSF81653 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis briggsae	loc495281 protein	1	P:GO:0000003	-		IPR000408; IPR009091; PTHR11254 (PANTHER), PTHR11254:SF8 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	phosphomevalo-te ki-se	10	P:GO:0040010; P:GO:0000003; P:GO:0018996; F:GO:0004631; F:GO:0005515; P:GO:0016310; P:GO:0006694; C:GO:0044464; P:GO:0009792; P:GO:0008299	-	EC:2.7.4.2	IPR005919; G3DSA:3.40.50.300 (GENE3D)
Caenorhabditis elegans	ring finger 1	1	F:GO:0005488	-		IPR000571; IPR001841; IPR013083; IPR017907; IPR018957; PTHR11224 (PANTHER), PTHR11224:SF19 (PANTHER), SSF57850 (SUPERFAMILY), SSF90229 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0000003		IPR001005
	-	0				-
Caenorhabditis elegans	protein ki-se domain containing protein	7	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0040018; P:GO:0040015; P:GO:0018996; P:GO:0040011	-		IPR011009; PTHR11909 (PANTHER), PTHR11909:SF11 (PANTHER)

Caenorhabditis elegans	protein ki-se domain containing protein	7	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0040018; P:GO:0040015; P:GO:0018996; P:GO:0040011	-		IPR011009; PTHR11909 (PANTHER), PTHR11909:SF11 (PANTHER)
Trichoplax adhaerens	histone deacetylase 11	7	F:GO:0004407; P:GO:0016575; C:GO:0000118; F:GO:0008134; C:GO:0005737; P:GO:0014003; C:GO:0005886	-		IPR000286; PTHR10625:SF9 (PANTHER), SSF52768 (SUPERFAMILY)
Caenorhabditis elegans	protein	1	F:GO:0005488	-		IPR015422; IPR015424
	-	0				-
	-	0				-
Caenorhabditis elegans	uncoordi-ted protein isoform partially confirmed by transcript evidence	8	F:GO:0004872; P:GO:0006629; F:GO:0005219; P:GO:0006816; P:GO:0006874; P:GO:0055085; F:GO:0005509; C:GO:0016021	-		IPR015925; PTHR13715:SF11 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	4-aminobutyrate mitochondrial	17	P:GO:0001666; P:GO:0009450; P:GO:0045776; C:GO:0032144; C:GO:0005739; P:GO:0045471; P:GO:0010039; F:GO:0003867; P:GO:0007620; P:GO:0007626; P:GO:0048148; P:GO:0042135; P:GO:0035094; C:GO:0019717; P:GO:0042493; F:GO:0042803; F:GO:0030170	-	EC:2.6.1.19	IPR004631; IPR005814; IPR015422; IPR015424
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	mterf domain-containing protein mitochondrial	0		C:GO:0005741; F:GO:0003674; P:GO:0006886; C:GO:0005575		IPR003690; PTHR13068 (PANTHER)
	-	0				-

Caenorhabditis elegans	suppressor of 3-like 1 (cerevisiae)	11	F:GO:0003678; P:GO:0040010; P:GO:0032508; F:GO:0003723; P:GO:0000003; C:GO:0042645; F:GO:0003677; P:GO:0002119; F:GO:0000166; P:GO:0006898; P:GO:0009792	-		IPR001650; IPR022192; G3DSA:3.40.50.300 (GENE3D), PTHR12131 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	suppressor of 3-like 1 (cerevisiae)	11	F:GO:0003678; P:GO:0040010; P:GO:0032508; F:GO:0003723; P:GO:0000003; C:GO:0042645; F:GO:0003677; P:GO:0002119; F:GO:0000166; P:GO:0006898; P:GO:0009792	-		IPR001650; IPR022192; G3DSA:3.40.50.300 (GENE3D), PTHR12131 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	suppressor of 3-like 1 (cerevisiae)	11	F:GO:0003678; P:GO:0040010; P:GO:0032508; F:GO:0003723; P:GO:0000003; C:GO:0042645; F:GO:0003677; P:GO:0002119; F:GO:0000166; P:GO:0006898; P:GO:0009792	-		IPR001650; IPR022192; G3DSA:3.40.50.300 (GENE3D), PTHR12131 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	rab3 gtpase-activating protein non-catalytic subunit	1	F:GO:0030234	-		PTHR12472 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	cg6459-pa	5	F:GO:0005515; C:GO:0005759; P:GO:0040010; P:GO:0040011; P:GO:0002009	-		-
Caenorhabditis briggsae	atp-binding sub-family c (cftr mrp) member 2	3	F:GO:0005488; C:GO:0044459; F:GO:0017111	-	EC:3.6.1.15	IPR001140; IPR003439; IPR003593; IPR011527; IPR017871; IPR017940; G3DSA:1.20.1560.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF36 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-ppk-3 protein	0		F:GO:0046872; F:GO:0005524; P:GO:0044267; P:GO:0046488; F:GO:0016307; F:GO:0008270; F:GO:0005515		-

Caenorhabditis elegans	glucose transporter	3	F:GO:0022891; C:GO:0016021; P:GO:0055085	-		IPR003663; IPR005828; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11600 (PANTHER), PTHR11600:SF107 (PANTHER), SignalP (SIGNALP)
Brugia malayi	nedd8 activating enzyme e1 subunit 1	7	C:GO:0005626; P:GO:0042981; P:GO:0031574; F:GO:0019781; P:GO:0045116; F:GO:0046982; C:GO:0005737	-		IPR000594; IPR009036; IPR016040; PTHR10953 (PANTHER), PTHR10953:SF29 (PANTHER)
Caenorhabditis briggsae	gamma-glutamyltranspeptidase family protein	1	F:GO:0003840	-	EC:2.3.2.2	IPR000101; SSF56235 (SUPERFAMILY)
Brugia malayi	coiled-coil domain-containing protein 58	1	C:GO:0005739	-		IPR019171
Loa loa	protein ki-se domain containing protein	5	P:GO:0006468; F:GO:0004672; F:GO:0005524; P:GO:0019915; P:GO:0006898	-		IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
Caenorhabditis elegans	gamma-secretase subunit aph-1	14	P:GO:0040010; C:GO:0043231; P:GO:0044267; P:GO:0048598; P:GO:0048599; P:GO:0060581; P:GO:0007219; P:GO:0034394; C:GO:0044425; C:GO:0044444; P:GO:0040011; P:GO:0009057; P:GO:0009792; P:GO:0060465	-		SignalP (SIGNALP)
Brugia malayi	low-density lipoprotein	3	F:GO:0004872; C:GO:0016021; F:GO:0005509	-		SignalP (SIGNALP)
Brugia malayi	ring finger protein 13	1	F:GO:0005488	-		IPR003137; G3DSA:3.50.30.30 (GENE3D), PTHR22765 (PANTHER), PTHR22765:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	phospholipid-transporting atpase 1 (aminophospholipid flippase 1)	8	P:GO:0006810; F:GO:0043492; P:GO:0046034; F:GO:0022892; F:GO:0046872; F:GO:0016820; F:GO:0000166; C:GO:0016020	-	EC:3.6.3.0	SignalP (SIGNALP)
Caenorhabditis elegans	mitochondrial ribosomal protein s22	4	P:GO:0002119; P:GO:0000003; P:GO:0040007; P:GO:0006898	-		IPR019374; PTHR13071 (PANTHER)
Caenorhabditis elegans	mitochondrial ribosomal protein s22	4	P:GO:0002119; P:GO:0000003; P:GO:0040007; P:GO:0006898	-		IPR019374; PTHR13071 (PANTHER)

Dictyostelium discoideum AX4	n-termi-l ki-se-like protein	0		F:GO:0016301; F:GO:0004672; F:GO:0005524; F:GO:0005488; P:GO:0006468		G3DSA:3.30.200.20 (GENE3D), PTHR12984 (PANTHER), PTHR12984:SF4 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-tag-151 protein	3	P:GO:0009792; P:GO:0040010; P:GO:0040011	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	5	P:GO:0045449; P:GO:0007399; P:GO:0030154; F:GO:0003700; C:GO:0044464	-		PTHR13029 (PANTHER), PTHR13029:SF7 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	riken cd- 2400010d15	1	F:GO:0005515	-		IPR009755; PTHR12897 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	ankyrin repeat-containing	0				IPR001452; IPR001660; IPR010993; IPR011511; IPR013761; IPR021129; G3DSA:2.30.30.40 (GENE3D), PTHR18958 (PANTHER), PTHR18958:SF31 (PANTHER)
Ancylostoma ceylanicum	serine protease	2	F:GO:0004867; F:GO:0008233	-		IPR002223; IPR020901; PTHR10083 (PANTHER), PTHR10083:SF39 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				IPR000436; IPR016060
Caenorhabditis briggsae	briggsae cbr-syn-2 protein	2	F:GO:0005515; P:GO:0016081	-		IPR006011; IPR010989; G3DSA:1.20.58.70 (GENE3D), PTHR19957 (PANTHER), PTHR19957:SF28 (PANTHER)
	-	0				-
Caenorhabditis elegans	pyridoxal ki-se	2	P:GO:0008615; F:GO:0008478	-	EC:2.7.1.35	IPR011611; G3DSA:3.40.1190.20 (GENE3D), PTHR10534 (PANTHER), SSF53613 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	ufm1-specific protease 2	1	F:GO:0008233	-		IPR012462; PTHR13226 (PANTHER), PTHR13226:SF5 (PANTHER)
Caenorhabditis elegans	ap-1 complex subunit mu-1	6	P:GO:0016183; P:GO:0007269; P:GO:0040025; F:GO:0005515; P:GO:0006886; C:GO:0030121	-		IPR001392; IPR008968; IPR011012; IPR018240; IPR022775; G3DSA:2.60.40.1170 (GENE3D), G3DSA:3.30.450.60 (GENE3D), PTHR11998 (PANTHER), PTHR11998:SF11 (PANTHER)
Brugia malayi	hypothetical protein Bm1_28590 [Brugia malayi]	0				-
Brugia malayi	fatty acid amide hydrolase	9	F:GO:0016788; F:GO:0005543; P:GO:0009062; P:GO:0000003; F:GO:0004040; C:GO:0044425; C:GO:0031090; F:GO:0042803; F:GO:0017064	-	EC:3.5.1.4	IPR000120; PTHR11895:SF4 (PANTHER)
	-	0				-

	-	0				-
Caenorhabditis briggsae	briggsae cbr-unc-26 protein	2	F:GO:0004437; F:GO:0005488	-		IPR015047
Brugia malayi	hypothetical protein [Brugia malayi]	0		P:GO:0009792		IPR020683; PTHR18958 (PANTHER), PTHR18958:SF203 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0003723; P:GO:0000003; F:GO:0005488; P:GO:0009792		SignalP (SIGNALP)
						IPR000923; IPR002172; PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER)
	-	0				-
Caenorhabditis sp. PS1010	hypothetical protein Csp3_JD07.006 [Caenorhabditis sp. PS1010]	0				-
Brugia malayi	lethal family member (let-805)	8	P:GO:0018996; P:GO:0009792; P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		-
Caenorhabditis briggsae	pat2_caebr ame: full=integrin alpha pat-2 ame: full=paralyzed arrest at two-fold protein 2 flags: precursor	8	P:GO:0009792; P:GO:0002119; P:GO:0018991; P:GO:0032940; P:GO:0040007; P:GO:0006898; C:GO:0016020; P:GO:0040039	-		G3DSA:2.60.40.1530 (GENE3D), PTHR23220 (PANTHER), PTHR23220:SF11 (PANTHER), SSF69179 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Geobacillus sp. G11MC16	hypothetical protein G11MC16DRAFT_3625 [Geobacillus sp. G11MC16]	0		C:GO:0016020; F:GO:0005515		-
Zea mays	unknown [Zea mays]	0				-
Lilium longiflorum	protein	0		F:GO:0005515		-
Lilium longiflorum	hypothetical protein [Lilium longiflorum]	0				-
Loa loa	ifa-1	3	C:GO:0005882; F:GO:0005198; F:GO:0005515	-		IPR001664; IPR016044; PD936484 (PRODOM), PTHR23239:SF13 (PANTHER)
	-	0				-
Caenorhabditis briggsae	dap (death associated protein ki-se) like ki-se family member (dlk-1)	0		F:GO:0016740; F:GO:0004674; C:GO:0045202; F:GO:0004672; C:GO:0030054; P:GO:0006468; F:GO:0000166; F:GO:0005524; F:GO:0016301; F:GO:0004709; F:GO:0005515; F:GO:0046872		PTHR23257 (PANTHER), PTHR23257:SF85 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis briggsae	mitochondrial ribosomal protein s2	7	P:GO:0009792; P:GO:0002119; F:GO:0003735; P:GO:0040010; C:GO:0015935; P:GO:0006898; P:GO:0006412	-	EC:3.6.5.3	IPR001865; IPR005706; IPR018130
	-	0				-
Loa loa	f-box and wd repeat domain containing 7	11	C:GO:0030424; C:GO:0005730; C:GO:0019005; P:GO:0046660; P:GO:0032876; P:GO:0016567; P:GO:0007062; F:GO:0005515; P:GO:0045746; P:GO:0031146; C:GO:0005654	-		IPR001680; IPR011044; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR22844 (PANTHER), PTHR22844:SF11 (PANTHER)
Loa loa	f-box and wd repeat domain containing 7	11	C:GO:0030424; C:GO:0005730; C:GO:0019005; P:GO:0046660; P:GO:0032876; P:GO:0016567; P:GO:0007062; F:GO:0005515; P:GO:0045746; P:GO:0031146; C:GO:0005654	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR22844 (PANTHER), PTHR22844:SF11 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-sec-5 protein	1	P:GO:0000003	-		PTHR13043 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	peptide methionine sulfoxide reductase	2	P:GO:0019538; F:GO:0016671	-	EC:1.8.4.0	IPR002569; PTHR10173 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	ubiquitin-conjugating enzyme e2-25kd	3	P:GO:0051246; F:GO:0019787; P:GO:0043687	-		IPR000449; IPR000608; IPR009060; IPR015940; IPR016135; G3DSA:1.10.8.10 (GENE3D), PTHR11621 (PANTHER), PTHR11621:SF28 (PANTHER)
Caenorhabditis briggsae	ubiquitin-conjugating enzyme e2-25kd	3	P:GO:0051246; F:GO:0019787; P:GO:0043687	-		IPR000449; IPR000608; IPR009060; IPR015940; IPR016135; G3DSA:1.10.8.10 (GENE3D), PTHR11621 (PANTHER), PTHR11621:SF28 (PANTHER)
Loa loa	exosome component 10	5	C:GO:0005730; P:GO:0006378; C:GO:0000176; F:GO:0003824; C:GO:0005652	-		IPR002121; IPR002562; IPR010997; IPR012337; G3DSA:3.30.420.10 (GENE3D), PTHR12124 (PANTHER), PTHR12124:SF2 (PANTHER)

Caenorhabditis elegans	aldh9a1a protein	15	C:GO:0005829; F:GO:0043176; C:GO:0015630; C:GO:0005739; P:GO:0001889; P:GO:0055114; P:GO:0045329; F:GO:0051287; F:GO:0019145; P:GO:0006081; P:GO:0042136; F:GO:0042803; F:GO:0047105; F:GO:0004029; C:GO:0005634	-	EC:1.2.1.19; EC:1.2.1.47; EC:1.2.1.3	SignalP (SIGNALP)
Caenorhabditis briggsae	rhomboid 5 homolog 2-like	1	C:GO:0016020	-		IPR002610; IPR022764; G3DSA:1.20.1540.10 (GENE3D), SignalP (SIGNALP), SSF144091 (SUPERFAMILY)
Caenorhabditis elegans	r- exonuclease 4	4	C:GO:0005730; F:GO:0003700; F:GO:0004518; P:GO:0006355	-		IPR006055; IPR012337; IPR013520; IPR018228; G3DSA:3.30.420.10 (GENE3D), PTHR12801 (PANTHER), PTHR12801:SF5 (PANTHER)
Caenorhabditis elegans	r- exonuclease 4	4	C:GO:0005730; F:GO:0003700; F:GO:0004518; P:GO:0006355	-		IPR006055; IPR012337; IPR013520; IPR018228; G3DSA:3.30.420.10 (GENE3D), PTHR12801 (PANTHER), PTHR12801:SF5 (PANTHER)
Loa loa	nuclear nucleic acid-binding protein c1d	2	F:GO:0005488; C:GO:0044424	-		IPR011082
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	ser thr-rich protein t10 in dgcr region	0				IPR008551
Caenorhabditis briggsae	dual specificity phosphatase 14-like	4	F:GO:0004725; F:GO:0008138; P:GO:0016311; C:GO:0044424	-	EC:3.1.3.48	IPR000340; IPR000387; IPR016130; IPR020417; IPR020420; IPR020422; G3DSA:3.90.190.10 (GENE3D), PTHR10159 (PANTHER), PTHR10159:SF21 (PANTHER), SSF52799 (SUPERFAMILY)
Gemmata obscuriglobus UQM 2246	serine racemase	1	F:GO:0003824	-		IPR000634; IPR001926; PTHR10314 (PANTHER), PTHR10314:SF17 (PANTHER)
Loa loa	enhancer of mr- decapping 4	1	C:GO:0044424	-		IPR011044; IPR015943; PTHR15598 (PANTHER)
Caenorhabditis briggsae	glycosyl hydrolases family 31 protein	3	F:GO:0030246; P:GO:0005975; F:GO:0004553	-	EC:3.2.1.0	IPR000322; IPR011013; PTHR22762:SF10 (PANTHER)
	-	0				-
Caenorhabditis briggsae	yms5_caeel ame: full=uncharacterized protein flags: precursor	0		P:GO:0007160; C:GO:0016021		SignalP (SIGNALP)

Pongo abelii	isoform cra_b	0		P:GO:0030030; P:GO:0001842; P:GO:0006468; C:GO:0005634; P:GO:0043200; P:GO:0006606; P:GO:0045792; P:GO:0030836; P:GO:0030010; C:GO:0030864; P:GO:0007015; P:GO:0000910; P:GO:0006928; C:GO:0030027; C:GO:0005737; P:GO:0001755; C:GO:0005829; C:GO:0005622; C:GO:0005856; C:GO:0031252; C:GO:0005576		-
	-	0				-
	-	0				-
Caenorhabditis elegans	scavenger receptor class member 2	2	P:GO:0040035; C:GO:0016020	-		IPR002159; PTHR11923:SF8 (PANTHER), SignalP (SIGNALP)
	-	0				-
Loa loa	elegans protein partially confirmed by transcript evidence	0		F:GO:0004500; P:GO:0006548		-
Ancylostoma ceylanicum	briggsae cbr-sas-5 protein	0		C:GO:0005737; P:GO:0007049; C:GO:0005856; P:GO:0007275; F:GO:0005515; C:GO:0005814		PD127281 (PRODOM)
Loa loa	dpy-30 homolog	1	F:GO:0005515	-		IPR007858; PTHR23356 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	phospholipid-transporting atpase 1 (aminophospholipid flippase 1)	3	F:GO:0005488; F:GO:0016817; F:GO:0005215	-		IPR001757; IPR018303; G3DSA:3.40.1110.10 (GENE3D), PTHR11939:SF14 (PANTHER), SSF56784 (SUPERFAMILY)
	-	0				-
Brugia malayi	zinc finger protein 161 homolog	4	F:GO:0003677; C:GO:0005622; F:GO:0005515; F:GO:0008270	-		IPR000210; IPR011333; IPR013069; PTHR23228 (PANTHER), PTHR23228:SF46 (PANTHER)
Caenorhabditis briggsae	zinc finger protein	0		F:GO:0008270; C:GO:0005622		IPR007087; IPR015880; SSF57667 (SUPERFAMILY)
Brugia malayi	thioredoxin domain-containing protein 11	0		C:GO:0005789; P:GO:0045454; C:GO:0016021; C:GO:0016020; C:GO:0005783		IPR012335; IPR012336
Caenorhabditis briggsae	Hypothetical protein CBG08318 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-flp-5 protein	0		P:GO:0007218		-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein ZK1248.15 [Caenorhabditis elegans]	0				IPR001202; G3DSA:2.20.70.10 (GENE3D)

Caenorhabditis briggsae	chloride intracellular channel	1	F:GO:0005488	-		IPR010987; PTHR11260 (PANTHER), PTHR11260:SF1 (PANTHER)
	-	0				-
Macaca mulatta	sh3 domain binding glutamic acid-rich protein like 3	6	P:GO:0045454; C:GO:0005737; P:GO:0008152; F:GO:0009055; F:GO:0015035; C:GO:0005634	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	ain family member (clp-1)	7	C:GO:0005737; P:GO:0016540; F:GO:0004198; F:GO:0005509; P:GO:0008219; C:GO:0016021; P:GO:0006508	-		IPR000169; IPR001300; IPR022684; G3DSA:3.90.70.10 (GENE3D), PTHR10183 (PANTHER), PTHR10183:SF45 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis elegans	ubiquitin-conjugating enzyme e2 variant 2	17	P:GO:0000209; F:GO:0005515; P:GO:0006355; P:GO:0008283; C:GO:0005829; F:GO:0016563; P:GO:0043524; P:GO:0032436; C:GO:0031372; P:GO:0043123; F:GO:0019787; P:GO:0010976; P:GO:0000729; P:GO:0051092; C:GO:0005634; P:GO:0045739; P:GO:0051965	-		-
	-	0				-
	-	0				-
Loa loa	f y-rich n-terminus family protein	0		F:GO:0046872; F:GO:0008168; F:GO:0016740; F:GO:0008270; F:GO:0005515; F:GO:0003677; C:GO:0005634		IPR018555
	-	0				-
Caenorhabditis briggsae	39s ribosomal protein	7	P:GO:0009792; P:GO:0002119; C:GO:0005762; F:GO:0003735; P:GO:0040007; P:GO:0006898; P:GO:0006412	-	EC:3.6.5.3	IPR019373; PTHR13409 (PANTHER)
Caenorhabditis elegans	hypothetical protein Y37E11AL.2 [Caenorhabditis elegans]	0		F:GO:0004864; P:GO:0043666; P:GO:0009966		-

Caenorhabditis briggsae	briggsae cbr-lgg-1 protein	17	F:GO:0050811; F:GO:0008017; C:GO:0005764; C:GO:0005875; C:GO:0000421; P:GO:0008340; C:GO:0005874; F:GO:0004872; P:GO:0000226; C:GO:0015629; P:GO:0007165; F:GO:0048487; P:GO:0031396; P:GO:0015031; C:GO:0005794; C:GO:0005790; C:GO:0005886	-		IPR004241; G3DSA:3.10.20.90 (GENE3D), PTHR10969:SF5 (PANTHER), SSF54236 (SUPERFAMILY)
Homo sapiens	complement c1r subcomponent precursor	6	F:GO:0004252; P:GO:0045087; F:GO:0005509; P:GO:0006958; C:GO:0005576; P:GO:0006508	-	EC:3.4.21.0	IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR19355 (PANTHER), PTHR19355:SF44 (PANTHER)
Caenorhabditis briggsae	endonuclease mitochondrial	8	P:GO:0006261; F:GO:0046872; F:GO:0004521; F:GO:0003676; F:GO:0004123; F:GO:0005515; C:GO:0005739; F:GO:0004520	-	EC:4.4.1.1	-
Caenorhabditis elegans	Hypothetical protein CBG16427 [Caenorhabditis briggsae]	0		C:GO:0005622; P:GO:0006810		-
Caenorhabditis elegans	solute carrier family member 28	10	P:GO:0055085; P:GO:0048250; P:GO:0040010; F:GO:0005488; F:GO:0005381; P:GO:0043249; C:GO:0016021; C:GO:0005743; P:GO:0035162; P:GO:0009792	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF77 (PANTHER)
Caenorhabditis elegans	ankyrin repeat domain 40	0				SignalP (SIGNALP)
Caenorhabditis elegans	zinc cchc domain containing 11	8	F:GO:0016779; P:GO:0016070; F:GO:0005488; P:GO:0010468; P:GO:0050794; P:GO:0007166; C:GO:0044424; P:GO:0001816	-	EC:2.7.7.0	SignalP (SIGNALP)
	-	0				-
	-	0				-

Caenorhabditis briggsae	chloride channel 7	7	P:GO:0055085; F:GO:0005247; C:GO:0016021; C:GO:0031410; P:GO:0006821; F:GO:0005515; P:GO:0009268	-		IPR001807; IPR006311; IPR014743; PTHR11689:SF15 (PANTHER)
Brugia malayi	apoptosis-inducing mitochondrion- 1	8	P:GO:0030263; C:GO:0005739; P:GO:0006309; F:GO:0009055; F:GO:0005515; C:GO:0000267; P:GO:0008630; C:GO:0005634	-		IPR001327; IPR013027; PR00411 (PRINTS), G3DSA:3.50.50.60 (GENE3D), PTHR22912 (PANTHER), PTHR22912:SF32 (PANTHER), SSF51905 (SUPERFAMILY)
Callithrix jacchus	ribosomal protein l4	5	F:GO:0003735; F:GO:0003723; F:GO:0005515; C:GO:0022625; P:GO:0006414	-		IPR002136; G3DSA:3.40.1370.10 (GENE3D), PTHR19431 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				IPR018122
	-	0				-
	-	0				IPR018122
	-	0				IPR018122
	-	0				-
Brugia malayi	cyclin c	0		F:GO:0016301; F:GO:0003674; P:GO:0006350; P:GO:0007275; P:GO:0045449; F:GO:0005515; C:GO:0005634		IPR006670; IPR006671; IPR011028; IPR013763; IPR015429; PIRSF028758 (PIR), PTHR10026:SF7 (PANTHER)
Brugia malayi	cyclin c	0		F:GO:0016301; F:GO:0003674; P:GO:0006350; P:GO:0007275; P:GO:0045449; F:GO:0005515; C:GO:0005634		IPR006670; IPR006671; IPR011028; IPR013763; IPR015429; PIRSF028758 (PIR), PTHR10026:SF7 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	dsh homolog 3	3	P:GO:0007275; F:GO:0004871; F:GO:0042802	-		-
Caenorhabditis briggsae	briggsae cbr-lin-33 protein	1	P:GO:0008219	-		-
Caenorhabditis briggsae	corneal wound healing-related protein	2	F:GO:0005515; C:GO:0005737	-		IPR007244; PTHR21373 (PANTHER)
Caenorhabditis briggsae	dihydroorotate dehydroge-se	6	F:GO:0004158; C:GO:0005743; P:GO:0055114; P:GO:0006222; P:GO:0050794; P:GO:0006207	-	EC:1.3.3.1	IPR001295; IPR005719; IPR012135; IPR013785; PTHR11938 (PANTHER), PTHR11938:SF7 (PANTHER), SSF51395 (SUPERFAMILY)
Caenorhabditis elegans	muscle lim protein	1	F:GO:0008270	-		IPR001781; PTHR18973 (PANTHER), PTHR18973:SF77 (PANTHER), SSF57716 (SUPERFAMILY)

Caenorhabditis briggsae	muscle lim protein	1	F:GO:0008270	-		IPR001781; PTHR18973 (PANTHER), PTHR18973:SF77 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis elegans	muscle lim protein	1	F:GO:0008270	-		IPR001781; PTHR18973 (PANTHER), PTHR18973:SF77 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis briggsae	ras-related protein rab-8a	16	C:GO:0030425; P:GO:0007264; P:GO:0048169; P:GO:0048210; P:GO:0051223; C:GO:0016023; C:GO:0055037; C:GO:0043025; F:GO:0019901; P:GO:0042384; C:GO:0014069; C:GO:0031513; P:GO:0006904; C:GO:0005794; F:GO:0005525; C:GO:0005886	-		IPR001806; IPR003579; IPR005225; IPR013753; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF229 (PANTHER), SSF52540 (SUPERFAMILY)
Acyrthosiphon pisum	cg32795 cg32795-pb	1	C:GO:0044464	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Pediculus humanus corporis	5 -nucleotidase domain-containing	0		F:GO:0008253; F:GO:0016787		-
Loa loa	zinc cchc domain containing 24	1	F:GO:0005488	-		IPR001878
	-	0				-
	-	0				-
Caenorhabditis briggsae	atpase aaa domain containing 1	11	P:GO:0010171; P:GO:0002119; F:GO:0016887; F:GO:0005515; F:GO:0005524; C:GO:0016021; P:GO:0040007; C:GO:0005739; P:GO:0006310; F:GO:0009378; P:GO:0006281	-		IPR003959; IPR003960; G3DSA:1.10.8.60 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23074 (PANTHER), PTHR23074:SF20 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				PS51257 (PROFILE), SignalP (SIGNALP)
Harpegnathos saltator	slc44a3 protein	0		C:GO:0016021; C:GO:0016020		IPR007603; SignalP (SIGNALP)
Caenorhabditis elegans	integral membrane protein	0				IPR019336; PTHR23252 (PANTHER), PTHR23252:SF3 (PANTHER), SignalP (SIGNALP)
Brugia malayi	mouse nedd8 related family member (ned-8)	8	P:GO:0008589; P:GO:0045116; P:GO:0051438; P:GO:0008283; F:GO:0005515; P:GO:0006511; P:GO:0030162; P:GO:0031647	-		IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), PTHR10666:SF11 (PANTHER), SSF54236 (SUPERFAMILY)

Loa loa	transcription initiation factor alpha subunit	8	F:GO:0030528; P:GO:0008340; F:GO:0003676; P:GO:0040035; P:GO:0050794; P:GO:0006898; P:GO:0009792; P:GO:0006350	-		IPR008851; PTHR13011 (PANTHER)
Caenorhabditis elegans	hypothetical protein Y37E11AL.5 [Caenorhabditis elegans]	0		P:GO:0007218; F:GO:0005509; P:GO:0007156; C:GO:0016021; C:GO:0016020; C:GO:0005886		SignalP (SIGNALP)
	-	0				-
	-	0				-
Meyerozyma guilliermondii ATCC 6260	protein phosphatase regulatory subunit 7	0		F:GO:0030234; P:GO:0000003; C:GO:0005634; F:GO:0030528; P:GO:0006355; P:GO:0016568; P:GO:0009792; P:GO:0008150; F:GO:0003682; C:GO:0005737; P:GO:0007165; F:GO:0004888; P:GO:0045449; C:GO:0031224; F:GO:0005515; P:GO:0045087; P:GO:0040010; F:GO:0008599		-
Loa loa	cyclin-dependent ki-se 2 associated protein 1	0		F:GO:0016301		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR22850 (PANTHER), PTHR22850:SF5 (PANTHER)
Loa loa	wd domain protein	0				IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR22850 (PANTHER), PTHR22850:SF17 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	acyl- thioesterase ii	2	P:GO:0019915; F:GO:0016787	-		IPR003703; G3DSA:3.10.129.10 (GENE3D), PTHR11066:SF3 (PANTHER), SSF54637 (SUPERFAMILY)
Caenorhabditis elegans	probable cation-transporting atpase in chromosome	5	F:GO:0016820; F:GO:0016887; F:GO:0000166; P:GO:0008152; C:GO:0016020	-	EC:3.6.3.0	IPR001757; G3DSA:3.40.1110.10 (GENE3D), G3DSA:3.40.50.1000 (GENE3D), PTHR11939:SF48 (PANTHER), SSF56784 (SUPERFAMILY), SSF81660 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-

Brugia malayi	briggsae cbr-ptb-1 protein	14	P:GO:0007219; P:GO:0008103; F:GO:0005515; P:GO:0008586; F:GO:0000166; F:GO:0000900; F:GO:0003730; C:GO:0005737; P:GO:0000398; P:GO:0008587; P:GO:0007319; F:GO:0008187; C:GO:0005634; C:GO:0030529	-		-
Caenorhabditis elegans	v-raf murine sarcoma viral oncogene homolog b1	2	F:GO:0016301; F:GO:0005515	-		IPR002219; IPR003116; G3DSA:3.10.20.90 (GENE3D), G3DSA:3.30.60.20 (GENE3D), PTHR23257 (PANTHER), PTHR23257:SF97 (PANTHER), SignalP (SIGNALP), SSF54236 (SUPERFAMILY), SSF57889 (SUPERFAMILY)
Caenorhabditis elegans	microtubule associated serine threonine ki-se 3	7	P:GO:0009792; P:GO:0006468; F:GO:0005515; F:GO:0005524; F:GO:0000287; P:GO:0000003; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR011009; IPR015022; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR22985 (PANTHER), PTHR22985:SF42 (PANTHER)
Caenorhabditis briggsae	d-glucuronyl c5-epimerase	6	P:GO:0044272; C:GO:0005794; P:GO:0030201; F:GO:0016857; C:GO:0016020; P:GO:0006024	-	EC:5.1.3.0	PTHR13174 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	ubiquitin specific peptidase 15	5	F:GO:0005488; P:GO:0044238; P:GO:0044260; P:GO:0009792; F:GO:0016787	-		IPR001394; PTHR10420 (PANTHER), PTHR10420:SF68 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis elegans	ubiquitin specific peptidase 15	5	F:GO:0005488; P:GO:0044238; P:GO:0044260; P:GO:0009792; F:GO:0016787	-		IPR001394; PTHR10420 (PANTHER), PTHR10420:SF68 (PANTHER), SSF54001 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	transcription elongation regulator 1	6	P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0016246; P:GO:0040011; P:GO:0040007	-		IPR001202; IPR002713; G3DSA:2.20.70.10 (GENE3D)
Caenorhabditis elegans	transcription elongation regulator 1	6	P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0016246; P:GO:0040011; P:GO:0040007	-		IPR001202; IPR002713; G3DSA:2.20.70.10 (GENE3D)

	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	d-se domain containing 2	0		F:GO:0016888; F:GO:0003674; F:GO:0016787; P:GO:0008150; F:GO:0004518; C:GO:0005634		IPR001130; IPR015992; IPR018228; G3DSA:3.20.20.140 (GENE3D), SSF51556 (SUPERFAMILY)
Teladorsagia circumcincta	nicotinic acetylcholine receptor alpha subunit	6	F:GO:0004872; C:GO:0045211; C:GO:0030054; P:GO:0006811; C:GO:0016021; F:GO:0004889	-		IPR006029; IPR006201; G3DSA:1.20.120.370 (GENE3D), PTHR18945:SF88 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	pan domain containing protein	0				-
Caenorhabditis briggsae	-dh dehydroge-se 1 beta 22kda	6	P:GO:0040010; P:GO:0022900; C:GO:0005747; P:GO:0002119; F:GO:0003954; P:GO:0006898	-	EC:1.6.99.3	PTHR12868 (PANTHER)
Caenorhabditis briggsae	-dh dehydroge-se	5	P:GO:0002119; C:GO:0005743; C:GO:0070469; P:GO:0040010; P:GO:0006898	-		PTHR12868 (PANTHER)
Caenorhabditis elegans	ctu2_caeel ame: full=cytoplasmic tr- 2-thiolation protein 2	2	C:GO:0005737; P:GO:0006400	-		PTHR20882 (PANTHER), PTHR20882:SF4 (PANTHER)
Brugia malayi	nuclear r- export factor 2	2	P:GO:0006810; C:GO:0031981	-		IPR005637; IPR009060; IPR018222; G3DSA:1.10.8.10 (GENE3D), G3DSA:3.10.450.50 (GENE3D), PTHR10662 (PANTHER), PTHR10662:SF21 (PANTHER), SSF54427 (SUPERFAMILY)
Caenorhabditis elegans	ell associated factor 2	4	C:GO:0005730; P:GO:0045449; F:GO:0005515; C:GO:0005654	-		IPR019194; PTHR15970 (PANTHER), PTHR15970:SF3 (PANTHER)
Ancylostoma caninum	tissue factor pathway isoform cra_a	1	P:GO:0065007	-		IPR002223; IPR020901; PTHR10083 (PANTHER), PTHR10083:SF17 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				IPR001810
	-	0				-
Caenorhabditis briggsae	phytanoyl- peroxisomal precursor	9	F:GO:0046872; F:GO:0048244; C:GO:0005777; F:GO:0031418; F:GO:0005515; P:GO:0055114; F:GO:0016702; P:GO:0001561; C:GO:0005739	-	EC:1.14.11.18; EC:1.13.11.0	IPR008775; G3DSA:2.60.120.620 (GENE3D), PTHR21308 (PANTHER), SSF51197 (SUPERFAMILY)
Caenorhabditis briggsae	intraflagellar transport 140 homolog	1	F:GO:0005488	-		PTHR15722 (PANTHER), PTHR15722:SF7 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG23816 [Caenorhabditis briggsae]	0				IPR015880

Angiostrongylus cantonensis	elegans protein confirmed by transcript evidence	2	P:GO:0009792; P:GO:0040002	-		IPR002486; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	serine threonine-protein phosphatase 2a regulatory subunit b	10	P:GO:0008340; P:GO:0000003; P:GO:0040010; C:GO:0044464; P:GO:0009792; P:GO:0002119; F:GO:0019888; F:GO:0003824; F:GO:0005488; P:GO:0043666	-		IPR004327; SSF140984 (SUPERFAMILY)
Caenorhabditis elegans	f-box domain containing protein	0		P:GO:0030163; F:GO:0001948; F:GO:0005515; C:GO:0019005		IPR001810; IPR022364; G3DSA:1.20.1280.50 (GENE3D)
Caenorhabditis elegans	suppressor of presenilin defect family member (spr-4)	0		F:GO:0005216; C:GO:0016021; C:GO:0016020; P:GO:0006813; C:GO:0005634; P:GO:0006811; P:GO:0006810; F:GO:0003676; F:GO:0003674; F:GO:0008270; C:GO:0005575; C:GO:0005622; P:GO:0055085; F:GO:0046872; F:GO:0005249		IPR007087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-epac-1 protein	4	P:GO:0007264; C:GO:0005622; F:GO:0005085; P:GO:0008152	-		IPR008937; PTHR23113:SF22 (PANTHER), SignalP (SIGNALP), SSF54236 (SUPERFAMILY)
Brugia malayi	lsm5 protein	4	F:GO:0003676; C:GO:0005681; C:GO:0030532; P:GO:0000398	-		IPR001163; IPR006649; IPR010920; G3DSA:2.30.30.100 (GENE3D), PTHR20971 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-ttr-47 protein	1	P:GO:0040011	-		SignalP (SIGNALP)
Loa loa	regulatory-associated protein of mtor	4	F:GO:0003993; F:GO:0005488; P:GO:0001934; P:GO:0006974	-	EC:3.1.3.2	IPR004083; PTHR12848:SF7 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	u6 snr--associated sm-like protein lsm8	5	F:GO:0017070; F:GO:0005515; C:GO:0030529; C:GO:0005634; P:GO:0000398	-		IPR001163; IPR006649; IPR010920; G3DSA:2.30.30.100 (GENE3D), PTHR15588 (PANTHER)
	-	0				-

Caenorhabditis elegans	patched family protein	13	P:GO:0009792; P:GO:0002119; F:GO:0008158; P:GO:0040018; P:GO:0001703; P:GO:0018996; P:GO:0000910; P:GO:0006810; P:GO:0040010; P:GO:0000003; P:GO:0040011; C:GO:0016021; F:GO:0005215	-		-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0000003; F:GO:0005089; P:GO:0035023; C:GO:0005622		-
Caenorhabditis elegans	eph receptor tyrosine ki-se	10	C:GO:0016021; P:GO:0016319; P:GO:0007391; F:GO:0005515; P:GO:0007409; F:GO:0000166; P:GO:0007165; F:GO:0005003; C:GO:0005886; P:GO:0006468	-		-
Caenorhabditis elegans	udp-glucose:glycoprotein glucosyltransferase containing protein	1	F:GO:0016757	-		IPR009448
	-	0				-
Homo sapiens	type alpha 1	31	P:GO:0060351; P:GO:0001957; P:GO:0071363; P:GO:0007605; P:GO:0034505; P:GO:0042542; P:GO:0001649; P:GO:0009612; P:GO:0001568; P:GO:0060325; F:GO:0005201; C:GO:0005615; P:GO:0048706; P:GO:0015031; F:GO:0048407; C:GO:0005737; P:GO:0043434; P:GO:0071300; P:GO:0007601; P:GO:0010812; C:GO:0005584; F:GO:0042802; P:GO:0060346; P:GO:0032964; P:GO:0030199; P:GO:0051591; P:GO:0031960;	-		SignalP (SIGNALP)

	-	0				-
Caenorhabditis elegans	vacuolar protein sorting 26 homolog b	5	C:GO:0030904; P:GO:0015031; C:GO:0005829; P:GO:0000003; P:GO:0007034	-		IPR005377; PTHR12233 (PANTHER)
	-	0				-
Haemochus contortus	briggsae cbr-gst- protein	4	P:GO:0008340; F:GO:0004364; P:GO:0040010; F:GO:0005515	-	EC:2.5.1.18	IPR004045; IPR010987; IPR012335; IPR012336; IPR017933; PTHR11571 (PANTHER), PTHR11571:SF6 (PANTHER)
Caenorhabditis elegans	monocarboxylate transporter	0		P:GO:0055085		IPR011701; IPR016196; G3DSA:1.20.1250.20 (GENE3D), PTHR11360 (PANTHER), PTHR11360:SF10 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	phosphatidylinositol 3-ki-se regulatory subunit	5	C:GO:0005622; P:GO:0040024; P:GO:0008340; F:GO:0019901; P:GO:0008286	-		-
Caenorhabditis elegans	hypothetical protein T01E8.5 [Caenorhabditis elegans]	0				-
	-	0				-
Loa loa	cell cycle regulator mat89bb homolog	1	P:GO:0007049	-		IPR019355; PTHR12955 (PANTHER)
	-	0				-
Caenorhabditis briggsae	transmembrane protein 144	1	P:GO:0002119	-		IPR012435; SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Brugia malayi	cyclin fold protein 1 variant b	1	P:GO:0048589	-		-
Caenorhabditis elegans	protein-tyrosine phosphatase containing protein	3	F:GO:0016791; P:GO:0009792; P:GO:0000003	-	EC:3.1.3.0	IPR000242; IPR000387; IPR016130; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR010558; SignalP (SIGNALP)
	-	0				IPR003124; IPR021854; PTHR23331 (PANTHER)
Caenorhabditis elegans	briggsae cbr-cid-1 protein	1	F:GO:0005488	-		IPR002058; G3DSA:3.30.460.10 (GENE3D), PTHR12271 (PANTHER), PTHR12271:SF15 (PANTHER), SSF81301 (SUPERFAMILY), SSF81631 (SUPERFAMILY)
Caenorhabditis elegans	zinc cchc domain containing 6	1	F:GO:0005488	-		IPR002058; G3DSA:3.30.460.10 (GENE3D), PTHR12271 (PANTHER), PTHR12271:SF15 (PANTHER), SSF81301 (SUPERFAMILY), SSF81631 (SUPERFAMILY)
Caenorhabditis elegans	zinc cchc domain containing 6	1	F:GO:0005488	-		IPR002058; G3DSA:3.30.460.10 (GENE3D), PTHR12271 (PANTHER), PTHR12271:SF15 (PANTHER), SSF81301 (SUPERFAMILY), SSF81631 (SUPERFAMILY)
Caenorhabditis elegans	leucyl-tr- synthetase	5	F:GO:0004823; P:GO:0006429; F:GO:0005515; F:GO:0005524; C:GO:0005829	-	EC:6.1.1.4	IPR014729; PTHR11946 (PANTHER), PTHR11946:SF6 (PANTHER), SSF52374 (SUPERFAMILY)

Loa loa	gpi mannosyltransferase 2	4	P:GO:0040007; P:GO:0040035; P:GO:0002119; P:GO:0009792	-		PF04188 (PFAM)
Teladorsagia circumcincta	protein disulfide isomerase	4	P:GO:0045454; F:GO:0003756; C:GO:0016020; C:GO:0005783	-	EC:5.3.4.1	-
	-	0				PR01228 (PRINTS)
	-	0				-
	-	0				PR01228 (PRINTS)
	-	0				PR01228 (PRINTS)
	-	0				PR01228 (PRINTS)
	-	0				PR01228 (PRINTS)
	-	0				-
Loa loa	selenocysteine lyase	3	P:GO:0009792; P:GO:0006520; F:GO:0003824	-		IPR000192; IPR015421; IPR015422; IPR015424; PTHR11601 (PANTHER)
						IPR003598; IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	ophagy (yeast atg homolog) family member (atg-11)	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-cdc- protein	0		F:GO:0005524; F:GO:0000166; F:GO:0017111		-
Angiostrongylus cantonensis	elegans protein confirmed by transcript evidence	5	F:GO:0003700; F:GO:0043565; F:GO:0046983; C:GO:0005634; P:GO:0006355	-		IPR001630; G3DSA:1.20.5.170 (GENE3D), PTHR22952 (PANTHER), PTHR22952:SF11 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	2	F:GO:0042302; C:GO:0016021	-		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	programmed cell death 2	7	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0005488; P:GO:0040010; C:GO:0044464; P:GO:0006898	-		IPR002893; PTHR12298 (PANTHER), PTHR12298:SF4 (PANTHER), SSF144232 (SUPERFAMILY)
Caenorhabditis elegans	nuclear pore complex protein family member (npp-13)	0		C:GO:0005643; P:GO:0006810		-
Caenorhabditis briggsae	class type	8	C:GO:0016021; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0015914; F:GO:0005515; F:GO:0000287; F:GO:0004012	-	EC:3.6.3.1	IPR001757; G3DSA:3.40.50.1000 (GENE3D), PTHR11939:SF19 (PANTHER), SSF56784 (SUPERFAMILY), SSF81665 (SUPERFAMILY)

Nematostella vectensis	endonuclease-reverse transcriptase	0		F:GO:0003723; F:GO:0004527; P:GO:0006278; F:GO:0004519; F:GO:0003964		-
	-	0				-
Loa loa	prefoldin subunit 6	2	C:GO:0005737; F:GO:0005515	-		IPR002777; IPR009053; G3DSA:1.10.287.370 (GENE3D), PTHR21431 (PANTHER)
Caenorhabditis elegans	integrator complex subunit 4	6	P:GO:0009987; P:GO:0007369; P:GO:0050789; P:GO:0040007; P:GO:0000003; P:GO:0010467	-		IPR011989; IPR016024; PTHR20938 (PANTHER), SignalP (SIGNALP)
Ancylostoma caninum	metalloprotease 1 precursor	1	F:GO:0008237	-		IPR001506; IPR006026; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SignalP (SIGNALP), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	gex interacting protein family member (gei-16)	1	F:GO:0005515	-		-
Loa loa	ankyrin repeat protein	0		P:GO:0006915; F:GO:0000166; F:GO:0017111; F:GO:0003674; F:GO:0005524; P:GO:0007165; F:GO:0005515; P:GO:0008150; F:GO:0005488		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	leucyl-tr- synthetase	4	C:GO:0005737; F:GO:0004823; P:GO:0006429; F:GO:0005524	-	EC:6.1.1.4	IPR002300; IPR009008; G3DSA:3.90.740.10 (GENE3D)
Caenorhabditis briggsae	general transcription factor 3c polypeptide 3	3	F:GO:0005488; P:GO:0040010; P:GO:0006898	-		SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-mlt-7 protein	4	F:GO:0020037; P:GO:0055114; F:GO:0004601; P:GO:0006979	-	EC:1.11.1.7	IPR002007; IPR006032; IPR010255; IPR019791; PTHR11475 (PANTHER), PTHR11475:SF9 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	tbc (tre-2 bub2 cdc16) domain family member (tbc-16)	0		P:GO:0032313; C:GO:0005622; F:GO:0005097		-
	-	0				IPR001778
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis briggsae	patched family protein	10	P:GO:0040025; F:GO:0008158; P:GO:0040018; P:GO:0018996; P:GO:0040002; P:GO:0000003; P:GO:0008340; P:GO:0040011; C:GO:0016021; P:GO:0019915	-		IPR000731; IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER), SignalP (SIGNALP), SSF82866 (SUPERFAMILY)
Ostertagia ostertagi	scaffold attachment factor b	2	F:GO:0003676; F:GO:0000166	-		-
Ostertagia ostertagi	scaffold attachment factor b	1	F:GO:0005488	-		IPR000504; IPR003034; IPR012677; G3DSA:1.10.720.30 (GENE3D), PTHR15683 (PANTHER), PTHR15683:SF2 (PANTHER), SSF54928 (SUPERFAMILY), SSF68906 (SUPERFAMILY)
Loa loa	fkbp-rapamycin associated	3	F:GO:0016773; F:GO:0016301; F:GO:0000166	-	EC:2.7.1.0	IPR000403; IPR011009; PTHR11139 (PANTHER), PTHR11139:SF9 (PANTHER)
Caenorhabditis briggsae	leishmanolysin-like peptidase	19	F:GO:0008270; P:GO:0008354; P:GO:0051225; P:GO:0007420; P:GO:0051298; P:GO:0007076; P:GO:0007052; P:GO:0007100; C:GO:0031252; P:GO:0051301; F:GO:0004222; P:GO:0006508; P:GO:0007155; P:GO:0007444; P:GO:0045842; P:GO:0008406; C:GO:0005737; P:GO:0006338; C:GO:0016020	-	EC:3.4.24.0	IPR001577; G3DSA:3.90.132.10 (GENE3D), SSF55486 (SUPERFAMILY)
	-	0				-

Acyrthosiphon pisum	isoform b	23	P:GO:0007411; P:GO:0031987; P:GO:0001964; P:GO:0007398; P:GO:0016360; P:GO:0007498; P:GO:0045747; P:GO:0042048; P:GO:0008356; P:GO:0045314; F:GO:0004842; P:GO:0030707; C:GO:0044425; P:GO:0007422; P:GO:0008104; P:GO:0007413; P:GO:0002121; P:GO:0030718; C:GO:0048471; C:GO:0005886; F:GO:0005488; P:GO:0007476; P:GO:0048854	-	EC:6.3.2.19	IPR006573
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis sp. PS1010	nicastrin	13	P:GO:0040010; P:GO:0018991; P:GO:0044260; P:GO:0048598; P:GO:0060581; F:GO:0016874; P:GO:0007219; P:GO:0019538; P:GO:0010467; P:GO:0009792; C:GO:0005737; P:GO:0060465; C:GO:0005886	-		-
Caenorhabditis elegans	coiled-coil domain-containing protein 85c-a	1	F:GO:0005515	-		IPR019359; PTHR13546 (PANTHER), PTHR13546:SF1 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	5	P:GO:0002119; P:GO:0018991; P:GO:0040010; P:GO:0006898; P:GO:0008406	-		-
	-	0				IPR008162
Loa loa	wdr9 form a	5	F:GO:0030528; P:GO:0006357; F:GO:0016740; F:GO:0005515; C:GO:0005634	-		IPR001680; IPR008162; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR16266 (PANTHER)

Loa loa	wdr9 form a	5	F:GO:0030528; P:GO:0006357; F:GO:0016740; F:GO:0005515; C:GO:0005634	-		IPR001680; IPR008162; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR16266 (PANTHER)
Loa loa	wdr9 form a	5	F:GO:0030528; P:GO:0006357; F:GO:0016740; F:GO:0005515; C:GO:0005634	-		IPR001680; IPR008162; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR16266 (PANTHER)
Loa loa	wdr9 form a	5	F:GO:0030528; P:GO:0006357; F:GO:0016740; F:GO:0005515; C:GO:0005634	-		IPR001680; IPR008162; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR16266 (PANTHER)
Caenorhabditis briggsae	fungal metazoan origin like protein variant 2	2	C:GO:0016020; C:GO:0005739	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	s-adenosylmethionine mitochondrial carrier protein	3	P:GO:0006810; C:GO:0016020; C:GO:0005739	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF45 (PANTHER)
	-	0				IPR000990; SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-inx- protein	6	P:GO:0040035; C:GO:0005921; P:GO:0040010; P:GO:0040011; P:GO:0019915; P:GO:0002009	-		IPR000990
Caenorhabditis elegans	i in family member (inx-17)	2	C:GO:0005921; P:GO:0000003	-		IPR000990
Brugia malayi	c6orf174 protein	0		F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150; C:GO:0005575		-
	-	0				-
Caenorhabditis elegans	histone h2a	14	P:GO:0006952; P:GO:0040010; C:GO:0000786; P:GO:0006281; P:GO:0018991; P:GO:0045449; P:GO:0040035; F:GO:0043565; P:GO:0002119; P:GO:0040011; P:GO:0006334; P:GO:0006997; P:GO:0009792; C:GO:0005634	-		IPR002119; IPR007125; IPR009072

Caenorhabditis elegans	histone h2a	14	P:GO:0006952; P:GO:0040010; C:GO:0000786; P:GO:0006281; P:GO:0018991; P:GO:0045449; P:GO:0040035; F:GO:0043565; P:GO:0002119; P:GO:0040011; P:GO:0006334; P:GO:0006997; P:GO:0009792; C:GO:0005634	-		IPR002119; IPR007125; IPR009072; SignalP (SIGNALP)
Pediculus humanus corporis	sex-determining protein fem-1	1	F:GO:0005515	-		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF131 (PANTHER)
Caenorhabditis briggsae	brca2 and cdkn1a interacting protein	3	P:GO:0007275; P:GO:0000003; P:GO:0009987	-		PTHR13261 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	topoisomerase iii beta	4	P:GO:0006268; F:GO:0003917; C:GO:0005694; P:GO:0006265	-	EC:5.99.1.2	IPR000380; IPR006171; G3DSA:3.40.50.140 (GENE3D)
Caenorhabditis elegans	d- topoisomerase 3-beta-1	7	P:GO:0006268; F:GO:0003917; F:GO:0005515; C:GO:0005694; P:GO:0006265; C:GO:0005634; F:GO:0000166	-	EC:5.99.1.2	IPR000380; IPR006171; G3DSA:3.40.50.140 (GENE3D)
Pediculus humanus corporis	wolf-hirschhorn syndrome candidate 1	4	F:GO:0005488; P:GO:0051789; P:GO:0018023; C:GO:0005634	-		-

Caenorhabditis elegans	briggsae cbr-nmy-2 protein	25	P:GO:0046664; F:GO:0017111; P:GO:0045200; P:GO:0035159; P:GO:0031036; C:GO:0016460; P:GO:0007443; P:GO:0007395; P:GO:0045214; P:GO:0035017; P:GO:0006936; P:GO:0007297; P:GO:0046663; F:GO:0032027; P:GO:0008258; P:GO:0051259; P:GO:0016203; C:GO:0032154; C:GO:0045179; P:GO:0045184; P:GO:0035317; C:GO:0030018; C:GO:0005886; P:GO:0007435; P:GO:0000910	-	EC:3.6.1.15	IPR004009; PTHR13140 (PANTHER), PTHR13140:SF23 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
Brugia malayi	elegans protein confirmed by transcript evidence	0		F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150		IPR006634; SignalP (SIGNALP)
Caenorhabditis briggsae	-dh-ubiquinone oxidoreductase fe-s protein 7	13	F:GO:0048038; P:GO:0006810; P:GO:0022900; F:GO:0008137; C:GO:0005739; F:GO:0046872; P:GO:0040035; F:GO:0051539; P:GO:0010171; P:GO:0002119; C:GO:0070469; P:GO:0009792; P:GO:0040018	-	EC:1.6.5.3	IPR006137; IPR006138; IPR014406; G3DSA:3.40.50.700 (GENE3D), SignalP (SIGNALP), SSF56770 (SUPERFAMILY)
Caenorhabditis elegans	malate l-lactate dehydroge-se family protein	2	F:GO:0016491; P:GO:0055114	-		IPR003767; G3DSA:3.30.1370.60 (GENE3D)
Caenorhabditis briggsae	Hypothetical protein CBG07069 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	dy-ctin 5	2	P:GO:0035046; C:GO:0005869	-		IPR011004; G3DSA:2.160.10.10 (GENE3D), PTHR13061 (PANTHER)

Pseudonaja textilis	tissue factor pathway inhibitor 2-like	0		F:GO:0004222; P:GO:0018298; P:GO:0006810; F:GO:0008270; C:GO:0005792; C:GO:0005578; F:GO:0008237; C:GO:0031012; P:GO:0010951; C:GO:0005576; F:GO:0030414; F:GO:0008233; P:GO:0009405; F:GO:0004867; P:GO:0051604; F:GO:0005488; P:GO:0010466		-
Caenorhabditis elegans	family with sequence similarity member isoform cra_a	0		P:GO:0008150; F:GO:0005515; C:GO:0005575		IPR007518
Caenorhabditis elegans	calcium-activated potassium channel	4	F:GO:0015269; P:GO:0006813; C:GO:0016021; F:GO:0005516	-		IPR004178; IPR015449; G3DSA:1.10.287.70 (GENE3D), PTHR10153:SF6 (PANTHER)
Nasonia vitripennis	acyl-coa-binding protein acbp	1	F:GO:0005488	-		IPR000582; IPR014352
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	U12964_12Hypothetical protein F26F4.9a [Caenorhabditis elegans]	0				IPR009703
Brugia malayi	cpsf a subunit region family protein	1	F:GO:0005515	-		IPR004871; PTHR10644 (PANTHER), PTHR10644:SF3 (PANTHER)
Caenorhabditis elegans	tetratricopeptide repeat domain 36	0		F:GO:0005488		IPR001440; IPR011990; IPR013026; IPR019734; PTHR21405 (PANTHER), SSF48452 (SUPERFAMILY)
Streptomyces flavogriseus ATCC 33331	glycosyl transferase family 51	0		C:GO:0009274; P:GO:0008360; F:GO:0008658; P:GO:0009273; F:GO:0016740; P:GO:0007047; F:GO:0003824; P:GO:0009252		-
	-	0				-
	-	0				-
	-	0				-
Frog virus 3	hypothetical protein FV3gorf43R [Frog virus 3]	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Teladorsagia circumcincta	galectin	3	F:GO:0005515; F:GO:0005529; P:GO:0000003	-		IPR001079; IPR008985; IPR013320; PTHR11346:SF29 (PANTHER)
	-	0				-
	-	0				-

Caenorhabditis elegans	xanthine dehydroge-se	19	C:GO:0005829; P:GO:0008340; P:GO:0007595; F:GO:0051537; C:GO:0005777; P:GO:0055114; F:GO:0009055; P:GO:0010044; F:GO:0004855; F:GO:0004854; F:GO:0043546; P:GO:0030856; F:GO:0042803; C:GO:0005576; F:GO:0050660; P:GO:0009115; F:GO:0005506; P:GO:0045453; F:GO:0030151	-	EC:1.17.3.2; EC:1.17.1.4	-
Caenorhabditis elegans	inositol polyphosphate ki-se family protein	0		F:GO:0016301; F:GO:0008440		IPR005522; PTHR12400:SF21 (PANTHER), SSF56104 (SUPERFAMILY)
Caenorhabditis briggsae	exosome component 10	2	P:GO:0044237; F:GO:0003824	-		IPR002562; IPR012337; PTHR12124 (PANTHER), PTHR12124:SF2 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-npp-14 protein	0				IPR015943; PTHR23193 (PANTHER), PTHR23193:SF1 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	nuclear pore complex protein family member (npp-16)	1	P:GO:0000003	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	coiled-coil and c2 domain containing 1a	1	F:GO:0005515	-		-
Brugia malayi	leucyl tr- synthetase family member (lrs-2)	0		F:GO:0016874; P:GO:0006418; F:GO:0000166; F:GO:0004823; C:GO:0005737; P:GO:0006412; F:GO:0005524; P:GO:0006429; F:GO:0004812		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-dys-1 protein	7	P:GO:0007271; F:GO:0005515; P:GO:0040017; C:GO:0016010; F:GO:0005277; P:GO:0015870; P:GO:0046716	-		-

Caenorhabditis briggsae	udp-glucose dehydroge-se	16	P:GO:0007427; F:GO:0003979; P:GO:0007224; P:GO:0016055; P:GO:0016319; P:GO:0055114; P:GO:0007507; F:GO:0042802; P:GO:0042048; P:GO:0015014; P:GO:0008543; F:GO:0051287; P:GO:0002121; P:GO:0007509; P:GO:0007428; P:GO:0030206	-	EC:1.1.1.22	IPR008927; IPR014026; IPR014027; IPR014028; IPR016040; IPR021157; PTHR11374:SF3 (PANTHER)
Caenorhabditis elegans	cytochrome p450	8	P:GO:0040018; F:GO:0004497; F:GO:0005506; P:GO:0040010; P:GO:0000003; P:GO:0008340; F:GO:0016705; P:GO:0040011	-		IPR001128; IPR002401; IPR017972; PTHR19383:SF176 (PANTHER)
Caenorhabditis elegans	inositol monophosphatase domain containing 1	9	C:GO:0016021; P:GO:0009791; P:GO:0030204; P:GO:0002063; P:GO:0001958; P:GO:0042733; F:GO:0004437; P:GO:0008299; F:GO:0008254	-	EC:3.1.3.6	IPR000760; G3DSA:3.30.540.10 (GENE3D), PTHR20854:SF8 (PANTHER), SSF56655 (SUPERFAMILY)
Homo sapiens	-dh dehydroge-se subunit 3	8	P:GO:0009642; P:GO:0006979; P:GO:0006810; P:GO:0009725; F:GO:0008137; C:GO:0005747; C:GO:0016021; P:GO:0006120	-	EC:1.6.5.3	-
Caenorhabditis elegans	alpha- -mannosylglycoprotein 6-beta-n-acetylglucosaminyltransferase a	3	P:GO:0006487; C:GO:0044464; F:GO:0008375	-		PTHR15075 (PANTHER)
Caenorhabditis elegans	alpha- -mannosylglycoprotein 6-beta-n-acetylglucosaminyltransferase a	3	P:GO:0006487; C:GO:0044464; F:GO:0008375	-		PTHR15075 (PANTHER)
	-	0				-
Caenorhabditis briggsae	temporarily assigned gene -me family member (tag-308)	0				-

Caenorhabditis elegans	vacuolar atp synthase subunit h	17	F:GO:0046961; F:GO:0005515; P:GO:0040007; P:GO:0015991; P:GO:0040011; P:GO:0040002; P:GO:0007035; P:GO:0018996; C:GO:0005829; P:GO:0050690; P:GO:0009792; P:GO:0015986; P:GO:0006897; P:GO:0002119; C:GO:0000221; C:GO:0005886; F:GO:0030234	-	EC:3.6.3.14	IPR004908; IPR011987; IPR016024
Caenorhabditis elegans	vacuolar atp synthase subunit h	18	F:GO:0046961; F:GO:0005515; P:GO:0040007; P:GO:0015991; P:GO:0040011; P:GO:0040002; P:GO:0007035; P:GO:0018996; C:GO:0005829; P:GO:0050690; P:GO:0009792; P:GO:0015986; P:GO:0006897; P:GO:0002119; C:GO:0000221; C:GO:0005886; P:GO:0044419; F:GO:0030234	-	EC:3.6.3.14	IPR004908; IPR011987; IPR016024
Caenorhabditis elegans	p-type had subfamily ic	5	P:GO:0006811; F:GO:0016820; F:GO:0000166; P:GO:0008152; C:GO:0016020	-	EC:3.6.3.0	IPR001757; G3DSA:3.40.1110.10 (GENE3D), PTHR11939:SF63 (PANTHER), SSF81660 (SUPERFAMILY)
	-	0				-
Haemonchus contortus	hc38	0				-
Caenorhabditis briggsae	protein tyrosine phosphatase family member (ptp-3)	8	P:GO:0007391; C:GO:0005912; C:GO:0005887; F:GO:0005001; F:GO:0005515; P:GO:0007399; P:GO:0006470; P:GO:0007185	-		IPR000242; IPR000387; IPR003961; IPR008957; IPR013783; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF48 (PANTHER), SignalP (SIGNALP), SSF52799 (SUPERFAMILY)
Caenorhabditis briggsae	protein tyrosine phosphatase family member (ptp-3)	5	F:GO:0004725; P:GO:0007391; C:GO:0005912; P:GO:0007399; P:GO:0006470	-	EC:3.1.3.48	IPR003961; IPR008957; IPR013783; PTHR10489 (PANTHER), SignalP (SIGNALP)
	-	0				-

Macaca mulatta	profilin 1	18	P:GO:0071363; F:GO:0005546; F:GO:0005102; C:GO:0015629; C:GO:0019717; C:GO:0005576; P:GO:0008064; C:GO:0005829; F:GO:0003779; F:GO:0070064; P:GO:0051054; P:GO:0001843; F:GO:0017048; P:GO:0050434; P:GO:0045944; P:GO:0051496; C:GO:0005634; C:GO:0045202	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	C:GO:0016021; C:GO:0009986; F:GO:0015171; P:GO:0055085	-		IPR002293; IPR004841; PTHR11785:SF76 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	riken cd- 2010309e21 gene	0		C:GO:0005739; F:GO:0003674; C:GO:0005737; P:GO:0008150		IPR008560
Caenorhabditis elegans	mitochondrial ribosomal protein s7	5	F:GO:0003735; F:GO:0003723; C:GO:0022627; P:GO:0006412; C:GO:0005739	-	EC:3.6.5.3	IPR000235; PTHR11205:SF12 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	mitochondrial ribosomal protein s7	5	F:GO:0003735; F:GO:0003723; C:GO:0022627; P:GO:0006412; C:GO:0005739	-	EC:3.6.5.3	IPR000235; PTHR11205:SF12 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	methyltransferase-like protein 4	0		F:GO:0003676; P:GO:0006139; F:GO:0008168; P:GO:0032259		IPR002052; IPR007757; PTHR14475 (PANTHER)
	-	0				-
Caenorhabditis briggsae	abc1 family protein	0		F:GO:0004672; F:GO:0005524; P:GO:0006468		IPR004147; IPR011009; PTHR10566 (PANTHER), PTHR10566:SF7 (PANTHER)
Caenorhabditis briggsae	abc1 family protein	0		F:GO:0004672; F:GO:0005524; P:GO:0006468		IPR004147; IPR011009; PTHR10566 (PANTHER), PTHR10566:SF7 (PANTHER)
Caenorhabditis briggsae	abc1 family protein	0		F:GO:0004672; F:GO:0005524; P:GO:0006468		IPR004147; IPR011009; PTHR10566 (PANTHER), PTHR10566:SF7 (PANTHER)

Pongo abelii	zyxin	13	F:GO:0008270; P:GO:0007267; C:GO:0005913; C:GO:0001725; P:GO:0007155; C:GO:0005925; F:GO:0005515; P:GO:0007165; P:GO:0044419; C:GO:0005737; P:GO:0050727; C:GO:0005634; C:GO:0005887	-		-
Caenorhabditis briggsae	briggsae cbr-asp-2 protein	4	P:GO:0008219; F:GO:0016787; F:GO:0005515; P:GO:0040011	-		IPR001461; IPR001969; IPR009007; IPR021109; PTHR13683:SF53 (PANTHER)
Caenorhabditis briggsae	proteasome subunit alpha type-1	17	P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0051437; P:GO:0040007; P:GO:0040011; P:GO:0051436; F:GO:0004298; P:GO:0002862; C:GO:0005737; P:GO:0018996; C:GO:0019773; F:GO:0001530; P:GO:0009792; P:GO:0002119; P:GO:0031145; C:GO:0005634	-	EC:3.4.25.0	IPR000426; IPR001353; G3DSA:3.60.20.10 (GENE3D), PTHR11599 (PANTHER), PTHR11599:SF12 (PANTHER), PS51475 (PROFILE), SSF56235 (SUPERFAMILY)
Angiostrongylus cantonensis	elegans protein confirmed by transcript evidence	3	F:GO:0005515; F:GO:0042302; C:GO:0016021	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	C:GO:0016021	-		-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F59G1.4 [Caenorhabditis elegans]	1	F:GO:0005488	-		-
Caenorhabditis elegans	hypothetical protein F59G1.4 [Caenorhabditis elegans]	1	F:GO:0005488	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	fan1_caeel ame: full=fanconi-associated nuclease 1 homolog	2	F:GO:0005515; P:GO:0006281	-		-
Caenorhabditis briggsae	nuclear transport factor 2 (ntf-2)	0		C:GO:0005622; P:GO:0006810		-
Caenorhabditis elegans	briggsae cbr-lin-13 protein	0		F:GO:0003674; P:GO:0040027; F:GO:0008270; C:GO:0005622; C:GO:0005634		IPR015880; IPR017956

Caenorhabditis briggsae	cellular senescence inhibited gene protein	10	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0044260; F:GO:0005488; C:GO:0005622; P:GO:0040010; P:GO:0010467; P:GO:0008340; P:GO:0044238	-		IPR002143; PTHR23105 (PANTHER), PTHR23105:SF3 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-prp-4 protein	0		P:GO:0008380		-
Haemonchus contortus	cysteine protei-se	7	P:GO:0009792; P:GO:0002119; F:GO:0008233; F:GO:0005515; P:GO:0040011; P:GO:0040007; P:GO:0006898	-		IPR000169; IPR000668; IPR013128; IPR015643; G3DSA:3.90.70.10 (GENE3D), SignalP (SIGNALP), SSF54001 (SUPERFAMILY)
Caenorhabditis elegans	ccch-type zinc finger transcription factor family member (ccch-3)	0		F:GO:0003676; F:GO:0046872; F:GO:0008270		IPR000571; G3DSA:4.10.1000.10 (GENE3D), SSF90229 (SUPERFAMILY)
Harpegnathos saltator	histone -like	5	C:GO:0000786; F:GO:0003677; P:GO:0006334; F:GO:0005515; C:GO:0005634	-		IPR000164; IPR007125; IPR009072
Loa loa	protein argo-ute-2	1	F:GO:0003676	-		PTHR22891 (PANTHER)
	-	0				IPR018378
Pongo abelii	ribosomal protein l6	6	F:GO:0003677; F:GO:0003735; F:GO:0003723; C:GO:0022625; P:GO:0006355; P:GO:0006414	-		IPR000915; IPR014722
Caenorhabditis elegans	zinc zz type family protein	17	C:GO:0030054; F:GO:0005277; P:GO:0015870; P:GO:0007528; P:GO:0007527; P:GO:0001954; F:GO:0046872; C:GO:0030864; F:GO:0051015; P:GO:0007271; C:GO:0005624; C:GO:0031594; P:GO:0046716; P:GO:0040017; C:GO:0030426; C:GO:0016010; P:GO:0006936	-		IPR001202; IPR015153; G3DSA:2.20.70.10 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF57 (PANTHER), SSF47473 (SUPERFAMILY)
	-	0				-
Camponotus floridanus	d- methyltransferase	5	F:GO:0003886; P:GO:0044260; F:GO:0003676; P:GO:0010467; P:GO:0090304	-	EC:2.1.1.37	-

Caenorhabditis briggsae	briggsae cbr-cej-1 protein	3	P:GO:0009792; P:GO:0000281; F:GO:0008061	-		IPR002557; G3DSA:2.170.140.10 (GENE3D), PTHR23301 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-cej-1 protein	3	P:GO:0009792; P:GO:0000281; F:GO:0008061	-		IPR002557; G3DSA:2.170.140.10 (GENE3D), PTHR23301 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-cej-1 protein	3	P:GO:0009792; P:GO:0000281; F:GO:0008061	-		IPR002557; G3DSA:2.170.140.10 (GENE3D), PTHR23301 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG11055 [Caenorhabditis briggsae]	0				-
	-	0				-
						IPR003599; IPR007110; IPR010939; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF9 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis briggsae	glycine dehydroge-se	10	F:GO:0004375; F:GO:0030170; F:GO:0016594; F:GO:0009055; P:GO:0055114; F:GO:0016829; C:GO:0005960; C:GO:0005739; F:GO:0042803; P:GO:0019464	-	EC:1.4.4.2	IPR015421; IPR015424; IPR020581
Caenorhabditis briggsae	glycine dehydroge-se	10	F:GO:0004375; F:GO:0030170; F:GO:0016594; F:GO:0009055; P:GO:0055114; F:GO:0016829; C:GO:0005960; C:GO:0005739; F:GO:0042803; P:GO:0019464	-	EC:1.4.4.2	IPR015421; IPR015424; IPR020581
	-	0				-
Caenorhabditis elegans	probable e3 ubiquitin-protein ligase mycbp2	4	F:GO:0008270; F:GO:0005515; P:GO:0030071; C:GO:0005680	-		PTHR12846 (PANTHER), PTHR12846:SF2 (PANTHER)
Caenorhabditis elegans	mgc89486 protein	7	P:GO:0040010; P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0040011; P:GO:0006898; P:GO:0009792	-		-
Loa loa	patatin-like phospholipase domain containing 4	1	P:GO:0008152	-		IPR002641; IPR016035; PTHR12406 (PANTHER)
	-	0				-
Caenorhabditis elegans	t family of potassium channels family member (twk-39)	0				-
Loa loa	f-box only protein 11	6	C:GO:0005737; P:GO:0007605; P:GO:0006464; F:GO:0005515; F:GO:0016274; C:GO:0005634	-		IPR001810; IPR006626; IPR011050; IPR012334; IPR022364; G3DSA:1.20.1280.50 (GENE3D), PTHR22990 (PANTHER), PTHR22990:SF6 (PANTHER)

Loa loa	f-box only protein 11	6	C:GO:0005737; P:GO:0007605; P:GO:0006464; F:GO:0005515; F:GO:0016274; C:GO:0005634	-		IPR001810; IPR006626; IPR011050; IPR012334; IPR022364; G3DSA:1.20.1280.50 (GENE3D), PTHR22990 (PANTHER), PTHR22990:SF6 (PANTHER)
Caenorhabditis elegans	vesicle trafficking protein sec22b	6	C:GO:0000139; C:GO:0005789; C:GO:0005793; F:GO:0005515; C:GO:0016021; P:GO:0006888	-		IPR001388; IPR010908; IPR011012; G3DSA:1.20.5.110 (GENE3D), PTHR21136 (PANTHER), PTHR21136:SF4 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Callithrix jacchus	40s ribosomal protein s27	8	P:GO:0008283; F:GO:0003677; F:GO:0003735; F:GO:0005515; C:GO:0022627; C:GO:0005634; F:GO:0008270; P:GO:0006414	-		IPR000592; IPR011332; G3DSA:2.20.25.100 (GENE3D)
Culex quinquefasciatus	e3 ubiquitin-protein ligase trim33 isoform 1	1	F:GO:0005488	-		IPR001841; IPR013083; PTHR13712 (PANTHER)
Caenorhabditis briggsae	retinol dehydroge-se 14	3	P:GO:0008152; C:GO:0044444; C:GO:0043231	-		IPR002198; IPR016040; PTHR19410:SF98 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis briggsae	retinol dehydroge-se 14	3	P:GO:0008152; C:GO:0044444; C:GO:0043231	-		IPR002198; IPR002347; IPR016040; PTHR19410:SF98 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0000003; P:GO:0040010; P:GO:0006898; P:GO:0002119; P:GO:0040007		IPR004296; PTHR21592 (PANTHER)
Caenorhabditis briggsae	denn madd domain containing 4c	0		F:GO:0003674; P:GO:0008150		PTHR12296 (PANTHER), PTHR12296:SF3 (PANTHER), PS51498 (PROFILE)
	-	0				-
	-	0				-
Teladorsagia circumcincta	briggsae cbr-flp-32 protein	0				-
Brugia malayi	innexin family protein	0		P:GO:0000003; C:GO:0016021; P:GO:0040011; P:GO:0040035; P:GO:0040010; P:GO:0002009; C:GO:0005921		IPR000990
Brugia malayi	innexin family protein	0		P:GO:0000003; C:GO:0016021; P:GO:0040011; P:GO:0040035; P:GO:0040010; P:GO:0002009; C:GO:0005921		IPR000990
	-	0				-

	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	lps glycosyltransferase family protein	5	P:GO:0040035; F:GO:0005515; P:GO:0040010; P:GO:0040011; P:GO:0002009	-		IPR002654; PTHR10730 (PANTHER)
Caenorhabditis elegans	mitochondrial carrier protein	6	F:GO:0005488; C:GO:0005743; F:GO:0022857; P:GO:0055085; P:GO:0006839; C:GO:0016021	-		IPR001993; IPR002067; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF38 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0000003; F:GO:0005488; C:GO:0016021; P:GO:0009792		IPR011990; IPR013026; PTHR16056 (PANTHER), SSF48452 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	uncoordi-ted family member (unc-115)	3	P:GO:0007010; F:GO:0003779; F:GO:0008270	-		IPR001781; PTHR18973 (PANTHER), PTHR18973:SF90 (PANTHER), SSF57716 (SUPERFAMILY)
Nippostrongylus brasiliensis	60s acidic ribosomal protein p1	5	P:GO:0009792; C:GO:0005840; F:GO:0003735; F:GO:0005515; P:GO:0006414	-		IPR001813; IPR001859; PTHR21141 (PANTHER), PTHR21141:SF6 (PANTHER)
	-	0				-
Caenorhabditis briggsae	isoform b	4	F:GO:0009982; F:GO:0003723; P:GO:0001522; P:GO:0008033	-	EC:5.4.99.12	IPR001406; IPR020095; IPR020097; IPR020103
Caenorhabditis elegans	adducin family member (add-2)	1	F:GO:0046872	-		IPR001303; PTHR10672 (PANTHER), PTHR10672:SF3 (PANTHER)
Caenorhabditis elegans	adducin family member (add-2)	1	F:GO:0046872	-		IPR001303; PTHR10672 (PANTHER), PTHR10672:SF3 (PANTHER)
Caenorhabditis elegans	hypothetical protein F52C12.2 [Caenorhabditis elegans]	0		F:GO:0004672; F:GO:0005524; F:GO:0003824; F:GO:0004713; P:GO:0006468		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	d- polymerase family exonuclease domain containing protein	5	P:GO:0040035; P:GO:0009792; P:GO:0006997; P:GO:0040011; P:GO:0002009	-		-
	-	0				-

Caenorhabditis briggsae	briggsae cbr-atn-1 protein	13	P:GO:0040010; C:GO:0030018; P:GO:0007016; F:GO:0005509; P:GO:0007629; C:GO:0055120; P:GO:0051017; P:GO:0031532; F:GO:0051015; F:GO:0042802; C:GO:0005925; P:GO:0007067; P:GO:0009792	-		IPR011992; IPR014837; IPR018249; PTHR11915 (PANTHER), PTHR11915:SF47 (PANTHER), SSF47473 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	brca1 interacting protein c-termi-l helicase 1	8	F:GO:0003676; P:GO:0071295; F:GO:0008026; P:GO:0008285; F:GO:0000166; P:GO:0006139; C:GO:0005737; C:GO:0005634	-		IPR006555; PTHR11472 (PANTHER), PTHR11472:SF6 (PANTHER)
Brugia malayi	13s condensin xcap-d2 partial	7	P:GO:0006996; F:GO:0005488; C:GO:0043234; P:GO:0007049; C:GO:0044446; C:GO:0000793; C:GO:0005634	-		IPR011989; IPR016024
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-lsm-1 protein	0		F:GO:0003676; C:GO:0030529		-
	-	0				-
Loa loa	transcriptio-l regulating factor 1-like	0		P:GO:0007283; C:GO:0005634; F:GO:0003677; F:GO:0003676; F:GO:0008270; F:GO:0003674; P:GO:0007275; P:GO:0030154; C:GO:0005622; F:GO:0046872; P:GO:0006350; P:GO:0008150; P:GO:0045449		IPR007087; IPR013087; IPR015880; PTHR23224 (PANTHER), PTHR23224:SF459 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis elegans	cyclin l2	7	P:GO:0009792; P:GO:0002119; P:GO:0000003; P:GO:0008340; P:GO:0040011; P:GO:0040007; C:GO:0005634	-		IPR004367; IPR006670; IPR011028; IPR013763; IPR015429; IPR015431
	-	0				-
	-	0				-

Caenorhabditis elegans	ap-2 complex subunit alpha-2	12	C:GO:0005829; F:GO:0008565; P:GO:0040010; F:GO:0008022; P:GO:0000003; F:GO:0008289; P:GO:0050690; C:GO:0030122; P:GO:0040011; P:GO:0006898; P:GO:0006886; P:GO:0009792	-		IPR002553; IPR011989; PTHR22780 (PANTHER), PTHR22780:SF4 (PANTHER)
Caenorhabditis elegans	ap-2 complex subunit alpha-2	12	C:GO:0005829; F:GO:0008565; P:GO:0040010; F:GO:0008022; P:GO:0000003; F:GO:0008289; P:GO:0050690; C:GO:0030122; P:GO:0040011; P:GO:0006898; P:GO:0006886; P:GO:0009792	-		IPR002553; IPR011989; PTHR22780 (PANTHER), PTHR22780:SF4 (PANTHER)
Caenorhabditis briggsae	mpv17 protein	2	C:GO:0016020; C:GO:0005739	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	marvel domain containing 2	0		C:GO:0008023; F:GO:0016944; C:GO:0016021; C:GO:0030054; C:GO:0016020; C:GO:0005923; P:GO:0006368		-
	-	0				-
	-	0				-
Loa loa	ph domain containing protein	4	C:GO:0005737; F:GO:0005515; C:GO:0043229; P:GO:0009987	-		PTHR21538 (PANTHER), PTHR21538:SF10 (PANTHER)
Loa loa	ph domain containing protein	4	C:GO:0005737; F:GO:0005515; C:GO:0043229; P:GO:0009987	-		PTHR21538 (PANTHER), PTHR21538:SF10 (PANTHER)
Caenorhabditis elegans	transcription termi-tion r- polymerase ii	12	F:GO:0008094; F:GO:0005515; C:GO:0008023; F:GO:0003717; P:GO:0030878; P:GO:0060023; C:GO:0005737; P:GO:0060022; F:GO:0003677; P:GO:0009887; F:GO:0003700; P:GO:0045893	-		IPR000330; PTHR10799 (PANTHER), PTHR10799:SF63 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-

Callithrix jacchus	ribophorin isoform cra_a	9	C:GO:0008250; C:GO:0019718; P:GO:0018279; C:GO:0016021; C:GO:0042470; P:GO:0015833; C:GO:0030867; F:GO:0005515; F:GO:0004579	-	EC:2.4.1.119	IPR007676
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0000003; P:GO:0040035; P:GO:0040010; P:GO:0009792; P:GO:0040007; P:GO:0019915; P:GO:0002009		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	zinc finger protein	17	F:GO:0030528; F:GO:0005515; P:GO:0006357; P:GO:0040010; P:GO:0006898; C:GO:0071011; P:GO:0040011; F:GO:0046872; P:GO:0000398; P:GO:0009792; P:GO:0002009; F:GO:0003677; P:GO:0002119; P:GO:0002121; P:GO:0010171; C:GO:0043232; P:GO:0040035	-		PTHR11208 (PANTHER), PTHR11208:SF5 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	C:GO:0031012	-		-
Brugia malayi	ppib protein	7	P:GO:0006457; C:GO:0005788; F:GO:0005515; C:GO:0042470; P:GO:0051169; F:GO:0042277; F:GO:0003755	-	EC:5.2.1.8	IPR002130; IPR015891; IPR020892; PTHR11071 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-hmt-1 protein	0		F:GO:0005524; F:GO:0016887; F:GO:0000166; C:GO:0016021; F:GO:0042626; F:GO:0017111; P:GO:0055085; P:GO:0006810		-
	-	0				-
	-	0				-

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0020037; F:GO:0005506; C:GO:0016021; F:GO:0009055; P:GO:0000003; P:GO:0040018; P:GO:0055114; F:GO:0016491; C:GO:0005575; P:GO:0008340; P:GO:0040011; P:GO:0040010; F:GO:0046872; F:GO:0004497		IPR001128; PTHR19383:SF176 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	2	P:GO:0040010; P:GO:0040011	-		IPR004888; PTHR10412 (PANTHER)
Caenorhabditis briggsae	-dh oxidase	4	P:GO:0008152; F:GO:0003824; P:GO:0043581; P:GO:0051301	-		IPR013785; PTHR22893 (PANTHER), PTHR22893:SF6 (PANTHER), SSF51395 (SUPERFAMILY)
Caenorhabditis briggsae	-dh oxidase	3	P:GO:0008152; F:GO:0003824; P:GO:0043581	-		IPR001155; IPR013785; PTHR22893 (PANTHER), PTHR22893:SF6 (PANTHER), SSF51395 (SUPERFAMILY)
Caenorhabditis elegans	kinesin-like protein family member (klp-12)	0		F:GO:0005524; P:GO:0009792; P:GO:0007018; P:GO:0007067; F:GO:0005515		-
Drosophila grimshawi	cug-bp- and etr-3-like factor 1	2	F:GO:0003676; F:GO:0000166	-		IPR015903; PTHR10432 (PANTHER)
Homo sapiens	cold shock domain containing r--binding	6	C:GO:0005737; F:GO:0003677; F:GO:0003723; F:GO:0005515; P:GO:0008584; P:GO:0006355	-		PTHR12913 (PANTHER)
Brugia malayi	dy-ctin 4	0		P:GO:0035046		-
	-	0				IPR000436; IPR016060; SignalP (SIGNALP)
	-	0				IPR000436; IPR016060; SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				IPR000436; IPR016060; SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				IPR000436; IPR016060; SignalP (SIGNALP)
	-	0				IPR000436; IPR016060; SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG16936 [Caenorhabditis briggsae]	0				IPR000436; IPR016060; SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-unc-14 protein	0				IPR004012
Caenorhabditis briggsae	cleavage and polyadenylation specific factor 1	4	P:GO:0006378; C:GO:0005847; F:GO:0003676; P:GO:0006379	-		SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-pqn-55 protein	0		F:GO:0008270		-

Caenorhabditis elegans	discoidin domain receptor member 2	13	P:GO:0040010; F:GO:0004674; C:GO:0016021; F:GO:0004872; P:GO:0007169; F:GO:0004713; F:GO:0005524; P:GO:0007155; F:GO:0005518; P:GO:0007165; C:GO:0016324; P:GO:0008284; P:GO:0006468	-	EC:2.7.11.0; EC:2.7.10.0	IPR000719; IPR001245; IPR008266; IPR011009; IPR020685; IPR020742; G3DSA:1.10.510.10 (GENE3D)
	-	0				-
Caenorhabditis briggsae	dead (asp-glu-ala-asp) box polypeptide 55	7	P:GO:0009987; P:GO:0040010; F:GO:0003676; P:GO:0000003; P:GO:0002119; F:GO:0000166; F:GO:0004386	-		IPR000629; IPR001650; IPR011545; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF26 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	microfibrillar-associated protein 1	17	P:GO:0016246; F:GO:0005515; P:GO:0040010; P:GO:0006898; C:GO:0071011; P:GO:0010389; P:GO:0018996; C:GO:0071013; P:GO:0000398; P:GO:0009792; C:GO:0005578; F:GO:0003711; C:GO:0043234; P:GO:0002119; P:GO:0032968; P:GO:0001703; P:GO:0040035	-		SignalP (SIGNALP)
Caenorhabditis sp. PS1010	eprs protein	5	C:GO:0005829; F:GO:0004827; F:GO:0005515; P:GO:0006418; F:GO:0004818	-	EC:6.1.1.15; EC:6.1.1.17	IPR000738; IPR009068
	-	0				-
Caenorhabditis elegans	kinesin-like protein family member (klp-4)	6	C:GO:0000235; P:GO:0007018; F:GO:0005515; F:GO:0005524; P:GO:0051294; F:GO:0003777	-		IPR022140; PTHR16012 (PANTHER), PTHR16012:SF65 (PANTHER)
Caenorhabditis elegans	mpp10 protein	6	P:GO:0040035; P:GO:0002119; P:GO:0040010; P:GO:0006364; P:GO:0006898; C:GO:0030529	-		-

Oscheius sp. (strain CEW1)	briggsae cbr-vit-5 protein	4	P:GO:0009792; P:GO:0008340; P:GO:0040010; F:GO:0005515	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Loa loa	briggsae cbr-ekl-1 protein	0		P:GO:0000003; P:GO:0016246; P:GO:0009792		-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	4	P:GO:0040010; P:GO:0009792; P:GO:0000003; P:GO:0040011	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	3	C:GO:0016021; P:GO:0008340; F:GO:0008378	-		PTHR23033 (PANTHER), PTHR23033:SF1 (PANTHER)
Brugia malayi	hypothetical protein Bm1_15295 [Brugia malayi]	0				-
Caenorhabditis briggsae	oxidoreductase htatip2 isoform b	8	P:GO:0034641; F:GO:0016491; P:GO:0009058; C:GO:0044424; F:GO:0050662; P:GO:0044238; P:GO:0050794; P:GO:0032502	-		IPR016040; SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		C:GO:0005739; C:GO:0016021; C:GO:0016020		IPR009688; PTHR21377 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	tetraspanin family protein	1	C:GO:0016021	-		IPR018499; PTHR19282 (PANTHER), PTHR19282:SF54 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis briggsae	Hypothetical protein CBG09061 [Caenorhabditis briggsae]	0				IPR016021
Brugia malayi	d- topoisomerase 2-beta-like	18	P:GO:0001764; F:GO:0005080; C:GO:0005829; P:GO:0030900; C:GO:0005730; P:GO:0006355; F:GO:0008022; C:GO:0070603; F:GO:0005524; P:GO:0007409; F:GO:0003700; F:GO:0003918; C:GO:0000792; F:GO:0046982; C:GO:0005654; P:GO:0006265; F:GO:0042826; F:GO:0003682	-	EC:5.99.1.3	IPR001154; IPR001241; IPR013759; IPR013760; PTHR10169 (PANTHER), PTHR10169:SF2 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; P:GO:0007186		IPR019427; G3DSA:1.20.1070.10 (GENE3D), PTHR22751 (PANTHER), PTHR22751:SF12 (PANTHER), SignalP (SIGNALP)

Caenorhabditis elegans	domain containing protein	3	C:GO:0005622; P:GO:0007165; F:GO:0016787	-		-
Caenorhabditis elegans	hypothetical protein F26F4.2 [Caenorhabditis elegans]	0		F:GO:0005515		-
	-	0				IPR000242; G3DSA:3.90.190.10 (GENE3D)
Brugia malayi	ser thr protein phosphatase family protein	1	F:GO:0016787	-		IPR004843; IPR006186; G3DSA:3.60.21.10 (GENE3D), SSF56300 (SUPERFAMILY)
Loa loa	kiaa1433 protein	1	F:GO:0005515	-		IPR019131; PTHR23166 (PANTHER), PTHR23166:SF6 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Loa loa	protein-tyrosine phosphatase containing protein	2	F:GO:0016791; P:GO:0000003	-	EC:3.1.3.0	IPR000242; IPR000387; IPR016130; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
Loa loa	protein-tyrosine phosphatase containing protein	2	F:GO:0016791; P:GO:0000003	-	EC:3.1.3.0	IPR000242; IPR000387; IPR016130; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Angiostrongylus cantonensis	elegans protein confirmed by transcript evidence	0				-
Angiostrongylus cantonensis	elegans protein confirmed by transcript evidence	0				-
Loa loa	sema domain containing protein	0		F:GO:0004872; P:GO:0007275; C:GO:0016020; C:GO:0005576		IPR001627; IPR015943; PS51257 (PROFILE), SignalP (SIGNALP)
	-	0				-
Haemonchus contortus	phosphoenolpyruvate carboxyki-se	8	P:GO:0006107; C:GO:0005625; C:GO:0005739; F:GO:0046872; P:GO:0051384; P:GO:0006094; F:GO:0004613; F:GO:0005525	-	EC:4.1.1.32	IPR008209; IPR013035; SSF53795 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	4	P:GO:0009792; P:GO:0002119; P:GO:0040010; P:GO:0006898	-		SignalP (SIGNALP)
	-	0				-
Dictyocaulus viviparus	troponin fast skeletal	1	F:GO:0005509	-		IPR002048; IPR011992; IPR018247; IPR018248; IPR018249; PTHR23050 (PANTHER), PTHR23050:SF10 (PANTHER), SSF47473 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	briggsae cbr-flp-33 protein	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	odulin family member (tmd-2)	2	C:GO:0005856; F:GO:0005523	-		IPR004934; PTHR10901:SF4 (PANTHER)
Brugia malayi	hypothetical protein Bm1_08935 [Brugia malayi]	0				-

Caenorhabditis elegans	zinc c2h2 type family protein	16	P:GO:0007427; P:GO:0007390; P:GO:0007417; P:GO:0016204; F:GO:0008270; F:GO:0003676; P:GO:0042440; P:GO:0007525; F:GO:0004757; P:GO:0055114; P:GO:0006729; P:GO:0045449; P:GO:0006911; P:GO:0007398; C:GO:0005634; F:GO:0003702	-	EC:1.1.1.153	IPR007087; IPR013087; IPR015880; PTHR10042 (PANTHER), PTHR10042:SF2 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis elegans	zinc c2h2 type family protein	19	P:GO:0021612; F:GO:0030528; P:GO:0030278; F:GO:0008270; P:GO:0032868; P:GO:0007611; P:GO:0048168; P:GO:0021660; P:GO:0008045; F:GO:0031625; P:GO:0014037; P:GO:0035284; F:GO:0003677; P:GO:0021666; P:GO:0007622; F:GO:0003700; P:GO:0045944; P:GO:0042552; C:GO:0005634	-		IPR007087; IPR013087; IPR015880; PTHR10042 (PANTHER), PTHR10042:SF2 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis elegans	yr51_caeel ame: full=uncharacterized protein	5	P:GO:0010171; P:GO:0002119; P:GO:0018996; P:GO:0040010; P:GO:0008152	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR001534
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR001534
Loa loa	hypothetical protein LOAG_00601 [Loa loa]	0				PTHR16206 (PANTHER)
Loa loa	hypothetical protein LOAG_00601 [Loa loa]	0				PTHR16206 (PANTHER)
Brugia malayi	small optic lobes homolog	5	F:GO:0003676; C:GO:0005622; P:GO:0006508; F:GO:0004198; F:GO:0008270	-		-
Brugia malayi	formin binding protein 11-related protein	6	P:GO:0009792; P:GO:0002119; P:GO:0018991; F:GO:0005515; P:GO:0040010; P:GO:0006898	-		IPR002713; PTHR11864 (PANTHER)

Caenorhabditis elegans	-dh dehydroge-se iron-sulfur protein mitochondrial precursor	4	F:GO:0003723; F:GO:0008137; P:GO:0055114; C:GO:0005747	-	EC:1.6.5.3	IPR001268; IPR010218; IPR020396; PTHR10884 (PANTHER), PTHR10884:SF5 (PANTHER), SSF143243 (SUPERFAMILY)
Loa loa	fragile site-associated protein	0		C:GO:0016021; C:GO:0016020		IPR018863
Caenorhabditis elegans	methionyl aminopeptidase 2	16	F:GO:0003743; P:GO:0007276; P:GO:0040010; P:GO:0016055; P:GO:0031365; F:GO:0046872; P:GO:0018206; F:GO:0004177; P:GO:0006508; F:GO:0005515; F:GO:0008235; P:GO:0006898; P:GO:0016485; P:GO:0009792; P:GO:0008406; C:GO:0005737	-	EC:3.4.11.0	-
Caenorhabditis elegans	methionyl aminopeptidase 2	16	F:GO:0003743; P:GO:0007276; P:GO:0040010; P:GO:0016055; P:GO:0031365; F:GO:0046872; P:GO:0018206; F:GO:0004177; P:GO:0006508; F:GO:0005515; F:GO:0008235; P:GO:0006898; P:GO:0016485; P:GO:0009792; P:GO:0008406; C:GO:0005737	-	EC:3.4.11.0	-
Caenorhabditis elegans	methionyl aminopeptidase 2	16	F:GO:0003743; P:GO:0007276; P:GO:0040010; P:GO:0016055; P:GO:0031365; F:GO:0046872; P:GO:0018206; F:GO:0004177; P:GO:0006508; F:GO:0005515; F:GO:0008235; P:GO:0006898; P:GO:0016485; P:GO:0009792; P:GO:0008406; C:GO:0005737	-	EC:3.4.11.0	IPR000994; IPR001714; IPR002468; IPR011991; SSF46785 (SUPERFAMILY)

Caenorhabditis elegans	methionyl aminopeptidase 2	16	F:GO:0003743; P:GO:0007276; P:GO:0040010; P:GO:0016055; P:GO:0031365; F:GO:0046872; P:GO:0018206; F:GO:0004177; P:GO:0006508; F:GO:0005515; F:GO:0008235; P:GO:0006898; P:GO:0016485; P:GO:0009792; P:GO:0008406; C:GO:0005737	-	EC:3.4.11.0	-
	-	0				-
Caenorhabditis elegans	alkylated d- repair protein alkb-like protein 8	4	F:GO:0005488; P:GO:0040010; P:GO:0008152; F:GO:0008168	-	EC:2.1.1.0	IPR013216; G3DSA:2.60.120.590 (GENE3D), G3DSA:3.40.50.150 (GENE3D), PTHR13069 (PANTHER), SSF51197 (SUPERFAMILY), SSF53335 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG15174 [Caenorhabditis briggsae]	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-sel-13 protein	0				-
Caenorhabditis elegans	guanylyl cyclase family member (gcy-28)	0		C:GO:0016020; F:GO:0004383; F:GO:0004672; P:GO:0009190; P:GO:0006182; P:GO:0006468; F:GO:0000166; F:GO:0005524; F:GO:0008528; F:GO:0016829; F:GO:0016849		-
	-	0				-
	-	0				IPR001810; IPR022364; G3DSA:1.20.1280.50 (GENE3D)
Caenorhabditis briggsae	autophagy protein 9	4	C:GO:0044444; C:GO:0043229; C:GO:0016020; P:GO:0006914	-		IPR007241; PTHR13038:SF11 (PANTHER), SignalP (SIGNALP)
Loa loa	elegans protein partially confirmed by transcript evidence	0		C:GO:0005643; P:GO:0016973		-
Caenorhabditis briggsae	cleft lip and palate transmembrane protein 1-like protein	2	C:GO:0016021; P:GO:0006915	-		IPR008429
	-	0				-
	-	0				-

synthetic construct	s100 calcium binding protein a11	10	C:GO:0001726; P:GO:0008156; F:GO:0005509; F:GO:0048154; P:GO:0008285; F:GO:0048306; P:GO:0007165; F:GO:0042803; C:GO:0005737; C:GO:0005634	-		IPR001751; IPR011992; IPR013787; IPR018247; IPR018248; IPR018249; PTHR11639 (PANTHER), PTHR11639:SF7 (PANTHER), SSF47473 (SUPERFAMILY)
	-	0				-
	-	0				-
Sclerotinia sclerotiorum 1980	d- polymerase iii subunits gamma and tau	0		F:GO:0016740; F:GO:0003677; P:GO:0006260; F:GO:0000166; F:GO:0003887; F:GO:0017111; F:GO:0005524; F:GO:0016779; C:GO:0009360		-
Sclerotinia sclerotiorum 1980	d- polymerase iii subunits gamma and tau	0		F:GO:0016740; F:GO:0003677; P:GO:0006260; F:GO:0000166; F:GO:0003887; F:GO:0017111; F:GO:0005524; F:GO:0016779; C:GO:0009360		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	hypoxia-inducible factor 1 alpha	1	P:GO:0045449	-		IPR000014; IPR013767; G3DSA:3.30.450.20 (GENE3D), PTHR23043 (PANTHER), SSF55785 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	ef-hand calcium binding domain 4b	10	F:GO:0005509; P:GO:0007264; P:GO:0006913; F:GO:0005515; P:GO:0032237; P:GO:0006886; C:GO:0005737; P:GO:0002115; C:GO:0005634; F:GO:0005525	-		IPR001806; IPR013753; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF253 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	cation-transporting atpase	5	F:GO:0005388; C:GO:0016021; P:GO:0006754; F:GO:0005524; P:GO:0006812	-	EC:3.6.3.8	IPR001757; IPR018303; G3DSA:3.40.1110.10 (GENE3D), PTHR11939:SF48 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Haemonchus contortus	elegans protein confirmed by transcript evidence	4	P:GO:0040019; P:GO:0009792; P:GO:0040010; P:GO:0002119	-		-

Caenorhabditis elegans	innexin protein 13	5	P:GO:0040035; C:GO:0005921; P:GO:0040010; P:GO:0040011; P:GO:0002009	-		SignalP (SIGNALP)
	-	0				-
Brugia malayi	rho guanine nucleotide exchange factor 7	4	P:GO:0043065; F:GO:0005085; P:GO:0007165; C:GO:0005737	-		IPR000219; PTHR22826 (PANTHER), PTHR22826:SF16 (PANTHER)
Caenorhabditis elegans	isoform b	2	P:GO:0009792; F:GO:0005488	-		IPR002181; IPR014715; IPR014716; PTHR19143 (PANTHER), PTHR19143:SF28 (PANTHER)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG04107 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	Hypothetical protein CBG04107 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR009673
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0006355; F:GO:0003676; C:GO:0016021; F:GO:0008270; C:GO:0005622; P:GO:0007186		IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)
Loa loa	elegans protein partially confirmed by transcript evidence	0		P:GO:0006355; F:GO:0003676; C:GO:0016021; F:GO:0008270; C:GO:0005622; P:GO:0007186		IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)
Loa loa	elegans protein partially confirmed by transcript evidence	0		P:GO:0006355; F:GO:0003676; C:GO:0016021; F:GO:0008270; C:GO:0005622; P:GO:0007186		IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)
Loa loa	elegans protein partially confirmed by transcript evidence	0		P:GO:0006355; F:GO:0003676; C:GO:0016021; F:GO:0008270; C:GO:0005622; P:GO:0007186		IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)
Loa loa	elegans protein partially confirmed by transcript evidence	0		P:GO:0006355; F:GO:0003676; C:GO:0016021; F:GO:0008270; C:GO:0005622; P:GO:0007186		IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0008150; C:GO:0005575		-
	-	0				-
Caenorhabditis briggsae	yw60_caeel ame: full=uncharacterized protein	0				SignalP (SIGNALP)

Rattus norvegicus	ribosomal protein l27	4	C:GO:0005840; C:GO:0005829; F:GO:0003735; P:GO:0006414	-		IPR001141; IPR005824; IPR014722
Caenorhabditis briggsae	short chain dehydroge-se reductase family protein	5	P:GO:0044237; C:GO:0016021; P:GO:0055114; F:GO:0016491; F:GO:0050662	-		IPR002198; PTHR19410:SF98 (PANTHER)
Caenorhabditis briggsae	wd repeat domain 55	4	P:GO:0040035; F:GO:0005515; P:GO:0006898; C:GO:0044424	-		IPR001680; IPR015943; PTHR22840 (PANTHER), PTHR22840:SF2 (PANTHER), SSF101908 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	zinc carboxypeptidase family protein	0		P:GO:0006508; F:GO:0004181; F:GO:0004180; F:GO:0008270		-
Caenorhabditis briggsae	novel protein glutamate receptor interacting protein 1	1	F:GO:0005515	-		-
Caenorhabditis briggsae	novel protein glutamate receptor interacting protein 1	1	F:GO:0005515	-		-
Caenorhabditis briggsae	briggsae cbr-eya-1 protein	1	F:GO:0005515	-		PTHR10190 (PANTHER), PTHR10190:SF3 (PANTHER), SignalP (SIGNALP)
Branchiostoma floridae	alkaline phosphatase	1	F:GO:0016787	-		IPR001952; IPR017849; IPR017850; PTHR11596 (PANTHER)
Photobacterium sp. SKA34	alkaline phosphatase	1	F:GO:0016787	-		IPR001952; IPR017849; IPR017850; PTHR11596 (PANTHER)
Caenorhabditis briggsae	nitrilase 1	11	F:GO:0047427; F:GO:0080109; F:GO:0047558; P:GO:0019762; P:GO:0046686; P:GO:0009970; P:GO:0051410; P:GO:0000003; P:GO:0019499; C:GO:0016020; F:GO:0080061	-	EC:3.5.5.4; EC:4.2.1.65	IPR000132; IPR003010
Caenorhabditis elegans	zinc-binding dehydroge-se family protein	4	P:GO:0008152; P:GO:0008340; F:GO:0003824; F:GO:0005488	-		IPR002085; IPR011032; IPR013149; IPR013154; IPR016040; G3DSA:3.90.180.10 (GENE3D), PTHR11695:SF15 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	tb2 hva22 family protein	1	F:GO:0005515	-		IPR004345; PTHR12300:SF13 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	5	C:GO:0016021; P:GO:0006865; C:GO:0009986; F:GO:0015171; P:GO:0055085	-		IPR002293; PTHR11785:SF76 (PANTHER)
Caenorhabditis elegans	briggsae cbr-rack-1 protein	0		F:GO:0016301; F:GO:0004872; F:GO:0005515		-

Caenorhabditis elegans	g-protein beta subunit	0		P:GO:0042335; P:GO:0007626; P:GO:0018991; C:GO:0071013; P:GO:0048477; C:GO:0071011; C:GO:0005875; C:GO:0005737; F:GO:0005080; F:GO:0016301; P:GO:0035220; P:GO:0000398; F:GO:0004872; F:GO:0005515		PTHR19868 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-rack-1 protein	10	C:GO:0005737; F:GO:0004872; F:GO:0016301; P:GO:0007205; C:GO:0005886; F:GO:0005102; F:GO:0019903; F:GO:0008270; C:GO:0043025; F:GO:0005080	-		IPR001680; IPR011046; IPR015943; PTHR19868 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-rack-1 protein	10	C:GO:0005737; F:GO:0004872; F:GO:0016301; P:GO:0007205; C:GO:0005886; F:GO:0005102; F:GO:0019903; F:GO:0008270; C:GO:0043025; F:GO:0005080	-		IPR001680; IPR011046; IPR015943; PTHR19868 (PANTHER)
Caenorhabditis elegans	activated c ki-se 1 receptor	13	F:GO:0005080; C:GO:0005875; P:GO:0035220; P:GO:0042335; P:GO:0018991; C:GO:0071011; F:GO:0004872; P:GO:0007626; P:GO:0000398; F:GO:0016301; C:GO:0071013; P:GO:0048477; C:GO:0005737	-		-

Caenorhabditis elegans	activated c ki-se 1 receptor	13	F:GO:0005080; C:GO:0005875; P:GO:0035220; P:GO:0042335; P:GO:0018991; C:GO:0071011; F:GO:0004872; P:GO:0007626; P:GO:0000398; F:GO:0016301; C:GO:0071013; P:GO:0048477; C:GO:0005737	-		-
Caenorhabditis briggsae	guanine nucleotide binding protein (g protein) beta polypeptide 2-like 1	12	C:GO:0005737; F:GO:0004872; P:GO:0008104; P:GO:0023034; F:GO:0016301; P:GO:0007205; C:GO:0005886; P:GO:0007165; F:GO:0005102; F:GO:0019903; C:GO:0043025; F:GO:0005080	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR19868 (PANTHER)
Caenorhabditis briggsae	guanine nucleotide binding protein (g protein) beta polypeptide 2-like 1	12	C:GO:0005737; F:GO:0004872; P:GO:0008104; P:GO:0023034; F:GO:0016301; P:GO:0007205; C:GO:0005886; P:GO:0007165; F:GO:0005102; F:GO:0019903; C:GO:0043025; F:GO:0005080	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR19868 (PANTHER)
Haemonchus contortus	thymus-specific serine protease	1	F:GO:0005515	-		IPR008758; G3DSA:3.40.50.1820 (GENE3D), PTHR11010:SF4 (PANTHER), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein K07B1.6 [Caenorhabditis elegans]	1	P:GO:0002119	-		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	dolichyl-phosphate beta-glucosyltransferase	3	F:GO:0016740; P:GO:0007379; P:GO:0009880	-		IPR001173; G3DSA:3.90.550.10 (GENE3D), PTHR10859 (PANTHER), SignalP (SIGNALP), SSF53448 (SUPERFAMILY)
Ailuropoda melanoleuca	polyadenylate-binding protein 1-like	9	P:GO:0006378; P:GO:0008380; P:GO:0048255; C:GO:0005681; F:GO:0008494; F:GO:0008022; C:GO:0005829; F:GO:0000166; F:GO:0008143	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF69 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	mterf domain-containing protein 2	0				IPR003690; PTHR13068 (PANTHER)

	-	0				-
Caenorhabditis briggsae	equilibrative nucleoside transporter	4	P:GO:0040035; P:GO:0018991; C:GO:0016020; P:GO:0002009	-		IPR002259; PTHR10332:SF6 (PANTHER)
Caenorhabditis elegans	hypothetical protein E04F6.6 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	dystrophin-like protein	7	P:GO:0007271; F:GO:0005515; P:GO:0040017; C:GO:0016010; F:GO:0005277; P:GO:0015870; P:GO:0046716	-		-
Loa loa	suppressor of defective silencing	0				IPR013907; PTHR21964 (PANTHER), PTHR21964:SF1 (PANTHER)
Caenorhabditis briggsae	cathepsin b-like cysteine protei-se precursor	3	C:GO:0016021; P:GO:0006508; F:GO:0008234	-		IPR000668; IPR013128; IPR015643; G3DSA:3.90.70.10 (GENE3D), SSF54001 (SUPERFAMILY)
Caenorhabditis elegans	molybdopterin synthase large	4	F:GO:0030366; P:GO:0006777; F:GO:0016740; C:GO:0005829	-		IPR003448; G3DSA:3.40.50.300 (GENE3D), PTHR23404 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
Leishmania infantum JPCM5	checkpoint with forkhead and ring finger domains	0		F:GO:0046872; F:GO:0008270; F:GO:0005515		IPR001841; IPR013083; IPR017907; IPR018957; PTHR13982 (PANTHER), PTHR13982:SF4 (PANTHER), SSF57850 (SUPERFAMILY)
	-	0				-
Loa loa	replication factor c (activator 1) 37kda	6	F:GO:0017111; C:GO:0005730; P:GO:0006260; F:GO:0003677; F:GO:0005524; C:GO:0005663	-	EC:3.6.1.15	G3DSA:1.10.8.60 (GENE3D), PTHR11669 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	i in (lysosomal protein) homolog family member (ctns-1)	5	P:GO:0015811; P:GO:0003333; F:GO:0015171; C:GO:0005765; C:GO:0031410	-		IPR006603; PTHR13131 (PANTHER), PF04193 (PFAM), SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-pup-2 protein	1	P:GO:0008340	-		-
	-	0				-
Caenorhabditis elegans	threonyl-tr- synthetase	5	C:GO:0005737; F:GO:0004829; F:GO:0005524; P:GO:0006435; P:GO:0007040	-	EC:6.1.1.3	-
	-	0				-
Caenorhabditis brenneri	purity of essence	3	P:GO:0042066; P:GO:0007291; F:GO:0005516	-		PTHR21725 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-qui-1 protein	0		F:GO:0005524; F:GO:0000166; F:GO:0017111		IPR001680; IPR011047; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR19871 (PANTHER)
Caenorhabditis briggsae	neuro-l symmetry protein isoform a	0				-

Caenorhabditis elegans	prostaglandin e synthase 2	0		P:GO:0045454; F:GO:0009055; F:GO:0015035		IPR010987; PTHR12782 (PANTHER)
Caenorhabditis briggsae	lambda 1	6	F:GO:0070403; P:GO:0044281; P:GO:0044237; F:GO:0050104; C:GO:0005829; P:GO:0044238	-	EC:1.1.1.45	IPR006108; IPR006176; IPR008927; IPR013328; IPR016040; PTHR23309 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	briggsae cbr-mppa-1 protein	0		F:GO:0046872; P:GO:0006508; F:GO:0003824; F:GO:0004222; F:GO:0008270		-
Caenorhabditis elegans	briggsae cbr-aap-1 protein	5	P:GO:0008340; P:GO:0008286; F:GO:0019901; C:GO:0044464; P:GO:0040024	-		IPR000980; IPR001720; SSF55550 (SUPERFAMILY)
	-	0				-
Rattus norvegicus	rr- promoter binding protein	4	F:GO:0003700; F:GO:0008134; P:GO:0009303; P:GO:0008283	-		-
	-	0				-
Caenorhabditis briggsae	dual oxidase	18	P:GO:0018149; P:GO:0006979; P:GO:0006952; F:GO:0016174; P:GO:0040032; F:GO:0005509; C:GO:0016021; P:GO:0042338; P:GO:0055114; P:GO:0040007; F:GO:0004601; F:GO:0009055; P:GO:0002119; P:GO:0040011; F:GO:0020037; F:GO:0050660; P:GO:0009792; C:GO:0005882	-	EC:1.6.3.1; EC:1.11.1.7	IPR002007; IPR010255; IPR019791; PTHR11475 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	P:GO:0009792; P:GO:0000003	-		-
	-	0				-
Loa loa	longevity assurance factor 1	1	C:GO:0016021	-		-

Caenorhabditis elegans	protein tyrosine receptor d	8	P:GO:0018996; P:GO:0009792; P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		IPR003961; IPR008957; IPR013783; PTHR10489 (PANTHER)
Caenorhabditis elegans	map ki-se-activated protein ki-se 3	6	C:GO:0005737; F:GO:0004683; P:GO:0006468; F:GO:0005515; F:GO:0005524; C:GO:0005634	-	EC:2.7.11.17	IPR000719; IPR008271; IPR011009; IPR017441; IPR017442; IPR020636; IPR020646; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
	-	0				-
Acyrthosiphon pisum	endonuclease-reverse transcriptase	0		F:GO:0003723; P:GO:0006278; F:GO:0004519; F:GO:0003964		-
Bombyx mori	endonuclease-reverse transcriptase	1	F:GO:0003824	-		-
Caenorhabditis briggsae	ras-related protein rab-30	8	C:GO:0005737; F:GO:0005525; F:GO:0005515; P:GO:0006913; F:GO:0004767; P:GO:0006886; C:GO:0005634; P:GO:0007264	-	EC:3.1.4.12	-
	-	0				-
Haemochus contortus	briggsae cbr-gst- protein	3	F:GO:0005515; F:GO:0004364; P:GO:0008340	-	EC:2.5.1.18	IPR004045; IPR012335; IPR012336; PTHR11571 (PANTHER), PTHR11571:SF6 (PANTHER)
	-	0				-
Caenorhabditis elegans	eb module family protein	0		F:GO:0004674; F:GO:0016810; F:GO:0004672; P:GO:0006468; F:GO:0000166; F:GO:0005524; P:GO:0005975; F:GO:0003824; F:GO:0005488		-
	-	0				-
Ancylostoma caninum	secreted protein asp-2	0		F:GO:0009055; P:GO:0019646; C:GO:0005576		IPR001283; IPR014044
Ancylostoma caninum	secreted protein asp-2	0		F:GO:0009055; P:GO:0019646; C:GO:0005576		IPR001283; IPR014044
Caenorhabditis briggsae	temporarily assigned gene -me family member (tag-163)	1	F:GO:0005515	-		-
Loa loa	zinc finger protein dhhc domain containing	1	F:GO:0046872	-		SignalP (SIGNALP)
Loa loa	zinc finger dhhc domain containing protein 5	0		F:GO:0046872; F:GO:0008270		-
	-	0				SignalP (SIGNALP)

Pan troglodytes	complement 1 subcomponent q polypeptide gamma	7	C:GO:0005730; P:GO:0006958; P:GO:0030853; P:GO:0045650; P:GO:0045087; C:GO:0005576; C:GO:0005737	-		-
Caenorhabditis briggsae	briggsae cbr-sax-3 protein	13	P:GO:0007411; P:GO:0001656; P:GO:0001657; P:GO:0050925; P:GO:0001554; P:GO:0050772; F:GO:0046982; C:GO:0009986; P:GO:0007420; P:GO:0007156; F:GO:0042802; P:GO:0032870; C:GO:0030673	-		IPR003598; IPR003961; IPR007110; IPR008957; IPR013098; IPR013783; PTHR10489 (PANTHER), PTHR10489:SF27 (PANTHER), SignalP (SIGNALP), SSF48726 (SUPERFAMILY)
Caenorhabditis briggsae	loc733382 protein	0		F:GO:0005529		IPR000922; PTHR12011 (PANTHER), PTHR12011:SF1 (PANTHER)
Pan troglodytes	interferon induced transmembrane protein 3 (1-8u)	8	F:GO:0005057; P:GO:0045087; P:GO:0008285; C:GO:0005886; P:GO:0007166; F:GO:0005515; C:GO:0016021; P:GO:0009615	-		IPR007593; PTHR13999 (PANTHER)
synthetic construct	interferon induced transmembrane protein 3 (1-8u)	8	F:GO:0005057; P:GO:0045087; P:GO:0008285; C:GO:0005886; P:GO:0007166; F:GO:0005515; C:GO:0016021; P:GO:0009615	-		IPR007593; PTHR13999 (PANTHER)
synthetic construct	interferon induced transmembrane protein 3 (1-8u)	5	C:GO:0016021; P:GO:0045087; P:GO:0009615; F:GO:0005515; C:GO:0005886	-		-
Pan troglodytes	interferon induced transmembrane protein 3 (1-8u)	5	C:GO:0016021; P:GO:0045087; P:GO:0009615; F:GO:0005515; C:GO:0005886	-		IPR007593; PTHR13999 (PANTHER)
Caenorhabditis elegans	#NAME?	3	F:GO:0016757; F:GO:0005515; C:GO:0016020	-		IPR001503; IPR010916; PTHR11929:SF7 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	bifunctio-l aminoacyl-tr- synthetase	6	P:GO:0006412; C:GO:0005829; F:GO:0004827; F:GO:0005515; P:GO:0043039; F:GO:0004818	-	EC:3.6.5.3; EC:6.1.1.15; EC:6.1.1.17	IPR000738; IPR009068

Caenorhabditis briggsae	r- binding identical	4	C:GO:0005622; P:GO:0009792; F:GO:0000166; F:GO:0003723	-		IPR000504; IPR012677; IPR015465; PTHR10432 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	r- binding identical	4	C:GO:0005622; P:GO:0009792; F:GO:0000166; F:GO:0003723	-		IPR000504; IPR012677; IPR015465; PTHR10432 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	solute carrier family 36 (proton amino acid symporter) member isoform cra_a	13	P:GO:0055085; F:GO:0015078; C:GO:0005764; F:GO:0005302; C:GO:0016021; F:GO:0015193; F:GO:0005280; F:GO:0015180; P:GO:0015824; P:GO:0015808; P:GO:0015816; P:GO:0015992; C:GO:0005886	-		IPR013057; PTHR22950 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-taf- protein	8	P:GO:0006367; P:GO:0045944; P:GO:0007517; F:GO:0016251; P:GO:0007283; F:GO:0005515; C:GO:0005669; P:GO:0048813	-		IPR003894; IPR007900; PTHR15138 (PANTHER), PTHR15138:SF4 (PANTHER)
Brugia malayi	nuclear receptor subfamily group member 2	9	P:GO:0007417; P:GO:0007270; F:GO:0004872; P:GO:0001752; P:GO:0042331; F:GO:0005515; C:GO:0005737; P:GO:0006350; P:GO:0007510	-		IPR001628; IPR001723; IPR008946; PTHR11865 (PANTHER), PTHR11865:SF190 (PANTHER), SSF57716 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	uncoordi-ted family member (unc-89)	0				-
Caenorhabditis elegans	exocyst complex component 8	6	P:GO:0009792; P:GO:0040018; P:GO:0000003; P:GO:0010171; P:GO:0002119; P:GO:0040011	-		IPR014812; PTHR21426 (PANTHER), PTHR21426:SF9 (PANTHER)
Caenorhabditis elegans	exocyst complex component 7	1	C:GO:0044464	-		-
	-	0				SignalP (SIGNALP)

Ailuropoda melanoleuca	endothelial differentiation-related factor 1	13	P:GO:0019216; P:GO:0043388; F:GO:0005516; P:GO:0006355; F:GO:0043565; F:GO:0003700; P:GO:0045446; P:GO:0007275; F:GO:0004402; F:GO:0003713; C:GO:0005669; C:GO:0005737; F:GO:0008168	-	EC:2.3.1.48; EC:2.1.1.0	-
Caenorhabditis briggsae	briggsae cbr-max-1 protein	4	C:GO:0005856; P:GO:0008340; F:GO:0005488; P:GO:0040010	-		-
Oryctolagus cuniculus	non-pou domain octamer-binding	11	C:GO:0042382; C:GO:0016363; F:GO:0003723; P:GO:0006310; P:GO:0006281; P:GO:0045449; F:GO:0042802; P:GO:0008380; F:GO:0003677; F:GO:0000166; P:GO:0006397	-		IPR000504; IPR012677; PTHR23189 (PANTHER), PTHR23189:SF15 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0005096; P:GO:0051056; C:GO:0005622		PTHR21344 (PANTHER)
Loa loa	serologically defined colon cancer antigen 1	2	C:GO:0005634; C:GO:0005737	-		IPR008616; PTHR15239 (PANTHER)
Brachypodium distachyon	mdr-like abc transporter	5	F:GO:0015440; F:GO:0008559; P:GO:0055085; F:GO:0005524; C:GO:0016021	-	EC:3.6.3.43; EC:3.6.3.44	IPR003439; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF96 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	prohibitin protein wph	3	P:GO:0009792; P:GO:0000003; C:GO:0016020	-		IPR000163; IPR001107; SSF117892 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	-dh-ubiquinone oxidoreductase b12 subunit	9	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0040018; F:GO:0008137; P:GO:0040010; P:GO:0008340; P:GO:0006898; C:GO:0005739	-	EC:1.6.5.3	-
Caenorhabditis elegans	small family member (sma-9)	1	F:GO:0005515	-		IPR007087; IPR013087; IPR015880; SSF57667 (SUPERFAMILY)
Pongo abelii	PREDICTED: hypothetical protein LOC100438967 [Pongo abelii]	0				IPR019543; PTHR23103 (PANTHER), PTHR23103:SF7 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein W02H5.2 [Caenorhabditis elegans]	0				-

Caenorhabditis briggsae	testis derived transcript	3	C:GO:0005737; F:GO:0046872; P:GO:0008340	-		IPR001781; IPR010442; PTHR18973 (PANTHER), PTHR18973:SF105 (PANTHER), SSF57716 (SUPERFAMILY)
	-	0				PTHR10845 (PANTHER), PTHR10845:SF14 (PANTHER)
Caenorhabditis elegans	briggsae cbr-wee- protein	9	C:GO:0019898; C:GO:0043231; F:GO:0004674; P:GO:0051447; P:GO:0002119; C:GO:0044444; P:GO:0048477; P:GO:0051327; P:GO:0009790	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11042 (PANTHER), PTHR11042:SF6 (PANTHER)
Caenorhabditis elegans	briggsae cbr-wee- protein	9	C:GO:0019898; C:GO:0043231; F:GO:0004674; P:GO:0051447; P:GO:0002119; C:GO:0044444; P:GO:0048477; P:GO:0051327; P:GO:0009790	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11042 (PANTHER), PTHR11042:SF6 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	cdt1 protein	3	P:GO:0007369; P:GO:0000003; C:GO:0044424	-		IPR014939; SSF46785 (SUPERFAMILY)
Caenorhabditis briggsae	e3 ubiquitin-protein ligase mib2	2	F:GO:0046872; F:GO:0003824	-		IPR001841; IPR013083; PTHR18958 (PANTHER), PTHR18958:SF268 (PANTHER)
Caenorhabditis briggsae	e3 ubiquitin-protein ligase mib2	2	F:GO:0046872; F:GO:0003824	-		IPR001841; IPR013083; PTHR18958 (PANTHER), PTHR18958:SF268 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Phthorimaea operculella granulovirus	ubiquitin	1	C:GO:0005737	-		-
Anopheles gambiae str. PEST	ubiquitin	0		F:GO:0003735; P:GO:0006412; C:GO:0005737; C:GO:0005840; C:GO:0005622		-
Caenorhabditis elegans	dead (asp-glu-ala-asp) box polypeptide 18	4	F:GO:0008026; F:GO:0003723; P:GO:0006200; F:GO:0005524	-		IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF23 (PANTHER), SSF52540 (SUPERFAMILY)
Mus musculus	small proline-rich protein 3	0		P:GO:0031424; F:GO:0005515		-
Ailuropoda melanoleuca	heterogeneous nuclear ribonucleoprotein m	10	F:GO:0003823; C:GO:0005730; C:GO:0005887; C:GO:0042382; F:GO:0019904; C:GO:0005681; F:GO:0003723; P:GO:0000380; C:GO:0016363; F:GO:0000166	-		IPR000504; IPR012677; PTHR23003 (PANTHER), PTHR23003:SF6 (PANTHER), SSF54928 (SUPERFAMILY)

Loa loa	asparaginyl-tr- synthetase mitochondrial	3	F:GO:0016874; P:GO:0006412; C:GO:0005739	-	EC:3.6.5.3	IPR004364; IPR004365; IPR006195; IPR012340; IPR016027; IPR018150; G3DSA:3.30.930.10 (GENE3D), PTHR22594:SF6 (PANTHER), SSF55681 (SUPERFAMILY)
Caenorhabditis elegans	fatty acid elongation protein 3	2	C:GO:0016021; P:GO:0007283	-		IPR002076
Caenorhabditis briggsae	60s ribosomal protein l17	10	P:GO:0000022; P:GO:0006412; P:GO:0040010; F:GO:0003735; P:GO:0000003; P:GO:0007413; P:GO:0002119; P:GO:0040011; P:GO:0009792; C:GO:0022625	-	EC:3.6.5.3	PTHR10010 (PANTHER), PTHR10010:SF4 (PANTHER)
Caenorhabditis elegans	60s ribosomal protein l17	9	P:GO:0006412; P:GO:0040010; F:GO:0003735; P:GO:0000003; C:GO:0015934; P:GO:0007413; P:GO:0002119; P:GO:0040011; P:GO:0009792	-	EC:3.6.5.3	SignalP (SIGNALP)
Caenorhabditis briggsae	leukocyte cell-derived chemotaxin 2	0		F:GO:0004222; P:GO:0030851; P:GO:0001501; C:GO:0005737; C:GO:0005576; P:GO:0006935; P:GO:0006508; P:GO:0030178; C:GO:0005615		IPR008663; IPR016047; G3DSA:2.70.70.10 (GENE3D)
Brugia malayi	myotubularin-related family protein	0		P:GO:0016311; F:GO:0016791		-
	-	0				-
	-	0				-
	-	0				-
Loa loa	r--binding protein pno1	4	C:GO:0005730; P:GO:0040035; P:GO:0009792; F:GO:0003723	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	yt31_caeel ame: full=uncharacterized protein	0				-
Caenorhabditis elegans	fanci (fanconi anemia complex component i) homolog family member (fnci-1)	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	6	C:GO:0005777; P:GO:0055114; P:GO:0006635; F:GO:0003995; F:GO:0050660; F:GO:0003997	-	EC:1.3.99.3; EC:1.3.3.6	IPR009100; IPR012258; IPR013786; PTHR10909 (PANTHER)

Caenorhabditis elegans	vitellogenin structural genes (yolk protein genes) family member (vit-6)	0		P:GO:0006869; F:GO:0005319; P:GO:0006886; F:GO:0045735; F:GO:0005515; C:GO:0005576; F:GO:0008565		IPR015816
Caenorhabditis elegans	vitellogenin structural genes (yolk protein genes) family member (vit-6)	0		P:GO:0006869; F:GO:0005319; F:GO:0045735; P:GO:0006886; C:GO:0005576; F:GO:0008565		IPR015819; SignalP (SIGNALP)
Caenorhabditis elegans	vitellogenin structural genes (yolk protein genes) family member (vit-6)	0		P:GO:0006869; F:GO:0005319; F:GO:0045735; P:GO:0006886; C:GO:0005576; F:GO:0008565		IPR015819; SignalP (SIGNALP)
Caenorhabditis briggsae	vitellogenin structural genes (yolk protein genes) family member (vit-6)	0		P:GO:0006869; F:GO:0005319; P:GO:0006886; F:GO:0045735; C:GO:0005576; F:GO:0008565		IPR015816
Oscheius sp. (strain CEW1)	vitellogenin structural genes (yolk protein genes) family member (vit-6)	5	P:GO:0006869; F:GO:0005319; P:GO:0006886; F:GO:0008565; F:GO:0005515	-		IPR001747; IPR015816; PTHR23345 (PANTHER)
Loa loa	40s ribosomal protein s13	7	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; P:GO:0000003; P:GO:0040007; P:GO:0006412	-	EC:3.6.5.3	
Loa loa	40s ribosomal protein s13	7	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; P:GO:0000003; P:GO:0040007; P:GO:0006412	-	EC:3.6.5.3	
Oscheius sp. (strain CEW1)	vitellogenin structural genes (yolk protein genes) family member (vit-6)	5	F:GO:0005319; F:GO:0005515; P:GO:0006869; F:GO:0008565; P:GO:0006886	-		IPR001747; IPR015816; IPR015819; PTHR23345 (PANTHER)

Loa loa	ribosomal protein s13	11	F:GO:0003729; C:GO:0005730; P:GO:0040007; F:GO:0003735; P:GO:0000003; P:GO:0006414; C:GO:0022627; P:GO:0033119; P:GO:0002119; F:GO:0005515; P:GO:0009792	-		
Loa loa	ribosomal protein s13	11	F:GO:0003729; C:GO:0005730; P:GO:0040007; F:GO:0003735; P:GO:0000003; P:GO:0006414; C:GO:0022627; P:GO:0033119; P:GO:0002119; F:GO:0005515; P:GO:0009792	-		
Ancylostoma caninum	c-type lectin family member (clec-266)	0		F:GO:0004888; C:GO:0016021; C:GO:0016020; F:GO:0005529; F:GO:0003674; C:GO:0009897; C:GO:0005575; C:GO:0005887; P:GO:0008150; F:GO:0005509; F:GO:0005488		-
Ancylostoma caninum	c-type lectin family member (clec-266)	0		F:GO:0004888; C:GO:0016021; C:GO:0016020; F:GO:0005529; F:GO:0003674; C:GO:0009897; C:GO:0005575; C:GO:0005887; P:GO:0008150; F:GO:0005509; F:GO:0005488		IPR001304; IPR013032; IPR016186; IPR016187; PTHR22802 (PANTHER), PTHR22802:SF15 (PANTHER), SignalP (SIGNALP)
Ancylostoma caninum	c-type lectin family member (clec-266)	0		F:GO:0004888; C:GO:0016021; C:GO:0016020; F:GO:0005529; F:GO:0003674; C:GO:0009897; C:GO:0005575; C:GO:0005887; P:GO:0008150; F:GO:0005509; F:GO:0005488		IPR001304; IPR013032; IPR016186; IPR016187; PTHR22802 (PANTHER), PTHR22802:SF15 (PANTHER)

Caenorhabditis briggsae	ectonucleoside triphosphate diphosphohydrolase 4	5	C:GO:0000139; P:GO:0030154; P:GO:0007506; F:GO:0017110; C:GO:0016021	-	EC:3.6.1.6	IPR000407; PTHR11782:SF5 (PANTHER)
Caenorhabditis elegans	histidyl-tr- cytoplasmic	4	C:GO:0005737; F:GO:0004812; P:GO:0006418; F:GO:0000166	-		IPR004154; IPR004516; G3DSA:3.30.930.10 (GENE3D), SSF55681 (SUPERFAMILY)
Brugia malayi	coiled-coil domain-containing protein 111	0		P:GO:0006260; F:GO:0003674; P:GO:0006269; P:GO:0008150; F:GO:0003896; C:GO:0005575		-
Caenorhabditis briggsae	wd-repeat protein	3	C:GO:0044444; P:GO:0040011; C:GO:0043229	-		IPR011047; IPR015943; IPR017986; IPR019781; IPR019782; PTHR14221 (PANTHER)
Loa loa	hypothetical protein LOAG_06732 [Loa loa]	0				-
Caenorhabditis briggsae	cdk5 and abl enzyme substrate 1	2	F:GO:0005515; C:GO:0005829	-		IPR006670; IPR006671; IPR011028; IPR013763; PTHR22896 (PANTHER)
	-	0				-
Caenorhabditis briggsae	pi-3-ki-se-related ki-se smg-1	3	F:GO:0005488; P:GO:0009987; F:GO:0016740	-		IPR000403; IPR003152; IPR011009; PTHR11139 (PANTHER), PTHR11139:SF9 (PANTHER)
Caenorhabditis elegans	chromosome 20 open reading frame 3	0		P:GO:0009058; C:GO:0009986; C:GO:0016021; C:GO:0016020; P:GO:0008150; F:GO:0016844; F:GO:0004064		-
Gallus gallus	mkiaa0236 protein	0				IPR015880
Caenorhabditis briggsae	briggsae cbr-abf-2 protein	0				SignalP (SIGNALP)
Homo sapiens	mhc class i antigen	9	C:GO:0000139; F:GO:0032393; C:GO:0005887; F:GO:0005515; C:GO:0031901; P:GO:0002474; P:GO:0006955; P:GO:0044419; C:GO:0042612	-		IPR003006; IPR003597; IPR013783; PTHR16675 (PANTHER), PTHR16675:SF53 (PANTHER), SSF48726 (SUPERFAMILY)
Callithrix jacchus	mhc class i antigen	10	F:GO:0032393; C:GO:0005887; C:GO:0005624; P:GO:0006952; F:GO:0005515; P:GO:0002474; C:GO:0005576; P:GO:0006955; P:GO:0044419; C:GO:0042612	-		IPR003006; IPR003597; IPR007110; IPR010579; IPR013783; PTHR16675 (PANTHER), PTHR16675:SF53 (PANTHER), SSF48726 (SUPERFAMILY)

Homo sapiens	mhc class i antigen	12	C:GO:0000139; F:GO:0032393; C:GO:0005887; C:GO:0005624; P:GO:0006952; F:GO:0005515; C:GO:0031901; P:GO:0002474; C:GO:0005576; P:GO:0006955; P:GO:0044419; C:GO:0042612	-			IPR003006; IPR003597; IPR010579; IPR013783; PTHR16675 (PANTHER), PTHR16675:SF53 (PANTHER), SSF48726 (SUPERFAMILY)
Homo sapiens	mhc class i antigen	9	C:GO:0000139; F:GO:0032393; C:GO:0005887; F:GO:0005515; C:GO:0031901; P:GO:0002474; P:GO:0006955; P:GO:0044419; C:GO:0042612	-			IPR003006; IPR003597; IPR007110; IPR013783; PTHR16675 (PANTHER), PTHR16675:SF53 (PANTHER), SSF48726 (SUPERFAMILY)
Homo sapiens	mhc class i antigen	9	C:GO:0000139; F:GO:0032393; C:GO:0005887; F:GO:0005515; C:GO:0031901; P:GO:0002474; P:GO:0006955; P:GO:0044419; C:GO:0042612	-			SignalP (SIGNALP)
Macaca mulatta	mhc class i antigen	10	F:GO:0032393; C:GO:0005887; C:GO:0005624; P:GO:0006952; F:GO:0005515; P:GO:0002474; C:GO:0005576; P:GO:0006955; P:GO:0044419; C:GO:0042612	-			IPR003006; IPR003597; IPR007110; IPR010579; IPR013783; PTHR16675 (PANTHER), PTHR16675:SF53 (PANTHER), SSF48726 (SUPERFAMILY)
Homo sapiens	mhc class ib antigen	9	C:GO:0000139; F:GO:0032393; C:GO:0005887; F:GO:0005515; C:GO:0031901; P:GO:0002474; P:GO:0006955; P:GO:0044419; C:GO:0042612	-			IPR003006; IPR003597; IPR007110; IPR013783; PTHR16675 (PANTHER), PTHR16675:SF53 (PANTHER), SSF48726 (SUPERFAMILY)

Homo sapiens	mhc class i antigen	11	C:GO:0000139; F:GO:0032393; C:GO:0005887; C:GO:0005624; P:GO:0006952; F:GO:0005515; C:GO:0031901; P:GO:0002474; P:GO:0006955; P:GO:0044419; C:GO:0042612	-		IPR003006; IPR003597; IPR007110; IPR010579; IPR013783; PTHR16675 (PANTHER), PTHR16675:SF53 (PANTHER), SSF48726 (SUPERFAMILY)
Homo sapiens	mhc class i antigen	9	C:GO:0000139; F:GO:0032393; C:GO:0005887; F:GO:0005515; C:GO:0031901; P:GO:0002474; P:GO:0006955; P:GO:0044419; C:GO:0042612	-		SignalP (SIGNALP)
Homo sapiens	major histocompatibility class c	7	P:GO:0006955; F:GO:0032393; C:GO:0005576; P:GO:0044419; C:GO:0005887; P:GO:0002474; C:GO:0042612	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	fatty acid desaturase	3	P:GO:0055114; F:GO:0016491; P:GO:0006629	-		IPR005804
Caenorhabditis briggsae	protein flightless-1 homolog	1	F:GO:0003779	-		IPR001611; IPR003591; G3DSA:3.80.10.10 (GENE3D), PTHR23155 (PANTHER), PTHR23155:SF37 (PANTHER), PS51450 (PROFILE), SSF52047 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0000003; P:GO:0006898; P:GO:0009792; P:GO:0002119; P:GO:0040007		SignalP (SIGNALP)
						IPR007110; IPR010939; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF9 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein Y48G9A.3 [Caenorhabditis elegans]	1	P:GO:0000003	-		IPR011989; PTHR23346 (PANTHER), PTHR23346:SF4 (PANTHER)

Caenorhabditis elegans	aldehyde dehydroge-se	13	F:GO:0004028; C:GO:0005773; F:GO:0004030; P:GO:0009269; F:GO:0004029; P:GO:0008218; P:GO:0055114; P:GO:0009737; C:GO:0016021; P:GO:0006081; C:GO:0005783; C:GO:0009536; P:GO:0009651	-	EC:1.2.1.5; EC:1.2.1.3	IPR012394; IPR015590; IPR016161; IPR016163
Caenorhabditis briggsae	atg2 autophagy related 2 homolog a	0		F:GO:0003674; C:GO:0005575		PTHR13190 (PANTHER), PTHR13190:SF2 (PANTHER)
Brugia pahangi	nuclear receptor nhr-6	1	F:GO:0005515	-		PTHR11865 (PANTHER), PTHR11865:SF168 (PANTHER)
Caenorhabditis elegans	ht004 protein	5	P:GO:0000003; P:GO:0010171; P:GO:0040010; P:GO:0002119; P:GO:0040011	-		PTHR12732 (PANTHER)
Caenorhabditis briggsae	bicaudal d homolog 1	2	C:GO:0043229; P:GO:0051179	-		SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0003677	-		IPR001766; IPR011991; SSF46785 (SUPERFAMILY)
Loa loa	transmembrane protein 93	3	P:GO:0009792; P:GO:0040007; P:GO:0002119	-		-
Caenorhabditis briggsae	briggsae cbr-xpc-1 protein	0		F:GO:0003684; P:GO:0006289; C:GO:0005634		-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	C:GO:0005887; P:GO:0006760; F:GO:0004181; P:GO:0006508	-	EC:3.4.17.0	G3DSA:3.40.630.10 (GENE3D), G3DSA:3.50.30.30 (GENE3D), PTHR10404 (PANTHER), PTHR10404:SF15 (PANTHER), SSF52025 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	transport and golgi organization-like	1	F:GO:0005515	-		IPR000210; IPR011333; IPR013069; IPR013089; PTHR23230:SF183 (PANTHER)
Caenorhabditis elegans	in family member (ttn-1)	3	P:GO:0009792; F:GO:0004672; F:GO:0000166	-		-
Loa loa	kiaa1018 protein	2	F:GO:0005515; P:GO:0006281	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis elegans	ubiquitin specific peptidase 24	0		F:GO:0004221; F:GO:0016787; F:GO:0003674; C:GO:0005575; P:GO:0006511; F:GO:0008234; F:GO:0008233; P:GO:0008150; F:GO:0005488		PTHR10420 (PANTHER), PTHR10420:SF3 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		C:GO:0016021; F:GO:0005375; P:GO:0006825		-
	-	0				IPR000175; PTHR11616:SF15 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	fatty acid amide hydrolase	10	P:GO:0009062; F:GO:0017064; F:GO:0016788; F:GO:0005543; C:GO:0031090; C:GO:0043231; C:GO:0044444; C:GO:0016021; F:GO:0004040; F:GO:0042803	-	EC:3.5.1.4	IPR000120; PTHR11895:SF4 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	atp-binding cassette sub-family e member 1	22	P:GO:0009615; C:GO:0005852; P:GO:0006413; P:GO:0006401; F:GO:0008428; P:GO:0040010; F:GO:0043024; P:GO:0040011; F:GO:0009055; F:GO:0051536; P:GO:0043524; P:GO:0009792; P:GO:0002119; P:GO:0010171; P:GO:0016049; F:GO:0016887; P:GO:0006200; P:GO:0016071; F:GO:0005524; P:GO:0040035; P:GO:0044419; C:GO:0005739	-		IPR003439; IPR003593; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR19248 (PANTHER), PTHR19248:SF5 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	myosin light polypeptide 1	4	P:GO:0018991; P:GO:0040010; F:GO:0005509; P:GO:0040011	-		IPR011992; IPR018249; PTHR23048 (PANTHER), SSF47473 (SUPERFAMILY)
	-	0				-
	-	0				-

Caenorhabditis briggsae	histidine triad nucleotide-binding protein 3	2	C:GO:0016021; F:GO:0003824	-		-
Caenorhabditis elegans	bc026590 protein	1	P:GO:0040011	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	calcium atpase	5	F:GO:0005388; C:GO:0016021; P:GO:0006754; F:GO:0005524; P:GO:0006816	-	EC:3.6.3.8	IPR001757; IPR008250; IPR018303; G3DSA:1.20.1110.10 (GENE3D), PTHR11939:SF76 (PANTHER), SSF56784 (SUPERFAMILY), SSF81653 (SUPERFAMILY), SSF81665 (SUPERFAMILY)
Caenorhabditis elegans	calcium atpase	5	F:GO:0005388; C:GO:0016021; P:GO:0006754; F:GO:0005524; P:GO:0006816	-	EC:3.6.3.8	IPR001757; IPR008250; IPR018303; G3DSA:1.20.1110.10 (GENE3D), PTHR11939:SF76 (PANTHER), SSF56784 (SUPERFAMILY), SSF81653 (SUPERFAMILY), SSF81665 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-ari-1 protein	1	F:GO:0005488	-		IPR006093; PTHR11685 (PANTHER), PTHR11685:SF16 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-ari-1 protein	1	F:GO:0005488	-		IPR006093; PTHR11685 (PANTHER), PTHR11685:SF16 (PANTHER)
	-	0				-
Caenorhabditis elegans	uncoordi-ted family member (unc-57)	6	F:GO:0042802; P:GO:0007417; C:GO:0005768; P:GO:0007165; F:GO:0016740; C:GO:0016020	-		IPR004148; PTHR10661 (PANTHER), PTHR10661:SF23 (PANTHER), SSF103657 (SUPERFAMILY)
Caenorhabditis elegans	gamma-glutamyltransferase 1-like	1	F:GO:0003840	-	EC:2.3.2.2	IPR000101; SignalP (SIGNALP), SSF56235 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	carboxypeptidase d	5	F:GO:0004181; C:GO:0005624; C:GO:0016021; P:GO:0006508; F:GO:0008270	-	EC:3.4.17.0	-
Brugia malayi	negative elongation factor b	1	C:GO:0044424	-		IPR010405
Loa loa	uncoordi-ted family member (unc-89)	0				-
Callithrix jacchus	eukaryotic translation elongation factor 1 beta 2	5	C:GO:0005829; F:GO:0003746; C:GO:0005853; F:GO:0005515; P:GO:0006414	-		IPR001326; IPR014038; IPR014717; PTHR11595 (PANTHER), PTHR11595:SF3 (PANTHER)
Caenorhabditis briggsae	-d dehydroge-se	4	C:GO:0005737; P:GO:0006546; F:GO:0016491; F:GO:0004047	-	EC:2.1.2.10	IPR013977; PTHR13847 (PANTHER), PTHR13847:SF6 (PANTHER), SSF101790 (SUPERFAMILY)

Loa loa	rb1-inducible coiled-coil protein 1	11	F:GO:0005515; P:GO:0007507; P:GO:0007254; C:GO:0000407; C:GO:0070969; P:GO:0045793; P:GO:0000045; P:GO:0001934; P:GO:0001889; C:GO:0005634; P:GO:0043066	-		IPR019460; PTHR13222 (PANTHER)
Caenorhabditis elegans	tar-binding protein	3	F:GO:0042802; P:GO:0007528; P:GO:0008344	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF6 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	solute carrier family member 37	8	P:GO:0048250; P:GO:0040010; F:GO:0005488; F:GO:0005381; C:GO:0016021; C:GO:0005743; P:GO:0034755; P:GO:0009792	-		-
Caenorhabditis elegans	gtp-ase activating protein for arf containing protein	6	F:GO:0008060; P:GO:0032312; F:GO:0008270; P:GO:0019915; P:GO:0002119; F:GO:0005515	-		-
Loa loa	er lipid raft associated 2	4	C:GO:0005789; F:GO:0005515; C:GO:0016021; P:GO:0030433	-		IPR001107; SignalP (SIGNALP)
Brugia malayi	chromosome 14 open reading frame 106	0		C:GO:0005694; C:GO:0005634; F:GO:0003677; P:GO:0007067; C:GO:0000775; P:GO:0051301; F:GO:0003674; C:GO:0005575; P:GO:0007049; P:GO:0008150; P:GO:0045449		IPR015216
Brugia malayi	chromosome 14 open reading frame 106	0		C:GO:0005694; C:GO:0005634; F:GO:0003677; P:GO:0007067; C:GO:0000775; P:GO:0051301; F:GO:0003674; C:GO:0005575; P:GO:0007049; P:GO:0008150; P:GO:0045449		IPR015216
	-	0				-
Caenorhabditis elegans	hypothetical protein Y55D5A.4 [Caenorhabditis elegans]	0				-
Angiostrongylus cantonensis	iq calmodulin-binding motif domain protein	0				SignalP (SIGNALP)

Caenorhabditis elegans	tbc (tre-2 bub2 cdc16) domain family member (tbc-20)	0		P:GO:0032313; C:GO:0005622; F:GO:0005097		IPR000195; G3DSA:1.10.8.270 (GENE3D), PTHR20913 (PANTHER), PTHR20913:SF7 (PANTHER)
Caenorhabditis elegans	tbc (tre-2 bub2 cdc16) domain family member (tbc-20)	0		P:GO:0032313; C:GO:0005622; F:GO:0005097		IPR000195; G3DSA:1.10.8.270 (GENE3D), PTHR20913 (PANTHER), PTHR20913:SF7 (PANTHER)
Angiostrongylus cantonensis	tubulin-specific chaperone a	6	F:GO:0051087; P:GO:0007023; F:GO:0051082; C:GO:0005829; P:GO:0007021; C:GO:0005874	-		IPR004226; G3DSA:1.20.58.90 (GENE3D)
	-	0				-
Caenorhabditis elegans	mannosyl-oligosaccharide alpha- -	7	F:GO:0004569; C:GO:0005788; F:GO:0004571; F:GO:0005509; P:GO:0006516; P:GO:0043161; C:GO:0016020	-	EC:3.2.1.130 ; EC:3.2.1.113	IPR001382; IPR010916; PTHR11742:SF8 (PANTHER), PS51257 (PROFILE), SignalP (SIGNALP)
Caenorhabditis elegans	er degradation-enhancing alpha-mannosidase-like 3	7	F:GO:0004569; C:GO:0005788; F:GO:0004571; F:GO:0005509; P:GO:0006516; P:GO:0043161; C:GO:0016020	-	EC:3.2.1.130 ; EC:3.2.1.113	IPR001382; IPR010916; PTHR11742:SF8 (PANTHER), PS51257 (PROFILE), SignalP (SIGNALP)
Brugia malayi	polymerase (d- directed) delta regulatory subunit	7	F:GO:0016772; P:GO:0040010; C:GO:0043625; P:GO:0006261; P:GO:0040035; P:GO:0040011; P:GO:0009792	-		IPR007185; PTHR10416 (PANTHER)
	-	0				IPR019317
	-	0				IPR019317
Caenorhabditis elegans	guanyl-nucleotide exchange factor	3	F:GO:0005085; P:GO:0007520; P:GO:0002121	-		IPR000048; IPR000904; G3DSA:1.10.1000.11 (GENE3D), G3DSA:1.10.220.20 (GENE3D), PTHR10663 (PANTHER), PTHR10663:SF12 (PANTHER)
Trichomonas vaginalis G3	ankyrin unc44	0		F:GO:0005216; P:GO:0006816; C:GO:0016021; C:GO:0016020; P:GO:0006811; P:GO:0006810; F:GO:0005262; C:GO:0000502; P:GO:0055085		-
	-	0				-
Caenorhabditis briggsae	slowpoke potassium channel family member (slo-2)	6	C:GO:0016020; P:GO:0006813; P:GO:0008152; F:GO:0003824; F:GO:0015269; F:GO:0005488	-		PTHR10027 (PANTHER), PTHR10027:SF6 (PANTHER)

Caenorhabditis briggsae	spermatogenesis-associated protein 20	0		F:GO:0003674; F:GO:0004476; P:GO:0006013; F:GO:0003824; C:GO:0005575		IPR008928; IPR012341; PTHR12145 (PANTHER)
Ixodes scapularis	conserved hypothetical protein [Ixodes scapularis]	0				-
	-	0				-
						IPR003598; IPR003961; IPR007110; IPR008957; IPR013098; IPR013783; PR00014 (PRINTS), PTHR19900 (PANTHER), PTHR19900:SF7 (PANTHER), SSF48726 (SUPERFAMILY)
Loa loa	chromosome 7 open reading frame 20	0		F:GO:0003674; P:GO:0008150; F:GO:0005515; C:GO:0005575		IPR007317
Caenorhabditis briggsae	isoform e	1	F:GO:0005515	-		IPR001849; IPR011993; PTHR17271 (PANTHER), PTHR17271:SF1 (PANTHER), SSF50729 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG22130 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)
Brugia malayi	ancient conserved domain protein	0				IPR000644; G3DSA:3.10.580.10 (GENE3D), PTHR12064 (PANTHER), PTHR12064:SF6 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	zinc finger	1	F:GO:0005515	-		IPR007087; IPR013087; IPR015880; IPR017956; PTHR23224 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis briggsae	diphosphomevalo-te decarboxylase	9	P:GO:0009792; P:GO:0002119; P:GO:0006694; P:GO:0044237; P:GO:0000003; P:GO:0040011; P:GO:0040007; F:GO:0016829; F:GO:0000166	-		IPR005935; G3DSA:3.30.70.890 (GENE3D), SSF55060 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	r--dependent helicase	8	P:GO:0009792; P:GO:0002119; F:GO:0003724; F:GO:0008026; F:GO:0003676; P:GO:0040010; F:GO:0005524; P:GO:0000003	-		SignalP (SIGNALP)
Caenorhabditis elegans	loc556764 protein	10	P:GO:0009792; P:GO:0002119; F:GO:0003724; F:GO:0008026; F:GO:0003676; P:GO:0040010; F:GO:0008186; F:GO:0005524; P:GO:0000003; P:GO:0006396	-		IPR000629; IPR001650; IPR011545; IPR014001; IPR014014; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF50 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)

Caenorhabditis briggsae	loc556764 protein	7	P:GO:0009792; P:GO:0002119; F:GO:0008026; F:GO:0003676; P:GO:0040010; F:GO:0005524; P:GO:0000003	-		IPR000629; IPR001650; IPR011545; IPR014001; IPR014014; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF50 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	loc556764 protein	10	P:GO:0009792; P:GO:0002119; F:GO:0003724; F:GO:0008026; F:GO:0003676; P:GO:0040010; F:GO:0008186; F:GO:0005524; P:GO:0000003; P:GO:0006396	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis briggsae	Hypothetical protein CBG02647 [Caenorhabditis briggsae]	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Loa loa	hypothetical protein LOAG_10533 [Loa loa]	0				-
Loa loa	hypothetical protein LOAG_10533 [Loa loa]	0				-
	-	0				SignalP (SIGNALP)
Brugia malayi	elegans protein partially confirmed by transcript evidence	0		F:GO:0003723; F:GO:0003674; P:GO:0007492; P:GO:0008150; C:GO:0005634; C:GO:0005575		IPR004087; IPR004088; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR10288 (PANTHER), SSF54791 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	F:GO:0016740	-		IPR013783
Caenorhabditis briggsae	hypothetical kda protein in chromosome	11	P:GO:0040010; P:GO:0016079; F:GO:0005488; P:GO:0000910; C:GO:0045202; C:GO:0000299; P:GO:0007602; P:GO:0006898; P:GO:0030100; P:GO:0009792; P:GO:0048488	-		PTHR12444 (PANTHER)
Caenorhabditis briggsae	splicing factor 3b	11	P:GO:0040035; P:GO:0009792; P:GO:0002119; C:GO:0005686; F:GO:0005515; P:GO:0018996; C:GO:0071011; P:GO:0040011; P:GO:0040007; P:GO:0000398; C:GO:0071013	-		IPR006568; IPR007180; PTHR12785 (PANTHER), PTHR12785:SF6 (PANTHER)
Caenorhabditis elegans	briggsae cbr-gak-1 protein	0		F:GO:0005515; F:GO:0003677		-

Caenorhabditis elegans	briggsae cbr-gak-1 protein	0		F:GO:0005515; F:GO:0003677		-
	-	0				-
Caenorhabditis elegans	novel protein vertebrate gamma-aminobutyric acid b 2	5	P:GO:0007186; C:GO:0016021; P:GO:0007165; F:GO:0004965; F:GO:0004930	-		IPR002455; IPR017978; PTHR10519 (PANTHER), PTHR10519:SF2 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	ykad_caeel ame: full=uncharacterized protein	0		F:GO:0046872; F:GO:0008270; F:GO:0005515		-
	-	0				-
Caenorhabditis briggsae	acyl binding protein	1	F:GO:0005488	-		IPR000582; IPR014352; PTHR23310:SF5 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Oesophagostomum dentatum	serine threonine protein phosphatase pp1 isozyme 1	4	P:GO:0006470; F:GO:0046872; F:GO:0004722; P:GO:0000003	-		IPR004843; IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF19 (PANTHER), SSF56300 (SUPERFAMILY)
Loa loa	pci domain containing 2	5	P:GO:0000003; P:GO:0010171; P:GO:0040010; P:GO:0002119; P:GO:0040011	-		PTHR12732 (PANTHER)
Caenorhabditis elegans	bestrophin family protein	2	P:GO:0040011; P:GO:0040018	-		IPR000615; IPR021134
Caenorhabditis elegans	hypothetical protein R02F2.7 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	d- polymerase gamma	12	P:GO:0006470; F:GO:0004383; P:GO:0030421; P:GO:0008340; F:GO:0003887; C:GO:0005760; P:GO:0006264; F:GO:0003677; F:GO:0004725; F:GO:0020037; P:GO:0008406; P:GO:0006182	-	EC:4.6.1.2; EC:2.7.7.7; EC:3.1.3.48	IPR001098; IPR002297
	-	0				-
Caenorhabditis elegans	apolipoprotein h	7	P:GO:0031100; P:GO:0034197; P:GO:0030195; C:GO:0034358; F:GO:0008289; P:GO:0048523; P:GO:0008152	-		IPR000436; IPR016060; PTHR19325 (PANTHER), PTHR19325:SF40 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-pdr-1 protein	3	P:GO:0009987; F:GO:0016874; F:GO:0005515	-		IPR002867; IPR003977; PTHR11685 (PANTHER), PTHR11685:SF4 (PANTHER), SSF57850 (SUPERFAMILY)
Brugia malayi	wd repeat domain 68	7	C:GO:0005737; F:GO:0005515; P:GO:0016567; C:GO:0080008; F:GO:0004402; C:GO:0005634; P:GO:0051216	-	EC:2.3.1.48	-

Caenorhabditis briggsae	vacuolar atp synthase subunit g	7	P:GO:0012501; F:GO:0015078; C:GO:0016471; P:GO:0006754; F:GO:0016820; P:GO:0015992; C:GO:0005886	-	EC:3.6.3.0	IPR005124; PTHR12713:SF4 (PANTHER)
Caenorhabditis briggsae	coiled-coil domain containing 132	0				PTHR13258 (PANTHER)
Haemonchus contortus	phosphoenolpyruvate carboxyki-se	6	C:GO:0005737; P:GO:0006094; F:GO:0046872; F:GO:0005525; F:GO:0016301; F:GO:0004613	-	EC:4.1.1.32	IPR008209; G3DSA:2.170.8.10 (GENE3D), SSF53795 (SUPERFAMILY)
Caenorhabditis elegans	translation initiation factor eif-2b epsilon subunit	5	P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0040018; P:GO:0040010	-		G3DSA:3.90.550.10 (GENE3D), PTHR22572 (PANTHER), PTHR22572:SF4 (PANTHER), SSF53448 (SUPERFAMILY)
Caenorhabditis briggsae	troponin c	7	P:GO:0055114; P:GO:0000003; P:GO:0040007; F:GO:0005509; F:GO:0005515; F:GO:0032440; P:GO:0002119	-	EC:1.3.1.74	IPR002048; IPR011992; IPR018247; IPR018248; IPR018249; PTHR23050 (PANTHER), PTHR23050:SF16 (PANTHER), SSF47473 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-lin-9 protein	0		C:GO:0070176		-
Brugia malayi	mediator of r- polymerase ii transcription subunit 21	6	P:GO:0045944; P:GO:0007413; P:GO:0001824; P:GO:0040011; C:GO:0016592; F:GO:0003713	-		IPR021384; PTHR13381 (PANTHER), SSF140718 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical kda protein in chromosome	4	P:GO:0009792; P:GO:0040010; F:GO:0005515; P:GO:0002119	-		-
Angiostrongylus cantonensis	pre-mr- splicing protein	10	P:GO:0007030; P:GO:0002119; P:GO:0018996; C:GO:0071011; P:GO:0000003; P:GO:0040011; P:GO:0040007; C:GO:0005829; P:GO:0000398; C:GO:0071013	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR19923 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021		-
Botryotinia fuckeliana B05.10	hypothetical protein BC1G_06829 [Botryotinia fuckelia-B05.10]	0		F:GO:0016787		-

Caenorhabditis elegans	lethal protein isoform d	8	P:GO:0018996; P:GO:0009792; P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		-
Loa loa	organic solute transporter alpha-like protein	0		C:GO:0016021; P:GO:0009792; F:GO:0005215; P:GO:0006810		IPR005178; PTHR23423:SF3 (PANTHER), SignalP (SIGNALP)
	-	0				-
Angiostrongylus cantonensis	uncoordi-ted family member (unc-87)	1	F:GO:0005515	-		-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Loa loa	briggsae cbr-ced-3 protein	7	C:GO:0005737; P:GO:0030972; F:GO:0005515; F:GO:0016787; P:GO:0000003; P:GO:0008340; C:GO:0016020	-		IPR001315; IPR002398; IPR011029; PTHR10454:SF21 (PANTHER)
Brugia malayi	splicing factor 45	0		F:GO:0003676; F:GO:0000166; C:GO:0005622		IPR000467; IPR000504; IPR012677; PTHR13288 (PANTHER), PTHR13288:SF8 (PANTHER), SSF54928 (SUPERFAMILY)
Brugia malayi	splicing factor 45	0		F:GO:0003676; F:GO:0000166; C:GO:0005622		IPR000467; IPR000504; IPR012677; PTHR13288 (PANTHER), PTHR13288:SF8 (PANTHER), SSF54928 (SUPERFAMILY)
Homo sapiens	prosaposin	19	P:GO:0055085; F:GO:0008047; P:GO:0043065; P:GO:0006687; P:GO:0045161; C:GO:0016021; C:GO:0005743; C:GO:0043202; C:GO:0005615; F:GO:0008289; P:GO:0006869; F:GO:0005515; P:GO:0009966; P:GO:0007585; F:GO:0005319; C:GO:0005578; F:GO:0005529; P:GO:0006919; C:GO:0005794	-		IPR007856; IPR008138; IPR008139; IPR011001; PTHR11480 (PANTHER), PTHR11480:SF3 (PANTHER)

Caenorhabditis elegans	zeta-coat protein	14	C:GO:0030126; P:GO:0008340; C:GO:0000808; P:GO:0048599; P:GO:0006260; P:GO:0032940; P:GO:0018996; P:GO:0006891; P:GO:0002119; F:GO:0005515; P:GO:0006898; P:GO:0006886; P:GO:0009792; C:GO:0005634	-		IPR011012; IPR022775; G3DSA:3.30.450.60 (GENE3D), PTHR11043 (PANTHER)
Caenorhabditis elegans	ferm domain (-ezrin-radixin-moesin) family member (frm-1)	0		F:GO:0005488; C:GO:0019898; F:GO:0008092; F:GO:0005515		-
Caenorhabditis elegans	splicing factor 3a subunit 2	12	C:GO:0005681; F:GO:0008270; F:GO:0003676; P:GO:0040007; P:GO:0040035; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0000398; P:GO:0006898; P:GO:0002009; P:GO:0009792	-		IPR000690; IPR003604; IPR015880; PTHR23205 (PANTHER)
Brugia malayi	ubx domain containing 8	0		C:GO:0005811; F:GO:0003674; C:GO:0005737; P:GO:0006986; C:GO:0005783; P:GO:0008150; F:GO:0005515; C:GO:0005575		IPR001012; G3DSA:3.10.20.90 (GENE3D), PTHR23322 (PANTHER), PTHR23322:SF1 (PANTHER), SSF54236 (SUPERFAMILY)
Caenorhabditis elegans	cog5 protein	3	P:GO:0009792; P:GO:0040010; P:GO:0040039	-		-
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
	-	0				-
Caenorhabditis elegans	isocitrate dehydroge-se	6	F:GO:0051287; P:GO:0055114; F:GO:0000287; P:GO:0006099; F:GO:0004449; C:GO:0005739	-	EC:1.1.1.41	IPR001804; IPR019818; PTHR11835:SF5 (PANTHER), SSF53659 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	vacuolar protein sorting-associated protein 53 homolog	0		C:GO:0010008; C:GO:0016020; C:GO:0005794; C:GO:0005768; P:GO:0015031		IPR007234; PTHR12820 (PANTHER)
	-	0				-
	-	0				-

Caenorhabditis briggsae	protein	2	F:GO:0005488; F:GO:0003824	-		IPR001841; IPR002867; IPR006058; IPR013083; IPR015880; IPR017907; PTHR11685 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis briggsae	thioesterase superfamily member 2	2	P:GO:0051289; F:GO:0016291	-		IPR003736; IPR006683; G3DSA:3.10.129.10 (GENE3D), PTHR21660 (PANTHER), SSF54637 (SUPERFAMILY)
Caenorhabditis elegans	acyl-protein thioesterase 1	1	F:GO:0016787	-		IPR003140; G3DSA:3.40.50.1820 (GENE3D), PTHR10655 (PANTHER), PTHR10655:SF6 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
	-	0				-
	-	0				-
Loa loa	non-smc condensin ii subunit d3	3	F:GO:0005488; P:GO:0007049; C:GO:0044424	-		IPR005829; IPR011989; IPR016024; PTHR14222 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	protein ki-se domain containing protein	4	P:GO:0006468; F:GO:0005524; P:GO:0040011; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
Loa loa	inositol -trisphosphate receptor	6	F:GO:0005488; P:GO:0006816; F:GO:0005220; P:GO:0055085; C:GO:0016021; C:GO:0005783	-		IPR015925; PTHR13715:SF2 (PANTHER)
Brugia malayi	adp-specific phosphofructoki-se glucoki-se conserved region family protein	3	F:GO:0016301; F:GO:0016773; P:GO:0005975	-	EC:2.7.1.0	IPR001227; IPR016035
Caenorhabditis elegans	briggsae cbr-spd-5 protein	1	F:GO:0005488	-		PD936484 (PRODOM)
Loa loa	phosphatidylinositide phosphatase sac1	6	P:GO:0009792; P:GO:0002119; P:GO:0040018; P:GO:0040010; P:GO:0008340; C:GO:0016021	-		IPR002013
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0007264; F:GO:0008270; C:GO:0005575; F:GO:0005085		IPR007515; IPR011057; IPR011323; PTHR13276 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				IPR000299; IPR019748
Loa loa	g-rich sequence factor-	7	C:GO:0043234; P:GO:0007311; P:GO:0006417; P:GO:0051276; P:GO:0045451; F:GO:0005515; P:GO:0007428	-		IPR000504; IPR012677; PTHR13976 (PANTHER), PTHR13976:SF3 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	P:GO:0006415; F:GO:0003747	-		SignalP (SIGNALP)
Caenorhabditis briggsae	gpn-loop gtpase 2	2	F:GO:0005515; F:GO:0000166	-		IPR004130; G3DSA:3.40.50.300 (GENE3D), PTHR21231 (PANTHER), PTHR21231:SF3 (PANTHER), SSF52540 (SUPERFAMILY)

	-	0				-
Clostridiales bacterium 1_7_47_FAA	#NAME?	0		F:GO:0004553; P:GO:0005978; P:GO:0005975; F:GO:0003824; F:GO:0043169; F:GO:0003844		-
	-	0				-
Caenorhabditis elegans	interferon gamma-inducible thiol reductase	0				IPR004911; PTHR13234:SF2 (PANTHER)
Caenorhabditis briggsae	membrane protein involved in er to golgi	1	P:GO:0016192	-		SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-npp-15 protein	0		F:GO:0003674; C:GO:0016021; P:GO:0040010		-
	-	0				-
Caenorhabditis briggsae	tyrosine sulfotransferase	1	F:GO:0008146	-	EC:2.8.2.0	G3DSA:3.40.50.300 (GENE3D), PTHR12788 (PANTHER), SSF52540 (SUPERFAMILY)
Angiostrongylus cantonensis	26s protease regulatory subunit 4	9	F:GO:0017111; C:GO:0000502; C:GO:0005730; P:GO:0051436; P:GO:0051437; P:GO:0031145; F:GO:0005524; F:GO:0005515; C:GO:0005737	-	EC:3.6.1.15	PTHR23073 (PANTHER), PTHR23073:SF9 (PANTHER)
Caenorhabditis elegans	briggsae cbr-deps-1 protein	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	protein sidekick	2	P:GO:0007155; C:GO:0016021	-		IPR003961; IPR008957; IPR013783; PTHR10489 (PANTHER), PTHR10489:SF57 (PANTHER)
Loa loa	transcription initiation factor tfiid subunit 7	0		C:GO:0005669; P:GO:0006367; F:GO:0016251; F:GO:0003743		IPR006751; PTHR12228 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	3	C:GO:0034703; F:GO:0005261; P:GO:0055080	-		SignalP (SIGNALP)
Caenorhabditis briggsae	queuine tr--ribosyltransferase	2	F:GO:0008479; P:GO:0008616	-	EC:2.4.2.29	IPR002616
	-	0				IPR015880
	-	0				-
Angiostrongylus cantonensis	elegans protein confirmed by transcript evidence	0				IPR021010; SSF141739 (SUPERFAMILY)
Angiostrongylus cantonensis	elegans protein confirmed by transcript evidence	0				IPR021010; SSF141739 (SUPERFAMILY)
Angiostrongylus cantonensis	elegans protein confirmed by transcript evidence	0				IPR021010; SSF141739 (SUPERFAMILY)

Caenorhabditis elegans	argo-ute 1	5	C:GO:0005737; P:GO:0008340; F:GO:0003743; P:GO:0009790; P:GO:0002119	-		-
Caenorhabditis elegans	argo-ute 1	5	C:GO:0005737; P:GO:0008340; F:GO:0003743; P:GO:0009790; P:GO:0002119	-		-
Caenorhabditis briggsae	latent transforming growth factor beta binding protein 1	6	P:GO:0001570; F:GO:0005488; P:GO:0040010; C:GO:0005578; P:GO:0048570; P:GO:0007179	-		IPR000152; IPR000742; IPR013032; IPR013091; IPR018097; G3DSA:2.10.25.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF84 (PANTHER), SSF57196 (SUPERFAMILY)
Loa loa	lobulin-like cell adhesion molecule family member (igcm-3)	1	P:GO:0019915	-		-
Caenorhabditis elegans	chromosome 9 open reading frame 114	4	P:GO:0009792; P:GO:0040010; P:GO:0006898; P:GO:0002119	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	exocyst complex component 1	5	P:GO:0007126; P:GO:0000003; P:GO:0040010; F:GO:0005515; P:GO:0040011	-		IPR019160; PTHR16092 (PANTHER), PTHR16092:SF1 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	atpase type 13a1	5	C:GO:0016021; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0006812	-		IPR001757; G3DSA:3.40.50.1000 (GENE3D), PTHR11939:SF48 (PANTHER)
Caenorhabditis elegans	atpase type 13a1	5	C:GO:0016021; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0006812	-		IPR001757; G3DSA:3.40.50.1000 (GENE3D), PTHR11939:SF48 (PANTHER)
Loa loa	protein mo25	1	F:GO:0005488	-		IPR002007; IPR013878; IPR016024; PTHR10182 (PANTHER), PTHR10182:SF3 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	atp synthase lipid-binding mitochondrial precursor	10	F:GO:0046933; C:GO:0000276; C:GO:0016021; P:GO:0045471; P:GO:0015986; P:GO:0040007; F:GO:0008289; P:GO:0002119; P:GO:0006898; P:GO:0009792	-	EC:3.6.3.14	IPR000454; IPR002379; IPR020537; PTHR10031 (PANTHER), SignalP (SIGNALP)

Loa loa	polymerase (d- directed) gamma	6	P:GO:0030421; P:GO:0008340; F:GO:0003676; P:GO:0006264; F:GO:0016791; P:GO:0008406	-	EC:3.1.3.0	-
	-	0				IPR003124
Caenorhabditis elegans	gata transcription factor gatac	3	F:GO:0046872; P:GO:0045449; F:GO:0003677	-		IPR000679; IPR013088; PTHR10071 (PANTHER), PTHR10071:SF15 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis briggsae	pecanex-like 3 isoform 1	0		F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150; C:GO:0005575		SignalP (SIGNALP)
Caenorhabditis briggsae	tpr domain containing protein	0		F:GO:0005488		-
Caenorhabditis elegans	proteasome (macropain) 26s non- 10	25	P:GO:0051436; P:GO:0045737; P:GO:0002119; P:GO:0090201; C:GO:0045111; P:GO:0032088; C:GO:0005838; C:GO:0015629; F:GO:0008134; P:GO:0031145; P:GO:0043409; P:GO:0040010; P:GO:0006898; P:GO:0043518; C:GO:0005737; P:GO:0043066; P:GO:0030307; P:GO:0051437; P:GO:0018996; P:GO:0070682; P:GO:0032436; P:GO:0007253; P:GO:0040011; C:GO:0005634; P:GO:0010553	-		IPR002110; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER), PTHR18958:SF176 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis elegans	membrane calcium atpase family member (mca-3)	7	F:GO:0005388; C:GO:0016021; P:GO:0006754; F:GO:0005524; P:GO:0006816; C:GO:0005737; P:GO:0030182	-	EC:3.6.3.8	IPR001757; IPR004014; G3DSA:2.70.150.10 (GENE3D), PTHR11939:SF76 (PANTHER), SSF81665 (SUPERFAMILY)
Caenorhabditis elegans	integrator complex subunit 7	0		F:GO:0005488; C:GO:0005737; C:GO:0005634		PTHR13322 (PANTHER)
Caenorhabditis elegans	integrator complex subunit 7	0		F:GO:0005488; C:GO:0005737; C:GO:0005634		PTHR13322 (PANTHER)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR009432; SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR009432; SignalP (SIGNALP)

	-	0				-
	-	0				-
Caenorhabditis elegans	39s ribosomal protein mitochondrial	5	P:GO:0040035; P:GO:0009792; P:GO:0002119; C:GO:0005840; P:GO:0040010	-		IPR002677
Caenorhabditis elegans	39s ribosomal protein mitochondrial	6	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0040010; C:GO:0015934; P:GO:0006412	-	EC:3.6.5.3	IPR002677
Caenorhabditis elegans	39s ribosomal protein mitochondrial	5	P:GO:0040035; P:GO:0009792; P:GO:0002119; C:GO:0005840; P:GO:0040010	-		IPR002677
Caenorhabditis elegans	39s ribosomal protein mitochondrial	6	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0040010; C:GO:0015934; P:GO:0006412	-	EC:3.6.5.3	IPR002677
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Brugia malayi	bromodomain containing protein	0		P:GO:0000003; P:GO:0010171; P:GO:0009792; P:GO:0002119; F:GO:0005515		-
Caenorhabditis elegans	cytochrome oxidase assembly protein	2	P:GO:0006461; C:GO:0016020	-		IPR000169; IPR003780; PTHR23289 (PANTHER), SignalP (SIGNALP)

Homo sapiens	cathepsin b	29	F:GO:0042277; P:GO:0009749; C:GO:0005764; F:GO:0030984; P:GO:0051789; C:GO:0009897; C:GO:0005625; C:GO:0005739; P:GO:0045471; P:GO:0042981; C:GO:0005901; P:GO:0009611; F:GO:0032403; C:GO:0005615; P:GO:0006508; P:GO:0043434; F:GO:0004197; C:GO:0042470; P:GO:0007519; P:GO:0014070; P:GO:0070670; C:GO:0048471; C:GO:0016324; C:GO:0042383; P:GO:0050790; P:GO:0014075; P:GO:0060548; P:GO:0006914;	-	EC:3.4.22.0	IPR000169; IPR000668; IPR013128; IPR015643; G3DSA:3.90.70.10 (GENE3D), SSF54001 (SUPERFAMILY)
	-	0				-
Arthroderma otae CBS 113480	transferase	2	C:GO:0016020; F:GO:0003824	-		IPR017849; SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein T04C4.1 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				IPR000571
	-	0				IPR000571
	-	0				-
Caenorhabditis elegans	replication factor c (activator 1) 145kda	19	C:GO:0005654; P:GO:0000003; F:GO:0005515; P:GO:0006261; P:GO:0040010; P:GO:0006898; C:GO:0005624; P:GO:0006297; F:GO:0008047; P:GO:0009792; F:GO:0008517; F:GO:0003689; P:GO:0002119; C:GO:0005663; P:GO:0015884; F:GO:0015350; P:GO:0007004; C:GO:0005887; F:GO:0005524	-		IPR008921; IPR013725; G3DSA:1.10.8.60 (GENE3D), PTHR23389 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis elegans	diacylglycerol ki-se	7	F:GO:0003676; P:GO:0007205; F:GO:0005515; P:GO:0007165; F:GO:0008270; F:GO:0004143; F:GO:0000166	-	EC:2.7.1.107	IPR000159; IPR022272; SSF54236 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	mitochondrial ribosomal protein s31	0		C:GO:0005840		PTHR13231 (PANTHER)
	-	0				-
Homo sapiens	-dh dehydroge-se subunit 6	0				PTHR11435 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	rho gtpase-activating protein 21	5	F:GO:0005100; P:GO:0007266; C:GO:0044444; C:GO:0043229; C:GO:0016020	-		-
Caenorhabditis briggsae	isocitrate dehydroge-se	10	P:GO:0006097; P:GO:0006103; C:GO:0005743; P:GO:0055114; P:GO:0006099; F:GO:0051287; F:GO:0004450; F:GO:0000287; P:GO:0006102; P:GO:0006950	-	EC:1.1.1.42	IPR001804; IPR004790; IPR019818; SignalP (SIGNALP), SSF53659 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG14129 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	archain 1	9	C:GO:0005829; P:GO:0006890; P:GO:0018996; C:GO:0030131; P:GO:0002119; F:GO:0005515; C:GO:0030663; P:GO:0048205; P:GO:0006886	-		IPR008968; G3DSA:2.60.40.1170 (GENE3D), PTHR10121 (PANTHER)
Caenorhabditis briggsae	ring finger protein 7	13	F:GO:0005507; P:GO:0008631; F:GO:0008270; P:GO:0000003; P:GO:0051775; P:GO:0045116; P:GO:0006916; P:GO:0008637; F:GO:0019788; F:GO:0005515; C:GO:0005737; P:GO:0006919; C:GO:0005634	-		IPR001841; IPR013083; IPR018363; PTHR11210 (PANTHER), PTHR11210:SF3 (PANTHER), SSF57850 (SUPERFAMILY)

Caenorhabditis elegans	hypothetical protein F55F10.1 [Caenorhabditis elegans]	0		C:GO:0005634; F:GO:0000166; F:GO:0008134; F:GO:0017111; F:GO:0005524; F:GO:0016887; P:GO:0006355; C:GO:0005622; P:GO:0043254		PTHR22908 (PANTHER), PTHR22908:SF13 (PANTHER)
	-	0				-
Caenorhabditis sp. PS1010	chromatin assembly factor 1 subunit b	5	P:GO:0009987; P:GO:0000003; F:GO:0005515; C:GO:0044444; C:GO:0044428	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR15271 (PANTHER)
Brugia malayi	hypothetical kda protein in chromosome	0		C:GO:0016021; C:GO:0016020; F:GO:0005215; P:GO:0006810		IPR000425; PTHR21191 (PANTHER), PTHR21191:SF2 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	f37c4_caeel ame: full=protein	1	F:GO:0005515	-		-
	-	0				IPR005829
Caenorhabditis briggsae	run domain containing protein	0		F:GO:0046872; C:GO:0005737; F:GO:0008270; P:GO:0023034; F:GO:0005515		IPR004012; PTHR22835 (PANTHER), PTHR22835:SF37 (PANTHER), SSF140741 (SUPERFAMILY)
Caenorhabditis elegans	polyglutamine-binding protein 1	0		F:GO:0005515		IPR001202; G3DSA:2.20.70.10 (GENE3D), PTHR21737 (PANTHER), PTHR21737:SF3 (PANTHER)
Brugia malayi	Conserved hypothetical protein [Brugia malayi]	0		F:GO:0003676; F:GO:0008270		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis elegans	subfamily member 13	3	P:GO:0006457; F:GO:0031072; F:GO:0051082	-		IPR001623; IPR011989; IPR015609; PTHR11821:SF23 (PANTHER)
Caenorhabditis elegans	subfamily member 13	3	P:GO:0006457; F:GO:0031072; F:GO:0051082	-		IPR001623; IPR015609; PTHR11821:SF23 (PANTHER)
Caenorhabditis elegans	loc446287 protein	2	P:GO:0008152; F:GO:0016627	-		IPR006090; IPR009075; PTHR10909 (PANTHER), PTHR10909:SF10 (PANTHER)
Caenorhabditis elegans	#NAME?	3	F:GO:0008417; F:GO:0005515; C:GO:0016020	-		SignalP (SIGNALP)
	-	0				-
Angiostrongylus cantonensis	peroxisomal membrane protein 11c	0		C:GO:0005777; F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150; C:GO:0005575; C:GO:0005778		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		IPR002223; IPR006150; IPR020901; PTHR10083 (PANTHER), PTHR10083:SF39 (PANTHER)
	-	0				-
	-	0				-

	-	0				-
Brugia malayi	collagen-binding adhesin	0		C:GO:0005618; P:GO:0007155; C:GO:0009986; F:GO:0005518; F:GO:0005515		IPR012340; IPR013955; IPR016027
Salinispora tropica CNB-440	collagen-binding adhesin	0		C:GO:0005618; P:GO:0007155; C:GO:0009986; F:GO:0005518; F:GO:0005515		-
Salinispora tropica CNB-440	collagen-binding adhesin	0		C:GO:0005618; P:GO:0007155; C:GO:0009986; F:GO:0005518; F:GO:0005515		IPR016027
Caenorhabditis briggsae	briggsae cbr-prx-14 protein	4	P:GO:0009792; P:GO:0002119; P:GO:0040010; C:GO:0044464	-		IPR006785; PTHR23058 (PANTHER)
Acyrthosiphon pisum	ubiquitin-conjugating enzyme e2e 1 (ubc4 5 yeast)	14	C:GO:0005829; P:GO:0033523; P:GO:0000209; P:GO:0051436; P:GO:0010390; P:GO:0032020; P:GO:0051437; P:GO:0070936; P:GO:0031145; F:GO:0004842; F:GO:0042296; F:GO:0005515; C:GO:0000151; C:GO:0005654	-	EC:6.3.2.19	IPR000608; IPR016135; PTHR11621 (PANTHER), PTHR11621:SF29 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	4	C:GO:0016021; P:GO:0006814; P:GO:0055085; F:GO:0005215	-		-
	-	0				-
Caenorhabditis elegans	hypothetical protein F25D7.5 [Caenorhabditis elegans]	0				-
Brugia malayi	microtubule associated protein	1	F:GO:0005488	-		IPR000357; IPR011989; IPR016024; IPR021133; PTHR12609 (PANTHER)
Caenorhabditis elegans	sterol regulatory element-binding protein cleavage-activating protein	6	P:GO:0006629; C:GO:0043231; C:GO:0044444; P:GO:0044281; P:GO:0009792; C:GO:0016020	-		-
	-	0				-
Caenorhabditis elegans	hypothetical protein W04B5.3 [Caenorhabditis elegans]	0		F:GO:0005529		PTHR12381 (PANTHER), PTHR12381:SF2 (PANTHER)
Caenorhabditis elegans	kiaa1450 partial	0				PTHR21634 (PANTHER), PTHR21634:SF9 (PANTHER)
	-	0				-

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	11	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040002; P:GO:0040011; C:GO:0016021; C:GO:0005576; P:GO:0019915; P:GO:0040007; P:GO:0006898; F:GO:0042302	-		IPR002486; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER), SignalP (SIGNALP)
Loa loa	briggsae cbr-smg-1 protein	0		F:GO:0016740; P:GO:0016310; F:GO:0004674; P:GO:0006974; C:GO:0005634; F:GO:0000166; C:GO:0005737; F:GO:0003674; F:GO:0005524; F:GO:0016301; P:GO:0006281; C:GO:0005575; P:GO:0000184; F:GO:0016773; F:GO:0046872; P:GO:0008150; F:GO:0005488		-
Caenorhabditis elegans	reticulon protein family member (ret-1)	1	F:GO:0005515	-		-
Caenorhabditis elegans	reticulon protein family member (ret-1)	2	C:GO:0044464; F:GO:0005515	-		IPR003388; PTHR10994:SF19 (PANTHER)
Caenorhabditis elegans	reticulon protein family member (ret-1)	2	C:GO:0044464; F:GO:0005515	-		IPR003388; PTHR10994:SF19 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	alanine-glyoxylate aminotransferase	2	F:GO:0030170; F:GO:0008483	-	EC:2.6.1.0	IPR005814; IPR015421; IPR015424; PTHR11986:SF23 (PANTHER)
Caenorhabditis elegans	briggsae cbr-pad-1 protein	2	P:GO:0015031; P:GO:0007275	-		PTHR14042 (PANTHER)
Caenorhabditis elegans	bromodomain and wd repeat domain containing 2	1	P:GO:0008286	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	briggsae cbr-ada-2 protein	8	P:GO:0009792; P:GO:0010171; P:GO:0040027; P:GO:0040010; P:GO:0000003; P:GO:0008340; P:GO:0040011; P:GO:0006898	-		IPR007087; IPR017969; PTHR12374 (PANTHER)
Branchiostoma floridae	vacuolar protein sorting 35	0				IPR005378; SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	general transcription factor polypeptide 52kda	8	C:GO:0005654; P:GO:0006366; F:GO:0016874; F:GO:0004672; P:GO:0045449; F:GO:0005488; C:GO:0044444; P:GO:0006281	-		IPR004598; IPR010916

Loa loa	bloom s syndrome protein homolog	3	P:GO:0006259; F:GO:0008026; F:GO:0000166	-		-
	-	0				-
Caenorhabditis elegans	cysteine protease atg4d	0		P:GO:0006914; C:GO:0005737; F:GO:0016787; F:GO:0008234; F:GO:0008233; F:GO:0004197; P:GO:0006810; P:GO:0015031		IPR005078; PTHR22624:SF15 (PANTHER)
Caenorhabditis brenneri	fk506 binding protein 13kda	6	P:GO:0006457; F:GO:0005528; F:GO:0005515; C:GO:0016020; C:GO:0005783; F:GO:0003755	-	EC:5.2.1.8	IPR001179; G3DSA:3.10.50.40 (GENE3D), PTHR10516:SF20 (PANTHER), SignalP (SIGNALP), SSF54534 (SUPERFAMILY)
	-	0				-
Macaca fascicularis	proteasome (macropain) beta 4	11	P:GO:0051436; P:GO:0051437; F:GO:0004298; C:GO:0045111; C:GO:0005813; P:GO:0031145; F:GO:0001530; P:GO:0002862; P:GO:0044419; C:GO:0005839; C:GO:0005634	-	EC:3.4.25.0	IPR001353; IPR016050; G3DSA:3.60.20.10 (GENE3D), PTHR11599 (PANTHER), PTHR11599:SF5 (PANTHER), PS51476 (PROFILE), SSF56235 (SUPERFAMILY)
Caenorhabditis elegans	u3 small nucleolar r--associated protein 15 homolog	2	C:GO:0005730; P:GO:0006364	-		PTHR19924 (PANTHER), PTHR19924:SF2 (PANTHER)
Loa loa	hypothetical protein LOAG_00601 [Loa loa]	0				IPR011991; SSF46785 (SUPERFAMILY)
Loa loa	hypothetical protein LOAG_00601 [Loa loa]	0				IPR011991; SSF46785 (SUPERFAMILY)
Anopheles gambiae str. PEST	phospholipase d3	5	F:GO:0008081; F:GO:0004620; P:GO:0008152; C:GO:0005783; C:GO:0044425	-	EC:3.1.4.0	IPR001736; G3DSA:3.30.870.10 (GENE3D), PTHR10185 (PANTHER), SSF56024 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	hd domain containing protein	1	F:GO:0003824	-		IPR003607; IPR006674; PTHR21262 (PANTHER), SSF109604 (SUPERFAMILY)
Caenorhabditis elegans	solute carrier family 27 (fatty acid transporter) member 4	13	F:GO:0005488; P:GO:0042760; C:GO:0016021; P:GO:0007584; C:GO:0031526; P:GO:0043588; F:GO:0004467; P:GO:0001676; P:GO:0001579; C:GO:0005902; C:GO:0005783; P:GO:0015909; F:GO:0031957	-	EC:6.2.1.3	IPR000873; G3DSA:3.30.300.30 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF15 (PANTHER), SSF56801 (SUPERFAMILY)

Caenorhabditis elegans	adp-ribose mitochondrial precursor	1	F:GO:0005488	-		IPR000086; IPR015797; PTHR13030 (PANTHER), PTHR13030:SF8 (PANTHER), PS51462 (PROFILE)
	-	0				-
Caenorhabditis elegans	dynein heavy chain	5	P:GO:0007018; C:GO:0030286; F:GO:0016887; F:GO:0005524; F:GO:0003777	-		IPR013602
	-	0				-
Populus trichocarpa	misshapen-like ki-se 1	0		F:GO:0004674; P:GO:0006950; F:GO:0004672; F:GO:0005083; F:GO:0003676; P:GO:0006468; F:GO:0000166; F:GO:0005525; F:GO:0005524; P:GO:0050790; F:GO:0016301; P:GO:0007275; P:GO:0007243; P:GO:0045060; F:GO:0003924		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-
Loa loa	#NAME?	9	P:GO:0009792; P:GO:0010171; F:GO:0004553; P:GO:0005975; F:GO:0043169; F:GO:0003844; F:GO:0031072; P:GO:0040010; P:GO:0000003	-	EC:3.2.1.0; EC:2.4.1.18	IPR006048; IPR013780; IPR013781; IPR017853; PTHR10357 (PANTHER), PTHR10357:SF27 (PANTHER), SSF51011 (SUPERFAMILY)
Homo sapiens	major histocompatibility class dp alpha 1	9	C:GO:0005789; C:GO:0005887; C:GO:0042613; C:GO:0005794; P:GO:0002504; C:GO:0005765; F:GO:0032395; C:GO:0010008; P:GO:0006955	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	10	C:GO:0005789; P:GO:0006467; P:GO:0002119; F:GO:0016671; F:GO:0005515; P:GO:0055114; P:GO:0000003; P:GO:0008340; F:GO:0050660; P:GO:0040007	-	EC:1.8.4.0	IPR007266

	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-polk-1 protein	3	F:GO:0003887; P:GO:0006281; F:GO:0003684	-	EC:2.7.7.7	-
Caenorhabditis briggsae	calpain 5	6	P:GO:0042004; C:GO:0005622; F:GO:0004198; P:GO:0019099; P:GO:0006508; C:GO:0016020	-		IPR001300; G3DSA:3.90.70.10 (GENE3D), PTHR10183 (PANTHER), PTHR10183:SF32 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis briggsae	family protein	3	P:GO:0000003; F:GO:0008121; P:GO:0040010	-	EC:1.10.2.2	SignalP (SIGNALP)
	-	0				-
Brugia malayi	aaa family protein	0		P:GO:0006260; F:GO:0005524; F:GO:0000166; C:GO:0005663; F:GO:0017111; F:GO:0003677; F:GO:0003689		-
	-	0				-
Caenorhabditis briggsae	peroxisomal biogenesis factor 3	2	P:GO:0040010; C:GO:0016020	-		IPR006966; PTHR22950 (PANTHER), PTHR22950:SF8 (PANTHER)
	-	0				-
Caenorhabditis elegans	high affinity copper uptake protein 1	3	C:GO:0016021; P:GO:0006825; F:GO:0005375	-		IPR007274; PTHR12483:SF7 (PANTHER)
Caenorhabditis elegans	protein ki-se domain containing protein	0		F:GO:0016301; F:GO:0004672; F:GO:0005524; F:GO:0000166; P:GO:0006468; F:GO:0004674		-
Caenorhabditis elegans	protein ki-se domain containing protein	0		F:GO:0016301; F:GO:0004672; F:GO:0005524; F:GO:0000166; P:GO:0006468; F:GO:0004674		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		-
	-	0				-
Homo sapiens	high density lipoprotein binding protein	9	C:GO:0005737; F:GO:0008289; C:GO:0005886; F:GO:0003723; F:GO:0005515; P:GO:0006869; P:GO:0008203; C:GO:0005634; C:GO:0034364	-		IPR004087; IPR004088; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR10627 (PANTHER), PTHR10627:SF9 (PANTHER), SSF54791 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-

Brugia malayi	receptor accessory protein 1	5	F:GO:0031849; P:GO:0008219; C:GO:0016021; C:GO:0031966; P:GO:0051205	-		IPR004345; PTHR12300:SF19 (PANTHER), SignalP (SIGNALP)
Loa loa	serine threonine-protein ki-se smg1	6	P:GO:0044260; F:GO:0016773; F:GO:0016301; P:GO:0090304; F:GO:0000166; C:GO:0044424	-	EC:2.7.1.0	-
	-	0				-
Caenorhabditis elegans	dihydropyrimidine dehydroge-se	16	C:GO:0005829; F:GO:0004158; P:GO:0006145; P:GO:0006212; F:GO:0046872; P:GO:0055114; F:GO:0009055; F:GO:0017113; F:GO:0051539; P:GO:0006222; P:GO:0006210; F:GO:0042803; F:GO:0050660; P:GO:0006207; F:GO:0050661; P:GO:0006214	-	EC:1.3.3.1; EC:1.3.1.2	IPR012135; IPR013785; PTHR11938 (PANTHER), PTHR11938:SF7 (PANTHER), SSF51395 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-ers-3 protein	4	F:GO:0005488; F:GO:0016876; P:GO:0006412; P:GO:0043039	-	EC:6.1.1.0; EC:3.6.5.3	IPR000924; IPR001412; IPR004527; IPR014729; IPR020058; IPR020061; G3DSA:3.90.800.10 (GENE3D), PTHR10119:SF1 (PANTHER), SSF52374 (SUPERFAMILY)
Caenorhabditis elegans	protein crooked neck	9	P:GO:0009792; P:GO:0002119; F:GO:0005488; P:GO:0018996; P:GO:0006397; P:GO:0000003; P:GO:0040011; P:GO:0040007; C:GO:0005634	-		-
Caenorhabditis elegans	las1-like (cerevisiae)	0		C:GO:0071339; F:GO:0005515; C:GO:0005730; C:GO:0005634		IPR007174
Caenorhabditis elegans	dehydrodolichyl diphosphate synthase	2	F:GO:0000166; F:GO:0016765	-		SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG08142 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	splicing factor subunit 3	7	P:GO:0040035; P:GO:0018996; P:GO:0010171; F:GO:0005515; P:GO:0040039; P:GO:0060218; C:GO:0005634	-		SignalP (SIGNALP)
	-	0				-

Caenorhabditis briggsae	mbk-1	11	P:GO:0040010; P:GO:0018108; F:GO:0004674; C:GO:0016607; F:GO:0043621; F:GO:0005524; P:GO:0007399; P:GO:0040011; P:GO:0001706; P:GO:0046777; F:GO:0004715	-	EC:2.7.11.0; EC:2.7.10.2	IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF116 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	deacetylase complex protein family member (dcp-66)	9	P:GO:0040010; F:GO:0005488; P:GO:0040027; P:GO:0040035; P:GO:0040026; P:GO:0040011; P:GO:0006898; P:GO:0002009; C:GO:0005634	-		PTHR13455 (PANTHER), PTHR13455:SF1 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	uncoordi-ted family member (unc-104)	4	P:GO:0007018; F:GO:0005524; F:GO:0003777; C:GO:0005874	-		IPR001849; IPR011993; PTHR16012 (PANTHER), PTHR16012:SF201 (PANTHER), SSF50729 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	jumonji domain containing 2c	3	F:GO:0005488; F:GO:0051864; P:GO:0016577	-	EC:1.14.11.27	IPR001965; IPR011011; IPR013083; IPR019786; PTHR13793 (PANTHER)
Caenorhabditis briggsae	zinc-finger protein zpr1	4	C:GO:0005737; C:GO:0005634; F:GO:0008270; F:GO:0005515	-		-
Caenorhabditis briggsae	jumonji domain containing 2c	4	F:GO:0005488; F:GO:0051864; F:GO:0032454; P:GO:0033169	-	EC:1.14.11.27	IPR003347; IPR003349; IPR013129; PTHR10694 (PANTHER), PTHR10694:SF7 (PANTHER), SSF51197 (SUPERFAMILY)
Caenorhabditis elegans	malic enzyme	8	F:GO:0004471; F:GO:0046872; F:GO:0051287; F:GO:0009055; C:GO:0005759; F:GO:0016619; P:GO:0006108; P:GO:0055114	-	EC:1.1.1.39; EC:1.1.1.38	IPR001891; IPR012301; G3DSA:3.40.50.10380 (GENE3D), PTHR23406 (PANTHER), PTHR23406:SF2 (PANTHER), SSF53223 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis briggsae	large subunit ribosomal protein 27	9	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0005525; F:GO:0003735; P:GO:0018996; P:GO:0000003; P:GO:0040007; P:GO:0006412	-	EC:3.6.5.3	IPR001141; IPR005824; IPR014722; IPR018262
Loa loa	briggsae cbr-pqn-38 protein	0				-
Caenorhabditis elegans	temporarily assigned gene -me family member (tag-308)	0				-
Heliconius melpomene	endonuclease-reverse transcriptase	0		F:GO:0003723; P:GO:0006508; P:GO:0006278; F:GO:0008270; F:GO:0004519; F:GO:0004197; C:GO:0005622; F:GO:0003964		IPR000477; IPR015706; PTHR19446:SF100 (PANTHER), SSF56672 (SUPERFAMILY)
Caenorhabditis elegans	glutamate carboxypeptidase	3	F:GO:0008237; P:GO:0006508; F:GO:0005515	-		IPR001261; IPR002933; G3DSA:3.40.630.10 (GENE3D), PTHR11014 (PANTHER), PTHR11014:SF15 (PANTHER), SSF53187 (SUPERFAMILY)
	-	0				PR01217 (PRINTS)
	-	0				PR01217 (PRINTS)
	-	0				-
Caenorhabditis elegans	hematopoietic sig-l peptide-containing membrane domain-containing 1	0				-
Caenorhabditis elegans	mov34 mpn pad-1 family protein	11	F:GO:0003743; P:GO:0006413; C:GO:0005829; P:GO:0040010; P:GO:0008340; P:GO:0040035; C:GO:0005852; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0006898	-		IPR000555; PTHR10540 (PANTHER), PTHR10540:SF6 (PANTHER)
Caenorhabditis briggsae	neutral alpha-glucosidase ab-like	1	F:GO:0005515	-		IPR000322; PTHR22762:SF7 (PANTHER)
Caenorhabditis briggsae	f-box domain containing protein	0				IPR001810; G3DSA:3.80.10.10 (GENE3D)
Caenorhabditis elegans	aldo keto reductase family protein	9	F:GO:0047939; C:GO:0005829; F:GO:0004032; P:GO:0042840; P:GO:0046185; P:GO:0043050; P:GO:0040011; C:GO:0016324; P:GO:0019853	-	EC:1.1.1.19; EC:1.1.1.21	IPR001395; IPR018170; IPR020471; IPR023210; PTHR11732:SF34 (PANTHER)

Caenorhabditis elegans	aldo keto reductase family protein	6	P:GO:0019752; P:GO:0044248; P:GO:0043050; F:GO:0004033; P:GO:0040011; C:GO:0044464	-		IPR001395; IPR018170; IPR020471; IPR023210; PTHR11732:SF34 (PANTHER)
Caenorhabditis elegans	aldo keto reductase family protein	2	P:GO:0043050; P:GO:0040011	-		IPR001395; IPR018170; IPR020471; IPR023210; PTHR11732:SF34 (PANTHER)
Caenorhabditis elegans	aldo keto reductase family protein	2	P:GO:0043050; P:GO:0040011	-		IPR001395; IPR018170; IPR020471; IPR023210; PTHR11732:SF34 (PANTHER)
Caenorhabditis elegans	aldo keto reductase family protein	2	P:GO:0043050; P:GO:0040011	-		IPR001395; IPR018170; IPR020471; IPR023210; PTHR11732:SF34 (PANTHER)
Caenorhabditis elegans	aldo keto reductase family protein	2	P:GO:0043050; P:GO:0040011	-		IPR001395; IPR018170; IPR020471; IPR023210; PTHR11732:SF34 (PANTHER)
Caenorhabditis elegans	briggsae cbr-ttll-5 protein	1	F:GO:0003824	-		IPR004344; PTHR12241:SF8 (PANTHER), SSF56059 (SUPERFAMILY)
						-
	-	0				-
Caenorhabditis briggsae	kiaa0020 protein	2	F:GO:0003723; P:GO:0018991	-		IPR011989; IPR012959; IPR016024; PTHR13389 (PANTHER)
Caenorhabditis briggsae	kiaa0020 protein	2	F:GO:0003723; P:GO:0018991	-		IPR011989; IPR012959; IPR016024; PTHR13389 (PANTHER)
Loa loa	zinc c2h2 type family protein	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		IPR007087; IPR013087; IPR015880; PTHR23224 (PANTHER), PTHR23224:SF473 (PANTHER), SSF57667 (SUPERFAMILY)
	-	0				PD133063 (PRODOM), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	mitochondrial ribosomal protein l48	7	P:GO:0006412; P:GO:0040010; C:GO:0005840; F:GO:0003735; P:GO:0002119; P:GO:0006898; P:GO:0009792	-	EC:3.6.5.3	IPR001848; PTHR13473 (PANTHER)
	-	0				-
Caenorhabditis elegans	uncharacterized methyltransferase wbscr22	2	F:GO:0008168; P:GO:0008152	-	EC:2.1.1.0	IPR013216; IPR022238; G3DSA:3.40.50.150 (GENE3D), PTHR12734 (PANTHER), SSF53335 (SUPERFAMILY)
	-	0				-
	-	0				-
Loa loa	hypothetical protein LOAG_10513 [Loa loa]	2	P:GO:0007186; C:GO:0016021	-		SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
Epinephelus coioides	40s ribosomal protein s23	5	F:GO:0045182; F:GO:0003735; F:GO:0005515; C:GO:0022627; P:GO:0006414	-		IPR005680; IPR006032; IPR012340; IPR016027

Loa loa	ccr4-not transcription subunit 1	0		P:GO:0006350; P:GO:0045449; F:GO:0005515		-
Caenorhabditis elegans	coenzyme q biosynthesis family member (coq-2)	9	F:GO:0003899; F:GO:0008412; P:GO:0008340; P:GO:0016094; C:GO:0016021; C:GO:0005743; P:GO:0006383; P:GO:0006744; C:GO:0005666	-	EC:2.7.7.6	IPR000537; IPR006370; PTHR11048 (PANTHER), PTHR11048:SF2 (PANTHER)
Caenorhabditis briggsae	slowpoke potassium channel family member (slo-2)	6	C:GO:0016020; P:GO:0006813; P:GO:0008152; F:GO:0003824; F:GO:0015269; F:GO:0005488	-		-
	-	0				-
Caenorhabditis elegans	a chain golgi alpha-mannosidase ii in complex with 5-substituted swainsonine a-log: -5- - swainsonine	10	C:GO:0000139; F:GO:0004559; C:GO:0005795; F:GO:0030246; P:GO:0006487; P:GO:0006013; F:GO:0004572; C:GO:0016021; F:GO:0008270; C:GO:0005783	-	EC:3.2.1.24; EC:3.2.1.114	IPR011013; IPR011682; G3DSA:2.70.98.30 (GENE3D), PTHR11607 (PANTHER), PTHR11607:SF4 (PANTHER)
Caenorhabditis elegans	hypothetical protein Y20F4.2 [Caenorhabditis elegans]	0				PTHR13589 (PANTHER), PTHR13589:SF2 (PANTHER)
Loa loa	rap ran-gap family protein	5	P:GO:0050896; P:GO:0023052; P:GO:0016043; P:GO:0048523; F:GO:0005488	-		PF11864 (PFAM)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	transmembrane and coiled-coil domain family 2	1	F:GO:0005515	-		IPR019394; PTHR17613 (PANTHER)
Caenorhabditis briggsae	transmembrane and coiled-coil domain family 2	1	F:GO:0005515	-		IPR019394; PTHR17613 (PANTHER)
Caenorhabditis elegans	hypothetical protein ZK622.1 [Caenorhabditis elegans]	0		F:GO:0004672; F:GO:0005524; P:GO:0006468; F:GO:0004713; F:GO:0004674		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0055085		-
Caenorhabditis elegans	briggsae cbr-snf-12 protein	0		F:GO:0015293; F:GO:0005328; C:GO:0016021; C:GO:0016020; P:GO:0006836; C:GO:0005887; P:GO:0006810		-
Caenorhabditis briggsae	phosphoribosylformylglyci-midine synthase	2	P:GO:0040010; F:GO:0003824	-		-

Caenorhabditis elegans	leucine-rich repeat ki-se	3	P:GO:0006468; F:GO:0004672; F:GO:0005524	-		IPR000719; IPR011009; IPR011042; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR23257 (PANTHER), PTHR23257:SF88 (PANTHER), SSF101898 (SUPERFAMILY)
Caenorhabditis elegans	amp-binding enzyme family protein	8	P:GO:0016358; P:GO:0060136; P:GO:0007611; C:GO:0031966; C:GO:0005777; F:GO:0004467; C:GO:0005783; P:GO:0019217	-	EC:6.2.1.3	IPR000873; IPR020459; IPR020845; G3DSA:2.30.38.10 (GENE3D), G3DSA:3.40.50.980 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF8 (PANTHER), SignalP (SIGNALP), SSF56801 (SUPERFAMILY)
Caenorhabditis elegans	rwd domain containing protein	0		F:GO:0046872; F:GO:0008270; F:GO:0005515		IPR001841; IPR006575; IPR013083; IPR016135; IPR018957
Brugia malayi	hypothetical protein Bm1_32955 [Brugia malayi]	0		P:GO:0006260; F:GO:0003896		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	major allergen	0		P:GO:0055114; F:GO:0009055; F:GO:0016491; P:GO:0006099; F:GO:0051536		SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0003674; P:GO:0008150		IPR002110; IPR020683
Caenorhabditis briggsae	Hypothetical protein CBG16019 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	queuine tr--ribosyltransferase	4	C:GO:0005739; F:GO:0046872; F:GO:0008479; P:GO:0008616	-	EC:2.4.2.29	IPR002616
Caenorhabditis briggsae	uncoordi-ted family member (unc-87)	1	F:GO:0005515	-		-
Brugia malayi	coiled-coil domain-containing	0				-
Caenorhabditis elegans	hypothetical protein F57C9.6 [Caenorhabditis elegans]	0		C:GO:0016021; P:GO:0007186		G3DSA:1.20.1070.10 (GENE3D)
Caenorhabditis elegans	sensory axon guidance family member (sax-1)	0				-
Caenorhabditis elegans	cg9153- isoform a	1	P:GO:0000003	-		PTHR11254 (PANTHER), PTHR11254:SF8 (PANTHER)
	-	0				-
Caenorhabditis briggsae	probable r--binding protein 19	6	C:GO:0005737; C:GO:0005730; C:GO:0005654; F:GO:0003676; P:GO:0040019; F:GO:0000166	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF64 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	loc402804 protein	0		C:GO:0005739; F:GO:0003674; P:GO:0008152; F:GO:0016787; P:GO:0008150		G3DSA:3.40.50.1820 (GENE3D), SSF53474 (SUPERFAMILY)

Caenorhabditis elegans	alp enigma encoding family member (alp-1)	1	F:GO:0042802	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR18973 (PANTHER), PTHR18973:SF57 (PANTHER)
Caenorhabditis elegans	peptidase family m3 containing protein	6	F:GO:0004222; P:GO:0045449; F:GO:0003702; P:GO:0006367; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	IPR001567; G3DSA:1.10.1370.10 (GENE3D), PTHR11804 (PANTHER), PTHR11804:SF4 (PANTHER), SSF55486 (SUPERFAMILY)
Loa loa	3 -phosphoadenosine 5 -phosphosulfate synthase 1	7	P:GO:0006790; P:GO:0001501; F:GO:0016301; F:GO:0004781; F:GO:0005524; P:GO:0000003; P:GO:0008340	-	EC:2.7.7.4	IPR002891; IPR015947; G3DSA:3.10.400.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR11055 (PANTHER), PTHR11055:SF1 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Brugia malayi	aryl hydrocarbon receptor interacting protein	11	P:GO:0045862; F:GO:0003712; F:GO:0004871; P:GO:0022417; P:GO:0006626; P:GO:0019915; C:GO:0044444; F:GO:0016853; F:GO:0051082; P:GO:0009792; C:GO:0005634	-		PTHR11242 (PANTHER)
Caenorhabditis briggsae	mr- turnover protein 4 homolog	1	C:GO:0043229	-		PTHR21141 (PANTHER), PTHR21141:SF1 (PANTHER)
Loa loa	btb poz domain containing protein	2	F:GO:0005515; C:GO:0016021	-		IPR000210; IPR011333; IPR013069; PTHR22744 (PANTHER)
	-	0				-
	-	0				IPR011009; G3DSA:1.10.510.10 (GENE3D)
Caenorhabditis briggsae	conserved atpase domain protein	7	P:GO:0006541; F:GO:0016812; F:GO:0016597; F:GO:0004086; F:GO:0005524; P:GO:0006207; F:GO:0004070	-	EC:3.5.2.0; EC:2.1.3.2	IPR005480; IPR013816; PTHR11405 (PANTHER), PTHR11405:SF3 (PANTHER), SSF56059 (SUPERFAMILY)
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
Caenorhabditis elegans	briggsae cbr-gck-4 protein	9	P:GO:0040010; P:GO:0000910; F:GO:0004674; P:GO:0010171; P:GO:0032879; P:GO:0002119; P:GO:0040011; P:GO:0010800; P:GO:0008283	-	EC:2.7.11.0	IPR022165; PD936484 (PRODOM), PTHR22986 (PANTHER), PTHR22986:SF67 (PANTHER)
	-	0				-
Caenorhabditis elegans	gcn1 general control of amino-acid synthesis 1-like 1	1	P:GO:0000003	-		IPR011989; PTHR23346 (PANTHER), PTHR23346:SF7 (PANTHER)

Caenorhabditis briggsae	adp-ribosylation factor 4	16	P:GO:0016192; P:GO:0040010; P:GO:0007264; P:GO:0007186; P:GO:0040035; P:GO:0018996; P:GO:0010171; P:GO:0002119; F:GO:0005215; P:GO:0040039; P:GO:0006886; P:GO:0009792; C:GO:0005794; C:GO:0005634; F:GO:0005525; C:GO:0005886	-		IPR005225; IPR006688; IPR006689; G3DSA:3.40.50.300 (GENE3D), PTHR11711:SF30 (PANTHER), PS51417 (PROFILE), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	ubiquitin-protein ligase e3b	3	C:GO:0005622; F:GO:0016881; P:GO:0006464	-	EC:6.3.2.0	IPR000569; PTHR11254 (PANTHER), PTHR11254:SF70 (PANTHER)
Dictyocaulus viviparus	mediator of r- polymerase ii transcription subunit 18	12	P:GO:0007411; P:GO:0040010; P:GO:0006357; F:GO:0016455; P:GO:0010171; P:GO:0007413; P:GO:0002119; F:GO:0005515; P:GO:0040011; C:GO:0016592; P:GO:0002009; P:GO:0009792	-		IPR019095; PTHR13321 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	uncoordi-ted protein isoform confirmed by transcript evidence	4	F:GO:0005089; C:GO:0005622; P:GO:0035023; F:GO:0016740	-		IPR000219; IPR001331; IPR001849; IPR011993; PTHR22826 (PANTHER), PTHR22826:SF47 (PANTHER), SSF50729 (SUPERFAMILY)
Angiostrongylus cantonensis	briggsae cbr-fos-1 protein	5	F:GO:0003700; F:GO:0043565; F:GO:0046983; C:GO:0005634; P:GO:0006355	-		-
Loa loa	stromal antigen	2	F:GO:0005515; P:GO:0009987	-		PTHR11199 (PANTHER)
Trypanosoma cruzi strain CL Brener	cb090_human ame: full= uncharacterized protein c2orf90	0				-
Caenorhabditis elegans	gtp binding protein bms1	2	F:GO:0032555; F:GO:0017111	-	EC:3.6.1.15	IPR007034; IPR012948; PTHR12858 (PANTHER), PTHR12858:SF2 (PANTHER)
	-	0				-
Brugia malayi	peptidyl-prolyl cis-trans isomerase h	5	P:GO:0006457; C:GO:0030532; C:GO:0071011; P:GO:0000398; F:GO:0003755	-	EC:5.2.1.8	IPR002130; IPR015891; IPR020892; PTHR11071 (PANTHER), PTHR11071:SF58 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		-

Loa loa	chain crystal structure of the d1d2 sub-complex from the human snrnp core	13	C:GO:0030532; F:GO:0003676; C:GO:0071011; P:GO:0040007; P:GO:0040027; P:GO:0032940; P:GO:0007052; F:GO:0005515; P:GO:0040011; P:GO:0000398; P:GO:0006898; C:GO:0071013; P:GO:0009792	-		IPR001163; IPR006649; IPR010920; G3DSA:2.30.30.100 (GENE3D), PTHR12777 (PANTHER)
Caenorhabditis briggsae	survival of motor neuron protein-interacting protein 1	2	P:GO:0006396; P:GO:0048676	-		IPR007022; PF04938 (PFAM)
Caenorhabditis elegans	briggsae cbr-polq-1 protein	0		F:GO:0003676; F:GO:0004386; P:GO:0006260; F:GO:0005524; F:GO:0003887; F:GO:0016787; F:GO:0008026; F:GO:0003677		PTHR11752 (PANTHER), PTHR11752:SF3 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG11342 [Caenorhabditis briggsae]	0		C:GO:0016021; P:GO:0007186		IPR017452; PTHR22751 (PANTHER), PTHR22751:SF8 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	ribosomal r- processing 12 homolog (cerevisiae)	0		F:GO:0003674; F:GO:0005488; C:GO:0016021; C:GO:0016020; P:GO:0008150; C:GO:0005575		IPR011989; IPR012978; IPR016024; PTHR21576 (PANTHER), PTHR21576:SF2 (PANTHER)
Loa loa	protein-tyrosine phosphatase containing protein	1	F:GO:0004721	-	EC:3.1.3.16	SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005488	-		IPR000949
Brugia malayi	conserved oligomeric golgi complex subunit 4	3	N:GO:0071842; P:GO:0048193; C:GO:0044431	-		IPR013167; PTHR10483 (PANTHER), PTHR10483:SF7 (PANTHER)
Caenorhabditis elegans	briggsae cbr-kin-29 protein	1	F:GO:0016740	-		-
Brugia malayi	phosphoinositide-3- regulatory subunit 4	5	F:GO:0005515; F:GO:0004672; P:GO:0019915; C:GO:0005829; F:GO:0000166	-		SignalP (SIGNALP)
Caenorhabditis elegans	major facilitator superfamily protein	2	P:GO:0055085; C:GO:0016021	-		IPR005828; IPR016196; G3DSA:1.20.1250.20 (GENE3D), PTHR11662 (PANTHER), PTHR11662:SF24 (PANTHER)
	-	0				-
Caenorhabditis elegans	zn finger motif protein	1	F:GO:0046872	-		-
	-	0				-
Caenorhabditis elegans	carbonic anhydrase xiii	0		F:GO:0046872; P:GO:0006730; F:GO:0008270; F:GO:0004089		IPR001148; IPR018338; PTHR18952:SF34 (PANTHER)
	-	0				-
	-	0				-
	-	0				-

Loa loa	set and mynd domain containing 3	1	F:GO:0005488	-		IPR002893; PTHR12197 (PANTHER), PTHR12197:SF9 (PANTHER), SSF144232 (SUPERFAMILY), SSF82199 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	death-associated protein ki-se 1	7	P:GO:0006917; F:GO:0004674; F:GO:0005524; F:GO:0005515; P:GO:0007165; C:GO:0044424; P:GO:0006468	-	EC:2.7.11.0	IPR000488; IPR011029; IPR020675; IPR020680
Haemonchus contortus	aspartyl protease family member (asp-2)	2	P:GO:0008219; F:GO:0005515	-		IPR001461; IPR001969; IPR009007; IPR012848; IPR021109; PTHR13683:SF53 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	clathrin coat assembly protein ap17	16	P:GO:0030100; C:GO:0030122; P:GO:0000003; P:GO:0048268; P:GO:0040007; P:GO:0007269; F:GO:0008565; P:GO:0006886; C:GO:0005829; F:GO:0030276; P:GO:0050690; P:GO:0009792; P:GO:0002119; C:GO:0008021; C:GO:0030121; P:GO:0010171	-		SignalP (SIGNALP)
Caenorhabditis briggsae	cold-shock d--binding domain-containing protein	7	F:GO:0008270; P:GO:0006355; F:GO:0003677; F:GO:0000166; P:GO:0001708; P:GO:0007275; C:GO:0005737	-		IPR002059; IPR011129; IPR012340; IPR016027; IPR019844; PTHR11544 (PANTHER), PTHR11544:SF3 (PANTHER)
Caenorhabditis elegans	ykaa_caeel ame: full=uncharacterized amino-acid permease	0		C:GO:0016021; C:GO:0016020; P:GO:0055085; P:GO:0006810		PTHR11827 (PANTHER), PTHR11827:SF7 (PANTHER)
Loa loa	mediator of r- polymerase ii subunit 12 homolog	13	F:GO:0030528; P:GO:0018991; P:GO:0006366; P:GO:0040010; P:GO:0040018; P:GO:0040026; P:GO:0040011; P:GO:0009792; C:GO:0044446; P:GO:0045449; P:GO:0010171; C:GO:0005634; P:GO:0040035	-		PTHR12796 (PANTHER)

	-	0				-
Caenorhabditis elegans	fatty acid amide hydrolase 2	3	C:GO:0016020; F:GO:0003824; C:GO:0005811	-		IPR000120; IPR020556; PTHR11895:SF5 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	F:GO:0017111; P:GO:0044238; C:GO:0005739; P:GO:0044237	-	EC:3.6.1.15	IPR011704; G3DSA:3.40.50.300 (GENE3D), PTHR21610 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
	-	0				PR00021 (PRINTS), PR00211 (PRINTS), SignalP (SIGNALP)
	-	0				PR00021 (PRINTS), PR00211 (PRINTS), SignalP (SIGNALP)
Caenorhabditis briggsae	probable 2-oxoglutarate dehydroge-se e1 component mitochondrial precursor	2	F:GO:0016624; P:GO:0008152	-	EC:1.2.4.0	G3DSA:3.40.50.970 (GENE3D), SSF52518 (SUPERFAMILY)
	-	0				IPR012879; SignalP (SIGNALP)
Trichostrongylus vitrinus	rio1 family protein	2	F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR000687; IPR011009; IPR018934; IPR018935; G3DSA:3.90.1200.10 (GENE3D), PTHR10593 (PANTHER), PTHR10593:SF5 (PANTHER)
Caenorhabditis elegans	adp-ribosylation factor-like protein 3	14	P:GO:0007049; F:GO:0004871; P:GO:0007264; C:GO:0000139; P:GO:0007186; F:GO:0046872; P:GO:0051301; F:GO:0019003; F:GO:0005515; P:GO:0034608; C:GO:0005819; P:GO:0006886; C:GO:0005634; F:GO:0005525	-		IPR006689; G3DSA:3.40.50.300 (GENE3D), PTHR11711:SF27 (PANTHER), PS51417 (PROFILE), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-hot-5 protein	0				IPR010558
Brugia malayi	actin	18	P:GO:0007126; P:GO:0007108; P:GO:0040007; P:GO:0007517; P:GO:0000281; P:GO:0040035; P:GO:0030036; C:GO:0005865; F:GO:0005524; C:GO:0005938; P:GO:0002119; F:GO:0016887; F:GO:0005515; C:GO:0005884; F:GO:0005200; P:GO:0040039; P:GO:0006898; P:GO:0009792	-		IPR004000; IPR004001; IPR020902; G3DSA:2.30.36.70 (GENE3D), G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), SSF53067 (SUPERFAMILY)
Caenorhabditis elegans	beta like 1	3	F:GO:0042802; C:GO:0005634; P:GO:0006917	-		PTHR14978 (PANTHER)
Caenorhabditis elegans	hypothetical protein C50E3.5 [Caenorhabditis elegans]	0				-

Caenorhabditis elegans	hypothetical protein C50E3.5 [Caenorhabditis elegans]	0				-
	-	0				-
synthetic construct	60s ribosomal protein l29-like	7	F:GO:0008201; F:GO:0003735; F:GO:0003723; F:GO:0005515; C:GO:0022625; P:GO:0007566; P:GO:0006414	-		IPR002673
Acyrthosiphon pisum	pre-mr- splicing factor	0		P:GO:0000003; P:GO:0032968; P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0006357; P:GO:0040007		-
	-	0				IPR018221
	-	0				-
Gallus gallus	chromosome 5 open reading frame 35	0				-
Caenorhabditis elegans	ctdspl2a protein	1	F:GO:0004721	-	EC:3.1.3.16	IPR004274; G3DSA:3.40.50.1000 (GENE3D), PTHR12210 (PANTHER), PTHR12210:SF12 (PANTHER), SSF56784 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-pcp- protein	3	P:GO:0009792; P:GO:0006508; F:GO:0008236	-		IPR008758; G3DSA:3.40.50.1820 (GENE3D), PTHR11010:SF6 (PANTHER), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR008574
	-	0				SignalP (SIGNALP)
	-	0				-
Brugia malayi	r- guanylyltransferase and 5 -phosphatase	18	P:GO:0008340; C:GO:0005654; P:GO:0000003; F:GO:0000166; F:GO:0004484; P:GO:0040010; P:GO:0006898; P:GO:0040017; F:GO:0016791; P:GO:0006259; P:GO:0018996; P:GO:0019915; F:GO:0008186; P:GO:0009792; P:GO:0002009; P:GO:0002119; P:GO:0010171; P:GO:0006370	-	EC:2.7.7.50; EC:3.1.3.0	IPR001339; IPR012340; IPR013846; IPR016027; G3DSA:3.30.470.30 (GENE3D), PTHR10367 (PANTHER), SSF56091 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	fan1_caebr ame: full=fanconi-associated nuclease 1 homolog	2	F:GO:0005488; P:GO:0006974	-		-
Caenorhabditis elegans	mh2 domain containing protein	3	C:GO:0005622; F:GO:0005515; P:GO:0006350	-		IPR001132; IPR008984; IPR013790; IPR017855; PTHR13703:SF12 (PANTHER)
Brugia malayi	n-alpha-acetyltransferase auxiliary subunit-like	0		F:GO:0005488; C:GO:0005737; F:GO:0005515		IPR019183; PTHR22767 (PANTHER), PTHR22767:SF3 (PANTHER)
Brugia malayi	briggsae cbr-kup-1 protein	0		F:GO:0000166		-
	-	0				SignalP (SIGNALP)

	-	0				-
Caenorhabditis briggsae	e3 ubiquitin-protein ligase march8	0		F:GO:0016874; C:GO:0016021; C:GO:0016020; C:GO:0005768; C:GO:0030659; F:GO:0008270; C:GO:0005794; C:GO:0005765; C:GO:0005764; C:GO:0031410; P:GO:0008152; F:GO:0046872; C:GO:0031902; C:GO:0031901; C:GO:0005886		IPR011016; IPR013083; IPR018957; PTHR23012 (PANTHER), PTHR23012:SF3 (PANTHER), SSF57850 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	plexin a1	1	C:GO:0016020	-		IPR002165; IPR003659; G3DSA:3.30.1680.10 (GENE3D), PTHR22625 (PANTHER), PTHR22625:SF11 (PANTHER)
Caenorhabditis elegans	plexin a1	1	C:GO:0016020	-		IPR002165; IPR003659; G3DSA:3.30.1680.10 (GENE3D), PTHR22625 (PANTHER), PTHR22625:SF11 (PANTHER)
Caenorhabditis briggsae	intraflagellar transport protein 140	0		F:GO:0003674; F:GO:0005488; F:GO:0003824; P:GO:0008150; C:GO:0005575		PTHR15722 (PANTHER)
Rattus norvegicus	coiled-coil domain-containing protein 93	0				IPR019159; PTHR16441 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; P:GO:0008152; F:GO:0003824		IPR004245; IPR017849; PTHR10974:SF5 (PANTHER)
Brugia malayi	zinc c2h2 type family protein	0		F:GO:0003676; F:GO:0046872; F:GO:0008270; F:GO:0005515; C:GO:0005622		IPR007087; IPR013087; IPR015880; PTHR23224 (PANTHER), SSF57667 (SUPERFAMILY)
Brugia malayi	taf1 r- polymerase tata box binding protein -associated factor	8	P:GO:0006351; P:GO:0080090; F:GO:0005515; P:GO:0031323; F:GO:0016740; P:GO:0043687; C:GO:0005634; P:GO:0060255	-		-
	-	0				-
Caenorhabditis elegans	heparan sulfate n-deacetylase n-sulfotransferase	3	C:GO:0016020; C:GO:0005794; F:GO:0008146	-	EC:2.8.2.0	IPR000863; G3DSA:3.40.50.300 (GENE3D), PTHR10605 (PANTHER), PTHR10605:SF2 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0008152; F:GO:0008080		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-

Caenorhabditis briggsae	trehalase family protein	4	P:GO:0009792; F:GO:0003824; P:GO:0040007; P:GO:0002119	-		IPR001661; IPR008928; IPR018232; PTHR23403:SF1 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-nlp-18 protein	0				-
	-	0				-
	-	0				-
Loa loa	ring zinc finger-containing protein	8	P:GO:0009792; P:GO:0010171; F:GO:0005488; P:GO:0040018; P:GO:0018996; P:GO:0040010; P:GO:0000003; P:GO:0008219	-		-
Loa loa	ring zinc finger-containing protein	8	P:GO:0009792; P:GO:0010171; F:GO:0005488; P:GO:0040018; P:GO:0018996; P:GO:0040010; P:GO:0000003; P:GO:0008219	-		-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG02451 [Caenorhabditis briggsae]	0		P:GO:0006898; P:GO:0000003; P:GO:0040018; P:GO:0002119; P:GO:0009792; P:GO:0040011; P:GO:0040010; P:GO:0040035; F:GO:0005488		-
	-	0				-
Caenorhabditis sp. PS1010	6720455i24rik homolog	5	P:GO:0007163; P:GO:0007411; P:GO:0007155; C:GO:0016020; P:GO:0007413	-		IPR000742; IPR006209; IPR006210; IPR013032; IPR013320; G3DSA:2.10.25.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF220 (PANTHER), SSF57196 (SUPERFAMILY)
Caenorhabditis elegans	u6 snr--associated sm-like protein lsm6	14	C:GO:0030532; P:GO:0040010; F:GO:0003723; P:GO:0040002; P:GO:0006364; P:GO:0008033; P:GO:0008380; P:GO:0010171; P:GO:0006402; P:GO:0002119; P:GO:0040011; F:GO:0046982; P:GO:0006397; C:GO:0005737	-		IPR001163; IPR006649; IPR010920; G3DSA:2.30.30.100 (GENE3D), PTHR11021 (PANTHER)

Caenorhabditis elegans	briggsae cbr-zyg-1 protein	0		F:GO:0016740; F:GO:0004674; F:GO:0004672; P:GO:0006468; F:GO:0000166; C:GO:0005737; F:GO:0005524; C:GO:0005814; P:GO:0007275; F:GO:0016301; F:GO:0004713; F:GO:0005515; P:GO:0007049; C:GO:0005856		-
Caenorhabditis elegans	bromodomain containing protein	1	P:GO:0040011	-		IPR001965; IPR011011; IPR013083; IPR019786; IPR019787; PTHR22880 (PANTHER), PTHR22880:SF4 (PANTHER)
Caenorhabditis briggsae	patched family protein	5	P:GO:0040018; P:GO:0018996; P:GO:0007275; P:GO:0040011; C:GO:0016020	-		IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER)
Caenorhabditis briggsae	cytochrome c oxidase subunit via polypeptide 1	6	P:GO:0040010; P:GO:0008340; C:GO:0005743; P:GO:0006091; P:GO:0000003; C:GO:0044425	-		IPR001349; IPR018507
Cyathostominae sp. JM-2007a	mgc84409 protein	1	F:GO:0008270	-		IPR001781; PTHR18973 (PANTHER), PTHR18973:SF106 (PANTHER), SSF57716 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	cytochrome p450 2g1-like	1	F:GO:0046872	-		IPR001128; IPR002401
Caenorhabditis briggsae	myosin heavy chain	6	C:GO:0032982; P:GO:0055114; F:GO:0005524; F:GO:0051015; F:GO:0003774; F:GO:0032440	-	EC:1.3.1.74	SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein Y47G6A.29 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				-
Angiostrongylus cantonensis	elongation factor 2	12	F:GO:0003746; P:GO:0040007; P:GO:0040035; P:GO:0006414; P:GO:0006184; P:GO:0002119; F:GO:0005515; F:GO:0003924; C:GO:0030529; P:GO:0009792; C:GO:0005737; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000640; IPR005517; IPR009022; IPR014721; IPR020568; G3DSA:3.30.70.870 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF4 (PANTHER)

Caenorhabditis elegans	uncoordi-ted family member (unc-44)	3	P:GO:0007165; F:GO:0004623; F:GO:0005515	-	EC:3.1.1.4	IPR000906; PTHR12582 (PANTHER)
Caenorhabditis elegans	uncoordi-ted family member (unc-44)	1	F:GO:0005515	-		IPR000488; IPR000906; IPR011029; PTHR18958 (PANTHER), PTHR18958:SF20 (PANTHER)
Caenorhabditis elegans	ankyrin-related unc-44	1	F:GO:0005515	-		-
Caenorhabditis elegans	uncoordi-ted family member (unc-44)	1	F:GO:0005515	-		IPR000488; IPR000906; IPR011029; PTHR18958 (PANTHER), PTHR18958:SF20 (PANTHER)
Caenorhabditis elegans	eukaryotic translation elongation factor	12	P:GO:0000022; C:GO:0005829; F:GO:0003746; C:GO:0005875; P:GO:0040007; P:GO:0040035; P:GO:0006414; P:GO:0002119; F:GO:0003924; P:GO:0009792; C:GO:0005811; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000640; IPR000795; IPR004161; IPR005517; IPR009000; IPR009022; IPR014721; IPR020568; G3DSA:2.40.30.10 (GENE3D), G3DSA:3.30.70.870 (GENE3D), G3DSA:3.40.50.300 (GENE3D), G3DSA:3.90.1430.10 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF4 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-tam-1 protein	0		F:GO:0008270; F:GO:0005515		-
Caenorhabditis briggsae	briggsae cbr-tam-1 protein	0		F:GO:0008270; F:GO:0005515		-
Caenorhabditis briggsae	briggsae cbr-tam-1 protein	0		F:GO:0008270; F:GO:0005515		-
Caenorhabditis briggsae	ap-3 complex subunit delta-1	8	P:GO:0009987; P:GO:0006810; P:GO:0040007; P:GO:0002376; P:GO:0010171; P:GO:0002119; C:GO:0044444; P:GO:0009792	-		IPR010474; PTHR22781 (PANTHER), PTHR22781:SF9 (PANTHER)
Caenorhabditis briggsae	ap-3 complex subunit delta-1	8	P:GO:0009987; P:GO:0006810; P:GO:0040007; P:GO:0002376; P:GO:0010171; P:GO:0002119; C:GO:0044444; P:GO:0009792	-		IPR010474; PTHR22781 (PANTHER), PTHR22781:SF9 (PANTHER)
Caenorhabditis elegans	hypothetical protein F25F8.1 [Caenorhabditis elegans]	0		F:GO:0003677		-
Caenorhabditis elegans	mevalo-te ki-se	10	C:GO:0005737; P:GO:0009792; P:GO:0002119; P:GO:0016310; P:GO:0008299; F:GO:0004496; F:GO:0005524; P:GO:0008340; P:GO:0040011; P:GO:0040007	-	EC:2.7.1.36	IPR006204; IPR006205; IPR014721; IPR020568; PTHR10457 (PANTHER)

Caenorhabditis elegans	mevalo-te ki-se	11	C:GO:0005737; F:GO:0042802; P:GO:0009792; P:GO:0002119; P:GO:0016310; P:GO:0008299; F:GO:0004496; F:GO:0005524; P:GO:0008340; P:GO:0040011; P:GO:0040007	-	EC:2.7.1.36	IPR006204; IPR006205; IPR006206; IPR014721; IPR020568; PTHR10457 (PANTHER)
Caenorhabditis elegans	a chain a high resolution crystal structure of human glutamate carboxypeptidase ii in a complex with a urea-based inhibitor	2	F:GO:0070011; C:GO:0016020	-		IPR007365; G3DSA:1.20.930.40 (GENE3D), PTHR10404 (PANTHER), PTHR10404:SF15 (PANTHER)
Drosophila ananassae	gastric mucin	0		F:GO:0008061; P:GO:0006030; F:GO:0016787; C:GO:0005576		-
Caenorhabditis elegans	hypothetical protein T06D8.1 [Caenorhabditis elegans]	0		F:GO:0008061; P:GO:0006030; F:GO:0016787; C:GO:0005576		-
	-	0				-
Caenorhabditis elegans	hypothetical protein T06D8.1 [Caenorhabditis elegans]	0		P:GO:0006629; F:GO:0008970		-
	-	0				-
Ailuropoda melanoleuca	casein ki-se beta polypeptide	21	C:GO:0005956; P:GO:0033211; P:GO:0006956; F:GO:0004674; P:GO:0042325; P:GO:0030177; F:GO:0042802; P:GO:0043623; P:GO:0008285; P:GO:0006508; F:GO:0005102; P:GO:0051101; F:GO:0019904; P:GO:0007249; F:GO:0008134; F:GO:0004252; C:GO:0005576; P:GO:0050790; C:GO:0005737; C:GO:0005886; F:GO:0019887	-	EC:2.7.11.0; EC:3.4.21.0	IPR000704; IPR016149; IPR016150

Drosophila melanogaster	katanin 60	12	P:GO:0051179; P:GO:0051329; F:GO:0008017; P:GO:0006996; C:GO:0043005; C:GO:0000922; F:GO:0005524; F:GO:0008568; C:GO:0044444; P:GO:0007017; F:GO:0046982; P:GO:0048699	-	EC:3.6.4.3	IPR003959; IPR003960; G3DSA:1.10.8.60 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23074 (PANTHER), PTHR23074:SF19 (PANTHER), SSF52540 (SUPERFAMILY)
Trichoplax adhaerens	ring finger protein 14	0		F:GO:0046872; C:GO:0005737; F:GO:0019787; F:GO:0008270; P:GO:0032355; P:GO:0016567; F:GO:0005515; C:GO:0005634		IPR001841; IPR002867; IPR013083; IPR017907; PTHR11685 (PANTHER), PTHR11685:SF7 (PANTHER), SSF57850 (SUPERFAMILY)
Polysphondylium pallidum PN500	hypothetical protein PPL_01926 [Polysphondylium pallidum PN500]	0		F:GO:0016787		-
Caenorhabditis briggsae	d-k protein	0		C:GO:0016021; F:GO:0032440; P:GO:0000902; F:GO:0000166; F:GO:0005524; P:GO:0055114; F:GO:0016491; C:GO:0005788; C:GO:0005783		IPR001023; IPR005829; IPR013126; G3DSA:1.20.1270.10 (GENE3D), G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), PTHR19375:SF7 (PANTHER), SignalP (SIGNALP), SSF100934 (SUPERFAMILY), SSF53067 (SUPERFAMILY)
Caenorhabditis briggsae	d-k protein	0		C:GO:0016021; F:GO:0032440; P:GO:0000902; F:GO:0000166; F:GO:0005524; P:GO:0055114; F:GO:0016491; C:GO:0005788; C:GO:0005783		IPR001023; IPR005829; IPR013126; G3DSA:1.20.1270.10 (GENE3D), G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), PTHR19375:SF7 (PANTHER), SignalP (SIGNALP), SSF100934 (SUPERFAMILY), SSF53067 (SUPERFAMILY)
Caenorhabditis briggsae	d-k protein	0		C:GO:0016021; F:GO:0032440; P:GO:0000902; F:GO:0000166; F:GO:0005524; P:GO:0055114; F:GO:0016491; C:GO:0005788; C:GO:0005783		IPR001023; IPR005829; IPR013126; G3DSA:1.20.1270.10 (GENE3D), G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), PTHR19375:SF7 (PANTHER), SignalP (SIGNALP), SSF100934 (SUPERFAMILY), SSF53067 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Trichomonas vaginalis G3	ankyrin repeat protein	0				IPR002110; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER), PTHR18958:SF306 (PANTHER)
Trichomonas vaginalis G3	ankyrin repeat protein	0				IPR002110; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER), PTHR18958:SF306 (PANTHER)

Caenorhabditis elegans	briggsae cbr-elpc-2 protein	1	P:GO:0009987	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR13729 (PANTHER)
	-	0				-
Loa loa	2fe-2s iron-sulfur cluster binding domain containing protein	1	F:GO:0005488	-		IPR001041; IPR012675; PTHR23426 (PANTHER), PTHR23426:SF1 (PANTHER)
Branchiostoma floridae	isoform cra_a	1	F:GO:0008415	-		IPR000182; IPR016181; PTHR23091 (PANTHER)
Mus musculus	type alpha isoform cra_a	31	P:GO:0060351; P:GO:0001957; P:GO:0071363; P:GO:0007605; P:GO:0034505; P:GO:0042542; P:GO:0001649; P:GO:0009612; P:GO:0001568; P:GO:0060325; F:GO:0005201; C:GO:0005615; P:GO:0048706; P:GO:0015031; F:GO:0048407; C:GO:0005737; P:GO:0043434; P:GO:0071300; P:GO:0007601; P:GO:0010812; C:GO:0005584; F:GO:0042802; P:GO:0060346; P:GO:0032964; P:GO:0030199; P:GO:0051591; P:GO:0031960;	-		IPR008160; PTHR10499 (PANTHER), PTHR10499:SF127 (PANTHER)
	-	0				-
Haemonchus contortus	heat shock protein family member (hsp-)	1	P:GO:0009408	-		-
Ostertagia ostertagi	heat shock protein family member (hsp-)	1	P:GO:0006950	-		-
Ostertagia ostertagi	heat shock protein family member (hsp-)	1	P:GO:0006950	-		IPR001436; IPR002068; IPR008978; G3DSA:2.60.40.790 (GENE3D), PTHR11527 (PANTHER), PTHR11527:SF28 (PANTHER)
Ostertagia ostertagi	heat shock protein family member (hsp-)	1	P:GO:0006950	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				IPR008160; PTHR10499 (PANTHER), PTHR10499:SF114 (PANTHER)
Caenorhabditis elegans	ypi7_caeel ame: full=uncharacterized f-box protein	0				-
Caenorhabditis remanei	spc-1	6	C:GO:0030863; C:GO:0044459; F:GO:0005515; F:GO:0005509; F:GO:0016787; C:GO:0044422	-		IPR002017; IPR018159; G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF6 (PANTHER), SSF46966 (SUPERFAMILY)
	-	0				-

Caenorhabditis briggsae	ab-hydrolase associated lipase region family protein	0		P:GO:0006629; F:GO:0016787; F:GO:0004806		G3DSA:3.40.50.1820 (GENE3D), PTHR11005 (PANTHER)
	-	0				SignalP (SIGNALP)
Acetivibrio cellulolyticus	mucin 1	1	C:GO:0044464	-		IPR000982; PR01217 (PRINTS)
	-	0				-
Caenorhabditis elegans	briggsae cbr-dct-11 protein	0				SignalP (SIGNALP)
Caenorhabditis elegans	nuclear pore complex protein family member (npp-22)	0		C:GO:0005643; P:GO:0015031; C:GO:0016021; C:GO:0016020; C:GO:0005634; P:GO:0006810; P:GO:0000003; P:GO:0009792; C:GO:0031965; P:GO:0051028; P:GO:0055085		-
	-	0				SignalP (SIGNALP)
Loa loa	transcription initiation factor tfiid subunit 6	0		F:GO:0005488; P:GO:0006352; F:GO:0003743; P:GO:0051090; F:GO:0003702; F:GO:0016986; F:GO:0003677; C:GO:0005634		IPR011442; PTHR10221 (PANTHER), PTHR10221:SF7 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	aminoadipate-semialdehyde dehydroge-se-phosphopantetheinyl transferase	3	P:GO:0009792; P:GO:0040010; P:GO:0040011	-		-
Caenorhabditis elegans	briggsae cbr-clec-1 protein	7	P:GO:0040035; P:GO:0010171; P:GO:0002119; F:GO:0005488; P:GO:0040018; P:GO:0040011; P:GO:0002009	-		-
Caenorhabditis elegans	stress-associated endoplasmic reticulum protein 2	15	P:GO:0001501; F:GO:0005515; P:GO:0009791; P:GO:0015031; C:GO:0016021; C:GO:0005789; P:GO:0010259; P:GO:0045727; P:GO:0048644; P:GO:0046622; P:GO:0006006; P:GO:0055085; P:GO:0060124; P:GO:0030968; P:GO:0032024	-		-
Ostertagia ostertagi	l3 es protein	0				-

Caenorhabditis briggsae	trehalase	5	P:GO:0009792; F:GO:0004135; P:GO:0005978; P:GO:0005991; F:GO:0004555	-	EC:3.2.1.33; EC:3.2.1.28	IPR001661; IPR008928; PTHR23403:SF1 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	F:GO:0016887; F:GO:0005524; C:GO:0005739	-		PTHR21610 (PANTHER), PTHR21610:SF4 (PANTHER)
Caenorhabditis elegans	r- dependent r- polymerase family protein	2	F:GO:0005515; P:GO:0009792	-		IPR000215; IPR007855
Loa loa	briggsae cbr-nmy-1 protein	4	F:GO:0003779; C:GO:0016459; F:GO:0005524; F:GO:0003774	-		IPR001609; PTHR13140 (PANTHER), PTHR13140:SF23 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Loa loa	c2orf29 protein	0		C:GO:0000123; P:GO:0016573; F:GO:0004402; P:GO:0045449; F:GO:0003713; C:GO:0005634		IPR019312
	-	0				-
Homo sapiens	protein nkg7	1	C:GO:0005887	-		IPR004032; PTHR10671:SF1 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	probable r--binding protein eif1ad	7	P:GO:0009792; P:GO:0002119; F:GO:0003676; F:GO:0005515; P:GO:0040010; P:GO:0000003; P:GO:0006898	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	caax prenyl protease 1 homolog	4	P:GO:0006508; C:GO:0044425; F:GO:0008235; C:GO:0005794	-		IPR001915; PTHR10120 (PANTHER), PTHR10120:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	elongation factor ts	5	P:GO:0009792; P:GO:0002119; P:GO:0040010; P:GO:0000003; P:GO:0006898	-		IPR000449; IPR001816; IPR006162; IPR009060; IPR014039; IPR018101; G3DSA:1.10.8.10 (GENE3D), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				PR01217 (PRINTS)
Caenorhabditis elegans	2-oxoglutarate and iron-dependent oxyge-se domain containing 1	1	P:GO:0045132	-		-
Caenorhabditis elegans	briggsae cbr-glrx-10 protein	4	P:GO:0045454; F:GO:0046872; F:GO:0009055; F:GO:0015035	-		IPR002109; IPR011767; IPR011899; IPR012335; IPR012336; IPR014025; PTHR10168 (PANTHER), PTHR10168:SF16 (PANTHER)

Caenorhabditis briggsae	adenosine ki-se	11	F:GO:0004001; C:GO:0005829; P:GO:0006166; P:GO:0040010; P:GO:0006175; P:GO:0000003; P:GO:0042102; P:GO:0046085; F:GO:0005515; P:GO:0016310; C:GO:0005634	-	EC:2.7.1.20	IPR001805; IPR002173; IPR011611; G3DSA:3.30.1110.10 (GENE3D), G3DSA:3.40.1190.20 (GENE3D), PTHR10584 (PANTHER), SSF53613 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	protein phosphatase 1d magnesium- delta isoform	3	P:GO:0009617; P:GO:0000086; F:GO:0016787	-		IPR001932; IPR014045; IPR015655; PTHR13832:SF94 (PANTHER)
Brugia malayi	thioester-containing protein	6	C:GO:0005615; P:GO:0008152; F:GO:0016491; F:GO:0005515; F:GO:0004866; F:GO:0016740	-		IPR001599; PTHR11412 (PANTHER), PTHR11412:SF30 (PANTHER)
	-	0				-
Caenorhabditis elegans	sushi domain	0		F:GO:0030414; C:GO:0005576		IPR000436; IPR016060
Caenorhabditis elegans	multiple pdz domain protein family member (mpz-1)	2	F:GO:0005515; C:GO:0016021	-		PTHR19964 (PANTHER), PTHR19964:SF5 (PANTHER)
synthetic construct	ribosomal protein s3	20	P:GO:0006413; C:GO:0032587; F:GO:0003684; P:GO:0006919; F:GO:0019901; P:GO:0006414; F:GO:0051536; P:GO:0045738; P:GO:0032088; C:GO:0030425; P:GO:0006917; P:GO:0009790; F:GO:0051059; F:GO:0004519; F:GO:0003735; C:GO:0012505; C:GO:0005634; F:GO:0003906; F:GO:0003729; C:GO:0022627	-	EC:4.2.99.18	IPR001351; IPR004044; IPR004087; IPR005703; IPR009019; IPR015946; IPR018280; PTHR11760 (PANTHER), PTHR11760:SF9 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-try-5 protein	0		P:GO:0006508; F:GO:0004252; C:GO:0031410; F:GO:0008236; F:GO:0016787; F:GO:0003824; F:GO:0008233; C:GO:0005576		IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR19355 (PANTHER), PTHR19355:SF58 (PANTHER)
Loa loa	structural mainte-nce of chromosomes protein 6	1	P:GO:0009987	-		PTHR19306 (PANTHER), PTHR19306:SF2 (PANTHER)

						IPR002126; IPR015919; PTHR10596 (PANTHER), PTHR10596:SF77 (PANTHER)
Loa loa	histone acetyltransferase	14	P:GO:0040010; F:GO:0008270; F:GO:0008415; P:GO:0006333; P:GO:0045449; P:GO:0000003; P:GO:0040027; P:GO:0010171; C:GO:0000785; P:GO:0006898; P:GO:0002009; P:GO:0009792; F:GO:0003682; C:GO:0005634	-		IPR002717; IPR016181; PTHR10615 (PANTHER), PTHR10615:SF30 (PANTHER)
	-	0				-
Caenorhabditis briggsae	class member 1	4	F:GO:0004571; F:GO:0005509; P:GO:0030433; C:GO:0016020	-	EC:3.2.1.113	IPR001382; PTHR11742:SF7 (PANTHER)
Caenorhabditis elegans	glyoxalase domain containing 4	1	C:GO:0005739	-		IPR004360; G3DSA:3.10.180.10 (GENE3D), PTHR10374 (PANTHER), SSF54593 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	hexamethylene bis-acetamide inducible 1	4	F:GO:0005488; F:GO:0016564; P:GO:0016481; C:GO:0044424	-		PTHR13469 (PANTHER), PTHR13469:SF4 (PANTHER)
	-	0				-
Caenorhabditis briggsae	protein tyrosine phosphatase-like (proline instead of catalytic arginine) member b	1	F:GO:0005515	-		IPR007482
	-	0				-
	-	0				-
Caenorhabditis elegans	zinc c2h2 type family protein	2	P:GO:0009987; P:GO:0007275	-		IPR007087; IPR013087; IPR015880; IPR020830; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis briggsae	zinc c2h2 type family protein	0		F:GO:0003676; F:GO:0008270; C:GO:0005634; C:GO:0005622		IPR007087; IPR013087; IPR015880; IPR020830; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis briggsae	lupus la ribonucleoprotein	0		F:GO:0003676; F:GO:0005488; C:GO:0030529		-
	-	0				-
Caenorhabditis briggsae	carbamoylphosphate synthetase aspartate transcarbamylase dihydroorotase	7	P:GO:0006541; F:GO:0016812; F:GO:0016597; F:GO:0004086; F:GO:0005524; P:GO:0006207; F:GO:0004070	-	EC:3.5.2.0; EC:2.1.3.2	IPR000991; IPR001317; IPR005481; IPR005483; IPR006220; IPR011702; IPR013817; IPR016185; IPR017926; G3DSA:3.40.50.880 (GENE3D), PTHR11405 (PANTHER), PTHR11405:SF3 (PANTHER), SSF52317 (SUPERFAMILY)
Microcoleus chthonoplastes PCC 7420	d- sulfur modification protein	0				-
Danio rerio	PREDICTED: cingulin-like [Danio rerio]	0				-
	-	0				-

Caenorhabditis elegans	dynein heavy chain	5	P:GO:0007018; C:GO:0030286; F:GO:0016887; F:GO:0005524; F:GO:0003777	-		IPR004273; PTHR10676 (PANTHER), PTHR10676:SF28 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	engulfment and cell	0		C:GO:0005856; P:GO:0006909		IPR006816; PTHR12771 (PANTHER), PTHR12771:SF2 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
NADP+; Short=DHPDHase; Short=DPD; AltName: Full=Dihydrothymine dehydrogenase; AltName: Full=Dihydrouracil dehydrogenase	dihydropyrimidine dehydroge-se	23	C:GO:0005829; F:GO:0004158; C:GO:0005625; P:GO:0006145; P:GO:0006212; F:GO:0046872; P:GO:0055114; P:GO:0007584; F:GO:0009055; F:GO:0017113; P:GO:0007623; F:GO:0051539; P:GO:0006222; P:GO:0051384; P:GO:0006210; P:GO:0042493; F:GO:0042803; F:GO:0002058; F:GO:0050660; P:GO:0006207; F:GO:0050661; P:GO:0006214; F:GO:0010181	-	EC:1.3.3.1; EC:1.3.1.2	IPR013027; G3DSA:3.50.50.60 (GENE3D), PTHR11938 (PANTHER), PTHR11938:SF6 (PANTHER), SSF51905 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-ptr-24 protein	0		C:GO:0016021; C:GO:0016020; F:GO:0005215; P:GO:0006810; F:GO:0008158		PTHR10796 (PANTHER), PTHR10796:SF12 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	myosin if	6	C:GO:0016461; F:GO:0003779; F:GO:0005524; F:GO:0003774; P:GO:0006508; F:GO:0005516	-		PTHR13140 (PANTHER), PTHR13140:SF31 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005488	-		-
	-	0				-
Caenorhabditis elegans	gex interacting protein family member (gei-16)	1	F:GO:0005515	-		-
Caenorhabditis briggsae	transmembrane and coiled-coil domains 4	0		F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150; C:GO:0005575		IPR007941

Caenorhabditis briggsae	mdn1 midasin family protein	6	P:GO:0043254; P:GO:0006355; F:GO:0005524; F:GO:0016887; F:GO:0008134; C:GO:0005634	-		G3DSA:3.40.50.300 (GENE3D), PTHR22908 (PANTHER), PTHR22908:SF13 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	sig-l peptidase complex subunit 1	12	F:GO:0008233; C:GO:0005787; P:GO:0006465; C:GO:0030176; P:GO:0040007; P:GO:0000003; P:GO:0006508; C:GO:0005792; P:GO:0002119; P:GO:0040011; P:GO:0006898; P:GO:0009792	-		IPR009542
Caenorhabditis elegans	r--binding protein 42	6	P:GO:0002088; F:GO:0003723; C:GO:0005737; P:GO:0000003; C:GO:0005634; F:GO:0000166	-		IPR000504; IPR012677; IPR015464; PTHR10432 (PANTHER), SSF54928 (SUPERFAMILY)
Tribolium castaneum	vesicular mannose-binding lectin	4	C:GO:0043231; P:GO:0032501; C:GO:0044444; C:GO:0016020	-		IPR005052; IPR008985; IPR013320; IPR019825; PTHR12223:SF6 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	leucine zipper-ef-hand containing transmembrane protein 1	4	P:GO:0009792; P:GO:0040018; P:GO:0000003; P:GO:0006898	-		IPR018249; PTHR14009 (PANTHER), PTHR14009:SF1 (PANTHER)
Caenorhabditis elegans	ankyrin repeat domain-containing protein 49	0		F:GO:0004623; F:GO:0016787		IPR002110; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER), PTHR18958:SF218 (PANTHER)
Loa loa	cytoplasmic linker associated protein 2	5	P:GO:0031110; F:GO:0008017; P:GO:0030900; C:GO:0005874; C:GO:0044444	-		PTHR21567 (PANTHER), PTHR21567:SF10 (PANTHER), SignalP (SIGNALP)
Brugia malayi	low quality protein: clip-associating protein 1-like	5	P:GO:0006996; F:GO:0005488; C:GO:0015630; C:GO:0044444; C:GO:0044430	-		IPR011989; IPR016024; IPR021133; PTHR21567 (PANTHER), PTHR21567:SF10 (PANTHER), PF12348 (PFAM)
Mus musculus	PREDICTED: hypothetical protein [Mus musculus]	0		F:GO:0003674; C:GO:0005575		IPR003582
	-	0				-
Brugia malayi	set binding factor 1	0		F:GO:0046872; P:GO:0016311; F:GO:0016791		IPR004182; PTHR10807 (PANTHER), PTHR10807:SF1 (PANTHER)
	-	0				-

Caenorhabditis elegans	excitatory gaba receptor exp-1a	6	P:GO:0010171; C:GO:0045211; C:GO:0030054; F:GO:0005230; P:GO:0006811; C:GO:0016021	-		IPR006201; IPR006202; PTHR18945:SF8 (PANTHER)
Caenorhabditis elegans	isoform a	2	P:GO:0006810; C:GO:0016020	-		IPR013657; PTHR10778 (PANTHER), PTHR10778:SF4 (PANTHER)
Homo sapiens	a chain structure of hsp90 with small molecule inhibitor bound	14	C:GO:0005829; P:GO:0042026; P:GO:0006839; F:GO:0030235; P:GO:0070096; C:GO:0042470; F:GO:0005524; F:GO:0030911; P:GO:0007165; F:GO:0051082; P:GO:0006986; P:GO:0045429; F:GO:0042803; P:GO:0034619	-		IPR001404; IPR003594; IPR020575; IPR020576
Caenorhabditis elegans	briggsae cbr-mut-2 protein	0		F:GO:0016779		SignalP (SIGNALP)
Caenorhabditis briggsae	tr--dihydrouridine synthase 2-like	4	F:GO:0016491; F:GO:0003723; P:GO:0008152; C:GO:0005739	-		-
Homo sapiens	complement component 3	16	F:GO:0048037; P:GO:0006957; F:GO:0005102; P:GO:0010951; P:GO:0050766; P:GO:0045766; C:GO:0005615; P:GO:0001798; P:GO:0007596; P:GO:0007165; P:GO:0010575; P:GO:0006935; P:GO:0007186; P:GO:0006958; F:GO:0004866; P:GO:0001970	-		IPR009048; PTHR11412 (PANTHER), PTHR11412:SF14 (PANTHER)
Caenorhabditis elegans	abnormal cell lineage family member (lin-29)	6	F:GO:0008270; F:GO:0003676; F:GO:0003700; P:GO:0016481; P:GO:0048749; C:GO:0005634	-		IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis elegans	fch domain only protein 2	0		C:GO:0030131; F:GO:0003674; P:GO:0016192; P:GO:0008150; P:GO:0006886; F:GO:0005515		IPR001060; PTHR23065 (PANTHER)
Nasonia vitripennis	peroxisomal -trans-enoyl- isomerase	2	F:GO:0003824; F:GO:0005515	-		IPR001753; G3DSA:3.90.226.10 (GENE3D), PTHR11941 (PANTHER), SSF52096 (SUPERFAMILY)

Caenorhabditis elegans	beta-lactamase-like protein 2	2	F:GO:0016787; C:GO:0005739	-		IPR001279; G3DSA:3.60.15.10 (GENE3D), PTHR23131 (PANTHER), SSF56281 (SUPERFAMILY)
Loa loa	d--directed r- polymerases i and iii subunit rpac2	4	F:GO:0003899; F:GO:0003677; P:GO:0006350; C:GO:0005634	-	EC:2.7.7.6	-
Caenorhabditis elegans	isy1 splicing factor homolog (cerevisiae)	4	P:GO:0040035; P:GO:0002119; P:GO:0018996; C:GO:0044428	-		IPR009360; PTHR13021:SF5 (PANTHER)
Caenorhabditis elegans	isoform a	2	F:GO:0030170; F:GO:0008483	-	EC:2.6.1.0	IPR005814; IPR015421; IPR015422; IPR015424; PTHR11986:SF23 (PANTHER)
	-	0				-
Ailuropoda melanoleuca	histone h2a type 1-like	0				-
Caenorhabditis briggsae	Hypothetical protein CBG06646 [Caenorhabditis briggsae]	0				-
Gallus gallus	multidrug resistance protein	4	F:GO:0042626; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF96 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	pre-mr--splicing factor atp-dependent r- helicase prp16	7	P:GO:0008380; F:GO:0008026; F:GO:0003676; C:GO:0005681; F:GO:0005515; P:GO:0006397; F:GO:0005524	-		IPR001650; IPR002464; IPR011545; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR18934 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	iron-responsive element-binding protein 1	6	P:GO:0006879; F:GO:0005515; F:GO:0051539; F:GO:0003994; P:GO:0008152; C:GO:0005829	-	EC:4.2.1.3	IPR001030; IPR015928; IPR015931; IPR015932; IPR015934; IPR015937; IPR018136
Caenorhabditis briggsae	fructose-bisphosphate aldolase	3	F:GO:0042802; P:GO:0006096; F:GO:0004332	-	EC:4.1.2.13	IPR000741; IPR013785; SSF51569 (SUPERFAMILY)
Caenorhabditis briggsae	fructose-bisphosphate aldolase	3	F:GO:0042802; P:GO:0006096; F:GO:0004332	-	EC:4.1.2.13	IPR000741; IPR013785; SSF51569 (SUPERFAMILY)
Caenorhabditis elegans	ankyrin repeat domain 50	3	F:GO:0005515; P:GO:0006974; P:GO:0008340	-		-
	-	0				-
						SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-fli-1 protein	2	F:GO:0016787; F:GO:0003779	-		IPR007122; IPR007123; G3DSA:3.40.20.10 (GENE3D), PTHR11977:SF6 (PANTHER), SSF55753 (SUPERFAMILY)

Granulibacter bethesdensis CGDNIH1	tr- modification gtpase	0		P:GO:0008033; C:GO:0005739; F:GO:0016787; F:GO:0000166; C:GO:0005737; F:GO:0005525; C:GO:0005622; P:GO:0006400; F:GO:0003924; F:GO:0046872; P:GO:0007264		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0005509; F:GO:0004571; C:GO:0016020		-
Caenorhabditis briggsae	Hypothetical protein CBG05778 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	midasin homolog	6	F:GO:0017111; P:GO:0050789; C:GO:0005622; P:GO:0006461; F:GO:0005515; F:GO:0000166	-	EC:3.6.1.15	IPR011704; G3DSA:3.40.50.300 (GENE3D), PTHR22908 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Ciona intestinalis	PREDICTED: hypothetical protein [Cio- intesti-lis]	0		F:GO:0046872; F:GO:0003676; P:GO:0055114; F:GO:0009055; F:GO:0016491; F:GO:0020037; F:GO:0005506; F:GO:0004497		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	atpase type 13a1	6	C:GO:0016021; F:GO:0046872; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0006812	-		IPR001757; IPR008250; G3DSA:2.70.150.10 (GENE3D), PTHR11939:SF48 (PANTHER), SSF81653 (SUPERFAMILY)
Caenorhabditis elegans	splicing factor 3b subunit 1	9	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0003676; P:GO:0040010; P:GO:0008340; P:GO:0040011; P:GO:0006898; C:GO:0030529	-		IPR011989; IPR016024; PTHR12097 (PANTHER)
Caenorhabditis briggsae	patched family protein	6	P:GO:0040025; P:GO:0040018; P:GO:0018996; P:GO:0000003; P:GO:0008340; P:GO:0040011	-		IPR000731; IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER), SignalP (SIGNALP), SSF82866 (SUPERFAMILY)

Caenorhabditis elegans	patched family protein	4	P:GO:0018996; C:GO:0016020; P:GO:0040018; P:GO:0040011	-		-
	-	0				-
Loa loa	patched family protein	3	P:GO:0040018; P:GO:0018996; P:GO:0040011	-		IPR000731; IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER), SSF82866 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis briggsae	Hypothetical protein CBG15976 [Caenorhabditis briggsae]	0		C:GO:0005737; C:GO:0016020		-
Caenorhabditis briggsae	af292052_1 5n224	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-unc-68 protein	1	P:GO:0006810	-		-
Caenorhabditis elegans	piwi-like protein 1	7	F:GO:0034584; P:GO:0031047; F:GO:0005515; C:GO:0043186; P:GO:0034587; P:GO:0007281; P:GO:0009653	-		IPR003165; IPR012337; PTHR22892 (PANTHER), PTHR22892:SF5 (PANTHER)
Caenorhabditis elegans	piwi-like protein 1	7	F:GO:0034584; P:GO:0031047; F:GO:0005515; C:GO:0043186; P:GO:0034587; P:GO:0007281; P:GO:0009653	-		IPR003165; IPR012337; PTHR22892 (PANTHER), PTHR22892:SF5 (PANTHER)
	-	0				SignalP (SIGNALP)
Loa loa	methyltransferase like 9	2	F:GO:0016740; F:GO:0005515	-		IPR007884; IPR018357; G3DSA:3.40.50.150 (GENE3D), SSF53335 (SUPERFAMILY)
Caenorhabditis briggsae	ribosomal protein l18a	7	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; P:GO:0040010; P:GO:0000003; P:GO:0006412	-	EC:3.6.5.3	-
Brugia malayi	peptidylprolyl isomerase -like 5	0		F:GO:0003674; P:GO:0008152; P:GO:0008150; F:GO:0005515; C:GO:0005575		-
Brugia malayi	poly(adp-ribose) glycohydrolase	0		F:GO:0004649; F:GO:0003735; P:GO:0006342; P:GO:0043484; F:GO:0016787; P:GO:0006412; P:GO:0006911; P:GO:0005975; C:GO:0005840; C:GO:0005654; P:GO:0035065; P:GO:0051457; P:GO:0009408; C:GO:0005622		IPR007724

Caenorhabditis briggsae	xpa-binding protein 2	11	P:GO:0040010; F:GO:0005488; P:GO:0000910; C:GO:0071011; P:GO:0000381; P:GO:0000003; P:GO:0006911; P:GO:0002119; C:GO:0071013; P:GO:0009792; P:GO:0001703	-		PTHR11246 (PANTHER), PTHR11246:SF5 (PANTHER)
Caenorhabditis briggsae	xpa-binding protein 2	11	P:GO:0040010; F:GO:0005488; P:GO:0000910; C:GO:0071011; P:GO:0000381; P:GO:0000003; P:GO:0006911; P:GO:0002119; C:GO:0071013; P:GO:0009792; P:GO:0001703	-		IPR003107; PTHR11246 (PANTHER), PTHR11246:SF5 (PANTHER)
	-	0				-
Caenorhabditis briggsae	dmx-like 2	1	C:GO:0044464	-		PTHR13950 (PANTHER), PTHR13950:SF1 (PANTHER)
Caenorhabditis elegans	phospholipase d member 4	4	C:GO:0016021; P:GO:0008152; F:GO:0003824; F:GO:0005515	-		-
Caenorhabditis elegans	intron-binding protein aquarius	1	F:GO:0005488	-		PTHR10887 (PANTHER), PTHR10887:SF5 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-sulp-8 protein	3	C:GO:0016020; P:GO:0006810; F:GO:0005215	-		IPR002645; PTHR11814 (PANTHER)
Nasonia vitripennis	PREDICTED: hypothetical protein [-sonia vitripennis]	0				-
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	arid bright d- binding domain containing protein	1	F:GO:0005488	-		IPR001606; PTHR12656 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	F:GO:0005509	-		IPR018249; PTHR13025 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	dtdp-glucose 4-6-dehydratase	3	P:GO:0044237; F:GO:0050662; F:GO:0003824	-		IPR001509; IPR016040; PTHR10366 (PANTHER), PTHR10366:SF35 (PANTHER), SignalP (SIGNALP), SSF51735 (SUPERFAMILY)
Caenorhabditis briggsae	tpr domain containing protein	1	F:GO:0005488	-		SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Homo sapiens	riken cd- 1810037i17 gene	1	C:GO:0016021	-		-
Caenorhabditis elegans	hypothetical protein K07C11.8 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	hypothetical protein K07C11.8 [Caenorhabditis elegans]	0				SignalP (SIGNALP)

Caenorhabditis briggsae	cyclin e	25	C:GO:0031981; P:GO:0006468; F:GO:0016301; P:GO:0051597; P:GO:0014074; P:GO:0045597; P:GO:0010243; P:GO:0051412; P:GO:0031100; P:GO:0006270; P:GO:0033197; P:GO:0045471; P:GO:0001547; P:GO:0031670; P:GO:0032570; P:GO:0034097; P:GO:0007088; C:GO:0005813; P:GO:0042493; F:GO:0016538; P:GO:0000082; P:GO:0019222; F:GO:0032403; P:GO:0001889; P:GO:0032355	-		IPR006670; IPR006671; IPR011028; IPR013763; IPR014400; PTHR10177 (PANTHER), PTHR10177:SF15 (PANTHER)
Caenorhabditis elegans	u493_caeel ame: full=upf0493 protein	1	P:GO:0040017	-		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	60s ribosome subunit biogenesis protein nip7 homolog	8	P:GO:0040010; F:GO:0003723; C:GO:0005730; P:GO:0040035; P:GO:0002119; F:GO:0005515; P:GO:0006898; P:GO:0042255	-		IPR002478; IPR005155; IPR015947; G3DSA:2.30.130.10 (GENE3D), PTHR23415 (PANTHER), PTHR23415:SF4 (PANTHER), SSF88802 (SUPERFAMILY)
						SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-tyr-4 protein	0		F:GO:0020037; P:GO:0006979; F:GO:0004222; F:GO:0016787; F:GO:0008270; P:GO:0055114; F:GO:0008237; F:GO:0016491; F:GO:0008233; P:GO:0006508; F:GO:0005515; F:GO:0004601; P:GO:0008152; F:GO:0046872		IPR003582; IPR013090

Oryctolagus cuniculus	cytochrome c oxidase subunit 6b1	6	C:GO:0005758; C:GO:0005743; P:GO:0034220; P:GO:0055114; P:GO:0015992; F:GO:0004129	-	EC:1.9.3.1	SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	F:GO:0016791	-	EC:3.1.3.0	IPR000242; IPR000387; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis elegans	nuclear vcp-like	3	C:GO:0005730; F:GO:0005524; F:GO:0017111	-	EC:3.6.1.15	IPR003959; IPR003960; G3DSA:3.40.50.300 (GENE3D), PTHR23077 (PANTHER), PTHR23077:SF16 (PANTHER), SSF52540 (SUPERFAMILY)
Loa loa	hypothetical protein LOAG_04493 [Loa loa]	0				-
Caenorhabditis briggsae	briggsae cbr-igcm-1 protein	0		C:GO:0016020		IPR003598; IPR003599; IPR007110; IPR013098; IPR013162; IPR013783; PTHR11640 (PANTHER), PTHR11640:SF2 (PANTHER), SignalP (SIGNALP), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	catenin (cadherin-associated protein) delta 2 (neural plakophilin-related arm-repeat protein)	5	P:GO:0007612; P:GO:0001763; P:GO:0048167; F:GO:0005515; C:GO:0044424	-		IPR000225; IPR011989; IPR016024; PTHR10372 (PANTHER), PTHR10372:SF4 (PANTHER)
Caenorhabditis briggsae	nucleolar protein c7b	1	F:GO:0005515	-		IPR004182; PTHR23354 (PANTHER), PTHR23354:SF4 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-pxn-2 protein	2	F:GO:0005488; P:GO:0000003	-		IPR002007; IPR010255; IPR019791; PTHR11475 (PANTHER), PTHR11475:SF10 (PANTHER)
Caenorhabditis elegans	aldehyde dehydroge-se 7 member a1	6	F:GO:0004029; P:GO:0055114; C:GO:0044444; P:GO:0006081; C:GO:0043231; P:GO:0007605	-	EC:1.2.1.3	SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0009792		PTHR10343 (PANTHER), PTHR10343:SF10 (PANTHER)
Brugia malayi	setd8b protein	3	F:GO:0016740; F:GO:0003714; P:GO:0016481	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	hypothetical protein LOAG_11764 [Loa loa]	0				-
Caenorhabditis briggsae	5-oxoproli-se (atp-hydrolysing)	1	F:GO:0016787	-		IPR002821; IPR008040; PTHR11365 (PANTHER)
Caenorhabditis elegans	briggsae cbr-set-6 protein	0		F:GO:0008168; F:GO:0016740; F:GO:0008270; F:GO:0018024; P:GO:0016568		IPR001214; IPR007728; IPR013032; G3DSA:2.170.270.10 (GENE3D), PTHR22884 (PANTHER), PTHR22884:SF21 (PANTHER), SignalP (SIGNALP), SSF82199 (SUPERFAMILY)
Ciona intestinalis	novel protein	0				-

	-	0				-
Caenorhabditis elegans	briggsae cbr-dhs-24 protein	0		P:GO:0055114; F:GO:0005488; F:GO:0016491; P:GO:0008152; F:GO:0003824		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	4	F:GO:0015269; P:GO:0006813; C:GO:0016021; F:GO:0005516	-		IPR015449; PTHR10153:SF6 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	probable inner membrane protein oxa1l2	0		C:GO:0016021; C:GO:0016020; P:GO:0051205		SignalP (SIGNALP)
Caenorhabditis briggsae	ect2 protein	0		F:GO:0017048; P:GO:0007422; P:GO:0008360; P:GO:0007111; P:GO:0051225; P:GO:0000902; P:GO:0007110; C:GO:0005634; P:GO:0050790; P:GO:0007155; P:GO:0000915; P:GO:0035023; F:GO:0005089; P:GO:0000910; P:GO:0050770; F:GO:0005085; P:GO:0008078; P:GO:0045184; P:GO:0007443; P:GO:0007399; P:GO:0023034; P:GO:0007509; C:GO:0005622; F:GO:0005515		IPR001357; G3DSA:3.40.50.10190 (GENE3D), PTHR16777 (PANTHER)
Loa loa	superkiller viralicidic activity 2-like 2	16	P:GO:0040010; C:GO:0005681; F:GO:0003676; P:GO:0031101; F:GO:0008026; P:GO:0006200; P:GO:0040035; P:GO:0008380; F:GO:0005524; P:GO:0002119; P:GO:0051781; F:GO:0005515; P:GO:0040011; P:GO:0006397; P:GO:0002009; P:GO:0009792	-		IPR011545; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR11752 (PANTHER), PTHR11752:SF2 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				PTHR14017 (PANTHER), PTHR14017:SF1 (PANTHER)

Loa loa	piwi domain-containing protein	1	P:GO:0007275	-		IPR003100; IPR003165; IPR012337; G3DSA:2.170.260.10 (GENE3D), PTHR22891 (PANTHER), SSF101690 (SUPERFAMILY)
Caenorhabditis briggsae	choline transporter-like family member (chtl-1)	6	P:GO:0002009; C:GO:0016021; P:GO:0040007; P:GO:0040035; P:GO:0040002; P:GO:0002119	-		IPR007603; PTHR12385:SF7 (PANTHER)
Caenorhabditis elegans	briggsae cbr-gska-3 protein	3	P:GO:0002119; F:GO:0004672; P:GO:0040010	-		-
Caenorhabditis elegans	isoform c	1	P:GO:0009792	-		IPR004182; PTHR23319 (PANTHER)
	-	0				-
Caenorhabditis elegans	g-protein coupled receptor	1	P:GO:0007186	-		IPR017452; IPR019427; G3DSA:1.20.1070.10 (GENE3D), PTHR22751 (PANTHER), PTHR22751:SF12 (PANTHER), SignalP (SIGNALP), SSF81321 (SUPERFAMILY)
Dictyocaulus viviparus	briggsae cbr-ccg-1 protein	0				-
Caenorhabditis elegans	2-hydroxyphytanoyl-coa lyase	3	F:GO:0030976; F:GO:0000287; F:GO:0003824	-		IPR012001; G3DSA:3.40.50.970 (GENE3D), PTHR18968 (PANTHER), PTHR18968:SF1 (PANTHER), SSF52467 (SUPERFAMILY), SSF52518 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein Y54G2A.52 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
Brugia malayi	mitogen-activated protein ki-se-binding protein 1	3	P:GO:0009792; P:GO:0040035; F:GO:0005515	-		IPR001680; IPR015943; PTHR22847 (PANTHER), PTHR22847:SF10 (PANTHER), SSF101908 (SUPERFAMILY)
Caenorhabditis briggsae	pantothe-te ki-se 4	8	P:GO:0040010; P:GO:0008340; P:GO:0000003; F:GO:0016740; P:GO:0002119; F:GO:0000166; P:GO:0009792; P:GO:0044237	-		-
Caenorhabditis elegans	briggsae cbr-soc-1 protein	0		P:GO:0008595; F:GO:0042169; C:GO:0005737; P:GO:0019730; P:GO:0008293; F:GO:0005515; F:GO:0005070; P:GO:0046578; C:GO:0005886; P:GO:0045500		IPR001849; IPR011993; PTHR12156 (PANTHER), PTHR12156:SF1 (PANTHER), SSF50729 (SUPERFAMILY)

Caenorhabditis elegans	briggsae cbr-soc-1 protein	0		P:GO:0008595; F:GO:0042169; C:GO:0005737; P:GO:0019730; P:GO:0008293; F:GO:0005515; F:GO:0005070; P:GO:0046578; C:GO:0005886; P:GO:0045500		IPR001849; IPR011993; PTHR12156 (PANTHER), PTHR12156:SF1 (PANTHER), SSF50729 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	uncoordi-ted family member (unc-52)	2	P:GO:0030239; C:GO:0005578	-		-
Brugia malayi	craniofacial development protein 1	0				-
Brugia malayi	myosin xviiia	0		C:GO:0005634; F:GO:0003677; F:GO:0003674; P:GO:0006916; F:GO:0005524; F:GO:0042802; F:GO:0008094; C:GO:0016459; P:GO:0008152; P:GO:0008150; F:GO:0000166; C:GO:0005737; P:GO:0006259; C:GO:0005794; C:GO:0005793; F:GO:0003774; C:GO:0005730; C:GO:0005856; F:GO:0005515		-
	-	0				-
	-	0				-
Homo sapiens	lactotransferrin precursor	10	F:GO:0008199; P:GO:0042742; P:GO:0006879; P:GO:0006959; P:GO:0006826; F:GO:0005515; F:GO:0004252; F:GO:0008201; C:GO:0030141; C:GO:0005576	-	EC:3.4.21.0	-
Caenorhabditis elegans	yth domain containing 2	5	F:GO:0003676; F:GO:0004672; F:GO:0008026; F:GO:0005524; P:GO:0006468	-		IPR001374; IPR002464; IPR011545; IPR014001; IPR014021; G3DSA:3.30.1370.50 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR18934 (PANTHER), SSF52540 (SUPERFAMILY), SSF82708 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-kin-29 protein	2	F:GO:0005488; F:GO:0016301	-		IPR020636; IPR020666

Caenorhabditis briggsae	briggsae cbr-ehbp-1 protein	5	F:GO:0008017; C:GO:0016324; F:GO:0003779; P:GO:0000910; P:GO:0006897	-		IPR001715; PTHR11915 (PANTHER), PTHR11915:SF47 (PANTHER)
	-	0				-
Taeniopygia guttata	elmo domain-containing protein 1	1	P:GO:0000910	-		IPR006816; PTHR12771 (PANTHER), PTHR12771:SF1 (PANTHER)
Ixodes scapularis	importin 7	4	F:GO:0042393; P:GO:0006606; F:GO:0005215; C:GO:0005634	-		IPR011989; IPR016024; PTHR10997 (PANTHER), PTHR10997:SF18 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Brugia malayi	CG3579-PA [Brugia malayi]	0		F:GO:0003824		SignalP (SIGNALP)
Brugia malayi	CG3579-PA [Brugia malayi]	0		F:GO:0003824		SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	male sterility protein	3	P:GO:0008152; F:GO:0003824; F:GO:0005515	-		IPR013120; IPR016040; PTHR11011 (PANTHER), PTHR11011:SF8 (PANTHER)
Brugia malayi	btb poz domain containing protein	2	F:GO:0005515; P:GO:0000003	-		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	5	P:GO:0009792; F:GO:0016491; P:GO:0040010; P:GO:0002119; P:GO:0040011	-		IPR001395; IPR018170; IPR020471; IPR023210; PTHR11732:SF34 (PANTHER)
Brugia malayi	kinesin-like protein klp10a	11	P:GO:0000278; P:GO:0006996; C:GO:0005874; P:GO:0000279; F:GO:0003774; F:GO:0005515; C:GO:0044444; P:GO:0007017; F:GO:0000166; C:GO:0005819; P:GO:0007275	-		IPR001752; IPR019821; PTHR16012 (PANTHER), PTHR16012:SF186 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	ercc4 domain containing protein	3	F:GO:0005488; P:GO:0006281; P:GO:0009792	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				IPR016160; PTHR13167 (PANTHER), PTHR13167:SF7 (PANTHER), SignalP (SIGNALP)
	-	0				PTHR18929 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis elegans	-d-dependent malic mitochondrial precursor	7	F:GO:0046872; F:GO:0051287; F:GO:0004470; P:GO:0006108; P:GO:0055114; F:GO:0016616; C:GO:0005739	-	EC:1.1.1.0	PTHR23406 (PANTHER), PTHR23406:SF2 (PANTHER)

Caenorhabditis elegans	d domain (prokaryotic heat shock protein) family member (dnj-17)	0		F:GO:0003676; P:GO:0000003; F:GO:0008270; C:GO:0005622		SignalP (SIGNALP)
Caenorhabditis elegans	#NAME?	0		F:GO:0016740; P:GO:0008152; F:GO:0003824; F:GO:0008483; F:GO:0030170		IPR000192; IPR015421; IPR015424; PTHR11601 (PANTHER)
Loa loa	dy-ctin subunit 6	0		C:GO:0005737; C:GO:0005856; F:GO:0016740; P:GO:0008150; P:GO:0007018		-
Loa loa	chromosome 9 open reading frame 41-like	0				IPR012901
Caenorhabditis briggsae	cytochrome c oxidase subunit va	6	P:GO:0009792; P:GO:0008340; P:GO:0000003; F:GO:0004129; P:GO:0040007; P:GO:0002119	-	EC:1.9.3.1	-
	-	0				-
Caenorhabditis elegans	acetyl- hydrolase transferase family protein	5	F:GO:0019239; C:GO:0005811; P:GO:0009168; P:GO:0006084; F:GO:0016787	-		IPR003702; G3DSA:3.30.750.70 (GENE3D), PTHR21432:SF11 (PANTHER), SSF100950 (SUPERFAMILY)
Caenorhabditis elegans	polymerase (d- directed) epsilon	17	F:GO:0008270; F:GO:0003887; P:GO:0006260; P:GO:0040035; P:GO:0006297; F:GO:0003677; P:GO:0000731; F:GO:0005515; F:GO:0000166; P:GO:0040011; P:GO:0006997; P:GO:0000082; F:GO:0004527; C:GO:0005654; P:GO:0002009; P:GO:0009792; F:GO:0003682	-	EC:2.7.7.7	PTHR10670 (PANTHER), SSF56672 (SUPERFAMILY)
Loa loa	cyclin k	3	F:GO:0005515; P:GO:0000079; P:GO:0006366	-		IPR006670; IPR006671; IPR011028; IPR013763; IPR015429; PTHR10026:SF11 (PANTHER)
Ailuropoda melanoleuca	pleckstrin homology domain family o member 1	3	C:GO:0005634; C:GO:0005737; C:GO:0005886	-		IPR001849; PTHR15871 (PANTHER), PTHR15871:SF1 (PANTHER)
Brugia malayi	trafficking protein particle complex 1	3	P:GO:0006888; C:GO:0030008; F:GO:0005515	-		-

Taeniopygia guttata	heterogeneous nuclear ribonucleoprotein k	12	C:GO:0005737; C:GO:0005730; P:GO:0008380; C:GO:0030530; C:GO:0005654; C:GO:0005681; F:GO:0003723; F:GO:0005515; F:GO:0003697; P:GO:0006397; P:GO:0007165; P:GO:0044419	-		IPR004087; IPR004088; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR10288 (PANTHER), PTHR10288:SF38 (PANTHER), SSF54791 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-immp-2 protein	2	C:GO:0044464; F:GO:0008234	-		IPR000223; IPR011056; IPR015927; IPR019756; IPR019759; PTHR12383 (PANTHER), PTHR12383:SF3 (PANTHER), SignalP (SIGNALP)
Hyalomma marginatum rufipes	ubiquitin c	2	C:GO:0005634; C:GO:0005737	-		IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), PTHR10666:SF9 (PANTHER), SSF54236 (SUPERFAMILY)
Loa loa	smc c-termi-l domain containing protein	9	F:GO:0005515; P:GO:0006974; P:GO:0006259; P:GO:0010564; C:GO:0000776; P:GO:0007067; P:GO:0048523; P:GO:0007062; C:GO:0005634	-		PTHR18937 (PANTHER), PTHR18937:SF12 (PANTHER)
Caenorhabditis sp. PS1010	ribosomal protein s3	22	P:GO:0008340; P:GO:0000003; C:GO:0032587; F:GO:0003684; P:GO:0006919; P:GO:0040007; F:GO:0019901; P:GO:0006412; P:GO:0045738; P:GO:0018996; P:GO:0032088; P:GO:0019915; P:GO:0009792; P:GO:0006917; P:GO:0002119; F:GO:0051059; F:GO:0004519; F:GO:0003735; C:GO:0005634; F:GO:0003906; F:GO:0003729; C:GO:0022627	-	EC:3.6.5.3; EC:4.2.99.18	-
Caenorhabditis elegans	briggsae cbr-pcp- protein	3	P:GO:0009792; F:GO:0004180; F:GO:0008236	-		IPR008758; PTHR11010:SF6 (PANTHER)

Caenorhabditis elegans	beta-ureidopropio-se	5	P:GO:0006807; C:GO:0005829; F:GO:0046872; P:GO:0000003; F:GO:0003837	-	EC:3.5.1.6	-
Caenorhabditis elegans	metallophosphoesterase 1	0		F:GO:0016787		-
Loa loa	wapl (drosophila wings apart-like cohesin interactor) family member (wapl-1)	3	P:GO:0018991; P:GO:0040010; P:GO:0040011	-		IPR012502; PTHR22100 (PANTHER), PTHR22100:SF7 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	-dph:adrenodoxin mitochondrial	7	C:GO:0005739; P:GO:0007552; P:GO:0042048; P:GO:0035073; P:GO:0006694; P:GO:0007591; F:GO:0003824	-		IPR013027; PR00419 (PRINTS), G3DSA:3.50.50.60 (GENE3D), PTHR11938 (PANTHER), PTHR11938:SF4 (PANTHER), SSF51971 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	monoacylglycerol o-acyltransferase 2	5	P:GO:0044238; F:GO:0008415; C:GO:0044425; P:GO:0009792; C:GO:0005783	-		IPR007130; SignalP (SIGNALP)
Callithrix jacchus	ribosomal protein l5	8	C:GO:0005730; P:GO:0006364; P:GO:0042273; F:GO:0003735; P:GO:0006414; F:GO:0005515; C:GO:0022625; F:GO:0008097	-		IPR005484; IPR005485; G3DSA:3.30.420.100 (GENE3D), SSF53137 (SUPERFAMILY)
Brugia malayi	dual specificity catalytic domain containing protein	2	P:GO:0006796; F:GO:0016791	-	EC:3.1.3.0	IPR000340; IPR000387; IPR016130; IPR020422; G3DSA:3.90.190.10 (GENE3D), PTHR10159 (PANTHER), SignalP (SIGNALP), SSF52799 (SUPERFAMILY)
Brugia malayi	dual specificity catalytic domain containing protein	2	P:GO:0006796; F:GO:0016791	-	EC:3.1.3.0	IPR000340; IPR000387; IPR016130; IPR020422; G3DSA:3.90.190.10 (GENE3D), PTHR10159 (PANTHER), SignalP (SIGNALP), SSF52799 (SUPERFAMILY)
Haemonchus contortus	briggsae cbr-vha-6 protein	5	F:GO:0015078; C:GO:0033177; P:GO:0015986; C:GO:0031410; P:GO:0001845	-		IPR002490; PTHR11629:SF23 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-nhr-97 protein	4	F:GO:0004872; F:GO:0005488; P:GO:0006350; P:GO:0000003	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)

Caenorhabditis briggsae	d- polymerase delta catalytic subunit	12	C:GO:0005875; P:GO:0000910; F:GO:0003887; P:GO:0006260; F:GO:0003677; P:GO:0035188; P:GO:0002119; F:GO:0008296; F:GO:0000166; P:GO:0006898; P:GO:0009792; P:GO:0006974	-	EC:2.7.7.7	IPR006133; IPR012337; G3DSA:3.30.420.10 (GENE3D), PTHR10322 (PANTHER), PTHR10322:SF4 (PANTHER)
Caenorhabditis briggsae	use1_caeel ame: full=vesicle transport protein use1 ame: full=use1-like protein	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	variable abnormal morphology family member (vab-8)	5	P:GO:0007275; F:GO:0003774; P:GO:0009987; F:GO:0000166; C:GO:0044424	-		-
Caenorhabditis elegans	briggsae cbr-rbc-1 protein	0		P:GO:0006355; C:GO:0016021; F:GO:0043565; C:GO:0016020; P:GO:0045449; F:GO:0003677; F:GO:0003700; C:GO:0005634		-
Caenorhabditis elegans	related to yeast vacuolar protein sorting factor family member (vps-39)	6	P:GO:0002009; P:GO:0008219; P:GO:0009792; P:GO:0000003; P:GO:0010171; F:GO:0005515	-		IPR001180
Caenorhabditis briggsae	uncoordi-ted family member (unc-89)	0		F:GO:0004672; F:GO:0005524; F:GO:0000166; F:GO:0005089; P:GO:0006468; P:GO:0035023; C:GO:0005622; F:GO:0004674		IPR000719; IPR011009; IPR017442; IPR020636; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis briggsae	Hypothetical protein CBG09264 [Caenorhabditis briggsae]	0		F:GO:0005515		PTHR13546 (PANTHER), PTHR13546:SF1 (PANTHER)
Caenorhabditis elegans	pre-mr--splicing factor syf2	3	P:GO:0008380; P:GO:0006397; C:GO:0005634	-		IPR013260
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	protein tyrosine phosphatase family member (ptp-1)	5	F:GO:0004726; C:GO:0005856; F:GO:0008092; P:GO:0006470; F:GO:0016740	-		IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF58 (PANTHER), SSF52799 (SUPERFAMILY)

Caenorhabditis elegans	ras-related protein rap-1b precursor	6	C:GO:0005911; F:GO:0005525; C:GO:0005829; P:GO:0060026; P:GO:0007264; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001806; IPR003577; IPR005225; IPR013753; IPR020849; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF126 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	translocase of outer mitochondrial membrane 34	1	F:GO:0005488	-		IPR001440; IPR011990; IPR013026; IPR019734; PTHR22904 (PANTHER), PTHR22904:SF32 (PANTHER), SSF48452 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	cg3683	0		F:GO:0008137; P:GO:0006120; F:GO:0003954		PTHR13344 (PANTHER)
Caenorhabditis elegans	cg3683	0		F:GO:0008137; P:GO:0006120; F:GO:0003954		PTHR13344 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		IPR007967; SSF103107 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		IPR007967; SSF103107 (SUPERFAMILY)
Caenorhabditis briggsae	formin homology 2 domain containing protein	1	F:GO:0005515	-		IPR010473; IPR016024; PTHR23213 (PANTHER), PTHR23213:SF12 (PANTHER)
Caenorhabditis elegans	gpi mannosyltransferase 3	12	P:GO:0006412; C:GO:0031224; P:GO:0040010; P:GO:0008340; P:GO:0000003; P:GO:0016254; P:GO:0010171; P:GO:0002119; F:GO:0004376; P:GO:0040011; P:GO:0009792; C:GO:0005789	-	EC:3.6.5.3	IPR005599
	-	0				IPR006578
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-zig-7 protein	0		F:GO:0004674; F:GO:0004672; P:GO:0006468; F:GO:0000166; F:GO:0008270; F:GO:0005524; C:GO:0005578; F:GO:0008237; C:GO:0005576; F:GO:0008233		-
Caenorhabditis briggsae	briggsae cbr-ril-2 protein	1	P:GO:0007275	-		-
	-	0				-

Loa loa	mkiaa0226 protein	0		F:GO:0003674; P:GO:0006914; P:GO:0008150; F:GO:0008270; C:GO:0005768; P:GO:0006897; F:GO:0005515; C:GO:0005575		PTHR12326 (PANTHER)
	-	0				IPR013090; SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis elegans	-tural resistance-associated macrophage protein	7	P:GO:0046688; F:GO:0005381; P:GO:0035162; P:GO:0006810; P:GO:0010039; C:GO:0016021; P:GO:0019725	-		IPR001046; PTHR11706:SF7 (PANTHER), SignalP (SIGNALP)
Ciona intestinalis	transposase for is1016	0		F:GO:0008270; C:GO:0005622		IPR007087; IPR015880
Caenorhabditis elegans	hypothetical protein F07F6.8 [Caenorhabditis elegans]	0		P:GO:0006869; F:GO:0008289; C:GO:0016021; F:GO:0005515; P:GO:0042157		IPR008405
	-	0				-
Caenorhabditis briggsae	argi-se agmati-se formiminoglutamase	5	P:GO:0006525; F:GO:0005515; F:GO:0016740; F:GO:0008270; F:GO:0004053	-	EC:3.5.3.1	IPR006035; IPR014033; SSF52768 (SUPERFAMILY)
Brugia malayi	fyve zinc finger family protein	1	F:GO:0046872	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	oxt	7	P:GO:0050650; C:GO:0043231; F:GO:0030158; P:GO:0042732; P:GO:0015012; C:GO:0044444; C:GO:0016020	-	EC:2.4.2.26	IPR002889; IPR003406; PTHR19297:SF1 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	yam5_caeel ame: full=upf0057 membrane protein	0		C:GO:0016021		IPR000612; SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	prp38 family protein	3	C:GO:0005681; P:GO:0006397; P:GO:0008380	-		IPR005037
Caenorhabditis briggsae	alkyldihydroxyacetonephosphate synthase	10	P:GO:0009792; P:GO:0002119; F:GO:0016491; F:GO:0008609; C:GO:0005777; P:GO:0008610; P:GO:0042221; P:GO:0040007; F:GO:0050660; C:GO:0005739	-	EC:2.5.1.26	IPR004113; IPR016164; IPR016171; PTHR11748 (PANTHER), PTHR11748:SF3 (PANTHER)

Caenorhabditis briggsae	briggsae cbr-pqn-45 protein	0		P:GO:0009792		-
Caenorhabditis briggsae	briggsae cbr-pqn-45 protein	0		P:GO:0009792		-
	-	0				-
Caenorhabditis briggsae	atp-binding sub-family b (mdr tap) member 10	4	F:GO:0042626; P:GO:0055085; F:GO:0005524; C:GO:0032592	-		IPR003439; IPR003593; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF76 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	sterol regulatory element-binding protein cleavage-activating protein	13	F:GO:0005515; P:GO:0008202; C:GO:0043231; P:GO:0031323; P:GO:0009889; P:GO:0019216; P:GO:0009792; C:GO:0031090; P:GO:0044281; C:GO:0044446; P:GO:0006950; C:GO:0012505; C:GO:0044444	-		-
	-	0				-
	-	0				-
	-	0				-
Ostertagia ostertagi	ll20 15kda ladder antigen	1	F:GO:0019841	-		-
Caenorhabditis briggsae	briggsae cbr-dgk-4 protein	0		P:GO:0007205; F:GO:0004143; P:GO:0023034		IPR001660; IPR010993; IPR013761; IPR021129; PTHR11255 (PANTHER), PTHR11255:SF10 (PANTHER)
Brugia malayi	homeobox domain containing protein	0		P:GO:0006355; F:GO:0043565; P:GO:0045449; F:GO:0005515; F:GO:0003677; F:GO:0003700; C:GO:0005634		PTHR15116 (PANTHER), PTHR15116:SF7 (PANTHER)
Caenorhabditis elegans	hypothetical protein C50F2.4 [Caenorhabditis elegans]	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis briggsae	glutathione s-transferase	0		F:GO:0016740		PTHR12289 (PANTHER), PTHR12289:SF17 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	2	P:GO:0055085; C:GO:0016021	-		PTHR11662 (PANTHER), PTHR11662:SF17 (PANTHER), SignalP (SIGNALP)
	-	0				-
Loa loa	cleavage stimulation factor subunit 3	8	P:GO:0006378; P:GO:0009792; P:GO:0008380; F:GO:0003723; F:GO:0005515; P:GO:0000003; C:GO:0005634; P:GO:0006379	-		IPR003107; IPR008847; PTHR19980 (PANTHER)
Caenorhabditis briggsae	mitochondrial translation optimization 1 homolog isoform b	5	C:GO:0005737; F:GO:0016491; F:GO:0009055; F:GO:0050660; P:GO:0002098	-		IPR002218; IPR020595; G3DSA:3.50.50.60 (GENE3D), PTHR11806 (PANTHER), SSF51905 (SUPERFAMILY)

Caenorhabditis elegans	phosphatidylcholine:ceramide cholinephosphotransferase	3	F:GO:0047493; C:GO:0016021; P:GO:0006686	-	EC:2.7.8.3	PTHR21290 (PANTHER), PTHR21290:SF3 (PANTHER)
Brugia malayi	thyroid adenoma-associated protein	0		F:GO:0003674; F:GO:0005488; P:GO:0008150; C:GO:0005575		-
Caenorhabditis elegans	heavy unconventio-l myosin family member (hum-2)	12	F:GO:0017137; F:GO:0035255; C:GO:0016459; P:GO:0032880; C:GO:0043197; F:GO:0005524; F:GO:0003774; C:GO:0019717; C:GO:0043025; C:GO:0048471; P:GO:0050790; P:GO:0015031	-		IPR001609; PTHR13140 (PANTHER), PTHR13140:SF15 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0008270; C:GO:0005622		IPR007087; IPR015880
Caenorhabditis elegans	transgelin 3	0		P:GO:0031032; P:GO:0007517; F:GO:0003674; F:GO:0003779; P:GO:0007417; P:GO:0008150; C:GO:0005575		IPR000557; IPR001715; IPR003096; PTHR18959 (PANTHER), PTHR18959:SF6 (PANTHER)
Caenorhabditis elegans	transgelin 3	0		P:GO:0031032; P:GO:0007517; F:GO:0003674; F:GO:0003779; P:GO:0007417; P:GO:0008150; C:GO:0005575		IPR000557; IPR001715; IPR003096; PTHR18959 (PANTHER), PTHR18959:SF6 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-aex-3 protein	11	P:GO:0016192; P:GO:0007618; P:GO:0030421; P:GO:0018991; C:GO:0016021; P:GO:0051726; P:GO:0042981; C:GO:0008021; F:GO:0017112; P:GO:0007269; P:GO:0000187	-		PTHR13008 (PANTHER)
Taeniopygia guttata	centrosomal protein of 97 kda	2	C:GO:0005813; F:GO:0005515	-		IPR001611; PR00019 (PRINTS), G3DSA:3.80.10.10 (GENE3D), PTHR10588 (PANTHER), PTHR10588:SF10 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)
Caenorhabditis elegans	trehalose 6-phosphate synthase	1	F:GO:0004805	-	EC:3.1.3.12	SSF56784 (SUPERFAMILY)
Caenorhabditis briggsae	endothelin-converting enzyme	3	C:GO:0016021; F:GO:0004222; P:GO:0006508	-	EC:3.4.24.0	-

	-	0				-
Loa loa	ctr9 protein	10	F:GO:0042169; P:GO:0043473; P:GO:0016574; P:GO:0040007; P:GO:0000003; P:GO:0002119; P:GO:0014032; P:GO:0006898; P:GO:0009792; C:GO:0005634	-		IPR001440; IPR011990; IPR013026; IPR019734; PTHR14027 (PANTHER), PTHR14027:SF2 (PANTHER), SSF48452 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	prenyl diphosphate subunit 1	8	P:GO:0040010; P:GO:0008340; P:GO:0018991; P:GO:0006744; F:GO:0000010; P:GO:0040017; F:GO:0046982; P:GO:0008299	-	EC:2.5.1.30	IPR000092; IPR008949; IPR017446; PTHR12001:SF22 (PANTHER)
Caenorhabditis elegans	briggsae cbr-xrn-1 protein	0		F:GO:0003676; F:GO:0004527; C:GO:0005622		-
synthetic construct	metalloprotei-se inhibitor 1 precursor	7	P:GO:0051045; P:GO:0043249; F:GO:0046872; C:GO:0005604; F:GO:0005515; F:GO:0008191; P:GO:0008284	-		SignalP (SIGNALP)
Caenorhabditis elegans	mitochondrial ribosomal	3	C:GO:0005762; F:GO:0003735; P:GO:0006412	-	EC:3.6.5.3	PTHR21244 (PANTHER)
Caenorhabditis briggsae	pre-rr- processing protein utp22	0		C:GO:0000794; F:GO:0003723; C:GO:0005634; C:GO:0005730		IPR005554
	-	0				-
Brugia malayi	ki-se suppressor of ras	6	P:GO:0007265; F:GO:0004672; P:GO:0008595; P:GO:0007426; P:GO:0007476; F:GO:0000166	-		IPR000719; IPR001245; IPR008266; IPR011009; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR23257 (PANTHER), PTHR23257:SF90 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-lig-4 protein	7	P:GO:0006260; F:GO:0003677; C:GO:0005622; F:GO:0005524; F:GO:0003910; P:GO:0006310; P:GO:0006281	-	EC:6.5.1.1	IPR012310; PTHR10459 (PANTHER), PTHR10459:SF7 (PANTHER), SSF56091 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	selenoprotein t	1	P:GO:0050794	-		IPR011893; IPR012335; IPR012336; IPR019389
	-	0				-

Loa loa	eukaryotic translation initiation factor 2	6	P:GO:0010605; P:GO:0010608; P:GO:0044238; F:GO:0003676; P:GO:0044260; C:GO:0044424	-		IPR014811; PTHR22891 (PANTHER)
Caenorhabditis briggsae	isoform c	1	P:GO:0019915	-		IPR006603; PTHR14856 (PANTHER), PTHR14856:SF8 (PANTHER), PF04193 (PFAM)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	8	C:GO:0005856; P:GO:0040018; C:GO:0031143; P:GO:0000003; P:GO:0040011; P:GO:0019915; C:GO:0044297; F:GO:0005198	-		IPR000535; IPR008962; PTHR22947 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	P:GO:0006468; F:GO:0005524; F:GO:0004672; F:GO:0005515	-		-
Caenorhabditis briggsae	yl32_caeel ame: full=uncharacterized protein	0				-
Caenorhabditis briggsae	briggsae cbr-kin-29 protein	3	F:GO:0004672; F:GO:0000166; C:GO:0044424	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	solute carrier family 35 member c2	4	C:GO:0016021; F:GO:0016491; F:GO:0008270; P:GO:0055085	-		PTHR11132 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	nuclear receptor nhr-114	5	F:GO:0046872; F:GO:0004879; F:GO:0003677; P:GO:0045449; F:GO:0005515	-		IPR001628; IPR008946; IPR013088; PR00350 (PRINTS), PTHR11865 (PANTHER), PTHR11865:SF235 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis elegans	peptidyl-prolyl cis-trans isomerase	4	P:GO:0006457; P:GO:0009792; F:GO:0003755; C:GO:0005886	-	EC:5.2.1.8	IPR002130; IPR015891; IPR020892; PTHR11071 (PANTHER)

Caenorhabditis elegans	-scent polypeptide-associated complex alpha subunit	18	P:GO:0008340; F:GO:0017111; P:GO:0040007; F:GO:0017025; P:GO:0006412; P:GO:0045132; P:GO:0015031; P:GO:0018996; P:GO:0040039; P:GO:0019915; P:GO:0009792; F:GO:0003713; F:GO:0042802; P:GO:0002119; P:GO:0010171; C:GO:0005854; C:GO:0005634; P:GO:0040035	-	EC:3.6.1.15; EC:3.6.5.3	IPR000449; IPR002715; PTHR21713 (PANTHER)
Brugia malayi	family with sequence similarity member b	3	C:GO:0005737; F:GO:0005488; C:GO:0043229	-		IPR011990; IPR013026; SignalP (SIGNALP), SSF48452 (SUPERFAMILY)
Caenorhabditis brenneri	abc transporter atp-binding protein	3	F:GO:0017111; F:GO:0005488; C:GO:0044464	-	EC:3.6.1.15	IPR003439; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR11384 (PANTHER), PTHR11384:SF3 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	g protein-coupled receptor	2	P:GO:0007186; C:GO:0016021	-		IPR017452; IPR019427; G3DSA:1.20.1070.10 (GENE3D), PTHR22751 (PANTHER), PTHR22751:SF8 (PANTHER), SignalP (SIGNALP), SSF81321 (SUPERFAMILY)
Brugia malayi	dead deah box helicase family protein	1	F:GO:0005488	-		IPR001650; IPR011545; IPR014001; IPR014014; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF57 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein ZC247.1 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	hypothetical protein Y71F9B.1 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0007600; P:GO:0007165; F:GO:0042802; F:GO:0005515		PTHR11188 (PANTHER), PTHR11188:SF13 (PANTHER)
Brugia malayi	hypothetical protein Bm1_19875 [Brugia malayi]	0				-
	-	0				-
Caenorhabditis elegans	p21	3	F:GO:0005097; C:GO:0005622; P:GO:0032313	-		IPR000195; G3DSA:1.10.8.270 (GENE3D), PTHR22957 (PANTHER), PTHR22957:SF44 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	nematode astacin protease protein 30	4	F:GO:0004222; P:GO:0009792; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	IPR001506; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis briggsae	mflj00229 protein	1	F:GO:0005524	-		IPR012860; SignalP (SIGNALP)

Caenorhabditis elegans	solute carrier organic anion transporter family member 3a1	4	C:GO:0016021; P:GO:0009792; P:GO:0055085; F:GO:0005215	-		IPR004156; PTHR11388:SF7 (PANTHER), SignalP (SIGNALP)
Ancylostoma ceylanicum	scp-like extracellular protein	0		P:GO:0040011; P:GO:0006898; C:GO:0005576		-
	-	0				-
Caenorhabditis elegans	protein	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	P:GO:0023052; F:GO:0004872	-		IPR000276; IPR017452; G3DSA:1.20.1070.10 (GENE3D), PTHR19264 (PANTHER), PTHR19264:SF33 (PANTHER), SignalP (SIGNALP), SSF81321 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	eh domain binding protein 1	0				PTHR11915 (PANTHER), PTHR11915:SF30 (PANTHER)
	-	0				G3DSA:3.80.10.10 (GENE3D)
Caenorhabditis elegans	glycosyltransferase 25 domain containing 1	6	P:GO:0040035; P:GO:0009103; F:GO:0005515; P:GO:0040010; P:GO:0040011; P:GO:0002009	-		-
Caenorhabditis elegans	epoxide hydrolase microsomal	4	F:GO:0016803; P:GO:0040010; P:GO:0042221; C:GO:0016020	-	EC:3.3.2.0	IPR000073; IPR000639; IPR010497; IPR016292; G3DSA:3.40.50.1820 (GENE3D), PTHR21661 (PANTHER), PTHR21661:SF2 (PANTHER), SSF53474 (SUPERFAMILY)
	-	0				-
	-	0				-
Haemonchus contortus	hc38	0		C:GO:0005576		IPR006994
	-	0				-
Caenorhabditis elegans	splicing factor 3a	15	F:GO:0008270; F:GO:0003676; C:GO:0071011; C:GO:0005686; P:GO:0040007; P:GO:0040035; P:GO:0007052; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0000398; P:GO:0006898; C:GO:0071013; P:GO:0002009; P:GO:0009792	-		-

Caenorhabditis elegans	general vesicular transport factor p115	14	C:GO:0005829; F:GO:0008565; P:GO:0045056; C:GO:0000139; P:GO:0048280; F:GO:0042802; P:GO:0032940; P:GO:0006891; P:GO:0019915; C:GO:0005792; C:GO:0048471; P:GO:0040039; P:GO:0006898; P:GO:0006886	-		IPR011989; PTHR10013 (PANTHER)
Caenorhabditis elegans	briggsae cbr-mrp-4 protein	0		F:GO:0042626; F:GO:0005215; C:GO:0016021; P:GO:0006810; F:GO:0000166; F:GO:0017111; F:GO:0005524; F:GO:0016887; P:GO:0055085		PTHR19242 (PANTHER), PTHR19242:SF15 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-tag-320 protein	6	P:GO:0045454; P:GO:0040007; F:GO:0016853; C:GO:0005811; P:GO:0002119; P:GO:0040011	-		IPR005746; IPR005788; IPR012335; IPR012336; IPR013766; IPR017936; IPR017937; PTHR18929 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	metabotropic glutamate receptor type 3	3	C:GO:0016020; P:GO:0023052; F:GO:0004872	-		-
Caenorhabditis briggsae	udp-galactose transporter	6	C:GO:0000139; P:GO:0015785; F:GO:0005351; P:GO:0006012; C:GO:0016021; F:GO:0005459	-		IPR007271; PTHR10231:SF13 (PANTHER), SignalP (SIGNALP), SSF103481 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG21314 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)
Caenorhabditis elegans	early endosome antigen 1-like	4	F:GO:0046872; C:GO:0005769; F:GO:0005515; C:GO:0005969	-		IPR000306; IPR011011; IPR013083; IPR017455; G3DSA:1.20.5.390 (GENE3D), PTHR23164 (PANTHER)

Caenorhabditis elegans	loc398457 protein	29	C:GO:0000785; P:GO:0031991; P:GO:0046777; F:GO:0004713; P:GO:0040011; F:GO:0019894; P:GO:0030261; F:GO:0046872; F:GO:0008017; F:GO:0051117; C:GO:0000775; P:GO:0009792; C:GO:0051233; C:GO:0005813; P:GO:0007059; F:GO:0035175; P:GO:0007126; P:GO:0045184; P:GO:0018108; P:GO:0090307; C:GO:0000794; P:GO:0007109; C:GO:0005876; C:GO:0032133; F:GO:0005524; P:GO:0051256; C:GO:0000922; P:GO:0043987;	-	EC:2.7.10.0	IPR000719; IPR008271; IPR011009; IPR017441; IPR017442; IPR020636; IPR020663; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
Caenorhabditis elegans	briggsae cbr-cnk-1 protein	1	P:GO:0040026	-		-
Brugia malayi	fructosamine-3-ki-se-related protein	0		F:GO:0016301; F:GO:0003674; P:GO:0016310; F:GO:0016740; P:GO:0008152; P:GO:0008150; C:GO:0005575		-
Ostertagia ostertagi	alpha tubulin	15	P:GO:0040010; C:GO:0005874; P:GO:0035046; P:GO:0051258; P:GO:0007018; P:GO:0002119; F:GO:0005515; P:GO:0040017; F:GO:0003924; P:GO:0040039; P:GO:0006898; F:GO:0005198; P:GO:0002009; P:GO:0009792; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000217; IPR002452; IPR003008; IPR017975

Caenorhabditis briggsae	tubulin alpha chain	15	P:GO:0040010; C:GO:0005874; P:GO:0035046; P:GO:0051258; P:GO:0007018; P:GO:0002119; F:GO:0005515; P:GO:0040017; F:GO:0003924; P:GO:0040039; P:GO:0006898; F:GO:0005198; P:GO:0002009; P:GO:0009792; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000217; IPR002452; IPR003008; IPR008280; IPR017975; IPR018316; IPR023123
Ostertagia ostertagi	elegans protein confirmed by transcript evidence	15	P:GO:0040010; C:GO:0005874; P:GO:0035046; P:GO:0051258; P:GO:0007018; P:GO:0002119; F:GO:0005515; P:GO:0040017; F:GO:0003924; P:GO:0040039; P:GO:0006898; F:GO:0005198; P:GO:0002009; P:GO:0009792; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000217; IPR002452; IPR003008; IPR017975
Caenorhabditis briggsae	tubulin alpha chain	15	P:GO:0040010; C:GO:0005874; P:GO:0035046; P:GO:0051258; P:GO:0007018; P:GO:0002119; F:GO:0005515; P:GO:0040017; F:GO:0003924; P:GO:0040039; P:GO:0006898; F:GO:0005198; P:GO:0002009; P:GO:0009792; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000217; IPR002452; IPR003008; IPR008280; IPR017975; IPR018316; IPR023123

Caenorhabditis briggsae	tubulin alpha chain	15	P:GO:0040010; C:GO:0005874; P:GO:0035046; P:GO:0051258; P:GO:0007018; P:GO:0002119; F:GO:0005515; P:GO:0040017; F:GO:0003924; P:GO:0040039; P:GO:0006898; F:GO:0005198; P:GO:0002009; P:GO:0009792; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000217; IPR002452; IPR003008; IPR008280; IPR017975; IPR018316; IPR023123
Caenorhabditis elegans	gdp-fucose transporter	4	C:GO:0005794; P:GO:0006810; P:GO:0030259; C:GO:0016021	-		IPR013657; PTHR11132 (PANTHER), SSF103481 (SUPERFAMILY)
Caenorhabditis elegans	gdp-fucose transporter	4	C:GO:0005794; P:GO:0006810; P:GO:0030259; C:GO:0016021	-		IPR013657; PTHR11132 (PANTHER), SSF103481 (SUPERFAMILY)
Caenorhabditis briggsae	tubulin alpha chain	15	P:GO:0040010; C:GO:0005874; P:GO:0035046; P:GO:0051258; P:GO:0007018; P:GO:0002119; F:GO:0005515; P:GO:0040017; F:GO:0003924; P:GO:0040039; P:GO:0006898; F:GO:0005198; P:GO:0002009; P:GO:0009792; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000217; IPR002452; IPR003008; IPR008280; IPR017975; IPR018316; IPR023123
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	15	P:GO:0040010; C:GO:0005874; P:GO:0035046; P:GO:0051258; P:GO:0007018; P:GO:0002119; F:GO:0005515; P:GO:0040017; F:GO:0003924; P:GO:0040039; P:GO:0006898; F:GO:0005198; P:GO:0002009; P:GO:0009792; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-

Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	15	P:GO:0040010; C:GO:0005874; P:GO:0035046; P:GO:0051258; P:GO:0007018; P:GO:0002119; F:GO:0005515; P:GO:0040017; F:GO:0003924; P:GO:0040039; P:GO:0006898; F:GO:0005198; P:GO:0002009; P:GO:0009792; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Caenorhabditis elegans	o ant response abnormal family member (odr-4)	1	F:GO:0005488	-		IPR002085; PTHR11695:SF3 (PANTHER)
Caenorhabditis elegans	d--directed r- polymerase ii subunit rpb7	15	F:GO:0003899; F:GO:0003723; P:GO:0006915; F:GO:0004672; P:GO:0006367; P:GO:0040007; P:GO:0000003; P:GO:0008380; C:GO:0005665; P:GO:0002119; F:GO:0005515; P:GO:0006368; P:GO:0006898; P:GO:0009792; P:GO:0001703	-	EC:2.7.7.6	-
Caenorhabditis elegans	d--directed r- polymerase ii subunit rpb7	15	F:GO:0003899; F:GO:0003723; P:GO:0006915; F:GO:0004672; P:GO:0006367; P:GO:0040007; P:GO:0000003; P:GO:0008380; C:GO:0005665; P:GO:0002119; F:GO:0005515; P:GO:0006368; P:GO:0006898; P:GO:0009792; P:GO:0001703	-	EC:2.7.7.6	IPR003029; IPR005576; IPR012340; IPR016027; PTHR12709 (PANTHER), PTHR12709:SF1 (PANTHER)

Caenorhabditis elegans	d--directed r- polymerase ii subunit rpb7	15	F:GO:0003899; F:GO:0003723; P:GO:0006915; F:GO:0004672; P:GO:0006367; P:GO:0040007; P:GO:0000003; P:GO:0008380; C:GO:0005665; P:GO:0002119; F:GO:0005515; P:GO:0006368; P:GO:0006898; P:GO:0009792; P:GO:0001703	-	EC:2.7.7.6	IPR003029; IPR005576; IPR012340; IPR016027; IPR022967; PTHR12709 (PANTHER), PTHR12709:SF1 (PANTHER)
Loa loa	btb poz domain containing protein	1	F:GO:0005488	-		IPR013089
	-	0				IPR010916
	-	0				IPR010916
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG02486 [Caenorhabditis briggsae]	0		C:GO:0016021; C:GO:0016020; P:GO:0055085; P:GO:0030001; F:GO:0046873		IPR003689; PTHR11040 (PANTHER), PTHR11040:SF5 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	ring finger protein 160	1	F:GO:0005488	-		IPR001841; IPR013083; PTHR12389 (PANTHER), PF11793 (PFAM), SSF57850 (SUPERFAMILY)
Caenorhabditis elegans	cleavage and polyadenylation specificity factor cpsf	6	P:GO:0006378; P:GO:0008380; C:GO:0005847; F:GO:0003730; F:GO:0005515; P:GO:0006379	-		IPR004871; PTHR10644 (PANTHER), PTHR10644:SF2 (PANTHER)
	-	0				-
Caenorhabditis elegans	integral membrane protein gpr180	0				PTHR23252 (PANTHER), PTHR23252:SF3 (PANTHER), SignalP (SIGNALP)
Penicillium marneffei ATCC 18224	myst histone acetyltransferase (monocytic leukemia) 3	13	C:GO:0000785; C:GO:0032991; F:GO:0030528; F:GO:0005515; F:GO:0016407; P:GO:0051216; P:GO:0007389; P:GO:0048706; C:GO:0044428; P:GO:0045449; P:GO:0048705; P:GO:0048598; P:GO:0016573	-		IPR007087; IPR015880; IPR016181; G3DSA:3.30.60.60 (GENE3D), PTHR10615 (PANTHER), PTHR10615:SF35 (PANTHER)
	-	0				-
	-	0				-
Brugia malayi	g protein pathway suppressor 1	3	P:GO:0000165; P:GO:0000003; F:GO:0005515	-		IPR019585; PTHR14145 (PANTHER), PTHR14145:SF2 (PANTHER)

Caenorhabditis briggsae	vascular endothelial growth factor receptor	0		P:GO:0070374; P:GO:0008283; C:GO:0005887; C:GO:0005886; F:GO:0004715; F:GO:0004714; F:GO:0004713; P:GO:0045785; C:GO:0016020; P:GO:0001700; P:GO:0007267; F:GO:0004674; F:GO:0004672; F:GO:0019955; P:GO:0007169; F:GO:0005011; P:GO:0007165; F:GO:0042803; F:GO:0005524; P:GO:0016337; P:GO:0007160; P:GO:0030334; F:GO:0016301; F:GO:0000166; C:GO:0043235; P:GO:0042127; P:GO:0006468;		IPR000719; IPR001245; G3DSA:1.10.510.10 (GENE3D), SignalP (SIGNALP)
Caenorhabditis elegans	vascular endothelial growth factor receptor	0		P:GO:0070374; P:GO:0008283; C:GO:0005887; C:GO:0005886; F:GO:0004715; F:GO:0004714; F:GO:0004713; P:GO:0045785; C:GO:0016020; P:GO:0001700; P:GO:0007267; F:GO:0004674; F:GO:0004672; F:GO:0019955; P:GO:0007169; F:GO:0005011; P:GO:0007165; F:GO:0042803; F:GO:0005524; P:GO:0016337; P:GO:0007160; P:GO:0030334; F:GO:0016301; F:GO:0000166; C:GO:0043235; P:GO:0042127; P:GO:0006468;		IPR000719; IPR001245; IPR011009; IPR020685; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)

Caenorhabditis elegans	briggsae cbr-chk-1 protein	14	P:GO:0000226; P:GO:0000003; F:GO:0016301; P:GO:0000075; P:GO:0006974; P:GO:0040010; P:GO:0040011; C:GO:0044424; P:GO:0000279; P:GO:0009792; P:GO:0007165; P:GO:0002119; P:GO:0010171; P:GO:0007346	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	atp-binding sub-family a member 1	19	P:GO:0055099; P:GO:0045332; F:GO:0005515; F:GO:0000166; F:GO:0005548; P:GO:0008203; P:GO:0010875; P:GO:0043691; P:GO:0006911; C:GO:0005794; F:GO:0008509; P:GO:0071300; P:GO:0002790; P:GO:0033700; F:GO:0016887; P:GO:0006497; P:GO:0071222; C:GO:0005887; F:GO:0017127	-		PTHR19229 (PANTHER), PTHR19229:SF25 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	transmembrane protein 144	2	P:GO:0009792; P:GO:0000003	-		IPR012435; SignalP (SIGNALP)
Caenorhabditis brenneri	isoform b	1	P:GO:0000003	-		IPR000326; IPR019388; PTHR23129 (PANTHER)
Caenorhabditis brenneri	isoform b	1	P:GO:0000003	-		IPR000326; IPR019388; PTHR23129 (PANTHER)
Caenorhabditis elegans	u4 tri-snrnp-associated protein 1	5	P:GO:0018996; P:GO:0040007; P:GO:0040035; P:GO:0002119; P:GO:0040011	-		IPR005011
Caenorhabditis elegans	phospholipase b-like 2-like	0		F:GO:0016787; C:GO:0043202; P:GO:0016042		-
	-	0				-

Caenorhabditis brenneri	isoleucyl-tr- synthetase	4	F:GO:0004812; F:GO:0046872; P:GO:0006418; F:GO:0000166	-		IPR002300; IPR002301; IPR014729; G3DSA:1.10.730.10 (GENE3D), PTHR11946 (PANTHER), SignalP (SIGNALP), SSF52374 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG04315 [Caenorhabditis briggsae]	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				IPR010916
Ostertagia ostertagi	latrophilin receptor family member (lat-1)	7	F:GO:0004930; F:GO:0005529; C:GO:0005886; P:GO:0007165; P:GO:0007420; C:GO:0016021; P:GO:0007218	-		IPR000832; IPR017981; PTHR12011 (PANTHER), PTHR12011:SF55 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-nhr-48 protein	5	F:GO:0046872; F:GO:0004879; F:GO:0003677; P:GO:0045449; F:GO:0005515	-		-
	-	0				SignalP (SIGNALP)
Brugia malayi	mediator complex subunit rgr-1	1	P:GO:0007275	-		-
Caenorhabditis briggsae	briggsae cbr-cdh-4 protein	6	P:GO:0007163; C:GO:0005886; P:GO:0007411; P:GO:0007155; C:GO:0016021; P:GO:0007413	-		IPR002126; IPR015919; SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Ostertagia ostertagi	calcium-dependent apyrase	0		F:GO:0005509; F:GO:0016787; F:GO:0016462		IPR009283; SignalP (SIGNALP)
Caenorhabditis elegans	cytoplasmic protein nck2	7	F:GO:0005515; P:GO:0044237; C:GO:0044464; P:GO:0042102; C:GO:0043227; P:GO:0007169; P:GO:0030838	-		IPR000108; IPR000980; IPR001452; IPR011511; G3DSA:2.30.30.40 (GENE3D), PTHR22820 (PANTHER), PTHR22820:SF9 (PANTHER), SSF55550 (SUPERFAMILY)
Caenorhabditis sp. PS1010	haspin protein ki-se	5	P:GO:0044238; F:GO:0004672; P:GO:0044260; C:GO:0005622; F:GO:0000166	-		IPR017441
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	2	P:GO:0023034; C:GO:0016021	-		-

Caenorhabditis briggsae	pten induced ki-se 1	9	P:GO:0010646; F:GO:0004672; F:GO:0046872; P:GO:0023060; P:GO:0048522; P:GO:0008219; P:GO:0043687; P:GO:0032501; C:GO:0005739	-		PTHR22972 (PANTHER)
Caenorhabditis elegans	dihydropyrimidi-se	12	C:GO:0005829; F:GO:0004157; F:GO:0008270; C:GO:0005625; P:GO:0006212; P:GO:0019482; P:GO:0006210; F:GO:0016597; P:GO:0051289; F:GO:0002058; C:GO:0005634; F:GO:0002059	-	EC:3.5.2.2	-
	-	0				-
	-	0				-
Haemonchus contortus	glutamate dehydroge-se	6	P:GO:0055114; P:GO:0000003; P:GO:0006520; F:GO:0005488; P:GO:0040010; F:GO:0016639	-	EC:1.4.1.0	G3DSA:1.10.287.140 (GENE3D)
	-	0				-
Caenorhabditis briggsae	phosphatidylinositide phosphatase sac1	6	P:GO:0009792; P:GO:0002119; P:GO:0040018; P:GO:0040010; P:GO:0008340; C:GO:0044425	-		-
Brugia malayi	hypothetical protein Bm1_01480 [Brugia malayi]	0		P:GO:0045449; F:GO:0003677		IPR000875; IPR001005
Brugia malayi	hypothetical protein Bm1_01480 [Brugia malayi]	0		P:GO:0045449; F:GO:0003677		IPR000875; IPR001005
Caenorhabditis briggsae	briggsae cbr-pme-5 protein	0				IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF255 (PANTHER)
Caenorhabditis elegans	phosphatidyltransferase	1	F:GO:0016740	-		IPR000462; PTHR10414 (PANTHER), PTHR10414:SF18 (PANTHER)
Caenorhabditis briggsae	possible metal-binding domain in r-se l rli family protein	3	P:GO:0006468; F:GO:0005524; F:GO:0004713	-	EC:2.7.10.0	IPR007087; IPR007177; IPR007209; PTHR20426 (PANTHER)
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	exosome component 10	0		F:GO:0004527; F:GO:0003723; F:GO:0016787; C:GO:0005634; F:GO:0003676; P:GO:0044237; F:GO:0003674; P:GO:0000184; F:GO:0008408; P:GO:0006139; P:GO:0008150; F:GO:0003824; F:GO:0000166; P:GO:0006396; P:GO:0006364; F:GO:0004518; C:GO:0005730; C:GO:0005622; C:GO:0000178; C:GO:0000176		IPR012588
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	coiled-coil domain-containing protein 12	0		F:GO:0003674; P:GO:0008150		-
	-	0				-
Loa loa	geranylgeranyl pyrophosphate synthetase	7	P:GO:0000022; C:GO:0005840; P:GO:0008354; P:GO:0035050; C:GO:0043025; F:GO:0004659; C:GO:0005811	-		IPR000092; IPR008949; IPR017446; PTHR12001:SF5 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		C:GO:0016021; F:GO:0005375; P:GO:0006825		IPR007274; PTHR12483:SF4 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				PTHR12187 (PANTHER), PTHR12187:SF2 (PANTHER)
Caenorhabditis elegans	wd repeat-containing protein 47	2	F:GO:0016740; F:GO:0005515	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR19863 (PANTHER), PTHR19863:SF2 (PANTHER)
Caenorhabditis briggsae	d- ligase 1	10	P:GO:0006260; F:GO:0046872; F:GO:0003677; P:GO:0007049; F:GO:0005524; C:GO:0005634; F:GO:0003910; P:GO:0006310; P:GO:0051301; P:GO:0006281	-	EC:6.5.1.1	IPR012309; IPR012310; IPR012340; IPR016027; IPR016059; G3DSA:3.30.1490.70 (GENE3D), PTHR10459 (PANTHER), PTHR10459:SF10 (PANTHER), SSF56091 (SUPERFAMILY)
Loa loa	androgen induced inhibitor of proliferation pds5	0		F:GO:0005488		PTHR12663 (PANTHER)

Caenorhabditis briggsae	protein-tyrosine phosphatase containing protein	4	P:GO:0016311; F:GO:0004721; P:GO:0009792; P:GO:0000003	-	EC:3.1.3.16	IPR000242; IPR000387; IPR003595; IPR016130; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis elegans	homogentisate -dioxyge-se	5	F:GO:0042802; F:GO:0004411; P:GO:0055114; P:GO:0006559; P:GO:0006570	-	EC:1.13.11.5	IPR005708; IPR011051
Caenorhabditis briggsae	dead (asp-glu-ala-asp) box polypeptide 52	3	F:GO:0004386; F:GO:0003676; F:GO:0000166	-		IPR011545; IPR014014; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF21 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	glucose transporter 1 transcript	3	C:GO:0016021; F:GO:0022891; P:GO:0055085	-		IPR005828; PTHR11600 (PANTHER), PTHR11600:SF103 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-apr-1 protein	6	C:GO:0044464; P:GO:0051179; P:GO:0048856; P:GO:0009790; P:GO:0050794; F:GO:0005488	-		PTHR12607 (PANTHER), PTHR12607:SF4 (PANTHER)
Caenorhabditis remanei	twitchin ki-se	0		F:GO:0016301; F:GO:0004672; F:GO:0005524; F:GO:0000166; P:GO:0006468; F:GO:0004674		-
Brugia malayi	r- binding protein	0		F:GO:0003676; F:GO:0000166		-
Caenorhabditis briggsae	3 -5 exonuclease family protein	0		P:GO:0006139; F:GO:0003676; F:GO:0004527; C:GO:0005622; F:GO:0008408		IPR012337; G3DSA:3.30.420.10 (GENE3D)
Caenorhabditis elegans	uncharacterized protein kiaa0467	0		P:GO:0009058; C:GO:0016021; C:GO:0005794; F:GO:0001733		-
Caenorhabditis briggsae	briggsae cbr-mdt-29 protein	0		P:GO:0006350; P:GO:0045449; F:GO:0005515; C:GO:0005634		IPR021018
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	temporarily assigned gene -me family member (tag-261)	0				G3DSA:1.10.1660.10 (GENE3D)

Caenorhabditis elegans	lon protease mitochondrial precursor	23	F:GO:0008236; F:GO:0004176; F:GO:0070361; F:GO:0070363; F:GO:0070362; P:GO:0007568; P:GO:0010044; F:GO:0043531; P:GO:0070407; F:GO:0003697; C:GO:0042645; F:GO:0003727; F:GO:0070364; P:GO:0001666; F:GO:0070182; F:GO:0051880; P:GO:0043623; P:GO:0032042; P:GO:0051260; P:GO:0006200; P:GO:0009725; F:GO:0005524; P:GO:0034599	-		-
Caenorhabditis elegans	lon protease mitochondrial precursor	24	P:GO:0034619; F:GO:0004252; F:GO:0004176; F:GO:0070361; F:GO:0070363; F:GO:0070362; P:GO:0007568; P:GO:0010044; F:GO:0043531; P:GO:0070407; F:GO:0003697; C:GO:0042645; F:GO:0003727; P:GO:0006515; F:GO:0070364; P:GO:0001666; F:GO:0070182; F:GO:0051880; P:GO:0032042; P:GO:0051260; P:GO:0006200; P:GO:0009725; F:GO:0005524; P:GO:0034599	-	EC:3.4.21.0	-

Caenorhabditis elegans	lon protease mitochondrial precursor	23	F:GO:0008236; F:GO:0004176; F:GO:0070361; F:GO:0070363; F:GO:0070362; P:GO:0007568; P:GO:0010044; F:GO:0043531; P:GO:0070407; F:GO:0003697; C:GO:0042645; F:GO:0003727; F:GO:0070364; P:GO:0001666; F:GO:0070182; F:GO:0051880; P:GO:0043623; P:GO:0032042; P:GO:0051260; P:GO:0006200; P:GO:0009725; F:GO:0005524; P:GO:0034599	-		-
Caenorhabditis briggsae	spastin	19	C:GO:0016020; C:GO:0043231; F:GO:0008568; P:GO:0051301; P:GO:0051013; C:GO:0005874; F:GO:0008017; P:GO:0031117; F:GO:0043014; P:GO:0045773; P:GO:0001578; C:GO:0048471; P:GO:0051260; F:GO:0048487; F:GO:0005524; P:GO:0007416; P:GO:0043066; P:GO:0021955; P:GO:0034214	-	EC:3.6.4.3	IPR003959; IPR003960; G3DSA:3.40.50.300 (GENE3D), PTHR23074 (PANTHER), PTHR23074:SF1 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	snw domain-containing protein 1	7	F:GO:0030528; C:GO:0005681; P:GO:0045449; F:GO:0005102; C:GO:0000785; P:GO:0000398; F:GO:0008134	-		IPR017862
Caenorhabditis briggsae	xenotropic and polytropic retrovirus receptor	6	P:GO:0010171; F:GO:0004930; C:GO:0005887; P:GO:0018991; P:GO:0040010; P:GO:0007186	-		IPR004342; PTHR10783 (PANTHER), PTHR10783:SF4 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	uncoordi-ted family member (unc-22)	3	P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	-

Brugia malayi	zinc c2h2 type family protein	0		F:GO:0008270; C:GO:0005622		IPR007087; IPR015880; PTHR23233 (PANTHER), PTHR23233:SF7 (PANTHER)
Caenorhabditis elegans	ubiquitin carboxyl-termi-l	1	F:GO:0016787	-		IPR001394; IPR018200; PTHR10420 (PANTHER), PTHR10420:SF62 (PANTHER), SignalP (SIGNALP), SSF54001 (SUPERFAMILY)
Caenorhabditis briggsae	grip1 associated protein 1	1	F:GO:0005515	-		PTHR23180 (PANTHER), PTHR23180:SF18 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Loa loa	phosphoglycerate mutase family protein	0				G3DSA:3.40.50.1240 (GENE3D), SSF53254 (SUPERFAMILY)
	-	0				IPR007889; IPR009057
	-	0				-
	-	0				-
Caenorhabditis elegans	mixed lineage protein ki-se	8	P:GO:0006357; F:GO:0004674; P:GO:0023034; F:GO:0005524; F:GO:0005515; P:GO:0046777; P:GO:0001672; C:GO:0005634	-	EC:2.7.11.0	IPR000719; IPR002290; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22974 (PANTHER), PTHR22974:SF1 (PANTHER)
Caenorhabditis elegans	mixed lineage protein ki-se	8	P:GO:0006357; F:GO:0004674; P:GO:0023034; F:GO:0005524; F:GO:0005515; P:GO:0046777; P:GO:0001672; C:GO:0005634	-	EC:2.7.11.0	IPR000719; IPR002290; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22974 (PANTHER), PTHR22974:SF1 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	exocyst complex component 2	1	P:GO:0000003	-		IPR002909; IPR013783; IPR014756; PTHR13043 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-tag-196 protein	2	F:GO:0016787; F:GO:0005515	-		IPR000010; G3DSA:3.10.450.10 (GENE3D), PTHR11413 (PANTHER), SignalP (SIGNALP), SSF54403 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein C15C7.5 [Caenorhabditis elegans]	2	P:GO:0040011; P:GO:0019915	-		-
Caenorhabditis elegans	heat repeat-containing protein 7a-like	0		F:GO:0003674; F:GO:0005488; P:GO:0008150		IPR011989; IPR016024
Pediculus humanus corporis	lsm2 u6 small nuclear r- associated	10	C:GO:0071011; P:GO:0000381; C:GO:0005688; P:GO:0006402; F:GO:0017070; F:GO:0019901; C:GO:0046540; C:GO:0071013; C:GO:0005737; P:GO:0000244	-		-

	-	0				-
Caenorhabditis elegans	ras-related protein rab-5a	29	P:GO:0030100; P:GO:0001525; C:GO:0045121; F:GO:0030742; P:GO:0007032; C:GO:0019717; P:GO:0016337; C:GO:0042470; F:GO:0005525; P:GO:0001702; P:GO:0015031; P:GO:0006184; C:GO:0030425; C:GO:0001726; C:GO:0030139; P:GO:0031623; P:GO:0007264; C:GO:0043025; F:GO:0051021; C:GO:0043234; C:GO:0030424; C:GO:0008021; P:GO:0048169; C:GO:0048471; F:GO:0019003; F:GO:0003924; C:GO:0005886; C:GO:0031901;	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Ancylostoma caninum	secreted protein asp-2	0		P:GO:0040011; C:GO:0005576		IPR001283; IPR014044; PTHR10334:SF11 (PANTHER)
Ancylostoma caninum	secreted protein asp-2	0		C:GO:0005576		IPR014044
	-	0				-
	-	0				SignalP (SIGNALP)
Ancylostoma caninum	secreted protein asp-2	0		P:GO:0040011; C:GO:0005576		IPR001283; IPR014044; IPR018244; PTHR10334:SF11 (PANTHER)
Ancylostoma caninum	secreted protein asp-2	0		P:GO:0040011; C:GO:0005576		IPR001283; IPR014044; PTHR10334:SF11 (PANTHER)
Ancylostoma caninum	secreted protein asp-2	0		P:GO:0040011; C:GO:0005576		IPR001283; IPR014044; PTHR10334:SF11 (PANTHER)
Brugia malayi	elegans protein confirmed by transcript evidence	0		F:GO:0005198		SignalP (SIGNALP)
Caenorhabditis elegans	uridine phosphorylase 2	4	C:GO:0005737; P:GO:0009166; F:GO:0004850; P:GO:0009116	-	EC:2.4.2.3	IPR010059; IPR018017; G3DSA:3.40.50.1580 (GENE3D), SSF53167 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
Loa loa	origin recognition complex subunit 5	0		P:GO:0006260; C:GO:0000808; C:GO:0005634		IPR020796
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein F42A10.5 [Caenorhabditis elegans]	0		F:GO:0005515		-
Caenorhabditis elegans	hypothetical protein F42A10.5 [Caenorhabditis elegans]	0		F:GO:0005515		-
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	steroid receptor-interacting snf2 domain	9	F:GO:0003712; P:GO:0045449; F:GO:0004872; F:GO:0003677; F:GO:0005524; F:GO:0016740; F:GO:0004386; F:GO:0019901; C:GO:0005634	-		PTHR10799 (PANTHER), PTHR10799:SF51 (PANTHER)
Loa loa	uncharacterized protein kiaa0241	0		F:GO:0003674; C:GO:0016020; P:GO:0008150; C:GO:0005575		IPR018307
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	6	F:GO:0008233; P:GO:0019538; F:GO:0022834; P:GO:0007271; P:GO:0000003; P:GO:0040011	-		-
Caenorhabditis elegans	phosphoribosylformylglyci-midine synthase	5	P:GO:0040010; C:GO:0009536; F:GO:0005515; P:GO:0006189; F:GO:0004642	-	EC:6.3.5.3	IPR017926; G3DSA:3.40.50.880 (GENE3D), PTHR10099 (PANTHER), SSF52317 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0040007; P:GO:0006898; P:GO:0002119	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0040007; P:GO:0006898; P:GO:0002119	-		-
Callithrix jacchus	ribosomal protein l35	6	C:GO:0005730; F:GO:0003729; F:GO:0003735; F:GO:0005515; C:GO:0022625; P:GO:0006414	-		SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-egg-3 protein	2	F:GO:0016791; F:GO:0005515	-	EC:3.1.3.0	PTHR19134 (PANTHER), PTHR19134:SF19 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	muscle positioning protein 4	2	F:GO:0005515; F:GO:0005509	-		IPR000152; IPR000742; IPR006209; IPR006210; G3DSA:2.10.25.10 (GENE3D), PTHR22992 (PANTHER), PTHR22992:SF12 (PANTHER), SSF57196 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	c2 domain containing protein	9	P:GO:0016079; C:GO:0008021; F:GO:0005544; F:GO:0035005; P:GO:0048167; F:GO:0005515; F:GO:0005215; P:GO:0046928; C:GO:0005886	-	EC:2.7.1.154	IPR000008; IPR008973; IPR018029; G3DSA:2.60.40.150 (GENE3D), PTHR10024 (PANTHER), PTHR10024:SF31 (PANTHER)
	-	0				SignalP (SIGNALP)

Caenorhabditis briggsae	ysr3_caeel ame: full=uncharacterized protein	0				-
Caenorhabditis elegans	gro-1 operon gene protein 1	0				IPR019155; PTHR21481 (PANTHER)
Caenorhabditis elegans	vacuolar protein	0		F:GO:0005488; F:GO:0008270; F:GO:0005515		PTHR23323 (PANTHER), PF00637 (PFAM)
	-	0				-
Macaca fascicularis	small subunit 1	8	C:GO:0005737; P:GO:0008284; C:GO:0005886; F:GO:0004198; F:GO:0005509; P:GO:0006508; C:GO:0005634; F:GO:0046982	-		-
Caenorhabditis briggsae	sand family protein	0				IPR004353
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	viral a-type inclusion protein	1	F:GO:0005488	-		IPR000237; IPR009053; PD968187 (PRODOM)
Caenorhabditis elegans	grip domain containing protein	1	F:GO:0005488	-		IPR000237; IPR009053; PD936484 (PRODOM)
	-	0				-
Brugia malayi	esophageal cancer associated	0		F:GO:0003674; C:GO:0005575		PTHR13673 (PANTHER)
Callithrix jacchus	subfamily member 3b	13	P:GO:0006924; F:GO:0005083; P:GO:0042102; P:GO:0007569; C:GO:0005829; P:GO:0032088; P:GO:0007264; P:GO:0009790; F:GO:0051082; P:GO:0033077; P:GO:0006264; C:GO:0005634; C:GO:0005739	-		IPR001623; IPR003095; IPR015609; PTHR11821:SF79 (PANTHER)
Caenorhabditis elegans	hypothetical protein T12B3.3 [Caenorhabditis elegans]	2	P:GO:0044238; F:GO:0008081	-	EC:3.1.4.0	IPR017946
Caenorhabditis elegans	briggsae cbr-opt-2 protein	0		P:GO:0006857; F:GO:0015198; C:GO:0016021; C:GO:0016020; F:GO:0005215; P:GO:0006810		-
	-	0				-
Caenorhabditis elegans	acid phosphatase-1	1	P:GO:0019915	-		-
Caenorhabditis elegans	major allergen	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	transport and golgi organization-like	0		F:GO:0005515		IPR011705; IPR013089; PTHR23230:SF183 (PANTHER)

Caenorhabditis elegans	merhead embryonic lethal family member (hmr-1)	7	P:GO:0007411; F:GO:0005515; P:GO:0007155; P:GO:0001745; P:GO:0048675; C:GO:0044425; C:GO:0005886	-		-
Caenorhabditis elegans	merhead embryonic lethal family member (hmr-1)	7	P:GO:0007411; F:GO:0005515; P:GO:0007155; P:GO:0001745; P:GO:0048675; C:GO:0044425; C:GO:0005886	-		-
	-	0				-
Brugia malayi	cleavage and polyadenylation specificity factor subunit 3	10	P:GO:0006378; F:GO:0046872; P:GO:0008380; F:GO:0004521; C:GO:0005847; F:GO:0003729; F:GO:0005515; P:GO:0006398; C:GO:0030529; F:GO:0008409	-		IPR001279; IPR022712; G3DSA:3.60.15.10 (GENE3D), PTHR11203 (PANTHER), PTHR11203:SF11 (PANTHER), SSF56281 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	P:GO:0043652; C:GO:0005886; P:GO:0012501; F:GO:0017111	-	EC:3.6.1.15	PTHR19229 (PANTHER), PTHR19229:SF18 (PANTHER), SignalP (SIGNALP)
Homo sapiens	ribosomal protein l13	5	F:GO:0003735; F:GO:0003723; F:GO:0005515; C:GO:0022625; P:GO:0006414	-		IPR001380; IPR018256
Caenorhabditis elegans	cg8129- isoform b	4	F:GO:0004794; P:GO:0008152; F:GO:0030170; F:GO:0016597	-	EC:4.3.1.19	IPR001926; IPR002912; G3DSA:3.30.70.260 (GENE3D), G3DSA:3.40.50.1100 (GENE3D), PTHR10314 (PANTHER), PTHR10314:SF17 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-asp-5 protein	6	C:GO:0016021; P:GO:0008219; P:GO:0006508; F:GO:0004190; F:GO:0005515; P:GO:0040011	-	EC:3.4.23.0	IPR001461; IPR009007; IPR021109; PTHR13683:SF53 (PANTHER)
Chlamydomonas reinhardtii	hypothetical kda protein in faa3-mas3 intergenic	0		F:GO:0003674; C:GO:0005737; P:GO:0008033; P:GO:0008150; C:GO:0005575		-
	-	0				-

Caenorhabditis elegans	phosphatidylinositol-3-phosphate phosphatidylinositol 5-type iii	14	P:GO:0042147; C:GO:0005829; C:GO:0031901; P:GO:0044238; F:GO:0008270; P:GO:0023034; P:GO:0034504; C:GO:0032593; F:GO:0016308; F:GO:0005515; C:GO:0045121; C:GO:0012506; P:GO:0006898; P:GO:0044237	-	EC:2.7.1.68	IPR002423; G3DSA:3.50.7.10 (GENE3D), PTHR11353:SF14 (PANTHER)
Loa loa	leucine rich repeat family protein	0		F:GO:0005515		-
Caenorhabditis briggsae	transcriptio-l regulator atrx	3	F:GO:0005524; F:GO:0004386; F:GO:0003677	-		IPR000330; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10799 (PANTHER), PTHR10799:SF53 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	zinc finger protein	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		IPR006797; IPR007087; IPR015880
Caenorhabditis elegans	d- polymerase zeta catalytic subunit	1	P:GO:0006281	-		IPR006134; PTHR10322 (PANTHER), PTHR10322:SF5 (PANTHER), SSF56672 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	ryanodine receptor homologue	5	C:GO:0005875; F:GO:0005262; P:GO:0006811; P:GO:0006936; C:GO:0016020	-		IPR001870; IPR003877; IPR015925; PTHR13715:SF11 (PANTHER)
Brugia malayi	activating sig-l cointegrator 1 complex subunit 3-like 1 isoform 1	12	P:GO:0018991; C:GO:0005681; F:GO:0008026; P:GO:0040007; F:GO:0003677; F:GO:0005524; P:GO:0007601; P:GO:0002119; F:GO:0005515; P:GO:0000354; C:GO:0005682; P:GO:0009792	-		G3DSA:3.40.50.300 (GENE3D), PTHR11752 (PANTHER), PTHR11752:SF7 (PANTHER)
Angiostrongylus cantonensis	poly polymerase cid (caffein-induced death protein)	3	C:GO:0005622; F:GO:0005515; F:GO:0003725	-		IPR002058; G3DSA:3.30.460.10 (GENE3D), PTHR12271 (PANTHER), PTHR12271:SF14 (PANTHER), SSF81301 (SUPERFAMILY), SSF81631 (SUPERFAMILY)

Caenorhabditis elegans	briggsae cbr-gex-2 protein	11	P:GO:0016477; P:GO:0007411; P:GO:0050807; P:GO:0008360; C:GO:0045202; P:GO:0006911; P:GO:0030866; F:GO:0005515; P:GO:0010172; C:GO:0005737; P:GO:0030031	-		IPR008081
Caenorhabditis elegans	low-density lipoprotein receptor-related protein 2	3	F:GO:0004872; C:GO:0016021; F:GO:0005509	-		IPR000033; IPR011042; PTHR10529 (PANTHER), SSF63825 (SUPERFAMILY)
Loa loa	leucine rich repeat family protein	0		F:GO:0005216; C:GO:0016021; C:GO:0016020; P:GO:0006811; P:GO:0006810; F:GO:0003674; F:GO:0005515; P:GO:0055085; P:GO:0008150		G3DSA:3.80.10.10 (GENE3D), PTHR23154 (PANTHER), PTHR23154:SF128 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)
Brugia malayi	lysine-specific histone demethylase 1	13	P:GO:0033169; P:GO:0043433; F:GO:0034648; F:GO:0016491; P:GO:0034720; F:GO:0050660; P:GO:0034339; F:GO:0032454; F:GO:0003682; F:GO:0030374; C:GO:0005634; F:GO:0050681; F:GO:0016564	-		IPR007526; IPR009057; IPR011991
Brugia malayi	lysine-specific histone demethylase 1	2	P:GO:0008152; F:GO:0003824	-		IPR007526; IPR009057; IPR011991
Loa loa	lysine-specific histone demethylase 1	13	P:GO:0033169; P:GO:0043433; F:GO:0034648; F:GO:0016491; P:GO:0034720; F:GO:0050660; P:GO:0034339; F:GO:0032454; F:GO:0003682; F:GO:0030374; C:GO:0005634; F:GO:0050681; F:GO:0016564	-		IPR007526; IPR009057; IPR011991

Loa loa	lysine-specific histone demethylase 1	13	P:GO:0033169; P:GO:0043433; F:GO:0034648; F:GO:0016491; P:GO:0034720; F:GO:0050660; P:GO:0034339; F:GO:0032454; F:GO:0003682; F:GO:0030374; C:GO:0005634; F:GO:0050681; F:GO:0016564	-		IPR007526; IPR009057; IPR011991
Brugia malayi	wd repeat domain 4	0		F:GO:0016740; F:GO:0008168; P:GO:0008033; C:GO:0005634; C:GO:0005737; C:GO:0005654; F:GO:0005515; P:GO:0006400; F:GO:0008176		IPR015943; PTHR16288 (PANTHER), SSF101908 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	sig-l recognition particle 68	10	F:GO:0005488; C:GO:0043231; P:GO:0040002; P:GO:0040035; P:GO:0002119; C:GO:0044444; C:GO:0030529; P:GO:0006898; P:GO:0009792; P:GO:0040018	-		PTHR12860 (PANTHER)
Caenorhabditis elegans	myc and mondo-like family member (mml-1)	4	P:GO:0009792; P:GO:0002119; P:GO:0040010; P:GO:0006898	-		PTHR15741 (PANTHER), PTHR15741:SF1 (PANTHER)
Loa loa	sympk protein	3	C:GO:0005737; C:GO:0005654; F:GO:0005515	-		IPR021850; PTHR15245 (PANTHER), PTHR15245:SF2 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0016787		IPR002018; G3DSA:3.40.50.1820 (GENE3D), PTHR11559:SF6 (PANTHER), SSF53474 (SUPERFAMILY)
Brugia malayi	hmg box family protein	0		F:GO:0003677; C:GO:0005634		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
Nematostella vectensis	predicted protein [Nematostella vectensis]	0				-
Caenorhabditis briggsae	atpase aaa domain containing 3a	4	C:GO:0005743; F:GO:0005524; F:GO:0017111; P:GO:0008152	-	EC:3.6.1.15	PTHR23075 (PANTHER)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		PTHR22934 (PANTHER), PTHR22934:SF14 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		PTHR22934 (PANTHER), PTHR22934:SF14 (PANTHER)

Brugia malayi	zinc knuckle family protein	6	P:GO:0009792; F:GO:0003676; P:GO:0001703; F:GO:0005515; C:GO:0005634; F:GO:0008270	-		IPR001841; IPR001878; IPR013083; IPR013084; IPR014891; IPR017907; PTHR15439 (PANTHER), SSF57756 (SUPERFAMILY), SSF57850 (SUPERFAMILY)
Ixodes scapularis	tpr repeat nuclear	9	F:GO:0042169; P:GO:0033523; P:GO:0010390; P:GO:0040007; P:GO:0000003; C:GO:0016593; P:GO:0002119; P:GO:0006898; P:GO:0009792	-		PTHR14027 (PANTHER), PTHR14027:SF2 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0005488		-
	-	0				-
	-	0				-
Caenorhabditis elegans	acetyl- hydrolase transferase family protein	3	C:GO:0005811; P:GO:0044237; F:GO:0003824	-		IPR003702; G3DSA:3.40.1080.10 (GENE3D), G3DSA:3.40.810.20 (GENE3D), PTHR21432:SF11 (PANTHER), SignalP (SIGNALP), SSF100950 (SUPERFAMILY)
Brugia malayi	co-chaperone protein mitochondrial	3	P:GO:0006974; C:GO:0005739; F:GO:0005515	-		IPR001623; IPR015609; PTHR11821:SF53 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	60s ribosomal protein l11	9	P:GO:0006412; P:GO:0040010; C:GO:0005840; P:GO:0006917; F:GO:0003735; P:GO:0040035; P:GO:0002119; P:GO:0040039; P:GO:0009792	-	EC:3.6.5.3	IPR002132; IPR020929; IPR022803; PTHR11994:SF2 (PANTHER)
Caenorhabditis briggsae	uncharacterized protein	2	F:GO:0046872; F:GO:0008237	-		IPR007863; IPR011249; PTHR11851 (PANTHER), PTHR11851:SF68 (PANTHER)
Caenorhabditis elegans	vesicle transport through interaction with t-s-res homolog 1a	7	F:GO:0005484; C:GO:0031201; C:GO:0008021; P:GO:0042147; P:GO:0006886; C:GO:0016021; C:GO:0043025	-		-
Loa loa	brain rptpmam4 isoform ii	6	F:GO:0004721; F:GO:0005515; P:GO:0044237; P:GO:0051179; C:GO:0044459; P:GO:0048523	-	EC:3.1.3.16	IPR000242; IPR000387; IPR016130; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), SSF52799 (SUPERFAMILY)
Loa loa	potential dual specificity phosphatase	5	P:GO:0006470; F:GO:0019900; F:GO:0016791; P:GO:0033133; C:GO:0005737	-	EC:3.1.3.0	PTHR10159 (PANTHER), PTHR10159:SF13 (PANTHER)

	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	cuticular collagen	4	P:GO:0019915; P:GO:0006952; P:GO:0010171; F:GO:0005515	-		IPR002486; IPR008160; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	g patch domain containing 1	3	P:GO:0019915; P:GO:0010171; P:GO:0002119	-		PTHR13384 (PANTHER), PTHR13384:SF8 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	prostaglandin reductase 2	4	P:GO:0055114; C:GO:0005737; F:GO:0016491; F:GO:0008270	-		IPR002085; IPR013149; IPR016040; PTHR11695:SF5 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	f26_caeel ame: full=probable 6-phosphofructo-2-ki-se fructose- -biphosphatase short=6pf-2-k fru- -p2ase short=pfk fbpase includes: ame: full=6-phosphofructo-2-ki-se includes: ame: full=fructose- -bisphosphatase	3	P:GO:0006003; F:GO:0005524; F:GO:0003873	-	EC:2.7.1.105	IPR003094; PTHR10606:SF11 (PANTHER)
Caenorhabditis elegans	yl54_caeel ame: full=uncharacterized protein	0				-
Caenorhabditis elegans	yl54_caeel ame: full=uncharacterized protein	0				-
Caenorhabditis elegans	af316599_1 paracaspase	11	P:GO:0000003; F:GO:0005515; P:GO:0046649; P:GO:0050778; P:GO:0044238; P:GO:0050794; P:GO:0043170; F:GO:0008233; P:GO:0035466; C:GO:0044444; P:GO:0032501	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	prion-like-(q n-rich)-domain-bearing protein family member (pqn-22)	1	P:GO:0009792	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	zinc carboxypeptidase	3	P:GO:0006508; F:GO:0004181; F:GO:0008270	-	EC:3.4.17.0	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), PTHR11705:SF12 (PANTHER), SSF53187 (SUPERFAMILY)
Caenorhabditis briggsae	small	2	F:GO:0032555; P:GO:0050794	-		-

Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-
Loa loa	iesterase family member (pde-2)	9	F:GO:0004118; P:GO:0046069; F:GO:0046872; F:GO:0030552; C:GO:0045121; P:GO:0007165; F:GO:0042803; F:GO:0030553; P:GO:0006198	-		IPR002073; PTHR11347 (PANTHER), PTHR11347:SF17 (PANTHER), SSF109604 (SUPERFAMILY)
Caenorhabditis briggsae	small subunit processome homolog	0		F:GO:0003674; P:GO:0008150		IPR006984; G3DSA:3.40.50.1010 (GENE3D), SSF88723 (SUPERFAMILY)
Caenorhabditis elegans	atp-binding cassette transporter 13-like	4	F:GO:0016887; P:GO:0006810; F:GO:0000166; F:GO:0005215	-		SignalP (SIGNALP)
Caenorhabditis briggsae	potential initiation factor 2 subunit family protein	0		F:GO:0046523; F:GO:0003743; P:GO:0044237; P:GO:0044249; F:GO:0016853		IPR000649; PTHR10233:SF6 (PANTHER), SSF100950 (SUPERFAMILY)
Loa loa	116 kda u5 small nuclear ribonucleoprotein component	16	F:GO:0003746; C:GO:0015030; P:GO:0000910; C:GO:0005681; P:GO:0040007; C:GO:0016607; P:GO:0000003; P:GO:0008380; P:GO:0018996; P:GO:0002119; F:GO:0005515; P:GO:0040011; F:GO:0003924; P:GO:0006397; P:GO:0009792; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000640; IPR004161; IPR005517; IPR009000; IPR009022; IPR014721; IPR020568; G3DSA:2.40.30.10 (GENE3D), G3DSA:3.30.70.870 (GENE3D), G3DSA:3.90.1430.10 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF5 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-abt-2 protein	0		F:GO:0005524; F:GO:0016887; F:GO:0000166; F:GO:0017111		SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG23745 [Caenorhabditis briggsae]	4	P:GO:0009792; P:GO:0016246; P:GO:0040007; P:GO:0002119	-		-
Brugia malayi	coiled-coil domain containing 49	0		P:GO:0055114; P:GO:0010171; P:GO:0040010; P:GO:0009792; P:GO:0006979; P:GO:0040019		-
	-	0				-

Homo sapiens	clusterin	20	P:GO:0009615; P:GO:0051788; P:GO:0048812; C:GO:0034366; P:GO:0045597; P:GO:0032463; P:GO:0043691; P:GO:0031018; C:GO:0016235; P:GO:0006916; P:GO:0008284; P:GO:0006629; P:GO:0006958; F:GO:0051787; C:GO:0048471; P:GO:0001836; P:GO:0045087; P:GO:0006979; C:GO:0031012; C:GO:0005739	-		IPR000753; IPR016016; PTHR10970 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	Hypothetical protein F49D11.10 [Caenorhabditis elegans]	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	prion-like-(q n-rich)-domain-bearing protein family member (pqn-42)	0				-
Caenorhabditis elegans	prion-like-(q n-rich)-domain-bearing protein family member (pqn-42)	0				-
	-	0				SignalP (SIGNALP)
Brugia malayi	ruvb-like 2	6	F:GO:0003678; C:GO:0071339; P:GO:0006310; F:GO:0005524; F:GO:0016887; P:GO:0016481	-		-
Xenopus (Silurana) tropicalis	methyltransferase like 9	0		F:GO:0008168; F:GO:0003674; F:GO:0016740; P:GO:0008150		IPR007884
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	F:GO:0005488; P:GO:0006810	-		PTHR12965 (PANTHER)
Caenorhabditis briggsae	6-phosphofructo-2-ki-se fructose- -biphosphatase isoform cra_a	12	P:GO:0006007; F:GO:0003873; C:GO:0005829; P:GO:0009749; F:GO:0019900; P:GO:0006090; F:GO:0004331; P:GO:0006089; F:GO:0005524; P:GO:0033133; P:GO:0006003; P:GO:0032024	-	EC:2.7.1.105; EC:3.1.3.46	IPR003094; IPR013078; G3DSA:3.40.50.1240 (GENE3D), PTHR10606:SF11 (PANTHER), SSF53254 (SUPERFAMILY)

Brugia malayi	egf-like domain containing protein	8	P:GO:0048519; P:GO:0007155; P:GO:0032879; C:GO:0016021; P:GO:0050794; C:GO:0044459; F:GO:0005488; P:GO:0032502	-		IPR001169; IPR013032; IPR013111; IPR015812; G3DSA:2.10.25.10 (GENE3D), PTHR10082:SF5 (PANTHER), SSF57196 (SUPERFAMILY)
Bombyx mori	endonuclease-reverse transcriptase	1	F:GO:0003824	-		-
Caenorhabditis briggsae	briggsae cbr-kin-4 protein	8	P:GO:0009792; P:GO:0006468; F:GO:0008415; F:GO:0005515; F:GO:0005524; F:GO:0000287; P:GO:0000003; F:GO:0004674	-	EC:2.7.11.0	IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR14191 (PANTHER)
Caenorhabditis elegans	upf0459 protein cg10681	0		P:GO:0008150; C:GO:0005575		-
Caenorhabditis elegans	briggsae cbr-phat-2 protein	1	F:GO:0005515	-		IPR003582; PTHR21724 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	4	F:GO:0005515; P:GO:0008340; P:GO:0008152; F:GO:0003824	-		IPR013781; IPR017853; PTHR23208 (PANTHER), PTHR23208:SF13 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	4	F:GO:0005515; P:GO:0008340; P:GO:0008152; F:GO:0003824	-		IPR013781; IPR017853; PTHR23208 (PANTHER), PTHR23208:SF13 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	4	F:GO:0005515; P:GO:0008340; P:GO:0008152; F:GO:0003824	-		IPR013781; IPR017853; PTHR23208 (PANTHER), PTHR23208:SF13 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	leucine-ruch repeat hypothetical protein phosphatase 1 regulatory	4	P:GO:0009792; P:GO:0040035; P:GO:0006898; P:GO:0040011	-		G3DSA:3.80.10.10 (GENE3D), PTHR10588 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
						IPR003598; IPR003599; IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF5 (PANTHER), SSF48726 (SUPERFAMILY)
						IPR003598; IPR003599; IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF5 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-

Caenorhabditis elegans	phospholipase d1	13	P:GO:0007265; F:GO:0004620; P:GO:0016042; P:GO:0006935; C:GO:0005768; F:GO:0008081; F:GO:0005515; C:GO:0031090; P:GO:0007154; F:GO:0035091; C:GO:0044431; P:GO:0008654; P:GO:0050830	-	EC:3.1.4.0	IPR001736; IPR001849; IPR015679; G3DSA:3.30.870.10 (GENE3D), PTHR18896:SF6 (PANTHER), SSF50729 (SUPERFAMILY), SSF56024 (SUPERFAMILY)
Caenorhabditis elegans	aquaporin 8	7	C:GO:0005929; P:GO:0006833; C:GO:0005886; C:GO:0045177; F:GO:0015250; C:GO:0043025; C:GO:0044425	-		IPR000425; IPR022357; PTHR19139:SF25 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	6	C:GO:0016021; P:GO:0040007; F:GO:0005524; P:GO:0010171; P:GO:0002119; F:GO:0016887	-		IPR013525; PTHR19241 (PANTHER), PTHR19241:SF30 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	golgi-specific brefeldin a-resistance guanine nucleotide exchange factor 1	16	F:GO:0005515; C:GO:0005788; P:GO:0016044; C:GO:0005777; F:GO:0016563; C:GO:0005829; C:GO:0005801; P:GO:0048193; F:GO:0003677; P:GO:0032012; C:GO:0005795; F:GO:0005086; P:GO:0045449; C:GO:0005634; P:GO:0046903; C:GO:0005739	-		PTHR10663 (PANTHER), PTHR10663:SF8 (PANTHER)

Caenorhabditis elegans	golgi-specific brefeldin a-resistance guanine nucleotide exchange factor 1	16	F:GO:0005515; C:GO:0005788; P:GO:0016044; C:GO:0005777; F:GO:0016563; C:GO:0005829; C:GO:0005801; P:GO:0048193; F:GO:0003677; P:GO:0032012; C:GO:0005795; F:GO:0005086; P:GO:0045449; C:GO:0005634; P:GO:0046903; C:GO:0005739	-		PTHR10663 (PANTHER), PTHR10663:SF8 (PANTHER)
	-	0				-
Caenorhabditis elegans	hypothetical protein C27A12.9 [Caenorhabditis elegans]	0		P:GO:0008152; F:GO:0003824		PTHR23071 (PANTHER)
Caenorhabditis elegans	related to islet cell diabetes autoantigen family member (ida-1)	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	zinc finger in n-recognin family protein	0		F:GO:0046872; F:GO:0051015; F:GO:0030674; F:GO:0008270; F:GO:0005515; F:GO:0004842		PTHR21497 (PANTHER), PTHR21497:SF3 (PANTHER)
Loa loa	zinc dhhc domain containing 18	4	C:GO:0016020; F:GO:0046872; P:GO:0034613; F:GO:0016409	-		IPR001594; PTHR22883 (PANTHER)
Caenorhabditis briggsae	r- lariat debranching	7	P:GO:0009792; F:GO:0016788; P:GO:0040010; P:GO:0000003; P:GO:0040011; P:GO:0006898; P:GO:0006396	-		IPR007708; PTHR12849 (PANTHER)
Loa loa	met proto-oncogene precursor	7	P:GO:0001764; F:GO:0005488; P:GO:0001889; F:GO:0004872; P:GO:0021707; F:GO:0004713; P:GO:0021522	-	EC:2.7.10.0	IPR000719; IPR001245; IPR011009; IPR020685; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
Caenorhabditis elegans	nucleolar complex associated 4 homolog (cerevisiae)	9	P:GO:0040010; P:GO:0000003; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0006898; P:GO:0009792; P:GO:0040018; C:GO:0005634	-		IPR005612; PTHR12455 (PANTHER)

Brugia malayi	ribonucleases p mrp protein subunit pop1 containing protein	0		P:GO:0010171; P:GO:0006396; P:GO:0006898; P:GO:0000003; P:GO:0009792; P:GO:0002119; F:GO:0004526; P:GO:0001682; P:GO:0040010; P:GO:0040007		IPR012590
Haemonchus contortus	hexoki-se	5	P:GO:0060361; F:GO:0005515; F:GO:0005524; P:GO:0006096; F:GO:0004396	-	EC:2.7.1.1	IPR001312; IPR019807; IPR022672; IPR022673; G3DSA:3.40.367.20 (GENE3D), SSF53067 (SUPERFAMILY)
Haemonchus contortus	hexoki-se family protein	5	P:GO:0060361; F:GO:0005515; F:GO:0005524; P:GO:0006096; F:GO:0004396	-	EC:2.7.1.1	IPR001312; IPR019807; IPR022672; IPR022673; G3DSA:3.30.420.40 (GENE3D), G3DSA:3.40.367.20 (GENE3D), SSF53067 (SUPERFAMILY)
Haemonchus contortus	hexoki-se	4	F:GO:0005515; F:GO:0005524; P:GO:0006096; F:GO:0004396	-	EC:2.7.1.1	IPR001312; IPR019807; IPR022672; IPR022673; G3DSA:3.40.367.20 (GENE3D), SSF53067 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	6-phosphogluconolacto-se	3	C:GO:0044464; P:GO:0006098; F:GO:0017057	-	EC:3.1.1.31	IPR005900; G3DSA:3.40.50.1360 (GENE3D), SSF100950 (SUPERFAMILY)
Caenorhabditis elegans	serpentine class sx family member (srsx-34)	0		C:GO:0016021; P:GO:0055085; P:GO:0008340		IPR011701; IPR016196; PTHR10074 (PANTHER), PTHR10074:SF12 (PANTHER)
Caenorhabditis briggsae	peptidoglycan- domain containing 2	1	P:GO:0019915	-		IPR018392; G3DSA:3.10.350.10 (GENE3D), PTHR20932 (PANTHER)
Caenorhabditis briggsae	deoxyribonuclease-2	1	F:GO:0004518	-		-
Brugia malayi	f-box and wd repeat domain containing 7	8	C:GO:0005654; F:GO:0005515; C:GO:0005730; C:GO:0019005; P:GO:0016567; P:GO:0031146; P:GO:0007062; P:GO:0032876	-		IPR001810; IPR022364; G3DSA:1.20.1280.50 (GENE3D), PTHR22844 (PANTHER), PTHR22844:SF11 (PANTHER)
	-	0				-

Caenorhabditis briggsae	type iii restriction res subunit family protein	0		F:GO:0004386; P:GO:0006974; C:GO:0005634; F:GO:0003677; F:GO:0016787; F:GO:0003676; F:GO:0000166; P:GO:0000003; F:GO:0008270; F:GO:0005524; F:GO:0008026; P:GO:0006281; C:GO:0005575; F:GO:0005515; F:GO:0046872		PTHR14025 (PANTHER), PTHR14025:SF10 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	dead (asp-glu-ala-asp) box polypeptide 1	9	F:GO:0003676; P:GO:0044260; C:GO:0010494; F:GO:0005515; F:GO:0000166; P:GO:0006139; P:GO:0007275; P:GO:0010467; F:GO:0003724	-		IPR001650; IPR001870; IPR003877; IPR008985; IPR011545; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF44 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	placental protein 11 related	4	F:GO:0005488; F:GO:0004519; P:GO:0019538; C:GO:0044424	-		IPR018998; PTHR12439 (PANTHER), SignalP (SIGNALP), SSF142877 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	transformer-2 alpha	12	P:GO:0040010; F:GO:0003723; P:GO:0040035; P:GO:0002119; F:GO:0000166; P:GO:0000398; P:GO:0040011; P:GO:0002009; P:GO:0048477; P:GO:0009792; P:GO:0008406; C:GO:0005634	-		IPR000504; IPR012677; PTHR15241 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	C:GO:0043231; C:GO:0044444	-		-
Loa loa	f-box and leucine-rich repeat protein 14b	0		C:GO:0009536; C:GO:0016023; P:GO:0008150; F:GO:0004842; P:GO:0016567; F:GO:0005515; C:GO:0005575; C:GO:0019005		G3DSA:3.80.10.10 (GENE3D), PTHR23125 (PANTHER), PTHR23125:SF64 (PANTHER), SSF52047 (SUPERFAMILY)
	-	0				-

Macaca mulatta	eukaryotic initiation factor 4ai	10	F:GO:0003729; C:GO:0016281; F:GO:0008026; F:GO:0005515; P:GO:0031100; F:GO:0005524; F:GO:0000339; F:GO:0003743; C:GO:0005829; P:GO:0006412	-	EC:3.6.5.3	IPR011545; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF2 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	mitochondrial glutamate	2	P:GO:0008340; C:GO:0016020	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF23 (PANTHER)
Gallus gallus	ribosomal protein l26	7	P:GO:0042273; F:GO:0003735; F:GO:0003723; F:GO:0005515; P:GO:0006364; C:GO:0022625; P:GO:0006414	-		IPR005756; IPR005824; IPR005825; IPR008991; IPR014723; PTHR11143:SF2 (PANTHER)
	-	0				-
	-	0				-
Loa loa	wd repeat domain isoform cra_a	3	F:GO:0005488; C:GO:0044428; P:GO:0008152	-		IPR001680; IPR015943; IPR019405; IPR019781; PTHR13211 (PANTHER), SSF101908 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	type ii inositol- -bisphosphate 4-	0				-
Loa loa	retinoblastoma-associated protein a domain containing protein	0		F:GO:0005515		-
Caenorhabditis elegans	daf-16 foxo germline tumor affecting family member (dct-10)	0				IPR021109; SignalP (SIGNALP)
Caenorhabditis elegans	daf-16 foxo germline tumor affecting family member (dct-10)	0				IPR021109; SignalP (SIGNALP)
Caenorhabditis briggsae	er lumen protein retaining receptor	9	F:GO:0004872; C:GO:0005789; C:GO:0005794; P:GO:0006621; F:GO:0005515; F:GO:0005046; P:GO:0016192; P:GO:0006886; C:GO:0016021	-		IPR000133; PTHR10585:SF10 (PANTHER), SignalP (SIGNALP)
Brugia malayi	elegans protein confirmed by transcript evidence	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis briggsae	kinesin-like protein kif3a	17	F:GO:0003777; C:GO:0035085; P:GO:0007224; P:GO:0048260; C:GO:0005874; C:GO:0008021; P:GO:0007507; F:GO:0005524; P:GO:0007018; F:GO:0005515; P:GO:0021904; C:GO:0032391; P:GO:0001822; P:GO:0007368; P:GO:0042384; P:GO:0001701; P:GO:0009952	-		IPR001752; IPR019821; PTHR16012 (PANTHER), PTHR16012:SF160 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Brugia malayi	cullin-associated nedd8-dissociated protein 1	11	P:GO:0040010; P:GO:0045899; P:GO:0016567; P:GO:0002119; P:GO:0043086; F:GO:0016563; P:GO:0030154; F:GO:0017025; C:GO:0000151; P:GO:0009792; C:GO:0005634	-		-
Caenorhabditis elegans	isoform a	0		F:GO:0020037; P:GO:0006919; F:GO:0009055; F:GO:0003964; F:GO:0003723; P:GO:0016567; P:GO:0006278; C:GO:0031463; F:GO:0005515; P:GO:0007291		IPR006652; IPR013089; IPR015915; PTHR23230:SF168 (PANTHER)
Caenorhabditis elegans	glutamyl-tr- b subunit	1	F:GO:0016874	-		IPR006075; IPR017959; SSF55931 (SUPERFAMILY)
	-	0				-
Loa loa	zinc c2h2 type family protein	0		F:GO:0008270; C:GO:0005622		IPR007087; IPR015880
Loa loa	protein zwilch homolog	0		C:GO:0005694; P:GO:0007067; C:GO:0000777; P:GO:0006810; C:GO:0000776; C:GO:0000775; F:GO:0003674; P:GO:0007093; P:GO:0051301; P:GO:0009792; F:GO:0008289; F:GO:0005515; P:GO:0008150; P:GO:0007049		IPR018630

Loa loa	protein zwilch homolog	0		C:GO:0005694; P:GO:0007067; C:GO:0000777; P:GO:0006810; C:GO:0000776; C:GO:0000775; F:GO:0003674; P:GO:0007093; P:GO:0051301; P:GO:0009792; F:GO:0008289; F:GO:0005515; P:GO:0008150; P:GO:0007049		IPR018630
Caenorhabditis elegans	sdk2 protein	1	C:GO:0016020	-		IPR003961; IPR008957; IPR013783; PR00014 (PRINTS), PTHR10489 (PANTHER), PTHR10489:SF57 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	hypothetical protein F55F10.1 [Caenorhabditis elegans]	0		C:GO:0005634; F:GO:0000166; F:GO:0008134; F:GO:0017111; F:GO:0005524; F:GO:0016887; P:GO:0006355; C:GO:0005622; P:GO:0043254		PTHR22908 (PANTHER), PTHR22908:SF13 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	P:GO:0040010	-		IPR002544; SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-sulp-4 protein	0		P:GO:0008272; C:GO:0016021; F:GO:0008271; C:GO:0016020; P:GO:0055085; F:GO:0005215; P:GO:0006810		IPR002645; IPR011547; PTHR11814 (PANTHER), PTHR11814:SF26 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	C:GO:0016020; P:GO:0006810; F:GO:0005215	-		-
Caenorhabditis briggsae	stip	6	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0040007	-		PTHR23329 (PANTHER), PTHR23329:SF1 (PANTHER)
Caenorhabditis elegans	protein ki-se domain containing protein	1	P:GO:0040010	-		IPR011009; PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
Caenorhabditis elegans	frataxin mitochondrial precursor	2	C:GO:0005739; P:GO:0006879	-		IPR001794; IPR002908; SignalP (SIGNALP)

Caenorhabditis elegans	solute carrier family 30 (zinc transporter) member 9	8	P:GO:0055085; C:GO:0005856; P:GO:0044260; P:GO:0090304; F:GO:0008324; P:GO:0006812; C:GO:0016020; C:GO:0005634	-		IPR002524; IPR009061; G3DSA:1.20.1510.10 (GENE3D), G3DSA:3.90.530.10 (GENE3D), PTHR13414 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-hum-2 protein	9	F:GO:0017137; F:GO:0035255; P:GO:0032880; C:GO:0043197; C:GO:0019717; F:GO:0000166; C:GO:0043025; C:GO:0048471; P:GO:0015031	-		IPR001609; PTHR13140 (PANTHER), PTHR13140:SF32 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	nuclear pore complex protein family member (npp-8)	0		P:GO:0000003; P:GO:0006913; P:GO:0009792; P:GO:0002119; P:GO:0006997; F:GO:0017056; F:GO:0005515; P:GO:0040007; P:GO:0040035		-
Caenorhabditis briggsae	cdk5 regulatory subunit associated protein 1-like 1	3	P:GO:0009451; F:GO:0003824; F:GO:0051539	-		IPR005839; IPR013848
	-	0				-
Caenorhabditis elegans	vitellogenin structural genes (yolk protein genes) family member (vit-2)	6	P:GO:0009792; F:GO:0005515; P:GO:0006810; P:GO:0040010; P:GO:0033036; P:GO:0008340	-		IPR015255; IPR015819; PTHR23345 (PANTHER)
Caenorhabditis elegans	vitellogenin structural genes (yolk protein genes) family member (vit-2)	4	P:GO:0009792; F:GO:0005515; P:GO:0040010; P:GO:0008340	-		IPR015255; IPR015819; PTHR23345 (PANTHER)
Caenorhabditis elegans	vitellogenin structural genes (yolk protein genes) family member (vit-2)	6	P:GO:0009792; F:GO:0005515; P:GO:0006810; P:GO:0040010; P:GO:0033036; P:GO:0008340	-		IPR015255; IPR015819; PTHR23345 (PANTHER)
Caenorhabditis elegans	briggsae cbr-vit-2 protein	0		P:GO:0006869; F:GO:0005319		-
Caenorhabditis elegans	briggsae cbr-vit-2 protein	0		P:GO:0006869; F:GO:0005319; P:GO:0040010; P:GO:0009792; P:GO:0008340; F:GO:0005515		-

Caenorhabditis elegans	vitellogenin structural genes (yolk protein genes) family member (vit-2)	7	P:GO:0006810; P:GO:0040010; P:GO:0008340; F:GO:0022892; F:GO:0005515; P:GO:0033036; P:GO:0009792	-		IPR011700; G3DSA:1.20.5.170 (GENE3D), PTHR23334 (PANTHER), PTHR23334:SF7 (PANTHER)
Caenorhabditis elegans	vitellogenin structural genes (yolk protein genes) family member (vit-2)	7	P:GO:0006810; P:GO:0040010; P:GO:0008340; F:GO:0022892; F:GO:0005515; P:GO:0033036; P:GO:0009792	-		IPR011700; G3DSA:1.20.5.170 (GENE3D), PTHR23334 (PANTHER), PTHR23334:SF7 (PANTHER)
Caenorhabditis elegans	vitellogenin structural genes (yolk protein genes) family member (vit-2)	7	P:GO:0006810; P:GO:0040010; P:GO:0008340; F:GO:0022892; F:GO:0005515; P:GO:0033036; P:GO:0009792	-		IPR011700; G3DSA:1.20.5.170 (GENE3D), PTHR23334 (PANTHER), PTHR23334:SF7 (PANTHER)
Caenorhabditis elegans	bzip transcription factor family member (zip-4)	0		P:GO:0006355; C:GO:0045202; C:GO:0005737; F:GO:0043565; F:GO:0046983; F:GO:0005515; F:GO:0003700; C:GO:0005634		
Caenorhabditis elegans	vitellogenin structural genes (yolk protein genes) family member (vit-2)	4	P:GO:0009792; F:GO:0005515; P:GO:0040010; P:GO:0008340	-		IPR015255; IPR015819; PTHR23345 (PANTHER)
Meloidogyne chitwoodi	transposase	0		F:GO:0004803; P:GO:0015074; P:GO:0006313; F:GO:0003677		PTHR23016 (PANTHER)
Meloidogyne chitwoodi	transposase	0		F:GO:0004803; P:GO:0015074; P:GO:0006313; F:GO:0003677		IPR001888; PTHR23016 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	gpi mannosyltransferase 1	5	P:GO:0000003; P:GO:0016254; F:GO:0016758; C:GO:0005783; C:GO:0044425	-	EC:2.4.1.0	IPR007704; SignalP (SIGNALP)
Loa loa	coiled-coil domain-containing protein mtmr15-like	6	P:GO:0000724; P:GO:0033683; F:GO:0043130; F:GO:0017108; C:GO:0005634; F:GO:0008409	-		IPR014883; SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-aex-1 protein	3	F:GO:0004871; C:GO:0005622; P:GO:0030421	-		-

Caenorhabditis elegans	polymerase iii (d- directed) polypeptide b	6	F:GO:0003899; P:GO:0032728; P:GO:0045089; F:GO:0003677; F:GO:0032549; P:GO:0006350	-	EC:2.7.7.6	IPR007644; G3DSA:3.90.1100.10 (GENE3D), SSF64484 (SUPERFAMILY)
Brugia malayi	r- dependent r- polymerase family protein	0		P:GO:0009792		-
	-	0				-
Caenorhabditis briggsae	sarcolemmal membrane-associated protein	0		F:GO:0051082; P:GO:0006457; C:GO:0016272		IPR000253; IPR008984; PTHR15715 (PANTHER), PTHR15715:SF4 (PANTHER)
Caenorhabditis briggsae	39s ribosomal protein mitochondrial	3	P:GO:0009792; F:GO:0046872; C:GO:0005622	-		IPR001857; PTHR15680:SF3 (PANTHER)
	-	0				-
Loa loa	ribophorin ii	1	C:GO:0044464	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Brugia malayi	briggsae cbr-mig-14 protein	19	C:GO:0044456; C:GO:0000139; P:GO:0016055; P:GO:0051223; P:GO:0001745; P:GO:0060341; P:GO:0051649; P:GO:0035017; C:GO:0016021; C:GO:0005789; P:GO:0008587; P:GO:0002790; P:GO:0007367; C:GO:0005769; P:GO:0048522; P:GO:0007480; C:GO:0044459; C:GO:0031300; C:GO:0010008	-		-
	-	0				-
Brugia malayi	hypothetical protein Bm1_33815 [Brugia malayi]	0				-
Caenorhabditis elegans	briggsae cbr-met-2 protein	6	P:GO:0044238; P:GO:0001833; P:GO:0044260; F:GO:0016740; F:GO:0005515; C:GO:0005634	-		IPR001214; G3DSA:2.170.270.10 (GENE3D), PTHR22884 (PANTHER), PTHR22884:SF24 (PANTHER), SSF82199 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	7	P:GO:0009792; P:GO:0010171; F:GO:0005515; P:GO:0040010; F:GO:0003774; P:GO:0045132; F:GO:0000166	-		IPR001752; PTHR16012 (PANTHER), PTHR16012:SF183 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	5	P:GO:0009792; P:GO:0010171; F:GO:0005515; P:GO:0040010; P:GO:0045132	-		IPR001752; PTHR16012 (PANTHER), PTHR16012:SF170 (PANTHER), SSF52540 (SUPERFAMILY)

Caenorhabditis elegans	briggsae cbr-klp- protein	8	P:GO:0040010; P:GO:0045132; C:GO:0005739; P:GO:0010171; F:GO:0003774; F:GO:0005515; F:GO:0000166; P:GO:0009792	-		IPR001752; PTHR16012 (PANTHER), PTHR16012:SF183 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	nuclear hormone receptor family protein isoform confirmed by transcript evidence	3	F:GO:0004872; F:GO:0005488; P:GO:0006350	-		IPR000536; IPR008946; PTHR11865 (PANTHER), PTHR11865:SF235 (PANTHER)
Homo sapiens	cytochrome b-c1 complex subunit 8	7	C:GO:0005743; F:GO:0008121; C:GO:0070469; P:GO:0034220; P:GO:0015992; C:GO:0016021; P:GO:0022900	-	EC:1.10.2.2	IPR004205
Caenorhabditis elegans	briggsae cbr-vps-16 protein	11	P:GO:0009792; P:GO:0010171; P:GO:0002119; C:GO:0031902; P:GO:0008340; P:GO:0006886; P:GO:0040011; P:GO:0008219; C:GO:0005765; P:GO:0040007; P:GO:0048565	-		PTHR12811 (PANTHER)
Caenorhabditis briggsae	guanosine monophosphate reductase	8	P:GO:0009792; P:GO:0002119; F:GO:0046872; P:GO:0009409; F:GO:0003920; P:GO:0055114; P:GO:0040007; P:GO:0009117	-	EC:1.7.1.7	IPR001093; IPR005993; IPR013785; IPR015875; PTHR11911 (PANTHER), PTHR11911:SF7 (PANTHER), SSF51412 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	gtp-binding protein 5	6	F:GO:0005525; C:GO:0005622; F:GO:0005515; C:GO:0016021; P:GO:0015684; F:GO:0015093	-		IPR002917; IPR006073; IPR006169; IPR014100; G3DSA:3.40.50.300 (GENE3D), PTHR11702 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Homo sapiens	elongation factor 2	7	C:GO:0005737; F:GO:0003746; F:GO:0005525; F:GO:0005515; C:GO:0030529; P:GO:0006414; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000795; G3DSA:3.40.50.300 (GENE3D), G3DSA:3.90.1430.10 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF15 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	ladder protein	0		F:GO:0008289; F:GO:0019841; F:GO:0005488		-

Nematostella vectensis	multidrug resistance-associated	1	F:GO:0003824	-		IPR001140; IPR011527; IPR017940; G3DSA:1.20.1560.10 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF22 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	denn madd domain containing 5a-like	0		F:GO:0017137; C:GO:0005794; F:GO:0005515		IPR001194; IPR005113; PTHR12296 (PANTHER), PTHR12296:SF3 (PANTHER)
	-	0				-
Caenorhabditis elegans	probable e3 ubiquitin-protein ligase mycbp2	10	C:GO:0015630; C:GO:0030424; F:GO:0008270; P:GO:0021785; P:GO:0051493; P:GO:0032880; P:GO:0021952; P:GO:0030071; F:GO:0042803; C:GO:0005680	-		IPR001841; IPR013083; PTHR12846 (PANTHER), PTHR12846:SF2 (PANTHER), SSF57850 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	lin1-like protein	1	F:GO:0005515	-		PTHR13138 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Macaca fascicularis	un-med protein product [Macaca fascicularis]	0				-
Caenorhabditis briggsae	leucyl-tr- synthetase	7	P:GO:0006423; F:GO:0004823; P:GO:0006429; F:GO:0005515; F:GO:0005524; C:GO:0005829; F:GO:0004817	-	EC:6.1.1.4; EC:6.1.1.16	IPR001412; IPR002300; IPR014729; PTHR11946 (PANTHER), PTHR11946:SF6 (PANTHER), SSF52374 (SUPERFAMILY)
Brugia malayi	ubiquitin-protein ligase e3c	1	P:GO:0000003	-		IPR000569; PTHR11254 (PANTHER), PTHR11254:SF31 (PANTHER)
Haemonchus contortus	ilin (drosophila ecm protein) homolog family member (ppn-1)	8	F:GO:0004867; F:GO:0008270; C:GO:0005604; F:GO:0004222; F:GO:0005515; F:GO:0005201; P:GO:0030198; C:GO:0005634	-	EC:3.4.24.0	IPR000884; IPR010294; IPR013273; G3DSA:2.20.100.10 (GENE3D), PTHR13723 (PANTHER), PTHR13723:SF18 (PANTHER), SignalP (SIGNALP)
	-	0				-
Brugia malayi	isoform a	0				IPR012875; IPR018506
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
Ancylostoma caninum	secreted protein 5 precursor	0		F:GO:0009055; P:GO:0019646; P:GO:0040011; P:GO:0006898; C:GO:0005576		IPR001283; IPR014044; PTHR10334:SF11 (PANTHER), SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	rab alpha subunit	10	P:GO:0009792; P:GO:0002119; F:GO:0005488; P:GO:0006464; P:GO:0040010; P:GO:0008340; P:GO:0040011; P:GO:0008219; F:GO:0016740; P:GO:0002009	-		IPR001611; IPR008940; G3DSA:3.80.10.10 (GENE3D), PTHR10588 (PANTHER), SSF52058 (SUPERFAMILY)
Caenorhabditis briggsae	ring finger protein 13	6	C:GO:0043231; F:GO:0008270; C:GO:0044446; F:GO:0005515; C:GO:0044444; C:GO:0031090	-		IPR001841; IPR013032; IPR013083; IPR018957; PTHR22765 (PANTHER), PTHR22765:SF1 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0016765		IPR001441; PTHR21528 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Ancylostoma ceylanicum	secreted protein 5 precursor	0		C:GO:0005576		-
Glycine max	chk1 checkpoint-like protein	0				-
Trichoplax adhaerens	chk1 checkpoint homolog (pombe)	3	P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	-
Trichoplax adhaerens	chk1 checkpoint homolog (pombe)	3	P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	-
Loa loa	cell cycle checkpoint protein rad17	3	P:GO:0050789; P:GO:0007049; P:GO:0006974	-		IPR004582; G3DSA:3.40.50.300 (GENE3D), PF03215 (PFAM), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	adam (disintegrin plus metalloprotease) family member (adm-4)	0		P:GO:0000003; P:GO:0006508; C:GO:0016021; F:GO:0008270; P:GO:0040010		-
Brugia malayi	calcium atpase	5	F:GO:0005388; C:GO:0016021; P:GO:0006754; F:GO:0005524; P:GO:0006816	-	EC:3.6.3.8	IPR001757; IPR004014; G3DSA:2.70.150.10 (GENE3D), PTHR11939:SF76 (PANTHER), SignalP (SIGNALP), SSF81665 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	grip1 associated protein 1	0		F:GO:0003674; P:GO:0008150; C:GO:0005769; C:GO:0005575		-
Loa loa	ankyrin repeat and zinc finger domain containing 1	0		F:GO:0046872; F:GO:0008270; C:GO:0005622		IPR007087; PTHR13182 (PANTHER)
	-	0				-

Caenorhabditis briggsae	poly polymerase cid (caffein-induced death protein)	0		F:GO:0005524; F:GO:0016779; C:GO:0005737; F:GO:0003887; F:GO:0016740; F:GO:0000166; P:GO:0006397		IPR002058; G3DSA:3.30.460.10 (GENE3D), PTHR12271 (PANTHER), PTHR12271:SF14 (PANTHER), SSF81301 (SUPERFAMILY), SSF81631 (SUPERFAMILY)
Caenorhabditis briggsae	poly polymerase cid (caffein-induced death protein)	0		F:GO:0005524; F:GO:0016779; C:GO:0005737; F:GO:0003887; F:GO:0016740; F:GO:0000166; P:GO:0006397		IPR002058; G3DSA:3.30.460.10 (GENE3D), PTHR12271 (PANTHER), PTHR12271:SF14 (PANTHER), SSF81301 (SUPERFAMILY), SSF81631 (SUPERFAMILY)
Caenorhabditis briggsae	poly polymerase cid (caffein-induced death protein)	0		F:GO:0005524; F:GO:0016779; C:GO:0005737; F:GO:0003887; F:GO:0016740; F:GO:0000166; P:GO:0006397		IPR002058; G3DSA:3.30.460.10 (GENE3D), PTHR12271 (PANTHER), PTHR12271:SF14 (PANTHER), SSF81301 (SUPERFAMILY), SSF81631 (SUPERFAMILY)
	-	0				-
Caenorhabditis brenneri	39s ribosomal protein mitochondrial	9	P:GO:0006412; P:GO:0040010; C:GO:0005739; F:GO:0003735; P:GO:0000002; C:GO:0015934; P:GO:0002119; P:GO:0009792; P:GO:0040019	-	EC:3.6.5.3	IPR005749; IPR021131; PTHR12934:SF1 (PANTHER)
Caenorhabditis elegans	adp-ribosylation factor-like 2	16	C:GO:0005829; P:GO:0000910; P:GO:0015870; F:GO:0005095; P:GO:0007049; F:GO:0004871; P:GO:0007264; C:GO:0005813; P:GO:0030540; F:GO:0005515; P:GO:0007021; F:GO:0003924; C:GO:0005794; F:GO:0005525; C:GO:0005886; P:GO:0009790	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR005225; IPR006688; IPR006689; G3DSA:3.40.50.300 (GENE3D), PTHR11711:SF26 (PANTHER), PS51417 (PROFILE), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	n-acetylglucosaminyl-phosphatidylinositol de-n-acetylase	4	F:GO:0016787; P:GO:0016254; C:GO:0016020; C:GO:0005783	-		IPR003737; G3DSA:3.40.50.10320 (GENE3D), PTHR12993:SF2 (PANTHER), SSF102588 (SUPERFAMILY)

Caenorhabditis elegans	myosin i	11	C:GO:0005737; P:GO:0042742; P:GO:0007368; C:GO:0005903; P:GO:0007498; F:GO:0003779; P:GO:0032528; C:GO:0016459; F:GO:0005524; F:GO:0003774; F:GO:0042623	-		IPR001609; PTHR13140 (PANTHER), PTHR13140:SF31 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	prolyl 4-hydroxylase	8	P:GO:0018401; F:GO:0031418; F:GO:0005506; F:GO:0005515; F:GO:0004656; P:GO:0055114; F:GO:0016702; C:GO:0005783	-	EC:1.14.11.2 ; EC:1.13.11.0	-
	-	0				-
Aspergillus clavatus NRRL 1	hypothetical protein ACLA_028940 [Aspergillus clavatus NRRL 1]	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-taf- protein	0		C:GO:0005669; P:GO:0006367; F:GO:0016251		SignalP (SIGNALP)
Caenorhabditis elegans	39s ribosomal protein mitochondrial	4	P:GO:0009792; C:GO:0005840; F:GO:0003735; P:GO:0006412	-	EC:3.6.5.3	IPR005822; IPR005823
	-	0				-
Homo sapiens	heat shock 27kda protein 1	16	P:GO:0009615; C:GO:0005626; C:GO:0030018; C:GO:0000502; C:GO:0005625; F:GO:0043130; F:GO:0042802; P:GO:0009408; C:GO:0009986; P:GO:0006916; P:GO:0006928; P:GO:0006446; C:GO:0005819; P:GO:0006986; C:GO:0005634; C:GO:0005886	-		IPR001436; IPR002068; IPR008978; G3DSA:2.60.40.790 (GENE3D), PTHR11527 (PANTHER), PTHR11527:SF33 (PANTHER)
Caenorhabditis briggsae	solute carrier organic anion transporter member 4a1	2	P:GO:0055085; C:GO:0016021	-		IPR004156; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), G3DSA:3.30.60.30 (GENE3D), PTHR11388:SF5 (PANTHER), PS51465 (PROFILE), SignalP (SIGNALP), SSF100895 (SUPERFAMILY)
Caenorhabditis elegans	solute carrier organic anion transporter member partial	2	P:GO:0055085; C:GO:0016021	-		IPR004156; IPR016196; PTHR11388:SF5 (PANTHER)

Caenorhabditis elegans	amin (actin binding protein) alpha family member (fl--1)	0		F:GO:0003779; P:GO:0009612		IPR001298; IPR013783; IPR014756; IPR017868; PTHR11915 (PANTHER), PTHR11915:SF55 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	3	P:GO:0008340; F:GO:0016491; F:GO:0005506	-		IPR001128; PTHR19383:SF59 (PANTHER)
Pongo abelii	stomatin -like 2	3	C:GO:0005743; C:GO:0005856; F:GO:0005102	-		IPR001972
Yarrowia lipolytica	chaperone domain protein	4	P:GO:0006457; F:GO:0046872; F:GO:0051082; F:GO:0031072	-		IPR001623; IPR015609; PTHR11821:SF79 (PANTHER)
Loa loa	coiled-coil domain containing 101	1	P:GO:0006350	-		IPR010750; PTHR21539 (PANTHER)
Caenorhabditis briggsae	xnop56 protein	9	P:GO:0006364; P:GO:0040035; P:GO:0002119; F:GO:0005515; F:GO:0030515; C:GO:0070761; C:GO:0031428; P:GO:0009792; P:GO:0040018	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	poly -binding	2	F:GO:0003676; F:GO:0000166	-		IPR015464; PTHR10432 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG09291 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	tbc (tre-2 bub2 cdc16) domain family member (tbc-19)	0		P:GO:0032313; C:GO:0005622; F:GO:0005097		IPR011047; IPR015943; IPR016160
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	slingshot homolog 2	9	P:GO:0032268; P:GO:0006470; P:GO:0000902; P:GO:0030036; F:GO:0003779; F:GO:0004721; C:GO:0005737; C:GO:0005886; P:GO:0071318	-	EC:3.1.3.16	-
Caenorhabditis elegans	yuqp_caeel ame: full=cral-trio domain-containing protein	1	P:GO:0040010	-		PTHR23324 (PANTHER), PTHR23324:SF3 (PANTHER)
Caenorhabditis elegans	transmembrane protein 184b	2	F:GO:0016301; C:GO:0016021	-		-
	-	0				-
Brugia malayi	cap-gly domain containing protein	2	F:GO:0051010; C:GO:0005881	-		IPR000938; IPR023092; PTHR18916 (PANTHER), PTHR18916:SF9 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	ribosomal protein l35	10	C:GO:0005730; P:GO:0009792; P:GO:0002119; F:GO:0003729; F:GO:0003735; F:GO:0005515; P:GO:0000003; C:GO:0022625; P:GO:0040007; P:GO:0006414	-		IPR001854; IPR018254; PTHR13872 (PANTHER), PTHR13872:SF2 (PANTHER)
Caenorhabditis elegans	leukotriene a4 hydrolase	9	F:GO:0008233; P:GO:0006954; F:GO:0046872; P:GO:0042221; P:GO:0006691; F:GO:0005515; F:GO:0004301; C:GO:0005737; C:GO:0005634	-	EC:3.3.2.10	IPR001930; IPR014782; PTHR11533:SF4 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	solute carrier family 30 (zinc transporter) member 9	7	P:GO:0006289; C:GO:0005856; F:GO:0003700; P:GO:0006812; P:GO:0006350; C:GO:0016020; C:GO:0005634	-		PTHR13414 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG14981 [Caenorhabditis briggsae]	2	P:GO:0040039; P:GO:0000003	-		-
Dracunculus medinensis	heat shock protein 70	5	F:GO:0005524; P:GO:0055114; P:GO:0006950; F:GO:0005515; F:GO:0032440	-	EC:1.3.1.74	IPR001023; IPR013126; IPR018181; G3DSA:3.30.30.30 (GENE3D), G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), PTHR19375:SF1 (PANTHER), SSF53067 (SUPERFAMILY)
Dracunculus medinensis	heat shock protein 70	5	F:GO:0005524; P:GO:0055114; P:GO:0006950; F:GO:0005515; F:GO:0032440	-	EC:1.3.1.74	IPR001023; IPR013126; IPR018181; G3DSA:3.30.30.30 (GENE3D), G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), PTHR19375:SF1 (PANTHER), SSF53067 (SUPERFAMILY)
Nippostrongylus brasiliensis	heat shock protein 70	3	F:GO:0005524; F:GO:0005515; P:GO:0006950	-		IPR019651; SignalP (SIGNALP)
Nippostrongylus brasiliensis	heat shock protein 70	3	F:GO:0005524; F:GO:0005515; P:GO:0006950	-		IPR019651; SignalP (SIGNALP)
Caenorhabditis briggsae	heat shock protein 70	5	F:GO:0005524; P:GO:0055114; P:GO:0006950; F:GO:0005515; F:GO:0032440	-	EC:1.3.1.74	IPR001023; IPR013126; IPR018181; G3DSA:2.60.34.10 (GENE3D), G3DSA:3.30.30.30 (GENE3D), G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), PTHR19375:SF1 (PANTHER), SSF100920 (SUPERFAMILY), SSF53067 (SUPERFAMILY)

Caenorhabditis briggsae	heat shock protein 70	5	F:GO:0005524; P:GO:0055114; P:GO:0006950; F:GO:0005515; F:GO:0032440	-	EC:1.3.1.74	IPR001023; IPR013126; IPR018181; G3DSA:2.60.34.10 (GENE3D), G3DSA:3.30.30.30 (GENE3D), G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), PTHR19375:SF1 (PANTHER), SSF100920 (SUPERFAMILY), SSF53067 (SUPERFAMILY)
Caenorhabditis elegans	heat shock protein 70	5	F:GO:0005524; P:GO:0055114; P:GO:0006950; F:GO:0005515; F:GO:0032440	-	EC:1.3.1.74	IPR001023; IPR013126; IPR018181; G3DSA:2.60.34.10 (GENE3D), G3DSA:3.30.30.30 (GENE3D), G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), PTHR19375:SF1 (PANTHER), SSF100920 (SUPERFAMILY), SSF100934 (SUPERFAMILY), SSF53067 (SUPERFAMILY)
Caenorhabditis elegans	heat shock protein 70	5	F:GO:0005524; P:GO:0055114; P:GO:0006950; F:GO:0005515; F:GO:0032440	-	EC:1.3.1.74	IPR001023; IPR013126; IPR018181; G3DSA:1.20.1270.10 (GENE3D), G3DSA:2.60.34.10 (GENE3D), G3DSA:3.30.30.30 (GENE3D), G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), PTHR19375:SF1 (PANTHER), SSF100920 (SUPERFAMILY), SSF100934 (SUPERFAMILY), SSF53067 (SUPERFAMILY)
Caenorhabditis briggsae	cell division cycle and apoptosis regulator protein 1	4	P:GO:0040027; F:GO:0005515; P:GO:0040017; P:GO:0040010	-		PTHR14304 (PANTHER), PTHR14304:SF3 (PANTHER)
Brugia malayi	cell division cycle and apoptosis regulator protein 1	4	P:GO:0040027; F:GO:0005515; P:GO:0040017; P:GO:0040010	-		IPR003034; G3DSA:1.10.720.30 (GENE3D), PTHR14304 (PANTHER), PTHR14304:SF3 (PANTHER), SSF68906 (SUPERFAMILY)
Brugia malayi	cell division cycle and apoptosis regulator protein 1	4	P:GO:0040027; F:GO:0005515; P:GO:0040017; P:GO:0040010	-		IPR003034; G3DSA:1.10.720.30 (GENE3D), PTHR14304 (PANTHER), PTHR14304:SF3 (PANTHER), SSF68906 (SUPERFAMILY)
Brugia malayi	cell division cycle and apoptosis regulator protein 1	4	P:GO:0040027; F:GO:0005515; P:GO:0040017; P:GO:0040010	-		IPR003034; G3DSA:1.10.720.30 (GENE3D), PTHR14304 (PANTHER), PTHR14304:SF3 (PANTHER), SSF68906 (SUPERFAMILY)
Caenorhabditis briggsae	adamtsl4 protein	3	F:GO:0008233; F:GO:0005515; C:GO:0005576	-		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	briggsae cbr-oct-2 protein	3	P:GO:0019915; C:GO:0016020; P:GO:0006810	-		IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11600 (PANTHER), PTHR11600:SF44 (PANTHER), SignalP (SIGNALP)

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0003723; P:GO:0009451; P:GO:0001522; F:GO:0009982		SignalP (SIGNALP)
Caenorhabditis elegans	creb binding protein	8	F:GO:0005515; P:GO:0048518; P:GO:0006355; C:GO:0044424; P:GO:0048513; P:GO:0009790; P:GO:0002119; P:GO:0022414	-		IPR001487; IPR003101; PTHR13808 (PANTHER)
Loa loa	dual oxidase 1	12	P:GO:0018149; P:GO:0006979; P:GO:0006952; P:GO:0040032; P:GO:0042338; F:GO:0046872; P:GO:0040007; F:GO:0016491; P:GO:0002119; P:GO:0040011; P:GO:0009792; C:GO:0005882	-		IPR011992; PTHR11972 (PANTHER), PTHR11972:SF1 (PANTHER), SSF47473 (SUPERFAMILY)
Loa loa	dual oxidase 1	12	P:GO:0018149; P:GO:0006979; P:GO:0006952; P:GO:0040032; P:GO:0042338; F:GO:0046872; P:GO:0040007; F:GO:0016491; P:GO:0002119; P:GO:0040011; P:GO:0009792; C:GO:0005882	-		IPR011992; PTHR11972 (PANTHER), PTHR11972:SF1 (PANTHER), SSF47473 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	ki-se ki-se family member (ckk-1)	10	F:GO:0005516; P:GO:0032147; C:GO:0005625; P:GO:0032793; F:GO:0005524; C:GO:0005737; P:GO:0019722; F:GO:0004683; C:GO:0005634; P:GO:0006468	-	EC:2.7.11.17	IPR000719; IPR008271; IPR011009; IPR017442; IPR020636; IPR020657; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
Aedes aegypti	brain chiti-se and chia	1	F:GO:0003824	-		IPR001223; IPR013781; IPR017853; PTHR11177 (PANTHER), PTHR11177:SF26 (PANTHER)
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis elegans	briggsae cbr-sec- protein	19	P:GO:0071711; P:GO:0040003; P:GO:0035158; P:GO:0008360; P:GO:0034394; P:GO:0009306; P:GO:0048081; P:GO:0007029; P:GO:0007030; C:GO:0070971; C:GO:0030134; P:GO:0035149; P:GO:0016203; P:GO:0022409; P:GO:0030011; P:GO:0046907; C:GO:0005811; F:GO:0005488; P:GO:0003331	-		IPR006895; IPR006896; G3DSA:3.40.50.410 (GENE3D), PTHR13803 (PANTHER), SSF53300 (SUPERFAMILY), SSF81995 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-sec- protein	19	P:GO:0071711; P:GO:0040003; P:GO:0035158; P:GO:0008360; P:GO:0034394; P:GO:0009306; P:GO:0048081; P:GO:0007029; P:GO:0007030; C:GO:0070971; C:GO:0030134; P:GO:0035149; P:GO:0016203; P:GO:0022409; P:GO:0030011; P:GO:0046907; C:GO:0005811; F:GO:0005488; P:GO:0003331	-		IPR006895; IPR006896; G3DSA:3.40.50.410 (GENE3D), PTHR13803 (PANTHER), SSF53300 (SUPERFAMILY), SSF81995 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-pssy-1 protein	1	P:GO:0040018	-		-
Caenorhabditis briggsae	briggsae cbr-tsp-17 protein	0		C:GO:0016021; C:GO:0016020		IPR018499; PTHR19282 (PANTHER), PTHR19282:SF34 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	cytochrome b5	3	C:GO:0005811; F:GO:0020037; C:GO:0005739	-		IPR001199; IPR018506; PTHR19359 (PANTHER)
Caenorhabditis briggsae	zinc finger protein	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		IPR007087
	-	0				-
Caenorhabditis elegans	frg1 protein	0		C:GO:0015030; P:GO:0006364; C:GO:0016607; P:GO:0042254; C:GO:0005634		IPR008999; IPR010414; IPR022272; G3DSA:2.80.10.50 (GENE3D)

Caenorhabditis elegans	uncoordi-ted family member (unc-43)	13	P:GO:0006952; F:GO:0005516; F:GO:0046872; C:GO:0005954; P:GO:0051932; P:GO:0000003; F:GO:0005524; P:GO:0040017; P:GO:0007067; C:GO:0005737; P:GO:0040018; F:GO:0004683; P:GO:0006468	-	EC:2.7.11.17	IPR000719; IPR008271; IPR011009; IPR015742; IPR017441; IPR017442; IPR020636; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
Brugia malayi	domon domain containing protein	2	P:GO:0006548; F:GO:0004500	-	EC:1.14.17.1	-
Caenorhabditis elegans	leishmanolysin-like (metallopeptidase m8 family)	8	C:GO:0005737; F:GO:0004222; P:GO:0007067; P:GO:0007155; P:GO:0006508; C:GO:0016020; F:GO:0008270; P:GO:0051301	-	EC:3.4.24.0	IPR001577; G3DSA:3.10.170.20 (GENE3D), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	nucleolar complex protein 3 homolog	1	C:GO:0031981	-		IPR005612
	-	0				-
Caenorhabditis briggsae	yrr5_caeel ame: full=uncharacterized protein	0				-
	-	0				-
Caenorhabditis brenneri	elegans protein confirmed by transcript evidence	1	P:GO:0016539	-		IPR001534; SignalP (SIGNALP)
Tribolium castaneum	serine-type protease inhibitor	0		F:GO:0008233		IPR013111
Drosophila willistoni	aromatic amino acid decarboxylase	1	F:GO:0004837	-	EC:4.1.1.25	IPR002129; IPR010977; IPR015421; IPR015424; G3DSA:1.20.1340.10 (GENE3D)
Loa loa	ck1 ttbk protein ki-se	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0000003; P:GO:0040011; F:GO:0008270; P:GO:0040010; P:GO:0006898; P:GO:0002119; P:GO:0040007; C:GO:0005622		IPR015880
	-	0				-
Caenorhabditis elegans	briggsae cbr-unc- protein	0				-
Xenopus laevis	tsc22 domain member 2	0		P:GO:0006355; F:GO:0003682; C:GO:0000785; P:GO:0006333; C:GO:0005634; F:GO:0003700		IPR000580; PTHR12348:SF2 (PANTHER)
Caenorhabditis elegans	innexin family protein	9	P:GO:0040035; P:GO:0009792; P:GO:0007631; P:GO:0040010; P:GO:0030421; P:GO:0040011; C:GO:0016021; P:GO:0019915; P:GO:0002009	-		IPR000990

	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		-
Culex quinquefasciatus	shc transforming protein	3	C:GO:0016020; F:GO:0005515; P:GO:0007265	-		IPR000980; PTHR10337 (PANTHER), SSF55550 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	protein gpr107	0		F:GO:0004872; C:GO:0016021; P:GO:0008150		IPR009637; PTHR21229:SF2 (PANTHER)
Branchiostoma floridae	5 -nucleotidase domain containing 2	0		F:GO:0046872; F:GO:0003674; F:GO:0016787; P:GO:0008150		IPR008380; PTHR12103:SF3 (PANTHER), SSF56784 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	target of rapamycin	18	F:GO:0016301; P:GO:0003006; F:GO:0005515; P:GO:0001558; P:GO:0048610; F:GO:0016773; P:GO:0044237; P:GO:0048468; P:GO:0050896; P:GO:0048513; P:GO:0051179; P:GO:0045927; P:GO:0008595; P:GO:0045793; P:GO:0048522; P:GO:0007276; P:GO:0035264; P:GO:0048598	-	EC:2.7.1.0	IPR011989; IPR016024; PTHR11139 (PANTHER), PTHR11139:SF9 (PANTHER), PF11865 (PFAM)
Caenorhabditis briggsae	ras and ef-hand domain containing	5	C:GO:0044444; F:GO:0000166; P:GO:0046907; P:GO:0007165; P:GO:0015031	-		IPR001806; IPR003579; IPR005225; IPR013753; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF253 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	protein phosphatase 2c	1	F:GO:0004721	-	EC:3.1.3.16	IPR000222; IPR001932; IPR014045; IPR015655; PTHR13832:SF94 (PANTHER)
Caenorhabditis elegans	briggsae cbr-ugt-58 protein	2	F:GO:0016758; P:GO:0008152	-	EC:2.4.1.0	IPR002213
Caenorhabditis briggsae	junctophilin 3-like	0				PTHR23085 (PANTHER), PTHR23085:SF3 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	solute carrier family 30 (zinc transporter) member 2	7	F:GO:0005385; P:GO:0071577; P:GO:0015674; C:GO:0016023; C:GO:0005770; P:GO:0061090; C:GO:0010008	-		IPR002524; G3DSA:1.20.1510.10 (GENE3D), SignalP (SIGNALP)
	-	0				-

Caenorhabditis briggsae	briggsae cbr-ptp-1 protein	5	F:GO:0016791; C:GO:0005886; F:GO:0005515; P:GO:0009987; C:GO:0005829	-	EC:3.1.3.0	IPR000299; IPR011993; IPR014847; IPR018980; PTHR23280 (PANTHER), SSF50729 (SUPERFAMILY)
Loa loa	d--directed r- polymerases and iii subunit rpabc1	6	P:GO:0040035; P:GO:0009792; F:GO:0003899; F:GO:0003677; P:GO:0006350; C:GO:0005634	-	EC:2.7.7.6	IPR000783; IPR005571; IPR014381; IPR020608; PTHR10535 (PANTHER)
Loa loa	ph domain containing protein	0				IPR001849; IPR011993; SSF50729 (SUPERFAMILY)
Caenorhabditis briggsae	fad dependent oxidoreductase	4	C:GO:0005737; P:GO:0006546; F:GO:0016491; F:GO:0004047	-	EC:2.1.2.10	IPR006076; G3DSA:3.50.50.60 (GENE3D), PTHR13847 (PANTHER), PTHR13847:SF16 (PANTHER), SSF51905 (SUPERFAMILY)
Loa loa	ku p80 d-	2	F:GO:0005488; C:GO:0044424	-		IPR002035; IPR005161; G3DSA:3.40.50.410 (GENE3D), SSF53300 (SUPERFAMILY)
	-	0				-
Loa loa	ubx domain-containing protein 6	1	F:GO:0005515	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	phosphatidylserine receptor	9	P:GO:0035212; P:GO:0046329; P:GO:0018395; P:GO:0090304; F:GO:0005515; P:GO:0010467; F:GO:0070815; P:GO:0043066; C:GO:0005634	-		IPR003347; IPR013129; PTHR12480 (PANTHER), SSF51197 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	ensangp00000014982 isoform 2	1	C:GO:0016020	-		PTHR21215 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	protein trs85 homolog	6	P:GO:0040010; P:GO:0018991; P:GO:0010171; P:GO:0007413; P:GO:0040017; P:GO:0040018	-		-
	-	0				-
Caenorhabditis briggsae	major facilitator superfamily protein	2	P:GO:0055085; C:GO:0016021	-		-

Brugia malayi	abnormal embryonic partitioning of cytoplasm family member (par-3)	16	P:GO:0007369; F:GO:0005515; P:GO:0007163; P:GO:0007155; C:GO:0043296; C:GO:0005913; P:GO:0045165; P:GO:0051301; C:GO:0016021; P:GO:0008406; C:GO:0005737; P:GO:0008105; P:GO:0040001; P:GO:0030707; N:GO:0071844; P:GO:0009994	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR16484 (PANTHER), PTHR16484:SF2 (PANTHER)
Caenorhabditis briggsae	zinc carboxypeptidase family protein	4	F:GO:0004181; F:GO:0005515; P:GO:0006508; F:GO:0008270	-	EC:3.4.17.0	IPR000834; IPR008969; IPR014766; G3DSA:3.40.630.10 (GENE3D), PTHR11532 (PANTHER), PTHR11532:SF5 (PANTHER), SignalP (SIGNALP), SSF53187 (SUPERFAMILY)
Caenorhabditis briggsae	zinc carboxypeptidase family protein	4	F:GO:0004181; F:GO:0005515; P:GO:0006508; F:GO:0008270	-	EC:3.4.17.0	IPR000834; IPR008969; IPR014766; G3DSA:3.40.630.10 (GENE3D), PTHR11532 (PANTHER), PTHR11532:SF5 (PANTHER), SignalP (SIGNALP), SSF53187 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-dao-5 protein	3	C:GO:0044428; P:GO:0009987; F:GO:0005488	-		IPR007718
Caenorhabditis briggsae	briggsae cbr-dao-5 protein	3	P:GO:0009987; F:GO:0005488; C:GO:0005654	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	acylamino-acid-releasing enzyme	1	F:GO:0008236	-		-
	-	0				-
Caenorhabditis briggsae	pseudouridylate synthase	2	P:GO:0009451; F:GO:0016853	-		IPR001406; IPR020094; IPR020097; IPR020103
Caenorhabditis elegans	choline ethanolaminephosphotransferase 1	3	C:GO:0005789; P:GO:0008654; F:GO:0016780	-	EC:2.7.8.0	SignalP (SIGNALP)
Ailuropoda melanoleuca	r--binding protein 42	4	C:GO:0005634; C:GO:0005737; F:GO:0000166; F:GO:0003723	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	eating: abnormal pharyngeal pumping family member (eat-18)	0				-
Caenorhabditis briggsae	protein ki-se domain containing protein	6	P:GO:0002119; F:GO:0005515; F:GO:0004672; P:GO:0040011; P:GO:0040007; F:GO:0000166	-		IPR000719; IPR005479; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)

Caenorhabditis briggsae	u4 u6 small nuclear	4	C:GO:0030532; C:GO:0071011; P:GO:0006898; P:GO:0000398	-		IPR013881; PTHR14212 (PANTHER)
	-	0				-
Caenorhabditis elegans	mboat family protein	2	C:GO:0016020; P:GO:0010171	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	smc2	0		F:GO:0045502; P:GO:0048477; C:GO:0005694; C:GO:0005828; P:GO:0051276; P:GO:0007018; P:GO:0001709; C:GO:0031616; P:GO:0051726; C:GO:0000785; P:GO:0007076; C:GO:0016021; P:GO:0000819; C:GO:0031224; P:GO:0000070; P:GO:0007422; F:GO:0005525; P:GO:0051299; F:GO:0005524; C:GO:0000776; P:GO:0007067; F:GO:0000166; P:GO:0016330; P:GO:0006886; P:GO:0042127; P:GO:0001754; P:GO:0001751;		PTHR18937 (PANTHER), PTHR18937:SF13 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	cullin family member (cul-2)	2	P:GO:0030163; F:GO:0005515	-		IPR001373; IPR016159; G3DSA:1.20.1310.10 (GENE3D), PTHR11932 (PANTHER), PTHR11932:SF10 (PANTHER)
Caenorhabditis elegans	aldo keto reductase	1	F:GO:0016616	-	EC:1.1.1.0	IPR001395; IPR018170; IPR020471; IPR023210; PTHR11732:SF34 (PANTHER)
Caenorhabditis elegans	connector enhancer of ksr family member (cnk-1)	1	P:GO:0040026	-		IPR001849; IPR011993; SSF50729 (SUPERFAMILY)
Loa loa	variable abnormal morphology family member (vab-10)	0		F:GO:0005509; P:GO:0007050; F:GO:0003779		IPR001101; G3DSA:3.90.1290.10 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF49 (PANTHER), SSF75399 (SUPERFAMILY)
	-	0				-
	-	0				IPR008962
Schizosaccharomyces japonicus yFS275	chromodomain protein	4	P:GO:0006333; C:GO:0000785; C:GO:0005634; F:GO:0003682	-		IPR000953; IPR016197; IPR017984; G3DSA:2.40.50.40 (GENE3D), PTHR22812 (PANTHER)

Caenorhabditis elegans	acetoacetyl- synthetase	6	P:GO:0009987; P:GO:0006629; F:GO:0016878; C:GO:0005737; P:GO:0032502; P:GO:0010033	-	EC:6.2.1.0	IPR000873; G3DSA:3.40.50.980 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF40 (PANTHER), SSF56801 (SUPERFAMILY)
Caenorhabditis briggsae	d-3-phosphoglycerate dehydroge-se	9	P:GO:0040010; P:GO:0006098; P:GO:0055114; F:GO:0004617; F:GO:0004455; F:GO:0051287; F:GO:0005515; P:GO:0009792; P:GO:0006564	-	EC:1.1.1.95; EC:1.1.1.86	IPR015508; IPR016040; PTHR10996 (PANTHER)
Caenorhabditis elegans	neurotransmitter-gated ion-channel ligand binding domain containing protein	5	C:GO:0016021; C:GO:0030054; C:GO:0045211; F:GO:0005230; P:GO:0006811	-		IPR006201; IPR006202; PTHR18945:SF12 (PANTHER)
Pan troglodytes	ribosomal protein s20	5	F:GO:0003735; F:GO:0003723; F:GO:0005515; C:GO:0022627; P:GO:0006414	-		-
Pongo abelii	chondroitin sulfate glucuronyltransferase	3	C:GO:0032580; F:GO:0050510; C:GO:0016021	-	EC:2.4.1.226	IPR008428
Caenorhabditis elegans	low-density lipoprotein receptor-related protein 2	5	F:GO:0005509; C:GO:0016021; F:GO:0004872; P:GO:0008152; P:GO:0006898	-		IPR000152; IPR001881; IPR006210; IPR013091; IPR018097; G3DSA:2.10.25.10 (GENE3D), PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER), SSF57196 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	wh1 domain containing protein	11	P:GO:0065008; P:GO:0007015; P:GO:0007391; F:GO:0005515; P:GO:0007409; P:GO:0051128; P:GO:0006928; P:GO:0046907; P:GO:0050794; P:GO:0048477; C:GO:0044464	-		IPR000697; IPR011993; IPR014885; PTHR11202 (PANTHER), PTHR11202:SF1 (PANTHER), SSF50729 (SUPERFAMILY)
Caenorhabditis elegans	sh2 domain containing protein	2	P:GO:0009987; P:GO:0032501	-		IPR000980; IPR001452; G3DSA:2.30.30.40 (GENE3D), SSF55550 (SUPERFAMILY)
Brugia malayi	btb poz domain-containing protein 9	0		F:GO:0003674; P:GO:0007155; P:GO:0008150; F:GO:0005515; C:GO:0005575		IPR000210; IPR011333; IPR011705; IPR013069; IPR013089; PTHR23230:SF181 (PANTHER)

Caenorhabditis briggsae	eb module family protein	0		F:GO:0008061; P:GO:0006030; P:GO:0005975; F:GO:0016810; F:GO:0003824; C:GO:0005576		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	protein phosphatase 2c containing protein	7	P:GO:0006470; C:GO:0005739; F:GO:0046872; C:GO:0008287; F:GO:0004741; P:GO:0010510; F:GO:0004724	-	EC:3.1.3.43	IPR000222; IPR001932; IPR015655; PTHR13832:SF98 (PANTHER)
Brugia malayi	arid bright d- binding domain containing protein	2	F:GO:0003676; C:GO:0043229	-		IPR001606; PTHR13964 (PANTHER)
Loa loa	arid bright d- binding domain containing protein	2	C:GO:0043229; F:GO:0003677	-		IPR001606; PTHR13964 (PANTHER), PTHR13964:SF2 (PANTHER)
Caenorhabditis briggsae	wnt inhibitory factor 1	0		C:GO:0016021; C:GO:0016020; P:GO:0007275; F:GO:0004713; C:GO:0005576; P:GO:0040010; P:GO:0016055; F:GO:0005509; F:GO:0005488		IPR000742; IPR006210; IPR013032; G3DSA:2.10.25.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF167 (PANTHER), SSF57196 (SUPERFAMILY)
Caenorhabditis briggsae	zinc carboxypeptidase family protein	1	F:GO:0004180	-		-
Monodelphis domestica	scy1-like 3 (cerevisiae)	2	F:GO:0005488; C:GO:0044464	-		IPR011989; PTHR12984 (PANTHER), PTHR12984:SF4 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-ppfr-2 protein	0				-
Loa loa	hypothetical protein LOAG_04772 [Loa loa]	0				-
	-	0				-
Caenorhabditis briggsae	multidrug resistance protein family member (mrp-5)	8	P:GO:0002119; F:GO:0016887; P:GO:0040002; P:GO:0040017; P:GO:0006810; P:GO:0040010; C:GO:0044464; F:GO:0000166	-		PTHR19242 (PANTHER), PTHR19242:SF14 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	transferase mitochondrial	2	P:GO:0006783; F:GO:0016740	-		-

Loa loa	briggsae cbr-rib-1 protein	12	C:GO:0031224; F:GO:0015020; P:GO:0016055; P:GO:0008354; P:GO:0015014; P:GO:0008589; P:GO:0008101; F:GO:0005515; P:GO:0030210; C:GO:0005794; C:GO:0005783; F:GO:0008375	-	EC:2.4.1.17	IPR004263; PTHR11062 (PANTHER), PTHR11062:SF7 (PANTHER)
Caenorhabditis elegans	excretory ca-l abnormal family member (exc-5)	1	F:GO:0046872	-		-
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
Caenorhabditis elegans	moesin ezrin radixin	17	C:GO:0035003; C:GO:0005884; P:GO:0007318; P:GO:0042048; P:GO:0045197; P:GO:0016336; F:GO:0003779; C:GO:0005819; P:GO:0032956; C:GO:0045169; P:GO:0016057; C:GO:0019898; P:GO:0007368; C:GO:0005912; P:GO:0045313; C:GO:0005634; C:GO:0005938	-		IPR000299; IPR000798; IPR008954; IPR011174; IPR011259; IPR011993; IPR014352; IPR018979; IPR018980; IPR019747; IPR019748; IPR019749; IPR019750; G3DSA:1.20.5.450 (GENE3D), G3DSA:3.10.20.90 (GENE3D), PTHR23281 (PANTHER), PTHR23281:SF3 (PANTHER), SSF50729 (SUPERFAMILY), SSF54236 (SUPERFAMILY)
Caenorhabditis elegans	glutathione s-transferase	0		F:GO:0016740; P:GO:0008150; C:GO:0005575		IPR004045; IPR010987; IPR012335; IPR012336; IPR017933; PTHR11571 (PANTHER), PTHR11571:SF11 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-rhy-1 protein	0		F:GO:0008415; F:GO:0016740; C:GO:0016021; P:GO:0040011; P:GO:0040035; F:GO:0016747; P:GO:0018991		-
Caenorhabditis briggsae	histidine acid phosphatase family protein	4	P:GO:0009987; C:GO:0043231; C:GO:0044446; C:GO:0044444	-		IPR000560; G3DSA:3.40.50.1240 (GENE3D), PTHR11567 (PANTHER), PTHR11567:SF18 (PANTHER), SSF53254 (SUPERFAMILY)
Caenorhabditis briggsae	histidine acid phosphatase family protein	4	C:GO:0043231; C:GO:0044444; P:GO:0008152; C:GO:0044446	-		IPR000560; G3DSA:3.40.50.1240 (GENE3D), PTHR11567 (PANTHER), PTHR11567:SF18 (PANTHER), SSF53254 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	protein tyrosine phosphatase family member (ptp-1)	5	F:GO:0004726; C:GO:0005856; F:GO:0008092; P:GO:0006470; C:GO:0016020	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR17130 (PANTHER)
Brugia malayi	hypothetical protein Bm1_04745 [Brugia malayi]	0				-
Loa loa	hypothetical protein LOAG_11910 [Loa loa]	0				-
	-	0				IPR001496; PTHR10385 (PANTHER), PTHR10385:SF17 (PANTHER)
Caenorhabditis sp. PS1010	uncoordi-ted family member (unc-73)	5	P:GO:0006915; P:GO:0023033; F:GO:0005085; P:GO:0050794; C:GO:0005737	-		IPR002017; IPR018159; G3DSA:1.20.58.60 (GENE3D), PTHR22826 (PANTHER), PTHR22826:SF47 (PANTHER), SSF46966 (SUPERFAMILY)
Macaca fascicularis	s-phase ki-se-associated protein 1-like	7	C:GO:0005829; P:GO:0051437; C:GO:0019005; F:GO:0004842; F:GO:0005515; P:GO:0031146; C:GO:0005654	-	EC:6.3.2.19	IPR001232; IPR011333; IPR016072; IPR016073; PTHR11165:SF21 (PANTHER)
Caenorhabditis elegans	lethal family member (let-805)	8	P:GO:0018996; P:GO:0009792; P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		SignalP (SIGNALP)
	-	0				-
Loa loa	novel protein containing six wd40 domains at c-terminus	6	C:GO:0030425; C:GO:0031931; P:GO:0001938; F:GO:0019901; C:GO:0043025; P:GO:0042325	-		IPR004083; IPR016024; PTHR12848:SF6 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG22082 [Caenorhabditis briggsae]	0		C:GO:0016021; P:GO:0007186		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	vacuolar protein sorting protein 18	0		F:GO:0008270; F:GO:0005515		PTHR23323 (PANTHER)
	-	0				-
	-	0				-
Ancylostoma ceylanicum	venom-allergen-like protein family member (vap-1)	1	P:GO:0040011	-		IPR001283; IPR014044
Caenorhabditis elegans	translocated promoter region	8	P:GO:0000003; C:GO:0016020; P:GO:0040015; P:GO:0040011; P:GO:0023060; P:GO:0002119; P:GO:0050794; C:GO:0044446	-		PD936484 (PRODOM)
	-	0				-
	-	0				-
Loa loa	retinoblastoma-associated protein rap140	0				IPR022188

Caenorhabditis elegans	prostaglandin e synthase 2	7	C:GO:0005829; C:GO:0005739; P:GO:0046903; P:GO:0045449; F:GO:0003677; F:GO:0003824; C:GO:0005634	-		IPR002109; IPR011767; IPR012335; IPR012336; PTHR12782 (PANTHER)
Caenorhabditis briggsae	pctaire protein ki-se 1	4	P:GO:0006468; F:GO:0005515; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF103 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-drr-1 protein	3	F:GO:0005515; C:GO:0016020; P:GO:0008340	-		SignalP (SIGNALP)
Caenorhabditis elegans	regulator of g protein sig-ling family member (rgs-5)	0		F:GO:0016301; F:GO:0004871		-
	-	0				-
Caenorhabditis elegans	saccharopine dehydroge-se	3	C:GO:0016021; P:GO:0008152; F:GO:0005488	-		IPR005097; PTHR12286 (PANTHER)
Pongo abelii	type alpha 1 (ehlers-danlos syndrome type autosomal domi-nt) isoform cra_b	22	P:GO:0009314; P:GO:0018149; P:GO:0030168; P:GO:0048565; P:GO:0043206; C:GO:0005586; P:GO:0007229; P:GO:0050777; P:GO:0007507; P:GO:0007160; C:GO:0005615; F:GO:0046332; P:GO:0001501; F:GO:0048407; P:GO:0043588; P:GO:0030199; F:GO:0005178; P:GO:0007179; P:GO:0034097; P:GO:0032964; F:GO:0005201; P:GO:0001568	-		SignalP (SIGNALP)
Caenorhabditis elegans	mixed lineage ki-se 4	1	F:GO:0016740	-		IPR000719; IPR001245; IPR001452; IPR008271; IPR011009; IPR017441; G3DSA:1.10.510.10 (GENE3D), G3DSA:2.30.30.40 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR23257 (PANTHER), PTHR23257:SF49 (PANTHER)
Caenorhabditis elegans	mixed lineage ki-se 4	1	F:GO:0016740	-		IPR000719; IPR001245; IPR001452; IPR008271; IPR011009; IPR017441; G3DSA:1.10.510.10 (GENE3D), G3DSA:2.30.30.40 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR23257 (PANTHER), PTHR23257:SF49 (PANTHER)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-

	-	0				PF10961 (PFAM), SignalP (SIGNALP)
	-	0				-
Brugia malayi	af4 fmr2 family member 1-like	0		P:GO:0007366; F:GO:0003700; F:GO:0003677; C:GO:0005634; P:GO:0045893; P:GO:0051493; P:GO:0007275; F:GO:0016563; P:GO:0042051; P:GO:0006350; P:GO:0008361; P:GO:0032368; P:GO:0045449		IPR007797; PTHR10528:SF2 (PANTHER)
Brugia malayi	af4 fmr2 family member 1-like	0		P:GO:0007366; F:GO:0003700; F:GO:0003677; C:GO:0005634; P:GO:0045893; P:GO:0051493; P:GO:0007275; F:GO:0016563; P:GO:0042051; P:GO:0006350; P:GO:0008361; P:GO:0032368; P:GO:0045449		IPR007797; PTHR10528:SF2 (PANTHER)
Brugia malayi	af4 fmr2 family member 1-like	0		P:GO:0007366; F:GO:0003700; F:GO:0003677; C:GO:0005634; P:GO:0045893; P:GO:0051493; P:GO:0007275; F:GO:0016563; P:GO:0042051; P:GO:0006350; P:GO:0008361; P:GO:0032368; P:GO:0045449		IPR007797; PTHR10528:SF2 (PANTHER)
	-	0				-
	-	0				-
Brugia malayi	snf2 family n-termi-l domain containing protein	0		F:GO:0003676; F:GO:0004386; F:GO:0005524; F:GO:0003677		-
Caenorhabditis briggsae	cytoplasmic intermediate filament protein	11	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0018991; P:GO:0018996; F:GO:0005515; C:GO:0005882; P:GO:0040010; P:GO:0040011; P:GO:0006898; F:GO:0005198	-		IPR001664; IPR016044; PTHR23239:SF13 (PANTHER)

	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-ain-1 protein	0				IPR001202
Caenorhabditis briggsae	briggsae cbr-ain-1 protein	0				IPR001202
Caenorhabditis briggsae	small zinc finger-like protein	8	C:GO:0005743; F:GO:0046872; P:GO:0045039; P:GO:0040035; C:GO:0042719; P:GO:0040011; P:GO:0009792; P:GO:0040018	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	regulator of telomere elongation helicase 1	7	P:GO:0006915; F:GO:0004003; P:GO:0000723; F:GO:0005524; F:GO:0005515; P:GO:0010569; C:GO:0005634	-		IPR006554; IPR010614; IPR014013; G3DSA:3.40.50.300 (GENE3D), PTHR11472 (PANTHER), PTHR11472:SF4 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Schistosoma mansoni	tyrosine ki-se	0		P:GO:0006468; P:GO:0040027; F:GO:0005524; F:GO:0016301; F:GO:0042169; P:GO:0018108; F:GO:0004674; P:GO:0009792; F:GO:0004672; P:GO:0042059; F:GO:0000166; C:GO:0005737; F:GO:0000287; F:GO:0004715; F:GO:0005515; F:GO:0004713; F:GO:0016740; C:GO:0005886		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	solute carrier family 39 (zinc transporter) member 14	5	F:GO:0015082; F:GO:0046915; P:GO:0055085; C:GO:0016021; P:GO:0000041	-		IPR003689; PTHR12191 (PANTHER)
Caenorhabditis elegans	solute carrier family 39 (zinc transporter) member 14	5	F:GO:0015082; F:GO:0046915; P:GO:0055085; C:GO:0016021; P:GO:0000041	-		IPR003689; PTHR12191 (PANTHER)
Caenorhabditis elegans	solute carrier family 39 (zinc transporter) member 14	5	F:GO:0015082; F:GO:0046915; P:GO:0055085; C:GO:0016021; P:GO:0000041	-		IPR003689; PTHR12191 (PANTHER)

	-	0				-
Dictyocaulus viviparus	major sperm protein	5	P:GO:0019915; C:GO:0005856; C:GO:0005737; F:GO:0005198; C:GO:0031143	-		IPR000535; IPR008962; PTHR22920 (PANTHER)
Nippostrongylus brasiliensis	major sperm protein	5	P:GO:0019915; C:GO:0005856; C:GO:0005737; F:GO:0005198; C:GO:0031143	-		IPR000535; IPR008962; PTHR22920 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	protein	1	C:GO:0005576	-		IPR001283; IPR014044; PTHR10334:SF8 (PANTHER)
Caenorhabditis briggsae	myoblast city	10	P:GO:0048869; P:GO:0043652; F:GO:0005083; P:GO:0007517; F:GO:0032403; F:GO:0019899; P:GO:0040039; P:GO:0009653; C:GO:0005886; F:GO:0017124	-		IPR010703; PTHR23317 (PANTHER), PTHR23317:SF16 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	tyrosyl-tr- synthetase	3	P:GO:0009792; P:GO:0000003; P:GO:0006412	-	EC:3.6.5.3	IPR002305; IPR014729
Brugia malayi	coiled-coil domain containing 88a	0		C:GO:0005737; P:GO:0000226; F:GO:0008017		PD936484 (PRODOM), PTHR18947 (PANTHER)
Saccoglossus kowalevskii	uroca-te hydratase	2	P:GO:0006548; F:GO:0016153	-	EC:4.2.1.49	IPR000193
Brugia malayi	cullin family protein	3	P:GO:0051533; P:GO:0006511; C:GO:0000151	-		IPR001373; IPR016159; G3DSA:1.20.1310.10 (GENE3D), PTHR11932 (PANTHER), PTHR11932:SF8 (PANTHER)
Ailuropoda melanoleuca	lamin a c	13	C:GO:0005626; C:GO:0016363; P:GO:0006998; P:GO:0035105; C:GO:0005638; P:GO:0007517; P:GO:0007283; N:GO:0090343; P:GO:0055015; F:GO:0005515; C:GO:0048471; C:GO:0005635; F:GO:0005198	-		IPR001322; IPR001664; G3DSA:2.60.40.1260 (GENE3D), PTHR23239:SF12 (PANTHER), SSF74853 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Ciona intestinalis	atp-dependent r- helicase ded1	1	F:GO:0005488	-		IPR011545; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), SSF52540 (SUPERFAMILY)

Caenorhabditis elegans	pyridine nucleotide-disulphide oxidoreductase family protein	5	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040010; P:GO:0000003	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	protein fam91a1-like	6	P:GO:0018991; F:GO:0003676; C:GO:0005622; F:GO:0008270; F:GO:0005515; P:GO:0040011	-		-
	-	0				-
	-	0				IPR000010; SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	brain protein	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	C:GO:0016020	-		IPR008253; PTHR22776 (PANTHER)
Brugia malayi	ubiquitin ribosomal protein cep52 fusion	4	C:GO:0005840; F:GO:0003735; C:GO:0005634; P:GO:0006412	-	EC:3.6.5.3	-
Apis mellifera	lysine-specific histone demethylase 1a	3	P:GO:0044238; P:GO:0044260; F:GO:0016491	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	hla-b associated transcript 1	23	F:GO:0015184; P:GO:0015804; C:GO:0016607; P:GO:0006461; F:GO:0043008; P:GO:0000245; C:GO:0005681; P:GO:0046784; F:GO:0042802; P:GO:0006520; F:GO:0017070; F:GO:0015175; C:GO:0005688; P:GO:0055085; C:GO:0000346; F:GO:0042605; C:GO:0005687; P:GO:0006200; C:GO:0005887; F:GO:0004004; F:GO:0005524; P:GO:0010501; F:GO:0030621	-		SignalP (SIGNALP)

Caenorhabditis elegans	hla-b associated transcript 1	23	F:GO:0015184; P:GO:0015804; C:GO:0016607; P:GO:0006461; F:GO:0043008; P:GO:0000245; C:GO:0005681; P:GO:0046784; F:GO:0042802; P:GO:0006520; F:GO:0017070; F:GO:0015175; C:GO:0005688; P:GO:0055085; C:GO:0000346; F:GO:0042605; C:GO:0005687; P:GO:0006200; C:GO:0005887; F:GO:0004004; F:GO:0005524; P:GO:0010501; F:GO:0030621	-		SignalP (SIGNALP)
Caenorhabditis elegans	hla-b associated transcript 1	23	F:GO:0015184; P:GO:0015804; C:GO:0016607; P:GO:0006461; F:GO:0043008; P:GO:0000245; C:GO:0005681; P:GO:0046784; F:GO:0042802; P:GO:0006520; F:GO:0017070; F:GO:0015175; C:GO:0005688; P:GO:0055085; C:GO:0000346; F:GO:0042605; C:GO:0005687; P:GO:0006200; C:GO:0005887; F:GO:0004004; F:GO:0005524; P:GO:0010501; F:GO:0030621	-		SignalP (SIGNALP)

Caenorhabditis elegans	hla-b associated transcript 1	23	F:GO:0015184; P:GO:0015804; C:GO:0016607; P:GO:0006461; F:GO:0043008; P:GO:0000245; C:GO:0005681; P:GO:0046784; F:GO:0042802; P:GO:0006520; F:GO:0017070; F:GO:0015175; C:GO:0005688; P:GO:0055085; C:GO:0000346; F:GO:0042605; C:GO:0005687; P:GO:0006200; C:GO:0005887; F:GO:0004004; F:GO:0005524; P:GO:0010501; F:GO:0030621	-		SignalP (SIGNALP)
Homo sapiens	otu domain-containing protein 4-like isoform 1	0		F:GO:0030246; F:GO:0016758; F:GO:0003674; P:GO:0005975; P:GO:0030259; C:GO:0005575; F:GO:0005515; C:GO:0005783; F:GO:0004577; P:GO:0008150		-
Homo sapiens	otu domain-containing protein 4-like isoform 1	0		F:GO:0030246; F:GO:0016758; F:GO:0003674; P:GO:0005975; P:GO:0030259; C:GO:0005575; F:GO:0005515; C:GO:0005783; F:GO:0004577; P:GO:0008150		-
	-	0				-
Caenorhabditis elegans	ryanodine receptor	7	P:GO:0006629; F:GO:0005219; P:GO:0006816; P:GO:0006874; P:GO:0055085; F:GO:0005509; C:GO:0016021	-		-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG09631 [Caenorhabditis briggsae]	3	C:GO:0005576; P:GO:0006954; F:GO:0005125	-		IPR010345; G3DSA:2.10.90.10 (GENE3D), SSF57501 (SUPERFAMILY)
Brugia malayi	small subunit processome component 20 homolog	3	C:GO:0005730; P:GO:0006364; F:GO:0005515	-		-

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; C:GO:0016020; F:GO:0008375		-
Loa loa	coenzyme q3 methyltransferase (cerevisiae)	6	P:GO:0006071; P:GO:0002119; P:GO:0006744; P:GO:0008340; F:GO:0008168; C:GO:0005739	-	EC:2.1.1.0	G3DSA:3.40.50.150 (GENE3D), PTHR23134 (PANTHER), SignalP (SIGNALP)
Loa loa	coenzyme q3 methyltransferase (cerevisiae)	6	P:GO:0006071; P:GO:0002119; P:GO:0006744; P:GO:0008340; F:GO:0008168; C:GO:0005739	-	EC:2.1.1.0	-
Caenorhabditis elegans	ribonuclease h2 subunit b	0		F:GO:0003674; P:GO:0008150; C:GO:0005634		IPR019024; PTHR13383 (PANTHER), PTHR13383:SF1 (PANTHER)
Caenorhabditis elegans	phosducin-like protein	1	F:GO:0005515	-		IPR001200; IPR012335; IPR012336; PTHR21148 (PANTHER), PTHR21148:SF12 (PANTHER), PF02114 (PFAM)
	-	0				-
Caenorhabditis elegans	proliferating cell nuclear antigen	9	P:GO:0042276; C:GO:0005730; P:GO:0051726; F:GO:0030337; F:GO:0003677; F:GO:0005515; C:GO:0043626; P:GO:0006275; C:GO:0005737	-		IPR000730; IPR022648; IPR022649; IPR022659; G3DSA:3.70.10.10 (GENE3D), SSF55979 (SUPERFAMILY)
Caenorhabditis elegans	proliferating cell nuclear antigen	9	P:GO:0042276; C:GO:0005730; P:GO:0051726; F:GO:0030337; F:GO:0003677; F:GO:0005515; C:GO:0043626; P:GO:0006275; C:GO:0005737	-		IPR000730; IPR022648; IPR022649; IPR022659; G3DSA:3.70.10.10 (GENE3D), SSF55979 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-pqn-20 protein	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	uncoordi-ted protein isoform partially confirmed by transcript evidence	8	F:GO:0004872; P:GO:0006629; F:GO:0005219; P:GO:0006816; P:GO:0006874; P:GO:0055085; F:GO:0005509; C:GO:0016021	-		IPR000699; IPR015925; PTHR13715:SF11 (PANTHER)
Caenorhabditis elegans	hypothetical protein Y54E10A.11 [Caenorhabditis elegans]	0		F:GO:0008270		-

Caenorhabditis elegans	structure-specific endonuclease subunit slx1	8	P:GO:0009792; P:GO:0006259; P:GO:0002119; F:GO:0046872; C:GO:0005622; F:GO:0004518; P:GO:0040007; P:GO:0006974	-		IPR000305; PTHR20208 (PANTHER), PTHR20208:SF6 (PANTHER)
Caenorhabditis elegans	structure-specific endonuclease subunit slx1	8	P:GO:0009792; P:GO:0002119; F:GO:0046872; F:GO:0004519; P:GO:0040007; C:GO:0005634; P:GO:0006310; P:GO:0006281	-		PTHR20208 (PANTHER), PTHR20208:SF6 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Brugia malayi	ubx domain containing protein	0				-
Caenorhabditis elegans	transmembrane protein 165	1	C:GO:0016021	-		IPR001727; SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	isoform a	0		F:GO:0016788; P:GO:0006886; C:GO:0031227		IPR007751; G3DSA:3.40.50.1820 (GENE3D), PTHR12482 (PANTHER), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	enoyl- hydratase isomerase domain-containing protein	2	F:GO:0016853; P:GO:0008152	-		IPR001753; IPR018376; G3DSA:3.90.226.10 (GENE3D), PTHR11941 (PANTHER), SSF52096 (SUPERFAMILY)
Caenorhabditis elegans	general vesicular transport factor p115	8	C:GO:0000139; P:GO:0048280; F:GO:0042802; P:GO:0032940; P:GO:0019915; P:GO:0040039; P:GO:0006898; P:GO:0006886	-		IPR006953; PTHR10013 (PANTHER)
Caenorhabditis elegans	briggsae cbr-hum-1 protein	4	C:GO:0016459; F:GO:0005524; F:GO:0003774; P:GO:0006508	-		SignalP (SIGNALP)
Brugia malayi	protein ki-se domain containing protein	0		P:GO:0007219; F:GO:0016301; F:GO:0004672; F:GO:0005524; P:GO:0006468; P:GO:0001745; F:GO:0031072; F:GO:0004674		IPR011009; G3DSA:1.10.510.10 (GENE3D), PTHR23172 (PANTHER), PTHR23172:SF21 (PANTHER)
	-	0				-
	-	0				-

Caenorhabditis elegans	lethal family member (let-805)	8	P:GO:0008340; P:GO:0000003; P:GO:0018996; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0006898; P:GO:0009792	-		IPR003961; IPR008957; IPR013783; PTHR10489 (PANTHER), PTHR10489:SF40 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-tag-63 protein	0				-
	-	0				-
	-	0				IPR022398
Caenorhabditis briggsae	dimethylglycine dehydroge-se	7	P:GO:0055085; F:GO:0004047; F:GO:0005488; C:GO:0005739; P:GO:0006546; F:GO:0016491; C:GO:0016020	-	EC:2.1.2.10	IPR006076; IPR006222; IPR013977; G3DSA:3.50.50.60 (GENE3D), PTHR13847 (PANTHER), PTHR13847:SF15 (PANTHER), SSF101790 (SUPERFAMILY), SSF103025 (SUPERFAMILY), SSF54373 (SUPERFAMILY)
Pongo abelii	serine-rich repeat-containing protein	0		F:GO:0003674; C:GO:0005618; F:GO:0005509; C:GO:0009986; C:GO:0016020; C:GO:0005575		-
	-	0				-
Caenorhabditis briggsae	lagen with endostatin domain family member (cle-1)	3	C:GO:0005604; C:GO:0030054; P:GO:0040035	-		IPR010515; PTHR10499 (PANTHER), PTHR10499:SF51 (PANTHER)
Brugia malayi	hypothetical protein Bm1_35105 [Brugia malayi]	0				IPR008606
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; P:GO:0055085; F:GO:0005215; P:GO:0006810		IPR005828; SignalP (SIGNALP)
Paenibacillus sp. JDR-2	collagen triple helix repeat protein	0				SignalP (SIGNALP)
Paenibacillus sp. JDR-2	collagen triple helix repeat protein	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Brugia malayi	briggsae cbr-kup-1 protein	0		F:GO:0000166		-
Caenorhabditis elegans	ube2q1 protein	6	F:GO:0005515; P:GO:0016567; F:GO:0005524; F:GO:0004842; F:GO:0016740; P:GO:0051246	-	EC:6.3.2.19	IPR000608; IPR016135; PTHR11621 (PANTHER), PTHR11621:SF6 (PANTHER)
Brugia malayi	domon domain containing protein	0		F:GO:0030246; F:GO:0004500; C:GO:0016021; F:GO:0003824; P:GO:0006548; P:GO:0016052		-
	-	0				-
Saccoglossus kowalevskii	PREDICTED: selectin, platelet-like [Saccoglossus kowalevskii]	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
	-	0				-

Caenorhabditis briggsae	coronin family member (cor-1)	1	P:GO:0000003	-		IPR001680; IPR011046; IPR015048; IPR015505; IPR015943; IPR017986; IPR019781; IPR019782
	-	0				-
Micromonas sp. RCC299	spindle pole body component alp6	0		C:GO:0000922; P:GO:0000226; C:GO:0005815		IPR007259
Strongylocentrotus purpuratus	high-mobility group 20a	0		C:GO:0005694; F:GO:0003700; F:GO:0003677; C:GO:0005634; P:GO:0016568; P:GO:0006355; C:GO:0005730; P:GO:0006325; F:GO:0005515; P:GO:0007049		-
Tribolium castaneum	xanthine dehydroge-se	2	F:GO:0003824; F:GO:0005488	-		IPR008274; PTHR11908 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0007165; C:GO:0005622		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	him-three paralog family member (htp-1)	0		F:GO:0046872; F:GO:0008270; F:GO:0005515; P:GO:0007067		IPR003511; PTHR21518 (PANTHER), SignalP (SIGNALP)
Danio rerio	wu:fo94f09 protein	0		F:GO:0003700; C:GO:0005634; F:GO:0003677; F:GO:0003676; F:GO:0008270; P:GO:0006355; C:GO:0005622; P:GO:0016032; F:GO:0046872		IPR001202; IPR007087; IPR015880; SSF57667 (SUPERFAMILY)
Caenorhabditis briggsae	neogenin homolog 1	2	P:GO:0016358; C:GO:0005887	-		IPR003961; IPR008957; IPR013783; PTHR10489 (PANTHER), PTHR10489:SF55 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0032501; P:GO:0006810; P:GO:0009987	-		IPR012501; PTHR12965 (PANTHER)
Brugia malayi	60s ribosomal protein l44	4	P:GO:0002119; P:GO:0018996; P:GO:0000003; P:GO:0040007	-		IPR000253; IPR008984
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0016301; F:GO:0005524; F:GO:0004672; F:GO:0000166; P:GO:0006468; F:GO:0004674		-
Caenorhabditis elegans	hypothetical protein F11A3.2 [Caenorhabditis elegans]	0		P:GO:0044237		-

Caenorhabditis elegans	delta chain (clathrin associated complex) family member (apd-3)	10	P:GO:0009792; P:GO:0010171; P:GO:0002119; F:GO:0005488; C:GO:0005794; C:GO:0030117; F:GO:0008565; P:GO:0016192; P:GO:0006886; P:GO:0040007	-		IPR002553; IPR011989; IPR016024; PTHR22781 (PANTHER), PTHR22781:SF9 (PANTHER)
Caenorhabditis briggsae	tar (hiv-1) r- binding protein 1	2	P:GO:0009987; F:GO:0016740	-		-
Caenorhabditis briggsae	briggsae cbr-dpy-22 protein	8	P:GO:0040010; P:GO:0018991; P:GO:0040035; P:GO:0010171; P:GO:0040026; P:GO:0040011; P:GO:0009792; P:GO:0040018	-		SignalP (SIGNALP)
Caenorhabditis briggsae	r- binding motif protein 8a	16	C:GO:0035145; P:GO:0040022; P:GO:0040010; F:GO:0003729; C:GO:0005730; P:GO:0016071; P:GO:0040035; P:GO:0008380; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0006898; P:GO:0002009; P:GO:0009792; P:GO:0001703; C:GO:0005737	-		IPR000504; IPR008111; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF50 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	polybromodomain protein	11	P:GO:0007306; P:GO:0040010; F:GO:0005488; C:GO:0005622; P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0007305; P:GO:0040011; P:GO:0002009; P:GO:0009792	-		IPR001487; PTHR16062 (PANTHER), PTHR16062:SF2 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0008276; C:GO:0005737; P:GO:0006479		-
Caenorhabditis briggsae	fyve zinc finger family protein	0		F:GO:0046872; F:GO:0008270		IPR000306; IPR011011; IPR013083; IPR017455; PTHR22835 (PANTHER), PTHR22835:SF12 (PANTHER)
	-	0				-

Caenorhabditis briggsae	tubulin gamma-1 chain	12	P:GO:0010457; F:GO:0051011; P:GO:0051726; C:GO:0005874; P:GO:0051306; C:GO:0008275; P:GO:0007052; P:GO:0051258; C:GO:0008274; F:GO:0003924; P:GO:0007020; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	activating sig-l cointegrator 1 complex subunit 3	3	F:GO:0005524; F:GO:0003677; F:GO:0008026	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG22251 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	zinc finger 1	2	F:GO:0005515; C:GO:0043231	-		IPR001841; IPR013083; PTHR12981 (PANTHER), SSF57850 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Loa loa	potassium channel tetramerisation domain containing 10	12	P:GO:0043161; F:GO:0005249; P:GO:0034765; C:GO:0005730; C:GO:0031463; F:GO:0004114; C:GO:0008076; F:GO:0004842; P:GO:0016567; N:GO:0071805; F:GO:0005515; C:GO:0005737	-	EC:3.1.4.17; EC:6.3.2.19	-
	-	0				-
Pongo abelii	cytochrome c oxidase subunit vic	5	C:GO:0005751; P:GO:0015992; C:GO:0016021; F:GO:0004129; P:GO:0006091	-	EC:1.9.3.1	IPR004204; SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Loa loa	inhibitor of growth protein 3	2	F:GO:0008270; F:GO:0005515	-		IPR001965; IPR011011; IPR013083; IPR019786; IPR019787; PTHR10333 (PANTHER), PTHR10333:SF13 (PANTHER)
Caenorhabditis briggsae	transmembrane and coiled-coil domains protein 1	1	C:GO:0016021	-		IPR002809; IPR008559
	-	0				-
Caenorhabditis elegans	guanylate cyclase 32e	3	P:GO:0044238; F:GO:0016829; P:GO:0044237	-		IPR001828; G3DSA:3.40.50.2300 (GENE3D), SSF53822 (SUPERFAMILY)

Trichomonas vaginalis G3	uncoordi-ted family member (unc-89)	0		F:GO:0003676; F:GO:0008168; F:GO:0016740; F:GO:0000166; F:GO:0008270; C:GO:0005634; C:GO:0005622		-
	-	0				-
Loa loa	mitogen-activated protein ki-se ki-se 1-interacting protein 1	1	F:GO:0005515	-		IPR015019; G3DSA:3.30.450.30 (GENE3D), SSF103196 (SUPERFAMILY)
	-	0				-
Pan troglodytes	prolyl 4- beta subunit isoform 5	0				SignalP (SIGNALP)
Brugia malayi	uv excision repair protein rad23 homolog a	3	F:GO:0003677; F:GO:0005515; P:GO:0006974	-		IPR000449; IPR000626; IPR004806; IPR006636; IPR009060; IPR015360; IPR015940; IPR019955; G3DSA:1.10.8.10 (GENE3D), G3DSA:3.10.20.90 (GENE3D), PTHR10621 (PANTHER), SSF54236 (SUPERFAMILY)
Loa loa	cpg binding protein	0		F:GO:0046872; F:GO:0008270; F:GO:0005515; F:GO:0003677		IPR022056; PTHR12321 (PANTHER)
Loa loa	cpg binding protein	0		F:GO:0046872; F:GO:0008270; F:GO:0005515; F:GO:0003677		IPR022056; PTHR12321 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-
Brugia malayi	tho complex subunit 2	7	P:GO:0045132; P:GO:0000003; P:GO:0040007; P:GO:0010171; F:GO:0005515; P:GO:0002119; P:GO:0040011	-		IPR021418; PTHR21597 (PANTHER)
	-	0				-
Caenorhabditis briggsae	vi related family member (viln-1)	0		P:GO:0045132; F:GO:0003779; P:GO:0007010		-
Caenorhabditis elegans	alanyl-tr- synthetase	3	P:GO:0009987; F:GO:0005488; F:GO:0016874	-		IPR002318; IPR018162; IPR018164; IPR018165; PTHR11777 (PANTHER)

Caenorhabditis briggsae	ca++ type member 1	24	F:GO:0004871; F:GO:0030145; P:GO:0016339; C:GO:0005802; C:GO:0030133; P:GO:0008544; C:GO:0000139; P:GO:0030026; C:GO:0005792; F:GO:0015410; P:GO:0032468; F:GO:0005509; C:GO:0016021; P:GO:0006754; P:GO:0043123; P:GO:0032472; F:GO:0005388; P:GO:0070588; C:GO:0030141; P:GO:0031532; P:GO:0006200; C:GO:0005886; F:GO:0005524; P:GO:0006828	-	EC:3.6.3.35; EC:3.6.3.8	IPR001757; IPR006068; G3DSA:1.20.1110.10 (GENE3D), PTHR11939:SF87 (PANTHER), SSF81665 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein Y37E11AL.6 [Caenorhabditis elegans]	0				-
	-	0				-
Oryza sativa Japonica Group	Os04g0654400 [Oryza sativa Japonica Group]	0		P:GO:0009058; F:GO:0016740		-
Mizuhopecten yessoensis	oocyte maturation arresting factor	0		F:GO:0046872; P:GO:0055114; P:GO:0006801		-
	-	0				-
Acidovorax avenae subsp. avenae ATCC 19860	urease accessory domain protein	0		F:GO:0051082; P:GO:0006461; C:GO:0005737; P:GO:0006457; F:GO:0016151; P:GO:0018307; P:GO:0019627		-
Brugia malayi	nmda receptor regulated 1	8	C:GO:0005667; F:GO:0043022; F:GO:0008080; F:GO:0005515; P:GO:0045893; C:GO:0005737; P:GO:0032502; P:GO:0006474	-		SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG08444 [Caenorhabditis briggsae]	0				PTHR23022 (PANTHER), PTHR23022:SF6 (PANTHER)
Caenorhabditis briggsae	progestin and adipoq receptor family member vii	0		P:GO:0030154; F:GO:0004872; P:GO:0048477; P:GO:0007275; C:GO:0016021; F:GO:0005496; C:GO:0005886		IPR004254; PTHR20855:SF5 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-

	-	0				-
Caenorhabditis elegans	membrane-associated guanylate ki-se	1	F:GO:0005515	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR23122 (PANTHER), PTHR23122:SF2 (PANTHER)
Caenorhabditis elegans	dead deah box helicase family protein	7	P:GO:0040010; P:GO:0040002; P:GO:0040035; P:GO:0002119; F:GO:0000166; F:GO:0004386; P:GO:0006898	-		IPR001650; IPR011545; IPR014001; IPR014014; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF20 (PANTHER), SSF52540 (SUPERFAMILY)
Brugia malayi	swi snf matrix actin dependent regulator of subfamily member 1	12	F:GO:0047485; P:GO:0006357; C:GO:0017053; C:GO:0000228; C:GO:0005730; F:GO:0003677; F:GO:0008080; C:GO:0016514; F:GO:0003713; P:GO:0045892; F:GO:0003682; P:GO:0006337	-		IPR000910; IPR009071; PTHR13711 (PANTHER), PTHR13711:SF13 (PANTHER)
	-	0				IPR013761; IPR021129; PTHR12247 (PANTHER), PTHR12247:SF1 (PANTHER)
Brugia malayi	mr--decapping enzyme 2	3	F:GO:0005515; P:GO:0071044; C:GO:0044424	-		IPR000086; IPR007722; IPR015797; IPR020084; IPR020476; PTHR23114 (PANTHER), PS51462 (PROFILE), SSF140586 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-tag-253 protein	0				IPR002737
Caenorhabditis briggsae	set domain	1	F:GO:0005488	-		IPR001965; IPR011011
Caenorhabditis briggsae	novel protein vertebrate sy-ptophysin	1	C:GO:0044464	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0005515		IPR000637; IPR017956
Caenorhabditis briggsae	thioredoxin-like protein	1	P:GO:0006974	-		IPR005746; IPR008979; IPR010400; IPR012335; IPR012336; IPR013766; IPR017936; IPR017937; G3DSA:2.60.120.470 (GENE3D), PTHR10438:SF18 (PANTHER)
Caenorhabditis briggsae	cbp p300 homolog family member (cbp-1)	13	F:GO:0008270; F:GO:0004402; P:GO:0040010; F:GO:0003712; P:GO:0040026; P:GO:0007283; P:GO:0018996; C:GO:0005737; P:GO:0040039; P:GO:0009792; P:GO:0045944; C:GO:0005634; P:GO:0040035	-	EC:2.3.1.48	IPR013178; PTHR13808 (PANTHER)

Caenorhabditis elegans	epsin 1	14	C:GO:0005737; P:GO:0009792; P:GO:0002119; C:GO:0005905; F:GO:0008289; C:GO:0005886; P:GO:0040017; P:GO:0040010; P:GO:0000003; P:GO:0019915; F:GO:0008134; P:GO:0006898; C:GO:0005634; P:GO:0051729	-		IPR001026; IPR008942; IPR013809; PTHR12276 (PANTHER), PTHR12276:SF13 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Ailuropoda melanoleuca	60s ribosomal protein l17	3	F:GO:0003735; C:GO:0015934; P:GO:0006412	-	EC:3.6.5.3	IPR001063; IPR005721; IPR018260
Ancylostoma ceylanicum	tissue factor pathway inhibitor a	0		F:GO:0030414; C:GO:0042151; P:GO:0007596; F:GO:0008233; F:GO:0004867; C:GO:0005576		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	6	P:GO:0006810; P:GO:0040010; P:GO:0000003; P:GO:0002119; P:GO:0009792; C:GO:0016020	-		IPR011701; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR10074 (PANTHER), PTHR10074:SF22 (PANTHER), SignalP (SIGNALP)
Brugia malayi	innexin family protein	5	P:GO:0040035; C:GO:0005921; P:GO:0040010; P:GO:0040011; P:GO:0002009	-		IPR000990; SignalP (SIGNALP)
	-	0				IPR000436; PTHR19325 (PANTHER), PTHR19325:SF25 (PANTHER)
Caenorhabditis briggsae	d- polymerase delta catalytic subunit	5	P:GO:0009792; P:GO:0002119; P:GO:0000910; P:GO:0035188; P:GO:0006898	-		IPR012337; PTHR10322 (PANTHER), PTHR10322:SF4 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	phosphatidylinositol transfer protein	9	P:GO:0000916; C:GO:0070732; P:GO:0007112; C:GO:0032154; P:GO:0000915; P:GO:0048137; P:GO:0043147; P:GO:0007111; P:GO:0007110	-		IPR001666; G3DSA:3.30.530.20 (GENE3D), SSF55961 (SUPERFAMILY)
	-	0				-

Pongo abelii	protein sec13 homolog isoform 2	6	C:GO:0031080; P:GO:0016044; C:GO:0000776; F:GO:0005515; P:GO:0006886; P:GO:0006888	-		-
Caenorhabditis briggsae	vacuolar protein sorting-associated protein 18 homolog	5	C:GO:0005768; C:GO:0043234; F:GO:0005515; C:GO:0005774; P:GO:0006996	-		IPR001841; IPR007087; IPR013083; PTHR23323 (PANTHER), PTHR23323:SF25 (PANTHER)
Loa loa	a-phase promoting complex subunit 11	8	P:GO:0008054; P:GO:0045132; F:GO:0046872; P:GO:0000003; P:GO:0040027; F:GO:0005515; P:GO:0009792; C:GO:0005634	-		-
Loa loa	a-phase promoting complex subunit 11	8	P:GO:0008054; P:GO:0045132; F:GO:0046872; P:GO:0000003; P:GO:0040027; F:GO:0005515; P:GO:0009792; C:GO:0005634	-		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	bsd domain containing 1	0		P:GO:0008150; C:GO:0005575		IPR005607; PTHR16019 (PANTHER), SSF140383 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG24039 [Caenorhabditis briggsae]	0				-
	-	0				-
Brugia malayi	polymerase ii (d- directed) polypeptide 33kda	9	F:GO:0003899; F:GO:0004672; P:GO:0006367; P:GO:0008380; C:GO:0005665; F:GO:0003677; F:GO:0046983; P:GO:0006368; C:GO:0005737	-	EC:2.7.7.6	IPR009025; IPR011262; IPR011263; G3DSA:3.30.1360.10 (GENE3D), PTHR11800 (PANTHER), PTHR11800:SF2 (PANTHER)
Methylobacter tundripaludum SV96	chromosome segregation protein smc	0		C:GO:0005694; F:GO:0005524; P:GO:0051276; F:GO:0005515; F:GO:0003774; C:GO:0016459		G3DSA:1.20.58.70 (GENE3D)

Caenorhabditis briggsae	briggsae cbr-npp-7 protein	0		P:GO:0006997; F:GO:0008270; P:GO:0009792; P:GO:0002119; P:GO:0040007; C:GO:0005622		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	zinc finger transcription factor family protein partially confirmed by transcript evidence	0		F:GO:0003676; C:GO:0016021; F:GO:0008270; P:GO:0009792; C:GO:0005622		IPR013032
Caenorhabditis elegans	ph domain containing protein	4	P:GO:0009987; P:GO:0048856; F:GO:0035091; C:GO:0016020	-		PTHR21630 (PANTHER), PTHR21630:SF6 (PANTHER)
Caenorhabditis elegans	acetyl- mitochondrial	14	F:GO:0003985; P:GO:0009725; P:GO:0042594; C:GO:0005743; P:GO:0007420; P:GO:0051260; F:GO:0019899; P:GO:0060612; P:GO:0014070; P:GO:0008152; C:GO:0005759; F:GO:0050662; P:GO:0072229; F:GO:0042803	-	EC:2.3.1.9	-
Callithrix jacchus	ribosomal protein l10a	7	F:GO:0003735; F:GO:0003723; P:GO:0009653; C:GO:0022625; C:GO:0005739; P:GO:0006414; P:GO:0006396	-		-
Loa loa	related to oncogene abl family member (abl-1)	2	F:GO:0005488; F:GO:0016740	-		-
Brugia malayi	mgc47001-prov protein	3	P:GO:0006259; F:GO:0004518; P:GO:0006974	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR14091 (PANTHER)

Caenorhabditis elegans	transcription initiation factor tfiid subunit 12	0		C:GO:0005669; F:GO:0003677; C:GO:0005634; C:GO:0030914; F:GO:0016986; C:GO:0000125; P:GO:0006914; P:GO:0006352; P:GO:0006350; F:GO:0003700; F:GO:0004222; F:GO:0004175; P:GO:0006367; P:GO:0006508; C:GO:0005737; F:GO:0005488; F:GO:0003713; P:GO:0045449; F:GO:0003743; C:GO:0033276; F:GO:0008270; F:GO:0005515; C:GO:0005886; F:GO:0004402; P:GO:0043966		IPR003228; IPR009072; PD012998 (PRODOM), PTHR12264 (PANTHER), PTHR12264:SF1 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-apa-2 protein	14	C:GO:0005829; F:GO:0008565; P:GO:0040010; F:GO:0008022; P:GO:0000003; C:GO:0030131; C:GO:0030666; P:GO:0050690; P:GO:0040011; P:GO:0006898; P:GO:0006886; C:GO:0030141; P:GO:0009792; C:GO:0005886	-		SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-apa-2 protein	14	C:GO:0005829; F:GO:0008565; P:GO:0040010; F:GO:0008022; P:GO:0000003; C:GO:0030131; C:GO:0030666; P:GO:0050690; P:GO:0040011; P:GO:0006898; P:GO:0006886; C:GO:0030141; P:GO:0009792; C:GO:0005886	-		SignalP (SIGNALP)

Caenorhabditis briggsae	briggsae cbr-apa-2 protein	14	C:GO:0005829; F:GO:0008565; P:GO:0040010; F:GO:0008022; P:GO:0000003; C:GO:0030131; C:GO:0030666; P:GO:0050690; P:GO:0040011; P:GO:0006898; P:GO:0006886; C:GO:0030141; P:GO:0009792; C:GO:0005886	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	2	F:GO:0008270; F:GO:0003676	-		IPR000571; G3DSA:4.10.1000.10 (GENE3D), PTHR12547 (PANTHER), SSF90229 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	2	F:GO:0008270; F:GO:0003676	-		IPR000571; G3DSA:4.10.1000.10 (GENE3D), PTHR12547 (PANTHER), SSF90229 (SUPERFAMILY)
Caenorhabditis elegans	ethanolamine ki-se 2	2	F:GO:0016301; P:GO:0007275	-		IPR002573; IPR011009; G3DSA:3.90.1200.10 (GENE3D), PTHR22603:SF7 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	tbc1 domain family member 9	4	F:GO:0005097; F:GO:0005509; C:GO:0005622; P:GO:0032313	-		IPR004182; PTHR23319 (PANTHER), SignalP (SIGNALP)
	-	0				-
Loa loa	protein ki-se domain containing protein	4	P:GO:0006468; F:GO:0005524; P:GO:0040011; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Brugia malayi	hypothetical protein Bm1_42720 [Brugia malayi]	0				-
	-	0				-
Brugia malayi	scribbled homolog isoform 4	7	P:GO:0048731; C:GO:0005911; P:GO:0048489; P:GO:0002009; P:GO:0030154; P:GO:0065007; P:GO:0016477	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR23119 (PANTHER)
Caenorhabditis elegans	26s proteasome non-atpase regulatory subunit 7	9	P:GO:0008340; P:GO:0051436; P:GO:0051437; P:GO:0040007; C:GO:0005838; P:GO:0000003; P:GO:0031145; P:GO:0002119; F:GO:0005515	-		IPR000555; PTHR10540 (PANTHER), PTHR10540:SF7 (PANTHER)

Ixodes scapularis	factor for adipocyte	0		P:GO:0008152; F:GO:0016787; F:GO:0016798; F:GO:0016162		IPR008957; IPR013783; PTHR19900 (PANTHER), PTHR19900:SF3 (PANTHER)
Caenorhabditis elegans	actin-related protein 2 3 complex subunit 1a	9	P:GO:0030833; P:GO:0040010; P:GO:0000003; P:GO:0002119; F:GO:0003779; C:GO:0015629; P:GO:0040011; P:GO:0009792; P:GO:0040018	-		PTHR10709 (PANTHER), PTHR10709:SF6 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-pqn-34 protein	0				-
Caenorhabditis elegans	loc496093 protein	4	C:GO:0005730; P:GO:0042127; F:GO:0005525; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000795; IPR002917; IPR014813; IPR023179; G3DSA:3.40.50.300 (GENE3D), PTHR11089 (PANTHER), PTHR11089:SF13 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	loc496093 protein	4	C:GO:0005730; P:GO:0042127; F:GO:0005525; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000795; IPR002917; IPR014813; IPR023179; G3DSA:3.40.50.300 (GENE3D), PTHR11089 (PANTHER), PTHR11089:SF13 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	slowpoke potassium channel family member (slo-2)	6	C:GO:0016020; P:GO:0006813; P:GO:0008152; F:GO:0003824; F:GO:0015269; F:GO:0005488	-		IPR013099; G3DSA:1.10.287.70 (GENE3D), PTHR10027 (PANTHER), PTHR10027:SF6 (PANTHER), SignalP (SIGNALP), SSF81324 (SUPERFAMILY)
	-	0				-
	-	0				-
Brugia malayi	tr- modification gtpase family protein	4	C:GO:0005622; P:GO:0008033; F:GO:0000166; P:GO:0050794	-		IPR021629
	-	0				-
Caenorhabditis elegans	methylmalonic aciduria (cobalamin deficiency) cbla type	4	F:GO:0005525; F:GO:0016787; F:GO:0005524; C:GO:0005739	-		IPR005129; G3DSA:1.20.5.170 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23408 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein Y119C1B.5 [Caenorhabditis elegans]	0		F:GO:0046872; C:GO:0016021; F:GO:0008270; F:GO:0005515		-
	-	0				-
Brugia malayi	retinoblastoma-like protein 2	3	C:GO:0043229; P:GO:0044238; P:GO:0044237	-		PTHR13742 (PANTHER), PTHR13742:SF8 (PANTHER), PF11934 (PFAM)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	iron zinc purple acid phosphatase-like	3	F:GO:0046872; P:GO:0009792; F:GO:0003993	-	EC:3.1.3.2	-
	-	0				IPR001283; IPR014044; PTHR10334:SF4 (PANTHER)
	-	0				SignalP (SIGNALP)

	-	0					-
	-	0					-
Caenorhabditis briggsae	isoform cra_a	55	P:GO:0032755; F:GO:0051087; C:GO:0046696; P:GO:0042026; P:GO:0032735; P:GO:0032729; C:GO:0005791; F:GO:0051082; P:GO:0043032; P:GO:0042542; P:GO:0032733; P:GO:0043065; C:GO:0005829; F:GO:0001530; P:GO:0032727; P:GO:0051085; C:GO:0005759; C:GO:0005615; C:GO:0045121; F:GO:0002039; P:GO:0042100; P:GO:0006986; F:GO:0002020; P:GO:0001666; P:GO:0006919; C:GO:0044459; F:GO:0043559;	-		SignalP (SIGNALP)
	-	0					-
	-	0					-
Caenorhabditis elegans	protein o-fucosyltransferase 1	12	P:GO:0016337; P:GO:0006493; F:GO:0008417; C:GO:0031410; P:GO:0007399; F:GO:0005112; P:GO:0006897; P:GO:0045746; P:GO:0030163; C:GO:0016020; C:GO:0005794; C:GO:0005783	-			IPR019378; PTHR21420 (PANTHER)
Caenorhabditis elegans	protein o-fucosyltransferase 1	12	P:GO:0016337; P:GO:0006493; F:GO:0008417; C:GO:0031410; P:GO:0007399; F:GO:0005112; P:GO:0006897; P:GO:0045746; P:GO:0030163; C:GO:0016020; C:GO:0005794; C:GO:0005783	-			IPR019378; PTHR21420 (PANTHER)

Caenorhabditis elegans	protein o-fucosyltransferase 1	12	P:GO:0016337; P:GO:0006493; F:GO:0008417; C:GO:0031410; P:GO:0007399; F:GO:0005112; P:GO:0006897; P:GO:0045746; P:GO:0030163; C:GO:0016020; C:GO:0005794; C:GO:0005783	-		IPR019378; PTHR21420 (PANTHER)
	-	0				-
Caenorhabditis elegans	nuclear hormone receptor family member (nhr-49)	7	F:GO:0003700; F:GO:0043565; P:GO:0008340; F:GO:0003707; C:GO:0005634; F:GO:0008270; P:GO:0006355	-		IPR000536; IPR008946; PTHR11865 (PANTHER), PTHR11865:SF197 (PANTHER)
Caenorhabditis elegans	cx module family protein	0		P:GO:0000003; P:GO:0040011; P:GO:0002119		IPR002619
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	laminin alpha- 2 chain	5	C:GO:0005606; P:GO:0030334; P:GO:0045995; P:GO:0030155; F:GO:0005102	-		IPR002049; IPR013032; PR00011 (PRINTS), G3DSA:2.10.25.10 (GENE3D), PTHR10574 (PANTHER), PTHR10574:SF36 (PANTHER), SSF57196 (SUPERFAMILY)
Caenorhabditis elegans	phospholipase b-like 2 precursor	0		F:GO:0016787; C:GO:0043202; P:GO:0016042		SignalP (SIGNALP)
Brugia malayi	unc-45 homolog b (elegans)	5	C:GO:0005737; P:GO:0030154; P:GO:0014706; P:GO:0007517; F:GO:0005488	-		-
Caenorhabditis elegans	presenilin family protein	5	C:GO:0016020; P:GO:0016048; P:GO:0007219; F:GO:0005515; P:GO:0007399	-		-
Caenorhabditis briggsae	dedicator of cytokinesis 1	8	P:GO:0043652; F:GO:0005083; F:GO:0032403; P:GO:0023052; F:GO:0019899; P:GO:0040039; C:GO:0005886; F:GO:0017124	-		PTHR23317 (PANTHER), PTHR23317:SF16 (PANTHER)

Caenorhabditis briggsae	dedicator of cytokinesis 1	8	P:GO:0043652; F:GO:0005083; F:GO:0032403; P:GO:0023052; F:GO:0019899; P:GO:0040039; C:GO:0005886; F:GO:0017124	-		PTHR23317 (PANTHER), PTHR23317:SF16 (PANTHER)
Loa loa	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		-
	-	0				-
Branchiostoma floridae	low density lipoprotein receptor-related protein 10	0		P:GO:0042733; C:GO:0016021; P:GO:0043113; C:GO:0016020; P:GO:0051124; P:GO:0001822; P:GO:0009954; P:GO:0009953; P:GO:0008104; F:GO:0004872; P:GO:0030178; P:GO:0001942; F:GO:0005515; P:GO:0048856; P:GO:0042475; C:GO:0005886; F:GO:0005509		IPR002172; PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER)
Ostreococcus tauri	condensin subunit cut3	0		C:GO:0005694; F:GO:0005524; P:GO:0051276; F:GO:0005515; F:GO:0003677		IPR010935; PTHR18937 (PANTHER), PTHR18937:SF13 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR007523; G3DSA:3.40.1230.10 (GENE3D)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	rogdi_caeel ame: full=protein rogdi homolog	0		P:GO:0006974; P:GO:0040010		-
Caenorhabditis elegans	transmembrane emp24 protein transport domain containing 5	2	C:GO:0016021; P:GO:0006810	-		IPR000348; IPR009038; IPR015717; PTHR22811 (PANTHER), SignalP (SIGNALP), SSF101576 (SUPERFAMILY)
Caenorhabditis elegans	transmembrane emp24 protein transport domain containing 5	2	C:GO:0016021; P:GO:0006810	-		IPR000348; IPR009038; IPR015717; PTHR22811 (PANTHER), SignalP (SIGNALP), SSF101576 (SUPERFAMILY)
Caenorhabditis elegans	transmembrane emp24 protein transport domain containing 5	2	C:GO:0016021; P:GO:0006810	-		IPR000348; IPR009038; IPR015717; PTHR22811 (PANTHER), SignalP (SIGNALP), SSF101576 (SUPERFAMILY)
Caenorhabditis elegans	daf-16 foxo germline tumor affecting family member (dct-6)	0				-
	-	0				-
	-	0				-
	-	0				-

	-	0				-
	-	0				-
Caenorhabditis briggsae	u327_caeel ame: full=upf0327 protein	0				IPR007512
	-	0				-
Caenorhabditis briggsae	succinyl- ligase	10	C:GO:0045244; P:GO:0006105; F:GO:0004777; P:GO:0006104; P:GO:0006099; F:GO:0019003; F:GO:0005524; F:GO:0046982; P:GO:0009792; F:GO:0004776	-	EC:1.2.1.24; EC:6.2.1.4	IPR005809; IPR013650; IPR013815; IPR013816; SSF56059 (SUPERFAMILY)
Ancylostoma ceylanicum	tpa_inf: eukaryotic translation elongation factor 1a	8	C:GO:0005737; P:GO:0009792; P:GO:0002119; P:GO:0007276; F:GO:0003746; F:GO:0005525; P:GO:0006414; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000795; G3DSA:3.40.50.300 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF37 (PANTHER), SSF52540 (SUPERFAMILY)
Ancylostoma ceylanicum	tpa_inf: eukaryotic translation elongation factor 1a	8	C:GO:0005737; P:GO:0009792; P:GO:0002119; P:GO:0007276; F:GO:0003746; F:GO:0005525; P:GO:0006414; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000795; G3DSA:3.40.50.300 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF37 (PANTHER), SSF52540 (SUPERFAMILY)
Dictyocaulus viviparus	tpa_inf: eukaryotic translation elongation factor 1a	8	C:GO:0005737; P:GO:0009792; P:GO:0002119; P:GO:0007276; F:GO:0003746; F:GO:0005525; P:GO:0006414; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000795; IPR004160; IPR004161; IPR009000; G3DSA:2.40.30.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF37 (PANTHER), SSF52540 (SUPERFAMILY)
Dictyocaulus viviparus	tpa_inf: eukaryotic translation elongation factor 1a	8	C:GO:0005737; P:GO:0009792; P:GO:0002119; P:GO:0007276; F:GO:0003746; F:GO:0005525; P:GO:0006414; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000795; IPR004160; IPR004161; IPR009000; G3DSA:2.40.30.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF37 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	rain ki-se homolog family member (mbk-2)	11	F:GO:0030145; P:GO:0006468; P:GO:0045725; F:GO:0005515; F:GO:0004713; P:GO:0042771; C:GO:0005737; F:GO:0004674; F:GO:0000287; C:GO:0005634; F:GO:0005524	-	EC:2.7.10.0; EC:2.7.11.0	PTHR11295 (PANTHER), PTHR11295:SF22 (PANTHER)
	-	0				-

Caenorhabditis sp. PS1010	gex interacting protein family member (gei-16)	1	F:GO:0005515	-		-
Caenorhabditis elegans	major intrinsic protein	8	C:GO:0016323; P:GO:0045087; P:GO:0055085; P:GO:0008340; P:GO:0050829; C:GO:0016021; P:GO:0015793; F:GO:0022838	-		IPR000425; IPR020904; IPR022357; PTHR19139:SF11 (PANTHER)
Caenorhabditis elegans	hypothetical protein F56C9.8 [Caenorhabditis elegans]	0		F:GO:0004221; P:GO:0006511		-
Caenorhabditis briggsae	leucine rich repeat containing 47	1	F:GO:0005488	-		IPR005146; PTHR10947 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis remanei	telomerase reverse transcriptase	0		F:GO:0003723; P:GO:0007004; F:GO:0003721; C:GO:0005697; F:GO:0003720; F:GO:0003677; C:GO:0005634; C:GO:0005694; P:GO:0022616; P:GO:0006916; C:GO:0030529; F:GO:0042803; P:GO:0043249; P:GO:0032203; P:GO:0006278; F:GO:0070034; F:GO:0003964; P:GO:0008152; P:GO:0008150; C:GO:0005737; F:GO:0016779; C:GO:0000781; C:GO:0005730; C:GO:0005654; F:GO:0005515; F:GO:0016740		-
Echinococcus granulosus	elegans protein partially confirmed by transcript evidence	0		F:GO:0004222; F:GO:0019870; F:GO:0008270; F:GO:0008237; C:GO:0005578; C:GO:0031012; C:GO:0005576; F:GO:0030414; F:GO:0008233; P:GO:0009405; F:GO:0004867; F:GO:0008200		SignalP (SIGNALP)
Caenorhabditis elegans	vacuolar protein sorting-associated protein 29	4	F:GO:0046872; C:GO:0010008; F:GO:0004647; P:GO:0015031	-	EC:3.1.3.3	IPR000979; IPR020935; G3DSA:3.60.21.10 (GENE3D), PTHR11124 (PANTHER), SSF56300 (SUPERFAMILY)

Meloidogyne incognita	dual oxidase 1	20	P:GO:0018149; P:GO:0006979; P:GO:0006952; F:GO:0016174; P:GO:0040032; F:GO:0005509; C:GO:0016021; P:GO:0042338; P:GO:0055114; P:GO:0040007; F:GO:0004601; F:GO:0009055; P:GO:0019221; P:GO:0002119; P:GO:0040011; F:GO:0020037; F:GO:0050660; P:GO:0009792; P:GO:0051591; C:GO:0005882	-	EC:1.6.3.1; EC:1.11.1.7	-
Brugia malayi	exonuclease family protein	0		F:GO:0003676; F:GO:0004527; F:GO:0008270; C:GO:0005622		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-ntl-2 protein	11	P:GO:0040010; P:GO:0008340; F:GO:0042802; P:GO:0040035; P:GO:0019915; P:GO:0002119; P:GO:0040011; P:GO:0006898; P:GO:0002009; P:GO:0009792; P:GO:0040018	-		-
Loa loa	fatty-acid amide hydrolase 1-like	2	F:GO:0016787; P:GO:0000003	-		IPR000120; PTHR11895:SF4 (PANTHER)
Bombyx mori	endonuclease-reverse transcriptase	0		F:GO:0003723; P:GO:0006278; F:GO:0008270; F:GO:0004519; F:GO:0003964; C:GO:0005622		-
Caenorhabditis briggsae	briggsae cbr-cyn-4 protein	9	P:GO:0006457; P:GO:0040022; F:GO:0005515; P:GO:0000209; C:GO:0005796; F:GO:0034450; C:GO:0005634; F:GO:0003755; C:GO:0000151	-	EC:5.2.1.8	IPR002130; IPR013083; IPR015891; IPR020892; PTHR11071 (PANTHER), PTHR11071:SF42 (PANTHER), PF04641 (PFAM), SSF57850 (SUPERFAMILY)

Caenorhabditis briggsae	carbamoyl-phosphate synthetase aspartate and dihydroorotase	7	P:GO:0006541; F:GO:0016812; F:GO:0016597; F:GO:0004086; F:GO:0005524; P:GO:0006207; F:GO:0004070	-	EC:3.5.2.0; EC:2.1.3.2	-
Caenorhabditis elegans	lysocardiolipin acyltransferase 1	4	F:GO:0008415; F:GO:0005515; C:GO:0016021; P:GO:0008152	-		IPR002123; PTHR10983 (PANTHER), PTHR10983:SF1 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	pre-mr--processing-splicing factor 8	17	P:GO:0050896; F:GO:0003723; C:GO:0005681; P:GO:0045132; P:GO:0040007; C:GO:0016607; P:GO:0040027; P:GO:0040035; P:GO:0018996; P:GO:0007601; F:GO:0005515; P:GO:0040011; P:GO:0000398; C:GO:0005682; P:GO:0006898; P:GO:0002009; P:GO:0009792	-		IPR012591; PTHR11140 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				IPR002097
	-	0				-
Caenorhabditis elegans	slit homolog 1	9	F:GO:0005102; P:GO:0051093; C:GO:0005576; P:GO:0050919; P:GO:0048846; P:GO:0022028; P:GO:0051960; P:GO:0048523; P:GO:0051129	-		IPR000372; IPR001611; IPR003591; PR00019 (PRINTS), G3DSA:3.80.10.10 (GENE3D), PTHR23154 (PANTHER), PTHR23154:SF44 (PANTHER), PS51450 (PROFILE), SignalP (SIGNALP), SSF52058 (SUPERFAMILY)

Caenorhabditis elegans	rac-beta serine threonine-protein ki-se	33	F:GO:0004674; P:GO:0010907; P:GO:0014850; P:GO:0043491; P:GO:0045429; C:GO:0032593; C:GO:0005625; P:GO:0043053; P:GO:0046326; P:GO:0010765; C:GO:0030027; C:GO:0005829; P:GO:0031667; C:GO:0005654; P:GO:0009967; P:GO:0046328; P:GO:0006970; C:GO:0005792; P:GO:0040010; P:GO:0043154; P:GO:0008340; P:GO:0045944; C:GO:0005886; P:GO:0019915; P:GO:0043066; C:GO:0005739; F:GO:0005524;	-	EC:2.7.11.0	IPR001849; IPR011993; IPR015744; PTHR22985 (PANTHER), SSF50729 (SUPERFAMILY)
Homo sapiens	aldolase fructose-bisphosphate	15	P:GO:0006941; F:GO:0070061; P:GO:0007015; P:GO:0008360; C:GO:0070062; F:GO:0042802; P:GO:0006754; C:GO:0031674; F:GO:0003779; P:GO:0046716; C:GO:0015629; P:GO:0006096; F:GO:0015631; F:GO:0004332; P:GO:0030388	-	EC:4.1.2.13	-
Polysphondylium pallidum PN500	ring finger and wd repeat domain 2	3	C:GO:0005654; F:GO:0004842; C:GO:0005829	-	EC:6.3.2.19	-
	-	0				-
Caenorhabditis briggsae	coiled-coil domain-containing protein 25	0		F:GO:0003674; C:GO:0005575		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	n-ethylmaleimide-sensitive factor attachment gamma	4	C:GO:0005783; C:GO:0005794; P:GO:0006886; F:GO:0005488	-		IPR000744; IPR011990; PTHR13768:SF2 (PANTHER), SignalP (SIGNALP), SSF48452 (SUPERFAMILY)
	-	0				-
Brugia malayi	hypothetical protein Bm1_43950 [Brugia malayi]	0				-

Caenorhabditis elegans	dehydroge-se reductase sdr family member 4	5	F:GO:0005488; F:GO:0016491; C:GO:0043231; P:GO:0055114; C:GO:0044444	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	spectrin beta chain	3	F:GO:0003779; F:GO:0005200; C:GO:0008091	-		G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF48 (PANTHER), SSF46966 (SUPERFAMILY)
Loa loa	cmgc cdk cdk9 protein ki-se	0				G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF111 (PANTHER)
Caenorhabditis briggsae	germ cell-specific gene 2	7	P:GO:0007243; F:GO:0004674; P:GO:0007049; F:GO:0003677; F:GO:0005524; C:GO:0005634; P:GO:0006468	-	EC:2.7.11.0	IPR000719; PF12330 (PFAM)
Caenorhabditis elegans	fanci (fanconi anemia complex component i) homolog family member (fnci-1)	0				-
	-	0				-
Caenorhabditis briggsae	bcl2 adenovirus e1b 19kda interacting protein 1	6	P:GO:0006996; P:GO:0042981; C:GO:0044446; C:GO:0044425; C:GO:0012505; C:GO:0005783	-		IPR005606; PTHR12825 (PANTHER)
Caenorhabditis briggsae	bcl2 adenovirus e1b 19kda interacting protein 1	6	P:GO:0006996; P:GO:0042981; C:GO:0044446; C:GO:0044425; C:GO:0012505; C:GO:0005783	-		IPR005606; PTHR12825 (PANTHER)
Caenorhabditis briggsae	iars2 protein	4	P:GO:0006412; F:GO:0005488; C:GO:0005739; F:GO:0004812	-	EC:3.6.5.3	IPR002300; IPR002301; IPR009008; IPR014729; G3DSA:3.90.740.10 (GENE3D), PTHR11946 (PANTHER), SSF52374 (SUPERFAMILY)
Caenorhabditis briggsae	macro domain-containing protein 1	0		C:GO:0005739; F:GO:0016779; F:GO:0003674; F:GO:0016740; F:GO:0003968; P:GO:0008150		IPR002589; G3DSA:3.40.220.10 (GENE3D), PTHR11106 (PANTHER), PTHR11106:SF3 (PANTHER), SSF52949 (SUPERFAMILY)
	-	0				-

Caenorhabditis elegans	cbp p300 homolog family member (cbp-1)	14	F:GO:0008270; F:GO:0004402; C:GO:0000123; P:GO:0040010; P:GO:0040026; P:GO:0007283; P:GO:0018996; C:GO:0005737; P:GO:0040039; P:GO:0009792; F:GO:0003713; P:GO:0045944; P:GO:0040035; P:GO:0016573	-	EC:2.3.1.48	IPR013178; PTHR13808 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-ric-3 protein	3	C:GO:0005783; C:GO:0044425; F:GO:0005515	-		PTHR21723 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	vitellogenin structural genes (yolk protein genes) family member (vit-6)	0		P:GO:0006869; F:GO:0005319; F:GO:0045735; P:GO:0006886; C:GO:0005576; F:GO:0008565		IPR015816
Caenorhabditis elegans	vitellogenin structural genes (yolk protein genes) family member (vit-6)	0		P:GO:0006869; F:GO:0005319; F:GO:0045735; P:GO:0006886; C:GO:0005576; F:GO:0008565		IPR015816
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	variable abnormal morphology family member (vab-10)	0		P:GO:0007050; F:GO:0005509		-
Caenorhabditis briggsae	uncharacterized aarf domain-containing protein ki-se 1	2	F:GO:0016740; C:GO:0005739	-		-
	-	0				-
Caenorhabditis elegans	general transcription factor polypeptide beta 34kda	13	P:GO:0006367; C:GO:0005673; P:GO:0000003; F:GO:0005515; P:GO:0040010; P:GO:0006898; P:GO:0040011; P:GO:0006259; F:GO:0003676; F:GO:0004386; P:GO:0009792; P:GO:0002119; P:GO:0010171	-		SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-tgt-1 protein	2	F:GO:0016757; P:GO:0006400	-		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-

Angiostrongylus cantonensis	briggsae cbr-mdl-1 protein	7	F:GO:0030528; F:GO:0003677; C:GO:0005634; F:GO:0008270; F:GO:0008168; P:GO:0006355; P:GO:0006281	-	EC:2.1.1.0	PTHR11969 (PANTHER), PTHR11969:SF3 (PANTHER)
Caenorhabditis elegans	adp-ribosylation factor-like protein 5a	8	C:GO:0005737; P:GO:0009792; F:GO:0005525; P:GO:0006886; C:GO:0005634; P:GO:0051729; P:GO:0008406; P:GO:0007264	-		IPR006689; G3DSA:3.40.50.300 (GENE3D), PTHR11711:SF31 (PANTHER), PS51417 (PROFILE), SSF52540 (SUPERFAMILY)
Brugia malayi	splicing arginine serine-	0		P:GO:0008380; P:GO:0006397; C:GO:0005634		IPR019147; PTHR13161 (PANTHER), PTHR13161:SF4 (PANTHER)
Caenorhabditis briggsae	r- polymerase domain 2 family protein	2	F:GO:0005488; F:GO:0016779	-	EC:2.7.7.0	-
Homo sapiens	hCG2030753 [Homo sapiens]	0				-
Loa loa	arginine-tr--protein transferase 1	1	F:GO:0016740	-		PTHR21367 (PANTHER)
Brugia malayi	translocated promoter region	0		C:GO:0045211; F:GO:0004872; F:GO:0004871; F:GO:0005216; F:GO:0005215; C:GO:0005886; P:GO:0007018; C:GO:0030054; C:GO:0016021; P:GO:0008150; P:GO:0043278; C:GO:0016020; P:GO:0035249; P:GO:0006412; C:GO:0005624; C:GO:0005654; C:GO:0045202; P:GO:0006606; P:GO:0007165; F:GO:0005524; C:GO:0005874; F:GO:0005234; C:GO:0000776; F:GO:0000166; P:GO:0043523; P:GO:0007094; P:GO:0034220;		-
Caenorhabditis briggsae	nematode kynurenine ransferase family member (nkat-3)	0		P:GO:0009058; F:GO:0016847; F:GO:0003824; F:GO:0016829; F:GO:0030170; F:GO:0016769		-
Caenorhabditis elegans	hypothetical protein K07B1.7 [Caenorhabditis elegans]	0				-

Ancylostoma caninum	briggsae cbr-sma-6 protein	4	P:GO:0006468; F:GO:0005024; F:GO:0005524; C:GO:0016020	-		IPR000472; G3DSA:2.10.60.10 (GENE3D), SignalP (SIGNALP), SSF57302 (SUPERFAMILY)
	-	0				-
Sorghum bicolor	cytochrome p450 like_tbp	2	P:GO:0055114; F:GO:0070330	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	C:GO:0016020	-		IPR003406; PTHR19297:SF3 (PANTHER)
	-	0				-
Caenorhabditis briggsae	fatty acid elongation protein 3	3	P:GO:0018996; P:GO:0008340; P:GO:0040010	-		IPR002076; SignalP (SIGNALP)
Caenorhabditis elegans	udp-glucose 4-epimerase	7	P:GO:0006694; P:GO:0000003; F:GO:0003854; F:GO:0050662; F:GO:0005515; F:GO:0003978; P:GO:0006012	-	EC:1.1.1.145; EC:5.1.3.2	IPR001509; IPR005886; IPR008089; IPR016040; G3DSA:3.90.25.10 (GENE3D), PTHR10366 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Loa loa	fatty acyl- reductase 1	8	P:GO:0006694; F:GO:0016620; F:GO:0003854; C:GO:0005777; F:GO:0005515; P:GO:0044237; F:GO:0050662; C:GO:0016020	-	EC:1.2.1.0; EC:1.1.1.145	IPR013120; IPR016040; PTHR11011 (PANTHER), PTHR11011:SF8 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis briggsae	fragile site-associated protein	0				-
Caenorhabditis briggsae	protein-tyrosine phosphatase containing protein	3	P:GO:0016311; F:GO:0004721; P:GO:0009792	-	EC:3.1.3.16	IPR000242; IPR000387; IPR003595; IPR016130; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
	-	0				-
	-	0				-
Bacillus cereus AH1273	lpxtg-motif cell wall anchor domain protein	0		F:GO:0005488; C:GO:0009986		-
Ciona intestinalis	phosphatidylinositol glycan anchor class g	0				-
Caenorhabditis elegans	R151.8B protein [Caenorhabditis elegans]	0				-
Brugia malayi	elegans protein confirmed by transcript evidence	2	F:GO:0005515; P:GO:0009792	-		IPR000504; IPR012677; PTHR10432 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	very long-chain specific acyl- mitochondrial	5	F:GO:0016627; P:GO:0006629; P:GO:0040010; P:GO:0044281; P:GO:0009792	-		-
Caenorhabditis briggsae	alanine-glyoxylate aminotransferase 2-like 2	3	F:GO:0030170; C:GO:0005739; F:GO:0008483	-	EC:2.6.1.0	-
Haemonchus contortus	forkhead transcription factor daf-16	4	F:GO:0003700; F:GO:0043565; C:GO:0005634; P:GO:0006355	-		-

Caenorhabditis elegans	hypothetical protein W05F2.4 [Caenorhabditis elegans]	3	P:GO:0040018; P:GO:0040035; P:GO:0002119	-		-
	-	0				IPR001810; G3DSA:1.20.1280.50 (GENE3D)
	-	0				-
	-	0				IPR005819
	-	0				-
Caenorhabditis elegans	uba and wwe domain containing 1	2	C:GO:0005622; P:GO:0009987	-		IPR000449; IPR009060; IPR015940; G3DSA:1.10.8.10 (GENE3D)
Caenorhabditis elegans	uba and wwe domain containing 1	2	C:GO:0005622; P:GO:0009987	-		IPR000449; IPR009060; IPR015940; G3DSA:1.10.8.10 (GENE3D)
Caenorhabditis elegans	midasin homolog	4	F:GO:0017111; P:GO:0050789; C:GO:0005622; F:GO:0000166	-	EC:3.6.1.15	PTHR22908 (PANTHER), PTHR22908:SF13 (PANTHER), SSF53300 (SUPERFAMILY)
Caenorhabditis briggsae	replication factor c subunit 1	10	P:GO:0000003; C:GO:0016020; P:GO:0006974; P:GO:0040010; P:GO:0006898; P:GO:0006350; P:GO:0009792; F:GO:0003677; P:GO:0002119; C:GO:0005634	-		IPR003959; G3DSA:3.40.50.300 (GENE3D), PTHR23389 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	smad nuclear-interacting protein 1	0		P:GO:0000003; P:GO:0040011; P:GO:0010171; P:GO:0006898; P:GO:0009792; P:GO:0002119; P:GO:0040007		-
Caenorhabditis briggsae	smad nuclear-interacting protein 1	1	P:GO:0032502	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	P:GO:0019915	-		-
Caenorhabditis briggsae	interacting protein 2	6	P:GO:0009792; P:GO:0002119; P:GO:0000003; P:GO:0040007; P:GO:0006898; P:GO:0002009	-		IPR014810; PTHR21686 (PANTHER), PTHR21686:SF11 (PANTHER)
	-	0				-
	-	0				IPR018276; SignalP (SIGNALP)
Loa loa	hypothetical protein LOAG_10948 [Loa loa]	0				-
Onchocerca volvulus	remodeling and spacing factor 1	12	F:GO:0042393; P:GO:0016584; C:GO:0031213; P:GO:0045892; P:GO:0043392; F:GO:0016563; P:GO:0006338; P:GO:0050434; P:GO:0006352; F:GO:0016887; P:GO:0006334; F:GO:0016564	-		PTHR10615 (PANTHER), PTHR10615:SF2 (PANTHER)

Caenorhabditis elegans	ph domain containing protein	0				IPR004012; SSF140741 (SUPERFAMILY)
Caenorhabditis briggsae	nuclear pore complex protein family member (npp-21)	14	P:GO:0006810; P:GO:0000003; F:GO:0005515; C:GO:0016020; P:GO:0060134; P:GO:0040015; C:GO:0019717; P:GO:0040011; P:GO:0043523; P:GO:0060079; P:GO:0035249; C:GO:0005635; P:GO:0002119; C:GO:0045202	-		PTHR18898 (PANTHER)
	-	0				-
Loa loa	zinc dhhc-type containing 6	0		F:GO:0046872; F:GO:0008415; F:GO:0016740; C:GO:0016021; C:GO:0016020; F:GO:0008270		IPR001594; PTHR22883 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR007621; SignalP (SIGNALP)
Loa loa	mannosyl (alpha- -)-glycoprotein beta- -n-acetylglucosaminyltransferase	3	C:GO:0000139; F:GO:0003827; P:GO:0006487	-	EC:2.4.1.101	IPR004139; G3DSA:3.90.550.10 (GENE3D)
	-	0				-
	-	0				-
	-	0				-
Branchiostoma floridae	deltex homolog 3	2	P:GO:0007219; F:GO:0005515	-		-
Branchiostoma floridae	deltex homolog 3	2	P:GO:0007219; F:GO:0005515	-		-
Caenorhabditis briggsae	alkbh protein	0		F:GO:0003735; P:GO:0055114; P:GO:0006412; F:GO:0016491; C:GO:0005840; C:GO:0005622		G3DSA:2.60.120.590 (GENE3D), SSF51197 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-snf-9 protein	1	C:GO:0016020	-		IPR000175; SignalP (SIGNALP)
Caenorhabditis elegans	t-cell immunomodulatory protein	4	P:GO:0009792; P:GO:0000003; P:GO:0040007; P:GO:0002119	-		G3DSA:2.130.10.130 (GENE3D), PTHR13412 (PANTHER), SignalP (SIGNALP), SSF69318 (SUPERFAMILY)
Caenorhabditis briggsae	pyruvate ki-se	6	P:GO:0009792; F:GO:0004743; F:GO:0005515; F:GO:0030955; F:GO:0000287; P:GO:0006096	-	EC:2.7.1.40	IPR001697; IPR011037; IPR015793; IPR015806; IPR015813
	-	0				-
Brugia malayi	acyltransferase family protein	3	P:GO:0008152; C:GO:0016021; F:GO:0008415	-		-

Caenorhabditis elegans	lin-26 related family member (lir-1)	5	P:GO:0002119; P:GO:0048856; F:GO:0005488; P:GO:0040007; P:GO:0048518	-		IPR015880; PTHR14596 (PANTHER), SSF57667 (SUPERFAMILY)
	-	0				-
Brugia malayi	general transcription factor polypeptide 102kda	8	P:GO:0042797; C:GO:0000127; P:GO:0040010; P:GO:0042791; F:GO:0003677; F:GO:0003709; F:GO:0005515; P:GO:0006898	-		IPR011990; IPR013026; SSF48452 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	transmembrane anterior posterior transformation protein 1 homolog	2	P:GO:0043009; C:GO:0016020	-		IPR008010; SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-apg-1 protein	13	P:GO:0016192; F:GO:0008565; P:GO:0040010; P:GO:0009306; P:GO:0000003; C:GO:0030131; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0006886; C:GO:0044431; P:GO:0009792; P:GO:0001703	-		IPR002553; IPR011989; IPR016024; PTHR22780 (PANTHER), PTHR22780:SF5 (PANTHER)
Loa loa	sodium- and chloride-dependent neurotransmitter transporter	3	C:GO:0005887; F:GO:0005328; P:GO:0006836	-		IPR000175; IPR010916; PTHR11616:SF12 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	la ribonucleoprotein domain member 1	0				IPR006607; PTHR22792 (PANTHER), PTHR22792:SF8 (PANTHER)
Caenorhabditis elegans	la ribonucleoprotein domain member 1	0		F:GO:0003674; P:GO:0008150		IPR006607; PTHR22792 (PANTHER), PTHR22792:SF8 (PANTHER)
Caenorhabditis elegans	la ribonucleoprotein domain member 1	0				IPR006607; PTHR22792 (PANTHER), PTHR22792:SF8 (PANTHER)
Caenorhabditis elegans	protein vac14-like protein	1	F:GO:0005515	-		IPR011989; IPR016024; PTHR16023 (PANTHER)
	-	0				-
Caenorhabditis elegans	2-amino-3-carboxymuco-te-6-semialdehyde decarboxylase	5	P:GO:0006568; P:GO:0006769; F:GO:0001760; C:GO:0005829; P:GO:0046874	-	EC:4.1.1.45	IPR006992; G3DSA:3.20.20.140 (GENE3D), PTHR21240 (PANTHER), SSF51556 (SUPERFAMILY)
Caenorhabditis elegans	peptidase s9 prolyl oligopeptidase active site domain protein	1	F:GO:0008236	-		-
Caenorhabditis elegans	sorbitol dehydroge-se	3	F:GO:0046872; F:GO:0016491; P:GO:0008152	-		IPR002085; IPR011032; IPR013149; IPR016040; G3DSA:3.90.180.10 (GENE3D), PTHR11695:SF38 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				-

Caenorhabditis elegans	uncoordi-ted family member (unc-5)	0		F:GO:0004872; P:GO:0007165; F:GO:0005515		IPR000906; PTHR12582 (PANTHER), PTHR12582:SF2 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Teladorsagia circumcincta	cytochrome c oxidase subunit iii	4	P:GO:0006123; C:GO:0016021; C:GO:0005739; F:GO:0004129	-	EC:1.9.3.1	-
Caenorhabditis briggsae	ankyrin unc44	1	C:GO:0044424	-		IPR002110; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER), PTHR18958:SF250 (PANTHER)
Caenorhabditis briggsae	chromosome transmission fidelity factor 18 homolog	1	P:GO:0009987	-		IPR003959; G3DSA:3.40.50.300 (GENE3D), PTHR13779 (PANTHER), PTHR13779:SF3 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-dys-1 protein	7	P:GO:0007271; F:GO:0005515; P:GO:0040017; C:GO:0016010; F:GO:0005277; P:GO:0015870; P:GO:0046716	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	adp atp translocase	15	F:GO:0008233; P:GO:0055085; P:GO:0040010; P:GO:0008340; C:GO:0016021; C:GO:0005743; P:GO:0040002; P:GO:0040035; P:GO:0010171; P:GO:0002119; F:GO:0005515; F:GO:0005215; P:GO:0006898; P:GO:0002009; P:GO:0009792	-		IPR001993; IPR002067; IPR002113; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF35 (PANTHER)
	-	0				-
Angiostrongylus cantonensis	s- protein	3	F:GO:0008270; F:GO:0003676; C:GO:0005622	-		IPR007087; IPR015880
Loa loa	spry domain containing protein	0		F:GO:0003676; P:GO:0040011; P:GO:0040010; P:GO:0009792; P:GO:0002119; P:GO:0019915; P:GO:0040007; P:GO:0002009		PTHR12381 (PANTHER), PTHR12381:SF7 (PANTHER)
Caenorhabditis briggsae	helix loop helix family member (hlh-30)	4	P:GO:0045449; P:GO:0000003; P:GO:0019915; C:GO:0005634	-		IPR001092; IPR011598; PTHR10014 (PANTHER), PTHR10014:SF7 (PANTHER)

Caenorhabditis briggsae	helix loop helix family member (hlh-30)	4	P:GO:0045449; P:GO:0000003; P:GO:0019915; C:GO:0005634	-		IPR001092; IPR011598; PTHR10014 (PANTHER), PTHR10014:SF7 (PANTHER)
	-	0				-
Caenorhabditis elegans	membrane calcium atpase family member (mca-3)	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0005515		IPR006578
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0005515		IPR006578
Caenorhabditis elegans	guanylate cyclase	20	P:GO:0006468; F:GO:0004383; F:GO:0017046; F:GO:0016941; P:GO:0023034; F:GO:0019901; P:GO:0048662; F:GO:0004672; F:GO:0005525; C:GO:0016021; P:GO:0042417; P:GO:0030828; F:GO:0008528; P:GO:0007165; P:GO:0007186; P:GO:0007168; C:GO:0005886; P:GO:0050880; F:GO:0005524; P:GO:0008217	-	EC:4.6.1.2	-
Caenorhabditis elegans	thioredoxin family protein	5	P:GO:0040035; P:GO:0045454; P:GO:0040010; P:GO:0019915; P:GO:0006898	-		IPR012335; IPR012336; IPR013766; IPR017936; PTHR18929 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	mov34 mpn pad-1 family protein	8	C:GO:0005737; P:GO:0009792; P:GO:0002119; P:GO:0040011; F:GO:0003743; P:GO:0006898; P:GO:0006412; P:GO:0007413	-	EC:3.6.5.3	PTHR10410 (PANTHER), PTHR10410:SF3 (PANTHER)
Caenorhabditis briggsae	uba and wwe domain containing 1	0		P:GO:0030154; F:GO:0016874; F:GO:0005488; F:GO:0016881; C:GO:0005634; F:GO:0003677; C:GO:0005622; P:GO:0006464		IPR010309

Caenorhabditis briggsae	tr--nucleotidyltransferase mitochondrial	10	P:GO:0008340; C:GO:0005739; F:GO:0004810; P:GO:0040007; P:GO:0006626; F:GO:0005524; P:GO:0002119; P:GO:0042780; P:GO:0006898; F:GO:0000049	-	EC:2.7.7.25	IPR002646; G3DSA:1.10.3090.10 (GENE3D), G3DSA:3.30.460.10 (GENE3D), PTHR13734 (PANTHER), PTHR13734:SF11 (PANTHER), SSF81301 (SUPERFAMILY), SSF81891 (SUPERFAMILY)
Pan troglodytes	keratin 17	11	C:GO:0005730; P:GO:0045109; P:GO:0031424; P:GO:0051798; P:GO:0045727; F:GO:0005515; C:GO:0045095; P:GO:0030307; F:GO:0005200; P:GO:0002009; C:GO:0005737	-		-
Caenorhabditis briggsae	plbl2_caeel ame: full= phospholipase b-like 2 ame: full=lama-like protein 2 ame: full=lami- ancestor homolog 2 flags: precursor	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	glycerol-3-phosphate dehydroge-se	9	F:GO:0004368; C:GO:0009331; F:GO:0005509; P:GO:0007629; C:GO:0005743; P:GO:0006127; F:GO:0009055; P:GO:0006072; C:GO:0005811	-	EC:1.1.99.5	SignalP (SIGNALP)
Loa loa	hyaluronidase family protein	0		P:GO:0008152; F:GO:0008080		IPR011496; IPR017853; PTHR13170 (PANTHER), PTHR13170:SF5 (PANTHER)
Caenorhabditis elegans	rap guanine nucleotide exchange factor 4	14	P:GO:0048731; P:GO:0007267; F:GO:0005515; P:GO:0032879; F:GO:0000166; P:GO:0010646; P:GO:0006887; C:GO:0005737; P:GO:0051239; C:GO:0030425; C:GO:0043234; C:GO:0044459; N:GO:0035556; F:GO:0005085	-		IPR000595; IPR014710; IPR018490; SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-epac-1 protein	2	P:GO:0050794; P:GO:0023052	-		IPR000591; IPR000595; IPR008937; IPR011991; IPR014710; IPR018490; PTHR23113:SF53 (PANTHER), SignalP (SIGNALP), SSF46785 (SUPERFAMILY)
	-	0				-
	-	0				-

Caenorhabditis elegans	hypothetical protein Y18H1A.3 [Caenorhabditis elegans]	0		F:GO:0005096; P:GO:0051056; C:GO:0005622		-
Loa loa	ph domain containing protein	0				SignalP (SIGNALP)
Loa loa	formin homology 2 domain containing protein	1	F:GO:0005515	-		IPR001265; IPR003104; IPR015425; PTHR23213 (PANTHER), PTHR23213:SF12 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG08509 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0008272; C:GO:0016021; F:GO:0008271; C:GO:0016020; P:GO:0055085; F:GO:0005215; P:GO:0006810		IPR002645; IPR011547; PTHR11814 (PANTHER), PTHR11814:SF26 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0008272; C:GO:0016021; F:GO:0008271; C:GO:0016020; P:GO:0055085; F:GO:0005215; P:GO:0006810		IPR002645; IPR011547; PTHR11814 (PANTHER), PTHR11814:SF26 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0008272; C:GO:0016021; F:GO:0008271; C:GO:0016020; P:GO:0055085; F:GO:0005215; P:GO:0006810		IPR002645; IPR011547; PTHR11814 (PANTHER), PTHR11814:SF26 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	adenine nucleotide translocator family member (ant-)	15	F:GO:0008233; P:GO:0055085; P:GO:0040010; P:GO:0008340; C:GO:0016021; C:GO:0005743; P:GO:0040002; P:GO:0040035; P:GO:0010171; P:GO:0002119; F:GO:0005515; F:GO:0005215; P:GO:0006898; P:GO:0002009; P:GO:0009792	-		IPR001993; IPR002067; IPR002113; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF35 (PANTHER)
Brugia malayi	la domain containing protein	2	F:GO:0003676; F:GO:0000166	-		IPR002344; IPR006630; IPR011991; PTHR22792 (PANTHER), PTHR22792:SF7 (PANTHER), SSF46785 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	exocyst complex component 1	5	P:GO:0007126; F:GO:0005515; P:GO:0040010; P:GO:0000003; P:GO:0040011	-		IPR019160; PTHR16092 (PANTHER), PTHR16092:SF1 (PANTHER)

Caenorhabditis elegans	cleft lip and palate associated transmembrane protein	4	C:GO:0016021; P:GO:0007275; P:GO:0030154; F:GO:0005515	-		IPR008429
Loa loa	set (trithorax polycomb) domain containing family member (set-2)	6	P:GO:0016568; F:GO:0003723; P:GO:0045449; C:GO:0016607; F:GO:0018024; F:GO:0000166	-	EC:2.1.1.43	IPR001214; IPR003616; IPR015722; G3DSA:2.170.270.10 (GENE3D), PTHR22884 (PANTHER), SSF82199 (SUPERFAMILY)
Canis familiaris	ribosomal protein x-linked	8	F:GO:0019843; F:GO:0003735; P:GO:0006414; C:GO:0022627; P:GO:0045727; C:GO:0005844; P:GO:0008284; P:GO:0007275	-		IPR000876; IPR002942; IPR005824; IPR013843; IPR013845; IPR018199
Caenorhabditis briggsae	glutaminyl-peptide cyclotransferase	6	P:GO:0019915; C:GO:0005576; C:GO:0016021; F:GO:0016603; P:GO:0006508; F:GO:0008233	-	EC:2.3.2.5	IPR007484; G3DSA:3.40.630.10 (GENE3D), PTHR12283 (PANTHER), SignalP (SIGNALP), SSF53187 (SUPERFAMILY)
Bos taurus	PREDICTED: hypothetical protein [Bos taurus]	0				-
Brugia malayi	protein mothers against	14	P:GO:0048514; P:GO:0003146; P:GO:0060030; P:GO:0009880; P:GO:0006355; C:GO:0005667; P:GO:0001947; P:GO:0030509; P:GO:0043049; F:GO:0005515; P:GO:0048264; F:GO:0003700; P:GO:0007179; P:GO:0007368	-		IPR003619; IPR013019; IPR013790; PTHR13703:SF19 (PANTHER)
Caenorhabditis briggsae	abnormal dauer formation family member (daf-12)	6	F:GO:0003700; F:GO:0043565; F:GO:0003707; C:GO:0005634; F:GO:0008270; P:GO:0006355	-		-
Caenorhabditis elegans	uncoordi-ted family member (unc-52)	2	P:GO:0030239; C:GO:0005578	-		IPR002172; PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER)
	-	0				IPR001969; IPR007087; IPR015880
	-	0				-
Caenorhabditis elegans	testis derived transcript	2	F:GO:0008270; P:GO:0008340	-		-

Caenorhabditis elegans	cdc42 protein	46	P:GO:0007179; P:GO:0030011; P:GO:0032970; F:GO:0005525; P:GO:0045185; P:GO:0048813; P:GO:0000132; C:GO:0030426; P:GO:0040027; P:GO:0007411; P:GO:0050770; F:GO:0004767; P:GO:0030031; C:GO:0005626; P:GO:0007396; P:GO:0015031; P:GO:0006911; P:GO:0030866; P:GO:0007349; P:GO:0040039; P:GO:0046843; C:GO:0030424; P:GO:0006898; C:GO:0005912; P:GO:0007254; P:GO:0042060; P:GO:0046664; P:GO:0040007;	-	EC:3.1.4.12; EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Brugia malayi	peptidase family m1 containing protein	0		P:GO:0006508; F:GO:0008237; F:GO:0004177; F:GO:0008270		IPR001930; IPR015568
	-	0				-

Caenorhabditis elegans	glycoprotein 350 220	0		P:GO:0032534; P:GO:0043206; C:GO:0043205; C:GO:0019031; P:GO:0050900; C:GO:0016021; P:GO:0007155; C:GO:0016020; C:GO:0005618; C:GO:0031528; F:GO:0005509; C:GO:0030027; P:GO:0007586; P:GO:0030335; C:GO:0045121; P:GO:0072175; P:GO:0019058; C:GO:0005737; P:GO:0033634; C:GO:0001726; P:GO:0007162; C:GO:0030175; F:GO:0005515; C:GO:0005886; C:GO:0016324; C:GO:0005576; F:GO:0005201		-
Loa loa	integrator complex subunit 3	0		F:GO:0003674; P:GO:0006281; P:GO:0008150; C:GO:0005634; C:GO:0005575		IPR019333; PTHR13587 (PANTHER)
Loktanella vestfoldensis SKA53	ribosomal r- large subunit methyltransferase j	0		F:GO:0003676; F:GO:0008168; C:GO:0005737; P:GO:0006364; F:GO:0016740; F:GO:0008173; P:GO:0031167; P:GO:0032259		-
Caenorhabditis briggsae	asparagine-linked glycosylation 11 homolog (alpha- -mannosyltransferase)	6	P:GO:0002119; P:GO:0000003; P:GO:0040011; P:GO:0040007; P:GO:0006898; C:GO:0016020	-		IPR001296; PTHR12526 (PANTHER), PTHR12526:SF23 (PANTHER), SignalP (SIGNALP), SSF53756 (SUPERFAMILY)
	-	0				-
	-	0				-

Caenorhabditis elegans	mitogen-activated protein ki-se 1	26	F:GO:0004705; P:GO:0006468; P:GO:0007369; F:GO:0005515; P:GO:0050803; P:GO:0048149; P:GO:0006974; P:GO:0007507; P:GO:0006355; P:GO:0034334; P:GO:0046534; P:GO:0007173; C:GO:0005737; P:GO:0006916; P:GO:0045500; P:GO:0007067; P:GO:0008293; P:GO:0008595; P:GO:0007474; P:GO:0050804; C:GO:0030054; P:GO:0045467; C:GO:0005634; F:GO:0005524; P:GO:0040025; P:GO:0000165	-		IPR011009; IPR017441; G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF70 (PANTHER)
Brugia malayi	d- primase large subunit	5	P:GO:0040035; P:GO:0009792; P:GO:0006997; P:GO:0000910; P:GO:0006898	-		IPR007238
Caenorhabditis briggsae	uncoordi-ted family member (unc-89)	0				IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	scy1 protein ki-se	3	P:GO:0006468; F:GO:0005524; F:GO:0004672	-		IPR011989; IPR016024
Xenopus (Silurana) tropicalis	sestrin 3	0		P:GO:0007050; C:GO:0005634		IPR006730
Loa loa	phosphatidylinositol glycan anchor class p	3	F:GO:0016740; C:GO:0016021; P:GO:0016254	-		IPR013717; PTHR21726 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	phospholipase b domain containing 1-like	0		F:GO:0016787; P:GO:0008150; C:GO:0043202; P:GO:0016042; C:GO:0005575		IPR007000
Caenorhabditis elegans	peptidase m20	3	F:GO:0005515; F:GO:0008237; P:GO:0006508	-		IPR002933; G3DSA:3.40.630.10 (GENE3D), PTHR11014 (PANTHER), PTHR11014:SF5 (PANTHER), SSF53187 (SUPERFAMILY)
Loa loa	mynd finger family protein	6	C:GO:0030425; C:GO:0030424; P:GO:0030512; P:GO:0040010; F:GO:0005102; F:GO:0008270	-		-
	-	0				-

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	C:GO:0016020	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	hypothetical protein Y34B4A.7 [Caenorhabditis elegans]	0		C:GO:0016021; F:GO:0003824		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	basic transcription factor 35 kd subunit	6	P:GO:0040010; P:GO:0044260; C:GO:0005622; P:GO:0090304; P:GO:0000003; P:GO:0009792	-		IPR004600; SignalP (SIGNALP)
Pongo abelii	lactotransferrin precursor	10	F:GO:0008199; P:GO:0042742; P:GO:0006879; P:GO:0006959; P:GO:0006826; F:GO:0005515; F:GO:0004252; F:GO:0008201; C:GO:0030141; C:GO:0005576	-	EC:3.4.21.0	SignalP (SIGNALP)
Tribolium castaneum	bcnt-like protein	0				-
Caenorhabditis elegans	lbp bpi cetp n-termi-l domain containing protein	6	P:GO:0002119; P:GO:0009792; P:GO:0000003; P:GO:0040007; F:GO:0008289; P:GO:0040011	-		IPR001124; G3DSA:3.15.20.10 (GENE3D), PTHR10504 (PANTHER), PTHR10504:SF14 (PANTHER)
Caenorhabditis elegans	hypothetical protein Y20F4.2 [Caenorhabditis elegans]	0				PTHR13589 (PANTHER), PTHR13589:SF2 (PANTHER)
Caenorhabditis elegans	spectrin alpha chain	1	F:GO:0005509	-		IPR002017; G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF6 (PANTHER), SSF46966 (SUPERFAMILY)
	-	0				-
Macaca mulatta	PREDICTED: hypothetical protein LOC100426317 [Macaca mulatta]	0				-
	-	0				-
Loa loa	hmg box family protein	2	F:GO:0019899; C:GO:0044424	-		IPR000910; IPR009071; PTHR10373 (PANTHER)
Caenorhabditis elegans	hexoki-se domain containing 1	8	P:GO:0006468; P:GO:0018193; F:GO:0004396; C:GO:0005730; C:GO:0005829; P:GO:0006096; F:GO:0005524; C:GO:0005739	-	EC:2.7.1.1	IPR001312; IPR022672; G3DSA:3.30.420.40 (GENE3D), SSF53067 (SUPERFAMILY)
	-	0				-
Drosophila melanogaster	salivary glue protein	0		F:GO:0004827; F:GO:0005524; P:GO:0006412; F:GO:0004812; C:GO:0005737; P:GO:0006433		-

Brugia malayi	d--directed r- polymerase ii largest	6	F:GO:0046872; F:GO:0003899; C:GO:0005665; F:GO:0003677; F:GO:0005515; P:GO:0006366	-	EC:2.7.7.6	IPR007080; PTHR19376 (PANTHER), PTHR19376:SF14 (PANTHER), SSF64484 (SUPERFAMILY)
Ailuropoda melanoleuca	protein unc-13 homolog a	17	F:GO:0047485; C:GO:0030054; C:GO:0043234; P:GO:0023034; F:GO:0046872; F:GO:0017075; P:GO:0006887; C:GO:0042734; P:GO:0007269; P:GO:0050435; P:GO:0016188; C:GO:0019717; F:GO:0019992; F:GO:0019904; F:GO:0046982; F:GO:0042803; C:GO:0005737	-		PTHR10480 (PANTHER)
Caenorhabditis elegans	uncoordi-ted family member (unc-89)	0		F:GO:0004672; F:GO:0005524; F:GO:0000166; P:GO:0006468; F:GO:0004674		IPR003599; IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				IPR013032; SignalP (SIGNALP)
	-	0				IPR013032
	-	0				-
Caenorhabditis elegans	alonic aciduria type a protein family member (mmaa-1)	2	F:GO:0016787; F:GO:0032555	-		IPR005129; PTHR23408 (PANTHER)
Brugia malayi	hypothetical protein Bm1_49755 [Brugia malayi]	0		P:GO:0044237		-
Angiostrongylus cantonensis	c2 domain containing protein	1	P:GO:0009792	-		IPR008973; G3DSA:2.60.40.150 (GENE3D), PTHR10774 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	nuclear hormone receptor family member (nhr-49)	5	F:GO:0046872; F:GO:0004879; F:GO:0003677; P:GO:0045449; F:GO:0005515	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; P:GO:0055085; P:GO:0008340		IPR011701; IPR016196; G3DSA:1.20.1250.20 (GENE3D), PTHR10074 (PANTHER), PTHR10074:SF12 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-

Acyrthosiphon pisum	casein ki-se ii beta subunit	15	C:GO:0005956; P:GO:0033211; F:GO:0004674; P:GO:0030177; F:GO:0042802; P:GO:0043623; P:GO:0008285; F:GO:0005102; P:GO:0051101; F:GO:0019904; P:GO:0007249; F:GO:0008134; C:GO:0005737; C:GO:0005886; F:GO:0019887	-	EC:2.7.11.0	-
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	1	P:GO:0019915	-		-
Brugia malayi	major sperm protein	0		C:GO:0005737; C:GO:0005856; F:GO:0005198; C:GO:0031143; C:GO:0042995		IPR000535; IPR008962
Caenorhabditis elegans	hypothetical protein F47G3.1 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	cation chloride cotransporter	2	P:GO:0055085; C:GO:0016021	-		IPR004841; PTHR11827 (PANTHER), PTHR11827:SF2 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0006508; F:GO:0008236; F:GO:0016787; C:GO:0005576		IPR000073; G3DSA:3.40.50.1820 (GENE3D), PTHR12277 (PANTHER), PTHR12277:SF8 (PANTHER), SSF53474 (SUPERFAMILY)
	-	0				-
	-	0				-

Danio rerio	breast cancer anti-estrogen resistance 1	0		P:GO:0051301; P:GO:0008286; P:GO:0007173; F:GO:0019901; P:GO:0008283; P:GO:0016477; P:GO:0048011; P:GO:0050853; P:GO:0050852; P:GO:0007155; P:GO:0007186; P:GO:0050851; P:GO:0007015; C:GO:0005925; F:GO:0004871; P:GO:0030335; P:GO:0042981; P:GO:0001558; C:GO:0030054; C:GO:0005737; P:GO:0048008; C:GO:0001726; P:GO:0007229; C:GO:0005829; C:GO:0005624; F:GO:0005515; F:GO:0017124		-
Loa loa	stat transcription factor family member (sta-1)	10	C:GO:0005737; F:GO:0042802; F:GO:0003700; F:GO:0004871; F:GO:0003677; P:GO:0007275; F:GO:0005509; P:GO:0007165; C:GO:0005634; P:GO:0006355	-		IPR001217; IPR012345; PTHR11801:SF10 (PANTHER)
Brugia malayi	protein vac14 homolog	8	C:GO:0005856; F:GO:0004872; F:GO:0019209; F:GO:0005515; P:GO:0006970; C:GO:0005774; P:GO:0007165; C:GO:0010008	-		IPR000357; IPR011989; IPR016024; PTHR16023 (PANTHER)
Caenorhabditis elegans	malic enzyme	7	F:GO:0046872; F:GO:0051287; F:GO:0004470; P:GO:0006108; P:GO:0055114; F:GO:0016616; C:GO:0005739	-	EC:1.1.1.0	IPR012302; IPR016040; PTHR23406 (PANTHER), PTHR23406:SF2 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				-

Ancylostoma caninum	casein ki-se alpha 1	22	C:GO:0005815; C:GO:0005829; F:GO:0042277; P:GO:0040010; P:GO:0016055; F:GO:0004674; C:GO:0005625; C:GO:0005730; F:GO:0001948; P:GO:0000902; P:GO:0007507; P:GO:0000003; P:GO:0007052; P:GO:0051301; F:GO:0005524; F:GO:0000287; P:GO:0007067; F:GO:0051219; P:GO:0007165; C:GO:0000777; P:GO:0009792; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF18 (PANTHER)
Ancylostoma caninum	casein ki-se alpha 1	22	C:GO:0005815; C:GO:0005829; F:GO:0042277; P:GO:0040010; P:GO:0016055; F:GO:0004674; C:GO:0005625; C:GO:0005730; F:GO:0001948; P:GO:0000902; P:GO:0007507; P:GO:0000003; P:GO:0007052; P:GO:0051301; F:GO:0005524; F:GO:0000287; P:GO:0007067; F:GO:0051219; P:GO:0007165; C:GO:0000777; P:GO:0009792; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF18 (PANTHER)
Caenorhabditis briggsae	mannose-p-dolichol utilization defect 1 protein	0		F:GO:0003674; C:GO:0016021; C:GO:0016020; C:GO:0005575		IPR006603; PTHR12226 (PANTHER), PF04193 (PFAM)
Caenorhabditis briggsae	zinc finger protein 629-like	1	F:GO:0005515	-		IPR007087; IPR013087; IPR015880; PTHR23224 (PANTHER), PTHR23224:SF182 (PANTHER), SSF57667 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-rbc-1 protein	2	P:GO:0009987; P:GO:0050789	-		PTHR13950 (PANTHER), PTHR13950:SF1 (PANTHER)
	-	0				-
	-	0				-
Dictyocaulus viviparus	hypothetical protein isoform a [Dictyocaulus viviparus]	0				-

Caenorhabditis elegans	pwwp domain containing protein	2	P:GO:0000003; P:GO:0006898	-		-
Caenorhabditis elegans	sp1070 cg9138-pa	0		F:GO:0005488; F:GO:0005509; F:GO:0004872; P:GO:0007155; C:GO:0016021		IPR003410
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	tnni3 interacting ki-se	7	C:GO:0005737; P:GO:0006468; F:GO:0005524; F:GO:0008022; C:GO:0005634; F:GO:0004674; F:GO:0031013	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR23257 (PANTHER), PTHR23257:SF63 (PANTHER)
						IPR001298; IPR013783; IPR014756; IPR017868; PTHR11915 (PANTHER), PTHR11915:SF24 (PANTHER)
	-	0				-
Streptomyces sp. ACT-1	lpxtg-motif cell wall anchor domain protein	0		C:GO:0009986		-
Caenorhabditis briggsae	autophagy-related protein 2 homolog a-like	0				PTHR13190 (PANTHER), PTHR13190:SF2 (PANTHER)
Caenorhabditis elegans	palmitoyltransferase zdhhc17	7	F:GO:0019706; F:GO:0004871; P:GO:0042953; F:GO:0015095; C:GO:0030660; P:GO:0043123; F:GO:0005515	-		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF137 (PANTHER)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG09214 [Caenorhabditis briggsae]	0		P:GO:0006270		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Homo sapiens	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 4	2	F:GO:0016740; C:GO:0016021	-		-
Caenorhabditis briggsae	transport integral membrane protein	3	C:GO:0016020; F:GO:0015250; P:GO:0006833	-		IPR000425; PTHR19139:SF11 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	tr--dihydrouridine synthase 2-like	6	F:GO:0003725; P:GO:0055114; F:GO:0050660; F:GO:0017150; P:GO:0008033; C:GO:0005739	-		IPR001269; IPR013785; SignalP (SIGNALP), SSF51395 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				PTHR23324 (PANTHER), PTHR23324:SF3 (PANTHER)
Caenorhabditis elegans	hypothetical protein VC5.2 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	transcription factor adf-1 (adh distal factor 1)	0		F:GO:0046872; F:GO:0008270; F:GO:0005515; F:GO:0003677		IPR006578
Caenorhabditis elegans	quinine non-avoider family member (qui-1)	0				-
	-	0				SignalP (SIGNALP)

	-	0				-
Caenorhabditis elegans	cleavage and polyadenylation specificity factor subunit 5	14	C:GO:0042382; P:GO:0040010; P:GO:0040035; P:GO:0008380; C:GO:0005813; F:GO:0017091; P:GO:0002119; P:GO:0040011; P:GO:0006397; F:GO:0042803; P:GO:0009792; F:GO:0016787; F:GO:0042826; P:GO:0016246	-		IPR000086; PTHR13047 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	P:GO:0040010	-		IPR002544; SignalP (SIGNALP)
Caenorhabditis briggsae	dipeptidyl anminopeptidase	1	F:GO:0008236	-		IPR001375; G3DSA:3.40.50.1820 (GENE3D), PTHR11731 (PANTHER), PTHR11731:SF7 (PANTHER), SSF53474 (SUPERFAMILY)
Brugia malayi	piwi domain containing protein	1	P:GO:0002119	-		IPR003165; IPR012337; PTHR22891 (PANTHER)
	-	0				-
Brugia malayi	vesicle-fusing atpase	10	P:GO:0009792; P:GO:0002119; F:GO:0005515; P:GO:0032940; F:GO:0005524; P:GO:0000003; P:GO:0040011; F:GO:0017111; P:GO:0040007; P:GO:0006898	-	EC:3.6.1.15	IPR003338; IPR004201; IPR009010; G3DSA:3.10.330.10 (GENE3D), PTHR23078 (PANTHER), SSF54585 (SUPERFAMILY)
	-	0				-
Loa loa	gtp-ase activating protein for arf containing protein	0		F:GO:0008060; P:GO:0032312; F:GO:0008270		-
	-	0				-
Caenorhabditis elegans	germi-l center ki-se family member (gck-1)	8	F:GO:0042802; P:GO:0006468; F:GO:0046872; P:GO:0006979; C:GO:0005794; F:GO:0005524; P:GO:0007165; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF95 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR009432
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR009432
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR009432
Brugia malayi	upf0558 protein	0				IPR019410; G3DSA:3.40.50.150 (GENE3D), PTHR21095 (PANTHER), SSF53335 (SUPERFAMILY)
Caenorhabditis elegans	wd repeat and fyve domain containing 3 isoform 1	1	F:GO:0005488	-		-
Caenorhabditis elegans	transmembrane amino acid transporter protein	3	P:GO:0019915; P:GO:0040010; P:GO:0040011	-		IPR013057; PTHR22950 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein F29B9.12 [Caenorhabditis elegans]	0				SignalP (SIGNALP)

Caenorhabditis elegans	mitochondrial ribosomal protein l36	4	C:GO:0005840; F:GO:0003735; P:GO:0040010; P:GO:0006412	-	EC:3.6.5.3	IPR000473; PD002101 (PRODOM), PTHR18804:SF5 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	6	C:GO:0016021; P:GO:0009792; P:GO:0040018; P:GO:0008340; P:GO:0040010; P:GO:0002119	-		-
	-	0				-
Caenorhabditis briggsae	mboat family protein	2	C:GO:0016020; P:GO:0010171	-		PTHR13906 (PANTHER), PTHR13906:SF2 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	zinc finger fyve domain-containing protein 19	0		F:GO:0046872; F:GO:0008270; C:GO:0005575		IPR000306; IPR011011; IPR013083; IPR017455; PTHR12673 (PANTHER), PTHR12673:SF5 (PANTHER)
Brugia malayi	xpa-binding protein 2	5	F:GO:0005488; P:GO:0000381; C:GO:0071011; P:GO:0006911; C:GO:0071013	-		IPR003107; IPR011990; PTHR11246 (PANTHER), PTHR11246:SF5 (PANTHER), SSF48452 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-tag-264 protein	5	P:GO:0040035; P:GO:0002119; P:GO:0040039; P:GO:0040018; P:GO:0006974	-		IPR010793
Brugia malayi	esophageal cancer associated protein	0		F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150		PTHR13673 (PANTHER)
	-	0				-
Caenorhabditis briggsae	leucine-rich repeat-containing protein 68	0		F:GO:0003674; P:GO:0008150		G3DSA:3.80.10.10 (GENE3D), PTHR13824 (PANTHER), PTHR13824:SF6 (PANTHER), SSF52047 (SUPERFAMILY)
Caenorhabditis briggsae	leucine-rich repeat-containing protein 68	0		F:GO:0003674; P:GO:0008150		G3DSA:3.80.10.10 (GENE3D), PTHR13824 (PANTHER), PTHR13824:SF6 (PANTHER), SSF52047 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	40s ribosomal protein s2	10	P:GO:0009792; P:GO:0002119; F:GO:0003735; C:GO:0005811; F:GO:0003723; F:GO:0005515; P:GO:0000003; C:GO:0022627; P:GO:0040007; P:GO:0006412	-	EC:3.6.5.3	IPR000851; IPR005324; IPR005711; IPR013810; IPR014720; IPR014721; IPR018192; IPR020568; PTHR13718:SF4 (PANTHER), SSF54768 (SUPERFAMILY)

Caenorhabditis briggsae	40s ribosomal protein s2	9	P:GO:0009792; P:GO:0002119; F:GO:0003735; F:GO:0003723; F:GO:0005515; P:GO:0040010; C:GO:0015935; P:GO:0000003; P:GO:0006412	-	EC:3.6.5.3	IPR001662; PTHR11260 (PANTHER), PTHR11260:SF2 (PANTHER)
Caenorhabditis briggsae	40s ribosomal protein s2	10	P:GO:0009792; P:GO:0002119; F:GO:0003735; C:GO:0005811; F:GO:0003723; F:GO:0005515; P:GO:0000003; C:GO:0022627; P:GO:0040007; P:GO:0006412	-	EC:3.6.5.3	IPR000851; IPR005324; IPR005711; IPR013810; IPR014720; IPR014721; IPR018192; IPR020568; PTHR13718:SF4 (PANTHER), SSF54768 (SUPERFAMILY)
Caenorhabditis briggsae	40s ribosomal protein s2	9	P:GO:0009792; P:GO:0002119; F:GO:0003735; F:GO:0003723; F:GO:0005515; P:GO:0040010; C:GO:0015935; P:GO:0000003; P:GO:0006412	-	EC:3.6.5.3	IPR001662; PTHR11260 (PANTHER), PTHR11260:SF2 (PANTHER)
Caenorhabditis briggsae	40s ribosomal protein s2	10	P:GO:0009792; P:GO:0002119; F:GO:0003735; C:GO:0005811; F:GO:0003723; F:GO:0005515; P:GO:0000003; C:GO:0022627; P:GO:0040007; P:GO:0006412	-	EC:3.6.5.3	IPR000851; IPR005324; IPR005711; IPR013810; IPR014720; IPR014721; IPR018192; IPR020568; PTHR13718:SF4 (PANTHER), SSF54768 (SUPERFAMILY)
Caenorhabditis briggsae	40s ribosomal protein s2	9	P:GO:0009792; P:GO:0002119; F:GO:0003735; F:GO:0003723; F:GO:0005515; P:GO:0040010; C:GO:0015935; P:GO:0000003; P:GO:0006412	-	EC:3.6.5.3	IPR001662; PTHR11260 (PANTHER), PTHR11260:SF2 (PANTHER)
	-	0				-
	-	0				-

Homo sapiens	cathepsin d	10	F:GO:0042277; C:GO:0005764; C:GO:0005739; P:GO:0008219; C:GO:0005615; P:GO:0000045; P:GO:0006508; C:GO:0042470; F:GO:0004190; C:GO:0031012	-	EC:3.4.23.0	IPR001461; IPR001969; IPR009007; IPR021109; PTHR13683:SF84 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-vab-9 protein	0		C:GO:0016021; C:GO:0016020		IPR015664; SignalP (SIGNALP)
Caenorhabditis sp. PS1010	chromatin assembly factor 1 subunit b	1	P:GO:0000003	-		PTHR15271 (PANTHER), SignalP (SIGNALP)
	-	0				-
Ostertagia ostertagi	metalloprotease 1 precursor	3	F:GO:0004222; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	-
	-	0				-
Caenorhabditis elegans	per1-like domain containing 1	4	F:GO:0005515; C:GO:0043231; C:GO:0044444; C:GO:0016020	-		IPR007217; SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0005524; F:GO:0004672; P:GO:0006468		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	briggsae cbr-him-17 protein	0				-
	-	0				-
						IPR002172; PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG19064 [Caenorhabditis briggsae]	0		F:GO:0005524		-
	-	0				-
Pristionchus pacificus	abnormal dauer formation family member (daf-12)	4	F:GO:0046872; F:GO:0004879; F:GO:0003677; P:GO:0045449	-		IPR008946
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	g protein-coupled receptor	0		F:GO:0004872; C:GO:0016021; P:GO:0007186		SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-emb-27 protein	3	P:GO:0000279; P:GO:0000003; P:GO:0007275	-		-
Brugia malayi	ino80 complex subunit d- partial	0				-
	-	0				SignalP (SIGNALP)

Brugia malayi	cd151 antigen	6	P:GO:0010171; P:GO:0002119; P:GO:0040002; P:GO:0000003; C:GO:0016021; P:GO:0040007	-		IPR018499; PTHR19282 (PANTHER), PTHR19282:SF27 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	abnormal go-d development family member (gon-2)	6	P:GO:0007067; P:GO:0055085; P:GO:0006811; C:GO:0016021; P:GO:0008406; F:GO:0005216	-		PTHR13800 (PANTHER)
	-	0				-
Caenorhabditis elegans	glycosyl hydrolases family 31 protein	2	P:GO:0008152; F:GO:0004553	-	EC:3.2.1.0	IPR000322; IPR017853; PTHR22762:SF10 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-mlt-7 protein	4	F:GO:0020037; P:GO:0055114; F:GO:0004601; P:GO:0006979	-	EC:1.11.1.7	-
Caenorhabditis elegans	tubulin--tyrosine ligase-like protein 12	1	C:GO:0009507	-		-
Caenorhabditis elegans	ras-related protein rab-7	3	P:GO:0015031; F:GO:0005525; P:GO:0007264	-		-
	-	0				-
Caenorhabditis elegans	a-phase promoting complex subunit 10	12	C:GO:0005654; P:GO:0070979; F:GO:0005515; P:GO:0051437; C:GO:0005680; P:GO:0051436; C:GO:0005829; F:GO:0004842; P:GO:0000090; P:GO:0031145; P:GO:0030071; P:GO:0000086	-	EC:6.3.2.19	-
Brugia malayi	probable molybdopterin binding domain containing protein	7	P:GO:0007416; F:GO:0032947; P:GO:0051260; C:GO:0045202; F:GO:0005102; F:GO:0042803; C:GO:0005737	-		IPR001453; IPR005110; IPR005111; IPR008284; IPR020817; G3DSA:2.170.190.11 (GENE3D), G3DSA:2.40.340.10 (GENE3D), G3DSA:3.90.105.10 (GENE3D), PTHR10192 (PANTHER)
Macaca mulatta	elongation factor 2	8	F:GO:0003746; P:GO:0006414; P:GO:0006184; F:GO:0005515; F:GO:0003924; C:GO:0030529; C:GO:0005737; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000640; IPR005517; IPR009022; IPR014721; IPR020568; G3DSA:3.30.70.870 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF4 (PANTHER)
Sordaria macrospora	un-med protein product [Sordaria macrospora]	0				-
	-	0				-

Thermomicrobium roseum DSM 5159	kinesin family protein	0		F:GO:0003723; C:GO:0005634; F:GO:0003674; F:GO:0005524; F:GO:0046872; F:GO:0016301; C:GO:0016020; P:GO:0007018; F:GO:0003700; F:GO:0004222; P:GO:0008150; F:GO:0003824; F:GO:0000166; C:GO:0005874; P:GO:0006508; F:GO:0008663; F:GO:0003777; F:GO:0003774; F:GO:0008270; C:GO:0005886; C:GO:0005575		-
Caenorhabditis elegans	briggsae cbr-nol-9 protein	0		P:GO:0000003; P:GO:0006974		G3DSA:3.40.50.300 (GENE3D), PF03205 (PFAM)
	-	0				SignalP (SIGNALP)
Loa loa	set1 ash2 histone methyltransferase complex subunit ash2-like	4	P:GO:0040007; P:GO:0040027; P:GO:0040035; F:GO:0005515	-		-
Caenorhabditis briggsae	mitogen-activated protein ki-se 8 isoform 2	3	P:GO:0009987; F:GO:0005488; F:GO:0016740	-		IPR000719; IPR006578; IPR011009; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF62 (PANTHER)
Caenorhabditis elegans	ubiquinone me-quinone biosynthesis methyltransferase	3	P:GO:0006744; P:GO:0008340; F:GO:0008168	-	EC:2.1.1.0	-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	valyl-tr- synthetase	2	F:GO:0016874; P:GO:0006412	-	EC:3.6.5.3	IPR002300; IPR002303; IPR009008; IPR014729; G3DSA:3.90.740.10 (GENE3D), PTHR11946 (PANTHER), SSF52374 (SUPERFAMILY)
	-	0				-
Loa loa	patched family protein	0		C:GO:0016021; C:GO:0016020; F:GO:0008158		IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	isoleucyl-tr- synthetase	6	F:GO:0005515; P:GO:0006428; F:GO:0005524; F:GO:0004822; C:GO:0005829; F:GO:0008270	-	EC:6.1.1.5	IPR001412; IPR002300; IPR002301; IPR009008; IPR014729; G3DSA:3.90.740.10 (GENE3D), PTHR11946 (PANTHER), SSF52374 (SUPERFAMILY)
Caenorhabditis elegans	sy-ptophysin sy-ptoporin family protein	1	C:GO:0016021	-		IPR008253; PTHR22776 (PANTHER), PTHR22776:SF6 (PANTHER), SignalP (SIGNALP)

Magnetococcus sp. MC-1	elegans protein confirmed by transcript evidence	0		P:GO:0060271; F:GO:0003674; P:GO:0060041; P:GO:0010842; P:GO:0008150; P:GO:0007018; F:GO:0005515		-
	-	0				-
Caenorhabditis elegans	udp-n-acetylglucosamine transporter	5	F:GO:0005515; P:GO:0000003; P:GO:0008643; C:GO:0016020; F:GO:0015144	-		-
	-	0				-
Caenorhabditis elegans	adp-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin a-inhibited)	14	F:GO:0050811; C:GO:0005829; P:GO:0040010; P:GO:0023034; C:GO:0000139; P:GO:0006887; P:GO:0000003; F:GO:0005085; P:GO:0002119; C:GO:0005802; P:GO:0040011; P:GO:0006898; F:GO:0017022; P:GO:0009792	-		PTHR10663 (PANTHER), PTHR10663:SF1 (PANTHER), SignalP (SIGNALP)
Homo sapiens	h+ lysosomal v1 subunit f	10	F:GO:0046933; C:GO:0016471; P:GO:0015986; P:GO:0006200; C:GO:0005624; F:GO:0005515; F:GO:0046961; F:GO:0042624; P:GO:0060041; C:GO:0033180	-	EC:3.6.3.14; EC:3.6.1.3	IPR005772; IPR008218; G3DSA:3.40.50.10580 (GENE3D)
Caenorhabditis elegans	pan domain containing protein	0				IPR003014; IPR003609
	-	0				-
Brugia malayi	tk fer protein ki-se	2	F:GO:0005488; F:GO:0016301	-		-
Caenorhabditis elegans	d- helicase hel308	4	F:GO:0003676; F:GO:0008026; F:GO:0000166; P:GO:0006139	-		IPR001650; IPR011545; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR11752 (PANTHER), PTHR11752:SF3 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	steroidogenic acute regulatory protein	6	P:GO:0010033; P:GO:0044237; P:GO:0006694; P:GO:0050794; C:GO:0044444; P:GO:0032501	-		IPR002913; G3DSA:3.30.530.20 (GENE3D), PTHR12136 (PANTHER), PTHR12136:SF11 (PANTHER), SSF55961 (SUPERFAMILY)
Populus trichocarpa	retrotransposon protein	0				-

Loa loa	tribbles homolog 3	8	P:GO:0032270; P:GO:0045859; P:GO:0031327; P:GO:0044093; P:GO:0043687; F:GO:0019899; C:GO:0005634; F:GO:0030234	-		IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22961 (PANTHER), PTHR22961:SF3 (PANTHER)
	-	0				-
Caenorhabditis elegans	myosin light polypeptide 5 regulatory	3	C:GO:0016020; P:GO:0009987; P:GO:0006810	-		IPR011701; IPR016196; G3DSA:1.20.1250.20 (GENE3D), PTHR10924 (PANTHER)
Caenorhabditis briggsae	alix (apoptosis-linked gene 2 interacting protein x) homolog family member (alx-1)	0				IPR004328; G3DSA:1.20.140.50 (GENE3D), G3DSA:1.25.40.280 (GENE3D), PTHR23030 (PANTHER)
Caenorhabditis elegans	d- binding protein elf-1	13	P:GO:0008360; P:GO:0007009; P:GO:0007426; P:GO:0040007; P:GO:0000003; F:GO:0003677; P:GO:0007399; P:GO:0002119; P:GO:0042127; F:GO:0003704; P:GO:0035159; P:GO:0008362; C:GO:0005634	-		-
	-	0				-
Caenorhabditis elegans	coiled-coil domain-containing protein 130	2	F:GO:0005515; P:GO:0009615	-		IPR007590
Caenorhabditis elegans	coiled-coil domain-containing protein 130	2	F:GO:0005515; P:GO:0009615	-		IPR007590
Caenorhabditis elegans	coiled-coil domain-containing protein 130	2	F:GO:0005515; P:GO:0009615	-		IPR007590
Caenorhabditis briggsae	par-6 at contacts (abnormal early localization of par-6) family member (pac-1)	2	F:GO:0005096; P:GO:0007165	-		IPR001849; PTHR23175 (PANTHER), PTHR23175:SF3 (PANTHER)
Caenorhabditis briggsae	ufl1_caebr ame: full=e3 ufm1-protein ligase 1 homolog	0		F:GO:0016874		-
Loa loa	repressor of r- polymerase iii transcription maf1-like protein	1	P:GO:0040010	-		IPR015257
Loa loa	repressor of r- polymerase iii transcription maf1-like protein	1	P:GO:0040010	-		IPR015257
	-	0				PR01217 (PRINTS)
Caenorhabditis elegans	autophagy-related protein 3	4	F:GO:0016879; P:GO:0006810; P:GO:0006996; P:GO:0006914	-		IPR007134; IPR018247; PTHR12866 (PANTHER)
Loa loa	ulp1 protease c-termi-l catalytic domain containing protein	0		C:GO:0005634; P:GO:0000003; P:GO:0002119; P:GO:0009792; F:GO:0008234; F:GO:0008233; P:GO:0006508; P:GO:0040010; P:GO:0040007		-

Loa loa	ulp1 protease c-termi-l catalytic domain containing protein	0		C:GO:0005634; P:GO:0000003; P:GO:0002119; P:GO:0009792; F:GO:0008234; F:GO:0008233; P:GO:0006508; P:GO:0040010; P:GO:0040007		-
Loa loa	dehydrodolichyl diphosphate synthase	2	F:GO:0000166; F:GO:0016765	-		IPR001441
	-	0				-
Caenorhabditis briggsae	ys48_caeel ame: full=uncharacterized protein	0		P:GO:0000003		-
Caenorhabditis elegans	lim domain family member (lim-9)	1	F:GO:0008270	-		IPR010442; PTHR18973 (PANTHER), PTHR18973:SF105 (PANTHER)
	-	0				-
	-	0				IPR008555
Heligmosomoides polygyrus	glutathione s-transferase	4	P:GO:0008340; P:GO:0040010; F:GO:0005515; F:GO:0016740	-		IPR004046; IPR010987; IPR017933; PTHR11571 (PANTHER), PTHR11571:SF6 (PANTHER)
Loa loa	methyl-cpg binding protein	2	C:GO:0043229; F:GO:0005488	-		PTHR12396 (PANTHER)
Loa loa	laminin a	2	C:GO:0005604; P:GO:0007155	-		IPR001791; IPR008985; IPR010916; IPR012680; IPR013320; PTHR10574 (PANTHER), PTHR10574:SF56 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-oct-2 protein	0		C:GO:0016021; P:GO:0055085; P:GO:0006810; F:GO:0005215		-
Caenorhabditis briggsae	Hypothetical protein CBG06638 [Caenorhabditis briggsae]	0				-
Loa loa	btb poz domain-containing protein 2	3	F:GO:0005515; P:GO:0040011; C:GO:0000932	-		IPR000210; IPR011333; IPR011705; IPR012983; IPR013069; IPR013089; PTHR23230:SF48 (PANTHER)
Loa loa	elegans protein partially confirmed by transcript evidence	4	F:GO:0008483; P:GO:0019915; P:GO:0008152; F:GO:0016829	-	EC:2.6.1.0	IPR001176; IPR004839; IPR015421; IPR015424; PTHR11751 (PANTHER), PTHR11751:SF38 (PANTHER)
Loa loa	elegans protein partially confirmed by transcript evidence	4	F:GO:0008483; P:GO:0019915; P:GO:0008152; F:GO:0016829	-	EC:2.6.1.0	IPR001176; IPR004839; IPR015421; IPR015424; PTHR11751 (PANTHER), PTHR11751:SF38 (PANTHER)
	-	0				-
Caenorhabditis elegans	hypothetical protein Y54H5A.2 [Caenorhabditis elegans]	0				-
Brugia malayi	mynd finger family protein	7	P:GO:0040010; P:GO:0030514; C:GO:0030424; F:GO:0008270; P:GO:0030512; C:GO:0030425; F:GO:0005102	-		IPR002893; PTHR13712 (PANTHER), PTHR13712:SF13 (PANTHER), SSF144232 (SUPERFAMILY)
Caenorhabditis elegans	protein ki-se domain containing protein	2	F:GO:0016301; P:GO:0000003	-		PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
	-	0				-

Caenorhabditis elegans	briggsae cbr-itsn-1 protein	5	C:GO:0005829; F:GO:0005085; F:GO:0005515; P:GO:0008624; C:GO:0005886	-		IPR001452; G3DSA:2.30.30.40 (GENE3D), PTHR11216 (PANTHER), PTHR11216:SF24 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-unc-112 protein	4	F:GO:0050839; C:GO:0005737; P:GO:0007160; P:GO:0007517	-		IPR001849; IPR011993; IPR014352; IPR019748; PTHR16160 (PANTHER), PTHR16160:SF3 (PANTHER), SSF50729 (SUPERFAMILY)
Caenorhabditis briggsae	iq calmodulin-binding motif family protein	4	C:GO:0016020; P:GO:0007165; P:GO:0007339; F:GO:0008603	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	8	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040011; P:GO:0019915; P:GO:0040007; P:GO:0006898; F:GO:0042302	-		IPR008160; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	8	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040011; P:GO:0019915; P:GO:0040007; P:GO:0006898; F:GO:0042302	-		IPR008160; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER)
Brugia malayi	methylenetetrahydrofolate reductase	5	F:GO:0005515; P:GO:0040010; P:GO:0055114; F:GO:0004489; P:GO:0006555	-	EC:1.5.1.20	IPR003171; G3DSA:3.20.20.220 (GENE3D), PTHR21091 (PANTHER), PTHR21091:SF1 (PANTHER), SSF51730 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	13	P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0006915; P:GO:0040018; F:GO:0003676; C:GO:0005622; P:GO:0040010; P:GO:0008340; P:GO:0040011; P:GO:0019915; F:GO:0008270; P:GO:0002009	-		-
Caenorhabditis elegans	protein kiaa0286	1	F:GO:0005515	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)

Homo sapiens	-dh dehydroge-se subunit 4	9	P:GO:0001666; P:GO:0006810; F:GO:0008137; C:GO:0005747; C:GO:0016021; P:GO:0021549; P:GO:0006120; P:GO:0007568; P:GO:0009790	-	EC:1.6.5.3	-
Loa loa	cg31690- isoform b	0		F:GO:0005524; F:GO:0005509; C:GO:0016021; F:GO:0042626; P:GO:0055085; F:GO:0005515; P:GO:0006810		-
Canis familiaris	cg31690- isoform b	0		F:GO:0005524; C:GO:0016021; F:GO:0042626; P:GO:0055085; P:GO:0006810		-
Caenorhabditis elegans	n-acetyl galactosaminyl transferase 6	7	C:GO:0000139; F:GO:0004653; F:GO:0005529; F:GO:0046872; C:GO:0005795; P:GO:0009312; C:GO:0016021	-	EC:2.4.1.41	PTHR11675 (PANTHER), SSF53448 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-sec-3 protein	5	P:GO:0007126; P:GO:0000003; P:GO:0040010; F:GO:0005515; P:GO:0040011	-		IPR011993
Caenorhabditis briggsae	briggsae cbr-toh-1 protein	3	F:GO:0004222; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	-
Caenorhabditis briggsae	novel protein human and mouse coiled-coil and c2 domain containing 1a	1	F:GO:0005515	-		PTHR13076 (PANTHER)
Homo sapiens	subfamily member 1	12	P:GO:0007283; F:GO:0046872; P:GO:0006457; F:GO:0050750; F:GO:0031072; P:GO:0030521; P:GO:0006986; F:GO:0005524; F:GO:0051082; C:GO:0016020; P:GO:0030317; P:GO:0009408	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	ysv3_caeel ame: full=uncharacterized protein	0				-

Brugia malayi	rap guanine nucleotide exchange factor 4	25	F:GO:0008603; C:GO:0001750; P:GO:0017157; P:GO:0019933; C:GO:0043197; F:GO:0005088; P:GO:0051056; P:GO:0017156; C:GO:0016323; C:GO:0005829; F:GO:0030552; P:GO:0001932; F:GO:0017016; C:GO:0060076; F:GO:0004692; C:GO:0005952; C:GO:0030424; P:GO:0030073; P:GO:0050790; F:GO:0032403; P:GO:0050805; C:GO:0001917; P:GO:0014911; C:GO:0016324; P:GO:0050773	-	EC:2.7.11.12	IPR000595; IPR002373; IPR008937; IPR014710; IPR018490; PTHR23113:SF53 (PANTHER)
	-	0				-
Caenorhabditis elegans	protein-tyrosine phosphatase containing protein	2	F:GO:0016791; F:GO:0005515	-	EC:3.1.3.0	IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF19 (PANTHER), SSF52799 (SUPERFAMILY)
Ancylostoma ceylanicum	secreted protein 5 precursor	0		P:GO:0040011; P:GO:0006898; C:GO:0005576		IPR014044
Caenorhabditis elegans	c2 domain containing protein	2	F:GO:0046872; C:GO:0016021	-		PTHR21119 (PANTHER), PTHR21119:SF1 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-ptr-8 protein	5	P:GO:0018996; C:GO:0016021; P:GO:0040018; F:GO:0008158; P:GO:0040011	-		IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG05384 [Caenorhabditis briggsae]	1	P:GO:0040011	-		-
Caenorhabditis elegans	c2 domain containing protein	0		F:GO:0046872; C:GO:0016021; P:GO:0023034		IPR000008; IPR008973; IPR018029; G3DSA:2.60.40.150 (GENE3D), PTHR21119 (PANTHER), PTHR21119:SF1 (PANTHER)
Hydra magnipapillata	forkhead transcription factor fkh1	4	P:GO:0010552; F:GO:0010843; P:GO:0042472; F:GO:0016563	-		IPR001766; IPR011991; IPR018122; SSF46785 (SUPERFAMILY)
Hydra magnipapillata	forkhead transcription factor fkh1	4	P:GO:0010552; F:GO:0010843; P:GO:0042472; F:GO:0016563	-		IPR001766; IPR011991; IPR018122; SSF46785 (SUPERFAMILY)

Caenorhabditis elegans	class type 10d	9	C:GO:0005739; C:GO:0016021; F:GO:0015662; P:GO:0006811; P:GO:0006754; F:GO:0005524; P:GO:0015914; F:GO:0000287; F:GO:0004012	-	EC:3.6.3.1	IPR001757; G3DSA:2.70.150.10 (GENE3D), PTHR11939:SF14 (PANTHER), SSF81665 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	atlastin gtpase 1	12	P:GO:0007029; C:GO:0016021; P:GO:0051260; F:GO:0042802; P:GO:0006184; C:GO:0005792; C:GO:0042995; P:GO:0007409; F:GO:0003924; C:GO:0005789; F:GO:0005525; C:GO:0000137	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR015894; G3DSA:3.40.50.300 (GENE3D), PTHR10751 (PANTHER), PTHR10751:SF3 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	mitochondrial 2-oxoglutarate malate carrier protein	6	F:GO:0004651; F:GO:0004016; P:GO:0006370; C:GO:0031533; F:GO:0005515; P:GO:0006171	-	EC:3.1.3.33; EC:4.6.1.1	IPR004206; IPR008172; PD009560 (PRODOM), G3DSA:2.40.320.10 (GENE3D), PTHR21028 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-brp-1 protein	0		F:GO:0005515		-
Caenorhabditis briggsae	briggsae cbr-brp-1 protein	0		F:GO:0005515		-
Caenorhabditis briggsae	briggsae cbr-brp-1 protein	0		F:GO:0005515		-
Caenorhabditis briggsae	briggsae cbr-brp-1 protein	0		F:GO:0005515		-
	-	0				SignalP (SIGNALP)
	-	0				-
Brugia malayi	immunoglobulin i-set domain containing protein	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	P:GO:0040010; P:GO:0040011	-		IPR004888; PTHR10412 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	ornithine decarboxylase	2	P:GO:0006596; F:GO:0004586	-	EC:4.1.1.17	IPR000183; IPR002433; IPR022644; IPR022653; G3DSA:3.20.20.10 (GENE3D), PTHR11482 (PANTHER), PTHR11482:SF4 (PANTHER), SSF51419 (SUPERFAMILY)
Ailuropoda melanoleuca	ribosomal protein l11	11	P:GO:0006917; C:GO:0005730; P:GO:0006364; P:GO:0042273; F:GO:0019843; F:GO:0003735; P:GO:0006414; P:GO:0006605; F:GO:0005515; C:GO:0022625; P:GO:0009790	-		IPR002132; IPR020929; IPR022803; PTHR11994:SF2 (PANTHER)

Homo sapiens	annexin a2	19	F:GO:0008092; P:GO:0001525; F:GO:0017137; C:GO:0043234; C:GO:0005625; F:GO:0005509; P:GO:0042730; F:GO:0005544; C:GO:0005604; P:GO:0001501; F:GO:0005546; P:GO:0007589; C:GO:0042470; C:GO:0005769; P:GO:0030199; C:GO:0048471; C:GO:0042383; F:GO:0004859; P:GO:0031340	-		IPR001464; IPR002389; IPR018252; IPR018502
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-dnj-22 protein	10	P:GO:0009792; P:GO:0002119; P:GO:0042127; P:GO:0040020; P:GO:0040010; P:GO:0000003; P:GO:0040019; P:GO:0006898; P:GO:0040039; P:GO:0002009	-		-
Ixodes scapularis	divergent aaa domain protein	0		F:GO:0004386; F:GO:0005524		IPR007421; PTHR10967 (PANTHER), PTHR10967:SF41 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-rnp-7 protein	8	C:GO:0030532; F:GO:0003729; C:GO:0071011; P:GO:0000381; P:GO:0048025; P:GO:0007052; F:GO:0000166; C:GO:0071013	-		IPR000504; IPR012677; IPR022023; PTHR13952 (PANTHER), SSF54928 (SUPERFAMILY)
Brugia malayi	u1 small nuclear ribonucleoprotein 70 kda	5	P:GO:0043484; C:GO:0005681; F:GO:0003723; F:GO:0005515; P:GO:0000398	-		-
Branchiostoma floridae	steroid-5-alpha- alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydroge-se alpha 1)	12	P:GO:0007530; C:GO:0016021; F:GO:0003865; P:GO:0055114; F:GO:0009055; P:GO:0046661; C:GO:0005792; P:GO:0030154; C:GO:0048471; P:GO:0042493; P:GO:0006702; C:GO:0005789	-	EC:1.3.99.5	IPR001104; PTHR10556 (PANTHER), PTHR10556:SF6 (PANTHER), SignalP (SIGNALP)

	-	0				-
Caenorhabditis briggsae	g-patch domain containing protein	0		F:GO:0003676; F:GO:0003723; F:GO:0003725; C:GO:0005622		PTHR12813 (PANTHER), PTHR12813:SF5 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG03866 [Caenorhabditis briggsae]	0		F:GO:0005488		SignalP (SIGNALP)
Brugia malayi	nuclear receptor co-repressor 1	12	F:GO:0003714; F:GO:0042826; C:GO:0017053; P:GO:0046329; P:GO:0051225; C:GO:0005737; P:GO:0010553; F:GO:0003677; P:GO:0021549; C:GO:0000118; C:GO:0005876; F:GO:0035257	-		IPR001005; IPR009057; IPR017884; PTHR13992 (PANTHER)
Caenorhabditis briggsae	udp-galactose transporter	2	P:GO:0006810; C:GO:0016020	-		IPR013657; PTHR10778 (PANTHER), PTHR10778:SF4 (PANTHER), SignalP (SIGNALP)
Xenopus laevis	phosphatidylinositol-specific phospholipase x domain containing 2	0		P:GO:0006629; F:GO:0016787; P:GO:0023034; P:GO:0016042; F:GO:0003674; F:GO:0008081; C:GO:0005575; F:GO:0004629; F:GO:0004871		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	lethal family member (let-805)	8	P:GO:0018996; P:GO:0009792; P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		IPR003961; IPR008957; IPR013783
Caenorhabditis elegans	charged multivesicular body protein 2a	3	P:GO:0015031; P:GO:0009792; C:GO:0031902	-		IPR005024; PTHR10476 (PANTHER), PTHR10476:SF4 (PANTHER)
Caenorhabditis elegans	suppressor of constitutive dauer formation family member (scd-1)	1	P:GO:0040010	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		C:GO:0005764; F:GO:0003674; P:GO:0040002; C:GO:0016021; P:GO:0046686; P:GO:0040010; P:GO:0002119; P:GO:0040007		IPR010987; PTHR12289 (PANTHER), PTHR12289:SF2 (PANTHER)
Caenorhabditis elegans	notch homolog scalloped wings	0		F:GO:0005488; F:GO:0005509; P:GO:0040010		-

Caenorhabditis briggsae	phosphoenolpyruvate carboxyki-se	4	C:GO:0005737; P:GO:0006094; F:GO:0005525; F:GO:0004613	-	EC:4.1.1.32	-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	P:GO:0009792; C:GO:0016021	-		-
Caenorhabditis briggsae	pseudouridylate synthase 10	2	P:GO:0009451; F:GO:0016853	-		IPR020103; PTHR21568 (PANTHER)
Caenorhabditis briggsae	pseudouridylate synthase 10	2	P:GO:0009451; F:GO:0016853	-		IPR020103; PTHR21568 (PANTHER)
Caenorhabditis briggsae	-galactosyltransferase 7	2	F:GO:0016757; P:GO:0005975	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
Drosophila willistoni	GK15899 [Drosophila willistoni]	0				-
	-	0				IPR017956
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Trichomonas vaginalis G3	viral a-type inclusion protein	0		C:GO:0000139; F:GO:0000166; C:GO:0005737; F:GO:0003779; F:GO:0005524; C:GO:0016459; F:GO:0003774; P:GO:0006886; P:GO:0048280; F:GO:0005488		PD968187 (PRODOM)
Brugia malayi	hypothetical protein Bm1_33560 [Brugia malayi]	0		P:GO:0007049; C:GO:0000775; P:GO:0007067; C:GO:0005634		-
Caenorhabditis elegans	ankyrin repeat and socs box-containing 8	0		P:GO:0009116; C:GO:0005737; F:GO:0003824; P:GO:0023034; C:GO:0005634		IPR001496; IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF263 (PANTHER)
Caenorhabditis elegans	ankyrin repeat and socs box-containing 8	0		P:GO:0009116; C:GO:0005737; F:GO:0003824; P:GO:0023034; C:GO:0005634		IPR001496; IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF263 (PANTHER)
Caenorhabditis elegans	r- dependent r- polymerase family protein	2	F:GO:0005515; P:GO:0009792	-		IPR007855
	-	0				IPR006578
	-	0				IPR006578
	-	0				-
Caenorhabditis briggsae	dipeptidyl anminopeptidase	3	P:GO:0006508; F:GO:0004252; F:GO:0004177	-	EC:3.4.21.0; EC:3.4.11.0	-
	-	0				-

Caenorhabditis elegans	dimethylaniline monooxyge-se	7	F:GO:0004499; F:GO:0050661; P:GO:0055114; P:GO:0000003; C:GO:0031227; C:GO:0016021; F:GO:0050660	-	EC:1.14.13.8	IPR020946; G3DSA:3.50.50.60 (GENE3D), PTHR23023 (PANTHER), PTHR23023:SF4 (PANTHER)
Ostertagia ostertagi	protein disulfide isomerase	8	P:GO:0006457; C:GO:0005875; F:GO:0008415; F:GO:0016757; C:GO:0005811; P:GO:0045454; F:GO:0003756; C:GO:0005783	-	EC:5.3.4.1	-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-pqn-85 protein	0		F:GO:0005488; P:GO:0034088; C:GO:0032116		-
Nematostella vectensis	endonuclease-reverse transcriptase	1	F:GO:0004518	-		PTHR23227 (PANTHER), PTHR23227:SF14 (PANTHER)
Ailuropoda melanoleuca	poly(adp-ribose) glycohydrolase	5	C:GO:0005829; F:GO:0004649; P:GO:0016045; C:GO:0005634; P:GO:0006974	-	EC:3.2.1.143	IPR007724
Ailuropoda melanoleuca	poly(adp-ribose) glycohydrolase	5	C:GO:0005829; F:GO:0004649; P:GO:0016045; C:GO:0005634; P:GO:0006974	-	EC:3.2.1.143	IPR007724
Macaca mulatta	PREDICTED: hypothetical protein LOC100426852 [Macaca mulatta]	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-rbc-1 protein	3	P:GO:0007424; P:GO:0007035; P:GO:0008593	-		PTHR13950 (PANTHER), PTHR13950:SF1 (PANTHER)
	-	0				-
Homo sapiens	myc-associated zinc finger protein (purine-binding transcription factor) isoform cra_f	8	F:GO:0003723; P:GO:0006369; F:GO:0008270; P:GO:0006367; P:GO:0045449; F:GO:0003677; F:GO:0005515; C:GO:0005634	-		-
	-	0				-
Caenorhabditis elegans	uncoordi-ted family member (unc-51)	9	P:GO:0009888; F:GO:0005488; P:GO:0023060; F:GO:0004672; P:GO:0040007; P:GO:0050808; P:GO:0010646; P:GO:0007275; P:GO:0044237	-		IPR000719; IPR002290; IPR008271; IPR011009; IPR013336; IPR017441; IPR017442; IPR020636; IPR022708; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)

Caenorhabditis elegans	uncoordi-ted family member (unc-51)	21	P:GO:0009653; P:GO:0006810; P:GO:0006468; P:GO:0009888; P:GO:0048589; C:GO:0005776; P:GO:0001558; P:GO:0010646; F:GO:0004672; P:GO:0031175; P:GO:0051239; P:GO:0048513; C:GO:0005829; C:GO:0070969; P:GO:0008104; P:GO:0050808; F:GO:0032403; P:GO:0048523; P:GO:0035466; P:GO:0010506; N:GO:0035556	-		IPR000719; IPR002290; IPR008271; IPR011009; IPR013336; IPR017441; IPR017442; IPR020636; IPR022708; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
	-	0				-
	-	0				IPR007246; SignalP (SIGNALP)
Caenorhabditis briggsae	serine protease family	0		F:GO:0003824; F:GO:0008233		-
Caenorhabditis briggsae	sideroflexin 3	6	F:GO:0005371; F:GO:0008324; P:GO:0055085; P:GO:0006812; C:GO:0016021; C:GO:0031966	-		IPR004686; PTHR11153:SF9 (PANTHER)
	-	0				-
Caenorhabditis elegans	novel protein	0		F:GO:0016874; P:GO:0071569; F:GO:0071568; F:GO:0003674; C:GO:0005575; F:GO:0005515; C:GO:0005783; P:GO:0008152; P:GO:0008150		-
Caenorhabditis elegans	novel protein	0		F:GO:0016874; P:GO:0071569; F:GO:0071568; F:GO:0003674; C:GO:0005575; F:GO:0005515; C:GO:0005783; P:GO:0008152; P:GO:0008150		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-mvb-12 protein	0		P:GO:0006629; F:GO:0005488; F:GO:0016787; F:GO:0003824; F:GO:0005529; F:GO:0004806		IPR018798; PS51498 (PROFILE)

Caenorhabditis briggsae	autophagy protein 9	1	P:GO:0009792	-		IPR007241; PTHR13038:SF1 (PANTHER), SignalP (SIGNALP)
	-	0				IPR008957; IPR013783
Caenorhabditis elegans	set domain and mariner transposase fusion gene	4	F:GO:0005488; F:GO:0004803; F:GO:0016740; P:GO:0006313	-		IPR001214; G3DSA:2.170.270.10 (GENE3D), PTHR22884 (PANTHER), PTHR22884:SF24 (PANTHER), SSF82199 (SUPERFAMILY)
Caenorhabditis briggsae	afg3(atpase family gene 3)-like 1	4	P:GO:0019538; F:GO:0016787; C:GO:0016020; F:GO:0000166	-		IPR011546; PTHR23076 (PANTHER), PTHR23076:SF11 (PANTHER)
Caenorhabditis briggsae	aldo keto reductase family protein	4	P:GO:0009792; P:GO:0040010; P:GO:0002119; P:GO:0040011	-		IPR001395; IPR018170; IPR020471; IPR023210; PTHR11732:SF34 (PANTHER)
Caenorhabditis elegans	c-termi-l binding protein	10	P:GO:0016055; F:GO:0008022; F:GO:0016616; P:GO:0000122; P:GO:0022416; F:GO:0051287; P:GO:0001700; F:GO:0003714; F:GO:0003713; C:GO:0005634	-	EC:1.1.1.0	IPR006139; IPR016040; PTHR10996 (PANTHER), PTHR10996:SF11 (PANTHER), SSF52283 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	tpr domain containing protein	0		F:GO:0005488		IPR011990
Loa loa	pre-b cell enhancing factor	0		F:GO:0004514; P:GO:0009435		PTHR11098 (PANTHER), PTHR11098:SF2 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	3	F:GO:0005515; F:GO:0005529; P:GO:0000003	-		IPR001079; IPR008985; IPR013320; PTHR11346:SF29 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	3	F:GO:0005515; F:GO:0005529; P:GO:0000003	-		IPR001079; IPR008985; IPR013320; PTHR11346:SF29 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				IPR008160; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER)
	-	0				-
Caenorhabditis elegans	slowpoke potassium channel family member (slo-2)	6	C:GO:0016020; P:GO:0006813; P:GO:0008152; F:GO:0003824; F:GO:0015269; F:GO:0005488	-		PTHR10027 (PANTHER), PTHR10027:SF6 (PANTHER)
Loa loa	zinc finger transcription factor family protein partially confirmed by transcript evidence	0		F:GO:0003676; C:GO:0016021; F:GO:0008270; P:GO:0009792; C:GO:0005622		IPR012337
	-	0				-
	-	0				-

Caenorhabditis briggsae	Hypothetical protein CBG09655 [Caenorhabditis briggsae]	4	P:GO:0019915; C:GO:0016021; P:GO:0006508; F:GO:0008233	-		-
Caenorhabditis briggsae	briggsae cbr-fli-1 protein	3	P:GO:0030239; F:GO:0003779; P:GO:0010004	-		-
Caenorhabditis briggsae	briggsae cbr-flp-19 protein	0				SignalP (SIGNALP)
Caenorhabditis briggsae	40s ribosomal protein s30	6	P:GO:0002119; C:GO:0005840; F:GO:0003735; P:GO:0040010; P:GO:0000003; P:GO:0006412	-	EC:3.6.5.3	IPR000626; IPR006846; G3DSA:3.10.20.90 (GENE3D), PTHR12650:SF3 (PANTHER), SSF54236 (SUPERFAMILY)
Caenorhabditis briggsae	40s ribosomal protein s30	6	P:GO:0002119; C:GO:0005840; F:GO:0003735; P:GO:0040010; P:GO:0000003; P:GO:0006412	-	EC:3.6.5.3	IPR000626; IPR006846; G3DSA:3.10.20.90 (GENE3D), PTHR12650:SF3 (PANTHER), SSF54236 (SUPERFAMILY)
Caenorhabditis briggsae	40s ribosomal protein s30	6	P:GO:0002119; C:GO:0005840; F:GO:0003735; P:GO:0040010; P:GO:0000003; P:GO:0006412	-	EC:3.6.5.3	IPR000626; IPR006846; G3DSA:3.10.20.90 (GENE3D), PTHR12650:SF3 (PANTHER), SSF54236 (SUPERFAMILY)
Caenorhabditis elegans	domain containing protein	0		P:GO:0051056; P:GO:0007264; F:GO:0005089; P:GO:0035023; F:GO:0003677; F:GO:0005085; C:GO:0005622		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-daf-15 protein	1	F:GO:0005488	-		IPR004083; PTHR12848:SF2 (PANTHER)
Brugia malayi	atp-dependent d- helicase	6	P:GO:0006310; F:GO:0003676; F:GO:0004672; C:GO:0005622; F:GO:0008026; F:GO:0005524	-		IPR004589; IPR011545; G3DSA:3.40.50.300 (GENE3D), SSF52540 (SUPERFAMILY)
Brugia malayi	atp-dependent d- helicase	7	P:GO:0006310; F:GO:0003676; F:GO:0004672; F:GO:0004003; C:GO:0005622; P:GO:0033554; F:GO:0005524	-		IPR004589; G3DSA:3.40.50.300 (GENE3D), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
Loa loa	tumor necrosis alpha-induced protein 8-like 3-like	0		F:GO:0009055; F:GO:0020037; F:GO:0005506; F:GO:0004497		IPR008477

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0006915; F:GO:0005515; C:GO:0016020	-		IPR006214; PTHR23291:SF14 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	fatty acid elongation protein 3	4	P:GO:0018996; C:GO:0016021; P:GO:0008340; P:GO:0040010	-		IPR002076; SignalP (SIGNALP)
Caenorhabditis elegans	fatty acid elongation protein 3	4	P:GO:0018996; C:GO:0016021; P:GO:0008340; P:GO:0040010	-		IPR002076; SignalP (SIGNALP)
Caenorhabditis elegans	o-sialoglycoprotein endopeptidase	4	F:GO:0004222; P:GO:0006508; F:GO:0008270; F:GO:0005515	-	EC:3.4.24.0	IPR000905; IPR017861
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-bam-2 protein	0		C:GO:0005887		-
Caenorhabditis elegans	ankyrin-repeat and fibronectin type iii domain containing 1	0		P:GO:0008150; P:GO:0007165; C:GO:0005575		PTHR21437 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0004500; C:GO:0016021; P:GO:0006548		IPR005018; PTHR23130 (PANTHER), PTHR23130:SF3 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	thioredoxin domain-containing protein 1	16	P:GO:0045454; P:GO:0006260; P:GO:0006916; C:GO:0005624; F:GO:0005515; P:GO:0045927; F:GO:0030612; P:GO:0006888; P:GO:0007165; P:GO:0045893; P:GO:0008283; P:GO:0045321; C:GO:0005789; F:GO:0015036; P:GO:0006950; C:GO:0005634	-		IPR012335; IPR012336; IPR013766; IPR017936; IPR017937; PTHR18929 (PANTHER), PS51257 (PROFILE), SignalP (SIGNALP)
	-	0				-
Oryctolagus cuniculus	heterochromatin protein 1-beta-like	4	P:GO:0009987; C:GO:0045120; C:GO:0000785; F:GO:0005515	-		IPR000953; IPR016197; G3DSA:2.40.50.40 (GENE3D), PTHR22812 (PANTHER), PTHR22812:SF4 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-kcc-3 protein	6	P:GO:0003333; P:GO:0007638; F:GO:0015171; P:GO:0006811; F:GO:0015379; C:GO:0016021	-		IPR004841; PTHR11827 (PANTHER), PTHR11827:SF2 (PANTHER)

Caenorhabditis elegans	briggsae cbr-kcc-3 protein	6	P:GO:0003333; P:GO:0007638; F:GO:0015171; P:GO:0006811; F:GO:0015379; C:GO:0016021	-		IPR004841; PTHR11827 (PANTHER), PTHR11827:SF2 (PANTHER)
Caenorhabditis elegans	hypothetical protein Y58G8A.4 [Caenorhabditis elegans]	1	P:GO:0000003	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Loa loa	dual specificity phosphatase 19	4	P:GO:0016070; P:GO:0006796; P:GO:0043412; F:GO:0004721	-	EC:3.1.3.16	-
	-	0				-
Loa loa	peptidylglycine alpha-amidating monooxyge-se	26	P:GO:0007595; P:GO:0060173; F:GO:0004598; P:GO:0007507; C:GO:0005624; P:GO:0009268; C:GO:0015630; P:GO:0051493; C:GO:0005615; P:GO:0006518; C:GO:0005829; P:GO:0051384; P:GO:0032880; P:GO:0046688; C:GO:0030424; P:GO:0042493; F:GO:0004504; P:GO:0021785; P:GO:0006464; F:GO:0042803; P:GO:0021952; C:GO:0030141; C:GO:0005887; F:GO:0005507; P:GO:0032355; C:GO:0043204	-	EC:4.3.2.5; EC:1.14.17.3	PTHR10680 (PANTHER), SignalP (SIGNALP)
Loa loa	sel-1 suppressor of lin-12-like (elegans)	2	F:GO:0005488; F:GO:0016787	-		IPR006597; IPR011990; PTHR11102 (PANTHER), PTHR11102:SF11 (PANTHER), SSF81901 (SUPERFAMILY)
Loa loa	sel-1 suppressor of lin-12-like (elegans)	2	F:GO:0005488; F:GO:0016787	-		IPR006597; IPR011990; PTHR11102 (PANTHER), PTHR11102:SF11 (PANTHER), SSF81901 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein T21F4.1 [Caenorhabditis elegans]	2	F:GO:0046872; F:GO:0016813	-	EC:3.5.3.0	-
Brugia malayi	wilms tumor 1 interacting protein	2	F:GO:0005488; C:GO:0044464	-		IPR001781; PTHR18973 (PANTHER), PTHR18973:SF64 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis briggsae	cadherin domain containing protein	1	C:GO:0016020	-		-
	-	0				-
	-	0				-

Caenorhabditis briggsae	adp-ribosylation arf	15	P:GO:0007264; P:GO:0007186; P:GO:0000003; P:GO:0006471; P:GO:0007269; F:GO:0003924; P:GO:0006898; P:GO:0006886; P:GO:0016197; P:GO:0009792; C:GO:0005737; P:GO:0048488; C:GO:0005634; F:GO:0005525; P:GO:0033227	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR005225; IPR006688; IPR006689; G3DSA:3.40.50.300 (GENE3D), PTHR11711:SF30 (PANTHER), PS51417 (PROFILE), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0042302	-		-
Caenorhabditis elegans	fk506 binding protein 12-rapamycin associated protein 1	3	F:GO:0016772; F:GO:0048565; F:GO:0005488	-		IPR011989; IPR016024; PTHR11139 (PANTHER), PTHR11139:SF9 (PANTHER), PF11865 (PFAM)
Callithrix jacchus	prefoldin subunit 2	3	P:GO:0006457; C:GO:0016272; F:GO:0051082	-		IPR002777; IPR009053; G3DSA:1.10.287.370 (GENE3D), PTHR13303 (PANTHER)
Caenorhabditis elegans	ndus8_caeel ame: full=probable -dh dehydroge-se iron-sulfur protein mitochondrial ame: full=complex i-23kd short=ci-23kd ame: full=-dh-ubiquinone oxidoreductase 23 kda subunit flags: precursor	0		F:GO:0051536; P:GO:0019684; F:GO:0009055; P:GO:0042493; P:GO:0002119; F:GO:0046872; P:GO:0006120; C:GO:0016020; P:GO:0008340; P:GO:0009792; P:GO:0040007; F:GO:0005506; C:GO:0005739; F:GO:0016651; P:GO:0055114; F:GO:0016491; P:GO:0040010; F:GO:0051539		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	arch_caebr ame: full=protein archease-like	3	P:GO:0040007; P:GO:0040035; P:GO:0002119	-		IPR002804; PD012969 (PRODOM), PTHR12682:SF8 (PANTHER)
Caenorhabditis briggsae	sig-l recognition particle 19 kda protein	1	C:GO:0048500	-		IPR002778
Brugia malayi	hypothetical protein Bm1_07015 [Brugia malayi]	0				-
Brugia malayi	briggsae cbr-dys-1 protein	7	P:GO:0007271; F:GO:0005515; P:GO:0040017; C:GO:0016010; F:GO:0005277; P:GO:0015870; P:GO:0046716	-		-
Caenorhabditis elegans	rio1 family protein	3	P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR011009; IPR015285; IPR018934; PTHR10593 (PANTHER), PTHR10593:SF1 (PANTHER), SSF46785 (SUPERFAMILY)

Caenorhabditis elegans	cef (clone eighty-four) protein binding transporter zinc ion binding	0		F:GO:0005215; P:GO:0006979; F:GO:0003676; F:GO:0008270; C:GO:0030127; C:GO:0005622; F:GO:0005515; P:GO:0016192; C:GO:0009507		-
Caenorhabditis elegans	c2h2 finger domain-containing protein	0		P:GO:0015031; F:GO:0005215; P:GO:0006979; P:GO:0006810; F:GO:0003676; F:GO:0008270; C:GO:0030127; P:GO:0006888; P:GO:0006886; C:GO:0005622; F:GO:0005515; P:GO:0016192; C:GO:0009507		-
	-	0				-
Caenorhabditis elegans	Hypothetical protein T20F7.1 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	sodium- and chloride-dependent neutral and basic amino acid transporter b(0+)	15	P:GO:0007274; F:GO:0005277; F:GO:0005328; P:GO:0001504; P:GO:0015870; C:GO:0016021; P:GO:0009636; P:GO:0015871; C:GO:0031526; F:GO:0015171; P:GO:0006520; F:GO:0030165; P:GO:0040017; C:GO:0045211; P:GO:0006865	-		IPR000175; PTHR11616:SF17 (PANTHER)
Caenorhabditis briggsae	transmembrane protein 53-b	0		F:GO:0003674; C:GO:0016021; P:GO:0008150		IPR008547
Caenorhabditis briggsae	dipeptidyl peptidase iii	3	C:GO:0005737; F:GO:0008239; P:GO:0006508	-		IPR005317; PTHR23422 (PANTHER)
Caenorhabditis briggsae	dipeptidyl peptidase iii	4	C:GO:0016020; C:GO:0005829; P:GO:0006508; F:GO:0008239	-		IPR005317; PTHR23422 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG12847 [Caenorhabditis briggsae]	0				-

Brugia malayi	briggsae cbr-scc-3 protein	28	F:GO:0005515; P:GO:0006412; P:GO:0016045; P:GO:0007141; C:GO:0005576; C:GO:0005730; P:GO:0007286; F:GO:0003677; C:GO:0005875; F:GO:0003735; P:GO:0045449; P:GO:0032494; P:GO:0008592; P:GO:0007379; C:GO:0005811; F:GO:0032500; P:GO:0006965; F:GO:0016019; C:GO:0005887; P:GO:0045087; C:GO:0035327; C:GO:0000922; C:GO:0005721; P:GO:0006260; C:GO:0008278; C:GO:0000780; C:GO:0022627;	-	EC:3.6.5.3	IPR013721; PTHR11199 (PANTHER)
Brugia malayi	briggsae cbr-scc-3 protein	28	F:GO:0005515; P:GO:0006412; P:GO:0016045; P:GO:0007141; C:GO:0005576; C:GO:0005730; P:GO:0007286; F:GO:0003677; C:GO:0005875; F:GO:0003735; P:GO:0045449; P:GO:0032494; P:GO:0008592; P:GO:0007379; C:GO:0005811; F:GO:0032500; P:GO:0006965; F:GO:0016019; C:GO:0005887; P:GO:0045087; C:GO:0035327; C:GO:0000922; C:GO:0005721; P:GO:0006260; C:GO:0008278; C:GO:0000780; C:GO:0022627	-	EC:3.6.5.3	IPR013721; PTHR11199 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)

Loa loa	protein-tyrosine phosphatase containing protein	1	F:GO:0016791	-	EC:3.1.3.0	IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis briggsae	thyroid hormone receptor interactor 13	11	P:GO:0000239; P:GO:0001556; P:GO:0007141; C:GO:0001673; P:GO:0006302; F:GO:0042802; P:GO:0007286; F:GO:0000166; P:GO:0007131; P:GO:0007144; P:GO:0009792	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0010172; P:GO:0009987; C:GO:0005634	-		IPR001699; IPR008967; IPR018186; PTHR11267:SF17 (PANTHER)
Gallus gallus	tripartite motif-containing protein 71	0		F:GO:0046872; C:GO:0005737; F:GO:0008270; F:GO:0005515; C:GO:0005622		IPR011042; SSF63829 (SUPERFAMILY)
Angiostrongylus cantonensis	major allergen	0		P:GO:0010171; F:GO:0009055; P:GO:0006099; P:GO:0002119; P:GO:0055114; F:GO:0016491; F:GO:0051536; P:GO:0040010; P:GO:0040007; P:GO:0018996		-
	-	0				-
Brugia malayi	3 -5 exoribonuclease csl4 homolog	3	C:GO:0005737; C:GO:0043229; C:GO:0000178	-		IPR019495; PTHR12686 (PANTHER)
Caenorhabditis elegans	thioredoxin domain containing 17	6	F:GO:0009055; F:GO:0005515; F:GO:0047134; F:GO:0004601; P:GO:0033209; C:GO:0005829	-	EC:1.8.1.8; EC:1.11.1.7	IPR010357; IPR012335; IPR012336
	-	0				-
Angiostrongylus cantonensis	max interactor 1	9	P:GO:0006281; F:GO:0008270; F:GO:0016564; F:GO:0003677; P:GO:0000122; F:GO:0005515; C:GO:0005737; F:GO:0008168; C:GO:0005634	-	EC:2.1.1.0	-
	-	0				-
Caenorhabditis elegans	briggsae cbr-rhy-1 protein	2	C:GO:0016021; F:GO:0016747	-	EC:2.3.1.0	IPR002656; SignalP (SIGNALP)

Caenorhabditis elegans	d- ligase	1	P:GO:0009987	-		IPR012310; IPR012340; IPR016027; IPR016059; G3DSA:3.30.1490.70 (GENE3D), G3DSA:3.30.470.30 (GENE3D), PTHR10459 (PANTHER), PTHR10459:SF7 (PANTHER), SSF56091 (SUPERFAMILY)
Loa loa	fh2 domain-containing protein 1	1	F:GO:0005488	-		IPR003104; IPR015425; PTHR23213 (PANTHER)
Caenorhabditis elegans	sedoheptuloki-se	0		F:GO:0016740; P:GO:0016310; F:GO:0000166; C:GO:0005737; F:GO:0005524; F:GO:0016301; P:GO:0005975; F:GO:0050277; F:GO:0016773		IPR000577; IPR018484; G3DSA:3.30.420.40 (GENE3D), PTHR10196:SF11 (PANTHER), SSF53067 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis briggsae	uncoordi-ted family member (unc-89)	0		F:GO:0004672; F:GO:0005524; F:GO:0005089; P:GO:0006468; P:GO:0035023; F:GO:0004674; C:GO:0005622		IPR003598; IPR003961; IPR007110; IPR008957; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF5 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
Caenorhabditis remanei	fog-3	0				IPR002087; IPR015676; PTHR17537:SF1 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Loa loa	splicing factor	0				IPR004882; PTHR12375:SF5 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				IPR000953; IPR016197; G3DSA:2.40.50.40 (GENE3D)
Caenorhabditis elegans	arginine ki-se	4	C:GO:0016021; F:GO:0005524; F:GO:0005515; F:GO:0004054	-	EC:2.7.3.3	IPR000749; IPR014746; IPR022413; IPR022414; IPR022415; PTHR11547:SF13 (PANTHER), SSF55931 (SUPERFAMILY)
Caenorhabditis elegans	arginine ki-se	4	C:GO:0016021; F:GO:0005524; F:GO:0005515; F:GO:0004054	-	EC:2.7.3.3	IPR000749; IPR014746; IPR022413; IPR022414; IPR022415; PTHR11547:SF13 (PANTHER), SSF55931 (SUPERFAMILY)
Caenorhabditis briggsae	uncharacterized conserved protein	1	P:GO:0008340	-		-
Caenorhabditis briggsae	uncoordi-ted family member (unc-44)	3	C:GO:0016020; P:GO:0007155; F:GO:0005515	-		-
Homo sapiens	lysozyme c precursor	8	P:GO:0042742; C:GO:0005615; P:GO:0006954; F:GO:0005515; P:GO:0019835; F:GO:0003796; P:GO:0007586; P:GO:0016998	-	EC:3.2.1.17	IPR000974; IPR001916; IPR019799; G3DSA:1.10.530.10 (GENE3D), PTHR11407 (PANTHER), PTHR11407:SF8 (PANTHER), SignalP (SIGNALP), SSF53955 (SUPERFAMILY)
Caenorhabditis briggsae	ke (drosophila actin-binding) homolog family member (ketn-1)	1	P:GO:0000003	-		-

Caenorhabditis elegans	transducin -like 3	7	P:GO:0040010; P:GO:0045132; P:GO:0006364; P:GO:0000003; C:GO:0032040; P:GO:0006898; P:GO:0009792	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR19854 (PANTHER), PTHR19854:SF2 (PANTHER)
synthetic construct	cd59 glycoprotein preproprotein	6	C:GO:0005624; P:GO:0007166; P:GO:0007596; F:GO:0005515; C:GO:0005576; C:GO:0031362	-		IPR001526; IPR016054; IPR018363; G3DSA:2.10.60.10 (GENE3D), PTHR10036 (PANTHER), SignalP (SIGNALP), SSF57302 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG18604 [Caenorhabditis briggsae]	0		F:GO:0046872; P:GO:0055114; F:GO:0009055; F:GO:0016491; F:GO:0020037; F:GO:0005506; F:GO:0004497		-
Brugia malayi	topoisomerase iii beta	6	P:GO:0006268; F:GO:0003917; F:GO:0005515; C:GO:0005694; P:GO:0006265; C:GO:0005634	-	EC:5.99.1.2	IPR000380; IPR002052; IPR003602; IPR013497; IPR013824; IPR013825
Brugia malayi	topoisomerase iii beta	6	P:GO:0006268; F:GO:0003917; F:GO:0005515; C:GO:0005694; P:GO:0006265; C:GO:0005634	-	EC:5.99.1.2	IPR000380; IPR002052; IPR003602; IPR013497; IPR013824; IPR013825
Caenorhabditis elegans	mitogen-activated protein ki-se ki-se ki-se 15	4	P:GO:0006468; F:GO:0005515; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	-
						-
Schistosoma japonicum	protein	0				-
Nicotiana tabacum	protein	1	F:GO:0016491	-		-
	-	0				-
Caenorhabditis briggsae	wwe domain containing protein	1	F:GO:0046872	-		-
Caenorhabditis elegans	skb1 methyltransferase family protein	1	F:GO:0016740	-		IPR007857; SSF53335 (SUPERFAMILY)
Loa loa	helix-loop-helix d--binding domain containing protein	1	P:GO:0006350	-		IPR001092; IPR011598; PTHR10985 (PANTHER), PTHR10985:SF18 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	glucosyl glucuronosyl transferases	1	P:GO:0040010	-		IPR002213; G3DSA:3.40.50.2000 (GENE3D), PTHR11926:SF3 (PANTHER), SSF53756 (SUPERFAMILY)

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	9	F:GO:0030528; P:GO:0007420; P:GO:0000122; F:GO:0043565; P:GO:0043193; F:GO:0008134; F:GO:0008094; P:GO:0006338; C:GO:0005634	-		IPR004022; IPR018501; PTHR22880 (PANTHER), PTHR22880:SF3 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-ilys-4 protein	3	P:GO:0009792; P:GO:0042742; F:GO:0003796	-	EC:3.2.1.17	IPR008597; PTHR11195:SF7 (PANTHER)
	-	0				-
Caenorhabditis elegans	actin binding	2	C:GO:0005739; F:GO:0005515	-		IPR003124; PTHR12902 (PANTHER)
Caenorhabditis elegans	lethal g0431 cg14788-pa	9	P:GO:0006412; P:GO:0040010; C:GO:0005840; F:GO:0003735; P:GO:0040035; P:GO:0002119; P:GO:0006898; P:GO:0009792; F:GO:0005525	-	EC:3.6.5.3	IPR002917; G3DSA:3.40.50.300 (GENE3D), PTHR11089 (PANTHER), PTHR11089:SF7 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	methyltransferase upf0383	0		F:GO:0003676; F:GO:0008168; C:GO:0005737; P:GO:0008033; F:GO:0016740; F:GO:0008270		IPR011671; G3DSA:3.40.50.150 (GENE3D), PTHR21210 (PANTHER), SSF53335 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	deoxyhypusine hydroxylase	9	P:GO:0009792; P:GO:0010171; P:GO:0040018; F:GO:0005515; P:GO:0008612; F:GO:0019135; P:GO:0040010; P:GO:0019915; P:GO:0006898	-	EC:1.14.99.29	IPR004155; IPR011989; IPR016024; IPR021133; PTHR12697 (PANTHER)
Caenorhabditis elegans	pdz domain containing 8	1	C:GO:0016020	-		-
Caenorhabditis elegans	secretory carrier membrane protein 2	4	P:GO:0006810; C:GO:0043231; C:GO:0044444; C:GO:0016020	-		IPR007273; PTHR10687:SF3 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	acyl- :lysophosphatidylglycerol acyltransferase 1	1	P:GO:0019915	-		IPR002123; PTHR10983 (PANTHER), PTHR10983:SF2 (PANTHER)

Loa loa	folylpolyglutamate synthase	10	F:GO:0004326; P:GO:0006139; P:GO:0044281; P:GO:0009058; P:GO:0031100; P:GO:0007420; P:GO:0042221; C:GO:0005829; C:GO:0005739; F:GO:0000166	-	EC:6.3.2.17	IPR001645; IPR013221; IPR018109; SignalP (SIGNALP)
Caenorhabditis elegans	e2f-associated phosphoprotein	2	C:GO:0043231; C:GO:0005737	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	trifunctio-l purine biosynthetic protein adenosine-3	4	F:GO:0016874; P:GO:0009168; F:GO:0005515; F:GO:0008168	-	EC:2.1.1.0	IPR002376; IPR010918; G3DSA:3.90.650.10 (GENE3D), PTHR10520 (PANTHER), PTHR10520:SF2 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-pqm-1 protein	6	P:GO:0006952; P:GO:0000003; C:GO:0005622; F:GO:0008270; F:GO:0005515; P:GO:0006898	-		IPR015880
Caenorhabditis elegans	tr- (nuclear export receptor for tr-s) isoform cra_a	4	P:GO:0046907; F:GO:0003723; C:GO:0044428; P:GO:0033036	-		PTHR15952 (PANTHER), PTHR15952:SF11 (PANTHER)
Ancylostoma caninum	scp-like extracellular protein	0		P:GO:0040011; P:GO:0006898; C:GO:0005576		IPR001283; IPR014044; PTHR10334:SF11 (PANTHER)
Caenorhabditis elegans	atp-dependent clp atp-binding subunit	4	P:GO:0044238; P:GO:0043170; F:GO:0005515; F:GO:0016787	-		IPR004487; PTHR11262 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	zinc finger protein 214-like	0		F:GO:0003677		IPR006578
	-	0				-
Caenorhabditis elegans	briggsae cbr-hda-4 protein	0		P:GO:0006350; F:GO:0016787; P:GO:0045449; P:GO:0016568; C:GO:0005634		-
Acyrthosiphon pisum	dynein heavy chain	2	F:GO:0017111; F:GO:0005515	-	EC:3.6.1.15	-
Caenorhabditis elegans	briggsae cbr-spp-15 protein	1	P:GO:0006629	-		-
Caenorhabditis elegans	briggsae cbr-col-113 protein	0		C:GO:0016021; F:GO:0042302		IPR002486; IPR008160; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER), SignalP (SIGNALP)
Brugia malayi	hypothetical protein [Brugia malayi]	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				IPR003124
Caenorhabditis briggsae	mitochondrial atp synthase alpha subunit	11	C:GO:0045261; P:GO:0040010; P:GO:0042777; P:GO:0008340; F:GO:0046933; P:GO:0000003; F:GO:0005524; P:GO:0002119; F:GO:0005515; F:GO:0046961; P:GO:0009792	-	EC:3.6.3.14	IPR000194; IPR000793; IPR004100; IPR005294; IPR017458; IPR018118; IPR020003; G3DSA:1.20.150.20 (GENE3D), G3DSA:2.40.30.20 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR15184 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	mitochondrial atp synthase alpha subunit	11	C:GO:0045261; P:GO:0040010; P:GO:0042777; P:GO:0008340; F:GO:0046933; P:GO:0000003; F:GO:0005524; P:GO:0002119; F:GO:0005515; F:GO:0046961; P:GO:0009792	-	EC:3.6.3.14	IPR000194; IPR000793; IPR004100; IPR005294; IPR017458; IPR018118; IPR020003; G3DSA:1.20.150.20 (GENE3D), G3DSA:2.40.30.20 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR15184 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	mitochondrial atp synthase alpha subunit	11	C:GO:0045261; P:GO:0040010; P:GO:0042777; P:GO:0008340; F:GO:0046933; P:GO:0000003; F:GO:0005524; P:GO:0002119; F:GO:0005515; F:GO:0046961; P:GO:0009792	-	EC:3.6.3.14	IPR000194; IPR000793; IPR004100; IPR005294; IPR017458; IPR018118; IPR020003; G3DSA:1.20.150.20 (GENE3D), G3DSA:2.40.30.20 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR15184 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	hypothetical protein W09G12.10 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
	-	0				-
	-	0				-

Homo sapiens	superoxide dismutase	43	P:GO:0048773; F:GO:0030145; P:GO:0048666; P:GO:0007626; F:GO:0005515; P:GO:0010332; P:GO:0042542; P:GO:0051289; P:GO:0001315; P:GO:0006357; C:GO:0005759; P:GO:0014823; P:GO:0007507; P:GO:0001306; P:GO:0042554; P:GO:0003032; P:GO:0009791; P:GO:0003069; C:GO:0005743; P:GO:0019430; P:GO:0055093; P:GO:0006916; P:GO:0043524; P:GO:0045429; P:GO:0055072; P:GO:0050665; F:GO:0019825;	-	EC:1.15.1.1	-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		PTHR18958 (PANTHER), PTHR18958:SF173 (PANTHER)
	-	0				-
Caenorhabditis elegans	xaa-pro aminopeptidase	3	C:GO:0005829; F:GO:0005515; F:GO:0004177	-	EC:3.4.11.0	IPR000587; IPR000994; G3DSA:3.40.350.10 (GENE3D), PTHR10804:SF4 (PANTHER), SSF53092 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	pseudouridylate synthase 3	2	F:GO:0009982; P:GO:0009451	-	EC:5.4.99.12	IPR001406; IPR020094; IPR020095; IPR020097; IPR020103
	-	0				IPR012337
Caenorhabditis elegans	scavenger receptor	3	F:GO:0005044; F:GO:0005488; C:GO:0016020	-		IPR006626; IPR016187
Caenorhabditis elegans	hypothetical protein Y69A2AR.28 [Caenorhabditis elegans]	0				-
Brugia malayi	trypsin family protein	0		P:GO:0006508; F:GO:0004252; F:GO:0003824		IPR018114; G3DSA:2.40.10.10 (GENE3D), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	btb poz domain containing protein	0		F:GO:0005515		-
Caenorhabditis elegans	btb poz domain containing protein	0		F:GO:0005515		-
	-	0				-

Caenorhabditis elegans	alpha 4 like	15	P:GO:0040010; C:GO:0005874; P:GO:0035046; P:GO:0051258; P:GO:0007018; P:GO:0002119; F:GO:0005515; P:GO:0040017; F:GO:0003924; P:GO:0040039; P:GO:0006898; F:GO:0005198; P:GO:0002009; P:GO:0009792; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
	-	0				-
Caenorhabditis brenneri	troponin c	5	P:GO:0002119; F:GO:0005515; P:GO:0000003; P:GO:0040007; F:GO:0005509	-		IPR002048; IPR011992; IPR018247; IPR018248; IPR018249; PTHR23050 (PANTHER), PTHR23050:SF16 (PANTHER), SSF47473 (SUPERFAMILY)
	-	0				-
	-	0				-
Bacillus thuringiensis serovar kurstaki str. T03a001	lpxtg-motif cell wall anchor domain protein	0		F:GO:0005488; C:GO:0009986		-
Bacillus thuringiensis serovar kurstaki str. T03a001	lpxtg-motif cell wall anchor domain protein	0		F:GO:0005488; C:GO:0009986; F:GO:0005515		-
Caenorhabditis elegans	glycosyl hydrolases family 31 protein	2	P:GO:0008152; F:GO:0004553	-	EC:3.2.1.0	IPR000322; IPR017853; PTHR22762:SF10 (PANTHER), SSF51011 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Loa loa	tata-box binding protein	10	P:GO:0007369; P:GO:0006367; P:GO:0006355; P:GO:0055114; F:GO:0032440; F:GO:0003677; F:GO:0005515; F:GO:0003700; C:GO:0005634; F:GO:0003702	-	EC:1.3.1.74	IPR000814; IPR012294; IPR012295
Caenorhabditis briggsae	tata-box binding protein	10	P:GO:0007369; P:GO:0006367; P:GO:0006355; P:GO:0055114; F:GO:0032440; F:GO:0003677; F:GO:0005515; F:GO:0003700; C:GO:0005634; F:GO:0003702	-	EC:1.3.1.74	IPR000814; IPR012294; IPR012295

Caenorhabditis briggsae	tata-box binding protein	10	P:GO:0007369; P:GO:0006367; P:GO:0006355; P:GO:0055114; F:GO:0032440; F:GO:0003677; F:GO:0005515; F:GO:0003700; C:GO:0005634; F:GO:0003702	-	EC:1.3.1.74	IPR000814; IPR012294; IPR012295
Caenorhabditis briggsae	tata-box binding protein	10	P:GO:0007369; P:GO:0006367; P:GO:0006355; P:GO:0055114; F:GO:0032440; F:GO:0003677; F:GO:0005515; F:GO:0003700; C:GO:0005634; F:GO:0003702	-	EC:1.3.1.74	IPR000814; IPR012294; IPR012295
Loa loa	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Loa loa	myosin xviiia	0		F:GO:0005524; F:GO:0000166; F:GO:0042623; F:GO:0003774; F:GO:0005515; C:GO:0016459		IPR001609; PTHR13140 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR021010; SSF141739 (SUPERFAMILY)
Caenorhabditis elegans	beta-ureidopropio-se	4	P:GO:0006807; C:GO:0005829; P:GO:0000003; F:GO:0003837	-	EC:3.5.1.6	IPR003010
Dictyocaulus viviparus	acetylcholinesterase 2	6	F:GO:0004104; P:GO:0001507; F:GO:0003990; C:GO:0005623; P:GO:0040012; F:GO:0042803	-	EC:3.1.1.8; EC:3.1.1.7	-
Caenorhabditis elegans	laminin alpha chain	5	C:GO:0005606; P:GO:0030334; P:GO:0045995; P:GO:0030155; F:GO:0005102	-		IPR001791; IPR008985; IPR012680; IPR013320
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	patched family protein	5	P:GO:0018996; C:GO:0016021; P:GO:0040018; F:GO:0008158; P:GO:0040011	-		IPR000731; IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER), SSF82866 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-

Caenorhabditis elegans	phospholipase a-2-activating protein	1	P:GO:0040010	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR19849 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-dhs-27 protein	7	F:GO:0018454; F:GO:0045703; F:GO:0005515; P:GO:0042761; C:GO:0016020; C:GO:0005783; P:GO:0009790	-	EC:1.1.1.36	IPR002198; IPR016040; PTHR19410:SF38 (PANTHER), SignalP (SIGNALP), SSF51735 (SUPERFAMILY)
Brugia malayi	msp domain containing protein	0		C:GO:0005856; F:GO:0005198		IPR000535; IPR008962; PTHR21513 (PANTHER), PTHR21513:SF1 (PANTHER)
Homo sapiens	complement component s subcomponent	8	F:GO:0005509; P:GO:0006958; P:GO:0045087; P:GO:0010001; P:GO:0006508; F:GO:0004252; C:GO:0005576; P:GO:0051591	-	EC:3.4.21.0	SignalP (SIGNALP)
Caenorhabditis elegans	myosin regulatory light chain	7	C:GO:0005856; F:GO:0005509; C:GO:0030016; P:GO:0055003; F:GO:0005515; P:GO:0042694; P:GO:0060048	-		IPR002048; IPR011992; IPR018247; IPR018249; PTHR23049 (PANTHER), PTHR23049:SF7 (PANTHER), SSF47473 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG02786 [Caenorhabditis briggsae]	0		F:GO:0005488		PTHR13298 (PANTHER), PTHR13298:SF1 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-unc-36 protein	2	F:GO:0005216; P:GO:0006810	-		PTHR10166 (PANTHER), PTHR10166:SF5 (PANTHER)
Loa loa	hypothetical protein LOAG_05929 [Loa loa]	0				-
Caenorhabditis elegans	d domain (prokaryotic heat shock protein) family member (dnj-8)	3	P:GO:0018991; P:GO:0040011; P:GO:0006898	-		-
	-	0				-
	-	0				IPR006058
Caenorhabditis elegans	briggsae cbr-zig-7 protein	0				PTHR10075 (PANTHER), PTHR10075:SF1 (PANTHER)
Caenorhabditis elegans	tgf-beta resistance-associated protein trag	0				IPR011046; IPR015943; IPR019782; PTHR12816 (PANTHER), PTHR12816:SF1 (PANTHER)
	-	0				SignalP (SIGNALP)
Dictyocaulus viviparus	hypothetical protein L3ni22 [Dictyocaulus viviparus]	0				-
	-	0				-
Caenorhabditis elegans	cathepsin z	2	F:GO:0008234; P:GO:0006508	-		IPR000169; IPR000668; IPR013128; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF14 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis briggsae	l-lactate dehydroge-se	5	C:GO:0005737; F:GO:0005488; F:GO:0004459; P:GO:0055114; P:GO:0006096	-	EC:1.1.1.27	IPR015955; IPR018177; IPR022383; PTHR11540 (PANTHER), PTHR11540:SF3 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)

	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	nhl repeat-containing	3	P:GO:0006915; F:GO:0008270; F:GO:0005515	-		IPR001258; IPR011042; IPR013017; PTHR13712 (PANTHER), PTHR13712:SF9 (PANTHER)
Brugia malayi	immunoglobulin i-set domain containing protein	0		F:GO:0004672; F:GO:0005524; F:GO:0000166; P:GO:0006468; F:GO:0004674		IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF7 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
Salmo salar	sh2 domain containing 4a	0		C:GO:0005737; F:GO:0005515		PTHR14388 (PANTHER)
Loa loa	uncoordi-ted family member (unc-32)	5	F:GO:0015078; C:GO:0033177; C:GO:0016021; P:GO:0015986; P:GO:0040013	-		IPR002490; PTHR11629:SF23 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				PTHR13417 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	pyridine nucleotide-disulfide oxidoreductase domain-containing protein 1	0		F:GO:0009055; F:GO:0003674; P:GO:0055114; F:GO:0016491; F:GO:0003824; C:GO:0005575; P:GO:0008152; P:GO:0008150; F:GO:0005488		IPR013027; G3DSA:3.50.50.60 (GENE3D), SSF51905 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	bromodomain containing protein	1	P:GO:0040011	-		-
Caenorhabditis elegans	mbk-1	9	P:GO:0040010; P:GO:0018108; F:GO:0004674; F:GO:0005524; F:GO:0005515; P:GO:0040011; P:GO:0046777; F:GO:0004715; C:GO:0005634	-	EC:2.7.11.0; EC:2.7.10.2	IPR011009; G3DSA:1.10.510.10 (GENE3D), PTHR23122 (PANTHER), PTHR23122:SF2 (PANTHER)
Caenorhabditis elegans	mbk-1	9	P:GO:0040010; P:GO:0018108; F:GO:0004674; F:GO:0005524; F:GO:0005515; P:GO:0040011; P:GO:0046777; F:GO:0004715; C:GO:0005634	-	EC:2.7.11.0; EC:2.7.10.2	IPR011009; G3DSA:1.10.510.10 (GENE3D), PTHR23122 (PANTHER), PTHR23122:SF2 (PANTHER)
	-	0				-

Caenorhabditis briggsae	major facilitator superfamily protein	0		C:GO:0016021; P:GO:0055085		IPR011701; IPR016196; G3DSA:1.20.1250.20 (GENE3D), PTHR11662 (PANTHER), PTHR11662:SF24 (PANTHER)
	-	0				-
Caenorhabditis briggsae	engulfment and cell motility protein 1	15	P:GO:0043652; F:GO:0070064; P:GO:0007015; P:GO:0031532; F:GO:0032403; F:GO:0019899; P:GO:0030334; P:GO:0060097; P:GO:0040025; C:GO:0044444; P:GO:0040039; P:GO:0009792; P:GO:0035262; C:GO:0005886; F:GO:0017124	-		PTHR12771 (PANTHER), PTHR12771:SF5 (PANTHER), PF11841 (PFAM)
	-	0				-
Angiostrongylus cantonensis	suppressor of tau pathology family member (sut-1)	0				-
	-	0				-
Caenorhabditis briggsae	peptidylprolyl isomerase -like 1	5	P:GO:0006457; P:GO:0008380; C:GO:0005681; P:GO:0006397; F:GO:0003755	-	EC:5.2.1.8	-
Brugia malayi	eukaryotic translation initiation factor 2 alpha ki-se pek	24	P:GO:0007595; P:GO:0032092; P:GO:0002063; P:GO:0048009; P:GO:0006919; P:GO:0046777; P:GO:0032057; C:GO:0005789; P:GO:0031018; P:GO:0006983; P:GO:0007029; P:GO:0045444; F:GO:0004694; P:GO:0030282; P:GO:0009967; F:GO:0042802; P:GO:0006926; P:GO:0030073; P:GO:0031642; P:GO:0019722; P:GO:0032933; P:GO:0051260; P:GO:0019217; P:GO:0030968	-		IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11042 (PANTHER), PTHR11042:SF12 (PANTHER)
Bos taurus	complement factor h precursor	0		P:GO:0006957; C:GO:0005576		IPR000436; IPR016060
	-	0				-

Caenorhabditis elegans	baculoviral iap repeat-containing 5	42	F:GO:0048037; P:GO:0008340; P:GO:0031536; P:GO:0043154; F:GO:0051087; F:GO:0030528; P:GO:0045941; P:GO:0018991; F:GO:0008270; C:GO:0005814; P:GO:0040010; P:GO:0007052; P:GO:0045931; P:GO:0051303; F:GO:0043027; F:GO:0008536; C:GO:0005881; C:GO:0005730; C:GO:0005829; P:GO:0006916; F:GO:0046982; P:GO:0040039; F:GO:0008017; C:GO:0031021; C:GO:0000775; P:GO:0009792; P:GO:0031577;	-			IPR001370; PTHR10044 (PANTHER), PTHR10044:SF15 (PANTHER), SSF57924 (SUPERFAMILY)
Caenorhabditis elegans	baculoviral iap repeat-containing 5	30	F:GO:0048037; P:GO:0008340; P:GO:0031536; P:GO:0043154; F:GO:0051087; F:GO:0008270; C:GO:0005814; P:GO:0045931; P:GO:0051303; F:GO:0043027; F:GO:0008536; C:GO:0005881; C:GO:0005730; C:GO:0005829; P:GO:0006916; F:GO:0046982; P:GO:0006996; F:GO:0008017; C:GO:0031021; C:GO:0000775; P:GO:0009792; P:GO:0031577; C:GO:0030496; C:GO:0000228; C:GO:0005876; F:GO:0042803; C:GO:0032133;	-			IPR001370; PTHR10044 (PANTHER), PTHR10044:SF15 (PANTHER), SSF57924 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-

Caenorhabditis elegans	activating sig-l cointegrator 1 complex subunit 3	4	F:GO:0008026; F:GO:0003677; C:GO:0005622; F:GO:0005524	-		IPR004179; G3DSA:1.10.3380.10 (GENE3D), PTHR11752 (PANTHER), PTHR11752:SF8 (PANTHER)
Loa loa	g-t family protein	0		P:GO:0006508; F:GO:0016740; P:GO:0008152; F:GO:0008080; F:GO:0008270		IPR016181
	-	0				-
	-	0				-
	-	0				-
Oscheius brevesophaga	ribosomal protein l27a	4	P:GO:0009792; C:GO:0005840; F:GO:0003735; P:GO:0006412	-	EC:3.6.5.3	IPR021131; G3DSA:3.100.10.10 (GENE3D), PTHR11721 (PANTHER)
	-	0				-
Caenorhabditis sp. PS1010	r- binding protein	0		F:GO:0003676; F:GO:0000166		-
	-	0				-
	-	0				SignalP (SIGNALP)
Danio rerio	poly(adp-ribose) polymerase	3	C:GO:0005739; C:GO:0005634; F:GO:0016757	-		-
Caenorhabditis elegans	-	2	F:GO:0015299; P:GO:0006812	-		IPR004709; IPR006153; IPR018413; IPR018422
Caenorhabditis brenneri	linker histone h1 and h5 family protein	4	C:GO:0000786; F:GO:0003677; P:GO:0006334; C:GO:0005634	-		IPR005818; IPR011991; PTHR11467 (PANTHER), SSF46785 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	atp-binding sub-family c (cftr mrp) member 4	6	P:GO:0055085; C:GO:0031088; F:GO:0022857; C:GO:0005624; F:GO:0003824; C:GO:0005886	-		IPR001140; IPR003439; IPR003593; IPR011527; IPR017871; IPR017940; G3DSA:1.20.1560.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF97 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	dehydroge-se reductase (sdr family) member 4	7	P:GO:0042574; F:GO:0005488; C:GO:0005777; P:GO:0009239; P:GO:0055114; F:GO:0008667; F:GO:0001758	-	EC:1.3.1.28; EC:1.2.1.36	IPR002198; IPR002347; IPR016040; PTHR19410:SF67 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	acyl- synthetase long-chain family member 1	7	C:GO:0005829; C:GO:0043231; P:GO:0046320; C:GO:0044446; P:GO:0007586; C:GO:0031090; F:GO:0004467	-	EC:6.2.1.3	IPR000873; IPR020459; IPR020845; G3DSA:3.40.50.980 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF8 (PANTHER), SSF56801 (SUPERFAMILY)

Caenorhabditis elegans	acyl- synthetase long-chain family member 1	7	C:GO:0005829; C:GO:0043231; P:GO:0046320; C:GO:0044446; P:GO:0007586; C:GO:0031090; F:GO:0004467	-	EC:6.2.1.3	IPR000873; IPR020459; IPR020845; G3DSA:3.40.50.980 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF8 (PANTHER), SSF56801 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	P:GO:0009792	-		IPR008574
Caenorhabditis briggsae	gex interacting protein family member (gei-16)	1	F:GO:0005515	-		-
	-	0				-
Caenorhabditis briggsae	glucosamine-6-phosphate isomerase 2	5	C:GO:0005737; F:GO:0016787; P:GO:0006044; F:GO:0005515; F:GO:0004342	-	EC:3.5.99.6	IPR004547; IPR006148; IPR018321; G3DSA:3.40.50.1360 (GENE3D), SSF100950 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	r- polymerase ii subunit a c-termi-l domain phosphatase	1	C:GO:0005622	-		G3DSA:3.40.50.1000 (GENE3D), PTHR23081 (PANTHER)
Caenorhabditis briggsae	zinc finger protein	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		IPR007087; IPR015880
Haemonchus contortus	nicotinic acetylcholine receptor alpha subunit	6	F:GO:0004872; C:GO:0045211; C:GO:0030054; P:GO:0006811; C:GO:0016021; F:GO:0004889	-		IPR002394; IPR006029; IPR006201; IPR006202; IPR018000; G3DSA:1.20.120.370 (GENE3D), PTHR18945:SF88 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	phosphatidylinositol 3- alpha polypeptide	17	P:GO:0008340; P:GO:0043491; C:GO:0005942; F:GO:0043560; F:GO:0046934; P:GO:0007611; P:GO:0000003; P:GO:0050920; P:GO:0043053; P:GO:0006916; F:GO:0016303; F:GO:0000166; P:GO:0006006; P:GO:0009792; C:GO:0030027; P:GO:0040014; P:GO:0006468	-	EC:2.7.1.153; EC:2.7.1.137	IPR000403; IPR001263; IPR011009; IPR015433; IPR016024; IPR018936; G3DSA:3.30.1010.10 (GENE3D), PTHR10048:SF14 (PANTHER)

Caenorhabditis briggsae	cytochrome c oxidase assembly	18	P:GO:0006367; P:GO:0045941; P:GO:0040007; P:GO:0006898; C:GO:0016021; F:GO:0003743; F:GO:0016531; F:GO:0016563; F:GO:0003702; P:GO:0045454; P:GO:0008535; P:GO:0009792; F:GO:0003677; P:GO:0002119; F:GO:0003824; C:GO:0005634; P:GO:0040035; C:GO:0005739	-		IPR003782; IPR012335; IPR012336
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	mrg family protein	0		F:GO:0016740; F:GO:0003682; C:GO:0000785; P:GO:0006333; C:GO:0005634		IPR000953; IPR008676; IPR016197; G3DSA:2.30.30.270 (GENE3D), PF11717 (PFAM)
	-	0				-
Caenorhabditis briggsae	cleavage and polyadenylation specific factor 3-like	4	C:GO:0005737; F:GO:0016787; P:GO:0016180; C:GO:0032039	-		G3DSA:3.60.15.10 (GENE3D), PTHR11203 (PANTHER), PTHR11203:SF8 (PANTHER), SSF56281 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	symplekin	0		P:GO:0006629; F:GO:0005488; C:GO:0005737; F:GO:0004629; P:GO:0006397; C:GO:0005634		IPR022075; PTHR15245 (PANTHER), PTHR15245:SF2 (PANTHER)
	-	0				-
Candida tropicalis MYA-3404	predicted protein [Candida tropicalis MYA-3404]	0				-
	-	0				-
Caenorhabditis elegans	nuclear nucleolar gtp-binding protein family member (ngp-1)	6	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0005525; C:GO:0005622; P:GO:0040010	-		IPR002917; IPR006073; IPR012971; G3DSA:3.40.50.300 (GENE3D), PTHR11089 (PANTHER), PTHR11089:SF9 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	hypothetical protein F45E1.1 [Caenorhabditis elegans]	0				-
Loa loa	transmembrane protein 129 precursor	0		C:GO:0016021; C:GO:0016020		IPR018801
	-	0				-
	-	0				-

Caenorhabditis elegans	kh domain containing protein	1	F:GO:0005515	-		IPR004087; IPR004088; IPR016021; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR20849 (PANTHER), SSF54791 (SUPERFAMILY)
Caenorhabditis elegans	kh domain containing protein	1	F:GO:0005515	-		IPR004087; IPR004088; IPR016021; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR20849 (PANTHER), SSF54791 (SUPERFAMILY)
Caenorhabditis elegans	kh domain containing protein	1	F:GO:0005515	-		IPR004087; IPR004088; IPR016021; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR20849 (PANTHER), SSF54791 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	scavenger receptor class a- c-type lectin (agap009143-pa)	2	F:GO:0004872; F:GO:0005488	-		IPR001190; IPR006626; IPR017448; G3DSA:3.10.250.10 (GENE3D), PTHR19331 (PANTHER), PTHR19331:SF24 (PANTHER)
Caenorhabditis elegans	pmr-type golgi atpase family member (pmr-1)	0				-
Caenorhabditis elegans	protein ki-se family member (kin-1)	30	C:GO:0005654; P:GO:0007243; P:GO:0018991; C:GO:0031594; F:GO:0019901; P:GO:0071374; P:GO:0046777; C:GO:0005624; P:GO:0009755; C:GO:0005794; P:GO:0034199; P:GO:0046827; C:GO:0005829; P:GO:0051447; P:GO:0018105; P:GO:0002009; P:GO:0043457; C:GO:0005952; P:GO:0002119; C:GO:0048471; F:GO:0032403; P:GO:0001707; P:GO:0051966; F:GO:0004862; C:GO:0005886; C:GO:0005625; F:GO:0005524;	-	EC:2.7.11.11	IPR000719; IPR000961; IPR002290; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22985 (PANTHER), PTHR22985:SF84 (PANTHER)
	-	0				-
	-	0				-

Caenorhabditis elegans	myo-inositol oxyge-se	12	C:GO:0005737; P:GO:0048016; P:GO:0009992; P:GO:0016044; F:GO:0050661; C:GO:0016234; F:GO:0005506; P:GO:0055114; F:GO:0004033; F:GO:0016651; P:GO:0019310; F:GO:0050113	-	EC:1.13.99.1	IPR007828; SSF109604 (SUPERFAMILY)
Dictyostelium discoideum AX4	hypothetical protein DDB_G0281503 [Dictyostelium discoideum AX4]	0				SignalP (SIGNALP)
Loa loa	cajalin 2-like	0				-
Brugia malayi	proteasome (macropain) 26s non- 13	6	C:GO:0000502; P:GO:0051436; P:GO:0051437; P:GO:0031145; P:GO:0007127; F:GO:0005515	-		PTHR10539 (PANTHER)
Caenorhabditis briggsae	eukaryotic translation initiation factor 3 subunit g	13	F:GO:0003743; P:GO:0006413; C:GO:0005829; P:GO:0040010; F:GO:0003723; F:GO:0008270; P:GO:0000003; C:GO:0005852; P:GO:0010171; P:GO:0002119; F:GO:0005515; F:GO:0000166; P:GO:0009792	-		IPR000504; IPR001878; IPR012677; IPR013084; PTHR10352 (PANTHER), PF12353 (PFAM), SSF54928 (SUPERFAMILY)
Teladorsagia circumcincta	nicotinic acetylcholine receptor non-alpha subunit	6	F:GO:0004872; C:GO:0045211; C:GO:0030054; P:GO:0006811; C:GO:0016021; F:GO:0004889	-		-
Caenorhabditis briggsae	transcription initiation factor tfiid subunit 1	6	P:GO:0006357; F:GO:0008270; F:GO:0003676; F:GO:0016563; F:GO:0017025; P:GO:0007140	-		PTHR13900 (PANTHER)
Angiostrongylus cantonensis	elegans protein confirmed by transcript evidence	0		C:GO:0016021; F:GO:0042302		-
	-	0				-
Loa loa	agc dmpk gek protein ki-se	0				-
	-	0				-
	-	0				-
Loa loa	twik (kcnk-like) family of potasium alpha subunit 40	3	C:GO:0016021; P:GO:0006813; F:GO:0005267	-		-
Xenopus (Silurana) tropicalis	bromodomain containing 3	0				-
	-	0				-

	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	cytochrome p450 family member (cyp-13b1)	2	F:GO:0016491; F:GO:0005506	-		-
	-	0				-
Caenorhabditis briggsae	uncoordi-ted family member (unc-22)	3	P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	mgc81819 protein	1	F:GO:0016787	-		SSF56235 (SUPERFAMILY)
	-	0				-
Brugia malayi	establishment of cohesion 1 homolog 2 (cerevisiae)	0		F:GO:0016740; F:GO:0003684; C:GO:0005634; F:GO:0003887; F:GO:0003674; P:GO:0006281; C:GO:0005575; F:GO:0008415; F:GO:0046872; P:GO:0007049; P:GO:0008150		IPR001126; PTHR11076:SF5 (PANTHER)
	-	0				-
Caenorhabditis elegans	probable dolichyl pyrophosphate glc1man9 c2 alpha- -glucosyltransferase	3	F:GO:0000033; P:GO:0006487; C:GO:0016020	-		IPR004856; SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	uncharacterized protein	2	F:GO:0046872; F:GO:0003824	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	P:GO:0000003	-		IPR013568
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	cationic amino acid transporter	5	P:GO:0019915; C:GO:0016021; P:GO:0006865; F:GO:0015171; P:GO:0055085	-		IPR002293; IPR004841; IPR015606; SignalP (SIGNALP)
Loa loa	r- polymerase ii associated homolog (cerevisiae)	8	C:GO:0016593; P:GO:0010390; F:GO:0005515; P:GO:0007031; P:GO:0033523; P:GO:0065007; C:GO:0005779; P:GO:0044249	-		IPR007133; PTHR23188:SF8 (PANTHER)
Caenorhabditis elegans	lim domain family member (lim-9)	4	F:GO:0003700; C:GO:0005634; F:GO:0008270; F:GO:0016740	-		IPR001781; PTHR18973 (PANTHER), PTHR18973:SF104 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis elegans	lim domain family member (lim-9)	4	F:GO:0003700; C:GO:0005634; F:GO:0008270; F:GO:0016740	-		IPR001781; PTHR18973 (PANTHER), PTHR18973:SF104 (PANTHER), SSF57716 (SUPERFAMILY)
	-	0				-
Gnathostoma spinigerum	tryptase alpha beta 1-like	1	F:GO:0016787	-		IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR19355 (PANTHER), PTHR19355:SF174 (PANTHER)

Gnathostoma spinigerum	tryptase alpha beta 1-like	2	P:GO:0006811; F:GO:0008236	-		IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR19355 (PANTHER), PTHR19355:SF174 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Dictyocaulus viviparus	glyceraldehyde-3-phosphate dehydroge-se	12	F:GO:0004365; P:GO:0008340; P:GO:0055114; F:GO:0051287; P:GO:0019915; P:GO:0002119; F:GO:0005515; P:GO:0006096; P:GO:0009792; P:GO:0008406; C:GO:0005737; P:GO:0040018	-	EC:1.2.1.12	IPR006424; IPR016040; IPR020828; IPR020829; IPR020830; IPR020831; G3DSA:3.30.360.10 (GENE3D), SSF51735 (SUPERFAMILY), SSF55347 (SUPERFAMILY)
Brugia malayi	protein hira	7	P:GO:0040010; P:GO:0007369; C:GO:0000790; P:GO:0000003; F:GO:0005515; P:GO:0009792; P:GO:0006350	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR13831 (PANTHER)
Caenorhabditis elegans	atpase family aaa domain-containing protein 3	13	C:GO:0032133; F:GO:0017111; P:GO:0000910; P:GO:0007423; P:GO:0016572; P:GO:0007052; F:GO:0005524; C:GO:0005938; C:GO:0000785; P:GO:0000236; P:GO:0045448; C:GO:0051233; P:GO:0008104	-	EC:3.6.1.15	IPR021911; PTHR23075 (PANTHER)
Ustilago maydis 521	hypothetical protein UM02748.1 [Ustilago maydis 521]	0		F:GO:0003917; F:GO:0003916; P:GO:0006265; C:GO:0005694; P:GO:0006259; F:GO:0003677; F:GO:0003676; F:GO:0008270; F:GO:0016853; P:GO:0006268		IPR001878; IPR013084; SSF57756 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	u493_caebr ame: full=upf0493 protein cbg04313	1	P:GO:0040011	-		-
Caenorhabditis elegans	hypothetical protein T10E9.2 [Caenorhabditis elegans]	0				-
	-	0				-

Caenorhabditis elegans	kynureni-se (l-kynurenine hydrolase)	9	C:GO:0005829; C:GO:0005625; C:GO:0005739; P:GO:0019441; P:GO:0009435; P:GO:0042221; F:GO:0030429; F:GO:0030170; P:GO:0019442	-	EC:3.7.1.3	IPR000192; IPR010111; IPR015421; IPR015424
	-	0				-
Caenorhabditis briggsae	pre-mr--processing-splicing factor 8	17	P:GO:0050896; F:GO:0003723; C:GO:0005681; P:GO:0045132; P:GO:0040007; C:GO:0016607; P:GO:0040027; P:GO:0040035; P:GO:0018996; P:GO:0007601; F:GO:0005515; P:GO:0040011; P:GO:0000398; C:GO:0005682; P:GO:0006898; P:GO:0002009; P:GO:0009792	-		IPR000555; IPR012984; IPR019580; IPR021983; PTHR11140 (PANTHER)
Loa loa	hypothetical protein LOAG_00279 [Loa loa]	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	F:GO:0009055; C:GO:0016020	-		-
	-	0				-
Caenorhabditis elegans	trrap-like (transcription transformation domain-associated protein) family member (trr-1)	0		F:GO:0005488; F:GO:0016773		-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-glr-1 protein	0		F:GO:0004970; F:GO:0005216; F:GO:0005215; C:GO:0016021; C:GO:0016020; C:GO:0045202; P:GO:0006811; P:GO:0006810; C:GO:0030054; F:GO:0005234; C:GO:0030288; F:GO:0004872; C:GO:0005886; C:GO:0045211		-
	-	0				-
Taeniopygia guttata	rad51-like 3 (cerevisiae)	1	P:GO:0006139	-		IPR013632; IPR020588; G3DSA:3.40.50.300 (GENE3D), PTHR22942 (PANTHER), PTHR22942:SF8 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0040011; F:GO:0005515		-
Loa loa	exostosin 1	1	C:GO:0044464	-		IPR004263; IPR015338; G3DSA:3.90.550.10 (GENE3D), PTHR11062 (PANTHER), PTHR11062:SF7 (PANTHER)
Caenorhabditis briggsae	pecanex-like protein 1	1	P:GO:0040011	-		PTHR12372 (PANTHER), SignalP (SIGNALP)
Loa loa	cell division cycle 16 homolog	13	C:GO:0005654; P:GO:0070979; P:GO:0051437; C:GO:0005680; P:GO:0051436; C:GO:0005829; P:GO:0009792; P:GO:0007067; C:GO:0005813; P:GO:0007126; C:GO:0005876; P:GO:0031145; P:GO:0040035	-		IPR011990; IPR013026; IPR019734; PTHR12558 (PANTHER), PTHR12558:SF9 (PANTHER), SSF48452 (SUPERFAMILY)
Caenorhabditis briggsae	tho complex 2 isoform 1	8	P:GO:0045132; P:GO:0040007; C:GO:0000445; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0046784	-		PTHR21597 (PANTHER)
	-	0				-
	-	0				-
	-	0				IPR002666; PTHR10686:SF6 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	solute carrier family 25 member 3	9	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0005488; C:GO:0005743; P:GO:0055085; P:GO:0040010; P:GO:0008340; C:GO:0016021	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF22 (PANTHER)
Caenorhabditis elegans	solute carrier family 25 member 3	9	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0005488; C:GO:0005743; P:GO:0055085; P:GO:0040010; P:GO:0008340; C:GO:0016021	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF22 (PANTHER)
Ancylostoma ceylanicum	spindle assembly abnormal protein sas-5	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F52H2.7 [Caenorhabditis elegans]	0				-

Caenorhabditis elegans	suppressor with morphological effect on genitalia family member (smg-1)	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-ugt-54 protein	0		P:GO:0008152; F:GO:0016758		-
	-	0				-
Brugia malayi	hydroxysteroid (17-beta) dehydroge-se 13	4	P:GO:0055114; F:GO:0016491; F:GO:0005488; P:GO:0009058	-		IPR002198; IPR002347; IPR016040; PTHR19410:SF36 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis briggsae	tm104_caebr ame: full=transmembrane protein 104 homolog	1	C:GO:0016020	-		IPR013057; PTHR16189 (PANTHER)
	-	0				IPR018544
Caenorhabditis briggsae	cysteine-rich protein 1	4	F:GO:0008270; F:GO:0005515; C:GO:0005737; P:GO:0008283	-		-
Caenorhabditis briggsae	histone deacetylase 1	16	P:GO:0008340; F:GO:0004407; F:GO:0003714; P:GO:0048813; P:GO:0016575; C:GO:0035098; C:GO:0016581; P:GO:0007517; P:GO:0006342; P:GO:0006099; C:GO:0005705; C:GO:0016580; P:GO:0007350; P:GO:0048477; C:GO:0031523; P:GO:0022904	-		IPR000286; IPR003084; SSF52768 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	F:GO:0016787	-		IPR000073; G3DSA:3.40.50.1820 (GENE3D), PTHR12277 (PANTHER), PTHR12277:SF8 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical kda protein in chromosome	2	P:GO:0000003; P:GO:0006898	-		IPR007356; PTHR13563:SF4 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-acl-6 protein	6	P:GO:0042221; C:GO:0016020; C:GO:0005829; P:GO:0019432; P:GO:0050794; F:GO:0004366	-	EC:2.3.1.15	IPR002123; PTHR12563 (PANTHER), PTHR12563:SF3 (PANTHER), SSF69593 (SUPERFAMILY)
Caenorhabditis briggsae	btb poz domain containing protein	2	F:GO:0005515; C:GO:0016021	-		IPR013069
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis elegans	inin receptor homolog family member (ckr-2)	5	F:GO:0004983; P:GO:0007165; P:GO:0007186; C:GO:0016021; P:GO:0019915	-		IPR000276; IPR017452; G3DSA:1.20.1070.10 (GENE3D), PTHR19264 (PANTHER), PTHR19264:SF283 (PANTHER), SSF81321 (SUPERFAMILY)
	-	0				-
Loa loa	rad1 homolog	1	F:GO:0005515	-		IPR003021; G3DSA:3.70.10.10 (GENE3D), SSF55979 (SUPERFAMILY)
Angiostrongylus cantonensis	nematode cuticle collagen n-termi-l domain containing protein	1	F:GO:0042302	-		IPR002486; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	e3 ubiquitin protein ligase	0		F:GO:0016874; F:GO:0008270		IPR011016; IPR013083; PTHR23012 (PANTHER), PTHR23012:SF3 (PANTHER)
Bos taurus	ubiquitin associated and sh3 domain a	0		P:GO:0050860; C:GO:0005737; C:GO:0005829; P:GO:0001817; C:GO:0005634		PTHR16469 (PANTHER)
Giardia lamblia ATCC 50803	te-scin-x precursor	0		F:GO:0030414; F:GO:0005509; C:GO:0016021; C:GO:0009279; C:GO:0016020; F:GO:0004867; C:GO:0005576; C:GO:0005886		PD936484 (PRODOM)
Caenorhabditis briggsae	atp-binding sub-family b (mdr tap) member 1	5	P:GO:0009792; F:GO:0042626; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		IPR001140; IPR011527; IPR017940; G3DSA:1.20.1560.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF96 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	atp-binding sub-family b (mdr tap) member 1	5	P:GO:0009792; F:GO:0042626; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		IPR001140; IPR011527; IPR017940; G3DSA:1.20.1560.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF96 (PANTHER), SSF52540 (SUPERFAMILY)

Caenorhabditis elegans	neural precursor cell developmentally down-regulated 4	27	F:GO:0043130; P:GO:0019089; C:GO:0016327; P:GO:0031175; P:GO:0006622; F:GO:0019871; F:GO:0031698; P:GO:0051592; F:GO:0070064; P:GO:0010768; F:GO:0004842; P:GO:0042921; F:GO:0045309; C:GO:0048471; P:GO:0044111; F:GO:0019904; P:GO:0050847; P:GO:0031623; P:GO:0014068; P:GO:0042787; C:GO:0000785; F:GO:0070063; P:GO:0032801; P:GO:0010766; P:GO:0046824; C:GO:0005938; P:GO:0045732	-	EC:6.3.2.19	IPR000008; IPR000569; IPR001202; IPR008973; IPR018029; G3DSA:2.20.70.10 (GENE3D), G3DSA:2.60.40.150 (GENE3D), PTHR11254 (PANTHER), PTHR11254:SF78 (PANTHER)
Caenorhabditis elegans	nedd4 protein	36	F:GO:0005112; F:GO:0043130; F:GO:0050815; P:GO:0019089; C:GO:0016327; P:GO:0006622; C:GO:0005829; F:GO:0019871; P:GO:0002092; F:GO:0031698; P:GO:0030948; P:GO:0051592; P:GO:0016199; P:GO:0070534; F:GO:0070064; P:GO:0051965; P:GO:0010768; F:GO:0004842; P:GO:0042921; C:GO:0048471; P:GO:0044111; F:GO:0019904; P:GO:0050847; C:GO:0000151; P:GO:0014068; P:GO:0042787; C:GO:0000785;	-	EC:6.3.2.19	IPR000008; IPR000569; IPR001202; IPR008973; IPR018029; G3DSA:2.20.70.10 (GENE3D), G3DSA:2.60.40.150 (GENE3D), PTHR11254 (PANTHER), PTHR11254:SF78 (PANTHER)
	-	0				IPR000436; IPR016060; SignalP (SIGNALP)

Loa loa	briggsae cbr-ced-3 protein	8	P:GO:0008340; P:GO:0000003; F:GO:0005515; C:GO:0016020; C:GO:0005737; P:GO:0030972; F:GO:0008233; P:GO:0043065	-		IPR001309; IPR002138; IPR002398; IPR011600; IPR015917; IPR016129; G3DSA:3.40.50.1460 (GENE3D), SSF52129 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-mef-2 protein	0		P:GO:0006355; P:GO:0006350; F:GO:0043565; P:GO:0045449; F:GO:0003677; F:GO:0003700; C:GO:0005634		-
Caenorhabditis briggsae	briggsae cbr-ran-5 protein	0		P:GO:0040011; P:GO:0010171; P:GO:0009792; P:GO:0046907		-
Caenorhabditis briggsae	atpase family aaa domain-containing protein 3	3	F:GO:0005524; F:GO:0017111; C:GO:0005739	-	EC:3.6.1.15	-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		-
Angiostrongylus cantonensis	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	briggsae cbr-clc-1 protein	2	P:GO:0018996; C:GO:0005911	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	nuclear pore complex protein protein isoform partially confirmed by transcript evidence	0		C:GO:0005643; P:GO:0006810		IPR007230; PTHR23198 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-npp-10 protein	0		C:GO:0005643; P:GO:0006810		-
Caenorhabditis elegans	nuclear pore complex protein nup98	0		C:GO:0005643; P:GO:0006810		PTHR23198 (PANTHER)
Caenorhabditis briggsae	nuclear pore complex protein protein isoform partially confirmed by transcript evidence	0		C:GO:0005643; P:GO:0006810		IPR007230; PTHR23198 (PANTHER)
Caenorhabditis briggsae	nuclear pore complex protein protein isoform partially confirmed by transcript evidence	0		C:GO:0005643; P:GO:0006810		IPR007230; PTHR23198 (PANTHER)
Pongo abelii	ribosomal protein l21-like	4	F:GO:0003735; F:GO:0003723; C:GO:0022625; P:GO:0006414	-		IPR001147
	-	0				-
Caenorhabditis elegans	hypothetical protein B0238.11 [Caenorhabditis elegans]	0		P:GO:0000003; P:GO:0040035; P:GO:0006898; P:GO:0002119; P:GO:0040007		-
Caenorhabditis elegans	very low-density lipoprotein receptor	8	C:GO:0005624; C:GO:0044424; P:GO:0030178; C:GO:0044425; F:GO:0032403; P:GO:0043277; P:GO:0008152; F:GO:0034185	-		-
Caenorhabditis briggsae	briggsae cbr-dys-1 protein	0				-

Caenorhabditis elegans	alkylglycerone phosphate synthase	9	P:GO:0009792; P:GO:0002119; F:GO:0016491; F:GO:0008609; C:GO:0005777; P:GO:0008610; P:GO:0040007; F:GO:0050660; C:GO:0016020	-	EC:2.5.1.26	IPR006094; IPR016166; IPR016167; IPR016168; PTHR11748 (PANTHER), PTHR11748:SF3 (PANTHER)
Loa loa	phospholipase a-2-activating protein	1	P:GO:0040010	-		IPR001680; IPR011046; IPR015155; IPR015943; IPR017986; IPR019781; IPR019782; PTHR19849 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	dead deah box helicase family protein	5	F:GO:0004004; F:GO:0003676; P:GO:0040010; F:GO:0005524; P:GO:0000003	-		IPR000629; IPR001650; IPR011545; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF48 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	dead deah box helicase family protein	5	F:GO:0004004; F:GO:0003676; P:GO:0040010; F:GO:0005524; P:GO:0000003	-		IPR000629; IPR001650; IPR011545; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF48 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	dead deah box helicase family protein	5	F:GO:0004004; F:GO:0003676; P:GO:0040010; F:GO:0005524; P:GO:0000003	-		IPR000629; IPR001650; IPR011545; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF48 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Heliconius melpomene	endonuclease-reverse transcriptase	2	F:GO:0003676; F:GO:0003824	-		-
Caenorhabditis briggsae	Hypothetical protein CBG07023 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	aldolase	7	F:GO:0042802; P:GO:0009792; P:GO:0018991; P:GO:0040010; P:GO:0040011; P:GO:0006096; F:GO:0004332	-	EC:4.1.2.13	IPR000741; IPR013785; SSF51569 (SUPERFAMILY)
Caenorhabditis elegans	aldolase	7	F:GO:0042802; P:GO:0009792; P:GO:0018991; P:GO:0040010; P:GO:0040011; P:GO:0006096; F:GO:0004332	-	EC:4.1.2.13	IPR000741; IPR013785; SSF51569 (SUPERFAMILY)
Caenorhabditis briggsae	aldolase	7	F:GO:0042802; P:GO:0009792; P:GO:0018991; P:GO:0040010; P:GO:0040011; P:GO:0006096; F:GO:0004332	-	EC:4.1.2.13	IPR000741; IPR013785; SSF51569 (SUPERFAMILY)

Caenorhabditis briggsae	aldolase	7	F:GO:0042802; P:GO:0009792; P:GO:0018991; P:GO:0040010; P:GO:0040011; P:GO:0006096; F:GO:0004332	-	EC:4.1.2.13	IPR000741; IPR013785; SSF51569 (SUPERFAMILY)
Caenorhabditis elegans	aldolase	7	F:GO:0042802; P:GO:0009792; P:GO:0018991; P:GO:0040010; P:GO:0040011; P:GO:0006096; F:GO:0004332	-	EC:4.1.2.13	IPR000741; IPR013785; SSF51569 (SUPERFAMILY)
Caenorhabditis elegans	aldolase	7	F:GO:0042802; P:GO:0009792; P:GO:0018991; P:GO:0040010; P:GO:0040011; P:GO:0006096; F:GO:0004332	-	EC:4.1.2.13	IPR000741; IPR013785; SSF51569 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Brugia malayi	alpha-galactosidase alpha-n-acetylgalactosaminidase	3	P:GO:0005975; F:GO:0004553; F:GO:0043169	-	EC:3.2.1.0	IPR000111; IPR002241; IPR013785; IPR017853; PTHR11452 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	atp-dependent r- helicase	5	F:GO:0008026; F:GO:0003676; C:GO:0005622; F:GO:0005524; F:GO:0008270	-		PTHR18934 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Bacillus cereus AH621	family protein	0		C:GO:0016021; F:GO:0003677; F:GO:0000166; F:GO:0003674; F:GO:0017111; P:GO:0051301; F:GO:0005524; P:GO:0007059; P:GO:0007049		SignalP (SIGNALP)
Loa loa	ankyrin repeat containing	0		P:GO:0001886; F:GO:0005488; P:GO:0048514; C:GO:0005856; P:GO:0001570; P:GO:0045602; P:GO:0003007		-
Heliconius melpomene	endonuclease-reverse transcriptase	0		F:GO:0003723; F:GO:0004527; P:GO:0006278; F:GO:0004519; F:GO:0003964		IPR005135; G3DSA:3.60.10.10 (GENE3D), PTHR23227 (PANTHER), PTHR23227:SF14 (PANTHER)

Heliconius melpomene	endonuclease-reverse transcriptase	0		F:GO:0003723; F:GO:0004527; P:GO:0006278; F:GO:0004519; F:GO:0003964		IPR005135; G3DSA:3.60.10.10 (GENE3D)
	-	0				-
Heliconius melpomene	endonuclease-reverse transcriptase	0		F:GO:0003723; F:GO:0004527; P:GO:0006278; F:GO:0004519; F:GO:0003964		IPR005135; G3DSA:3.60.10.10 (GENE3D), PTHR23227 (PANTHER), PTHR23227:SF14 (PANTHER)
Heliconius melpomene	endonuclease-reverse transcriptase	0		F:GO:0003723; F:GO:0004527; P:GO:0006278; F:GO:0004519; F:GO:0003964		IPR005135; G3DSA:3.60.10.10 (GENE3D), PTHR23227 (PANTHER), PTHR23227:SF14 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Brugia malayi	vinculin	8	C:GO:0005737; F:GO:0005200; P:GO:0007016; F:GO:0003779; C:GO:0005925; P:GO:0007155; P:GO:0006911; C:GO:0015629	-		IPR006077; G3DSA:1.20.120.230 (GENE3D), G3DSA:1.20.1490.10 (GENE3D)
Brugia malayi	vinculin	8	C:GO:0005737; F:GO:0005200; P:GO:0007016; F:GO:0003779; C:GO:0005925; P:GO:0007155; P:GO:0006911; C:GO:0015629	-		IPR006077; G3DSA:1.20.120.230 (GENE3D), G3DSA:1.20.1490.10 (GENE3D)
Caenorhabditis briggsae	dm d- binding domain containing protein	7	F:GO:0003700; F:GO:0016491; F:GO:0003677; P:GO:0007548; P:GO:0055114; C:GO:0005634; P:GO:0006355	-		IPR001275; PTHR12322 (PANTHER)
Angiostrongylus cantonensis	briggsae cbr-mdl-1 protein	2	P:GO:0045449; F:GO:0005515	-		PTHR11969 (PANTHER), PTHR11969:SF3 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR001534; SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-

	ap-2 complex subunit mu-1	12	P:GO:0016192; C:GO:0005829; C:GO:0030132; C:GO:0005739; F:GO:0008289; C:GO:0030131; C:GO:0005778; C:GO:0030666; P:GO:0050690; F:GO:0005515; F:GO:0005215; P:GO:0006886	-		IPR008968; IPR015629; IPR018240; G3DSA:2.60.40.1170 (GENE3D), PTHR11998 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	atypical abc1 abc1-c protein ki-se	0				-
Caenorhabditis briggsae	atypical abc1 abc1-c protein ki-se	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	phosphatidylinositol 4-ki-se alpha	3	P:GO:0000003; P:GO:0008219; F:GO:0016772	-		IPR015433; PTHR10048:SF15 (PANTHER)
Caenorhabditis briggsae	calcitonin receptor	5	P:GO:0007186; C:GO:0016021; P:GO:0007165; C:GO:0005886; F:GO:0004930	-		IPR000832; IPR017983; PTHR12011 (PANTHER), PTHR12011:SF14 (PANTHER), SignalP (SIGNALP)
Loa loa	a-phase-promoting complex subunit 7	0		F:GO:0005488; P:GO:0007049; P:GO:0051301; P:GO:0008150; F:GO:0005515; C:GO:0005575		IPR011990; IPR019734; PTHR12558 (PANTHER), PTHR12558:SF7 (PANTHER), SSF48452 (SUPERFAMILY)
Danio rerio	viral a-type inclusion protein	0		P:GO:0007018; F:GO:0003700; C:GO:0005634; C:GO:0005874; F:GO:0000166; C:GO:0005737; F:GO:0005524; F:GO:0003777; C:GO:0016459; P:GO:0006886; P:GO:0006355; C:GO:0030016; F:GO:0003774; C:GO:0005622; C:GO:0032982; F:GO:0003899		-
Caenorhabditis elegans	map ki-se ki-se	2	F:GO:0005515; P:GO:0019915	-		IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF20 (PANTHER)
	-	0				-
Loa loa	peptidase family m13 containing protein	3	P:GO:0019538; F:GO:0016787; C:GO:0016020	-		IPR000718; IPR018497; G3DSA:3.40.390.10 (GENE3D), SSF55486 (SUPERFAMILY)
	-	0				-

Loa loa	hypothetical protein LOAG_12942 [Loa loa]	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021		-
Loa loa	d- mismatch repair protein containing protein	21	P:GO:0051257; F:GO:0005515; P:GO:0045950; P:GO:0043060; P:GO:0007283; C:GO:0005712; P:GO:0000712; P:GO:0006303; P:GO:0008630; P:GO:0007060; C:GO:0000795; P:GO:0016446; C:GO:0001673; P:GO:0000239; P:GO:0048477; F:GO:0032137; P:GO:0000289; C:GO:0032389; P:GO:0006298; F:GO:0005524; P:GO:0045190	-		IPR002099; IPR003594; IPR011186; IPR014762
	-	0				IPR004296
Loa loa	briggsae cbr-acy-4 protein	5	F:GO:0004016; P:GO:0009190; C:GO:0016021; F:GO:0042302; F:GO:0000166	-	EC:4.6.1.1	IPR001054; PTHR11920 (PANTHER), PTHR11920:SF14 (PANTHER)
Loa loa	plastid acetyl- carboxylase	4	P:GO:0044249; F:GO:0005488; P:GO:0044238; F:GO:0016874	-		IPR005481; IPR011764; IPR013817; IPR016185; PTHR18866 (PANTHER), PTHR18866:SF6 (PANTHER)
Angiostrongylus cantonensis	homeo box d1	14	P:GO:0007411; F:GO:0030528; P:GO:0016337; P:GO:0006355; F:GO:0043565; P:GO:0010171; P:GO:0007413; P:GO:0002119; F:GO:0003700; P:GO:0040011; C:GO:0005737; P:GO:0040018; C:GO:0005634; P:GO:0009790	-		PTHR19418 (PANTHER), PTHR19418:SF174 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis briggsae	lam-2	2	P:GO:0007155; C:GO:0005578	-		IPR000034; IPR002049; IPR013032; PTHR10574 (PANTHER), PTHR10574:SF48 (PANTHER), SSF57196 (SUPERFAMILY)
	-	0				-

Caenorhabditis elegans	lrp1 protein	0		F:GO:0032570; F:GO:0005509; F:GO:0004872; P:GO:0008283; C:GO:0043025; C:GO:0005887; C:GO:0005886; F:GO:0004714; P:GO:0010875; F:GO:0032403; P:GO:0006898; P:GO:0006897; C:GO:0016021; C:GO:0016020; P:GO:0043277; P:GO:0007205; C:GO:0005624; P:GO:0030178; F:GO:0016787; P:GO:0032429; P:GO:0042157; C:GO:0005905; C:GO:0030425; P:GO:0006629; C:GO:0030136; F:GO:0070325; F:GO:0034185; F:GO:0016740;		SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	2	F:GO:0008270; F:GO:0005515	-		-
Caenorhabditis briggsae	rrp12-like protein	0		C:GO:0031965; F:GO:0005488; C:GO:0016021; C:GO:0016020; P:GO:0008150; F:GO:0005515; C:GO:0005634; C:GO:0005730		PTHR21576 (PANTHER), PTHR21576:SF2 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-asp-1 protein	5	C:GO:0005623; P:GO:0008219; F:GO:0005515; F:GO:0004175; P:GO:0030163	-		IPR001461; IPR001969; IPR009007; IPR021109; PTHR13683:SF53 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-glh-1 protein	2	F:GO:0016787; F:GO:0042802	-		IPR000629; IPR001650; IPR011545; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF61 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR008253; SignalP (SIGNALP)
	-	0				IPR009730
Brugia malayi	hypothetical protein [Brugia malayi]	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG09291 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)

Caenorhabditis elegans	anis1_anisi ame: full=major allergen ani s 1 ame: full=21 kda allergen ame: full=excretory gland allergen ans1 ame: allergen=ani s 1 flags: precursor	0		P:GO:0006915; F:GO:0030414; F:GO:0004867; C:GO:0005576		IPR002223; PTHR10083 (PANTHER), PTHR10083:SF17 (PANTHER)
	-	0				-
	-	0				-
Haemonchus contortus	acetylcholine regulator unc-	1	P:GO:0006904	-		IPR001619; G3DSA:1.25.40.60 (GENE3D), G3DSA:3.40.50.1910 (GENE3D), G3DSA:3.40.50.2060 (GENE3D), PTHR11679:SF7 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-clc-5 protein	0		F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150		IPR010761; SignalP (SIGNALP)
Caenorhabditis elegans	gpi ethanolamine phosphate	2	P:GO:0008152; F:GO:0003824	-		IPR007070; SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	phospholipase d3	2	C:GO:0044464; F:GO:0003824	-		G3DSA:3.30.870.10 (GENE3D), SignalP (SIGNALP), SSF56024 (SUPERFAMILY)
	-	0				PTHR19897 (PANTHER), PTHR19897:SF9 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0015078; P:GO:0015986; F:GO:0005488; C:GO:0033177; P:GO:0040010		-
Callithrix jacchus	ribophorin isoform cra_a	9	C:GO:0008250; C:GO:0019718; P:GO:0018279; C:GO:0016021; C:GO:0042470; P:GO:0015833; C:GO:0030867; F:GO:0005515; F:GO:0004579	-	EC:2.4.1.119	IPR007676
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	splicing arginine serine-rich 1	7	F:GO:0003723; F:GO:0050733; P:GO:0006376; F:GO:0000166; C:GO:0044428; P:GO:0001701; P:GO:0060048	-		IPR000504; IPR012677; PTHR10548 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	splicing arginine serine-rich 1	5	P:GO:0009792; P:GO:0008380; F:GO:0003723; F:GO:0005515; F:GO:0000166	-		-

Caenorhabditis elegans	arginine serine-rich splicing factor	5	P:GO:0009792; P:GO:0008380; F:GO:0003723; F:GO:0005515; F:GO:0000166	-		-
Caenorhabditis elegans	arginine serine-rich splicing factor	5	P:GO:0009792; P:GO:0008380; F:GO:0003723; F:GO:0005515; F:GO:0000166	-		-
	-	0				-
Brugia malayi	r- binding motif protein 25	7	C:GO:0005737; F:GO:0003729; P:GO:0006915; P:GO:0000381; F:GO:0005515; C:GO:0016607; F:GO:0000166	-		IPR000504; IPR012677; PTHR18806 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	fibulin 1	4	F:GO:0016504; F:GO:0005515; P:GO:0030198; C:GO:0005604	-		IPR006210; IPR013032; IPR013091; IPR018097; G3DSA:2.10.25.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF89 (PANTHER), SSF57196 (SUPERFAMILY)
Caenorhabditis briggsae	28s ribosomal protein mitochondrial	4	P:GO:0000003; P:GO:0040007; P:GO:0006898; P:GO:0002119	-		IPR019266
	-	0				-
Caenorhabditis elegans	protein aveugle	6	C:GO:0005737; P:GO:0042675; C:GO:0005886; P:GO:0007173; P:GO:0007165; P:GO:0001751	-		IPR001660; IPR010993; IPR011510; IPR013761; PTHR20843 (PANTHER)
Loa loa	probable 26s proteasome non-atpase regulatory subunit	0		P:GO:0042176; P:GO:0000003; P:GO:0002119; P:GO:0009792; F:GO:0030234; C:GO:0000502; P:GO:0008340; F:GO:0005515; P:GO:0040007; F:GO:0005488		-
Caenorhabditis elegans	briggsae cbr-dhs-5 protein	5	C:GO:0016021; P:GO:0055114; F:GO:0016491; P:GO:0006508; F:GO:0005515	-		-
Caenorhabditis briggsae	type-1 corticotropin-releasing hormone receptor alpha isoform	5	F:GO:0004930; C:GO:0005886; P:GO:0007165; P:GO:0007186; C:GO:0016021	-		IPR000832; IPR001879; IPR017981; IPR017983; PTHR12011 (PANTHER), PTHR12011:SF15 (PANTHER), SSF111418 (SUPERFAMILY)
Loa loa	hypothetical protein LOAG_12354 [Loa loa]	0				-
Angiostrongylus cantonensis	yot9_caeel ame: full=uncharacterized protein	0				-

Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0006629; C:GO:0016021; F:GO:0016787; F:GO:0004806		IPR002921; G3DSA:3.40.50.1820 (GENE3D), SSF53474 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Aspergillus clavatus NRRL 1	gas2 domain protein	0		P:GO:0007050		-
Brugia malayi	phosphatase and tensin-like	29	P:GO:0010035; P:GO:0007507; P:GO:0031174; P:GO:0046856; P:GO:0030336; C:GO:0005829; P:GO:0051895; F:GO:0004438; F:GO:0051800; P:GO:0046855; P:GO:0010033; P:GO:0010975; F:GO:0051717; F:GO:0016314; P:GO:0060070; F:GO:0004722; P:GO:0008285; P:GO:0007417; P:GO:0050821; F:GO:0030165; P:GO:0006470; F:GO:0004725; P:GO:0000079; F:GO:0019899; C:GO:0005634; P:GO:0051898; P:GO:0051091;	-	EC:3.1.3.64; EC:3.1.3.67; EC:3.1.3.48	IPR000340; IPR014019; IPR014020; IPR016130; G3DSA:3.90.190.10 (GENE3D), PTHR12305 (PANTHER), PTHR12305:SF6 (PANTHER), SSF52799 (SUPERFAMILY)

Brugia malayi	phosphatase and tensin-like	29	P:GO:0001933; P:GO:0010035; P:GO:0007507; P:GO:0031174; P:GO:0046856; P:GO:0030336; C:GO:0005829; P:GO:0051895; F:GO:0004438; F:GO:0051800; P:GO:0046855; P:GO:0010033; P:GO:0010975; F:GO:0051717; F:GO:0016314; P:GO:0060070; F:GO:0004722; P:GO:0008285; P:GO:0007417; P:GO:0050821; F:GO:0030165; P:GO:0006470; F:GO:0004725; P:GO:0000079; F:GO:0019899; C:GO:0005634; P:GO:0051898; P:GO:0051091;	-	EC:3.1.3.64; EC:3.1.3.67; EC:3.1.3.48	IPR000340; IPR014019; IPR014020; IPR016130; G3DSA:3.90.190.10 (GENE3D), PTHR12305 (PANTHER), PTHR12305:SF6 (PANTHER), SSF52799 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	ibr domain containing protein	3	F:GO:0003676; F:GO:0008270; F:GO:0005515	-		IPR001841; IPR002867; IPR013083; PTHR11685 (PANTHER), PTHR11685:SF5 (PANTHER), SSF57850 (SUPERFAMILY)
Brugia malayi	novel protein human ankyrin repeat and sterile alpha motif domain containing 1a	2	F:GO:0005515; C:GO:0044424	-		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF116 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Loa loa	f-box only protein 11	2	F:GO:0008270; F:GO:0004842	-	EC:6.3.2.19	SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	transmembrane protein 104	1	C:GO:0016021	-		IPR013057; PTHR16189 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	2	F:GO:0035299; F:GO:0005524	-	EC:2.7.1.158	IPR009286
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	3	P:GO:0040007; P:GO:0008340; P:GO:0040011	-		IPR010993; IPR013761; IPR021129

Caenorhabditis elegans	s-like r-se	0		F:GO:0003723; F:GO:0033897; F:GO:0016787; F:GO:0004519; F:GO:0004518; C:GO:0005576		IPR001568; IPR018188; PTHR11240:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	dienelactone hydrolase family protein	1	F:GO:0016787	-		IPR002925; G3DSA:3.40.50.1820 (GENE3D), PTHR22946 (PANTHER), SSF53474 (SUPERFAMILY)
Caenorhabditis briggsae	tetratricopeptide repeat protein 39b	1	F:GO:0005488	-		IPR019412; SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	cyclin-related protein fam58a-like isoform 2	0		P:GO:0048133; P:GO:0007179; F:GO:0005515		IPR006671; IPR011028; IPR013032; IPR013763; IPR015429
	-	0				-
Brugia malayi	mediator of r- polymerase ii transcription subunit 7	7	P:GO:0006357; F:GO:0008270; F:GO:0003676; C:GO:0005667; F:GO:0016455; F:GO:0005515; C:GO:0016592	-		-
Brugia malayi	elegans protein confirmed by transcript evidence	14	F:GO:0004197; P:GO:0008340; P:GO:0031638; P:GO:0007417; P:GO:0006919; P:GO:0007291; P:GO:0016540; P:GO:0007516; P:GO:0008258; P:GO:0046672; P:GO:0035071; F:GO:0042803; P:GO:0035081; C:GO:0005739	-	EC:3.4.22.0	IPR015672; IPR022535; SignalP (SIGNALP)
Caenorhabditis elegans	ytv2_caeel ame: full=uncharacterized zinc metalloprotease	0		P:GO:0006508; F:GO:0008233		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	protein o-fucosyltransferase 2	5	P:GO:0007283; P:GO:0010171; P:GO:0040025; F:GO:0016757; P:GO:0018991	-		IPR019378; PTHR13398 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR001466; IPR012338; G3DSA:3.40.710.10 (GENE3D), PTHR10566 (PANTHER), PTHR10566:SF6 (PANTHER)
Caenorhabditis briggsae	tho complex subunit 7 homolog	3	P:GO:0009987; P:GO:0006810; C:GO:0044424	-		IPR008501; IPR018018
Loa loa	protein ki-se	2	F:GO:0004713; F:GO:0000166	-	EC:2.7.10.0	SignalP (SIGNALP)
Caenorhabditis briggsae	let-2	4	C:GO:0005587; F:GO:0005488; F:GO:0030020; P:GO:0016043	-		IPR008160; PTHR10499 (PANTHER), PTHR10499:SF114 (PANTHER)

	-	0				-
Caenorhabditis elegans	chch domain containing protein	0		C:GO:0005739; C:GO:0005758; P:GO:0055085; F:GO:0005515; P:GO:0015031		-
Brugia malayi	member ras oncogene family	10	P:GO:0006928; F:GO:0005525; C:GO:0016023; C:GO:0005886; P:GO:0007049; P:GO:0007264; C:GO:0005739; F:GO:0019003; F:GO:0003924; P:GO:0015031	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001806; IPR002078; IPR003579; IPR005225; IPR013753; IPR015595; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	islet cell autoantigen 1	3	C:GO:0005737; P:GO:0046928; P:GO:0042221	-		IPR010504; PTHR10164 (PANTHER), SSF103657 (SUPERFAMILY)
Caenorhabditis elegans	peroxisomal coenzyme a diphosphatase nudt7	0		F:GO:0000287; F:GO:0016787; C:GO:0016021; F:GO:0016818; P:GO:0009132; F:GO:0030145		IPR000086; IPR015797; IPR020084; PTHR12992 (PANTHER), PS51462 (PROFILE)
	-	0				-
	-	0				-
Ancylostoma ceylanicum	elegans protein partially confirmed by transcript evidence	1	F:GO:0008233	-		IPR001506; IPR006026; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SignalP (SIGNALP), SSF55486 (SUPERFAMILY)
Ancylostoma ceylanicum	elegans protein partially confirmed by transcript evidence	1	F:GO:0008233	-		IPR001506; IPR006026; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SignalP (SIGNALP), SSF55486 (SUPERFAMILY)
Haemonchus contortus	beta-tubulin isotype 1	6	P:GO:0007018; F:GO:0005525; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Haemonchus contortus	beta-tubulin isotype 1	6	P:GO:0007018; F:GO:0005525; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Haemonchus contortus	beta-tubulin isotype 1	6	P:GO:0007018; F:GO:0005525; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-

Haemonchus contortus	beta-tubulin isotype 1	6	P:GO:0007018; F:GO:0005525; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Haemonchus contortus	beta-tubulin isotype 1	6	P:GO:0007018; F:GO:0005525; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Haemonchus contortus	beta-tubulin isotype 1	6	P:GO:0007018; F:GO:0005525; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Cooperia oncophora	beta-tubulin isotype 1	6	P:GO:0007018; F:GO:0005525; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000217; IPR002453; IPR003008; IPR008280; IPR013838; IPR017975; IPR018316
Cooperia oncophora	beta-tubulin isotype 1	6	P:GO:0007018; F:GO:0005525; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000217; IPR002453; IPR003008; IPR008280; IPR013838; IPR017975; IPR018316
Caenorhabditis brenneri	beta-tubulin isotype 1	6	P:GO:0007018; F:GO:0005525; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Haemonchus contortus	beta-tubulin isotype 1	6	P:GO:0007018; F:GO:0005525; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Haemonchus contortus	beta-tubulin isotype 1	6	P:GO:0007018; F:GO:0005525; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Haemonchus contortus	beta-tubulin isotype 1	6	P:GO:0007018; F:GO:0005525; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-

Haemonchus contortus	beta-tubulin isotype 1	6	P:GO:0007018; F:GO:0005525; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Haemonchus contortus	beta-tubulin isotype 1	6	P:GO:0007018; F:GO:0005525; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Caenorhabditis elegans	abhydrolase domain containing 12	0		P:GO:0008152; F:GO:0016787; C:GO:0016021; F:GO:0047372; C:GO:0016020		IPR000073; G3DSA:3.40.50.1820 (GENE3D), PTHR12277 (PANTHER), PTHR12277:SF4 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	abhydrolase domain containing 12	0		P:GO:0008152; F:GO:0016787; C:GO:0016021; F:GO:0047372; C:GO:0016020		IPR000073; G3DSA:3.40.50.1820 (GENE3D), PTHR12277 (PANTHER), PTHR12277:SF4 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F45E4.5 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	family with sequence similarity member b1	0		P:GO:0006508; F:GO:0003674; F:GO:0008236; F:GO:0016787; P:GO:0008150; C:GO:0005576; C:GO:0005575		-
Caenorhabditis elegans	-d-dependent malic mitochondrial precursor	9	F:GO:0046872; P:GO:0006090; F:GO:0051287; C:GO:0005759; F:GO:0016619; F:GO:0030060; P:GO:0006108; P:GO:0055114; F:GO:0004473	-	EC:1.1.1.38; EC:1.1.1.37; EC:1.1.1.40	IPR012302; IPR016040; PTHR23406 (PANTHER), PTHR23406:SF2 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	isocitrate dehydroge-se	12	C:GO:0005962; P:GO:0045926; P:GO:0006103; C:GO:0005730; P:GO:0006734; P:GO:0055114; F:GO:0004449; P:GO:0006099; F:GO:0005524; F:GO:0051287; F:GO:0000287; P:GO:0006102	-	EC:1.1.1.41	IPR001804; PTHR11835:SF5 (PANTHER), SSF53659 (SUPERFAMILY)

Caenorhabditis briggsae	c6orf153 protein	5	P:GO:0009792; P:GO:0002119; P:GO:0000003; P:GO:0040007; P:GO:0006898	-		IPR009292
Onchocerca volvulus	peptidyl-prolyl isomerase cwc27	2	F:GO:0003755; P:GO:0006457	-	EC:5.2.1.8	IPR002130; IPR015891; PTHR11071 (PANTHER), PTHR11071:SF33 (PANTHER)
	-	0				SignalP (SIGNALP)
Loa loa	activated r- polymerase ii transcriptio-l coactivator p15	5	C:GO:0031981; P:GO:0006355; P:GO:0000003; F:GO:0003677; F:GO:0005515	-		IPR003173; IPR009044
	-	0				-
	-	0				-
Caenorhabditis elegans	variable abnormal morphology family member (vab-10)	0		F:GO:0005509; P:GO:0007050		G3DSA:1.20.58.60 (GENE3D), SSF46966 (SUPERFAMILY)
Caenorhabditis elegans	d- repair protein rad4 containing protein	7	P:GO:0000718; P:GO:0000075; F:GO:0003684; F:GO:0005515; F:GO:0003697; C:GO:0005654; P:GO:0000715	-		IPR004583; IPR018327; IPR018328
Caenorhabditis briggsae	tetratricopeptide repeat protein 38	0		F:GO:0005488; P:GO:0008150; C:GO:0005575		IPR011990; SSF48452 (SUPERFAMILY)
	-	0				-
	-	0				-
Loa loa	microtubule-associated protein rp eb family member 1	14	P:GO:0000022; P:GO:0031115; C:GO:0005829; C:GO:0005875; P:GO:0035372; F:GO:0051010; P:GO:0007629; P:GO:0051225; P:GO:0007423; C:GO:0005876; P:GO:0007059; C:GO:0005881; P:GO:0030589; C:GO:0030981	-		IPR001715; IPR004953; PTHR10623 (PANTHER), SignalP (SIGNALP), SSF140612 (SUPERFAMILY)
Camponotus floridanus	uncharacterized transposase-like protein	0		F:GO:0046872; P:GO:0055114; F:GO:0009055; F:GO:0016491; F:GO:0020037; F:GO:0005506; F:GO:0004497		IPR007087; IPR015880
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	P:GO:0006810	-		SignalP (SIGNALP)
	-	0				-

Caenorhabditis briggsae	briggsae cbr-flp-2 protein	0		P:GO:0007218; P:GO:0040010; P:GO:0009792; P:GO:0002119; P:GO:0040007		SignalP (SIGNALP)
Caenorhabditis elegans	bro1 domain-containing protein brox	0		C:GO:0016020		G3DSA:1.25.40.280 (GENE3D), PTHR23032 (PANTHER)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG06447 [Caenorhabditis briggsae]	0				-
	-	0				-
Caenorhabditis elegans	immunoglobulin i-set domain containing protein	0		C:GO:0005737; F:GO:0003779; C:GO:0030017; C:GO:0005634		IPR003599; IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF11 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	temporarily assigned gene -me family member (tag-333)	0		F:GO:0005488; P:GO:0007165; F:GO:0005515		IPR000159; IPR003123; PTHR23101 (PANTHER), PTHR23101:SF3 (PANTHER), SSF109993 (SUPERFAMILY)
Caenorhabditis elegans	tbc domain containing protein	1	F:GO:0005515	-		-
Caenorhabditis briggsae	Hypothetical protein CBG15695 [Caenorhabditis briggsae]	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Loa loa	hypothetical protein LOAG_07466 [Loa loa]	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-nlr-1 protein	0				PTHR10127 (PANTHER), PTHR10127:SF2 (PANTHER)
Caenorhabditis elegans	vacuolar proton atpases	3	C:GO:0033177; C:GO:0016021; P:GO:0015986	-		IPR002490; PTHR11629:SF23 (PANTHER)
Caenorhabditis elegans	small family member (sma-9)	1	F:GO:0005515	-		-
Macaca mulatta	sig-l sequence delta	7	F:GO:0004872; C:GO:0005784; F:GO:0005515; F:GO:0005509; P:GO:0006886; P:GO:0007165; C:GO:0016021	-		IPR008855; SignalP (SIGNALP)
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				IPR018483
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				IPR018483
Caenorhabditis briggsae	calcium atpase	5	F:GO:0005388; C:GO:0016021; P:GO:0006754; F:GO:0005524; P:GO:0006816	-	EC:3.6.3.8	IPR001757; IPR022141; PTHR11939:SF5 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				IPR011047; IPR015943
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-

Taeniopygia guttata	uridine-cytidine ki-se 2	10	C:GO:0005829; P:GO:0071453; F:GO:0004849; F:GO:0016773; P:GO:0006911; F:GO:0005524; C:GO:0005792; P:GO:0016579; P:GO:0048678; P:GO:0007631	-	EC:2.7.1.48; EC:2.7.1.0	-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	gram domain containing protein	0				-
Brugia malayi	gram domain containing protein	0				-
Brugia malayi	gram domain containing protein	0				-
Brugia malayi	gram domain containing protein	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein T07E3.4 [Caenorhabditis elegans]	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-jph-1 protein	0				IPR003409; G3DSA:2.20.110.10 (GENE3D), PTHR23085 (PANTHER), PTHR23085:SF3 (PANTHER), SSF82185 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-jph-1 protein	0				IPR003409; G3DSA:2.20.110.10 (GENE3D), PTHR23085 (PANTHER), PTHR23085:SF3 (PANTHER), SSF82185 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-jph-1 protein	0				IPR003409; G3DSA:2.20.110.10 (GENE3D), PTHR23085 (PANTHER), PTHR23085:SF3 (PANTHER), SSF82185 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	nuclear vcp-like	0		F:GO:0005524; F:GO:0000166; F:GO:0017111		PTHR23077 (PANTHER), PTHR23077:SF16 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	skp1 related (ubiquitin ligase complex component) protein 18-like	4	P:GO:0002009; P:GO:0040035; P:GO:0006898; P:GO:0040011	-		-
Caenorhabditis briggsae	d- ligase i	5	F:GO:0008408; F:GO:0003697; P:GO:0000003; P:GO:0006289; P:GO:0007004	-		PTHR23240 (PANTHER), PTHR23240:SF1 (PANTHER)
	-	0				-
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
	-	0				-
	-	0				-

Loa loa	prp6 pre-mr- splicing factor 6 homolog	18	P:GO:0000003; C:GO:0046540; P:GO:0040010; P:GO:0040015; P:GO:0006898; F:GO:0043021; P:GO:0000244; P:GO:0018996; P:GO:0000245; P:GO:0040039; C:GO:0005681; P:GO:0009792; F:GO:0003713; P:GO:0002119; C:GO:0005682; C:GO:0071001; P:GO:0045944; F:GO:0050681	-		IPR011990; IPR013026; PTHR11246 (PANTHER), PTHR11246:SF1 (PANTHER), SSF48452 (SUPERFAMILY)
Caenorhabditis briggsae	cyclopropane-fatty-acyl-phospholipid synthase	2	P:GO:0008610; F:GO:0008825	-	EC:2.1.1.79	IPR003333; G3DSA:3.40.50.150 (GENE3D), SSF53335 (SUPERFAMILY)
Caenorhabditis elegans	ubiquitin-activating enzyme e1 domain-containing	9	C:GO:0005737; F:GO:0046872; F:GO:0005515; F:GO:0071566; F:GO:0005524; F:GO:0016616; F:GO:0048037; C:GO:0005634; P:GO:0071569	-	EC:1.1.1.0	-
Angiostrongylus cantonensis	yy2 transcription factor	1	F:GO:0005488	-		IPR007087; IPR013087; IPR015880; PTHR14003 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-sgn-1 protein	5	P:GO:0007010; C:GO:0016021; P:GO:0040013; C:GO:0016012; F:GO:0005515	-		IPR006875; PTHR12939 (PANTHER), PTHR12939:SF1 (PANTHER)
Caenorhabditis briggsae	ras association domain-containing protein 1	12	P:GO:0007265; F:GO:0008270; P:GO:0006974; C:GO:0044430; P:GO:0071157; C:GO:0015630; P:GO:0031398; F:GO:0047485; P:GO:0050821; F:GO:0042802; C:GO:0044444; C:GO:0005634	-		IPR002219; IPR008937; IPR020454; G3DSA:3.30.60.20 (GENE3D), PTHR23113:SF19 (PANTHER), SSF57889 (SUPERFAMILY)
Caenorhabditis elegans	homeobox family member (ceh-38)	1	P:GO:0000003	-		-
Caenorhabditis briggsae	mgc82750 protein	1	F:GO:0005488	-		IPR007810; PTHR23323 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG22096 [Caenorhabditis briggsae]	2	P:GO:0048856; P:GO:0007275	-		IPR011989
	-	0				-

Caenorhabditis elegans	potassium subfamily member 1	3	P:GO:0006811; C:GO:0016020; F:GO:0005216	-		IPR003280; IPR005408; IPR013099; G3DSA:1.10.287.70 (GENE3D), PTHR11003 (PANTHER), PTHR11003:SF26 (PANTHER), SignalP (SIGNALP), SSF81324 (SUPERFAMILY)
	-	0				-
Pongo abelii	preli domain containing 1	4	P:GO:0006955; C:GO:0005730; P:GO:0007275; C:GO:0005739	-		IPR006797; PTHR11158 (PANTHER), PTHR11158:SF16 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	pap-inositol- -phosphatase	1	F:GO:0004437	-		IPR000760; IPR020550; G3DSA:3.30.540.10 (GENE3D), G3DSA:3.40.190.80 (GENE3D), PTHR20854:SF7 (PANTHER), SignalP (SIGNALP), SSF56655 (SUPERFAMILY)
Caenorhabditis elegans	tfiih basal transcription factor complex helicase subunit	7	P:GO:0006283; P:GO:0006917; F:GO:0043139; F:GO:0004003; F:GO:0003677; F:GO:0005524; C:GO:0005634	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	P:GO:0040010; P:GO:0000003	-		IPR015419
Gallus gallus	non-structural mainte-nce of chromosome subunit of d-repair	0		P:GO:0008150; C:GO:0005575		IPR014854
Caenorhabditis elegans	hypothetical protein F46F11.7 [Caenorhabditis elegans]	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	P:GO:0002119; P:GO:0040010	-		-
	-	0				-
	-	0				-
Pongo abelii	60s acidic ribosomal protein p2	4	F:GO:0003735; F:GO:0003723; C:GO:0022625; P:GO:0006414	-		IPR001813; PTHR21141 (PANTHER), PTHR21141:SF5 (PANTHER)
Caenorhabditis elegans	dihydroorotate dehydroge-se	5	P:GO:0043065; C:GO:0005743; F:GO:0004152; P:GO:0006221; P:GO:0090140	-	EC:1.3.99.11	IPR013785; PTHR11938 (PANTHER), PTHR11938:SF7 (PANTHER), SSF51395 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-elpc-1 protein	0		F:GO:0016301; F:GO:0005488		IPR006849
Caenorhabditis briggsae	briggsae cbr-kin-29 protein	0		F:GO:0016740; F:GO:0004674; F:GO:0004672; C:GO:0005634; P:GO:0006468; F:GO:0000166; C:GO:0005737; F:GO:0005524; P:GO:0007275; F:GO:0016301; F:GO:0046872		-
	-	0				-

Ancylostoma caninum	bone morphogenetic protein type ib	6	P:GO:0048263; P:GO:0006468; F:GO:0005024; P:GO:0030509; F:GO:0005524; C:GO:0016020	-		IPR000719; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR23255 (PANTHER), PTHR23255:SF14 (PANTHER)
	-	0				-
	-	0				-
Heliconius melpomene	endonuclease-reverse transcriptase	0		F:GO:0003723; P:GO:0006278; F:GO:0004519; F:GO:0003677; F:GO:0003964		IPR000477; IPR015706; PTHR19446:SF100 (PANTHER), SignalP (SIGNALP), SSF56672 (SUPERFAMILY)
Caenorhabditis elegans	laminin see also lmb- protein 1	5	P:GO:0000003; P:GO:0010171; P:GO:0040010; F:GO:0005515; P:GO:0040011	-		-
Caenorhabditis briggsae	ykad_caeel ame: full=uncharacterized protein	0				-
	-	0				-
	-	0				-
Dictyocaulus viviparus	nematode polyprotein allergen related family member (npa-1)	2	P:GO:0008340; F:GO:0008289	-		PTHR21693 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	transcriptio-l regulating factor 1	0		F:GO:0008301; P:GO:0006707; F:GO:0003700; F:GO:0003677; C:GO:0005634; F:GO:0030374; P:GO:0045893; P:GO:0046885; F:GO:0008134; F:GO:0008270; P:GO:0007275; P:GO:0042592; C:GO:0005622; F:GO:0016455; F:GO:0046872; P:GO:0006694; P:GO:0045449		PTHR16089 (PANTHER), PTHR16089:SF9 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	unkempt homolog -like	7	F:GO:0003676; P:GO:0008152; C:GO:0005737; C:GO:0005634; F:GO:0008270; F:GO:0005515; F:GO:0016874	-		IPR000571; PTHR14493 (PANTHER), PTHR14493:SF1 (PANTHER)

Loa loa	ccr4-not transcription subunit isoform cra_b	11	P:GO:0040010; F:GO:0003676; F:GO:0046872; P:GO:0000003; F:GO:0004842; F:GO:0005515; P:GO:0051865; P:GO:0040017; P:GO:0009792; C:GO:0005737; C:GO:0005634	-	EC:6.3.2.19	IPR000504; IPR001841; IPR012677; IPR013083; PTHR12603 (PANTHER), SSF54928 (SUPERFAMILY), SSF57850 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		IPR005373
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		IPR005373
Pan troglodytes	ribosomal protein l14	7	P:GO:0042273; F:GO:0003735; F:GO:0003723; F:GO:0005515; P:GO:0006364; C:GO:0022625; P:GO:0006414	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	cub domain containing protein	0				IPR000859; PTHR10127 (PANTHER), PTHR10127:SF33 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG22545 [Caenorhabditis briggsae]	0		F:GO:0008270; C:GO:0005622		IPR007087; IPR015880
Caenorhabditis briggsae	zinc finger protein	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		IPR007087; IPR015880
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG09291 [Caenorhabditis briggsae]	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	exodeoxyribonuclease iii family protein	4	C:GO:0005622; F:GO:0008408; P:GO:0006974; F:GO:0003906	-	EC:4.2.99.18	IPR000097; IPR004808; IPR005135; IPR020848; G3DSA:3.60.10.10 (GENE3D)
Caenorhabditis briggsae	Hypothetical protein CBG16268 [Caenorhabditis briggsae]	0		F:GO:0016787		-
	-	0				-
Caenorhabditis elegans	hypothetical protein Y61A9LA.3 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	alpha-l- plasma	3	P:GO:0006004; F:GO:0004560; F:GO:0043169	-	EC:3.2.1.51	IPR000933; IPR013781; IPR016286; IPR017853; IPR018526
Caenorhabditis elegans	ankyrin repeat and mynd domain containing 2	0		F:GO:0046872; F:GO:0008270		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF211 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Brugia malayi	f-box domain containing protein	0				-

Caenorhabditis briggsae	clathrin-associated protein	7	P:GO:0016183; C:GO:0008021; P:GO:0007269; C:GO:0030122; F:GO:0005515; P:GO:0006886; P:GO:0033227	-		IPR001392; IPR008968; IPR015629; G3DSA:2.60.40.1170 (GENE3D), PTHR11998 (PANTHER)
Caenorhabditis elegans	cytochrome b5 domain containing 2	2	C:GO:0016021; F:GO:0016491	-		PTHR10281 (PANTHER), PTHR10281:SF4 (PANTHER)
Caenorhabditis elegans	cytochrome b5 domain containing 2	2	C:GO:0016021; F:GO:0016491	-		PTHR10281 (PANTHER), PTHR10281:SF4 (PANTHER)
	-	0				-
Caenorhabditis elegans	vacuolar protein sorting 13d	1	P:GO:0008104	-		-
Caenorhabditis elegans	briggsae cbr-eel-1 protein	4	C:GO:0005622; F:GO:0016881; F:GO:0005488; P:GO:0006464	-	EC:6.3.2.0	SignalP (SIGNALP)
	-	0				PTHR15245 (PANTHER), PTHR15245:SF2 (PANTHER)
Caenorhabditis elegans	diacylglycerol ki-se protein isoform partially confirmed by transcript evidence	0		P:GO:0007205; F:GO:0004143; P:GO:0023034		IPR002219; G3DSA:3.30.60.20 (GENE3D), PTHR11255 (PANTHER), PTHR11255:SF10 (PANTHER), SSF57889 (SUPERFAMILY)
Caenorhabditis elegans	malic enzyme -dp(+)- mitochondrial	8	F:GO:0046872; P:GO:0006090; F:GO:0051287; C:GO:0005759; F:GO:0016619; P:GO:0006108; P:GO:0055114; F:GO:0004473	-	EC:1.1.1.38; EC:1.1.1.40	IPR001891; IPR012301; G3DSA:3.40.50.10380 (GENE3D), PTHR23406 (PANTHER), PTHR23406:SF2 (PANTHER), SSF53223 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	protein phosphatase catalytic subunit	5	P:GO:0000082; F:GO:0004722; F:GO:0005515; P:GO:0006470; C:GO:0005829	-		IPR004843; IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF26 (PANTHER), SSF56300 (SUPERFAMILY)
Apis mellifera	yippee-like 1	1	C:GO:0005634	-		IPR004910; PTHR13847 (PANTHER)
	-	0				-
	-	0				-
Brugia malayi	haloacid dehaloge-se-like hydrolase domain containing 2	1	F:GO:0003824	-		G3DSA:3.40.50.1000 (GENE3D), PTHR19288 (PANTHER), PTHR19288:SF1 (PANTHER), SSF56784 (SUPERFAMILY)
Homo sapiens	peroxiredoxin 5	11	P:GO:0006954; C:GO:0005777; P:GO:0045454; C:GO:0044445; P:GO:0055114; F:GO:0004601; F:GO:0043027; F:GO:0051920; P:GO:0034614; P:GO:0043066; C:GO:0005739	-	EC:1.11.1.7; EC:1.11.1.15	IPR012335; IPR012336; IPR013740; PTHR10430 (PANTHER), PTHR10430:SF3 (PANTHER)

Caenorhabditis elegans	ww domain-containing oxidoreductase	10	P:GO:0006915; P:GO:0055114; P:GO:0030178; F:GO:0016491; P:GO:0032501; F:GO:0046983; F:GO:0050662; P:GO:0008202; P:GO:0032502; C:GO:0005794	-		IPR001202; G3DSA:2.20.70.10 (GENE3D), PTHR13436 (PANTHER), PTHR13436:SF2 (PANTHER)
Caenorhabditis briggsae	adrenoleukodystrophy related protein	9	P:GO:0055085; C:GO:0005779; P:GO:0007031; F:GO:0005325; F:GO:0042626; P:GO:0033540; F:GO:0042802; F:GO:0005524; P:GO:0015919	-	EC:3.6.3.47	IPR010509; PTHR11384 (PANTHER), PTHR11384:SF12 (PANTHER)
	-	0				-
Caenorhabditis briggsae	yrn9_caeel ame: full=uncharacterized protein	0				-
Drosophila grimshawi	zinc finger protein 14	3	F:GO:0008270; F:GO:0003676; C:GO:0005622	-		-
Brugia malayi	r- exonuclease 1 homolog	1	F:GO:0016787	-		IPR006055; IPR012337; IPR013520; G3DSA:3.30.420.10 (GENE3D), PTHR12801 (PANTHER), PTHR12801:SF19 (PANTHER)
	-	0				SignalP (SIGNALP)
Homo sapiens	keratin 7	10	P:GO:0006417; C:GO:0005730; P:GO:0051325; P:GO:0007010; P:GO:0006260; F:GO:0005515; C:GO:0045095; P:GO:0044419; F:GO:0005198; C:GO:0005737	-		IPR001664; IPR003054; IPR016044; IPR018039; G3DSA:1.20.5.170 (GENE3D)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	lysosomal acid phosphatase	0		F:GO:0016787; C:GO:0016021; C:GO:0016020; F:GO:0003993; P:GO:0008150; C:GO:0005575		IPR000560; G3DSA:3.40.50.1240 (GENE3D), PTHR11567 (PANTHER), PTHR11567:SF13 (PANTHER), SignalP (SIGNALP), SSF53254 (SUPERFAMILY)
Caenorhabditis elegans	likely c1-tetrahydrofolate synthase	5	P:GO:0043581; F:GO:0005524; P:GO:0009396; F:GO:0003824; C:GO:0009536	-		IPR000559; G3DSA:3.40.50.300 (GENE3D), PTHR10025 (PANTHER), PTHR10025:SF4 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein C25H3.11 [Caenorhabditis elegans]	0				-

Caenorhabditis briggsae	solute carrier family 22 (organic cation transporter) member isoform cra_a	11	P:GO:0055085; P:GO:0015893; F:GO:0015238; C:GO:0016021; F:GO:0031625; P:GO:0006811; F:GO:0015291; C:GO:0044444; C:GO:0016324; C:GO:0005635; F:GO:0015075	-		IPR016196; G3DSA:1.20.1250.20 (GENE3D), PTHR10074 (PANTHER), PTHR10074:SF56 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Xenopus (Silurana) tropicalis	macrophage mannose receptor 1-like	0		F:GO:0005488; F:GO:0005529		IPR001304; IPR013032; IPR016186; IPR016187; PTHR22739 (PANTHER)
Ciona intestinalis	u6 snr--associated sm-like protein lsm3	5	C:GO:0046540; C:GO:0005681; F:GO:0005515; P:GO:0000398; F:GO:0030629	-		IPR001163; IPR006649; IPR010920; G3DSA:2.30.30.100 (GENE3D), PTHR13110 (PANTHER)
Ciona intestinalis	u6 snr--associated sm-like protein lsm3	5	C:GO:0046540; C:GO:0005681; F:GO:0005515; P:GO:0000398; F:GO:0030629	-		IPR001163; IPR006649; IPR010920; G3DSA:2.30.30.100 (GENE3D), PTHR13110 (PANTHER)
Caenorhabditis briggsae	e3 ufm1-protein ligase 1	1	F:GO:0016874	-		IPR018611
Caenorhabditis briggsae	e3 ufm1-protein ligase 1	1	F:GO:0016874	-		IPR018611
Caenorhabditis elegans	uncoordi-ted family member (unc-89)	1	F:GO:0008092	-		IPR003599; IPR007110; IPR013098; IPR013783; PTHR19900 (PANTHER), PTHR19900:SF1 (PANTHER), SSF48726 (SUPERFAMILY)
Saccoglossus kowalevskii	cell division control protein 2 homolog 2	2	P:GO:0009987; F:GO:0004674	-	EC:2.7.11.0	-
	-	0				-
Caenorhabditis elegans	homogentisate -dioxyge-se	5	F:GO:0042802; P:GO:0006572; F:GO:0004411; P:GO:0055114; P:GO:0006559	-	EC:1.13.11.5	-
Caenorhabditis elegans	briggsae cbr-tol-1 protein	1	F:GO:0005515	-		IPR001611; G3DSA:3.80.10.10 (GENE3D), PTHR23154 (PANTHER), PS51450 (PROFILE), SignalP (SIGNALP), SSF52058 (SUPERFAMILY)
Caenorhabditis briggsae	uridine 5 -monophosphate synthase	6	C:GO:0005737; F:GO:0004590; P:GO:0006222; F:GO:0005515; F:GO:0004588; C:GO:0005634	-	EC:4.1.1.23; EC:2.4.2.10	IPR001754; IPR011060; IPR013785
	-	0				SignalP (SIGNALP)

Caenorhabditis briggsae	tetratricopeptide repeat protein 35	6	F:GO:0005515; P:GO:0040017; P:GO:0040010; P:GO:0000003; P:GO:0006898; C:GO:0005783	-		PTHR12760 (PANTHER)
Brugia malayi	rab3 gtpase-activating protein catalytic subunit	1	F:GO:0030695	-		-
Caenorhabditis briggsae	hypothetical tyrosi-se-like protein in chromosome	1	F:GO:0005515	-		IPR002227; IPR003582; IPR008922; PTHR11474 (PANTHER), PTHR11474:SF1 (PANTHER)
Caenorhabditis elegans	transcription initiation factor tfiid subunit 10	4	F:GO:0003676; F:GO:0003702; P:GO:0006352; C:GO:0005634	-		IPR003923
Bos taurus	heat shock protein hsp 90-beta	13	C:GO:0005739; P:GO:0006457; F:GO:0030235; P:GO:0060334; P:GO:0001890; C:GO:0042470; F:GO:0005524; P:GO:0032435; F:GO:0030911; P:GO:0060338; F:GO:0051082; P:GO:0006986; P:GO:0045429	-		SignalP (SIGNALP)
	-	0				PR01217 (PRINTS)
Homo sapiens	clusterin	20	P:GO:0009615; P:GO:0051788; P:GO:0048812; C:GO:0034366; P:GO:0045597; P:GO:0032463; P:GO:0043691; P:GO:0031018; C:GO:0016235; P:GO:0006916; P:GO:0008284; P:GO:0006629; P:GO:0006958; F:GO:0051787; C:GO:0048471; P:GO:0001836; P:GO:0045087; P:GO:0006979; C:GO:0031012; C:GO:0005739	-		IPR000753; IPR016014; IPR016015; IPR016016; PTHR10970 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	protein mon2-like protein	0		F:GO:0005488; P:GO:0006810; P:GO:0015031		-
Caenorhabditis elegans	uncharacterized protein kiaa0892	3	P:GO:0007059; C:GO:0044428; P:GO:0007067	-		PTHR21394 (PANTHER)
Caenorhabditis elegans	dhx35_caeel ame: full=probable atp-dependent r- helicase dhx35 homolog	2	F:GO:0004386; F:GO:0000166	-		-

Caenorhabditis elegans	macoilin	1	C:GO:0016021	-		IPR019130; PTHR13289 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	zinc finger protein c3h homolog	6	F:GO:0008270; P:GO:0010468; C:GO:0044424; P:GO:0006402; P:GO:0051252; F:GO:0003723	-		IPR000571; G3DSA:4.10.1000.10 (GENE3D), PTHR12547 (PANTHER), SSF90229 (SUPERFAMILY)
Caenorhabditis elegans	zinc finger protein c3h homolog	6	F:GO:0008270; P:GO:0010468; C:GO:0044424; P:GO:0006402; P:GO:0051252; F:GO:0003723	-		IPR000571; G3DSA:4.10.1000.10 (GENE3D), PTHR12547 (PANTHER), SSF90229 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0005515		-
	-	0				-
Caenorhabditis elegans	3 saliva family protein	2	C:GO:0016021; P:GO:0019915	-		IPR004316; IPR018179
Caenorhabditis elegans	pap 25a associated domain containing protein	9	F:GO:0016779; P:GO:0040010; F:GO:0043221; P:GO:0040035; P:GO:0007062; P:GO:0007281; P:GO:0042493; P:GO:0009792; C:GO:0005634	-	EC:2.7.7.0	IPR002934; G3DSA:3.30.460.10 (GENE3D), PTHR23092 (PANTHER), PTHR23092:SF4 (PANTHER), SSF81301 (SUPERFAMILY), SSF81631 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-vps-41 protein	9	F:GO:0005488; P:GO:0007034; P:GO:0040007; P:GO:0006624; P:GO:0002119; P:GO:0033036; P:GO:0009792; C:GO:0005773; P:GO:0043066	-		IPR001680; IPR011046; IPR015943; PTHR12616 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	fibronectin type-iii domain-containing protein 3a	0		C:GO:0016021; C:GO:0016020; F:GO:0016787; F:GO:0003674; P:GO:0008152; F:GO:0004896; F:GO:0016162; P:GO:0008150; F:GO:0016798		IPR003961; IPR008957; IPR013783; PTHR19900 (PANTHER), PTHR19900:SF3 (PANTHER)
	-	0				-
Caenorhabditis briggsae	udp-n-acetylglucosamine transporter	10	F:GO:0005461; F:GO:0005464; F:GO:0005463; F:GO:0005456; P:GO:0015757; P:GO:0015785; P:GO:0015789; C:GO:0016020; P:GO:0015782; F:GO:0005459	-		IPR007271; PTHR10231:SF9 (PANTHER), SignalP (SIGNALP)

Caenorhabditis elegans	cg4658- isoform a	1	P:GO:0008340	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	chromosome 1 open reading frame 123	1	F:GO:0000166	-		IPR008584; SignalP (SIGNALP), SSF141678 (SUPERFAMILY)
Caenorhabditis elegans	phosphoenolpyruvate carboxyki-se	7	P:GO:0006107; F:GO:0005488; C:GO:0005625; C:GO:0005739; P:GO:0051384; P:GO:0006094; F:GO:0004613	-	EC:4.1.1.32	IPR008209; IPR008210
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG17891 [Caenorhabditis briggsae]	0				-
	-	0				-
uncultured organism	hypothetical protein [uncultured organism]	0				-
Loa loa	folylpolyglutamate synthase	7	F:GO:0004326; P:GO:0006139; P:GO:0006730; F:GO:0005524; P:GO:0009396; C:GO:0005829; C:GO:0005739	-	EC:6.3.2.17	IPR001645; IPR013221; IPR018109
Caenorhabditis briggsae	schlafen-like protein 1-like	0		F:GO:0003676; F:GO:0005524; F:GO:0005488; F:GO:0000166; F:GO:0008270		IPR007421; PTHR10967 (PANTHER), PTHR10967:SF41 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	class member 2	7	C:GO:0000139; F:GO:0004559; F:GO:0030246; P:GO:0006013; F:GO:0004572; C:GO:0016021; F:GO:0008270	-	EC:3.2.1.24; EC:3.2.1.114	IPR000602; IPR011330; PTHR11607 (PANTHER), PTHR11607:SF4 (PANTHER)
Brugia malayi	inositol -trisphosphate receptor	4	F:GO:0004872; F:GO:0005262; P:GO:0006811; C:GO:0016020	-		IPR015925; PTHR13715:SF2 (PANTHER), SignalP (SIGNALP)
	-	0				-

Caenorhabditis briggsae	adenylosucci-te lyase	15	C:GO:0005829; F:GO:0004018; P:GO:0040010; P:GO:0018991; P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0051262; P:GO:0006167; F:GO:0070626; P:GO:0040011; P:GO:0006997; P:GO:0006898; P:GO:0002009; P:GO:0009792	-	EC:4.3.2.2	IPR008948; G3DSA:1.10.275.10 (GENE3D), PTHR11444 (PANTHER), PTHR11444:SF2 (PANTHER)
	-	0				-
Caenorhabditis elegans	hypothetical protein R144.11 [Caenorhabditis elegans]	6	P:GO:0040035; P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040018; P:GO:0002009	-		SignalP (SIGNALP)
Caenorhabditis briggsae	protein methyltransferase	0		F:GO:0008168; C:GO:0005737; F:GO:0016740		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	4	P:GO:0048599; F:GO:0003676; F:GO:0008270; F:GO:0005515	-		IPR000571; G3DSA:4.10.1000.10 (GENE3D), PTHR12547 (PANTHER), SSF90229 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-mdt-15 protein	14	P:GO:0030730; P:GO:0040010; P:GO:0008340; P:GO:0000003; P:GO:0002119; P:GO:0019217; P:GO:0040011; P:GO:0006898; F:GO:0035257; F:GO:0003713; P:GO:0045893; P:GO:0009792; P:GO:0040014; C:GO:0005634	-		-
Brugia malayi	briggsae cbr-mdt-15 protein	13	P:GO:0030730; P:GO:0040010; P:GO:0008340; P:GO:0000003; P:GO:0002119; P:GO:0019217; P:GO:0040011; P:GO:0006898; F:GO:0035257; F:GO:0003713; P:GO:0045893; P:GO:0009792; P:GO:0040014	-		IPR019087; PTHR23189 (PANTHER), PTHR23189:SF1 (PANTHER)

Caenorhabditis elegans	giy-yig catalytic domain containing protein	3	P:GO:0009792; P:GO:0002119; P:GO:0040007	-		SignalP (SIGNALP)
Trichoplax adhaerens	mgc81975 protein	0				IPR000717; PTHR15350 (PANTHER), PTHR15350:SF2 (PANTHER)
Caenorhabditis briggsae	chromosome 20 open reading frame 7	4	C:GO:0031314; P:GO:0008152; F:GO:0008168; P:GO:0032981	-	EC:2.1.1.0	IPR013216; G3DSA:3.40.50.150 (GENE3D), PTHR13090 (PANTHER), SignalP (SIGNALP), SSF53335 (SUPERFAMILY)
Caenorhabditis briggsae	chromosome 20 open reading frame 7	4	C:GO:0031314; P:GO:0008152; F:GO:0008168; P:GO:0032981	-	EC:2.1.1.0	IPR013216; G3DSA:3.40.50.150 (GENE3D), PTHR13090 (PANTHER), SignalP (SIGNALP), SSF53335 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-eat-18 protein	0				-
Caenorhabditis briggsae	briggsae cbr-eat-18 protein	0				IPR002172; PTHR10127 (PANTHER), PTHR10127:SF33 (PANTHER)
Caenorhabditis elegans	abnormal cell lineage family member (lin-10)	1	F:GO:0005515	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR12345 (PANTHER), PTHR12345:SF2 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-unc-79 protein	0		F:GO:0005488; F:GO:0008270		PTHR21696 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Haemonchus contortus	heat shock protein family member (hsp-)	1	P:GO:0009408	-		IPR001436; IPR002068; IPR008978; G3DSA:2.60.40.790 (GENE3D), PTHR11527 (PANTHER), PTHR11527:SF28 (PANTHER)
Caenorhabditis briggsae	melanin-concentrating hormone receptor 2	0		F:GO:0004872; F:GO:0004930; F:GO:0004871; C:GO:0016021; P:GO:0007165; F:GO:0005000; P:GO:0007186		-
Caenorhabditis elegans	protein trs85 homolog	5	P:GO:0045927; P:GO:0032501; P:GO:0009653; P:GO:0000003; P:GO:0040011	-		PTHR12975 (PANTHER)
	-	0				-
Caenorhabditis briggsae	cytoskeletal structural protein	0		P:GO:0007165		PTHR21437 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	scavenger receptor class member 2	1	C:GO:0016020	-		IPR002159; PTHR11923:SF8 (PANTHER)
	-	0				-
Nematostella vectensis	centromeric protein e	0		F:GO:0005524; F:GO:0000166; F:GO:0003777; F:GO:0003774; P:GO:0007018; C:GO:0005874		IPR001752; IPR019821; PTHR16012 (PANTHER), SSF52540 (SUPERFAMILY)

Brugia malayi	cbp p300 homolog family member (cbp-1)	0		P:GO:0000003; P:GO:0002119; C:GO:0005634; P:GO:0040026; P:GO:0006355; P:GO:0009792; P:GO:0009790; P:GO:0040039; P:GO:0040035; P:GO:0045944; C:GO:0005737; P:GO:0045449; F:GO:0003712; F:GO:0008270; P:GO:0018996; F:GO:0005515; F:GO:0004402; P:GO:0007283; P:GO:0040010		-
Caenorhabditis briggsae	aspartyl-tr- synthetase 2	4	C:GO:0005739; F:GO:0000166; F:GO:0004812; P:GO:0006418	-		IPR002312; IPR004115; IPR004364; IPR004365; IPR006195; IPR012340; IPR016027; IPR018150; IPR018153; G3DSA:3.30.930.10 (GENE3D), SignalP (SIGNALP), SSF55681 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	60s ribosomal protein l7 l12	5	P:GO:0002119; C:GO:0005622; F:GO:0005515; P:GO:0040010; P:GO:0008340	-		IPR008932; IPR013823; IPR014719; IPR015607; PTHR11809 (PANTHER)
	-	0				-
Caenorhabditis briggsae	serine threonine-protein ki-se 38 (ndr2 protein ki-se)	8	P:GO:0007243; F:GO:0046872; F:GO:0005524; P:GO:0050773; F:GO:0004697; C:GO:0005737; C:GO:0005634; P:GO:0006468	-	EC:2.7.11.13	IPR000719; IPR011009; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR22985 (PANTHER), PTHR22985:SF33 (PANTHER)
Caenorhabditis briggsae	intermediate in toll sig-l transduction	2	P:GO:0006952; F:GO:0005515	-		IPR010418
Caenorhabditis briggsae	intermediate in toll sig-l transduction	2	P:GO:0006952; F:GO:0005515	-		IPR010418
Ixodes scapularis	secreted mucin	0		F:GO:0016787		-
	-	0				-
Arabidopsis thaliana	r- recognition motif -containing protein	0		F:GO:0003676; F:GO:0003723; F:GO:0000166; P:GO:0008150; C:GO:0005575		-
Caenorhabditis elegans	pbx knotted 1 homeobox 1	3	P:GO:0030154; P:GO:0048513; C:GO:0044424	-		-

Caenorhabditis elegans	expulsion defective family member (aex-3)	6	P:GO:0007618; P:GO:0007268; P:GO:0018991; C:GO:0005623; P:GO:0030421; F:GO:0017112	-		PTHR13008 (PANTHER)
Loa loa	replication factor c (activator 1) 37kda	9	F:GO:0017111; P:GO:0006297; F:GO:0003677; F:GO:0005524; P:GO:0006271; F:GO:0005515; C:GO:0005654; P:GO:0048015; C:GO:0005663	-	EC:3.6.1.15	-
Caenorhabditis elegans	hypothetical protein T07D4.1 [Caenorhabditis elegans]	0		C:GO:0016021; P:GO:0007186		G3DSA:1.20.1070.10 (GENE3D), PTHR19264 (PANTHER), PTHR19264:SF286 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	transmembrane protein 144	3	F:GO:0015144; C:GO:0016021; P:GO:0002119	-		IPR012435; SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	briggsae cbr-gon-1 protein	1	F:GO:0008233	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	dead deah box helicase family protein	7	P:GO:0040035; P:GO:0002119; F:GO:0005488; F:GO:0004386; P:GO:0040002; P:GO:0040010; P:GO:0006898	-		-
Caenorhabditis elegans	aminoacylase 1	4	C:GO:0005625; F:GO:0005488; P:GO:0030163; F:GO:0016787	-		IPR002933; IPR010159; IPR011650; G3DSA:3.30.70.360 (GENE3D), G3DSA:3.40.630.10 (GENE3D), PTHR11014 (PANTHER), PTHR11014:SF8 (PANTHER), SSF53187 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	sam domain- and hd domain-containing protein 1	3	P:GO:0006952; P:GO:0000003; P:GO:0006955	-		PTHR11373 (PANTHER), PTHR11373:SF9 (PANTHER), SSF109604 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-mog-5 protein	4	F:GO:0003676; F:GO:0004386; F:GO:0000166; F:GO:0005515	-		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	7	P:GO:0009792; P:GO:0002119; F:GO:0003735; C:GO:0015935; P:GO:0000003; P:GO:0040007; P:GO:0006412	-	EC:3.6.5.3	SignalP (SIGNALP)
	-	0				-

Loa loa	zinc finger protein	13	P:GO:0040010; F:GO:0003723; F:GO:0008270; C:GO:0071011; P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0040011; P:GO:0000398; P:GO:0006898; P:GO:0002121; P:GO:0002009; P:GO:0009792	-		IPR004087; IPR004088; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR11208 (PANTHER), PTHR11208:SF6 (PANTHER), SSF54791 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	sig-l peptidase complex subunit 3	12	F:GO:0008233; C:GO:0005787; P:GO:0040010; P:GO:0006465; C:GO:0016021; P:GO:0000003; P:GO:0018996; C:GO:0005792; P:GO:0002119; P:GO:0040011; P:GO:0006898; P:GO:0009792	-		IPR007653; SignalP (SIGNALP)
Caenorhabditis elegans	sig-l peptidase complex subunit 3	12	F:GO:0008233; C:GO:0005787; P:GO:0040010; P:GO:0006465; C:GO:0016021; P:GO:0000003; P:GO:0018996; C:GO:0005792; P:GO:0002119; P:GO:0040011; P:GO:0006898; P:GO:0009792	-		-
Caenorhabditis briggsae	pab-dependent poly -specific ribonuclease subunit 2	2	F:GO:0016788; C:GO:0005622	-		IPR012337; IPR013520; G3DSA:3.30.420.10 (GENE3D), PTHR15728 (PANTHER)
Caenorhabditis briggsae	pab-dependent poly -specific ribonuclease subunit 2	2	F:GO:0016788; C:GO:0005622	-		IPR012337; IPR013520; G3DSA:3.30.420.10 (GENE3D), PTHR15728 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Branchiostoma floridae	tetraspan net-6	1	C:GO:0016020	-		-
Danio rerio	briggsae cbr-spe-26 protein	5	P:GO:0009987; P:GO:0048856; P:GO:0003006; P:GO:0008152; P:GO:0007275	-		IPR006652; IPR013089; IPR015915; PR00501 (PRINTS), PTHR23230:SF184 (PANTHER), SSF117281 (SUPERFAMILY)
	-	0				-
Loa loa	briggsae cbr-inx-1 protein	2	C:GO:0005921; C:GO:0016021	-		-
	-	0				-

Caenorhabditis briggsae	alkylglycerone phosphate synthase	7	P:GO:0009792; P:GO:0002119; F:GO:0008609; C:GO:0005777; P:GO:0042221; P:GO:0040007; C:GO:0005739	-	EC:2.5.1.26	-
Loa loa	hypothetical kda protein in chromosome	0				-
	-	0				-
Caenorhabditis elegans	d--directed r- polymerase i subunit rpa1	7	F:GO:0046872; F:GO:0003899; C:GO:0005654; F:GO:0003677; C:GO:0005736; F:GO:0005515; P:GO:0006350	-	EC:2.7.7.6	IPR007083; IPR015699; PTHR19376 (PANTHER), SSF64484 (SUPERFAMILY)
	-	0				-
Loa loa	ribosome biogenesis protein	6	C:GO:0005730; P:GO:0009792; F:GO:0005515; P:GO:0040010; P:GO:0040011; P:GO:0042255	-		IPR007034; PTHR12858 (PANTHER), PTHR12858:SF1 (PANTHER)
	-	0				-
Oryctolagus cuniculus	catenin beta-1	139	P:GO:0034097; F:GO:0019901; P:GO:0010552; P:GO:0043065; F:GO:0019903; P:GO:0030997; F:GO:0042153; P:GO:0010909; P:GO:0030521; P:GO:0071681; N:GO:0061154; P:GO:0000578; C:GO:0005915; P:GO:0048489; P:GO:0035117; P:GO:0007016; C:GO:0030057; C:GO:0030877; F:GO:0003704; P:GO:0001711; F:GO:0032403; P:GO:0060769; P:GO:0003337; P:GO:0048145; P:GO:0007403; P:GO:0043123; P:GO:0045765;	-		IPR000225; PTHR23315 (PANTHER), PTHR23315:SF13 (PANTHER)

Caenorhabditis elegans	isoform f	9	P:GO:0009790; P:GO:0006915; F:GO:0003677; P:GO:0007525; P:GO:0045924; P:GO:0001751; P:GO:0007422; C:GO:0005634; F:GO:0008270	-		SignalP (SIGNALP)
Caenorhabditis elegans	isoform f	9	P:GO:0009790; P:GO:0006915; F:GO:0003677; P:GO:0007525; P:GO:0045924; P:GO:0001751; P:GO:0007422; C:GO:0005634; F:GO:0008270	-		IPR000571; PTHR12675 (PANTHER)
Caenorhabditis elegans	muscleblind-like protein a	3	F:GO:0046872; F:GO:0003676; C:GO:0005634	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	eps (human endocytosis) related family member (eps-8)	1	F:GO:0005515	-		PTHR12287 (PANTHER), PTHR12287:SF6 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				PTHR21839 (PANTHER)
Caenorhabditis elegans	viral a-type inclusion protein repeat containing protein	3	P:GO:0007126; P:GO:0006898; P:GO:0040039	-		-
Caenorhabditis briggsae	viral a-type inclusion protein repeat containing protein	3	P:GO:0007126; P:GO:0006898; P:GO:0040039	-		-
Caenorhabditis elegans	briggsae cbr-rgs-6 protein	1	F:GO:0004871	-		-
	-	0				-
Brugia malayi	protein ki-se domain containing protein	0		F:GO:0016301; F:GO:0004672; F:GO:0005524; F:GO:0000166; P:GO:0006468; F:GO:0004674		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-gfi-2 protein	8	P:GO:0040035; P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040018; P:GO:0040010; P:GO:0008340; P:GO:0006898	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	hypothetical protein F41G3.1 [Caenorhabditis elegans]	0				-

Homo sapiens	lactate dehydroge-se a	8	P:GO:0031668; C:GO:0019861; F:GO:0005515; F:GO:0004459; P:GO:0055114; P:GO:0006096; C:GO:0005829; C:GO:0005739	-		EC:1.1.1.27	IPR015955; IPR018177; IPR022383; PTHR11540 (PANTHER), PTHR11540:SF3 (PANTHER)
Ailuropoda melanoleuca	low quality protein: tubulin alpha-1c chain-like	7	P:GO:0007018; F:GO:0005525; F:GO:0005515; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-		EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000217; IPR002452; IPR003008; PTHR11588:SF11 (PANTHER)
Caenorhabditis elegans	sig-l peptide peptidase	16	P:GO:0040010; F:GO:0005488; P:GO:0018991; P:GO:0044260; P:GO:0090304; P:GO:0018996; P:GO:0010171; P:GO:0002119; P:GO:0040011; F:GO:0004190; C:GO:0044428; P:GO:0010467; P:GO:0002009; P:GO:0009792; P:GO:0040015; P:GO:0040018	-		EC:3.4.23.0	-
Caenorhabditis elegans	sig-l peptide peptidase	19	C:GO:0030532; F:GO:0042500; P:GO:0040010; P:GO:0018991; C:GO:0016021; C:GO:0000790; P:GO:0008380; P:GO:0018996; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0002009; P:GO:0007424; P:GO:0009792; P:GO:0033619; P:GO:0040015; P:GO:0040018; C:GO:0005783	-			-
	-	0					-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0					-

Loa loa	d- polymerase epsilon	12	F:GO:0008270; F:GO:0003887; P:GO:0006260; P:GO:0040035; F:GO:0003677; F:GO:0000166; P:GO:0040011; P:GO:0006997; F:GO:0004527; P:GO:0002009; P:GO:0009792; C:GO:0005634	-	EC:2.7.7.7	IPR006134; PTHR10670 (PANTHER), SSF56672 (SUPERFAMILY)
Caenorhabditis elegans	matrix metalloprotei-se	0		P:GO:0030574; F:GO:0016787; P:GO:0030154; P:GO:0051591; F:GO:0003674; F:GO:0046872; F:GO:0008237; C:GO:0016020; P:GO:0001542; F:GO:0008233; C:GO:0031012; F:GO:0005509; F:GO:0004222; P:GO:0008152; P:GO:0007275; P:GO:0001525; P:GO:0006508; P:GO:0001554; C:GO:0031225; F:GO:0008270; C:GO:0005578; C:GO:0005576; C:GO:0005886; P:GO:0009725; C:GO:0005575		IPR001818; G3DSA:3.40.390.10 (GENE3D), PTHR10201 (PANTHER), PTHR10201:SF5 (PANTHER), SSF55486 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	protein ki-se domain containing protein	8	C:GO:0005929; C:GO:0030425; F:GO:0016301; F:GO:0005515; P:GO:0034606; C:GO:0030424; P:GO:0034608; C:GO:0043025	-		IPR000719; IPR001245; IPR008266; IPR011009; IPR020685; IPR020764; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
Caenorhabditis briggsae	mitochondrial -dh:ubiquinone oxidoreductase	5	P:GO:0009792; P:GO:0002119; P:GO:0040010; P:GO:0000003; P:GO:0040019	-		IPR009346
Caenorhabditis elegans	bromodomain containing protein	1	P:GO:0040011	-		IPR013136

Caenorhabditis elegans	d--binding protein smubp-2	0		F:GO:0003677; F:GO:0016787; F:GO:0000166; F:GO:0017111; F:GO:0003674; F:GO:0005524; C:GO:0005575; P:GO:0008150; C:GO:0009536		IPR003593; IPR007807; IPR014001; G3DSA:3.40.50.300 (GENE3D), PTHR10887 (PANTHER), PTHR10887:SF23 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	protein-tyrosine sulfotransferase a	2	C:GO:0005794; F:GO:0008476	-	EC:2.8.2.20	G3DSA:3.40.50.300 (GENE3D), PTHR12788 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
	-	0				-
Loa loa	srrm2 protein	4	P:GO:0040035; P:GO:0040027; P:GO:0008340; P:GO:0040007	-		IPR013170
Caenorhabditis briggsae	homeobox domain containing protein	19	F:GO:0008270; P:GO:0040010; P:GO:0006898; P:GO:0006355; P:GO:0040011; P:GO:0007050; C:GO:0005667; P:GO:0007420; P:GO:0002009; P:GO:0045664; P:GO:0002119; F:GO:0003700; P:GO:0045662; P:GO:0045663; F:GO:0010843; F:GO:0019899; P:GO:0040035; F:GO:0016564; C:GO:0005739	-		PTHR18973 (PANTHER), PTHR18973:SF19 (PANTHER)
Caenorhabditis elegans	mgc83087 protein	0		F:GO:0008168; F:GO:0016740; P:GO:0008152; C:GO:0016021; F:GO:0003824		-
Loa loa	translation initiation factor eif-2b subunit epsilon	5	P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0040018; P:GO:0040010	-		IPR003307; IPR016021; IPR016024; PTHR23001 (PANTHER), PTHR23001:SF1 (PANTHER)
	-	0				-
Brugia malayi	hypothetical protein Bm1_42390 [Brugia malayi]	0		F:GO:0005515		-

Caenorhabditis briggsae	clathrin heavy chain	14	C:GO:0030132; P:GO:0035002; F:GO:0005198; F:GO:0005515; P:GO:0035159; P:GO:0030198; P:GO:0007269; P:GO:0033227; P:GO:0016183; C:GO:0030130; P:GO:0006886; P:GO:0007291; C:GO:0030129; C:GO:0005811	-		IPR000547; IPR011990; IPR016024; PTHR10292 (PANTHER), PTHR10292:SF1 (PANTHER), PF00637 (PFAM)
Sus scrofa	cytoplasmic 1	16	C:GO:0005829; C:GO:0030863; C:GO:0030424; C:GO:0005625; F:GO:0019894; F:GO:0042802; C:GO:0035267; F:GO:0005524; P:GO:0007409; F:GO:0050998; P:GO:0006928; F:GO:0019901; F:GO:0005200; C:GO:0030529; C:GO:0070688; P:GO:0051592	-		IPR004000; IPR004001; IPR020902; G3DSA:2.30.36.70 (GENE3D), G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), SSF53067 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	stan	6	F:GO:0004930; P:GO:0007156; C:GO:0005886; F:GO:0005509; C:GO:0016021; P:GO:0007218	-		-
Caenorhabditis briggsae	26s non-atpase regulatory subunit	6	F:GO:0005515; P:GO:0006511; P:GO:0000003; C:GO:0000502; C:GO:0005634; P:GO:0009651	-		PTHR10410 (PANTHER), PTHR10410:SF5 (PANTHER)

Pan troglodytes	annexin a2	23	P:GO:0001501; P:GO:0001525; F:GO:0005546; C:GO:0005604; P:GO:0007589; F:GO:0017137; C:GO:0005624; C:GO:0042470; F:GO:0005509; P:GO:0031340; F:GO:0008092; C:GO:0042383; P:GO:0042730; C:GO:0043234; P:GO:0030199; C:GO:0005769; F:GO:0005544; P:GO:0050790; C:GO:0001725; C:GO:0030054; C:GO:0048471; F:GO:0004859; C:GO:0005625	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG15266 [Caenorhabditis briggsae]	0		F:GO:0008289		-
	-	0				-
Brugia malayi	hypothetical protein Bm1_50385 [Brugia malayi]	0				-
Brugia malayi	ubiquitously transcribed tetratricopeptide x chromosome	5	P:GO:0009792; P:GO:0040018; P:GO:0040010; P:GO:0040035; P:GO:0040011	-		IPR003347; IPR013129; PTHR14017 (PANTHER), PTHR14017:SF5 (PANTHER), SSF51197 (SUPERFAMILY)
Loa loa	degenerin unc-8	3	C:GO:0016021; F:GO:0005272; P:GO:0006814	-		IPR001873; G3DSA:1.10.287.770 (GENE3D), PTHR11690:SF17 (PANTHER)
Caenorhabditis briggsae	bub1 budding uninhibited by benzimidazoles 1 homolog	14	P:GO:0000278; F:GO:0016301; P:GO:0071173; F:GO:0005515; P:GO:0033043; P:GO:0051983; P:GO:0040011; C:GO:0000776; P:GO:0009792; P:GO:0002009; P:GO:0002119; P:GO:0040035; C:GO:0000779; P:GO:0000910	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-

Brugia malayi	cpb-1	7	F:GO:0008187; C:GO:0005737; P:GO:0007275; P:GO:0030154; F:GO:0000166; P:GO:0007283; F:GO:0005515	-		IPR000504; IPR012677; PTHR12566 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	hypothetical protein Y54E10A.11 [Caenorhabditis elegans]	0		F:GO:0008270		-
Caenorhabditis elegans	hypothetical protein Y54E10A.11 [Caenorhabditis elegans]	0		F:GO:0008270		-
Caenorhabditis elegans	hypothetical protein Y54E10A.11 [Caenorhabditis elegans]	0		F:GO:0008270		-
Caenorhabditis elegans	chromosome 6 open reading frame isoform cra_c	1	F:GO:0005515	-		-
Anopheles gambiae str. PEST	histone-lysine n-methyltransferase	8	P:GO:0016568; P:GO:0051038; F:GO:0008270; F:GO:0018024; F:GO:0003677; P:GO:0007275; P:GO:0048477; C:GO:0005634	-	EC:2.1.1.43	IPR000167; IPR001214; G3DSA:2.170.270.10 (GENE3D), PTHR22884 (PANTHER), PTHR22884:SF24 (PANTHER), SSF82199 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	endonuclease mitochondrial	4	F:GO:0016787; F:GO:0003676; F:GO:0005515; F:GO:0046872	-		IPR001604; IPR018524; IPR020821; PTHR13966 (PANTHER), SSF54060 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-nsy-1 protein	4	P:GO:0006468; F:GO:0005515; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR001660
Brugia malayi	c2 domain containing protein	6	C:GO:0016020; C:GO:0008021; F:GO:0005515; P:GO:0006810; F:GO:0005215; P:GO:0040011	-		-
	-	0				-
Caenorhabditis elegans	ef-hand 2	9	C:GO:0005829; P:GO:0006289; P:GO:0032465; P:GO:0007283; C:GO:0005814; C:GO:0032391; P:GO:0007099; F:GO:0031683; C:GO:0005932	-		IPR011992; IPR018249; PTHR10891 (PANTHER), PTHR10891:SF41 (PANTHER), SSF47473 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; P:GO:0007186		-
Caenorhabditis briggsae	atp-dependent d- helicase pif1	2	F:GO:0005488; F:GO:0017111	-	EC:3.6.1.15	IPR010285; G3DSA:3.40.50.300 (GENE3D), PTHR23274 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	chloride channel protein 2	3	C:GO:0005886; P:GO:0006810; F:GO:0005216	-		-
	-	0				-
	-	0				-

Caenorhabditis briggsae	Hypothetical protein CBG18289 [Caenorhabditis briggsae]	0		F:GO:0004672; F:GO:0005524; F:GO:0000166; P:GO:0006468		-
	-	0				-
	-	0				-
Loa loa	r--binding protein 16	6	P:GO:0009792; F:GO:0003676; P:GO:0010467; C:GO:0016363; P:GO:0016070; F:GO:0043175	-		IPR006569; IPR006903; IPR008942; PTHR14124 (PANTHER)
Caenorhabditis briggsae	ki-se-like protein splice variant 2	1	F:GO:0005515	-		IPR000357; IPR011989; IPR016024; IPR021133; PTHR12984 (PANTHER), PTHR12984:SF3 (PANTHER)
Caenorhabditis briggsae	ki-se-like protein splice variant 2	1	F:GO:0005515	-		IPR000357; IPR011989; IPR016024; IPR021133; PTHR12984 (PANTHER), PTHR12984:SF3 (PANTHER)
Caenorhabditis briggsae	protein rft1 homolog	5	P:GO:0040015; P:GO:0040017; P:GO:0006810; P:GO:0040010; C:GO:0016020	-		IPR007594
Loa loa	patatin-like phospholipase family protein	2	F:GO:0047499; P:GO:0016042	-		IPR002641; IPR016035; G3DSA:3.40.1090.10 (GENE3D), PTHR18958 (PANTHER), PTHR18958:SF94 (PANTHER)
	-	0				SignalP (SIGNALP)
	glutathione s-transferase pi	10	C:GO:0005737; P:GO:0007417; F:GO:0004364; P:GO:0006805; F:GO:0005515; P:GO:0006749; F:GO:0008144; P:GO:0006916; C:GO:0005634; F:GO:0043295	-	EC:2.5.1.18	IPR004045; IPR012335; IPR012336; PTHR11571 (PANTHER), PTHR11571:SF2 (PANTHER)
Caenorhabditis briggsae	acetyl- hydrolase transferase family protein	6	F:GO:0019239; C:GO:0005811; P:GO:0009168; P:GO:0006084; F:GO:0016787; F:GO:0016740	-		IPR003702; G3DSA:3.40.1080.10 (GENE3D), PTHR21432:SF11 (PANTHER), SSF100950 (SUPERFAMILY)
Brugia malayi	mgc80099 protein	1	P:GO:0009792	-		-
Oesophagostomum dentatum	serine threonine protein phosphatase pp1 isozyme 1	2	P:GO:0000003; F:GO:0004721	-	EC:3.1.3.16	IPR004843; IPR006186; G3DSA:3.60.21.10 (GENE3D), SSF56300 (SUPERFAMILY)
Caenorhabditis elegans	phospholipid scramblase 1	2	F:GO:0005515; P:GO:0006955	-		IPR005552; PTHR23248:SF5 (PANTHER)
	-	0				-

Ailuropoda melanoleuca	guanine nucleotide binding protein (g protein) beta polypeptide 1	13	P:GO:0007603; P:GO:0007265; F:GO:0004871; P:GO:0007213; C:GO:0001750; P:GO:0050909; P:GO:0007200; P:GO:0007204; C:GO:0005834; P:GO:0009755; F:GO:0003924; F:GO:0031702; P:GO:0008283	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR19850 (PANTHER)
	-	0				-
Oesophagostomum dentatum	serine threonine phosphatase	2	P:GO:0000003; F:GO:0004721	-	EC:3.1.3.16	SignalP (SIGNALP)
Caenorhabditis elegans	multidrug resistance protein family member (mrp-5)	8	P:GO:0002119; F:GO:0042626; P:GO:0040002; P:GO:0040017; P:GO:0055085; P:GO:0040010; F:GO:0005524; C:GO:0016021	-		IPR017940; PTHR19242 (PANTHER), PTHR19242:SF14 (PANTHER), SignalP (SIGNALP)
Brugia malayi	protein ki-se domain containing protein	4	F:GO:0004672; P:GO:0040010; P:GO:0019915; F:GO:0000166	-		-
Caenorhabditis briggsae	briggsae cbr-maoc-1 protein	4	P:GO:0019915; P:GO:0006952; P:GO:0008340; F:GO:0042802	-		G3DSA:3.10.129.10 (GENE3D)
Caenorhabditis elegans	vav 2 guanine nucleotide exchange factor	5	C:GO:0005829; F:GO:0005085; F:GO:0005515; P:GO:0007165; P:GO:0008624	-		-
Caenorhabditis elegans	briggsae cbr-taf-2 protein	0		F:GO:0008237; F:GO:0008270		-
Loa loa	ring finger protein 145	2	F:GO:0046872; C:GO:0005622	-		-
	-	0				-
Brugia malayi	elegans protein confirmed by transcript evidence	0		C:GO:0016020		SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	myosin heavy chain	34	P:GO:0046664; P:GO:0045200; C:GO:0016461; P:GO:0035159; P:GO:0031036; P:GO:0035072; P:GO:0007443; P:GO:0007395; P:GO:0045214; P:GO:0035017; P:GO:0007297; C:GO:0031672; P:GO:0046663; F:GO:0003779; F:GO:0000146; P:GO:0001736; F:GO:0008307; F:GO:0032027; P:GO:0008258; P:GO:0051259; P:GO:0016203; C:GO:0032154; C:GO:0045179; P:GO:0045184; C:GO:0005863; P:GO:0035317; P:GO:0007427;	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	lycerol ki-se family member (dgk-1)	7	F:GO:0004143; F:GO:0008270; F:GO:0003676; F:GO:0005515; F:GO:0000166; P:GO:0007165; P:GO:0007205	-	EC:2.7.1.107	IPR000756; PTHR11255 (PANTHER), PTHR11255:SF8 (PANTHER)
Caenorhabditis elegans	aspergillus nuclear division related family member (nud-2)	0				-
	-	0				-
Hypocrea lixii	family protein	0		F:GO:0005509; F:GO:0030414; C:GO:0016021; C:GO:0009279; C:GO:0016020; F:GO:0004867; C:GO:0005576; C:GO:0005886		-
Brugia malayi	fragile site-associated protein	0				IPR018863
Brugia malayi	notch-like transmembrane receptor lin-12	10	P:GO:0048468; N:GO:2000026; P:GO:0009888; C:GO:0044464; P:GO:0009653; P:GO:0048513; P:GO:0030182; P:GO:0045595; P:GO:0048523; F:GO:0005488	-		IPR000152; IPR000742; IPR000800; IPR006209; IPR006210; IPR013032; G3DSA:2.10.25.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF13 (PANTHER), SSF57196 (SUPERFAMILY)

	-	0				-
Dictyocaulus viviparus	hypothetical protein isoform a [Dictyocaulus viviparus]	0				-
Caenorhabditis briggsae	briggsae cbr-ego-1 protein	0		F:GO:0005515		-
Caenorhabditis elegans	endoribonuclease dicer	17	P:GO:0001525; F:GO:0004525; C:GO:0043005; P:GO:0030324; F:GO:0005515; P:GO:0035116; P:GO:0030422; C:GO:0005737; P:GO:0019827; F:GO:0004386; F:GO:0003677; P:GO:0048754; P:GO:0035196; F:GO:0003725; F:GO:0003993; P:GO:0055013; F:GO:0005524	-	EC:3.1.26.3; EC:3.1.3.2	-
Caenorhabditis elegans	uncoordi-ted family member (unc-89)	0				PTHR19897 (PANTHER), PTHR19897:SF5 (PANTHER)
	-	0				-
Caenorhabditis briggsae	adiponectin receptor 2	4	F:GO:0004872; P:GO:0007165; C:GO:0016021; P:GO:0006355	-		IPR004254; PTHR20855:SF13 (PANTHER)
	-	0				-
Loa loa	gtpase activating protein and vps9 domains 1	1	P:GO:0007165	-		-
Angiostrongylus cantonensis	60s ribosomal protein l7	10	P:GO:0009792; P:GO:0002119; F:GO:0030528; F:GO:0003735; F:GO:0005515; P:GO:0040010; P:GO:0000003; C:GO:0015934; P:GO:0006508; P:GO:0006412	-	EC:3.6.5.3	IPR005998; IPR012988; IPR016082; IPR018038; PTHR11524 (PANTHER)
Angiostrongylus cantonensis	60s ribosomal protein l7	10	P:GO:0009792; P:GO:0002119; F:GO:0030528; F:GO:0003735; F:GO:0005515; P:GO:0040010; P:GO:0000003; C:GO:0015934; P:GO:0006508; P:GO:0006412	-	EC:3.6.5.3	IPR005998; IPR012988; IPR016082; IPR018038; PTHR11524 (PANTHER)
Caenorhabditis briggsae	phenylethanolamine n-methyltransferase	2	F:GO:0005515; F:GO:0008168	-	EC:2.1.1.0	IPR000940; G3DSA:3.40.50.150 (GENE3D), PTHR10867:SF3 (PANTHER), SSF53335 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	polymerase iii (d- directed) polypeptide g like	4	P:GO:0002009; P:GO:0040010; P:GO:0040035; P:GO:0002119	-		-

Ailuropoda melanoleuca	ribosomal protein l23a	6	F:GO:0003735; F:GO:0005515; C:GO:0022625; F:GO:0019843; F:GO:0000166; P:GO:0006414	-		IPR001014; IPR005633; IPR012677; IPR012678; IPR013025; IPR019985; PTHR11620 (PANTHER)
Caenorhabditis briggsae	-dh-ubiquinone oxidoreductase subunit	9	P:GO:0040010; P:GO:0008340; F:GO:0008137; C:GO:0016021; C:GO:0005743; P:GO:0006120; P:GO:0002119; P:GO:0006898; P:GO:0009792	-	EC:1.6.5.3	IPR009423; SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-lem-3 protein	0		P:GO:0007413; C:GO:0005635		IPR003887; IPR011015; PTHR12019 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	srebp cleavage activating protein homolog family member (scp-1)	1	P:GO:0009792	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782
Melithaea caledonica	tissue factor pathway inhibitor-like	1	F:GO:0004867	-		IPR010916; SignalP (SIGNALP)
Melithaea caledonica	tissue factor pathway inhibitor-like	1	F:GO:0004867	-		SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-sax-2 protein	11	F:GO:0005515; P:GO:0048601; P:GO:0016055; P:GO:0042052; P:GO:0008407; F:GO:0016563; P:GO:0045860; P:GO:0048800; P:GO:0035317; P:GO:0048814; C:GO:0005938	-		PTHR12295 (PANTHER), PTHR12295:SF6 (PANTHER)
Apis mellifera	kiaa0319 protein	0		C:GO:0016021; C:GO:0005886		IPR000601; IPR022409; PTHR10083 (PANTHER), PTHR10083:SF14 (PANTHER)
Brugia malayi	n t family member (cit-)	0				IPR006670; IPR006671; IPR011028; IPR013763; IPR015429; PTHR10026:SF9 (PANTHER)
Caenorhabditis elegans	periodic tryptophan protein 1 homolog	0		F:GO:0003674; P:GO:0008150; C:GO:0005634; C:GO:0005575		IPR001680; IPR015943; PTHR14091 (PANTHER), SSF101908 (SUPERFAMILY)
Caenorhabditis elegans	periodic tryptophan protein 1 homolog	0		F:GO:0003674; P:GO:0008150; C:GO:0005634; C:GO:0005575		IPR001680; IPR015943; PTHR14091 (PANTHER), SSF101908 (SUPERFAMILY)
Caenorhabditis briggsae	ribosome production factor 1	9	P:GO:0006412; F:GO:0003723; C:GO:0005730; P:GO:0040007; F:GO:0005524; P:GO:0002119; P:GO:0042254; F:GO:0004812; P:GO:0006898	-	EC:3.6.5.3	IPR004154; IPR007109; G3DSA:3.40.50.10480 (GENE3D), PTHR22734 (PANTHER)

	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	negative regulator of mitosis	1	F:GO:0005515	-		IPR020003
Loa loa	taf1 r- polymerase tata box binding protein -associated factor	22	F:GO:0002039; P:GO:0006367; P:GO:0000080; F:GO:0008270; F:GO:0004402; P:GO:0018107; F:GO:0017025; P:GO:0046777; P:GO:0010552; C:GO:0005730; P:GO:0032436; P:GO:0018105; F:GO:0004674; F:GO:0003713; P:GO:0006368; F:GO:0003677; C:GO:0045120; P:GO:0042493; C:GO:0005669; F:GO:0070577; P:GO:0016573; C:GO:0071339	-	EC:2.3.1.48; EC:2.7.11.0	IPR022591; PTHR13900 (PANTHER)
Homo sapiens	eukaryotic translation elongation factor 1 gamma	6	F:GO:0003746; C:GO:0005853; F:GO:0005515; C:GO:0005829; P:GO:0009615; P:GO:0006414	-		IPR004045; IPR004046; IPR010987; IPR012335; IPR012336; IPR017933; PTHR11260 (PANTHER), PTHR11260:SF7 (PANTHER)
Caenorhabditis briggsae	pab-dependent poly -specific ribonuclease subunit 3	1	F:GO:0005515	-		PTHR12272 (PANTHER), PTHR12272:SF6 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	huntingtin interacting protein k	0				-
Tetraodon nigroviridis	malate dehydroge-se	4	P:GO:0018991; P:GO:0055114; F:GO:0016491; P:GO:0040011	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	serine palmitoyltransferase	5	P:GO:0009792; P:GO:0040027; P:GO:0040010; P:GO:0040011; F:GO:0003824	-		PTHR13693 (PANTHER), PTHR13693:SF2 (PANTHER)
	-	0				-
Pan troglodytes	hepatocellular carcinoma-associated antigen 112	1	C:GO:0016021	-		-
	-	0				-

Brugia malayi	transcription initiation factor tfiid subunit 8	0		P:GO:0030154; C:GO:0005737; P:GO:0001833; P:GO:0007275; P:GO:0045449; C:GO:0005634; F:GO:0003677		IPR006565; IPR009072
Caenorhabditis elegans	sorting nexin-18	5	P:GO:0009792; P:GO:0040027; F:GO:0035091; F:GO:0005515; P:GO:0007154	-		IPR001683; IPR019497; G3DSA:2.30.30.40 (GENE3D), PTHR10555 (PANTHER), PTHR10555:SF11 (PANTHER)
	-	0				-
Caenorhabditis elegans	secreted protein	0		F:GO:0001848; C:GO:0016021; P:GO:0045916		IPR000436; IPR016060; PTHR19325 (PANTHER), PTHR19325:SF25 (PANTHER)
	-	0				-
	-	0				-
Homo sapiens	-dh dehydroge-se	5	P:GO:0006810; F:GO:0008137; C:GO:0005747; P:GO:0006120; P:GO:0032981	-	EC:1.6.5.3	-
Danio rerio	novel protein	0		P:GO:0007154; P:GO:0006816; C:GO:0016021; C:GO:0016020; C:GO:0005575; P:GO:0055085; P:GO:0008150; F:GO:0005432; F:GO:0005488		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	isoform 2	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	tp53rk binding protein	3	C:GO:0005829; F:GO:0019901; C:GO:0005634	-		IPR013926; PTHR15840 (PANTHER), PTHR15840:SF5 (PANTHER), SSF143870 (SUPERFAMILY)
	-	0				-

Loa loa	shortsighted class 1	19	P:GO:0035282; P:GO:0030307; P:GO:0045746; P:GO:0001751; P:GO:0046843; P:GO:0006355; P:GO:0008101; P:GO:0009996; P:GO:0007297; C:GO:0005737; F:GO:0003702; P:GO:0008284; P:GO:0007422; P:GO:0035071; P:GO:0001709; F:GO:0003700; F:GO:0042803; C:GO:0005634; P:GO:0043066	-		IPR000580; PTHR12348:SF8 (PANTHER)
	-	0				-
Caenorhabditis elegans	zinc finger protein 699	0		P:GO:0006355; F:GO:0046872; F:GO:0003676; P:GO:0045449; F:GO:0008270; F:GO:0003677; C:GO:0005634; C:GO:0005622		IPR007087; IPR013087; IPR015880; PTHR23229 (PANTHER), PTHR23229:SF13 (PANTHER)
Caenorhabditis briggsae	protein ki-se domain containing protein	9	C:GO:0030424; C:GO:0030425; F:GO:0004713; C:GO:0005929; F:GO:0005515; F:GO:0000166; C:GO:0043025; P:GO:0034608; P:GO:0034606	-	EC:2.7.10.0	IPR000719; IPR001245; IPR011009; IPR020685; IPR020764; G3DSA:1.10.510.10 (GENE3D)
Caenorhabditis briggsae	vacuolar membrane protein pep11	9	P:GO:0009792; P:GO:0010171; P:GO:0040018; P:GO:0018996; F:GO:0005515; P:GO:0040010; P:GO:0000003; P:GO:0008219; F:GO:0008270	-		PTHR23323 (PANTHER), PTHR23323:SF24 (PANTHER)
Caenorhabditis elegans	pan domain containing protein	0				-
	-	0				-
Caenorhabditis brenneri	brain protein 44	0		F:GO:0003674; P:GO:0008150		IPR005336; PTHR14154 (PANTHER), PTHR14154:SF2 (PANTHER)
	-	0				-
Brugia malayi	interleukin enhancer binding factor 2	7	C:GO:0005730; F:GO:0003677; F:GO:0003725; F:GO:0005515; C:GO:0030529; P:GO:0045893; F:GO:0003702	-		-

Caenorhabditis briggsae	r- binding motif protein 19	6	C:GO:0005737; C:GO:0005730; C:GO:0005654; F:GO:0003676; P:GO:0040019; F:GO:0000166	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF64 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	sig-l transducer and activator of transcription	18	F:GO:0003700; F:GO:0004871; P:GO:0003006; P:GO:0006519; P:GO:0048732; P:GO:0019752; P:GO:0042981; P:GO:0007165; C:GO:0005737; F:GO:0042802; F:GO:0003677; P:GO:0048523; P:GO:0065008; P:GO:0045621; F:GO:0005509; C:GO:0005634; P:GO:0009308; P:GO:0006355	-		IPR001217; IPR008967; IPR012345; IPR013800; IPR015988; PTHR11801:SF9 (PANTHER)
Ascaris suum	serine threonine protein phosphatase pp1 isozyme 1	1	F:GO:0016787	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	trafficking protein particle complex subunit 4	5	C:GO:0044456; C:GO:0030008; F:GO:0005515; P:GO:0006888; C:GO:0016020	-		IPR007233; IPR011012; G3DSA:3.30.450.70 (GENE3D), PTHR23249:SF2 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	transcription initiation factor iif alpha	11	P:GO:0008340; P:GO:0006367; P:GO:0040035; F:GO:0003677; F:GO:0016563; P:GO:0006898; P:GO:0009792; F:GO:0003824; C:GO:0005634; F:GO:0003702; P:GO:0045941	-		IPR008851; IPR011039; PTHR13011 (PANTHER)
Caenorhabditis elegans	tr- modification gtpase	4	F:GO:0017111; C:GO:0005622; P:GO:0008033; F:GO:0000166	-	EC:3.6.1.15	IPR018948; G3DSA:1.20.120.430 (GENE3D), PTHR11649 (PANTHER), PTHR11649:SF14 (PANTHER), SSF103025 (SUPERFAMILY), SSF116878 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	c4b-binding protein beta	0		F:GO:0030414; F:GO:0016787; C:GO:0005576		IPR000436; IPR016060; PTHR19325 (PANTHER), PTHR19325:SF40 (PANTHER)
	-	0				-
Caenorhabditis elegans	protein	0		P:GO:0006508; F:GO:0004176		SignalP (SIGNALP)
	-	0				-

Brugia malayi	origin recognition complex subunit 1	5	F:GO:0005488; P:GO:0040007; P:GO:0040035; P:GO:0002119; P:GO:0009792	-		-
	-	0				-
Caenorhabditis elegans	kti12 homolog	0		F:GO:0005524; F:GO:0000166; P:GO:0008150		IPR013641; G3DSA:3.40.50.300 (GENE3D), PTHR12435 (PANTHER), SSF52540 (SUPERFAMILY)
synthetic construct	small nuclear ribonucleoprotein sm d2	8	C:GO:0005654; F:GO:0003676; P:GO:0000387; C:GO:0005681; F:GO:0005515; C:GO:0030532; C:GO:0005829; P:GO:0000245	-		SignalP (SIGNALP)
Caenorhabditis elegans	temporarily assigned gene -me family member (tag-308)	0				-
Loa loa	rap ran-gap family protein	13	P:GO:0008340; P:GO:0006974; P:GO:0046621; P:GO:0006911; C:GO:0005737; P:GO:0008285; P:GO:0051726; P:GO:0006629; P:GO:0030308; P:GO:0007165; P:GO:0046627; F:GO:0019900; P:GO:0007584	-		IPR000331; SSF111347 (SUPERFAMILY)
Caenorhabditis elegans	o-phosphoseryl-tr- selenium	6	C:GO:0005737; F:GO:0042802; F:GO:0030170; F:GO:0016740; F:GO:0016829; P:GO:0006412	-	EC:3.6.5.3	IPR008829; IPR019872
Homo sapiens	growth hormone inducible transmembrane protein	2	C:GO:0016021; C:GO:0005739	-		IPR006214; PTHR23291:SF1 (PANTHER), SignalP (SIGNALP)
						IPR003961; IPR008957; IPR013783; PR00014 (PRINTS), PTHR19900 (PANTHER), PTHR19900:SF7 (PANTHER)
Naegleria gruberi	missing oocyte	3	P:GO:0007294; P:GO:0006302; P:GO:0040020	-		PTHR16453 (PANTHER), PTHR16453:SF9 (PANTHER)
	-	0				-
Caenorhabditis elegans	hypothetical protein M70.4 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	dopamine transporter	3	C:GO:0016021; P:GO:0006810; F:GO:0015293	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	zinc finger	1	F:GO:0003676	-		IPR008906; IPR012337; PTHR23272 (PANTHER)

Caenorhabditis elegans	daf-16 foxo germline tumor affecting family member (dct-6)	0				-
Caenorhabditis elegans	briggsae cbr-sec-8 protein	0		P:GO:0006904; C:GO:0000145; P:GO:0015031		IPR007191; PTHR14146 (PANTHER)
	-	0				-
Brugia malayi	wgr domain containing protein	0		F:GO:0003676; F:GO:0003950; P:GO:0006471; F:GO:0008270; F:GO:0051287; C:GO:0005622; F:GO:0003677; C:GO:0005634		-
	-	0				-
Ostertagia ostertagi	excretory secretory antigen	1	F:GO:0019841	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	placental protein 11 related	8	C:GO:0005737; F:GO:0046872; F:GO:0004521; F:GO:0003723; P:GO:0007565; C:GO:0005576; F:GO:0008236; P:GO:0006508	-		IPR018998; PTHR12439 (PANTHER), SSF142877 (SUPERFAMILY)
Loa loa	mutator family member (mut-7)	1	F:GO:0005488	-		IPR002782
	-	0				-
Caenorhabditis elegans	phosphatidylinositol class c	1	F:GO:0016740	-		IPR009450; SignalP (SIGNALP)
Pan troglodytes	PREDICTED: hypothetical protein [Pan troglodytes]	0				-
Caenorhabditis elegans	procollagen- 2-oxoglutarate 5-dioxyge-se 3	9	P:GO:0055114; F:GO:0008475; F:GO:0031418; F:GO:0005515; P:GO:0032870; P:GO:0008045; F:GO:0005506; C:GO:0005783; P:GO:0006464	-	EC:1.14.11.4	PTHR10730 (PANTHER), PTHR10730:SF1 (PANTHER)
Brugia malayi	recq-mediated genome instability protein 1	0		P:GO:0006260; C:GO:0005634		PTHR14790 (PANTHER)
Caenorhabditis briggsae	arginine serine-rich coiled-coil protein 2	0				-
Caenorhabditis elegans	sy-ptotagmin i	5	F:GO:0035005; C:GO:0008021; P:GO:0006810; C:GO:0016020; F:GO:0005215	-	EC:2.7.1.154	G3DSA:2.60.40.150 (GENE3D), PTHR10024 (PANTHER), PTHR10024:SF40 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-pro-1 protein	4	P:GO:0030154; P:GO:0007506; P:GO:0006364; C:GO:0005634	-		-
	-	0				-
	-	0				SignalP (SIGNALP)

Danio rerio	v-ski sarcoma viral oncogene homolog	8	P:GO:0048468; P:GO:0090101; P:GO:0007399; F:GO:0005515; P:GO:0043010; P:GO:0008285; C:GO:0044451; P:GO:0009887	-		IPR003380; IPR009061; IPR010919; IPR014890; PTHR10005 (PANTHER)
	-	0				-
	-	0				-
Homo sapiens	PREDICTED: hypothetical protein XP_002343179 [Homo sapiens]	0				-
Caenorhabditis briggsae	cbf mak21 family protein	0		P:GO:0000003; F:GO:0005488; P:GO:0006898; P:GO:0002119; P:GO:0009792; P:GO:0040007		-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-mau-8 protein	1	F:GO:0005515	-		SignalP (SIGNALP)
Caenorhabditis elegans	transmembrane protein 57	0		C:GO:0016021		PTHR13289 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	tyrosyl-tr- synthetase	3	F:GO:0004812; P:GO:0006418; F:GO:0000166	-		IPR002305; IPR002307; IPR014729; SSF52374 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	briggsae cbr-rev-1 protein	9	P:GO:0009411; P:GO:0040010; P:GO:0042276; C:GO:0005622; F:GO:0046872; F:GO:0005515; F:GO:0017125; P:GO:0006898; P:GO:0009792	-		IPR001126; IPR017961; PTHR11076:SF13 (PANTHER), PF11799 (PFAM)
Loa loa	collagen protein confirmed by transcript evidence	3	P:GO:0032502; F:GO:0005515; C:GO:0060103	-		IPR002486; IPR008160; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein F07C6.4 [Caenorhabditis elegans]	0				-
Loa loa	cleavage and polyadenylation specificity factor subunit 2	5	P:GO:0040035; P:GO:0009792; P:GO:0000910; P:GO:0016246; F:GO:0016787	-		IPR022712; PTHR11203 (PANTHER), PTHR11203:SF5 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG01887 [Caenorhabditis briggsae]	0				-
Brugia malayi	-related lipid transfer domain containing 13	0		P:GO:0007165; C:GO:0005622		IPR019809
Caenorhabditis elegans	homogentisate -dioxyge-se	6	F:GO:0042802; F:GO:0046872; F:GO:0004411; P:GO:0055114; P:GO:0006559; P:GO:0006570	-	EC:1.13.11.5	IPR005708; IPR011051; SignalP (SIGNALP)
Homo sapiens	immunoglobulin heavy chain	0				IPR007110; IPR013106; IPR013783; PTHR23266 (PANTHER), PTHR23266:SF7 (PANTHER), SignalP (SIGNALP), SSF48726 (SUPERFAMILY)

Caenorhabditis briggsae	Hypothetical protein CBG05143 [Caenorhabditis briggsae]	3	C:GO:0016021; P:GO:0006508; F:GO:0008234	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	solute carrier family 41 member 1	4	F:GO:0008324; P:GO:0006812; C:GO:0016021; F:GO:0000166	-		IPR006667
	-	0				-
Caenorhabditis elegans	guanine deami-se	2	F:GO:0016787; F:GO:0008270	-		IPR002125; IPR016193; G3DSA:3.40.140.10 (GENE3D), PTHR11079 (PANTHER), PTHR11079:SF9 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	phosphatidylinositol-glycan biosynthesis class f protein	1	C:GO:0044464	-		IPR009580; SignalP (SIGNALP)
Loa loa	hypothetical protein LOAG_01466 [Loa loa]	0				-
Loa loa	hypothetical protein LOAG_01466 [Loa loa]	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
Haemonchus contortus	b chain structure of p-glycoprotein reveals a molecular basis for poly-specific drug binding	20	P:GO:0046685; P:GO:0007595; C:GO:0000139; F:GO:0005515; P:GO:0033280; P:GO:0048545; P:GO:0006855; P:GO:0014070; P:GO:0014045; C:GO:0009986; P:GO:0006629; F:GO:0008559; P:GO:0046686; P:GO:0010212; P:GO:0006200; C:GO:0046581; C:GO:0005887; F:GO:0005524; C:GO:0016324; C:GO:0005739	-	EC:3.6.3.44	IPR003439; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF96 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	ankyrin partial	0		F:GO:0004674; F:GO:0004672; P:GO:0006468; F:GO:0000166; F:GO:0005525; F:GO:0005524; F:GO:0016301; F:GO:0005515; C:GO:0005622; P:GO:0007264		IPR002110; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER)
Caenorhabditis briggsae	a in (actin filament binding protein) homolog family member (afd-1)	0		P:GO:0040010; P:GO:0007165; F:GO:0005515		IPR000159

Caenorhabditis elegans	cyclin d2	9	P:GO:0040007; F:GO:0019901; P:GO:0006898; P:GO:0045737; P:GO:0040039; P:GO:0001934; C:GO:0000307; P:GO:0009725; P:GO:0032501	-		IPR006670; IPR006671; IPR011028; IPR013763; IPR015451; PTHR10177 (PANTHER)
Caenorhabditis elegans	protein amp- beta 2 non-catalytic subunit	5	P:GO:0006631; C:GO:0043234; F:GO:0005515; P:GO:0050794; C:GO:0044424	-		PTHR10343 (PANTHER), PTHR10343:SF10 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	yqt2_caeel ame: full=uncharacterized protein	0		P:GO:0040035		-
	-	0				-
Caenorhabditis elegans	briggsae cbr-inx- protein	7	P:GO:0009792; P:GO:0007631; P:GO:0048856; P:GO:0040010; P:GO:0030421; P:GO:0000003; C:GO:0044425	-		IPR000408; IPR000990
Caenorhabditis briggsae	box h aca	0		P:GO:0042254; P:GO:0010171; P:GO:0006898; C:GO:0030529; P:GO:0006412; P:GO:0000003; P:GO:0009792; P:GO:0002119; C:GO:0005840; C:GO:0005622; P:GO:0040007		-
Heligmosomoides polygyrus	cytosolic glutathione s-transferase 1	4	P:GO:0008340; P:GO:0040010; F:GO:0005515; F:GO:0016740	-		-
	-	0				-
Ailuropoda melanoleuca	polyadenylate-binding protein 1-like	9	P:GO:0006378; P:GO:0008380; P:GO:0048255; C:GO:0005681; F:GO:0008494; F:GO:0008022; C:GO:0005829; F:GO:0000166; F:GO:0008143	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF69 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
	-	0				-
Brugia malayi	vacuolar protein-sorting-associated protein 25	4	P:GO:0030488; F:GO:0016429; P:GO:0006810; P:GO:0040010	-	EC:2.1.1.36	IPR008570; IPR014041; SSF46785 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		IPR006150; PTHR11201 (PANTHER), PTHR11201:SF241 (PANTHER)

	-	0				-
Caenorhabditis briggsae	lethal 07882	3	P:GO:0009792; P:GO:0002119; P:GO:0006898	-		IPR007276
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	5	P:GO:0040035; P:GO:0018991; P:GO:0008340; C:GO:0016020; P:GO:0002009	-		IPR002259; PTHR10332:SF6 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	sterol regulatory element binding transcription factor 1	3	F:GO:0030528; F:GO:0005515; C:GO:0005634	-		-
	-	0				-
Branchiostoma floridae	sorbitol dehydroge-se	9	C:GO:0005625; F:GO:0051287; C:GO:0005624; P:GO:0051160; P:GO:0046370; P:GO:0055114; F:GO:0003939; F:GO:0008270; P:GO:0006062	-	EC:1.1.1.14	IPR002085; IPR013149; IPR016040; PTHR11695:SF38 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	glycyl-tr- synthetase	7	C:GO:0016021; P:GO:0006426; P:GO:0015966; F:GO:0005524; F:GO:0046983; C:GO:0005737; F:GO:0004820	-	EC:6.1.1.14	IPR002314; IPR002315; G3DSA:3.30.930.10 (GENE3D), SSF55681 (SUPERFAMILY)
Caenorhabditis elegans	transbilayer amphipath transporters (subfamily iv p-type atpase) family member (tat-2)	7	C:GO:0016021; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0015914; F:GO:0000287; F:GO:0004012	-	EC:3.6.3.1	IPR001757; IPR018303; G3DSA:3.40.1110.10 (GENE3D), PTHR11939:SF19 (PANTHER), SignalP (SIGNALP), SSF56784 (SUPERFAMILY)
Caenorhabditis elegans	bed-type zinc finger transcription factor family member (bed-2)	2	F:GO:0005515; F:GO:0003677	-		-
Ailuropoda melanoleuca	eukaryotic translation initiation factor 3 subunit c	6	C:GO:0005852; F:GO:0005515; P:GO:0045948; F:GO:0003743; C:GO:0005829; F:GO:0043022	-		IPR000717; IPR011991; PTHR13937 (PANTHER), SSF46785 (SUPERFAMILY)
Loa loa	ribonucleases p mrp protein subunit pop1 containing protein	0		P:GO:0010171; P:GO:0006396; P:GO:0006898; P:GO:0000003; P:GO:0009792; P:GO:0002119; F:GO:0004526; P:GO:0001682; P:GO:0040010; P:GO:0040007		-

Brugia malayi	phosphatidylcholine:ceramide cholinephosphotransferase	7	F:GO:0047493; P:GO:0050789; C:GO:0016021; P:GO:0006686; P:GO:0051716; C:GO:0005794; P:GO:0010033	-	EC:2.7.8.3	PTHR21290 (PANTHER), PTHR21290:SF3 (PANTHER), SignalP (SIGNALP)
Loa loa	fasciclin-1 precursor (fasciclin i) (fas i)	0		P:GO:0007411; P:GO:0007158; P:GO:0007156; F:GO:0050839; C:GO:0005886; P:GO:0016338; P:GO:0008038		-
Caenorhabditis elegans	alkmo_caeel ame: full=alkylglycerol monooxyge-se homolog ame: full=transmembrane protein 195 homolog	0		P:GO:0055114; F:GO:0016491; F:GO:0005506; C:GO:0005783; P:GO:0006633		SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG13452 [Caenorhabditis briggsae]	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	protein ki-se c and casein ki-se substrate in neurons 2	4	C:GO:0005737; F:GO:0005515; P:GO:0009987; P:GO:0016043	-		IPR001060; IPR001452; G3DSA:2.30.30.40 (GENE3D), PTHR10959 (PANTHER)
Ornithorhynchus anatinus	mannosyl (alpha- -)-glycoprotein beta- -n-acetyl-glucosaminyltransferase	2	F:GO:0016757; C:GO:0016020	-		PTHR15075 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	tr- guanosine-2 -o-methyltransferase trm11 homolog	2	P:GO:0044237; F:GO:0016740	-		IPR000241; PTHR13370 (PANTHER)
	-	0				SignalP (SIGNALP)
Brugia malayi	elegans protein partially confirmed by transcript evidence	14	P:GO:0023033; P:GO:0007424; P:GO:0065008; N:GO:0071842; P:GO:0001700; F:GO:0005096; C:GO:0005622; P:GO:0009887; P:GO:0060562; P:GO:0048565; P:GO:0016331; P:GO:0007399; P:GO:0048523; P:GO:0016477	-		PTHR12659 (PANTHER)
Canis familiaris	syntaxin 18	2	P:GO:0006810; C:GO:0044464	-		IPR019529; PTHR15959 (PANTHER)

Mus musculus	ribosomal protein l24	11	F:GO:0003723; P:GO:0000027; F:GO:0003735; P:GO:0010458; P:GO:0006414; F:GO:0005515; P:GO:0060041; P:GO:0031290; P:GO:0031575; P:GO:0021554; C:GO:0022625	-		SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein ZC487.1 [Caenorhabditis elegans]	0		F:GO:0005524; F:GO:0003824		-
Loa loa	proteasome (macropain) activator subunit 4	0		F:GO:0005488; C:GO:0000502		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				G3DSA:3.40.50.300 (GENE3D), PTHR11089 (PANTHER), PTHR11089:SF1 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				G3DSA:3.40.50.300 (GENE3D), PTHR11089 (PANTHER), PTHR11089:SF1 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				G3DSA:3.40.50.300 (GENE3D), PTHR11089 (PANTHER), PTHR11089:SF1 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG22473 [Caenorhabditis briggsae]	1	F:GO:0005515	-		SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG22473 [Caenorhabditis briggsae]	1	F:GO:0005515	-		SignalP (SIGNALP)
Caenorhabditis briggsae	protein	0		P:GO:0006355; F:GO:0043565; F:GO:0003700; P:GO:0015031		IPR005024; PTHR22761 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F43D9.1 [Caenorhabditis elegans]	0		C:GO:0016020; F:GO:0008158		PTHR10796 (PANTHER), PTHR10796:SF13 (PANTHER), SignalP (SIGNALP)

Homo sapiens	cathepsin b	29	P:GO:0009749; C:GO:0005764; F:GO:0030984; P:GO:0051789; C:GO:0009897; C:GO:0005625; C:GO:0005739; P:GO:0045471; P:GO:0042981; C:GO:0005901; P:GO:0009611; F:GO:0032403; C:GO:0005615; P:GO:0006508; P:GO:0043434; F:GO:0004197; C:GO:0042470; P:GO:0007519; P:GO:0014070; P:GO:0070670; C:GO:0048471; C:GO:0016324; C:GO:0042383; P:GO:0050790; P:GO:0014075; P:GO:0060548;	-	EC:3.4.22.0	IPR000169; IPR000668; IPR012599; IPR013128; IPR015643; G3DSA:3.90.70.10 (GENE3D), SignalP (SIGNALP), SSF54001 (SUPERFAMILY)
Homo sapiens	glutathione peroxidase 1	41	P:GO:0006914; P:GO:0006641; F:GO:0017124; P:GO:0009609; P:GO:0018158; P:GO:0010332; P:GO:0043403; P:GO:0010269; P:GO:0001659; C:GO:0005829; P:GO:0001885; P:GO:0043523; P:GO:0007605; P:GO:0042311; P:GO:0006749; P:GO:0008631; P:GO:0014902; F:GO:0004602; P:GO:0060055; P:GO:0033194; P:GO:0006916; P:GO:0043154; P:GO:0043534; P:GO:0009650; P:GO:0033599; P:GO:0045444; P:GO:0051450;	-	EC:1.11.1.9	IPR000889; IPR012335; IPR012336
	-	0				-

Ailuropoda melanoleuca	rr- 2 -o-methyltransferase fibrillarin-like	9	C:GO:0001652; C:GO:0031428; C:GO:0015030; F:GO:0003723; F:GO:0005515; P:GO:0016074; P:GO:0006364; F:GO:0008168; P:GO:0008033	-	EC:2.1.1.0	IPR000692; IPR020813; G3DSA:3.40.50.150 (GENE3D), SSF53335 (SUPERFAMILY)
Candida dubliniensis CD36	potential histone deacetylase complex component sin3p	0		P:GO:0006355; F:GO:0005488; C:GO:0005634		IPR003822; PTHR12346 (PANTHER), PS51477 (PROFILE)
Perkinsus marinus ATCC 50983	dentin matrix acidic phosphoprotein 1	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	low-density lipoprotein receptor-related protein 2	3	C:GO:0016021; F:GO:0004872; F:GO:0005509	-		IPR000033; IPR011042; PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER), SSF63825 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	gamma-glutamyltranspeptidase family protein	1	F:GO:0003840	-	EC:2.3.2.2	-
Caenorhabditis briggsae	proteasome (macropain) 26s non- 13	6	P:GO:0051436; P:GO:0051437; C:GO:0005838; P:GO:0031145; P:GO:0007127; F:GO:0005515	-		SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	nol1 nop2 sun domain member 4	0		F:GO:0008168; F:GO:0003674; F:GO:0016740; P:GO:0008152; P:GO:0008150; P:GO:0032259; C:GO:0005575		IPR001678; G3DSA:3.40.50.150 (GENE3D), PTHR22808 (PANTHER), PTHR22808:SF3 (PANTHER), SSF53335 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	torsin family member b (torsin b)	3	F:GO:0005515; C:GO:0005783; F:GO:0000166	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein B0399.1 [Caenorhabditis elegans]	0		F:GO:0015269; C:GO:0016021; P:GO:0006813; F:GO:0005516		-

Caenorhabditis elegans	can cell migration defective family member (cam-1)	14	P:GO:0007411; P:GO:0007166; C:GO:0031594; P:GO:0045200; P:GO:0008285; C:GO:0030425; C:GO:0030424; P:GO:0007165; F:GO:0004714; C:GO:0032809; C:GO:0005887; F:GO:0017147; P:GO:0030335; P:GO:0040035	-	EC:2.7.10.1	IPR000719; IPR001245; IPR008266; IPR011009; IPR017441; IPR020635; IPR020685; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR23256:SF149 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0016787	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0016787		PTHR23131 (PANTHER)
Caenorhabditis briggsae	3 saliva family protein	5	F:GO:0004181; C:GO:0016021; P:GO:0007476; P:GO:0006911; P:GO:0019915	-	EC:3.4.17.0	IPR004316; IPR018179; SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	periodic tryptophan protein 2 homolog	4	F:GO:0004871; P:GO:0055085; P:GO:0007165; C:GO:0016021	-		IPR001680; IPR011046; IPR015943; IPR017441; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR19858 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				IPR009311; PTHR16932:SF3 (PANTHER)
	-	0				-
	-	0				-
Loa loa	transcription elongation factor b	6	F:GO:0005488; P:GO:0008340; C:GO:0008023; P:GO:0006368; F:GO:0016944; P:GO:0016246	-		IPR010684; PTHR15141 (PANTHER)
Caenorhabditis elegans	variable abnormal morphology family member (vab-10)	14	P:GO:0016199; P:GO:0007026; P:GO:0016319; C:GO:0030426; P:GO:0048813; P:GO:0035147; P:GO:0030716; C:GO:0000235; F:GO:0008092; P:GO:0035149; P:GO:0016203; C:GO:0045169; C:GO:0005912; P:GO:0030516	-		IPR002017; IPR018159; G3DSA:1.20.58.60 (GENE3D), SSF46966 (SUPERFAMILY)

Caenorhabditis elegans	hypothetical protein F48E3.2 [Caenorhabditis elegans]	3	C:GO:0016020; P:GO:0009792; P:GO:0006810	-		PTHR11600 (PANTHER), PTHR11600:SF12 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-cogc-1 protein	1	F:GO:0005515	-		-
Monodelphis domestica	chromosome 7 open reading frame 25	0				IPR010733
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-tag-184 protein	0		F:GO:0005488		-
Brugia malayi	selenocysteine lyase	4	F:GO:0030170; P:GO:0009792; P:GO:0008152; F:GO:0008483	-	EC:2.6.1.0	IPR015422; IPR015424; PTHR11601 (PANTHER)
Angiostrongylus cantonensis	briggsae cbr-pqn-68 protein	3	C:GO:0005737; F:GO:0016788; P:GO:0019478	-		IPR003732; PTHR10472:SF3 (PANTHER)
Callithrix jacchus	proteasome (macropain) 26s 4	10	C:GO:0000502; C:GO:0005739; P:GO:0051436; P:GO:0051437; P:GO:0031145; F:GO:0005524; F:GO:0016887; F:GO:0005515; P:GO:0001824; C:GO:0005634	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	nfu1 iron-sulfur cluster scaffold homolog (cerevisiae)	7	P:GO:0016226; F:GO:0005506; F:GO:0005515; F:GO:0051539; C:GO:0005634; C:GO:0005829; C:GO:0005739	-		IPR001075; IPR014824; IPR017065; PTHR11178 (PANTHER), SSF117916 (SUPERFAMILY)
Caenorhabditis briggsae	nfu1 iron-sulfur cluster scaffold homolog (cerevisiae)	7	P:GO:0016226; F:GO:0005506; F:GO:0005515; F:GO:0051539; C:GO:0005634; C:GO:0005829; C:GO:0005739	-		IPR001075; IPR014824; IPR017065; PTHR11178 (PANTHER), SSF117916 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein Y37E11AL.3 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	hypothetical protein Y37E11AL.3 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	briggsae cbr-mut-2 protein	0		F:GO:0016779		IPR002934; G3DSA:3.30.460.10 (GENE3D), SSF81301 (SUPERFAMILY)
Caenorhabditis elegans	dual oxidase maturation factor 1	2	P:GO:0008104; C:GO:0016020	-		IPR018469
	-	0				-
Homo sapiens	hCG1648136 [Homo sapiens]	0				-
	-	0				-
	-	0				-

Haemonchus contortus	serine threonine ki-se	4	P:GO:0006468; F:GO:0005515; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR001772; IPR002290; IPR008271; IPR011009; IPR015940; IPR017441; IPR017442; IPR020636; IPR020670; G3DSA:1.10.510.10 (GENE3D), G3DSA:1.10.8.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), G3DSA:3.30.310.80 (GENE3D), SSF103243 (SUPERFAMILY)
Haemonchus contortus	serine threonine ki-se	4	P:GO:0006468; F:GO:0005515; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR001772; IPR002290; IPR008271; IPR011009; IPR015940; IPR017441; IPR017442; IPR020636; IPR020670; G3DSA:1.10.510.10 (GENE3D), G3DSA:1.10.8.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), G3DSA:3.30.310.80 (GENE3D), SSF103243 (SUPERFAMILY)
Haemonchus contortus	serine threonine ki-se	4	P:GO:0006468; F:GO:0005515; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR001772; IPR002290; IPR008271; IPR011009; IPR015940; IPR017441; IPR017442; IPR020636; IPR020670; G3DSA:1.10.510.10 (GENE3D), G3DSA:1.10.8.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), G3DSA:3.30.310.80 (GENE3D), SSF103243 (SUPERFAMILY)
Haemonchus contortus	serine threonine ki-se	4	P:GO:0006468; F:GO:0005515; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR001772; IPR002290; IPR008271; IPR011009; IPR015940; IPR017441; IPR017442; IPR020636; IPR020670; G3DSA:1.10.510.10 (GENE3D), G3DSA:1.10.8.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), G3DSA:3.30.310.80 (GENE3D), SSF103243 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Xenopus laevis	inhibitor of growth member 2	1	F:GO:0046872	-		IPR001965; IPR011011; IPR013083; IPR019786; IPR019787; PTHR10333 (PANTHER), PTHR10333:SF21 (PANTHER)
Caenorhabditis briggsae	calcium-binding atopy-related autoantigen 1	2	C:GO:0016021; F:GO:0005509	-		PTHR12294 (PANTHER), PTHR12294:SF1 (PANTHER)
Caenorhabditis elegans	quinine non-avoider family member (qui-1)	0				-
Caenorhabditis briggsae	briggsae cbr-eat-18 protein	0		C:GO:0005615; F:GO:0016787		IPR000859; PTHR10127 (PANTHER), PTHR10127:SF33 (PANTHER)
	-	0				-
Brugia malayi	creb-regulated transcription coactivator 1	0				-
	-	0				-

Caenorhabditis briggsae	ribosomal protein s6	22	P:GO:0006924; P:GO:0007369; F:GO:0005515; C:GO:0005844; P:GO:0000028; P:GO:0048821; P:GO:0006414; P:GO:0031929; P:GO:0001890; C:GO:0005730; P:GO:0002309; P:GO:0022605; P:GO:0007067; P:GO:0033077; F:GO:0003735; P:GO:0031575; C:GO:0048471; P:GO:0006364; P:GO:0043066; P:GO:0042593; P:GO:0043065; C:GO:0022627	-		IPR001377; IPR014401; IPR018282; PTHR11502:SF1 (PANTHER)
Caenorhabditis elegans	wiskott-aldrich syndrome protein	6	P:GO:0050789; C:GO:0005856; P:GO:0008154; P:GO:0006461; F:GO:0005515; N:GO:0071844	-		IPR000095; IPR000697; IPR011026; IPR011993; G3DSA:3.90.810.10 (GENE3D), PTHR12779 (PANTHER), SSF50729 (SUPERFAMILY)
Caenorhabditis elegans	wiskott-aldrich syndrome protein	8	F:GO:0005515; P:GO:0008154; P:GO:0006461; C:GO:0005737; P:GO:0050896; C:GO:0005856; P:GO:0065007; N:GO:0071844	-		IPR000095; IPR000697; IPR011026; IPR011993; G3DSA:3.90.810.10 (GENE3D), PTHR12779 (PANTHER), SSF50729 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Loa loa	lim domain containing protein	0		F:GO:0005488; F:GO:0016491; P:GO:0008152; F:GO:0003824; F:GO:0008270		-
	-	0				-

Ailuropoda melanoleuca	melanoma antigen family 1	13	F:GO:0004705; P:GO:0006357; P:GO:0043193; P:GO:0090190; C:GO:0005829; P:GO:0008624; F:GO:0003713; P:GO:0043406; F:GO:0042802; C:GO:0043234; P:GO:0050680; P:GO:0032582; C:GO:0005886	-		-
	-	0				-
	-	0				IPR007087; IPR015880; SignalP (SIGNALP), SSF57667 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-sel-2 protein	6	P:GO:0008104; F:GO:0051018; P:GO:0042675; C:GO:0043231; C:GO:0044444; C:GO:0016020	-		IPR008985; IPR013320
Caenorhabditis elegans	cytochrome family subfamily polypeptide 2	3	F:GO:0016491; F:GO:0005506; C:GO:0016020	-		IPR001128; IPR002401; IPR017972; PTHR19383:SF165 (PANTHER)
Brugia malayi	arp6 actin-related protein 6 homolog	0		F:GO:0003674; C:GO:0005737; C:GO:0005856; P:GO:0008150; F:GO:0005515; C:GO:0005575		IPR004000; G3DSA:3.30.420.40 (GENE3D), PTHR11937:SF21 (PANTHER), SSF53067 (SUPERFAMILY)
Caenorhabditis briggsae	actin-related protein 6	1	F:GO:0005515	-		IPR004000; G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), PTHR11937:SF21 (PANTHER), SSF53067 (SUPERFAMILY)
Caenorhabditis elegans	excision repair cross-complementing rodent repair complementation group 4	7	P:GO:0006289; P:GO:0006310; F:GO:0004519; F:GO:0003677; P:GO:0007127; P:GO:0009792; C:GO:0000109	-		IPR020819; PTHR10150 (PANTHER)
Caenorhabditis briggsae	mitochondrial ribosomal protein l38	2	P:GO:0009792; P:GO:0002119	-		IPR008914; PTHR11362 (PANTHER)
Caenorhabditis sp. PS1010	briggsae cbr-cdh-4 protein	4	P:GO:0007163; P:GO:0007411; C:GO:0016020; P:GO:0007413	-		IPR002126; IPR015919; IPR020894; PTHR10596 (PANTHER), PTHR10596:SF74 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG04056 [Caenorhabditis briggsae]	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	alanine-glyoxylate aminotransferase 2-like 1	2	F:GO:0008483; P:GO:0008152	-	EC:2.6.1.0	IPR005814; IPR015421; PTHR11986:SF23 (PANTHER)
	-	0				-
	-	0				-

Caenorhabditis elegans	ribosome biogenesis protein	4	F:GO:0003924; C:GO:0005634; P:GO:0042254; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000795; G3DSA:3.40.50.300 (GENE3D), PTHR12858 (PANTHER), PTHR12858:SF2 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	fad synthase	5	C:GO:0005829; F:GO:0003919; P:GO:0040010; P:GO:0006747; F:GO:0000166	-	EC:2.7.7.2	IPR002500; IPR014729; PTHR23293 (PANTHER), SSF52402 (SUPERFAMILY)
Caenorhabditis briggsae	heat repeat-containing protein 7a	1	F:GO:0005488	-		IPR000357; IPR011989; IPR016024
Homo sapiens	apolipoprotein e	69	P:GO:0007186; P:GO:0010468; P:GO:0050728; F:GO:0042803; C:GO:0031232; C:GO:0034364; C:GO:0042627; P:GO:0006707; F:GO:0016209; P:GO:0007010; P:GO:0019934; F:GO:0008201; P:GO:0010875; P:GO:0007263; P:GO:0043691; C:GO:0034363; F:GO:0005543; P:GO:0051651; P:GO:0010544; F:GO:0046911; P:GO:0042311; P:GO:0046907; P:GO:0002021; P:GO:0045471; P:GO:0034375; F:GO:0001540; P:GO:0006874;	-		-
Caenorhabditis elegans	mitochondrial translatio-l initiation factor 2	12	F:GO:0015093; P:GO:0015684; P:GO:0040010; P:GO:0006898; F:GO:0043024; F:GO:0005525; C:GO:0016021; F:GO:0003743; P:GO:0007264; P:GO:0006446; F:GO:0003924; C:GO:0005739	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR004161; IPR009000; IPR015760; G3DSA:2.40.30.10 (GENE3D), PTHR23115 (PANTHER)
	-	0				-
	-	0				-
Brugia malayi	probable coatomer beta subunit	0		C:GO:0030117; P:GO:0016192; F:GO:0005198; P:GO:0006886; F:GO:0005515		-

Brugia malayi	probable coatomer beta subunit	0		C:GO:0030117; P:GO:0016192; F:GO:0005198; P:GO:0006886; F:GO:0005515		-
Caenorhabditis briggsae	cathepsin b	3	C:GO:0016021; P:GO:0006508; F:GO:0008234	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	loc496104 protein	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-abcx-1 protein	0		F:GO:0005524; F:GO:0016887; F:GO:0005488		-
	-	0				-
Callithrix jacchus	poly binding cytoplasmic isoform cra_c	9	P:GO:0006378; P:GO:0008380; P:GO:0048255; C:GO:0005681; F:GO:0008494; F:GO:0008022; C:GO:0005829; F:GO:0000166; F:GO:0008143	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF69 (PANTHER), SSF54928 (SUPERFAMILY)
Bombyx mori	protein	1	F:GO:0003824	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		C:GO:0016021; F:GO:0005375; P:GO:0006825		IPR007274; PTHR12483:SF4 (PANTHER)
	-	0				-
Caenorhabditis elegans	gtpase kras-like	16	P:GO:0007265; F:GO:0030275; F:GO:0019002; C:GO:0005739; P:GO:0043406; P:GO:0035176; P:GO:0019221; F:GO:0019003; P:GO:0051384; P:GO:0051000; C:GO:0045121; F:GO:0003924; P:GO:0051092; F:GO:0005525; C:GO:0005886; P:GO:0051385	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001806; IPR003577; IPR005225; IPR013753; IPR015592; IPR020849; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), SSF52540 (SUPERFAMILY)
Homo sapiens	major histocompatibility class dp beta 1	8	C:GO:0005789; C:GO:0042613; C:GO:0005794; P:GO:0002504; C:GO:0005765; C:GO:0016021; C:GO:0010008; P:GO:0006955	-		IPR003006; IPR003597; IPR007110; IPR013783; PTHR19944 (PANTHER), PTHR19944:SF26 (PANTHER), SSF48726 (SUPERFAMILY)

Homo sapiens	major histocompatibility class dp beta 1	8	C:GO:0005789; C:GO:0042613; C:GO:0005794; P:GO:0002504; C:GO:0005765; C:GO:0016021; C:GO:0010008; P:GO:0006955	-		-
synthetic construct	class member 1	8	C:GO:0005625; F:GO:0004559; C:GO:0005764; P:GO:0006013; P:GO:0006517; F:GO:0008270; P:GO:0007611; F:GO:0005537	-	EC:3.2.1.24	SignalP (SIGNALP)
Loa loa	rap ran-gap family protein	0		F:GO:0005096; P:GO:0051056; C:GO:0005622		-
Brugia malayi	cyclin-dependent ki-se 7	25	P:GO:0009299; P:GO:0006367; P:GO:0000718; P:GO:0006468; F:GO:0008094; F:GO:0008022; F:GO:0004693; C:GO:0005624; P:GO:0008283; P:GO:0030521; P:GO:0051301; P:GO:0000079; C:GO:0005829; C:GO:0005675; P:GO:0009792; F:GO:0003713; P:GO:0006368; C:GO:0005856; P:GO:0045448; P:GO:0045944; F:GO:0008353; F:GO:0032403; F:GO:0005524; F:GO:0050681; C:GO:0005739	-	EC:2.7.11.22; EC:2.7.11.23	IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF93 (PANTHER)
Caenorhabditis elegans	-dh oxidase	2	P:GO:0008152; F:GO:0003824	-		IPR001155; IPR013785; PTHR22893 (PANTHER), PTHR22893:SF6 (PANTHER), SSF51395 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	F:GO:0003824; P:GO:0008152	-		IPR002198; IPR002347; IPR016040; PTHR19410:SF18 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-smgl-1 protein	0				-
Caenorhabditis briggsae	btb poz domain containing protein	1	F:GO:0042802	-		IPR000210; IPR002083; IPR008974; IPR011333; IPR013069; IPR013089; IPR013322; PTHR23230:SF176 (PANTHER)

Caenorhabditis briggsae	btb poz domain containing protein	1	F:GO:0042802	-		IPR000210; IPR002083; IPR008974; IPR011333; IPR013069; IPR013089; IPR013322; PTHR23230:SF176 (PANTHER)
Caenorhabditis briggsae	myosin heavy chain	4	C:GO:0032982; F:GO:0003779; F:GO:0005524; F:GO:0003774	-		-
Caenorhabditis elegans	ect2 (mammalian rho gef) homolog family member (ect-2)	0		F:GO:0005089; P:GO:0035023; C:GO:0005622		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	yl54_caeel ame: full=uncharacterized protein	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	erythrocyte membrane protein	0		F:GO:0016874; C:GO:0016021; P:GO:0006898; F:GO:0008270; P:GO:0019915; P:GO:0009792; P:GO:0002119; P:GO:0040017; P:GO:0016246; P:GO:0040011; P:GO:0040010		-
Caenorhabditis elegans	leucyl-tr- synthetase	2	F:GO:0016874; P:GO:0006412	-	EC:3.6.5.3	-
	-	0				-
	-	0				-
Caenorhabditis briggsae	ubiquitin specific protease 24	0		F:GO:0004221; F:GO:0016787; F:GO:0003674; C:GO:0005575; P:GO:0006511; F:GO:0008234; F:GO:0008233; P:GO:0008150; F:GO:0005488		-
Caenorhabditis elegans	hydroxymethylglutaryl- synthase 1	10	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0018996; P:GO:0040010; P:GO:0008610; P:GO:0000003; P:GO:0040011; F:GO:0016740; P:GO:0006898	-		SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG06641 [Caenorhabditis briggsae]	0				IPR004114
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	novel protein	5	P:GO:0008380; C:GO:0005681; F:GO:0003723; F:GO:0005515; P:GO:0006397	-		IPR003890; IPR003891; IPR016021; IPR016024; PTHR18034 (PANTHER), PTHR18034:SF3 (PANTHER)

Caenorhabditis elegans	briggsae cbr-pri-1 protein	8	P:GO:0000910; P:GO:0040007; P:GO:0040035; F:GO:0016740; P:GO:0002119; C:GO:0044428; P:GO:0002009; P:GO:0009792	-		IPR002755; IPR014052; G3DSA:3.90.920.10 (GENE3D), SSF56747 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	muscle positioning protein 4	4	C:GO:0016021; F:GO:0004872; F:GO:0005509; F:GO:0005515	-		IPR000742; IPR006209; IPR006210; G3DSA:2.10.25.10 (GENE3D), PTHR22992 (PANTHER), PTHR22992:SF12 (PANTHER)
Caenorhabditis elegans	elongation factor-2 ki-se	2	F:GO:0005488; F:GO:0004674	-	EC:2.7.11.0	IPR006597; IPR011990; PTHR14187 (PANTHER), PTHR14187:SF2 (PANTHER), SSF81901 (SUPERFAMILY)
	-	0				-
Callithrix jacchus	glucose phosphate isomerase	10	P:GO:0001525; F:GO:0005125; C:GO:0005615; F:GO:0004347; P:GO:0006959; P:GO:0006096; P:GO:0007599; P:GO:0006094; C:GO:0005737; F:GO:0008083	-	EC:5.3.1.9	-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-tag-312 protein	0		F:GO:0003735; P:GO:0015031; F:GO:0000166; C:GO:0005737; P:GO:0006412; F:GO:0005525; P:GO:0006913; C:GO:0048471; C:GO:0005840; P:GO:0007165; P:GO:0006886; F:GO:0005515; C:GO:0005622; P:GO:0007264; F:GO:0005509		-
Caenorhabditis elegans	probable dolichyl pyrophosphate glc1man9 c2 alpha- -glucosyltransferase	3	F:GO:0000033; P:GO:0006487; C:GO:0016020	-		IPR004856; SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	hypothetical tyrosi-se-like protein in chromosome	4	F:GO:0005515; F:GO:0046872; F:GO:0016491; P:GO:0008152	-		IPR002227; IPR008922
Brugia malayi	n-glyca-se 1 isoform 2	3	C:GO:0005737; F:GO:0005488; P:GO:0006516	-		IPR002931; PTHR12143 (PANTHER), PTHR12143:SF2 (PANTHER), SSF54001 (SUPERFAMILY)
	-	0				-

Caenorhabditis elegans	erv1 alr family protein	4	P:GO:0045454; P:GO:0055114; F:GO:0016972; C:GO:0016020	-	EC:1.8.3.2	-
Brugia malayi	d- repair endonuclease xpf	9	P:GO:0000712; F:GO:0000014; P:GO:0000724; F:GO:0005515; F:GO:0003697; P:GO:0006296; P:GO:0009792; C:GO:0000110; P:GO:0000710	-		PTHR10150 (PANTHER)
Caenorhabditis briggsae	histone h2b	11	P:GO:0040010; C:GO:0000786; P:GO:0018991; P:GO:0040035; F:GO:0043565; C:GO:0035267; P:GO:0002119; P:GO:0040011; P:GO:0006334; P:GO:0009792; C:GO:0005811	-		IPR000558; IPR007125; IPR009072
Caenorhabditis briggsae	suppressor of 3-like 1	8	P:GO:0040010; F:GO:0005488; C:GO:0005739; P:GO:0000003; P:GO:0002119; P:GO:0006898; P:GO:0009792; F:GO:0016787	-		SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-prx-5 protein	12	F:GO:0005052; P:GO:0048699; C:GO:0016020; F:GO:0008022; P:GO:0016561; F:GO:0047485; P:GO:0030900; C:GO:0005829; P:GO:0006631; P:GO:0051262; C:GO:0005782; P:GO:0016477	-		IPR001440; IPR011990; IPR013026; IPR019734; PTHR10130 (PANTHER), SSF48452 (SUPERFAMILY)
Caenorhabditis elegans	ring finger and transmembrane domain-containing protein 2	0		F:GO:0046872; F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150; F:GO:0008270; F:GO:0005515; C:GO:0005575		PTHR15860 (PANTHER)
	-	0				-
	-	0				-
Brugia malayi	odr-3	2	F:GO:0019001; P:GO:0023052	-		IPR001019; IPR011025; G3DSA:3.40.50.300 (GENE3D), PTHR10218:SF60 (PANTHER), SSF52540 (SUPERFAMILY)

	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	-	5	F:GO:0015385; P:GO:0055085; P:GO:0006885; C:GO:0016021; P:GO:0006814	-		IPR018416; IPR018422
	-	0				-
Brugia malayi	guanylate cyclase	10	F:GO:0004383; F:GO:0004672; F:GO:0004872; F:GO:0005524; P:GO:0016199; P:GO:0007165; P:GO:0008045; C:GO:0005886; P:GO:0006468; P:GO:0006182	-	EC:4.6.1.2	IPR000719; IPR001054; IPR001245; IPR011009; IPR018297; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11920 (PANTHER), PTHR11920:SF50 (PANTHER)
Caenorhabditis briggsae	monoacylglycerol o-acyltransferase 2	8	C:GO:0016021; F:GO:0003846; F:GO:0016407; P:GO:0019432; P:GO:0006651; P:GO:0009792; P:GO:0050892; C:GO:0005783	-	EC:2.3.1.22	-
	-	0				-
	-	0				-
Caenorhabditis elegans	swi snf-related matrix-associated actin-dependent regulator of chromatin subfamily e member 1-related	5	C:GO:0043229; F:GO:0005488; P:GO:0045132; P:GO:0000003; P:GO:0006325	-		IPR000910; IPR009071; PTHR13711 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F45H11.3 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein F45H11.3 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein F45H11.3 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
	-	0				IPR003582; SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	ccr4-associated factor	15	P:GO:0006357; F:GO:0003676; P:GO:0000289; C:GO:0000932; P:GO:0007517; F:GO:0016251; P:GO:0040035; P:GO:0010171; P:GO:0002119; C:GO:0043186; P:GO:0048666; P:GO:0009792; F:GO:0016787; P:GO:0051729; C:GO:0005634	-		IPR006941; IPR012337; G3DSA:3.30.420.10 (GENE3D), PTHR10797 (PANTHER)

Caenorhabditis elegans	ccr4-associated factor	15	P:GO:0006357; F:GO:0003676; P:GO:0000289; C:GO:0000932; P:GO:0007517; F:GO:0016251; P:GO:0040035; P:GO:0010171; P:GO:0002119; C:GO:0043186; P:GO:0048666; P:GO:0009792; F:GO:0016787; P:GO:0051729; C:GO:0005634	-		IPR006941; IPR012337; G3DSA:3.30.420.10 (GENE3D), PTHR10797 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG14902 [Caenorhabditis briggsae]	6	P:GO:0010171; P:GO:0040018; P:GO:0018991; P:GO:0040017; P:GO:0040010; P:GO:0007413	-		-
Caenorhabditis elegans	cg9602 protein	3	P:GO:0051246; F:GO:0019787; P:GO:0043687	-		-
Caenorhabditis elegans	dad family protein	8	P:GO:0040035; P:GO:0002119; P:GO:0040011; P:GO:0040007; P:GO:0006898; P:GO:0045132; C:GO:0071013; P:GO:0002009	-		-
Caenorhabditis briggsae	multidrug resistance protein family member (mrp-1)	12	P:GO:0007427; P:GO:0055085; P:GO:0006941; F:GO:0008307; C:GO:0005863; F:GO:0000146; C:GO:0016021; F:GO:0042626; C:GO:0031672; F:GO:0005524; F:GO:0042803; P:GO:0030241	-		IPR001140; IPR003439; IPR003593; IPR011527; IPR017871; IPR017940; G3DSA:1.20.1560.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF35 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	lbp bpi cetp c-termi-l domain containing protein	6	P:GO:0009792; P:GO:0000003; P:GO:0040007; F:GO:0008289; P:GO:0002119; P:GO:0040011	-		IPR017942; IPR017943; G3DSA:3.15.10.10 (GENE3D), PTHR10504 (PANTHER), PTHR10504:SF14 (PANTHER)
Loa loa	myotubularin-related family protein	0		F:GO:0046872; P:GO:0016311; F:GO:0016791		IPR022096; PTHR10807 (PANTHER), PTHR10807:SF1 (PANTHER)
Caenorhabditis elegans	hypothetical protein R09F10.3 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				-
Loa loa	speckle-type poz protein	2	F:GO:0005515; P:GO:0000003	-		IPR000210; IPR011333; IPR013069

Brugia malayi	actin family protein	0		F:GO:0005515		-
Loa loa	pre-mr--processing-splicing factor 8	17	P:GO:0050896; F:GO:0003723; C:GO:0005681; P:GO:0045132; P:GO:0040007; C:GO:0016607; P:GO:0040027; P:GO:0040035; P:GO:0018996; P:GO:0007601; F:GO:0005515; P:GO:0040011; P:GO:0000398; C:GO:0005682; P:GO:0006898; P:GO:0002009; P:GO:0009792	-		IPR012591; PTHR11140 (PANTHER)
Caenorhabditis elegans	small subunit processome component 20 homolog	2	P:GO:0006364; C:GO:0005634	-		IPR011989; IPR016024
Caenorhabditis briggsae	briggsae cbr-sqv-8 protein	2	C:GO:0016020; F:GO:0015018	-	EC:2.4.1.135	SignalP (SIGNALP)
	-	0				-
	-	0				-
Nasonia vitripennis	polyribonucleotide nucleotidyltransferase 1	6	P:GO:0006402; C:GO:0005758; F:GO:0000175; F:GO:0003723; F:GO:0004654; P:GO:0006396	-	EC:2.7.7.8	IPR012162; IPR015847; SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; P:GO:0009792; F:GO:0005515		-
Caenorhabditis briggsae	phosphatidylinositol glycan anchor class n	4	C:GO:0005789; F:GO:0008484; F:GO:0016780; P:GO:0016254	-	EC:3.1.6.0; EC:2.7.8.0	IPR007070; IPR017852; SignalP (SIGNALP)
Caenorhabditis briggsae	tetratricopeptide repeat domain 1	2	P:GO:0006457; F:GO:0051082	-		IPR011990; IPR013026; IPR019734; IPR023114; PTHR22904 (PANTHER), PTHR22904:SF38 (PANTHER), SSF48452 (SUPERFAMILY)
Caenorhabditis briggsae	tetratricopeptide repeat domain 1	2	P:GO:0006457; F:GO:0051082	-		IPR011990; IPR013026; PTHR22904 (PANTHER), PTHR22904:SF38 (PANTHER), SSF48452 (SUPERFAMILY)
	-	0				-
Nematostella vectensis	mucin 1	1	P:GO:0008152	-		PR01217 (PRINTS)
	-	0				SignalP (SIGNALP)
Heliconius melpomene	endonuclease-reverse transcriptase	0		F:GO:0003723; P:GO:0006278; F:GO:0004519; F:GO:0003677; F:GO:0003964		IPR000477; IPR015706; PTHR19446:SF100 (PANTHER)
Caenorhabditis elegans	aarf domain containing ki-se 2	1	F:GO:0016740	-		SignalP (SIGNALP)
Brugia malayi	hr1 repeat family protein	1	F:GO:0016740	-		-
	-	0				-

Loa loa	elegans protein partially confirmed by transcript evidence	7	P:GO:0009792; P:GO:0002119; P:GO:0016246; P:GO:0040017; P:GO:0040010; P:GO:0019915; P:GO:0006898	-		-
Homo sapiens	lsm7 u6 small nuclear r- associated (cerevisiae)	6	P:GO:0006402; F:GO:0017070; C:GO:0030529; C:GO:0005634; F:GO:0046982; P:GO:0000398	-		IPR001163; IPR010920; G3DSA:2.30.30.100 (GENE3D), PTHR10553 (PANTHER), PTHR10553:SF1 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG08374 [Caenorhabditis briggsae]	0		F:GO:0005515		-
Brugia malayi	transmembrane 9 superfamily protein member 2	1	C:GO:0016021	-		IPR004240; PTHR10766:SF13 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	domain-containing protein	1	F:GO:0031072	-		PTHR15606 (PANTHER), PTHR15606:SF1 (PANTHER)
Caenorhabditis elegans	animal haem peroxidase family protein	4	F:GO:0020037; P:GO:0055114; F:GO:0004601; P:GO:0006979	-	EC:1.11.1.7	-
Caenorhabditis elegans	breast carcinoma amplified sequence 2	3	C:GO:0071011; P:GO:0000398; C:GO:0071013	-		IPR008409; PTHR13296 (PANTHER)
Caenorhabditis elegans	breast carcinoma amplified sequence 2	3	C:GO:0071011; P:GO:0000398; C:GO:0071013	-		IPR008409; PTHR13296 (PANTHER)
Loa loa	cpsf a subunit region family protein	5	P:GO:0006378; C:GO:0005847; F:GO:0003730; F:GO:0005515; P:GO:0006379	-		IPR004871; PTHR10644 (PANTHER), PTHR10644:SF2 (PANTHER)
Pongo abelii	matrix metalloprotei-se 11	7	F:GO:0004222; P:GO:0007275; C:GO:0005578; P:GO:0006508; F:GO:0005509; F:GO:0008270; P:GO:0030574	-	EC:3.4.24.0	SignalP (SIGNALP)
Caenorhabditis briggsae	domain member 1b	3	F:GO:0005088; C:GO:0005622; P:GO:0051056	-		IPR001895; IPR008937; PTHR23113:SF20 (PANTHER)
Caenorhabditis elegans	exosome complex exonuclease rrp45	7	P:GO:0040010; P:GO:0000003; P:GO:0002119; F:GO:0005515; P:GO:0009792; F:GO:0016787; C:GO:0005634	-		IPR015847; PTHR11097 (PANTHER), PTHR11097:SF8 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	P:GO:0009792	-		IPR011685
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	P:GO:0009792	-		IPR011685; SignalP (SIGNALP)

Brugia malayi	pyruvate ki-se	11	P:GO:0009792; F:GO:0004743; F:GO:0016830; C:GO:0005811; P:GO:0006725; P:GO:0016310; F:GO:0005515; F:GO:0030955; F:GO:0000287; P:GO:0006096; C:GO:0005829	-	EC:2.7.1.40	IPR001697; IPR015793; IPR015806; IPR015813
	-	0				PS51257 (PROFILE), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	abhydrolase domain containing 3	0		F:GO:0003674; F:GO:0016787; C:GO:0016021; C:GO:0016020; P:GO:0008150; F:GO:0004091; C:GO:0005575		IPR000073; IPR012020; G3DSA:3.40.50.1820 (GENE3D), PTHR10794 (PANTHER), PTHR10794:SF8 (PANTHER), SSF53474 (SUPERFAMILY)
Caenorhabditis briggsae	abhydrolase domain containing 3	0		F:GO:0003674; P:GO:0008152; F:GO:0016787; C:GO:0016021; C:GO:0016020; P:GO:0008150; F:GO:0004091; C:GO:0005575		IPR000073; IPR012020; G3DSA:3.40.50.1820 (GENE3D), PTHR10794 (PANTHER), PTHR10794:SF8 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
	-	0				-
	-	0				IPR013032
Caenorhabditis briggsae	histidyl-tr- synthetase	3	F:GO:0004812; P:GO:0006418; F:GO:0000166	-		IPR004516
Caenorhabditis elegans	calcium activated nucleotidase 1	6	P:GO:0040010; P:GO:0008340; F:GO:0017110; F:GO:0005515; C:GO:0005789; P:GO:0009191	-	EC:3.6.1.6	IPR009283; SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-pcp- protein	0		P:GO:0006508; F:GO:0008236		IPR008758; PTHR11010:SF6 (PANTHER)
						IPR003599; IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	homeobox protein	3	F:GO:0003677; P:GO:0045449; F:GO:0005515	-		IPR001356; IPR009057; IPR012287; IPR017970; PTHR19418 (PANTHER), PTHR19418:SF99 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG04746 [Caenorhabditis briggsae]	0		P:GO:0006898; P:GO:0002119; P:GO:0040007		-

Brugia malayi	protein arginine methyltransferase 8	14	P:GO:0040010; P:GO:0043393; F:GO:0035241; P:GO:0019919; F:GO:0008469; P:GO:0040011; F:GO:0046982; F:GO:0042803; P:GO:0002009; C:GO:0005737; C:GO:0005634; C:GO:0005886; F:GO:0035242; P:GO:0016571	-	EC:2.1.1.125	IPR010456; IPR018181; G3DSA:2.70.160.11 (GENE3D), G3DSA:3.40.50.150 (GENE3D), PTHR11006 (PANTHER), PTHR11006:SF19 (PANTHER), SSF53335 (SUPERFAMILY)
Brugia malayi	protein arginine methyltransferase 8	14	P:GO:0040010; P:GO:0043393; F:GO:0035241; P:GO:0019919; F:GO:0008469; P:GO:0040011; F:GO:0046982; F:GO:0042803; P:GO:0002009; C:GO:0005737; C:GO:0005634; C:GO:0005886; F:GO:0035242; P:GO:0016571	-	EC:2.1.1.125	-
Caenorhabditis elegans	cytohesin 3	7	C:GO:0005737; F:GO:0005085; P:GO:0045785; C:GO:0005886; F:GO:0005515; C:GO:0001726; F:GO:0005547	-		IPR000904; G3DSA:1.10.1000.11 (GENE3D), G3DSA:1.10.220.20 (GENE3D), PTHR10663 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	sig-l recognition particle 68	11	F:GO:0003729; P:GO:0040002; F:GO:0008312; P:GO:0040035; P:GO:0010507; P:GO:0002119; P:GO:0006898; P:GO:0009792; P:GO:0006614; P:GO:0040018; P:GO:0007040	-		PTHR12860 (PANTHER)
	-	0				SignalP (SIGNALP)
Rana catesbeiana	rho gdp-dissociation inhibitor 2	2	C:GO:0005737; F:GO:0005094	-		IPR000406; IPR014756; PTHR10980:SF5 (PANTHER)
	-	0				-

Caenorhabditis briggsae	golgin subfamily a member 5	5	C:GO:0031985; P:GO:0007030; P:GO:0048193; F:GO:0042803; C:GO:0016020	-		PTHR13815 (PANTHER)
Caenorhabditis briggsae	golgin subfamily a member 5	5	C:GO:0031985; P:GO:0007030; P:GO:0048193; F:GO:0042803; C:GO:0016020	-		PTHR13815 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Pongo abelii	insulin-like growth factor binding protein 7	13	P:GO:0051414; P:GO:0050810; P:GO:0007566; P:GO:0001558; C:GO:0005615; P:GO:0009408; P:GO:0008285; P:GO:0007155; P:GO:0032870; P:GO:0014070; F:GO:0005520; P:GO:0032526; C:GO:0031012	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	germ cell-less homolog 1	3	P:GO:0009987; F:GO:0042802; C:GO:0044428	-		PTHR23231 (PANTHER), PTHR23231:SF2 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	2-oxoglutarate and iron-dependent oxyge-se domain-containing protein 1	3	P:GO:0045132; F:GO:0016491; F:GO:0005488	-		IPR006620; PTHR12117 (PANTHER)
Loa loa	par-6 protein	16	F:GO:0005080; P:GO:0007369; C:GO:0043234; C:GO:0005923; P:GO:0045217; C:GO:0016021; P:GO:0040001; C:GO:0005938; P:GO:0007155; F:GO:0030742; P:GO:0030010; F:GO:0008134; P:GO:0016032; P:GO:0008406; F:GO:0017048; C:GO:0005634	-		SignalP (SIGNALP)

Caenorhabditis elegans	c-1-tetrahydrofolate cytoplasmic	14	P:GO:0046653; P:GO:0009086; P:GO:0006164; C:GO:0005739; P:GO:0006548; F:GO:0004488; P:GO:0055114; F:GO:0004477; F:GO:0016155; P:GO:0006730; F:GO:0005524; F:GO:0005515; F:GO:0004329; P:GO:0009396	-	EC:1.5.1.5; EC:3.5.4.9; EC:1.5.1.6; EC:6.3.4.3	IPR000559; IPR020628; G3DSA:3.30.1510.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR10025 (PANTHER), PTHR10025:SF4 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	briggsae cbr-ugt-62 protein	0		F:GO:0016740; F:GO:0030246; C:GO:0016021; F:GO:0016758; F:GO:0016757; P:GO:0005975; P:GO:0030259; P:GO:0040010; P:GO:0008152		SignalP (SIGNALP)
Caenorhabditis elegans	d--directed r- polymerase i subunit rpa1	7	F:GO:0003899; P:GO:0009303; C:GO:0005654; F:GO:0003677; C:GO:0005736; F:GO:0005515; F:GO:0008270	-	EC:2.7.7.6	IPR015699; PTHR19376 (PANTHER), SSF64484 (SUPERFAMILY)
Nematostella vectensis	n -(beta-n-acetylglucosaminyl)-l-asparagi-se	1	F:GO:0016787	-		IPR000246; PTHR10188:SF6 (PANTHER), SSF56235 (SUPERFAMILY)
Syngamus trachea	af370722_1intracellular globin	3	C:GO:0005576; F:GO:0005506; P:GO:0006810	-		IPR000971; IPR009050; IPR012292; SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	immunoglobulin i-set domain containing protein	0		C:GO:0005575		IPR003598; IPR003599; IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF11 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		-
Brugia malayi	hat family dimerisation domain containing protein	0		F:GO:0003676; F:GO:0046983		-
Caenorhabditis elegans	hypothetical protein Y54F10AR.2 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		-
Loa loa	zo- pellucida-like domain containing protein	0		F:GO:0005515		IPR001507; PTHR22907 (PANTHER)
	-	0				-
Pediculus humanus corporis	transportin 2 (importin karyopherin beta 2b)	4	F:GO:0005515; F:GO:0008565; F:GO:0008139; P:GO:0006886	-		IPR000357; IPR011989; IPR016024; PTHR10527 (PANTHER), PTHR10527:SF3 (PANTHER)
	-	0				-

	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0001851; C:GO:0005634; P:GO:0030449; C:GO:0005737; C:GO:0005576; F:GO:0043499; F:GO:0008201; P:GO:0006957; C:GO:0005886; C:GO:0005615; P:GO:0007155; F:GO:0005488		IPR000436; IPR016060; SignalP (SIGNALP)
	-	0				IPR000436; IPR016060; SignalP (SIGNALP)
Caenorhabditis elegans	-dh-ubiquinone oxidoreductase 42 kda subunit	8	P:GO:0009792; P:GO:0002119; P:GO:0006139; F:GO:0016773; P:GO:0040010; F:GO:0005524; P:GO:0000003; P:GO:0008340	-	EC:2.7.1.0	IPR002624; G3DSA:3.40.50.300 (GENE3D), PTHR10513:SF2 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
Loa loa	tpr repeat nuclear	5	P:GO:0009792; P:GO:0000003; P:GO:0040007; P:GO:0006898; P:GO:0002119	-		IPR011990; IPR013026; PTHR14027 (PANTHER), PTHR14027:SF2 (PANTHER), SSF48452 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	collagen protein confirmed by transcript evidence	0		C:GO:0016021; F:GO:0042302; P:GO:0009792		PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER)
Loa loa	elegans protein partially confirmed by transcript evidence	0				IPR019392
Caenorhabditis elegans	l-3-hydroxyacyl-coenzyme a short chain	12	P:GO:0006635; F:GO:0003857; F:GO:0005515; P:GO:0032868; P:GO:0014823; C:GO:0005743; P:GO:0046676; C:GO:0042645; F:GO:0050662; P:GO:0042493; F:GO:0016829; F:GO:0003985	-	EC:1.1.1.35; EC:2.3.1.9	IPR006108; IPR006176; IPR006180; IPR008927; IPR013328; IPR016040; PTHR23309 (PANTHER), SSF51735 (SUPERFAMILY)
Haemonchus contortus	galectin	2	F:GO:0005529; P:GO:0009987	-		-
	-	0				-
Caenorhabditis elegans	3-oxoacid transferase 1	3	P:GO:0046952; C:GO:0005739; F:GO:0008260	-	EC:2.8.3.5	IPR004163; IPR004165; G3DSA:3.40.1080.10 (GENE3D), PTHR13707:SF1 (PANTHER), SSF100950 (SUPERFAMILY)
Angiostrongylus cantonensis	mida_caeel ame: full=protein mida mitochondrial	0		F:GO:0003674; P:GO:0008150		IPR003788; PTHR12049 (PANTHER), SSF53335 (SUPERFAMILY)
	-	0				-

Caenorhabditis briggsae	wd repeat domain 43	0		F:GO:0003674; P:GO:0008150; C:GO:0005730; C:GO:0005634; C:GO:0005575		IPR007148
Caenorhabditis briggsae	wd repeat domain 43	0		F:GO:0003674; P:GO:0008150; C:GO:0005730; C:GO:0005634; C:GO:0005575		IPR007148
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Homo sapiens	immunoglobulin lambda light chain vlj region	0				IPR003596; IPR007110; IPR013106; IPR013783; PTHR23267 (PANTHER), PTHR23267:SF10 (PANTHER), SignalP (SIGNALP), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	general transcription factor iih subunit 2	16	P:GO:0006367; P:GO:0000718; F:GO:0008094; P:GO:0002031; P:GO:0040010; P:GO:0040011; F:GO:0047485; P:GO:0009411; F:GO:0046872; C:GO:0005675; P:GO:0009792; P:GO:0006368; F:GO:0008135; P:GO:0002119; P:GO:0010171; F:GO:0008353	-	EC:2.7.11.23	IPR000433; IPR004595; IPR007087; IPR015880; G3DSA:3.10.370.10 (GENE3D), PTHR12695 (PANTHER), PTHR12695:SF2 (PANTHER), SSF57889 (SUPERFAMILY)
Caenorhabditis elegans	microsomal triglyceride transfer protein	1	P:GO:0040011	-		PTHR13024 (PANTHER)
	-	0				-
	-	0				-
Loa loa	nematode cuticle collagen n-termi-l domain containing protein	4	P:GO:0009792; C:GO:0060107; F:GO:0005515; C:GO:0060111	-		IPR002486; SignalP (SIGNALP)
	-	0				-
	-	0				-
Brugia malayi	iron-sulfur cluster assembly 1 homolog (cerevisiae)	10	P:GO:0009792; P:GO:0002119; F:GO:0046872; P:GO:0016226; F:GO:0003676; F:GO:0051536; P:GO:0040010; P:GO:0006898; C:GO:0005739; F:GO:0005198	-		-
	-	0				-
Saccoglossus kowalevskii	major facilitator superfamily domain-containing protein 5	0		C:GO:0016021; C:GO:0016020; P:GO:0006810		IPR008509; SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-

Loa loa	hypothetical protein LOAG_06899 [Loa loa]	0				-
Loa loa	hypothetical protein LOAG_06899 [Loa loa]	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	7	P:GO:0045454; P:GO:0009792; F:GO:0016491; P:GO:0040007; F:GO:0016209; F:GO:0005515; P:GO:0002119	-		-
Caenorhabditis elegans	polymerase ii (d- directed) polypeptide 33kda	7	F:GO:0004672; P:GO:0006367; P:GO:0008380; C:GO:0005665; F:GO:0005515; P:GO:0006368; C:GO:0005737	-		IPR011262; IPR011263; PTHR11800 (PANTHER), PTHR11800:SF2 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG16021 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-col-142 protein	0		C:GO:0016021; P:GO:0040011; F:GO:0042302		IPR002486; SignalP (SIGNALP)
Caenorhabditis elegans	phospholipase b-like 2 precursor (lami- ancestor homolog 2) (lama-like protein 2) (76 kda protein) (kda protein)	0		F:GO:0016787; P:GO:0008150; C:GO:0043202; P:GO:0016042; C:GO:0005575		IPR007000
Caenorhabditis elegans	l-isoaspartyl protein carboxyl methyltransferase	3	C:GO:0005737; P:GO:0006464; F:GO:0004719	-	EC:2.1.1.77	SignalP (SIGNALP)
Caenorhabditis elegans	l-isoaspartyl protein carboxyl methyltransferase	3	C:GO:0005737; P:GO:0006464; F:GO:0004719	-	EC:2.1.1.77	-
Oryctolagus cuniculus	n-acetyltransferase 10	5	C:GO:0005730; F:GO:0008080; F:GO:0005515; F:GO:0005524; P:GO:0008152	-		PTHR10925 (PANTHER), PTHR10925:SF5 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Loa loa	glycosyl hydrolases family 31 protein	8	P:GO:0009792; P:GO:0002119; P:GO:0005975; C:GO:0005875; F:GO:0030246; F:GO:0005515; F:GO:0004558; P:GO:0040007	-	EC:3.2.1.20	IPR000322; IPR017853; PTHR22762:SF7 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	C:GO:0005576	-		-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	initiation factor 4g family member (ifg-1)	0		F:GO:0005488; P:GO:0016070; F:GO:0005515; C:GO:0005575		IPR003890; IPR016021; IPR016024; PTHR23253 (PANTHER), PTHR23253:SF4 (PANTHER)
Caenorhabditis elegans	initiation factor 4g family member (ifg-1)	0		F:GO:0005488; P:GO:0016070; F:GO:0005515; C:GO:0005575		IPR003890; IPR016021; IPR016024; PTHR23253 (PANTHER), PTHR23253:SF4 (PANTHER)

Caenorhabditis elegans	utp21 specific wd40 associated domain containing protein	0		C:GO:0032040; P:GO:0006364		-
Caenorhabditis elegans	briggsae cbr-tag-123 protein	1	C:GO:0016021	-		SignalP (SIGNALP)
Caenorhabditis briggsae	membrane palmitoylated 5 (maguk p55 subfamily member 5)	6	C:GO:0005737; P:GO:0009792; C:GO:0005886; F:GO:0005515; P:GO:0040010; C:GO:0005634	-		IPR001452; IPR001478; IPR011511; G3DSA:2.30.30.40 (GENE3D), G3DSA:2.30.42.10 (GENE3D), PTHR23122 (PANTHER), PTHR23122:SF5 (PANTHER)
Caenorhabditis briggsae	membrane palmitoylated 5 (maguk p55 subfamily member 5)	6	C:GO:0005737; P:GO:0009792; C:GO:0005886; F:GO:0005515; P:GO:0040010; C:GO:0005634	-		IPR001452; IPR001478; IPR011511; G3DSA:2.30.30.40 (GENE3D), G3DSA:2.30.42.10 (GENE3D), PTHR23122 (PANTHER), PTHR23122:SF5 (PANTHER)
Caenorhabditis elegans	uncharacterized protein	3	F:GO:0004222; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	IPR007863; IPR011237; IPR011249; IPR011765; PTHR11851 (PANTHER), PTHR11851:SF68 (PANTHER)
Caenorhabditis elegans	ryanodine receptor 2	20	F:GO:0005219; P:GO:0032026; C:GO:0005792; P:GO:0006816; C:GO:0019717; P:GO:0051592; F:GO:0051018; F:GO:0005509; C:GO:0016021; C:GO:0033017; P:GO:0051480; P:GO:0006629; C:GO:0043234; P:GO:0042493; P:GO:0050794; C:GO:0030018; P:GO:0055085; F:GO:0004872; P:GO:0007584; P:GO:0031000	-		IPR001870; IPR003877; IPR008985; IPR015925; PTHR13715:SF11 (PANTHER)
Brugia malayi	mediator complex subunit rgr-1	5	P:GO:0040007; P:GO:0045449; P:GO:0002119; P:GO:0009792; C:GO:0005634	-		IPR013947; PTHR12809 (PANTHER)
Brugia malayi	mediator complex subunit rgr-1	5	P:GO:0040007; P:GO:0045449; P:GO:0002119; P:GO:0009792; C:GO:0005634	-		IPR013947; PTHR12809 (PANTHER)
Brugia malayi	mediator complex subunit rgr-1	5	P:GO:0040007; P:GO:0045449; P:GO:0002119; P:GO:0009792; C:GO:0005634	-		IPR013947; PTHR12809 (PANTHER)
Caenorhabditis briggsae	alanine-glyoxylate aminotransferase (oxalosis i hyperoxaluria i glycolicaciduria serine-pyruvate aminotransferase)	2	P:GO:0008152; F:GO:0008483	-	EC:2.6.1.0	IPR015421; IPR015424; PTHR21152 (PANTHER), PTHR21152:SF5 (PANTHER), SignalP (SIGNALP)

Ancylostoma ceylanicum	metalloprotease 1 precursor	3	F:GO:0004222; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	IPR001506; IPR006026; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	cdc-42 guanine nucleotide exchange factor family member (cgef-1)	0		F:GO:0003676; P:GO:0015074; F:GO:0005089; P:GO:0035023; P:GO:0023034; F:GO:0003677; F:GO:0005085; C:GO:0005622		-
Loa loa	fibroblast growth factor receptor substrate 3	2	P:GO:0009792; P:GO:0000003	-		IPR002404; IPR011993; PTHR21258 (PANTHER), SSF50729 (SUPERFAMILY)
Ciona intestinalis	phospholipid-transporting atpase 1-like protein	5	F:GO:0043492; F:GO:0005488; F:GO:0022892; F:GO:0016820; C:GO:0016020	-	EC:3.6.3.0	-
	-	0				-
	-	0				-
Caenorhabditis elegans	nitrilase	3	F:GO:0016810; P:GO:0000003; P:GO:0006807	-		IPR000132; IPR003010; PTHR23088 (PANTHER)
Caenorhabditis elegans	sand family protein	0				IPR004353
Caenorhabditis elegans	sand family protein	0				IPR004353
Drosophila mojavensis	kek2 precursor	0		F:GO:0005515; C:GO:0005886		-
Caenorhabditis elegans	hypothetical protein F54A3.1 [Caenorhabditis elegans]	0				IPR021133
Candidatus Nitrospira defluvii	atp-dependent protease la	10	C:GO:0009295; P:GO:0006259; F:GO:0004176; F:GO:0043565; F:GO:0005524; F:GO:0004252; P:GO:0016485; C:GO:0005782; P:GO:0006950; P:GO:0006515	-	EC:3.4.21.0	IPR001984; IPR008269; IPR020568; PTHR10046 (PANTHER)
Loa loa	protein ki-se domain containing protein	4	P:GO:0040022; F:GO:0016301; F:GO:0005515; P:GO:0051729	-		IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
Caenorhabditis elegans	cg16787 cg16787-pa	0				IPR018790
	-	0				-
	-	0				-
Loa loa	proteolipid protein m6-1	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Ciona intestinalis	PREDICTED: hypothetical protein [Cio- intesti-lis]	0				-
Loa loa	plasmid mainte-nce protein containing protein	3	C:GO:0031224; F:GO:0016740; C:GO:0005783	-		IPR005599; SignalP (SIGNALP)
	-	0				-

Caenorhabditis briggsae	Hypothetical protein CBG08796 [Caenorhabditis briggsae]	4	P:GO:0040010; P:GO:0040035; P:GO:0002119; P:GO:0006898	-		-
	-	0				-
Caenorhabditis briggsae	prp38 pre-mr- processing factor 38 domain containing b	1	F:GO:0004437	-		IPR005037
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	P:GO:0044238; P:GO:0006915	-		IPR002213; G3DSA:3.40.50.2000 (GENE3D), PTHR11926:SF3 (PANTHER), SSF53756 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	domain-containing histone demethylation protein 1d	9	F:GO:0032454; F:GO:0071558; F:GO:0046914; P:GO:0071557; P:GO:0030901; F:GO:0016706; P:GO:0033169; F:GO:0005515; P:GO:0045893	-	EC:1.14.11.0	IPR003347; PTHR23123 (PANTHER), SSF51197 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	autophagy-related protein 101	0		C:GO:0000407; P:GO:0006914; C:GO:0005737; P:GO:0000045; F:GO:0032403		IPR012445
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		-
Caenorhabditis elegans	briggsae cbr-nlp-36 protein	1	F:GO:0005515	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Vanderwaltozyma polyspora DSM 70294	mucin 30e	1	F:GO:0005488	-		-

Vanderwaltozyma polyspora DSM 70294	mucin 30e	0		P:GO:0006030; P:GO:0000902; F:GO:0016787; P:GO:0006468; F:GO:0004553; P:GO:0005975; F:GO:0008658; C:GO:0030016; F:GO:0005524; F:GO:0016301; F:GO:0008237; C:GO:0016021; C:GO:0016020; F:GO:0031432; F:GO:0004674; F:GO:0008061; C:GO:0005618; F:GO:0004568; F:GO:0008233; F:GO:0004672; F:GO:0016798; F:GO:0043169; F:GO:0004222; P:GO:0008152; F:GO:0003824; F:GO:0000166; P:GO:0007599;		-
Loa loa	tata binding protein associated factor	0		F:GO:0008237; F:GO:0008270		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	transmembrane cell adhesion receptor mua-3	4	C:GO:0016021; F:GO:0004872; F:GO:0005509; F:GO:0005515	-		IPR000082; IPR000152; IPR000742; IPR006209; IPR006210; G3DSA:2.10.25.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF245 (PANTHER), SSF57196 (SUPERFAMILY)
Caenorhabditis elegans	d-aspartate oxidase	6	P:GO:0009792; P:GO:0055114; F:GO:0003884; F:GO:0005488; F:GO:0008445; F:GO:0047821	-	EC:1.4.3.3; EC:1.4.3.1; EC:1.4.3.7	PTHR11530 (PANTHER)
Caenorhabditis briggsae	mitochondrial r- polymerase	4	P:GO:0040010; P:GO:0000003; P:GO:0007413; P:GO:0006898	-		IPR002092; G3DSA:1.10.1320.10 (GENE3D), SSF56672 (SUPERFAMILY)
Caenorhabditis elegans	proteasome a-type and b-type family protein	9	P:GO:0009792; P:GO:0002119; F:GO:0004175; C:GO:0005839; P:GO:0000003; P:GO:0008340; P:GO:0040011; P:GO:0040007; P:GO:0051603	-		-
Caenorhabditis elegans	phosphatase regulatory subunit family protein	0				IPR005036; PTHR12307 (PANTHER)

Brugia malayi	d--directed r- polymerases and iii subunit rpabc5	10	F:GO:0003899; F:GO:0008270; P:GO:0006356; F:GO:0004672; P:GO:0006367; P:GO:0008380; C:GO:0005665; F:GO:0003677; P:GO:0006368; P:GO:0009792	-	EC:2.7.7.6	-
	-	0				-
	-	0				-
	-	0				IPR008518
Caenorhabditis elegans	briggsae cbr-dhs-7 protein	3	P:GO:0008152; F:GO:0016491; F:GO:0005488	-		IPR002198; IPR002347; IPR016040; PTHR19410:SF99 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	malic enzyme -dp(+)- mitochondrial	10	P:GO:0009060; F:GO:0046872; P:GO:0006090; F:GO:0051287; C:GO:0005759; F:GO:0016619; P:GO:0006108; P:GO:0055114; F:GO:0004473; P:GO:0006800	-	EC:1.1.1.38; EC:1.1.1.40	IPR012302; IPR016040; PTHR23406 (PANTHER), PTHR23406:SF2 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis briggsae	cell cycle control atpase	5	P:GO:0006357; F:GO:0016455; C:GO:0016592; F:GO:0003824; F:GO:0030170	-		IPR011063; IPR014729; PTHR11807 (PANTHER), PTHR11807:SF4 (PANTHER), SSF52402 (SUPERFAMILY)
Loa loa	traf interacting protein	3	P:GO:0006917; P:GO:0008283; F:GO:0005515	-		IPR001841; IPR007087; IPR013083; IPR018957; PTHR22937 (PANTHER), PTHR22937:SF6 (PANTHER), SignalP (SIGNALP), SSF57850 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Ailuropoda melanoleuca	ribosomal protein s13	7	F:GO:0003729; C:GO:0005730; F:GO:0003735; P:GO:0006414; C:GO:0022627; P:GO:0033119; F:GO:0005515	-		IPR012606; PTHR11885 (PANTHER), PTHR11885:SF1 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	glutaredoxin 2	4	P:GO:0045454; C:GO:0043231; C:GO:0044444; F:GO:0015035	-		IPR002109; IPR012335; IPR012336; IPR014025; PTHR10168 (PANTHER), PTHR10168:SF19 (PANTHER)
	-	0				-

Caenorhabditis elegans	suppressor of ypt1	5	P:GO:0031101; P:GO:0018996; P:GO:0006904; P:GO:0000003; P:GO:0006898	-		IPR001619; G3DSA:3.40.50.2060 (GENE3D), PTHR11679:SF2 (PANTHER)
	-	0				-
Pongo abelii	ubiquitin-like modifier activating enzyme 1	6	P:GO:0008219; F:GO:0005524; F:GO:0008641; F:GO:0005515; P:GO:0006464; F:GO:0016874	-		IPR000127; IPR009036; IPR016040; IPR018965; PTHR10953 (PANTHER), PTHR10953:SF1 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0005488		IPR003961; IPR008957; IPR013783; PR00014 (PRINTS), PTHR19900 (PANTHER), PTHR19900:SF7 (PANTHER)
Caenorhabditis briggsae	fatty acid synthase	15	F:GO:0008144; F:GO:0004312; P:GO:0006633; F:GO:0016788; F:GO:0008270; F:GO:0016829; C:GO:0005625; C:GO:0005739; P:GO:0055114; P:GO:0006084; F:GO:0000036; F:GO:0016491; F:GO:0070402; F:GO:0042803; C:GO:0042587	-	EC:2.3.1.85	-
Caenorhabditis briggsae	briggsae cbr-pad-1 protein	1	P:GO:0006810	-		-
Kordia algicida OT-1	late embryogenesis abundant protein	0		F:GO:0032934		PTHR23241 (PANTHER), PTHR23241:SF11 (PANTHER)
Kordia algicida OT-1	conserved domain protein	0				PTHR23241 (PANTHER), PTHR23241:SF11 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	mediator complex subunit 4	9	P:GO:0018991; P:GO:0006357; P:GO:0007517; F:GO:0016455; C:GO:0016592; F:GO:0003713; P:GO:0002009; P:GO:0009792; P:GO:0048813	-		IPR019258; PTHR13208 (PANTHER)
Caenorhabditis elegans	pdf (arthropod pigment dispersing factor) homolog family member (pdf-1)	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	domain member 1b	3	F:GO:0005085; C:GO:0005622; P:GO:0051056	-		IPR000651; IPR008937; G3DSA:1.20.870.10 (GENE3D), PTHR23113:SF20 (PANTHER)
	-	0				-
	-	0				-

Caenorhabditis elegans	hypothetical protein T24B8.7 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	hypothetical kda protein in chromosome	2	P:GO:0040010; P:GO:0009792	-		-
Caenorhabditis elegans	hypothetical kda protein in chromosome	2	P:GO:0040010; P:GO:0009792	-		SignalP (SIGNALP)
Caenorhabditis briggsae	cd63 antigen	0		C:GO:0016021; C:GO:0016020		IPR008952; IPR018499; G3DSA:1.10.1450.10 (GENE3D), PTHR19282 (PANTHER), PTHR19282:SF13 (PANTHER)
Brugia malayi	5 -nucleotidase	2	F:GO:0016787; F:GO:0005488	-		IPR006434; PF05822 (PFAM), SSF56784 (SUPERFAMILY)
	-	0				-
	-	0				-
Homo sapiens	-dh dehydroge-se	14	C:GO:0005654; P:GO:0017148; F:GO:0005515; F:GO:0008137; P:GO:0030262; C:GO:0016021; P:GO:0045892; P:GO:0022900; P:GO:0008624; C:GO:0005747; P:GO:0030308; P:GO:0006606; F:GO:0005524; P:GO:0006800	-	EC:1.6.5.3	-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis briggsae	briggsae cbr-ttr-45 protein	0				IPR001534; SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR001534; SignalP (SIGNALP)
	-	0				-
	-	0				-
Tetraodon nigroviridis	ca-licular multispecific organic anion transporter 1	2	F:GO:0003824; C:GO:0016020	-		IPR005291; PTHR19242 (PANTHER)
Caenorhabditis elegans	zinc c2h2 type family protein	6	P:GO:0009792; P:GO:0000003; C:GO:0005622; P:GO:0040007; F:GO:0008270; P:GO:0002119	-		IPR015880; PTHR23224 (PANTHER), PTHR23224:SF469 (PANTHER), SSF57667 (SUPERFAMILY)
Branchiostoma floridae	homologous-pairing protein 2 homolog	0		F:GO:0004872; P:GO:0008150; P:GO:0006310; P:GO:0007126; C:GO:0005634; C:GO:0005575		IPR010776
Branchiostoma floridae	homologous-pairing protein 2 homolog	0		F:GO:0004872; P:GO:0008150; P:GO:0006310; P:GO:0007126; C:GO:0005634; C:GO:0005575		IPR010776

Medicago truncatula	gtp-binding protein ypt3	8	C:GO:0005768; F:GO:0005525; C:GO:0009504; C:GO:0005886; P:GO:0000910; F:GO:0016787; P:GO:0007264; P:GO:0015031	-		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	isocitrate dehydroge-se	21	P:GO:0006979; P:GO:0006097; C:GO:0005829; P:GO:0008340; P:GO:0048545; P:GO:0006103; C:GO:0005777; C:GO:0005625; C:GO:0005739; P:GO:0008585; P:GO:0055114; P:GO:0006749; P:GO:0006099; F:GO:0051287; F:GO:0004450; F:GO:0000287; P:GO:0014070; P:GO:0006740; P:GO:0006102; F:GO:0042803; F:GO:0050661	-	EC:1.1.1.42	-
Caenorhabditis elegans	hypothetical protein C34G6.1 [Caenorhabditis elegans]	1	F:GO:0005488	-		-
Caenorhabditis elegans	furry homolog	1	F:GO:0005515	-		PTHR12295 (PANTHER), PTHR12295:SF6 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-tag-281 protein	0				IPR019319; PTHR13411 (PANTHER)
Caenorhabditis elegans	protein fam20c	0				IPR009581; PTHR12450:SF8 (PANTHER), PF06702 (PFAM), SignalP (SIGNALP)
Haemonchus contortus	microsomal aminopeptidase	5	C:GO:0016021; F:GO:0008237; P:GO:0006508; F:GO:0008270; F:GO:0004177	-	EC:3.4.11.0	IPR001930; PTHR11533:SF29 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	btb poz domain containing protein	0		F:GO:0005515		-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG02620 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	hypothetical protein K12B6.4 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	inositol -trisphosphate receptor	5	P:GO:0006816; F:GO:0005220; P:GO:0055085; C:GO:0016021; C:GO:0005783	-		IPR000699; IPR015925; PTHR13715:SF2 (PANTHER)

	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0005515		-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0005515		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-twk-2 protein	4	C:GO:0016021; P:GO:0006813; F:GO:0005267; P:GO:0055085	-		IPR013099; G3DSA:1.10.287.70 (GENE3D), PTHR11003 (PANTHER), PTHR11003:SF7 (PANTHER), SignalP (SIGNALP), SSF81324 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein F55E10.7 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	thioredoxin-like protein 4a	8	C:GO:0071011; P:GO:0000245; P:GO:0007052; P:GO:0051301; F:GO:0005515; P:GO:0007067; C:GO:0005682; C:GO:0005737	-		IPR004123; IPR012335; IPR012336
	-	0				-
Caenorhabditis briggsae	protein pelota homolog	4	F:GO:0005488; F:GO:0004518; P:GO:0006412; C:GO:0044424	-	EC:3.6.5.3	IPR004405; IPR005142; G3DSA:3.30.1330.30 (GENE3D), SSF55315 (SUPERFAMILY)
Caenorhabditis elegans	lung seven transmembrane receptor family protein	0		F:GO:0004872; C:GO:0016021		-
Caenorhabditis elegans	lon peptidase peroxisomal	11	F:GO:0008236; F:GO:0000166; P:GO:0006465; P:GO:0006139; P:GO:0014070; P:GO:0006508; F:GO:0016887; F:GO:0019899; C:GO:0005634; C:GO:0005782; P:GO:0044248	-		IPR001984; IPR003111; IPR003593; IPR003959; IPR008268; IPR008269; IPR015947; IPR020568; G3DSA:1.10.8.60 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR10046 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	mitochondrial ribosomal protein	8	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; P:GO:0040010; P:GO:0000003; P:GO:0006412; C:GO:0005739	-	EC:3.6.5.3	SignalP (SIGNALP)
Caenorhabditis elegans	toll-interacting protein	5	F:GO:0035325; P:GO:0016310; C:GO:0044464; P:GO:0007165; F:GO:0019900	-		IPR000008; IPR003892; IPR008973; IPR009060; G3DSA:1.10.8.10 (GENE3D), G3DSA:2.60.40.150 (GENE3D)

Homo sapiens	galactoside- 3 binding protein	9	F:GO:0005044; C:GO:0005615; F:GO:0005515; P:GO:0007155; P:GO:0007165; C:GO:0016020; C:GO:0005634; C:GO:0005578; P:GO:0006968	-		-
	-	0				-
Caligus rogercresseyi	beta-ureidopropio-se	5	P:GO:0006807; C:GO:0005829; F:GO:0046872; P:GO:0000003; F:GO:0003837	-	EC:3.5.1.6	IPR003010; PTHR23088 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG12788 [Caenorhabditis briggsae]	0		F:GO:0046872; P:GO:0045132; F:GO:0008270		IPR001781; PTHR18973 (PANTHER), PTHR18973:SF98 (PANTHER)
Brugia malayi	lim domain containing protein	1	F:GO:0008270	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-dnj-1 protein	4	P:GO:0006457; P:GO:0040011; F:GO:0031072; F:GO:0051082	-		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	C:GO:0005829; F:GO:0019901; F:GO:0019887	-		IPR002110; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER), PTHR18958:SF283 (PANTHER)
Loa loa	novel protein vertebrate denn madd domain containing 1 family	0				IPR005113; PTHR13196 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	rab gtpase activating protein 1-like	6	F:GO:0005097; P:GO:0032880; C:GO:0005769; P:GO:0032313; C:GO:0005794; C:GO:0005634	-		IPR000195; G3DSA:1.10.8.270 (GENE3D), PTHR22957 (PANTHER), PTHR22957:SF40 (PANTHER)
Homo sapiens	heat shock protein hsp 90-beta	13	C:GO:0005739; P:GO:0006457; F:GO:0030235; P:GO:0060334; P:GO:0001890; C:GO:0042470; F:GO:0005524; P:GO:0032435; F:GO:0030911; P:GO:0060338; F:GO:0051082; P:GO:0006986; P:GO:0045429	-		IPR001404; IPR020576; SSF110942 (SUPERFAMILY)
	-	0				-
	-	0				-

Loa loa	briggsae cbr-let-19 protein	3	P:GO:0050794; P:GO:0009792; P:GO:0006366	-		PTHR12950 (PANTHER), PTHR12950:SF3 (PANTHER)
Loa loa	briggsae cbr-let-19 protein	3	P:GO:0050794; P:GO:0009792; P:GO:0006366	-		PTHR12950 (PANTHER), PTHR12950:SF3 (PANTHER)
Loa loa	briggsae cbr-let-19 protein	3	P:GO:0050794; P:GO:0009792; P:GO:0006366	-		PTHR12950 (PANTHER), PTHR12950:SF3 (PANTHER)
Caenorhabditis elegans	uncoordi-ted family member (unc-26)	10	C:GO:0012506; P:GO:0050803; F:GO:0000166; F:GO:0004445; F:GO:0003723; P:GO:0016311; F:GO:0004439; C:GO:0043195; P:GO:0048790; P:GO:0048488	-	EC:3.1.3.56; EC:3.1.3.36	IPR005135; G3DSA:3.60.10.10 (GENE3D), PTHR11200 (PANTHER), PTHR11200:SF10 (PANTHER)
Caenorhabditis briggsae	glucose-6-phosphate dehydroge-se	4	P:GO:0006006; F:GO:0004345; P:GO:0055114; F:GO:0005488	-	EC:1.1.1.49	IPR001282; IPR022675; G3DSA:3.30.360.10 (GENE3D), SSF55347 (SUPERFAMILY)
Caenorhabditis briggsae	glucose-6-phosphate dehydroge-se	4	P:GO:0006006; F:GO:0004345; P:GO:0055114; F:GO:0005488	-	EC:1.1.1.49	IPR001282; IPR022675; G3DSA:3.30.360.10 (GENE3D), SSF55347 (SUPERFAMILY)
	-	0				-
	-	0				-
Ailuropoda melanoleuca	cyclin-dependent ki-se 2-associated protein 1	8	C:GO:0005737; P:GO:0006261; P:GO:0000084; P:GO:0006468; F:GO:0003677; F:GO:0016301; F:GO:0005515; C:GO:0005634	-		IPR019187; PTHR22607 (PANTHER)
Pongo abelii	c10	0		F:GO:0003674; P:GO:0008150		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	6	P:GO:0009792; F:GO:0042626; C:GO:0005886; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		IPR003439; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF96 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0019915; P:GO:0040018; P:GO:0040011	-		IPR000615; IPR021134; SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	C:GO:0005739	-		PTHR11089 (PANTHER), PTHR11089:SF1 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	C:GO:0005739	-		PTHR11089 (PANTHER), PTHR11089:SF1 (PANTHER)
	-	0				-
	-	0				-
	-	0				-

Takifugu obscurus	slc26a5 6-like anion exchanger	4	C:GO:0016021; F:GO:0008271; P:GO:0008272; P:GO:0055085	-		PTHR11814 (PANTHER), PTHR11814:SF25 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	spectrin alpha	10	C:GO:0005829; F:GO:0005516; C:GO:0015630; F:GO:0005509; C:GO:0005624; C:GO:0008091; F:GO:0004725; F:GO:0003779; F:GO:0005200; P:GO:0051693	-	EC:3.1.3.48	IPR002017; IPR018159; G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF6 (PANTHER), SSF46966 (SUPERFAMILY)
Loa loa	egg laying defective family member (egl-15)	2	F:GO:0005488; F:GO:0016301	-		IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF7 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	cytochrome c oxidase assembly protein cox11 containing protein	4	F:GO:0005507; C:GO:0005743; F:GO:0016787; F:GO:0008270	-		IPR007533; SignalP (SIGNALP)
Camponotus floridanus	rcc1 domain-containing protein 1	0				IPR000408; IPR009091; PTHR22870 (PANTHER), PTHR22870:SF27 (PANTHER)
Caenorhabditis elegans	metallo-beta-lactamase superfamily protein	0		P:GO:0008033; C:GO:0005634; F:GO:0016787; C:GO:0005739; C:GO:0005575; F:GO:0005515; F:GO:0004519; F:GO:0046872; F:GO:0004518; P:GO:0008150		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis briggsae	presenilin 1	45	C:GO:0043198; P:GO:0016048; C:GO:0016324; P:GO:0016485; P:GO:0007268; C:GO:0005783; P:GO:0048534; P:GO:0009790; C:GO:0031594; C:GO:0035253; P:GO:0030900; C:GO:0012505; P:GO:0007220; C:GO:0045121; P:GO:0006509; P:GO:0032469; P:GO:0006916; C:GO:0030424; P:GO:0007165; P:GO:0007219; F:GO:0004175; P:GO:0048518; P:GO:0010646; P:GO:0030182; C:GO:0005887; C:GO:0048471; C:GO:0005794;	-		IPR001108; IPR001686; IPR006639
	-	0				-
	-	0				SignalP (SIGNALP)
						IPR003599; IPR003961; IPR008957; IPR013098; IPR013783; PR00014 (PRINTS), PTHR19900 (PANTHER), PTHR19900:SF7 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	homology domain containing protein	0				-
Caenorhabditis elegans	tomosyn sy-ptic protein family member (tom-1)	2	P:GO:0016079; C:GO:0044464	-		IPR001680; IPR011046; IPR015943; PTHR10241 (PANTHER), PTHR10241:SF11 (PANTHER)
Caenorhabditis briggsae	mitochondrial ribosomal protein l3	3	C:GO:0005840; F:GO:0003735; P:GO:0006412	-	EC:3.6.5.3	IPR000597; IPR009000; G3DSA:2.40.30.10 (GENE3D), G3DSA:4.10.960.10 (GENE3D), PTHR11229 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	yl54_caeel ame: full=uncharacterized protein	0				-
Caenorhabditis elegans	a (sy-ptic dy-min binding protein) homolog family member (sdpn-1)	1	F:GO:0005515	-		IPR001060; PTHR10959 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-

Caenorhabditis briggsae	archain 1	8	C:GO:0030126; P:GO:0006890; P:GO:0018996; P:GO:0006891; C:GO:0030131; P:GO:0002119; F:GO:0005515; P:GO:0006886	-		IPR011012; IPR022775; G3DSA:3.30.450.60 (GENE3D), PTHR10121 (PANTHER)
Caenorhabditis elegans	ubiquitin specific peptidase 46	7	F:GO:0004843; P:GO:0016579; F:GO:0005515; P:GO:0032228; P:GO:0006511; F:GO:0004221; P:GO:0007610	-	EC:3.1.2.15	IPR001394; PTHR10420 (PANTHER), PTHR10420:SF54 (PANTHER), SSF54001 (SUPERFAMILY)
Trypanosoma brucei gambiense DAL972	golgin subfamily a member 5	5	P:GO:0009987; F:GO:0005515; C:GO:0044431; F:GO:0016787; C:GO:0016020	-		PD936484 (PRODOM)
	-	0				-
Brugia malayi	u6 snr--specific termi-l uridylyltransferase 1	0		F:GO:0016740; P:GO:0071044; F:GO:0050265; C:GO:0005634; F:GO:0003676; F:GO:0000166; F:GO:0003674; F:GO:0008270; F:GO:0003723; F:GO:0016779; C:GO:0005575; C:GO:0005730; C:GO:0005622; P:GO:0008152; P:GO:0008150		PTHR12271 (PANTHER), PTHR12271:SF11 (PANTHER), SSF81631 (SUPERFAMILY)
Brugia malayi	u6 snr--specific termi-l uridylyltransferase 1	0		F:GO:0016740; P:GO:0071044; F:GO:0050265; C:GO:0005634; F:GO:0003676; F:GO:0000166; F:GO:0003674; F:GO:0008270; F:GO:0003723; F:GO:0016779; C:GO:0005575; C:GO:0005730; C:GO:0005622; P:GO:0008152; P:GO:0008150		PTHR12271 (PANTHER), PTHR12271:SF11 (PANTHER), SSF81301 (SUPERFAMILY), SSF81631 (SUPERFAMILY)

Brugia malayi	u6 snr--specific termi-l uridylyltransferase 1	0		F:GO:0016740; P:GO:0071044; F:GO:0050265; C:GO:0005634; F:GO:0003676; F:GO:0000166; F:GO:0003674; F:GO:0008270; F:GO:0003723; F:GO:0016779; C:GO:0005575; C:GO:0005730; C:GO:0005622; P:GO:0008152; P:GO:0008150		PTHR12271 (PANTHER), PTHR12271:SF11 (PANTHER), SSF81301 (SUPERFAMILY), SSF81631 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	dihydropyrimidi-se-like 3	5	C:GO:0030425; F:GO:0016810; P:GO:0009987; P:GO:0008152; C:GO:0043025	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	deoxyribonuclease tatd	1	F:GO:0016888	-	EC:3.1.21.0	IPR001130; IPR012278; IPR015992; IPR018228; G3DSA:3.20.20.140 (GENE3D), SSF51556 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	transposase	0				PTHR23022 (PANTHER), PTHR23022:SF6 (PANTHER)
	-	0				-
Caenorhabditis elegans	neuroendocrine convertase	6	F:GO:0004252; P:GO:0016486; P:GO:0002165; C:GO:0005576; P:GO:0006508; P:GO:0035187	-	EC:3.4.21.0	IPR000209; IPR009020; IPR015500; IPR022398; G3DSA:3.30.70.850 (GENE3D), PTHR10795:SF11 (PANTHER), SignalP (SIGNALP)
	-	0				PTHR13994 (PANTHER)
Caenorhabditis briggsae	nuclear hormone receptor family protein isoform confirmed by transcript evidence	7	F:GO:0042802; F:GO:0043565; P:GO:0000003; F:GO:0003707; C:GO:0005634; F:GO:0008270; P:GO:0006355	-		-
	-	0				-
	-	0				-
Trichoplax adhaerens	transmembrane protein 222	2	F:GO:0005515; C:GO:0016020	-		IPR008496; SignalP (SIGNALP)
	-	0				IPR019793; SignalP (SIGNALP)
	-	0				-
Loa loa	mlh1	1	F:GO:0005488	-		IPR002099; IPR011186; IPR013507; IPR014721; IPR020568
	-	0				-

Caenorhabditis elegans	3-demethylubiquinone-9 3-methyltransferase	4	P:GO:0002119; P:GO:0006744; P:GO:0008340; F:GO:0008168	-	EC:2.1.1.0	IPR007848; G3DSA:3.40.50.150 (GENE3D), PTHR23134 (PANTHER), SSF53335 (SUPERFAMILY)
Caenorhabditis elegans	26s proteasome non-atpase regulatory subunit 14	6	C:GO:0005875; F:GO:0004175; C:GO:0008541; F:GO:0005515; P:GO:0009987; P:GO:0006508	-		IPR000555; G3DSA:3.40.140.10 (GENE3D), PTHR10410 (PANTHER), PTHR10410:SF5 (PANTHER), SSF102712 (SUPERFAMILY)
	-	0				-
Macaca mulatta	fas-activated serine threonine ki-se isoform 1	7	F:GO:0033867; P:GO:0006468; F:GO:0005515; F:GO:0005524; P:GO:0008624; P:GO:0007165; C:GO:0005739	-	EC:2.7.11.8	IPR013584; IPR015715; PTHR21228 (PANTHER)
Caenorhabditis briggsae	dihydropyrimidi-se	11	C:GO:0005829; F:GO:0004157; F:GO:0008270; P:GO:0006212; P:GO:0019482; P:GO:0006210; F:GO:0016597; P:GO:0051289; F:GO:0002058; C:GO:0005634; F:GO:0002059	-	EC:3.5.2.2	IPR006680; IPR011059; G3DSA:2.30.40.10 (GENE3D), G3DSA:3.20.20.140 (GENE3D), PTHR11647 (PANTHER), PTHR11647:SF1 (PANTHER), SSF51556 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-abf-2 protein	0				SignalP (SIGNALP)
Caenorhabditis elegans	d- polymerase epsilon	11	F:GO:0008270; F:GO:0003887; P:GO:0006260; P:GO:0040035; F:GO:0003677; F:GO:0000166; P:GO:0040011; P:GO:0006997; P:GO:0002009; P:GO:0009792; C:GO:0005634	-	EC:2.7.7.7	PTHR10670 (PANTHER), SSF56672 (SUPERFAMILY)
Caenorhabditis elegans	cog2 protein	9	P:GO:0040035; P:GO:0009792; P:GO:0030334; P:GO:0002119; F:GO:0005515; P:GO:0040010; P:GO:0035262; P:GO:0040039; P:GO:0048477	-		IPR009316

Caenorhabditis elegans	cog2 protein	9	P:GO:0040035; P:GO:0009792; P:GO:0030334; P:GO:0002119; F:GO:0005515; P:GO:0040010; P:GO:0035262; P:GO:0040039; P:GO:0048477	-		IPR009316
	-	0				-
Loa loa	briggsae cbr-rheb-1 protein	12	C:GO:0005829; P:GO:0040010; C:GO:0005681; P:GO:0007264; F:GO:0046872; P:GO:0000003; F:GO:0005515; P:GO:0040011; F:GO:0003924; P:GO:0040015; F:GO:0005525; C:GO:0005886	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001806; IPR013753; IPR015602; IPR020849; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	P:GO:0009987	-		IPR006605; IPR009017
Caenorhabditis briggsae	branched chain aminotransferase cytosolic	6	F:GO:0042802; F:GO:0004084; P:GO:0009083; P:GO:0009082; C:GO:0005829; C:GO:0005739	-	EC:2.6.1.42	-
	-	0				-
	-	0				-
	-	0				-
Loa loa	chitobiosyldiphosphodolichol beta-	0		P:GO:0009058; F:GO:0016740; F:GO:0016757		PTHR13036 (PANTHER)
Caenorhabditis elegans	tight junction protein	7	P:GO:0007254; P:GO:0016337; P:GO:0007391; C:GO:0005913; P:GO:0035147; F:GO:0005515; P:GO:0035156	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR13865 (PANTHER), PTHR13865:SF13 (PANTHER)
Caenorhabditis elegans	small subunit processome component 20 homolog	3	F:GO:0005488; C:GO:0031981; P:GO:0006364	-		IPR011430
Loa loa	ser thr protein phosphatase family protein	2	F:GO:0048037; F:GO:0004724	-		IPR004843; IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF16 (PANTHER), SSF56300 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)

Loa loa	wnt-4 protein	44	P:GO:0030237; P:GO:0045892; P:GO:0030501; F:GO:0004871; P:GO:0007223; N:GO:0039018; P:GO:0018345; P:GO:0045669; P:GO:0007507; P:GO:0032349; N:GO:2000066; P:GO:0009880; P:GO:0001889; C:GO:0005615; N:GO:0061205; P:GO:0002009; P:GO:0001837; P:GO:0090002; F:GO:0003714; P:GO:0042074; P:GO:0006702; P:GO:0045941; P:GO:0090263; P:GO:0071560; C:GO:0005737; P:GO:0035239; F:GO:0005201;	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Hypophthalmichthys nobilis	ribosomal protein l27	4	C:GO:0005840; C:GO:0005829; F:GO:0003735; P:GO:0006414	-		IPR001141
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	tpa: glycoprotein hormone-beta5	0		F:GO:0005179; C:GO:0005576		IPR006208; G3DSA:2.10.90.10 (GENE3D), SignalP (SIGNALP), SSF57501 (SUPERFAMILY)
Loa loa	fad synthetase	5	F:GO:0016779; P:GO:0040010; P:GO:0044238; P:GO:0009108; P:GO:0044271	-	EC:2.7.7.0	IPR001453; PTHR23293 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	F:GO:0016779; P:GO:0040010; P:GO:0008152	-	EC:2.7.7.0	PTHR23293 (PANTHER)
Caenorhabditis elegans	gtpase activating protein family member (gap-2)	5	C:GO:0005737; P:GO:0046580; P:GO:0040010; P:GO:0000003; F:GO:0005099	-		IPR000008; IPR001849; G3DSA:2.60.40.150 (GENE3D), PTHR10194 (PANTHER), PTHR10194:SF25 (PANTHER)

Caenorhabditis elegans	choline dehydroge-se	5	P:GO:0006066; C:GO:0005743; F:GO:0008812; P:GO:0000003; F:GO:0050660	-	EC:1.1.99.1	IPR000172; G3DSA:3.30.560.10 (GENE3D), G3DSA:3.50.50.60 (GENE3D), G3DSA:4.10.450.10 (GENE3D), PTHR11552 (PANTHER), PTHR11552:SF11 (PANTHER), PS51257 (PROFILE), SSF51905 (SUPERFAMILY)
	-	0				IPR010472
	-	0				IPR010472
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	iroquois-class homeodomain protein irx	13	P:GO:0045941; F:GO:0005515; P:GO:0046843; P:GO:0045317; P:GO:0006355; F:GO:0016563; P:GO:0001700; P:GO:0007422; F:GO:0043565; P:GO:0007224; F:GO:0003700; C:GO:0005634; P:GO:0007476	-		IPR001356; IPR002119; IPR009057; IPR012287; IPR017970; PTHR11211 (PANTHER), PTHR11211:SF2 (PANTHER)
	-	0				-
Saccoglossus kowalevskii	zinc finger protein	0		F:GO:0003676; F:GO:0003723; P:GO:0006508; P:GO:0015074; F:GO:0004190; P:GO:0006278; F:GO:0003677; F:GO:0003964		IPR001584; IPR012337; G3DSA:3.30.420.10 (GENE3D), PTHR10178 (PANTHER), PTHR10178:SF14 (PANTHER)
Aphelenchus avenae	trehalose 6-phosphate synthase	3	F:GO:0003825; P:GO:0034608; P:GO:0005992	-	EC:2.4.1.15	SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	5	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0040010; P:GO:0008340	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	5	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0040010; P:GO:0008340	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	C:GO:0016021; P:GO:0019915	-		IPR010291; IPR016196; G3DSA:1.20.1250.20 (GENE3D), PTHR23294 (PANTHER), SignalP (SIGNALP)

Caenorhabditis briggsae	n-termi-l conserved region family protein	16	P:GO:0000910; P:GO:0000070; P:GO:0007029; P:GO:0034504; P:GO:0031468; P:GO:0032940; P:GO:0007052; P:GO:0007078; P:GO:0019915; P:GO:0002119; P:GO:0040011; C:GO:0005635; C:GO:0005654; P:GO:0009792; P:GO:0040018; C:GO:0005783	-		IPR007651; IPR013209; G3DSA:3.40.50.1000 (GENE3D), PTHR12181 (PANTHER), PTHR12181:SF7 (PANTHER), SSF56784 (SUPERFAMILY)
Caenorhabditis briggsae	n-termi-l conserved region family protein	16	P:GO:0000910; P:GO:0000070; P:GO:0007029; P:GO:0034504; P:GO:0031468; P:GO:0032940; P:GO:0007052; P:GO:0007078; P:GO:0019915; P:GO:0002119; P:GO:0040011; C:GO:0005635; C:GO:0005654; P:GO:0009792; P:GO:0040018; C:GO:0005783	-		IPR007651; IPR013209; G3DSA:3.40.50.1000 (GENE3D), PTHR12181 (PANTHER), PTHR12181:SF7 (PANTHER), SSF56784 (SUPERFAMILY)
Caenorhabditis briggsae	n-termi-l conserved region family protein	16	P:GO:0000910; P:GO:0000070; P:GO:0007029; P:GO:0034504; P:GO:0031468; P:GO:0032940; P:GO:0007052; P:GO:0007078; P:GO:0019915; P:GO:0002119; P:GO:0040011; C:GO:0005635; C:GO:0005654; P:GO:0009792; P:GO:0040018; C:GO:0005783	-		IPR007651; IPR013209; G3DSA:3.40.50.1000 (GENE3D), PTHR12181 (PANTHER), PTHR12181:SF7 (PANTHER), SSF56784 (SUPERFAMILY)
Loa loa	dolichyl pyrophosphate man9 c2 alpha- -glucosyltransferase	5	P:GO:0006487; F:GO:0046527; P:GO:0000003; C:GO:0005783; C:GO:0044425	-		IPR004856; SignalP (SIGNALP)
Caenorhabditis elegans	yc91_caeel ame: full=uncharacterized mfs-type transporter	0		C:GO:0016021; P:GO:0040011; P:GO:0055085; P:GO:0007413		-

Caenorhabditis elegans	nicoti-te phosphoribosyltransferase	10	P:GO:0006979; C:GO:0005829; F:GO:0004514; P:GO:0009435; P:GO:0040007; P:GO:0019358; P:GO:0040035; F:GO:0004516; P:GO:0002119; P:GO:0009792	-	EC:2.4.2.19; EC:2.4.2.11	IPR007229; G3DSA:3.20.140.10 (GENE3D), PTHR11098 (PANTHER), SSF54675 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	dihydropyrimidine dehydroge-se	11	F:GO:0004158; P:GO:0006212; F:GO:0046872; P:GO:0055114; F:GO:0009055; F:GO:0017113; F:GO:0051539; P:GO:0006222; P:GO:0006207; C:GO:0005737; P:GO:0006214	-	EC:1.3.3.1; EC:1.3.1.2	IPR009051; IPR012285; PTHR11938 (PANTHER), PTHR11938:SF6 (PANTHER)
Caenorhabditis elegans	dihydropyrimidine dehydroge-se	11	F:GO:0004158; P:GO:0006212; F:GO:0046872; P:GO:0055114; F:GO:0009055; F:GO:0017113; F:GO:0051539; P:GO:0006222; P:GO:0006207; C:GO:0005737; P:GO:0006214	-	EC:1.3.3.1; EC:1.3.1.2	IPR009051; IPR012285; PTHR11938 (PANTHER), PTHR11938:SF6 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	thioredoxin family trp26	0		P:GO:0008150; C:GO:0005575		IPR008979; IPR010400; G3DSA:2.60.120.470 (GENE3D), PTHR12175 (PANTHER)
Caenorhabditis elegans	pwwp domain containing protein	0				-
	-	0				-
	-	0				-
Xenopus (Silurana) tropicalis	aurora ki-se a	9	P:GO:0018105; F:GO:0008017; F:GO:0004674; F:GO:0019894; C:GO:0000922; P:GO:0090307; C:GO:0005876; C:GO:0005813; P:GO:0046777	-	EC:2.7.11.0	IPR000719; IPR002290; IPR008271; IPR011009; IPR017441; IPR017442; IPR020636; IPR020663; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)

Xenopus laevis	aurora ki-se a	10	P:GO:0018105; F:GO:0008017; F:GO:0004674; F:GO:0019894; C:GO:0000922; P:GO:0090307; C:GO:0005876; C:GO:0005813; F:GO:0000166; P:GO:0046777	-	EC:2.7.11.0	IPR000719; IPR002290; IPR008271; IPR011009; IPR017441; IPR017442; IPR020636; IPR020663; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	tgf-beta resistance-associated protein trag	0				-
Caenorhabditis briggsae	hed family member (ptc-3)	7	P:GO:0009792; P:GO:0002119; P:GO:0040018; P:GO:0018996; P:GO:0000003; P:GO:0040011; C:GO:0016020	-		PTHR10796 (PANTHER), PTHR10796:SF34 (PANTHER)
synthetic construct	lipolysis stimulated lipoprotein receptor	11	P:GO:0009790; C:GO:0005730; F:GO:0004872; C:GO:0034362; C:GO:0005794; C:GO:0005886; C:GO:0042627; P:GO:0001889; C:GO:0016021; P:GO:0019216; C:GO:0034361	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	uncoordi-ted protein isoform partially confirmed by transcript evidence	3	P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	-
	-	0				-
Caenorhabditis briggsae	d- polymerase i family protein	5	P:GO:0006260; P:GO:0000003; P:GO:0007005; P:GO:0007275; F:GO:0003824	-		-
Caenorhabditis elegans	tomosyn sy-ptic protein family member (tom-1)	2	F:GO:0005515; C:GO:0016020	-		IPR001388; IPR013905; G3DSA:1.20.5.110 (GENE3D), PTHR10241 (PANTHER), PTHR10241:SF7 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-dep-1 protein	3	P:GO:0040026; P:GO:0040027; F:GO:0016791	-	EC:3.1.3.0	SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				IPR021662

Caenorhabditis briggsae	endonuclease v	1	F:GO:0003824	-		IPR004856; IPR007581; SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-elpc-4 protein	1	C:GO:0044424	-		IPR008728; SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	-dh dehydroge-se	8	P:GO:0006810; F:GO:0008137; C:GO:0005747; F:GO:0046872; F:GO:0051539; F:GO:0051287; P:GO:0006120; F:GO:0010181	-	EC:1.6.5.3	IPR001949; IPR011537; IPR011538; IPR019554; IPR019575; PTHR11780 (PANTHER), SSF140490 (SUPERFAMILY), SSF142019 (SUPERFAMILY), SSF142984 (SUPERFAMILY)
Loa loa	wd repeat and fyve domain-containing protein 3	1	F:GO:0008270	-		G3DSA:2.30.29.40 (GENE3D)
Caenorhabditis elegans	btb poz domain-containing protein 7	0		F:GO:0005515		IPR011333; IPR011705; PTHR16064 (PANTHER)
Haemonchus contortus	aminopeptidase n	5	C:GO:0016021; F:GO:0008237; P:GO:0006508; F:GO:0008270; F:GO:0004177	-	EC:3.4.11.0	IPR001930; IPR014782; PTHR11533:SF29 (PANTHER), SSF55486 (SUPERFAMILY), SSF63737 (SUPERFAMILY)
Haemonchus contortus	aminopeptidase n (alanyl aminopeptidase) (microsomal aminopeptidase) (aminopeptidase m) (kidney zn peptidase) (cd13 antigen)	5	C:GO:0016021; F:GO:0008237; P:GO:0006508; F:GO:0008270; F:GO:0004177	-	EC:3.4.11.0	IPR001930; IPR014782; PTHR11533:SF29 (PANTHER), SSF55486 (SUPERFAMILY), SSF63737 (SUPERFAMILY)
Caenorhabditis elegans	uncoordi-ted family member (unc-52)	2	P:GO:0030239; C:GO:0005578	-		IPR003598; IPR007110; IPR013098; IPR013783; PTHR10574 (PANTHER), PTHR10574:SF20 (PANTHER), SSF48726 (SUPERFAMILY)
Loa loa	sphingosine ki-se 2	6	P:GO:0006915; P:GO:0000003; P:GO:0032501; P:GO:0016310; F:GO:0016301; P:GO:0007610	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	ferm domain (-ezrin-radixin-moesin) family member (frm-1)	1	F:GO:0005515	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	85 kda calcium-independent phospholipase	1	P:GO:0006629	-		IPR016035; G3DSA:3.40.1090.10 (GENE3D), PTHR18958 (PANTHER), PTHR18958:SF94 (PANTHER)
Caenorhabditis elegans	phosphatidylinositol 4-ki-se alpha	9	P:GO:0008219; P:GO:0000003; C:GO:0030660; P:GO:0006661; P:GO:0007268; F:GO:0005515; P:GO:0016310; P:GO:0007165; F:GO:0004428	-		-

Caenorhabditis briggsae	phosphatidylinositol 4-ki-se type 3 alpha	5	F:GO:0005488; P:GO:0008219; P:GO:0000003; P:GO:0016310; F:GO:0004428	-		-
Caenorhabditis briggsae	phosphatidylinositol 4-ki-se alpha	6	F:GO:0005488; P:GO:0008219; P:GO:0000003; C:GO:0030660; P:GO:0016310; F:GO:0004428	-		-
Caenorhabditis elegans	alp enigma encoding family member (alp-1)	1	F:GO:0042802	-		IPR006643; PTHR18973 (PANTHER), PTHR18973:SF57 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-nex-3 protein	0		F:GO:0005509; F:GO:0005544; F:GO:0005515		IPR001464; IPR018502; PTHR10502:SF13 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-cln- protein	4	C:GO:0016020; C:GO:0005737; P:GO:0008340; P:GO:0046662	-		IPR003492
Camponotus floridanus	nuclear factor 1 a-type	9	C:GO:0005737; P:GO:0006260; P:GO:0019079; F:GO:0003700; F:GO:0003677; C:GO:0005886; F:GO:0008134; C:GO:0005634; P:GO:0006355	-		IPR000647; IPR019548; IPR020604
	-	0				-
	-	0				-
Brugia malayi	hypothetical protein Bm1_05795 [Brugia malayi]	0				SignalP (SIGNALP)
Loa loa	single stranded d- binding protein 3	3	F:GO:0003677; P:GO:0045449; C:GO:0005634	-		IPR006594; IPR008116; PTHR12610:SF1 (PANTHER)
Caenorhabditis briggsae	mitochondrial translation optimization 1 homolog (cerevisiae)	4	F:GO:0050660; F:GO:0003824; P:GO:0002098; C:GO:0005739	-		IPR002218; IPR013027; PR00411 (PRINTS), G3DSA:3.50.50.60 (GENE3D), PTHR11806 (PANTHER), SignalP (SIGNALP), SSF51905 (SUPERFAMILY)
Caenorhabditis briggsae	c4b-binding protein beta	0		F:GO:0030414; F:GO:0016787; C:GO:0005576		IPR000436; IPR016060; PTHR19325 (PANTHER), PTHR19325:SF40 (PANTHER)
	-	0				-
Loa loa	myelodysplasia myeloid leukemia isoform e	2	C:GO:0005737; C:GO:0043229	-		IPR019376; PTHR13105 (PANTHER), PTHR13105:SF1 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	P:GO:0044237; F:GO:0003824; P:GO:0048523; F:GO:0005488	-		IPR002591; IPR017849; IPR017850; PTHR10151 (PANTHER), PTHR10151:SF28 (PANTHER)

Caenorhabditis elegans	galactosyltransferase family protein	10	P:GO:0007293; P:GO:0001744; P:GO:0075015; F:GO:0046981; P:GO:0007298; F:GO:0008376; P:GO:0042248; P:GO:0006688; P:GO:0007166; P:GO:0007299	-		IPR002659; PTHR11214:SF14 (PANTHER)
Caenorhabditis elegans	tetratricopeptide repeat protein 27	1	F:GO:0005515	-		IPR011990; IPR013026; IPR019734; PTHR16193 (PANTHER), SSF48452 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	rab6ip1-like protein	0				IPR001024; IPR008976; PTHR10877 (PANTHER), PTHR10877:SF3 (PANTHER)
	-	0				-
Caenorhabditis elegans	protein phosphatase regulatory subunit 12c	2	F:GO:0005515; C:GO:0005737	-		IPR022671; PTHR18958 (PANTHER), PTHR18958:SF166 (PANTHER)
Caenorhabditis elegans	protein phosphatase regulatory subunit 12c	2	F:GO:0005515; C:GO:0005737	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Loa loa	platelet-activating factor acetylhydrolase 2	0		P:GO:0006629; P:GO:0006916; C:GO:0005737; P:GO:0008152; F:GO:0016787; F:GO:0005543; F:GO:0003847; P:GO:0016042		IPR005065; G3DSA:3.40.50.1820 (GENE3D), PF03403 (PFAM), SSF53474 (SUPERFAMILY)
Brugia malayi	brf1 subunit of r- polymerase iii transcription initiation factor iiib (cerevisiae)	13	P:GO:0006383; P:GO:0000003; F:GO:0030528; F:GO:0005515; P:GO:0040007; P:GO:0006898; P:GO:0006412; P:GO:0043488; C:GO:0044424; P:GO:0002119; P:GO:0006352; N:GO:2000112; F:GO:0003729	-	EC:3.6.5.3	IPR000812; IPR011665; G3DSA:1.20.5.650 (GENE3D), PTHR11618:SF4 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-egg-3 protein	3	P:GO:0016311; F:GO:0004721; F:GO:0005515	-	EC:3.1.3.16	PTHR19134 (PANTHER), PTHR19134:SF19 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	#NAME?	2	P:GO:0008652; F:GO:0016491	-		IPR004313; IPR011051; IPR014710

Caenorhabditis briggsae	-dh:ubiquinone reductase 23kd subunit precursor	15	P:GO:0006979; P:GO:0006810; P:GO:0040010; P:GO:0008340; P:GO:0019684; F:GO:0008137; C:GO:0005747; F:GO:0009055; F:GO:0051539; P:GO:0006120; P:GO:0002119; P:GO:0042493; P:GO:0032981; P:GO:0009792; F:GO:0005506	-	EC:1.6.5.3	IPR001450; IPR010226; IPR012285; IPR017896; IPR017900; PTHR10849 (PANTHER), SSF54862 (SUPERFAMILY)
Loa loa	-dh dehydroge-se	15	P:GO:0006979; P:GO:0006810; P:GO:0040010; P:GO:0008340; P:GO:0019684; F:GO:0008137; C:GO:0005747; F:GO:0009055; F:GO:0051539; P:GO:0006120; P:GO:0002119; P:GO:0042493; P:GO:0032981; P:GO:0009792; F:GO:0005506	-	EC:1.6.5.3	IPR001450; IPR010226; IPR012285; IPR017896; IPR017900; PTHR10849 (PANTHER), SSF54862 (SUPERFAMILY)
Caenorhabditis elegans	ras suppressor	0		F:GO:0005515		-
Dictyostelium discoideum AX4	tpr repeat containing protein	0		P:GO:0007047; P:GO:0008360; C:GO:0009274; P:GO:0009273; F:GO:0016763; P:GO:0046677; F:GO:0003677; P:GO:0006464; F:GO:0003824; F:GO:0008658; F:GO:0008233; C:GO:0005622; F:GO:0016881; P:GO:0009252; F:GO:0005488		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Canis familiaris	small edrk-rich factor 2	0		F:GO:0003674; C:GO:0005575		-
	-	0				SignalP (SIGNALP)
	-	0				-
Candida tropicalis MYA-3404	adp-ribosylation factor	4	P:GO:0007264; P:GO:0030036; C:GO:0005737; F:GO:0005525	-		-

Caenorhabditis elegans	rab5 gdp gtp exchange factor	1	F:GO:0005488	-		IPR002653; PTHR23101 (PANTHER), PTHR23101:SF2 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis elegans	rab5 gdp gtp exchange factor	1	F:GO:0005488	-		IPR002653; PTHR23101 (PANTHER), PTHR23101:SF2 (PANTHER), SSF57716 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	transmembrane protein 41b	1	C:GO:0016020	-		IPR015414; PTHR12677 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	flowering locus t	0				-
	-	0				-
Tribolium castaneum	atp-binding sub-family member 10	0		F:GO:0042626; C:GO:0016021; C:GO:0016020; P:GO:0006810; P:GO:0006200; F:GO:0000166; F:GO:0003674; F:GO:0017111; F:GO:0005524; F:GO:0016887; C:GO:0005575; P:GO:0055085; P:GO:0008152; C:GO:0005886; P:GO:0008150		IPR001140; IPR011527; IPR017940; G3DSA:1.20.1560.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF22 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	-dph--cytochrome p450 reductase	1	C:GO:0044464	-		IPR008254; IPR015702; G3DSA:3.40.50.360 (GENE3D), PTHR19384 (PANTHER), SignalP (SIGNALP), SSF52218 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	pan domain containing protein	0				IPR003014; IPR003609; SSF57414 (SUPERFAMILY)

Brugia malayi	low density lipoprotein receptor-related protein 6	27	P:GO:0030326; P:GO:0048593; P:GO:0007369; P:GO:0001501; P:GO:0030111; P:GO:0007507; P:GO:0016043; P:GO:0016477; P:GO:0050793; P:GO:0009798; P:GO:0042127; P:GO:0010646; P:GO:0048646; P:GO:0009952; F:GO:0005515; P:GO:0060443; P:GO:0048523; P:GO:0021872; P:GO:0045449; P:GO:0048522; P:GO:0065008; P:GO:0021915; C:GO:0043229; P:GO:0051239; C:GO:0044444; C:GO:0016020; P:GO:0060562	-		IPR006210; IPR011042; G3DSA:2.10.25.10 (GENE3D), PTHR10529 (PANTHER), SSF57196 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG18221 [Caenorhabditis briggsae]	0				-
	-	0				-
Loa loa	nik and ikk binding protein	0				PTHR21512 (PANTHER), PTHR21512:SF6 (PANTHER)
Loa loa	nik and ikk binding protein	0				PTHR21512 (PANTHER), PTHR21512:SF6 (PANTHER)
Loa loa	nik and ikk binding protein	0				PTHR21512 (PANTHER), PTHR21512:SF6 (PANTHER)
Caenorhabditis elegans	odd oz protein	1	F:GO:0003824	-		IPR013032; PTHR11219 (PANTHER), PTHR11219:SF4 (PANTHER)
	-	0				-
Caenorhabditis elegans	uncoordi-ted family member (unc-103)	4	F:GO:0005249; P:GO:0055085; P:GO:0006813; C:GO:0016021	-		PTHR10217 (PANTHER), PTHR10217:SF15 (PANTHER)
	-	0				-
Caenorhabditis briggsae	phosphodiesterase 8a	7	P:GO:0007411; P:GO:0000160; F:GO:0004871; F:GO:0046872; F:GO:0004115; P:GO:0007165; P:GO:0008152	-		IPR002073; IPR023088; IPR023174; PTHR11347 (PANTHER), PTHR11347:SF38 (PANTHER), SSF109604 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	protein	2	F:GO:0016787; P:GO:0044262	-		-
	-	0				-
Loa loa	elegans protein partially confirmed by transcript evidence	1	F:GO:0046872	-		IPR017907
	-	0				-
	-	0				-

synthetic construct	vesicle-associated membrane protein 8	10	P:GO:0006461; P:GO:0006944; C:GO:0005769; P:GO:0006892; C:GO:0012505; C:GO:0005624; C:GO:0031201; F:GO:0005515; C:GO:0016021; C:GO:0005739	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Homo sapiens	high mobility group at-hook isoform cra_e	16	C:GO:0000785; F:GO:0046965; P:GO:0006345; P:GO:0006461; P:GO:0006268; F:GO:0042975; P:GO:0006337; C:GO:0005829; C:GO:0005667; P:GO:0019047; F:GO:0003700; F:GO:0003680; F:GO:0019899; F:GO:0030374; P:GO:0019059; P:GO:0044419	-		-
Caenorhabditis elegans	ngfi-a binding protein 2	9	P:GO:0042552; F:GO:0030528; P:GO:0045682; P:GO:0014037; P:GO:0045449; P:GO:0040035; F:GO:0005515; P:GO:0001958; P:GO:0002009	-		IPR006988; IPR013761; PTHR12623 (PANTHER), PTHR12623:SF8 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				IPR003378
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F57B10.14 [Caenorhabditis elegans]	0		F:GO:0008121; F:GO:0009055; P:GO:0006122; C:GO:0031966		-
Caenorhabditis elegans	immunoglobulin i-set domain containing protein	0		F:GO:0005509		IPR007110; IPR013098; IPR013783; PTHR10075 (PANTHER), PTHR10075:SF2 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	stomatin-like protein 2	3	C:GO:0005743; C:GO:0005856; F:GO:0005102	-		-

Loa loa	paxillin	14	P:GO:0034614; P:GO:0040010; C:GO:0005875; F:GO:0008013; F:GO:0008270; F:GO:0017166; P:GO:0007155; C:GO:0005925; P:GO:0002119; P:GO:0007172; P:GO:0007165; P:GO:0009792; C:GO:0030027; P:GO:0006936	-		SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0005488		-
Caenorhabditis elegans	hypothetical protein T08B1.1 [Caenorhabditis elegans]	6	C:GO:0016021; P:GO:0009792; P:GO:0040010; P:GO:0055085; F:GO:0005215; P:GO:0002119	-		PTHR11600 (PANTHER), PTHR11600:SF28 (PANTHER)
	-	0				-
	-	0				-
Loa loa	sel-1 suppressor of lin-12-like (elegans)	4	F:GO:0005515; F:GO:0016787; C:GO:0016021; C:GO:0005783	-		IPR006597; IPR011990; PTHR11102 (PANTHER), PTHR11102:SF11 (PANTHER), SSF81901 (SUPERFAMILY)
Loa loa	sel-1 suppressor of lin-12-like (elegans)	4	F:GO:0005515; F:GO:0016787; C:GO:0016021; C:GO:0005783	-		IPR006597; IPR011990; PTHR11102 (PANTHER), PTHR11102:SF11 (PANTHER), SSF81901 (SUPERFAMILY)
	-	0				-
Pongo abelii	keratinocyte associated protein 2	4	C:GO:0008250; C:GO:0016021; F:GO:0004579; P:GO:0018279	-	EC:2.4.1.119	SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	hypothetical protein F41B4.1 [Caenorhabditis elegans]	1	F:GO:0005515	-		-
Loa loa	imp1 inner mitochondrial membrane peptidase-like	4	F:GO:0008236; P:GO:0006508; C:GO:0016020; C:GO:0005739	-		IPR000223; IPR011056; IPR015927; IPR019759; PTHR12383 (PANTHER), PTHR12383:SF2 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Loa loa	protein-tyrosine phosphatase containing protein	4	F:GO:0004725; P:GO:0006470; P:GO:0009792; P:GO:0000003	-	EC:3.1.3.48	IPR000242; IPR000387; IPR016130; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
						IPR003598; IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-kcc-3 protein	5	F:GO:0022891; P:GO:0007638; P:GO:0055085; F:GO:0022804; C:GO:0016020	-		IPR004841; SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	briggsae cbr-acc-1 protein	1	C:GO:0016020	-		IPR006201; PTHR18945:SF12 (PANTHER)
Caenorhabditis elegans	briggsae cbr-twk-16 protein	3	C:GO:0016021; P:GO:0006813; F:GO:0005267	-		-
Caenorhabditis elegans	dead h (asp-glu-ala-asp his) box polypeptide 11 (chl1-like helicase cerevisiae)	6	F:GO:0003676; F:GO:0008026; P:GO:0000003; F:GO:0000166; P:GO:0006139; P:GO:0009792	-		-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Brugia malayi	autophagy-related protein 13	3	P:GO:0000045; F:GO:0005515; C:GO:0070969	-		IPR018731; PTHR13430 (PANTHER)
Caenorhabditis elegans	hypothetical protein C29E4.13 [Caenorhabditis elegans]	0		P:GO:0000003; P:GO:0040010; P:GO:0006898; F:GO:0008270; C:GO:0005622		IPR007087; IPR015880
Caenorhabditis elegans	hypothetical protein C29E4.13 [Caenorhabditis elegans]	0		P:GO:0000003; P:GO:0040010; P:GO:0006898; F:GO:0008270; C:GO:0005622		IPR007087; IPR015880
	-	0				-
Brugia malayi	rad9 family protein	0		P:GO:0006281		IPR007268
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	atp-binding domain-containing protein	12	P:GO:0006412; C:GO:0005829; P:GO:0034227; P:GO:0048598; P:GO:0048599; P:GO:0007283; F:GO:0005524; F:GO:0016740; P:GO:0040025; P:GO:0002098; F:GO:0000049; P:GO:0006974	-	EC:3.6.5.3	PTHR11807 (PANTHER), PTHR11807:SF3 (PANTHER)
	-	0				IPR000276
Caenorhabditis elegans	transducin beta-like protein 3	8	P:GO:0040010; P:GO:0045132; P:GO:0006364; P:GO:0000003; C:GO:0032040; P:GO:0006898; P:GO:0009792; C:GO:0005634	-		IPR001680; IPR011047; IPR015943; IPR017986; IPR019781; IPR019782; PTHR19854 (PANTHER), PTHR19854:SF2 (PANTHER)

Caenorhabditis elegans	msp-domain protein 1 variant	6	P:GO:0040018; F:GO:0005515; C:GO:0031143; P:GO:0000003; P:GO:0019915; C:GO:0044297	-		-
Caenorhabditis elegans	msp-domain protein 1 variant	6	P:GO:0040018; F:GO:0005515; C:GO:0031143; P:GO:0000003; P:GO:0019915; C:GO:0044297	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	alix (apoptosis-linked gene 2 interacting protein x) homolog family member (alx-1)	0				IPR004328; G3DSA:1.25.40.280 (GENE3D), PTHR23030 (PANTHER), PTHR23030:SF11 (PANTHER)
	-	0				-
Angiostrongylus cantonensis	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Ailuropoda melanoleuca	stip1 homology and u-box containing protein 1	24	P:GO:0000209; P:GO:0051865; F:GO:0030544; P:GO:0006457; F:GO:0034450; P:GO:0071218; P:GO:0051604; C:GO:0042405; P:GO:0031398; F:GO:0051879; P:GO:0030579; F:GO:0030911; P:GO:0031943; C:GO:0005737; F:GO:0030674; C:GO:0000151; P:GO:0032436; P:GO:0006515; P:GO:0090035; F:GO:0051787; F:GO:0042803; C:GO:0031371; F:GO:0019900; F:GO:0046332	-		IPR003613; IPR013083; PTHR22904 (PANTHER), PTHR22904:SF27 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis elegans	ribonuclease h1	5	F:GO:0004523; P:GO:0006264; C:GO:0005634; C:GO:0005739; F:GO:0042803	-	EC:3.1.26.4	IPR002156; IPR011320; IPR012337; G3DSA:3.30.420.10 (GENE3D), PTHR10642 (PANTHER)

Caenorhabditis brenneri	c ntenin alcadein homolog family member (casy-1)	9	P:GO:0009792; C:GO:0005615; P:GO:0007156; F:GO:0005515; C:GO:0032809; P:GO:0008355; C:GO:0043231; F:GO:0005509; C:GO:0016021	-		PTHR14139 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein Y54H5A.2 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	beta-lactamase family protein	0				IPR001466; IPR012338; G3DSA:3.40.710.10 (GENE3D), PTHR10566 (PANTHER), PTHR10566:SF6 (PANTHER), SignalP (SIGNALP)
Loa loa	trehalase	3	P:GO:0009792; F:GO:0004553; P:GO:0044262	-	EC:3.2.1.0	IPR001661; IPR008928; PTHR23403:SF1 (PANTHER), SignalP (SIGNALP)
Loa loa	elegans protein confirmed by transcript evidence	0		P:GO:0055114; F:GO:0016491		IPR001395; IPR018170; IPR020471; IPR023210; PTHR11732:SF34 (PANTHER)
Caenorhabditis elegans	briggsae cbr-ham-1 protein	0				-
Caenorhabditis briggsae	tata-binding protein-associated factor 172	6	F:GO:0003677; F:GO:0005524; F:GO:0003700; F:GO:0004386; P:GO:0016481; C:GO:0005634	-		IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR10799 (PANTHER), PTHR10799:SF72 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-coq-8 protein	0				-
Caenorhabditis briggsae	nodal modulator 1	1	P:GO:0000003	-		IPR008970; IPR013783; PTHR23303 (PANTHER), PTHR23303:SF1 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	leucine rich repeat containing 59	4	P:GO:0009792; C:GO:0043231; C:GO:0044444; C:GO:0044446	-		IPR001611; IPR003591; G3DSA:3.80.10.10 (GENE3D), PTHR23155 (PANTHER), PTHR23155:SF7 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)
Pongo abelii	chaperonin containing subunit 5	7	C:GO:0005730; P:GO:0006457; C:GO:0005815; C:GO:0005832; F:GO:0005524; F:GO:0051082; P:GO:0009615	-		SignalP (SIGNALP)
Caenorhabditis elegans	variable abnormal morphology family member (vab-10)	0		F:GO:0005509; P:GO:0007050; F:GO:0003779		G3DSA:3.90.1290.10 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF49 (PANTHER), SSF75399 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
Loa loa	beta-lactamase family protein	0				-
Loa loa	hypothetical protein LOAG_04165 [Loa loa]	0				-

Loa loa	chromodomain helicase d- binding protein 1-like	6	F:GO:0008026; F:GO:0005515; P:GO:0006338; P:GO:0006974; C:GO:0005634; F:GO:0000166	-		IPR000330; PTHR10799 (PANTHER), PTHR10799:SF74 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein B0041.5 [Caenorhabditis elegans]	3	P:GO:0007411; P:GO:0019915; P:GO:0007413	-		PTHR23051 (PANTHER), SignalP (SIGNALP)
Brugia malayi	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		SignalP (SIGNALP)
Caenorhabditis briggsae	cg4236	33	F:GO:0000122; F:GO:0042393; C:GO:0005700; P:GO:0007307; F:GO:0042826; F:GO:0004402; F:GO:0046974; P:GO:0048813; P:GO:0016571; F:GO:0016251; C:GO:0035098; P:GO:0016584; P:GO:0007517; P:GO:0006335; P:GO:0006342; C:GO:0005737; C:GO:0070176; C:GO:0005667; F:GO:0003676; C:GO:0016589; C:GO:0016590; P:GO:0009792; F:GO:0035035; F:GO:0046976; P:GO:0042766; P:GO:0007346; F:GO:0003682; P:GO:0000289;	-	EC:2.3.1.48	IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; IPR022052; PTHR22850 (PANTHER), PTHR22850:SF27 (PANTHER)
Loa loa	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		SignalP (SIGNALP)

Caenorhabditis briggsae	cg4236	33	F:GO:0000122; F:GO:0042393; C:GO:0005700; P:GO:0007307; F:GO:0042826; F:GO:0004402; F:GO:0046974; P:GO:0048813; P:GO:0016571; F:GO:0016251; C:GO:0035098; P:GO:0016584; P:GO:0007517; P:GO:0006335; P:GO:0006342; C:GO:0005737; C:GO:0070176; C:GO:0005667; F:GO:0003676; C:GO:0016589; C:GO:0016590; P:GO:0009792; F:GO:0035035; F:GO:0046976; P:GO:0042766; P:GO:0007346; F:GO:0003682; P:GO:0000289;	-	EC:2.3.1.48	IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; IPR022052; PTHR22850 (PANTHER), PTHR22850:SF27 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0046872; F:GO:0005488; P:GO:0030001		-
Caenorhabditis elegans	yhb8_caeel ame: full=uncharacterized protein flags: precursor	0				-
Caenorhabditis elegans	protein arginine n-methyltransferase	12	C:GO:0005829; P:GO:0018216; F:GO:0035243; F:GO:0043021; P:GO:0010468; F:GO:0035241; P:GO:0000387; F:GO:0005515; F:GO:0008469; F:GO:0016277; C:GO:0005634; P:GO:0016571	-	EC:2.1.1.125 ; EC:2.1.1.126	IPR010456; G3DSA:3.40.50.150 (GENE3D), PTHR11006 (PANTHER), PTHR11006:SF4 (PANTHER), SSF53335 (SUPERFAMILY)
Caenorhabditis briggsae	unc-82	3	P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	-
Caenorhabditis elegans	briggsae cbr-tgt-2 protein	2	F:GO:0016757; P:GO:0006400	-		-
	-	0				-
Caenorhabditis elegans	leucyl-tr- synthetase	3	P:GO:0006412; F:GO:0016874; C:GO:0005737	-	EC:3.6.5.3	IPR002300; IPR002302; IPR014729; G3DSA:3.90.740.10 (GENE3D), PTHR11946 (PANTHER), SSF52374 (SUPERFAMILY)

Acyrthosiphon pisum	f-box-like wd repeat-containing protein tbl1xr1	0		F:GO:0003677; C:GO:0005634; P:GO:0010553; F:GO:0003674; P:GO:0060070; P:GO:0016568; P:GO:0006350; F:GO:0016563; C:GO:0017053; F:GO:0010843; F:GO:0047485; F:GO:0004872; C:GO:0005876; F:GO:0042393; P:GO:0008150; F:GO:0008013; P:GO:0045944; P:GO:0043161; F:GO:0003714; P:GO:0045449; C:GO:0005730; P:GO:0045892; C:GO:0000118; F:GO:0005515; C:GO:0005575		-
Caenorhabditis elegans	variable abnormal morphology family member (vab-10)	0				IPR018114
Caenorhabditis elegans	protein ki-se domain containing protein	6	F:GO:0046872; P:GO:0032502; F:GO:0005515; F:GO:0004672; P:GO:0009987; F:GO:0000166	-		IPR000719; IPR008271; IPR011009; IPR015737; IPR017442; IPR020636; G3DSA:1.10.510.10 (GENE3D)
Caenorhabditis elegans	endoplasmic reticulum metallopeptidase 1	1	C:GO:0044464	-		PTHR12147 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	swib complex baf60b domain-containing protein	0		P:GO:0006259; F:GO:0003674; F:GO:0005509; P:GO:0008150; F:GO:0004518; F:GO:0005515; C:GO:0005575; F:GO:0003677		IPR003121; IPR019835; PTHR13844 (PANTHER)
Caenorhabditis elegans	endonuclease exonuclease phosphatase family protein	2	F:GO:0016788; P:GO:0000003	-		G3DSA:3.60.10.10 (GENE3D)
Ailuropoda melanoleuca	fibrillarin	9	C:GO:0001652; C:GO:0031428; C:GO:0015030; F:GO:0003723; F:GO:0005515; P:GO:0016074; P:GO:0006364; F:GO:0008168; P:GO:0008033	-	EC:2.1.1.0	-
Caenorhabditis elegans	acylpeptide hydrolase	0		P:GO:0006508; F:GO:0004252; F:GO:0008236; F:GO:0016787		SignalP (SIGNALP)
Ancylostoma caninum	secreted protein 6 precursor	0		C:GO:0005576		IPR014044

Caenorhabditis elegans	lbp bpi cetp n-termi-l domain containing protein	6	P:GO:0002119; P:GO:0009792; P:GO:0000003; P:GO:0040007; F:GO:0008289; P:GO:0040011	-		SignalP (SIGNALP)
Caenorhabditis elegans	inositol -trisphosphate receptor	10	F:GO:0005515; P:GO:0006816; F:GO:0070679; P:GO:0051592; C:GO:0031095; C:GO:0044428; P:GO:0055085; C:GO:0005783; C:GO:0005887; F:GO:0005220	-		IPR000493; IPR000699; IPR015925; G3DSA:1.25.10.30 (GENE3D), PTHR13715:SF2 (PANTHER), SSF100909 (SUPERFAMILY)
Caenorhabditis briggsae	zinc c2h2 type family protein	7	P:GO:0009792; F:GO:0003676; C:GO:0005622; F:GO:0005515; P:GO:0040010; P:GO:0000003; F:GO:0008270	-		-
	-	0				-
Caenorhabditis elegans	hypothetical protein T28B8.3 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	histone methyltransferase-like family member (met-1)	0		F:GO:0016740; F:GO:0008168; P:GO:0006259; F:GO:0003677; C:GO:0005634; F:GO:0018024; P:GO:0006281; F:GO:0003824; F:GO:0005515; F:GO:0004518		IPR003616; G3DSA:2.170.270.10 (GENE3D), PTHR22884 (PANTHER), PTHR22884:SF36 (PANTHER), SSF82199 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				PTHR10900 (PANTHER), PTHR10900:SF10 (PANTHER)
Caenorhabditis briggsae	haloacid dehaloge-se-like hydrolase family protein	0		F:GO:0008967; F:GO:0016787; P:GO:0008152; F:GO:0003824		SignalP (SIGNALP), SSF56784 (SUPERFAMILY)
	-	0				-

Homo sapiens	alpha 4	21	P:GO:0001666; F:GO:0047485; C:GO:0030863; C:GO:0043234; F:GO:0005509; P:GO:0051271; C:GO:0005730; P:GO:0042981; P:GO:0051017; F:GO:0051015; F:GO:0001882; P:GO:0051272; C:GO:0001725; P:GO:0048549; C:GO:0031143; F:GO:0005178; C:GO:0048471; C:GO:0030529; F:GO:0042803; P:GO:0015031; P:GO:0032417	-		IPR011992; IPR014837; IPR018249; PTHR11915 (PANTHER), PTHR11915:SF47 (PANTHER), SSF47473 (SUPERFAMILY)
Caenorhabditis elegans	daf-16 foxo germline tumor affecting family member (dct-6)	0				-
Caenorhabditis briggsae	briggsae cbr-nhl-1 protein	4	P:GO:0006915; C:GO:0005622; F:GO:0008270; F:GO:0005515	-		-
	-	0				-
Loa loa	solute carrier family member e1	0		F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150; C:GO:0005575; P:GO:0006810		IPR004853; PTHR11132 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	i uaiaretic acid resistant family member (ndg-4)	3	P:GO:0009792; P:GO:0010171; P:GO:0040010	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	uncharacterized protein	0		F:GO:0005488		-
Caenorhabditis elegans	uncharacterized protein	0		F:GO:0005488		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Brugia malayi	myotubularin-related family protein	3	P:GO:0016311; F:GO:0016791; P:GO:0000278	-	EC:3.1.3.0	-
	-	0				-
Angiostrongylus cantonensis	elegans protein confirmed by transcript evidence	7	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040011; P:GO:0019915; P:GO:0040007; P:GO:0006898	-		IPR002486; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER), SignalP (SIGNALP)

Caenorhabditis elegans	uncoordi-ted family member (unc-89)	0		F:GO:0004672; F:GO:0005524; F:GO:0005089; P:GO:0006468; P:GO:0035023; F:GO:0004674; C:GO:0005622		IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	steroid receptor-interacting snf2 domain protein	5	F:GO:0004386; F:GO:0003677; F:GO:0005515; F:GO:0005524; C:GO:0016021	-		IPR000330; PTHR10799 (PANTHER), PTHR10799:SF51 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	microtubule interacting and domain containing 1	1	C:GO:0044464	-		PTHR21222 (PANTHER)
Loa loa	transmembrane protein 16c	0		C:GO:0016021		IPR007632; SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	egf-like domain containing protein	1	P:GO:0040010	-		IPR000742; IPR006210; IPR013032; PTHR11201 (PANTHER), PTHR11201:SF162 (PANTHER)
Caenorhabditis briggsae	transmembrane protein 131	1	F:GO:0005515	-		IPR000896
	-	0				-
	-	0				PS51257 (PROFILE)
	-	0				-
Acyrthosiphon pisum	galactoki-se 1	4	P:GO:0005975; F:GO:0005488; P:GO:0044237; F:GO:0016740	-		IPR006203; IPR006204; IPR006206; IPR014721; IPR020568; G3DSA:3.30.70.890 (GENE3D), PTHR10457 (PANTHER), PTHR10457:SF6 (PANTHER), SSF55060 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	frizzled homolog 7b	7	P:GO:0007186; F:GO:0004926; C:GO:0016021; P:GO:0007165; P:GO:0007275; P:GO:0016055; F:GO:0004930	-		IPR015526; IPR020067; PTHR11309:SF20 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	t-complex protein 1 subunit theta	5	C:GO:0005737; C:GO:0005856; P:GO:0006457; F:GO:0005524; F:GO:0051082	-		IPR001969; IPR002423; IPR012721; G3DSA:1.10.560.10 (GENE3D), G3DSA:3.30.260.10 (GENE3D), G3DSA:3.50.7.10 (GENE3D), SSF52029 (SUPERFAMILY), SSF54849 (SUPERFAMILY)
Caenorhabditis elegans	chaperonin containing subunit 8	8	C:GO:0005856; P:GO:0006457; P:GO:0035095; F:GO:0005524; F:GO:0051082; F:GO:0042623; C:GO:0005634; C:GO:0005829	-		IPR001969; IPR002194; IPR002423; IPR012721; IPR017998; G3DSA:1.10.560.10 (GENE3D), G3DSA:3.30.260.10 (GENE3D), G3DSA:3.50.7.10 (GENE3D), SSF52029 (SUPERFAMILY), SSF54849 (SUPERFAMILY)

Caenorhabditis elegans	chaperonin containing subunit 8	8	C:GO:0005856; P:GO:0006457; P:GO:0035095; F:GO:0005524; F:GO:0051082; F:GO:0042623; C:GO:0005634; C:GO:0005829	-		IPR001969; IPR002194; IPR002423; IPR012721; IPR017998; G3DSA:1.10.560.10 (GENE3D), G3DSA:3.30.260.10 (GENE3D), G3DSA:3.50.7.10 (GENE3D), SSF52029 (SUPERFAMILY), SSF54849 (SUPERFAMILY)
Caenorhabditis elegans	chaperonin containing subunit 8	8	C:GO:0005856; P:GO:0006457; P:GO:0035095; F:GO:0005524; F:GO:0051082; F:GO:0042623; C:GO:0005634; C:GO:0005829	-		IPR001969; IPR002194; IPR002423; IPR012721; IPR017998; G3DSA:1.10.560.10 (GENE3D), G3DSA:3.30.260.10 (GENE3D), G3DSA:3.50.7.10 (GENE3D), SSF52029 (SUPERFAMILY), SSF54849 (SUPERFAMILY)
Brugia malayi	structural mainte-nce of chromosomes 2	4	P:GO:0051276; F:GO:0005488; P:GO:0007049; C:GO:0005694	-		IPR010935; PD936484 (PRODOM), PTHR18937 (PANTHER), PTHR18937:SF9 (PANTHER)
Caenorhabditis elegans	chaperonin containing subunit 8	8	C:GO:0005856; P:GO:0006457; P:GO:0035095; F:GO:0005524; F:GO:0051082; F:GO:0042623; C:GO:0005634; C:GO:0005829	-		IPR001969; IPR002194; IPR002423; IPR012721; IPR017998; G3DSA:1.10.560.10 (GENE3D), G3DSA:3.30.260.10 (GENE3D), G3DSA:3.50.7.10 (GENE3D), SSF52029 (SUPERFAMILY), SSF54849 (SUPERFAMILY)
Caenorhabditis elegans	actin	18	P:GO:0007126; P:GO:0007108; P:GO:0040007; P:GO:0007517; P:GO:0000281; P:GO:0040035; P:GO:0030036; C:GO:0005865; F:GO:0005524; C:GO:0005938; P:GO:0002119; F:GO:0016887; F:GO:0005515; C:GO:0005884; F:GO:0005200; P:GO:0040039; P:GO:0006898; P:GO:0009792	-		IPR004000; IPR004001; IPR020902; G3DSA:2.30.36.70 (GENE3D), G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), SSF53067 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Brugia malayi	nli interacting factor-like phosphatase family protein	0		F:GO:0004721; C:GO:0005622; C:GO:0005634		PTHR23081 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				PR01217 (PRINTS)
Loa loa	ck1 ttbk protein ki-se	0				-

Caenorhabditis briggsae	brca1 interacting protein c-termi-l helicase 1	5	P:GO:0006357; F:GO:0005515; C:GO:0044444; F:GO:0004386; C:GO:0005634	-		IPR002464; IPR010614; IPR014013; G3DSA:3.40.50.300 (GENE3D), PTHR11472 (PANTHER), PTHR11472:SF6 (PANTHER), SSF52540 (SUPERFAMILY)
Ascaris suum	collagen-binding adhesin	1	F:GO:0005488	-		-
Ascaris suum	collagen-binding adhesin	1	F:GO:0005488	-		-
	-	0				-
Homo sapiens	gamma-inducible protein 30	7	F:GO:0016491; P:GO:0019886; C:GO:0005764; P:GO:0048147; P:GO:0055114; P:GO:0050821; C:GO:0005576	-		IPR004911; PTHR13234:SF7 (PANTHER), SignalP (SIGNALP)
Brugia malayi	negative elongation factor a homolog	0		F:GO:0003746		SignalP (SIGNALP)
	-	0				-
Loa loa	zinc finger protein 706	3	C:GO:0005622; P:GO:0040010; F:GO:0008270	-		IPR007087; IPR007513; IPR015880; G3DSA:4.10.1050.10 (GENE3D), PTHR21213 (PANTHER), SSF118359 (SUPERFAMILY)
Danio rerio	briggsae cbr-dao-5 protein	0		P:GO:0015031; F:GO:0005089; P:GO:0035023; F:GO:0004674; C:GO:0016020; F:GO:0008565; F:GO:0004672; P:GO:0006468; F:GO:0005524; C:GO:0030288; F:GO:0005515; C:GO:0005622		-
	-	0				-
Monodelphis domestica	sig-l cub egf-like 1	2	F:GO:0005488; C:GO:0005886	-		IPR001368; IPR009030; IPR011641; PTHR11201 (PANTHER), PTHR11201:SF72 (PANTHER)
Loa loa	caf1 family ribonuclease containing protein	1	F:GO:0005515	-		-
Caenorhabditis elegans	solute carrier family member 1	9	P:GO:0048878; P:GO:0015672; F:GO:0015377; C:GO:0016324; P:GO:0001822; F:GO:0005515; P:GO:0055085; P:GO:0030001; P:GO:0007588	-		IPR004841; PTHR11827 (PANTHER), PTHR11827:SF2 (PANTHER)
Caenorhabditis briggsae	clathrin coat assembly protein	4	F:GO:0005515; P:GO:0006886; C:GO:0030131; P:GO:0006897	-		IPR008968; PTHR11998 (PANTHER), PTHR11998:SF1 (PANTHER)

Brugia malayi	groucho tle n-termi-l q-rich domain containing protein	12	P:GO:0045879; C:GO:0043234; P:GO:0007015; P:GO:0030178; P:GO:0009887; F:GO:0003677; P:GO:0000122; F:GO:0003714; P:GO:0007541; P:GO:0007165; P:GO:0048813; C:GO:0005634	-		IPR005617; PTHR10814 (PANTHER)
Necator americanus	venom-allergen-like protein family member (vap-1)	0		P:GO:0040011; C:GO:0005576		IPR014044; SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein Y48G9A.3 [Caenorhabditis elegans]	1	P:GO:0000003	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	f-box and leucine-rich repeat protein 2	4	C:GO:0005737; F:GO:0004842; P:GO:0006508; P:GO:0006464	-	EC:6.3.2.19	IPR006553; G3DSA:3.80.10.10 (GENE3D), PTHR23125 (PANTHER), PTHR23125:SF69 (PANTHER), SSF52047 (SUPERFAMILY)
Caenorhabditis briggsae	bat2d protein	0		F:GO:0003674; P:GO:0008150		-
Caenorhabditis elegans	hypothetical tyrosi-se-like protein in chromosome	2	F:GO:0003824; F:GO:0005515	-		-
Caenorhabditis elegans	hypothetical tyrosi-se-like protein in chromosome	2	F:GO:0003824; F:GO:0005515	-		-
Caenorhabditis elegans	hypothetical tyrosi-se-like protein in chromosome	2	F:GO:0003824; F:GO:0005515	-		-
Caenorhabditis briggsae	ymm3_caeel ame: full=uncharacterized protein	0				-
Caenorhabditis elegans	hypothetical protein ZC581.3 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	hypothetical protein ZK1248.13 [Caenorhabditis elegans]	0				-
Cooperia oncophora	latrophilin-like protein 2	6	P:GO:0007218; C:GO:0016021; P:GO:0007165; C:GO:0005886; F:GO:0005529; F:GO:0004930	-		IPR000832; PTHR12011 (PANTHER), PTHR12011:SF56 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	c (cysteine rich motor neuron protein) homolog family member (crm-1)	6	P:GO:0000003; F:GO:0042802; P:GO:0018996; P:GO:0040015; P:GO:0040018; C:GO:0016020	-		IPR000867; IPR001007; IPR004094; IPR011061; IPR018112; PTHR11339 (PANTHER), PTHR11339:SF39 (PANTHER), SSF57603 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	cysteine synthase	3	P:GO:0008152; F:GO:0030170; F:GO:0003824	-		IPR001926; G3DSA:3.40.50.1100 (GENE3D), PTHR10314 (PANTHER), PTHR10314:SF8 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR009673; SignalP (SIGNALP)
	-	0				-
Pongo abelii	heme binding protein 2	1	C:GO:0005739	-		IPR006917; IPR011256; PTHR11220:SF3 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0040010; P:GO:0009792; P:GO:0000003	-		IPR009724; SignalP (SIGNALP)
Loa loa	hypothetical protein LOAG_04146 [Loa loa]	0				IPR009565
Saccoglossus kowalevskii	glutathione s-transferase kappa 1	2	C:GO:0030288; F:GO:0015035	-		IPR001853; IPR012336; PTHR13887 (PANTHER)

Caenorhabditis briggsae	Hypothetical protein CBG02786 [Caenorhabditis briggsae]	0		F:GO:0005488		PTHR13298 (PANTHER), PTHR13298:SF1 (PANTHER)
Caenorhabditis briggsae	kettin	0		P:GO:0000902; P:GO:0006468; P:GO:0001701; F:GO:0003677; C:GO:0030018; C:GO:0030017; C:GO:0030016; P:GO:0007512; P:GO:0007264; F:GO:0005524; P:GO:0035023; C:GO:0031430; F:GO:0004672; F:GO:0005089; P:GO:0003007; F:GO:0005085; F:GO:0003824; C:GO:0000786; P:GO:0043056; P:GO:0006334; F:GO:0005488; P:GO:0014866; P:GO:0045214; C:GO:0031674; C:GO:0031672; F:GO:0008307;		IPR003599; IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis briggsae	insulin-degrading enzyme	9	P:GO:0010815; F:GO:0008270; C:GO:0005777; F:GO:0004222; P:GO:0050435; P:GO:0006508; P:GO:0065007; F:GO:0042803; F:GO:0005524	-	EC:3.4.24.0	IPR007863; IPR011237; IPR011249; PTHR11851 (PANTHER), PTHR11851:SF64 (PANTHER)
	-	0				-
Hydra magnipapillata	alkaline phosphatase	0		P:GO:0033280; C:GO:0016020; P:GO:0046677; F:GO:0004035; F:GO:0016791; F:GO:0016787; C:GO:0031225; F:GO:0003824; F:GO:0046872; P:GO:0008152; C:GO:0005886		IPR001952; IPR017849; PTHR11596 (PANTHER)
	-	0				-
Caenorhabditis elegans	interferon gamma-inducible thiol reductase	0		C:GO:0005576		IPR004911; PTHR13234:SF2 (PANTHER)
	-	0				-
	-	0				-

Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0006629; F:GO:0016787; F:GO:0008081; C:GO:0016021; P:GO:0040010; P:GO:0006071; F:GO:0008889; C:GO:0005575		IPR017946
Caenorhabditis elegans	odd oz ten-m homolog 4	0		C:GO:0016021; C:GO:0009279; C:GO:0016020; C:GO:0005886		-
Caenorhabditis briggsae	mitochondrial ribosomal protein s35	6	P:GO:0009792; C:GO:0005763; P:GO:0002119; P:GO:0042769; P:GO:0043043; P:GO:0040007	-		PTHR13490 (PANTHER)
Caenorhabditis briggsae	mitochondrial ribosomal protein s35	6	P:GO:0009792; C:GO:0005763; P:GO:0002119; P:GO:0042769; P:GO:0043043; P:GO:0040007	-		PTHR13490 (PANTHER)
Selaginella moellendorffii	topoisomerase ii	4	P:GO:0044260; F:GO:0003677; P:GO:0090304; F:GO:0016853	-		IPR013506; IPR014721; IPR020568; PTHR10169 (PANTHER), PTHR10169:SF2 (PANTHER)
Caenorhabditis briggsae	solute carrier family 35 (udp-glucuronic acid udp-n-acetylgalactosamine dual transporter) member d1	7	F:GO:0005463; C:GO:0030176; P:GO:0015789; P:GO:0006065; P:GO:0030206; C:GO:0005794; F:GO:0005461	-		IPR004853; PTHR11132 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	d- primase large subunit	9	P:GO:0000910; F:GO:0051536; P:GO:0040035; F:GO:0003896; P:GO:0006269; P:GO:0006997; P:GO:0006898; C:GO:0005654; P:GO:0009792	-		IPR007238
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis briggsae	aspartyl aminopeptidase	2	F:GO:0008233; P:GO:0043581	-		IPR001948; G3DSA:3.40.630.10 (GENE3D), SSF53187 (SUPERFAMILY)
	-	0				-
Loa loa	elegans protein partially confirmed by transcript evidence	1	F:GO:0016740	-		IPR005027; PTHR10896:SF2 (PANTHER)
	-	0				-

Caenorhabditis elegans	peroxisomal -trans-enoyl- isomerase	5	C:GO:0005777; F:GO:0016863; C:GO:0005739; P:GO:0006635; F:GO:0005515	-	EC:5.3.3.0	IPR001753; G3DSA:3.90.226.10 (GENE3D), PTHR11941 (PANTHER), SSF52096 (SUPERFAMILY)
Caenorhabditis briggsae	d- polymerase delta catalytic subunit	19	P:GO:0009411; P:GO:0000084; P:GO:0000910; F:GO:0003887; C:GO:0043625; P:GO:0006297; F:GO:0003677; F:GO:0008408; P:GO:0000731; P:GO:0045004; P:GO:0035188; P:GO:0006287; P:GO:0002119; F:GO:0005515; F:GO:0000166; P:GO:0006898; C:GO:0005654; P:GO:0009792; F:GO:0003682	-	EC:2.7.7.7	PTHR10322 (PANTHER), PTHR10322:SF4 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	4	C:GO:0016020; F:GO:0008324; P:GO:0006812; P:GO:0055085	-		-
Caenorhabditis briggsae	dead box atp-dependent r- helicase	7	C:GO:0005682; F:GO:0004004; F:GO:0003676; C:GO:0071011; F:GO:0005524; P:GO:0000398; C:GO:0071013	-		PTHR10967 (PANTHER), PTHR10967:SF47 (PANTHER)
Branchiostoma floridae	bita_bitar ame: full=bitiscetin subunit alpha	0		F:GO:0030247; F:GO:0004888; C:GO:0016021; C:GO:0016020; F:GO:0005529; F:GO:0004930; P:GO:0007166; C:GO:0005576; F:GO:0005044; F:GO:0004872; F:GO:0005515; P:GO:0009405; P:GO:0007186; F:GO:0005509; P:GO:0007155; F:GO:0005488; P:GO:0006955		IPR001304; IPR016186; IPR016187
	-	0				-
Caenorhabditis elegans	g protein alpha subunit	4	P:GO:0007186; F:GO:0019001; P:GO:0007165; P:GO:0008152	-		-

Caenorhabditis elegans	ubx domain protein 6	0		C:GO:0000300; C:GO:0019898; P:GO:0046324; C:GO:0009898; F:GO:0008270; P:GO:0042593; C:GO:0048471; C:GO:0005792; P:GO:0006886; C:GO:0005575; F:GO:0005515; C:GO:0012506; C:GO:0005622; C:GO:0005829; P:GO:0008150		PTHR23153 (PANTHER), PTHR23153:SF14 (PANTHER)
Angiostrongylus cantonensis	briggsae cbr-nhl-1 protein	3	F:GO:0008270; F:GO:0005515; P:GO:0006915	-		-
Caenorhabditis briggsae	tubulin-specific chaperone d	7	P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0046785; P:GO:0040011; P:GO:0040007; P:GO:0002009	-		IPR022577; PTHR12658 (PANTHER)
Caenorhabditis elegans	metabotropic gaba-b receptor subtype 2	3	C:GO:0016020; P:GO:0023052; F:GO:0004888	-		PTHR10519 (PANTHER), PTHR10519:SF2 (PANTHER), SSF53822 (SUPERFAMILY)
Brugia malayi	multidrug resistance protein family member (mrp-5)	11	P:GO:0055085; P:GO:0040010; F:GO:0042626; P:GO:0040002; F:GO:0008514; C:GO:0005624; F:GO:0005524; P:GO:0002119; P:GO:0040017; C:GO:0005887; P:GO:0010033	-		IPR001140; IPR011527; IPR017940; G3DSA:1.20.1560.10 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF14 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	extracellular protein	1	F:GO:0005515	-		-
Caenorhabditis briggsae	extracellular protein	1	F:GO:0005515	-		IPR006670; IPR006671; IPR011028; IPR013763; PTHR10177 (PANTHER), PTHR10177:SF4 (PANTHER)
Caenorhabditis elegans	sy-ptotagmin 1	10	P:GO:0016079; F:GO:0005509; F:GO:0005544; C:GO:0030672; C:GO:0030666; F:GO:0005515; C:GO:0044425; F:GO:0005215; C:GO:0042598; C:GO:0005886	-		IPR000008; IPR008973; IPR018029; G3DSA:2.60.40.150 (GENE3D), PTHR10024 (PANTHER), PTHR10024:SF28 (PANTHER)
	-	0				-
Streptomyces antibioticus	aldehyde dehydroge-se	2	F:GO:0016491; P:GO:0008152	-		IPR012394; IPR015590; IPR016161; IPR016162; SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	briggsae cbr-exc-7 protein	3	F:GO:0005515; F:GO:0000166; F:GO:0003723	-		IPR000504; IPR002343; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF55 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	receptor mediated endocytosis family member (rme-8)	1	F:GO:0031072	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	pab-dependent poly -specific ribonuclease subunit 3	1	F:GO:0005515	-		IPR011009; PTHR12272 (PANTHER), PTHR12272:SF6 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	homolog subfamily b member 6	0		C:GO:0048471; C:GO:0005737; P:GO:0008150; F:GO:0031072; C:GO:0005634; C:GO:0005575		IPR001623; IPR015609; IPR018253; PTHR11821:SF63 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG07646 [Caenorhabditis briggsae]	0				PTHR10984 (PANTHER), PTHR10984:SF1 (PANTHER)
Brugia malayi	prpf39 protein	0		F:GO:0005488; P:GO:0008380; P:GO:0006397; P:GO:0006396; C:GO:0005634; C:GO:0005622		IPR003107; PTHR17204 (PANTHER), PTHR17204:SF5 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	silent information regulator protein sir2	4	F:GO:0005488; P:GO:0045449; F:GO:0016787; P:GO:0006974	-		G3DSA:3.40.50.1220 (GENE3D), SSF52467 (SUPERFAMILY)
Camponotus floridanus	hypothetical protein EAG_09297 [Camponotus floridanus]	0				-
	-	0				-
Caenorhabditis briggsae	afg3 atpase family gene 3-like 2	13	F:GO:0008270; F:GO:0017111; P:GO:0048747; C:GO:0016021; F:GO:0004222; F:GO:0051082; P:GO:0016043; P:GO:0030163; P:GO:0006508; P:GO:0007399; P:GO:0065007; F:GO:0005524; C:GO:0005739	-	EC:3.6.1.15; EC:3.4.24.0	IPR000642; PTHR23076 (PANTHER), PTHR23076:SF11 (PANTHER), SSF140990 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	t family of potassium channels family member (twk-39)	1	F:GO:0005216	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	lysophosphatidylcholine acyltransferase 3	2	P:GO:0010171; C:GO:0016021	-		IPR004299; PTHR13906 (PANTHER), PTHR13906:SF2 (PANTHER), SignalP (SIGNALP)

Caenorhabditis elegans	rac gtpase	16	P:GO:0007390; P:GO:0007254; P:GO:0035099; P:GO:0030032; P:GO:0008258; P:GO:0007435; P:GO:0007264; C:GO:0005622; P:GO:0051017; F:GO:0004767; P:GO:0051301; F:GO:0003924; P:GO:0007394; C:GO:0016020; F:GO:0005525; P:GO:0006974	-	EC:3.1.4.12; EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001806; IPR003578; IPR005225; IPR013753; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF285 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	transcription factor tfb2 family protein	2	P:GO:0044260; P:GO:0090304	-		-
	-	0				-
Caenorhabditis elegans	ras-gef domain-containing family member 1b	3	F:GO:0005085; C:GO:0005622; P:GO:0051056	-		IPR001895; IPR008937; PTHR23113:SF20 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	microfibrillar-associated protein 1	9	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0001703; P:GO:0018996; P:GO:0016246; P:GO:0040010; C:GO:0005576; P:GO:0006898	-		-
Loa loa	hypothetical protein LOAG_08020 [Loa loa]	0				IPR003492; SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	small nuclear r- activating polypeptide 190kda	9	P:GO:0040010; P:GO:0006383; P:GO:0040035; P:GO:0002119; P:GO:0040011; P:GO:0009301; P:GO:0009792; C:GO:0005634; P:GO:0006366	-		IPR001005; IPR009057; IPR012287; IPR014778; IPR015495; IPR017877; IPR017930; PTHR10641:SF13 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0000003; F:GO:0008270; P:GO:0009792		-
Caenorhabditis briggsae	phosphofurin acidic cluster sorting protein 2	0				IPR019381; PTHR13280 (PANTHER), PTHR13280:SF4 (PANTHER)
	-	0				IPR021933; PTHR13165 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	5 nucleotidase family	4	P:GO:0009792; P:GO:0000003; P:GO:0040007; P:GO:0002119	-		IPR008380; PTHR12103:SF1 (PANTHER), SSF56784 (SUPERFAMILY)

Caenorhabditis elegans	inositol polyphosphate-5- 40kda	3	P:GO:0009987; F:GO:0004437; F:GO:0042731	-		G3DSA:3.60.10.10 (GENE3D), PTHR12997 (PANTHER), PTHR12997:SF2 (PANTHER)
Caenorhabditis elegans	cytochrome c oxidase assembly protein cox19	1	C:GO:0005739	-		-
	-	0				IPR019515
	-	0				-
Caenorhabditis elegans	phosphomannomutase 2	2	P:GO:0008152; F:GO:0016853	-		IPR005002; IPR006379; G3DSA:3.40.50.1000 (GENE3D), SSF56784 (SUPERFAMILY)
Brugia malayi	hypothetical protein Bm1_34635 [Brugia malayi]	0		F:GO:0003676		PTHR13058 (PANTHER), PTHR13058:SF1 (PANTHER)
Caenorhabditis elegans	briggsae cbr-acl-9 protein	4	F:GO:0008415; F:GO:0005515; C:GO:0016021; P:GO:0008152	-		PTHR13058 (PANTHER), PTHR13058:SF1 (PANTHER)
Caenorhabditis briggsae	orotidine 5 -phosphate decarboxylase	4	P:GO:0055086; F:GO:0005515; F:GO:0016740; F:GO:0016829	-		IPR001754; IPR011060; IPR013785
Homo sapiens	guanylate ki-se 1	3	F:GO:0004385; F:GO:0005524; P:GO:0006163	-	EC:2.7.4.8	IPR008144; IPR008145; IPR020590; G3DSA:3.30.63.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23117 (PANTHER), PTHR23117:SF1 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	kinesin family member 13a	7	P:GO:0007018; F:GO:0005515; F:GO:0005524; P:GO:0008152; F:GO:0003777; P:GO:0015031; C:GO:0005874	-		IPR001752; PTHR16012 (PANTHER), PTHR16012:SF65 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	viral a-type inclusion protein repeat containing protein	1	F:GO:0005515	-		SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein T14B4.1 [Caenorhabditis elegans]	0				-
Loa loa	mgc84124 protein	0		F:GO:0003676; F:GO:0005353; C:GO:0016021; F:GO:0022891; C:GO:0016020; P:GO:0055085; F:GO:0005215; P:GO:0006810		IPR002775; PTHR13516 (PANTHER), SSF82704 (SUPERFAMILY)

Drosophila mojavensis	receptor protein serine threonine ki-se	0		P:GO:0005025; P:GO:0045887; F:GO:0005024; P:GO:0042078; P:GO:0007179; P:GO:0007178; P:GO:0045595; F:GO:0004872; C:GO:0005886; P:GO:0048636; P:GO:0007304; P:GO:0030509; C:GO:0016020; P:GO:0007391; F:GO:0016566; F:GO:0004675; P:GO:0001763; F:GO:0004674; P:GO:0035215; P:GO:0090254; F:GO:0004672; P:GO:0007424; P:GO:0022407; F:GO:0005524; F:GO:0004702; F:GO:0000166; C:GO:0005771; P:GO:0006468;		PTHR23255 (PANTHER), PTHR23255:SF14 (PANTHER)
Caenorhabditis elegans	tb2 hva22 family protein	2	P:GO:0019915; P:GO:0009792	-		IPR004345; SignalP (SIGNALP)
Loa loa	eukaryotic translation initiation factor 5b (eif-5b) (translation initiation factor if-2)	9	P:GO:0009792; P:GO:0002119; F:GO:0003746; F:GO:0005525; F:GO:0004781; P:GO:0000003; F:GO:0003743; P:GO:0040007; F:GO:0003924	-	EC:2.7.7.4; EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000795; IPR004161; IPR005225; IPR009000; IPR015760; IPR023115; G3DSA:2.40.30.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23115 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	related to yeast vacuolar protein sorting factor family member (vps-41)	9	P:GO:0009792; P:GO:0002119; F:GO:0046872; C:GO:0005773; P:GO:0006624; P:GO:0040007; P:GO:0007034; P:GO:0043066; P:GO:0015031	-		PTHR12616 (PANTHER)
Caenorhabditis briggsae	deah (asp-glu-ala-his) box polypeptide 16	4	F:GO:0003676; F:GO:0005524; F:GO:0005515; F:GO:0008026	-		PTHR18934 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-

Caenorhabditis briggsae	d- polymerase kappa	1	F:GO:0003677	-		IPR001126; IPR017963; G3DSA:1.10.150.20 (GENE3D), G3DSA:3.30.70.270 (GENE3D), PTHR11076:SF12 (PANTHER), PF11798 (PFAM), SSF56672 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG13916 [Caenorhabditis briggsae]	0				IPR016017; SSF110035 (SUPERFAMILY)
Caenorhabditis briggsae	d- replication licensing factor mcm5	6	P:GO:0009792; P:GO:0006260; P:GO:0001703; P:GO:0000910; P:GO:0040010; F:GO:0000166	-		-
	-	0				-
Caenorhabditis briggsae	cdp-alcohol phosphatidyltransferase family protein	3	C:GO:0016020; F:GO:0016780; P:GO:0008654	-	EC:2.7.8.0	IPR000462; PTHR10414 (PANTHER), PTHR10414:SF4 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	yl54_caeel ame: full=uncharacterized protein	0				-
	-	0				-
Caenorhabditis briggsae	large tumor suppressor 1	12	P:GO:0045736; P:GO:0007243; F:GO:0004674; C:GO:0000922; F:GO:0005524; P:GO:0009755; P:GO:0090090; F:GO:0005515; P:GO:0035329; P:GO:0000082; C:GO:0005634; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR002290; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22985 (PANTHER), PTHR22985:SF91 (PANTHER)
Nasonia vitripennis	beta-arrestin 1	0		P:GO:0007600; P:GO:0007165		IPR014753; IPR014756
	-	0				-
	-	0				-
	-	0				-
synthetic construct	atp synthase subunit mitochondrial-like	5	F:GO:0015078; C:GO:0000276; P:GO:0042776; F:GO:0016887; F:GO:0005515	-		IPR006808; PTHR12386 (PANTHER), PTHR12386:SF3 (PANTHER)
Loa loa	briggsae cbr-ppfr-2 protein	0				IPR015267; PTHR16487 (PANTHER)
Caenorhabditis briggsae	acyl- dehydroge-se-like protein	8	P:GO:0006468; F:GO:0004713; P:GO:0055114; F:GO:0016787; F:GO:0005524; F:GO:0003995; F:GO:0050660; P:GO:0006508	-	EC:2.7.10.0; EC:1.3.99.3	IPR000169; IPR006090; IPR006091; IPR009075; IPR009100; PTHR10909 (PANTHER), PTHR10909:SF10 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		IPR007967; SSF103107 (SUPERFAMILY)
	-	0				-
	-	0				-

Caenorhabditis briggsae	niemann-pick type c2	0		C:GO:0005576		IPR003172; IPR014756; PTHR11306 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Strongylocentrotus purpuratus	: shorter than wild-type family member (dpy-23)	6	C:GO:0030122; F:GO:0008289; F:GO:0005515; P:GO:0016192; P:GO:0006886; C:GO:0005739	-		IPR001392; IPR011012; IPR015629; G3DSA:3.30.450.60 (GENE3D), PTHR11998 (PANTHER)
Brugia malayi	schip-1-d241 253	0		F:GO:0004553; C:GO:0042597		IPR015649
	-	0				-
	-	0				-
	-	0				-
	-	0				IPR001548; PTHR10514:SF7 (PANTHER)
Caenorhabditis briggsae	udp-galactose transporter family protein	5	P:GO:0015785; P:GO:0015788; C:GO:0030173; F:GO:0005462; F:GO:0005459	-		-
	-	0				-
	-	0				-
Pongo abelii	host cell factor 1	11	C:GO:0071339; P:GO:0045787; P:GO:0043254; P:GO:0045449; F:GO:0042802; P:GO:0019046; F:GO:0003700; C:GO:0070688; F:GO:0003713; C:GO:0005737; P:GO:0006366	-		IPR006652; IPR011498; IPR015915; PTHR23244 (PANTHER), PTHR23244:SF36 (PANTHER), SSF117281 (SUPERFAMILY)
	-	0				-
Homo sapiens	tr- methyltransferase 112 homolog	4	C:GO:0043234; F:GO:0008276; F:GO:0005515; P:GO:0018364	-		-
Caenorhabditis briggsae	ww domain-containing protein	0		F:GO:0005515		IPR006596; G3DSA:3.40.50.1010 (GENE3D), SSF88723 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	dymeclin	4	P:GO:0009792; P:GO:0000003; F:GO:0005515; P:GO:0002119	-		IPR019142; PTHR12895 (PANTHER), PTHR12895:SF2 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	7	F:GO:0005488; P:GO:0030421; P:GO:0008340; P:GO:0006264; F:GO:0016791; F:GO:0016740; P:GO:0008406	-	EC:3.1.3.0	-

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; P:GO:0007186		IPR017452; PTHR22751 (PANTHER), PTHR22751:SF8 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	small subunit processome component 20 homolog	3	F:GO:0005488; C:GO:0031981; P:GO:0006364	-		SignalP (SIGNALP)
Caenorhabditis elegans	solute carrier family 41 member 1	2	F:GO:0008324; P:GO:0006812	-		IPR006667; PTHR16228 (PANTHER), SignalP (SIGNALP)
	-	0				-
Loa loa	ring finger protein 185	1	F:GO:0005488	-		IPR001841; IPR013083; IPR017907; IPR018957; PTHR12313 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis elegans	serine threonine-protein ki-se mrck beta	12	F:GO:0005083; F:GO:0004674; C:GO:0005856; P:GO:0007163; P:GO:0031532; C:GO:0031252; F:GO:0005524; C:GO:0005911; F:GO:0000287; P:GO:0007165; F:GO:0017048; P:GO:0006468	-	EC:2.7.11.0	IPR011009; G3DSA:3.30.200.20 (GENE3D), PTHR22988 (PANTHER), PTHR22988:SF2 (PANTHER)
Caenorhabditis elegans	briggsae cbr-fhod-1 protein	2	F:GO:0003779; P:GO:0030036	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	atp-dependent r- helicase a	11	C:GO:0070937; F:GO:0003676; P:GO:0070934; C:GO:0005730; F:GO:0008026; P:GO:0008380; C:GO:0005813; F:GO:0005515; C:GO:0030529; P:GO:0034605; F:GO:0003724	-		IPR001159; IPR014720; G3DSA:3.40.50.300 (GENE3D), PTHR18934 (PANTHER), SSF52540 (SUPERFAMILY), SSF54768 (SUPERFAMILY)
Loa loa	acyl- synthetase long-chain family member 5	9	P:GO:0048518; P:GO:0010033; P:GO:0044255; P:GO:0009792; C:GO:0031090; P:GO:0044281; C:GO:0044446; F:GO:0003824; C:GO:0005739	-		IPR000873; G3DSA:3.40.50.980 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF8 (PANTHER), SSF56801 (SUPERFAMILY)
Brugia malayi	gem-associated protein 7	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-dhs-14 protein	5	P:GO:0009792; F:GO:0005515; P:GO:0044237; P:GO:0040010; F:GO:0003824	-		IPR002198; IPR002347; IPR016040; PTHR19410:SF76 (PANTHER), SSF51735 (SUPERFAMILY)

Caenorhabditis briggsae	tetratricopeptide repeat protein 4	7	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0040018; P:GO:0040010; P:GO:0040011; P:GO:0006898	-		-
	-	0				-
Caenorhabditis elegans	hypothetical protein F37E3.3 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	Hypothetical protein CBG16818 [Caenorhabditis briggsae]	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	solute carrier family 25 (mitochondrial carrier oxoglutarate carrier) member 11	6	F:GO:0015367; C:GO:0005887; F:GO:0005488; C:GO:0005743; P:GO:0055085; P:GO:0006839	-		-
Caenorhabditis briggsae	related to yeast vacuolar protein sorting factor family member (vps-34)	5	F:GO:0005488; C:GO:0005942; P:GO:0046854; F:GO:0016303; P:GO:0048015	-	EC:2.7.1.137	IPR000403; IPR011009; IPR015433; IPR018936; G3DSA:3.30.1010.10 (GENE3D), PTHR10048:SF7 (PANTHER)
	-	0				-
Caenorhabditis elegans	cornichon	9	P:GO:0008314; P:GO:0046843; P:GO:0023034; P:GO:0045450; P:GO:0030722; P:GO:0045451; P:GO:0008069; P:GO:0006888; C:GO:0005887	-		IPR003377; PTHR12290 (PANTHER), PTHR12290:SF3 (PANTHER), SignalP (SIGNALP)
Loa loa	protein ki-se domain containing protein	0		F:GO:0016301; F:GO:0004672; F:GO:0005524; F:GO:0000166; P:GO:0006468; F:GO:0004674		IPR011009; IPR017441; G3DSA:3.30.200.20 (GENE3D), PTHR22974 (PANTHER), PTHR22974:SF5 (PANTHER)
	-	0				IPR000631; G3DSA:3.40.1190.20 (GENE3D)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	glutamic acid decarboxylase	3	F:GO:0030170; P:GO:0019752; F:GO:0016831	-	EC:4.1.1.0	IPR002129; IPR015421; IPR015422; IPR015424; PTHR11999:SF13 (PANTHER)
Caenorhabditis elegans	1-acylglycerol-3-phosphate acyltransferase	4	F:GO:0008415; C:GO:0016021; P:GO:0009792; P:GO:0008152	-		PTHR10983 (PANTHER), PTHR10983:SF2 (PANTHER)
Caenorhabditis elegans	diacylglycerol acyltransferase family protein	4	P:GO:0009792; F:GO:0016747; C:GO:0016021; P:GO:0008152	-	EC:2.3.1.0	IPR007130; SignalP (SIGNALP)

Pongo abelii	collagen alpha-2 chain-like	17	P:GO:0042476; F:GO:0030674; P:GO:0070208; P:GO:0043589; P:GO:0008217; F:GO:0042802; C:GO:0005615; F:GO:0046332; P:GO:0001501; F:GO:0048407; C:GO:0005584; P:GO:0030199; P:GO:0007179; F:GO:0005201; P:GO:0001568; P:GO:0007266; C:GO:0005886	-		IPR008160; PTHR10499 (PANTHER), PTHR10499:SF123 (PANTHER)
Brugia malayi	iesterase family member (pde-2)	9	F:GO:0004118; P:GO:0046069; F:GO:0046872; F:GO:0030552; C:GO:0045121; P:GO:0007165; F:GO:0042803; F:GO:0030553; P:GO:0006198	-		G3DSA:3.30.450.40 (GENE3D), SSF55781 (SUPERFAMILY)
Pristionchus pacificus	aldo-keto reductase	2	P:GO:0040010; P:GO:0040011	-		IPR001395; IPR023210; PTHR11732:SF34 (PANTHER)
Caenorhabditis briggsae	dachsous 1	5	P:GO:0016337; P:GO:0050794; P:GO:0007275; C:GO:0044464; P:GO:0007166	-		IPR002126; IPR015919; PTHR10596 (PANTHER), PTHR10596:SF74 (PANTHER)
Caenorhabditis briggsae	#NAME?	5	P:GO:0040010; P:GO:0009086; P:GO:0055114; F:GO:0005515; F:GO:0004489	-	EC:1.5.1.20	IPR003171; G3DSA:3.20.20.220 (GENE3D), SSF51730 (SUPERFAMILY)
Caenorhabditis briggsae	#NAME?	5	P:GO:0040010; P:GO:0009086; P:GO:0055114; F:GO:0005515; F:GO:0004489	-	EC:1.5.1.20	-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	reverse transcriptase	4	F:GO:0004519; F:GO:0003723; F:GO:0003964; P:GO:0006278	-	EC:2.7.7.49	-
Chlorella variabilis	nuclear protein hcc-1	0		F:GO:0003676; P:GO:0009792; F:GO:0005515		IPR003034; G3DSA:1.10.720.30 (GENE3D)
	-	0				SignalP (SIGNALP)

Ciona intestinalis	elegans protein partially confirmed by transcript evidence	0		F:GO:0004348; C:GO:0005764; P:GO:0006665; P:GO:0007040; P:GO:0005975; F:GO:0003824; F:GO:0043169		IPR001139; SignalP (SIGNALP), SSF51011 (SUPERFAMILY)
Loa loa	set domain containing protein	0		F:GO:0046872; P:GO:0006355; F:GO:0003676; F:GO:0008270; C:GO:0005634; C:GO:0005622		IPR001214; G3DSA:2.170.270.10 (GENE3D), SSF82199 (SUPERFAMILY)
Drosophila mojavensis	partner of drosha	5	P:GO:0007446; P:GO:0031053; F:GO:0003725; F:GO:0005515; C:GO:0005634	-		IPR001202
Brugia malayi	shq1 homolog (cerevisiae)	0		P:GO:0006508; F:GO:0003674; F:GO:0008234; C:GO:0005575		IPR007009; PTHR12967 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-cln- protein	9	P:GO:0008340; P:GO:0006665; C:GO:0005794; P:GO:0046662; P:GO:0009792; C:GO:0044425; P:GO:0016043; C:GO:0044446; P:GO:0006873	-		-
Brugia malayi	g protein-coupled receptor 107	2	C:GO:0016021; F:GO:0004872	-		-
Loa loa	patched family protein	6	P:GO:0048856; P:GO:0040018; P:GO:0018996; P:GO:0007275; P:GO:0040011; C:GO:0016020	-		IPR000731; IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER), SignalP (SIGNALP)
Loa loa	hemimethylated d- binding domain containing protein	0				-
Brugia malayi	ciao1_caeel ame: full=probable cytosolic iron-sulfur protein assembly protein ciao1 homolog	0		F:GO:0005488; P:GO:0016226; C:GO:0005856		IPR015943; IPR017986; IPR019781; IPR019782
Caenorhabditis elegans	leucine-rich repeat serine threonine-protein ki-se 1	7	P:GO:0006468; F:GO:0005525; C:GO:0005622; F:GO:0005515; F:GO:0005524; F:GO:0004674; P:GO:0007264	-	EC:2.7.11.0	IPR001245; G3DSA:3.30.200.20 (GENE3D), PTHR23257 (PANTHER), PTHR23257:SF88 (PANTHER)
Caenorhabditis briggsae	pentatricopeptide repeat domain 3	4	P:GO:0009792; P:GO:0016246; P:GO:0040007; P:GO:0002119	-		PTHR16276 (PANTHER), SignalP (SIGNALP)

Caenorhabditis briggsae	pentatricopeptide repeat domain 3	4	P:GO:0009792; P:GO:0016246; P:GO:0040007; P:GO:0002119	-		PTHR16276 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	failed axon connections protein	0				-
	-	0				IPR006942
Caenorhabditis briggsae	acyl- thioesterase ii	1	P:GO:0019915	-		IPR003703; G3DSA:3.10.129.10 (GENE3D), PTHR11066:SF7 (PANTHER), SSF54637 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0016787		IPR002018; PTHR11559:SF6 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	isovaleryl coenzyme a dehydroge-se	3	F:GO:0050660; P:GO:0055114; F:GO:0003995	-	EC:1.3.99.3	IPR006092; IPR009100; IPR013786; PTHR10909 (PANTHER), PTHR10909:SF10 (PANTHER)
Caenorhabditis briggsae	histone deacetylase 6	11	F:GO:0016811; C:GO:0005737; P:GO:0006511; F:GO:0008092; P:GO:0006996; P:GO:0006476; C:GO:0043234; P:GO:0050794; C:GO:0043229; F:GO:0033558; P:GO:0043241	-	EC:3.5.1.0	IPR000286; PTHR10625:SF19 (PANTHER), SSF52768 (SUPERFAMILY)
	-	0				-
Callithrix jacchus	eukaryotic translation initiation factor subunit e	9	F:GO:0003743; C:GO:0005829; F:GO:0047485; P:GO:0045948; C:GO:0005852; C:GO:0000785; C:GO:0016605; P:GO:0045947; P:GO:0000184	-		SignalP (SIGNALP)
Clostridium sporogenes ATCC 15579	collagen triple helix repeat protein	0				IPR022226; PTHR15606 (PANTHER), PTHR15606:SF2 (PANTHER)
Clostridium sporogenes ATCC 15579	collagen triple helix repeat protein	0				IPR022226; PTHR15606 (PANTHER), PTHR15606:SF2 (PANTHER)
Caenorhabditis briggsae	udp-glucose 4-epimerase	7	P:GO:0006694; F:GO:0003854; F:GO:0005515; F:GO:0003978; P:GO:0000003; P:GO:0006012; F:GO:0050662	-	EC:1.1.1.145 ; EC:5.1.3.2	IPR001509; IPR005886; IPR016040; PTHR10366 (PANTHER), SignalP (SIGNALP), SSF51735 (SUPERFAMILY)
	-	0				-
	-	0				-
Brugia malayi	mgc14327-like protein	0		C:GO:0016021; P:GO:0008150		SignalP (SIGNALP)
Caenorhabditis elegans	ubiquitin-fold modifier 1	4	C:GO:0005737; C:GO:0005634; F:GO:0005515; P:GO:0071569	-		IPR005375; G3DSA:3.10.20.90 (GENE3D), SSF54236 (SUPERFAMILY)

Caenorhabditis elegans	ubiquitin-fold modifier 1	4	C:GO:0005737; C:GO:0005634; F:GO:0005515; P:GO:0071569	-		IPR005375; G3DSA:3.10.20.90 (GENE3D), SSF54236 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	family with sequence similarity member a	1	F:GO:0005515	-		PTHR22875 (PANTHER), PTHR22875:SF1 (PANTHER)
Caenorhabditis elegans	family with sequence similarity member a	1	F:GO:0005515	-		PTHR22875 (PANTHER), PTHR22875:SF1 (PANTHER)
Caenorhabditis elegans	pdz domain containing protein	5	P:GO:0009792; P:GO:0040007; P:GO:0040035; F:GO:0005515; P:GO:0002119	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR19964 (PANTHER), PTHR19964:SF5 (PANTHER)
Pongo abelii	neudesin precursor	4	C:GO:0005615; F:GO:0008083; P:GO:0043410; F:GO:0020037	-		-
Loa loa	glutamine-oxaloacetic transami-se	6	F:GO:0030170; P:GO:0006536; P:GO:0006531; P:GO:0006103; P:GO:0009058; F:GO:0004069	-	EC:2.6.1.1	IPR000796; IPR015422; IPR015424
Caenorhabditis briggsae	receptor type guanylyl cyclase	7	F:GO:0004383; F:GO:0004672; F:GO:0008528; F:GO:0005524; C:GO:0016020; P:GO:0006468; P:GO:0006182	-	EC:4.6.1.2	-
Caenorhabditis elegans	amp-binding enzyme family protein	6	P:GO:0010890; F:GO:0004467; C:GO:0005811; P:GO:0007411; P:GO:0008152; C:GO:0005783	-	EC:6.2.1.3	-
Caenorhabditis elegans	golgi s-p receptor complex member 1	0		F:GO:0004872; F:GO:0005484; C:GO:0016020; P:GO:0042147; C:GO:0000139; P:GO:0006886; C:GO:0005794		PTHR21094 (PANTHER)
	-	0				-
Brugia malayi	exosome complex exonuclease rrp40	1	C:GO:0005737	-		IPR022967; PTHR21321 (PANTHER), PTHR21321:SF1 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-spg-7 protein	9	F:GO:0004222; P:GO:0030163; F:GO:0005524; C:GO:0016021; F:GO:0017111; P:GO:0006508; F:GO:0008270; C:GO:0005783; C:GO:0005739	-	EC:3.4.24.0; EC:3.6.1.15	IPR003593; IPR003959; G3DSA:3.40.50.300 (GENE3D), PTHR23076 (PANTHER), PTHR23076:SF11 (PANTHER), SSF52540 (SUPERFAMILY)

Synechococcus sp. RS9916	short-chain dehydroge-se reductase superfamily protein	0		P:GO:0055114; F:GO:0005488; F:GO:0016491; P:GO:0008152; F:GO:0016630; F:GO:0003824		-
Caenorhabditis elegans	scy1-like 2 protein	3	P:GO:0006468; F:GO:0005524; F:GO:0004672	-		PTHR12984 (PANTHER), PTHR12984:SF3 (PANTHER)
Caenorhabditis briggsae	transmembrane protein 87b	2	F:GO:0004872; C:GO:0016021	-		-
Caenorhabditis briggsae	briggsae cbr-phy-2 protein	7	P:GO:0018401; F:GO:0031418; F:GO:0005506; F:GO:0004656; P:GO:0055114; F:GO:0016702; C:GO:0005783	-	EC:1.14.11.2; EC:1.13.11.0	IPR011990; IPR013547; PTHR10869 (PANTHER), PTHR10869:SF13 (PANTHER)
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	2	P:GO:0009792; P:GO:0000003	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-lam-3 protein	5	C:GO:0005606; P:GO:0030334; P:GO:0045995; P:GO:0030155; F:GO:0005102	-		IPR000034; PTHR10574 (PANTHER), PTHR10574:SF25 (PANTHER)
	-	0				-
Caenorhabditis elegans	protein	0		P:GO:0016998; P:GO:0016042; C:GO:0005576; F:GO:0005179; P:GO:0006644; P:GO:0009253; F:GO:0003796; F:GO:0005509; F:GO:0004623		-
Caenorhabditis briggsae	alkaline phosphatase specific for p-nitrophenyl phosphate	0		F:GO:0016791; P:GO:0008152; F:GO:0016787; F:GO:0003824; F:GO:0003869		G3DSA:3.40.50.1000 (GENE3D), PTHR19288 (PANTHER), PTHR19288:SF11 (PANTHER)
Ostertagia ostertagi	secreted protein asp-2	1	P:GO:0040011	-		IPR001283; IPR014044; IPR018244; PTHR10334:SF11 (PANTHER)
Caenorhabditis briggsae	slowpoke potassium channel family member (slo-2)	6	C:GO:0016020; P:GO:0006813; P:GO:0008152; F:GO:0003824; F:GO:0015269; F:GO:0005488	-		IPR003929; IPR016040; PTHR10027 (PANTHER), PTHR10027:SF6 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	molybdenum cofactor synthesis 3	10	P:GO:0018192; F:GO:0016779; C:GO:0005829; P:GO:0034227; P:GO:0006777; F:GO:0004792; P:GO:0040035; F:GO:0042292; F:GO:0005515; P:GO:0002098	-	EC:2.7.7.0; EC:2.8.1.1	IPR000594; IPR007901; IPR009036; IPR016040; PTHR10953 (PANTHER)
Brugia malayi	polycomb protein	9	P:GO:0016574; P:GO:0006333; P:GO:0006342; F:GO:0004842; C:GO:0000785; F:GO:0005515; C:GO:0000151; F:GO:0003682; C:GO:0005634	-	EC:6.3.2.19	IPR000953; IPR016197; IPR017984; G3DSA:2.40.50.40 (GENE3D), PTHR22812 (PANTHER), PTHR22812:SF7 (PANTHER)
Caenorhabditis elegans	i in (lysosomal protein) homolog family member (ctns-1)	8	P:GO:0015811; P:GO:0003333; C:GO:0045335; F:GO:0015171; F:GO:0005515; P:GO:0007165; C:GO:0005765; C:GO:0016021	-		PTHR13131 (PANTHER)
Caenorhabditis briggsae	adenylyl cyclase family member (acy-3)	0				-
Loa loa	structural mainte-nce of chromosomes protein 3	1	F:GO:0005488	-		PTHR18937 (PANTHER), PTHR18937:SF8 (PANTHER)
	-	0				-
Heligmosomoides polygyrus	-ttectin precursor	0		F:GO:0005488; F:GO:0005509; P:GO:0007155; F:GO:0005529		IPR001304; IPR016186; IPR016187; PTHR22801 (PANTHER), PTHR22801:SF9 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	fgf receptor activating protein isoform cra_c	8	F:GO:0008565; P:GO:0006506; C:GO:0000139; P:GO:0006916; F:GO:0005515; C:GO:0005789; C:GO:0005634; P:GO:0006974	-		IPR019402; PTHR12892 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				IPR007087; IPR015880; SSF57667 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				IPR007087; IPR015880; SSF57667 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	uncharacterized protein c19orf47	0				IPR001660; IPR010993; IPR011510; IPR013761; PTHR21359 (PANTHER)
Caenorhabditis elegans	uncharacterized protein c19orf47	0				IPR001660; IPR010993; IPR011510; IPR013761; PTHR21359 (PANTHER)

Caenorhabditis briggsae	eb module family protein	0		F:GO:0004674; F:GO:0016810; F:GO:0004672; P:GO:0006468; F:GO:0000166; F:GO:0005524; P:GO:0005975; F:GO:0016491; F:GO:0003824; F:GO:0005515; F:GO:0004867; F:GO:0005488		IPR006149; IPR006210
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	mitochondrial ribosomal	8	P:GO:0006412; P:GO:0040010; C:GO:0005840; F:GO:0003735; P:GO:0000003; P:GO:0002119; P:GO:0006898; P:GO:0009792	-	EC:3.6.5.3	SignalP (SIGNALP)
Loa loa	integrator complex subunit 3	7	C:GO:0070876; F:GO:0005515; P:GO:0010212; P:GO:0016180; P:GO:0031576; P:GO:0006281; C:GO:0032039	-		PTHR13587 (PANTHER)
Caenorhabditis briggsae	atp-dependent r- helicase	3	F:GO:0008026; F:GO:0003676; F:GO:0005524	-		IPR007502; PTHR18934 (PANTHER), SignalP (SIGNALP)
	-	0				-
Brugia malayi	protein o-fucosyltransferase 2	5	P:GO:0007283; P:GO:0010171; P:GO:0040025; F:GO:0016757; P:GO:0018991	-		IPR019378; PTHR13398 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-rbc-1 protein	0				PTHR13950 (PANTHER), PTHR13950:SF1 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Camponotus floridanus	transposase-like	0				IPR005471; IPR009057; IPR011991
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	dymeclin	4	P:GO:0002119; F:GO:0005515; P:GO:0009792; P:GO:0000003	-		IPR019142; PTHR12895 (PANTHER), PTHR12895:SF2 (PANTHER)
Caenorhabditis elegans	gex interacting protein family member (gei-16)	1	F:GO:0005515	-		-
	-	0				-

Caenorhabditis elegans	plasma membrane proteolipid 3	0		F:GO:0003674; P:GO:0043581; C:GO:0016021; C:GO:0016020; P:GO:0008150; P:GO:0006810; C:GO:0005886		IPR000612; SignalP (SIGNALP)
Caenorhabditis elegans	mitochondrial ribosomal	6	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0040018; P:GO:0008340; P:GO:0006898	-		-
	-	0				-
Caenorhabditis elegans	hypothetical protein F39G3.5 [Caenorhabditis elegans]	0		F:GO:0005515		IPR004877; IPR006593; PTHR10106 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	polk (d- polymerase kappa) homolog family member (polk-1)	1	C:GO:0016020	-		IPR001126; IPR017961; IPR017962; PTHR11076:SF12 (PANTHER), PF11799 (PFAM)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	2	C:GO:0005856; F:GO:0000166	-		IPR000857; PTHR13140 (PANTHER), PTHR13140:SF27 (PANTHER)
Caenorhabditis elegans	dis3 mitotic control homolog (cerevisiae)	4	F:GO:0005515; F:GO:0004518; F:GO:0016219; C:GO:0044424	-		PTHR23355 (PANTHER), PTHR23355:SF13 (PANTHER)
Caenorhabditis elegans	dis3 mitotic control homolog (cerevisiae)	3	F:GO:0005488; F:GO:0004518; C:GO:0044424	-		PTHR23355 (PANTHER), PTHR23355:SF13 (PANTHER)
	-	0				-
Caenorhabditis elegans	type alpha 2	0		C:GO:0005594; F:GO:0042302		IPR008160; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER), SignalP (SIGNALP)
Loa loa	stromal antigen 2	6	P:GO:0032876; P:GO:0007062; C:GO:0000785; F:GO:0005515; C:GO:0015629; C:GO:0005634	-		PTHR11199 (PANTHER)
Loa loa	stromal antigen 2	6	P:GO:0032876; P:GO:0007062; C:GO:0000785; F:GO:0005515; C:GO:0015629; C:GO:0005634	-		PTHR11199 (PANTHER)
	-	0				SignalP (SIGNALP)
Brugia malayi	mbt repeat family protein	0		P:GO:0045449; F:GO:0008270; C:GO:0005634		IPR004092; G3DSA:2.30.30.160 (GENE3D), PTHR12247 (PANTHER), PTHR12247:SF1 (PANTHER), SSF63748 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG06766 [Caenorhabditis briggsae]	1	P:GO:0006915	-		IPR002223; PTHR10083 (PANTHER), PTHR10083:SF38 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	gtp cyclohydrolase 1 feedback regulatory protein	5	P:GO:0050789; F:GO:0005515; P:GO:0008152; F:GO:0003824; C:GO:0044424	-		-

Caenorhabditis briggsae	peptidase s9 prolyl oligopeptidase active site domain protein	1	F:GO:0016787	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	acyl-coenzyme a oxidase palmitoyl	11	F:GO:0003995; P:GO:0006693; F:GO:0016401; C:GO:0005739; P:GO:0033540; P:GO:0055114; P:GO:0006091; P:GO:0007283; C:GO:0005778; F:GO:0050660; F:GO:0005504	-	EC:1.3.99.3	IPR006091; IPR009075; IPR009100; IPR012258; PTHR10909 (PANTHER)
Brugia malayi	hypothetical protein Bm1_19575 [Brugia malayi]	0		F:GO:0005515		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	sodium hydrogen exchanger 3	5	F:GO:0015385; P:GO:0055085; P:GO:0006885; C:GO:0016021; P:GO:0006814	-		IPR006153; IPR018416; IPR018422; SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-vit-4 protein	4	P:GO:0009792; F:GO:0005515; P:GO:0040010; P:GO:0008340	-		IPR001846; PTHR11339 (PANTHER), PTHR11339:SF43 (PANTHER)
Caenorhabditis elegans	briggsae cbr-vit-4 protein	4	P:GO:0009792; F:GO:0005515; P:GO:0040010; P:GO:0008340	-		IPR001846; PTHR11339 (PANTHER), PTHR11339:SF43 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0003723; P:GO:0009451; P:GO:0001522; F:GO:0009982		-
Caenorhabditis briggsae	briggsae cbr-rhy-1 protein	2	C:GO:0016021; F:GO:0016747	-	EC:2.3.1.0	PTHR11161 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	tar-binding protein	1	F:GO:0042802	-		-
	-	0				-
Caenorhabditis briggsae	d- repair protein rev1	6	P:GO:0040010; F:GO:0005488; P:GO:0042276; F:GO:0017125; P:GO:0006898; P:GO:0009792	-		IPR001357; G3DSA:3.40.50.10190 (GENE3D)
Pongo abelii	prostate tumor-overexpressed gene 1	4	P:GO:0045449; C:GO:0005886; C:GO:0005634; C:GO:0048471	-		IPR021394; PTHR12433 (PANTHER), PTHR12433:SF3 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-rbc-2 protein	0				-

	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0000003; P:GO:0010171; P:GO:0040018		-
	-	0				-
Caenorhabditis elegans	tr- isopentenyltransferase	5	C:GO:0005622; F:GO:0005524; F:GO:0016740; F:GO:0008270; P:GO:0008033	-		IPR002627; G3DSA:3.40.50.300 (GENE3D), PTHR11088:SF21 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-unc-26 protein	11	P:GO:0048790; F:GO:0003723; F:GO:0004439; P:GO:0016311; C:GO:0043195; C:GO:0012506; F:GO:0000166; F:GO:0004445; F:GO:0004518; P:GO:0050803; P:GO:0048488	-	EC:3.1.3.36; EC:3.1.3.56	-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-pgp-9 protein	0		F:GO:0005524; F:GO:0016887; C:GO:0016021; F:GO:0000166; F:GO:0042626; F:GO:0017111; P:GO:0055085; P:GO:0006810		SignalP (SIGNALP)
Caenorhabditis elegans	phe-zine biosynthesis-like domain-containing protein	0		P:GO:0009058; F:GO:0003674; F:GO:0003824; P:GO:0008150; C:GO:0005575; F:GO:0016853		IPR003719; G3DSA:3.10.310.10 (GENE3D), SSF54506 (SUPERFAMILY)
Caenorhabditis elegans	wd repeat and sof domain-containing protein 1	9	C:GO:0080008; P:GO:0040010; F:GO:0005488; F:GO:0008415; P:GO:0040035; P:GO:0002119; P:GO:0040039; P:GO:0006898; C:GO:0005634	-		IPR007287; PTHR22851 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Loa loa	fkbp12-rapamycin complex-associated protein	1	F:GO:0016740	-		SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein Y38F2AR.3 [Caenorhabditis elegans]	1	P:GO:0000003	-		-
Haemonchus contortus	lectin galactoside-binding soluble 4	0		P:GO:0007155; C:GO:0005829; F:GO:0005529; C:GO:0005886		SignalP (SIGNALP)
	-	0				-

Xenopus (Silurana) tropicalis	venom c-type lectin mannose binding isoform 4	0		F:GO:0005488; F:GO:0005044; P:GO:0007155; C:GO:0016020; F:GO:0005529; C:GO:0005576; P:GO:0009405		IPR001304; IPR016186; IPR016187
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	F:GO:0005089; C:GO:0005622; P:GO:0035023	-		IPR000219; PTHR22826 (PANTHER), PTHR22826:SF50 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-nrs-1 protein	3	F:GO:0004812; P:GO:0006418; F:GO:0000166	-		-
Loa loa	briggsae cbr-scc-3 protein	1	F:GO:0005515	-		-
	-	0				IPR022272
Caenorhabditis elegans	erin family member (cdh-6)	2	C:GO:0016020; P:GO:0007155	-		IPR000832; SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	centromere protein b	2	F:GO:0003677; C:GO:0043229	-		IPR004906; IPR006600; IPR009057; IPR012287; PTHR19303 (PANTHER), PTHR19303:SF11 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		IPR007967; SSF103107 (SUPERFAMILY)
Loa loa	jmjc domain containing protein	7	F:GO:0051864; F:GO:0008270; C:GO:0005730; F:GO:0016564; F:GO:0005515; P:GO:0016577; C:GO:0005737	-	EC:1.14.11.27	IPR003347; PTHR10694 (PANTHER), PTHR10694:SF7 (PANTHER)
	-	0				-
Caenorhabditis briggsae	ipase c family member (plc-1)	10	F:GO:0005085; P:GO:0006629; F:GO:0004871; C:GO:0005622; F:GO:0004435; P:GO:0040010; F:GO:0005509; P:GO:0009566; P:GO:0032836; P:GO:0007264	-	EC:3.1.4.11	PTHR10336 (PANTHER), PTHR10336:SF6 (PANTHER), SignalP (SIGNALP)
Apis mellifera	isoform c	0				IPR006573; PTHR12429 (PANTHER)
	-	0				-
Caenorhabditis elegans	protein ki-se domain containing protein	2	F:GO:0016301; F:GO:0000166	-		IPR001611; G3DSA:3.80.10.10 (GENE3D), PS51450 (PROFILE), SignalP (SIGNALP)
Loa loa	vav 2 oncogene	3	F:GO:0005085; C:GO:0005622; F:GO:0005515	-		IPR000219; IPR011993; PTHR22826 (PANTHER), PTHR22826:SF53 (PANTHER), SSF50729 (SUPERFAMILY)
Ancylostoma caninum	kunitz-like protease inhibitor precursor	0		F:GO:0008233; F:GO:0004867		SignalP (SIGNALP)
	-	0				IPR001577; IPR016160; G3DSA:2.30.34.10 (GENE3D)

Caenorhabditis elegans	poly atp -d	3	F:GO:0016301; F:GO:0016773; F:GO:0005515	-	EC:2.7.1.0	IPR002504; IPR016064; IPR017437
Loa loa	briggsae cbr-dpy-26 protein	0				-
Caenorhabditis elegans	briggsae cbr-ced-5 protein	7	F:GO:0005083; P:GO:0043652; C:GO:0005886; F:GO:0032403; F:GO:0019899; P:GO:0040039; F:GO:0017124	-		PTHR23317 (PANTHER), PTHR23317:SF16 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0016740; F:GO:0004648; F:GO:0004965; C:GO:0016021; C:GO:0016020; F:GO:0016757; P:GO:0007010; F:GO:0004930; F:GO:0008483; F:GO:0003779; P:GO:0007165; F:GO:0004872; F:GO:0004871; P:GO:0007186; P:GO:0007050; F:GO:0003843		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	myotubularin-related protein 2	7	F:GO:0004437; P:GO:0051262; P:GO:0016311; F:GO:0004721; C:GO:0005774; C:GO:0005634; F:GO:0042803	-	EC:3.1.3.16	IPR000340; IPR000387; IPR004182; IPR010569; IPR016130; IPR017906; G3DSA:3.90.190.10 (GENE3D), PTHR10807 (PANTHER), PTHR10807:SF7 (PANTHER), SignalP (SIGNALP), SSF50729 (SUPERFAMILY), SSF52799 (SUPERFAMILY)
	-	0				-
	-	0				-
Homo sapiens	type alpha 2	8	F:GO:0005201; F:GO:0030674; C:GO:0005615; P:GO:0016337; C:GO:0005578; P:GO:0009749; P:GO:0030198; C:GO:0042383	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	heat repeat family protein	0		F:GO:0005488		-
	-	0				-
	-	0				-
	-	0				-

	-	0				-
	-	0				-
Ailuropoda melanoleuca	cellular retinoic acid-binding protein 1	7	C:GO:0005737; F:GO:0016918; P:GO:0007165; P:GO:0007275; F:GO:0019841; P:GO:0006810; F:GO:0005215	-		IPR000463; IPR000566; IPR011038; IPR012674
	-	0				IPR008962; SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-eea-1 protein	0		P:GO:0007018; C:GO:0005694; F:GO:0016787; C:GO:0005874; F:GO:0000166; F:GO:0005524; F:GO:0003777; P:GO:0051276; C:GO:0016459; F:GO:0003774; C:GO:0005622; F:GO:0005515; F:GO:0003899		PD936484 (PRODOM), PTHR23164 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	membrane-associated ring finger 3	1	C:GO:0044464	-		IPR011016; IPR013083; IPR018957; PTHR23012 (PANTHER), PTHR23012:SF2 (PANTHER), SSF57850 (SUPERFAMILY)
Brugia malayi	elegans protein partially confirmed by transcript evidence	2	P:GO:0007275; F:GO:0005488	-		IPR007587
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Oryctolagus cuniculus	thiamin pyrophosphoki-se 1	2	F:GO:0004788; P:GO:0006772	-	EC:2.7.6.2	IPR007371; PTHR13622 (PANTHER), PTHR13622:SF1 (PANTHER)
Tetraodon nigroviridis	mitogen-activated protein ki-se ki-se ki-se 2	8	C:GO:0005829; F:GO:0046872; P:GO:0007257; F:GO:0005524; F:GO:0004709; F:GO:0019901; P:GO:0008283; C:GO:0005634	-	EC:2.7.11.25	IPR000719; IPR011009; IPR015748; IPR017441; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR22986 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG14225 [Caenorhabditis briggsae]	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		C:GO:0016021; C:GO:0016020		-

Caenorhabditis briggsae	serine long chain base subunit 1	9	P:GO:0040010; P:GO:0009058; F:GO:0004758; F:GO:0016769; P:GO:0040027; C:GO:0035339; P:GO:0040011; P:GO:0009792; F:GO:0030170	-	EC:2.3.1.50	IPR004839; IPR015421; IPR015424; PTHR13693 (PANTHER), PTHR13693:SF2 (PANTHER)
Ailuropoda melanoleuca	polyadenylate-binding protein 1-like	9	P:GO:0006378; P:GO:0008380; P:GO:0048255; C:GO:0005681; F:GO:0008494; F:GO:0008022; C:GO:0005829; F:GO:0000166; F:GO:0008143	-		PTHR10432 (PANTHER), PTHR10432:SF52 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR017907
Loa loa	briggsae cbr-apg-1 protein	6	P:GO:0007369; P:GO:0040007; F:GO:0005515; P:GO:0015031; P:GO:0051649; C:GO:0005794	-		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	discoidin domain receptor family member (ddr-2)	1	P:GO:0040010	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	upf0632 protein c2orf89-like	0				-

	f chain crystal structure of g85r als mutant of human superoxide dismutase at a resolution	60	F:GO:0051087; F:GO:0042803; P:GO:0032287; P:GO:0006309; C:GO:0005777; F:GO:0005507; P:GO:0001541; P:GO:0042542; P:GO:0002262; P:GO:0060088; C:GO:0043234; P:GO:0043065; P:GO:0042554; C:GO:0005829; P:GO:0001895; P:GO:0051881; P:GO:0007605; P:GO:0040014; P:GO:0031667; P:GO:0006749; P:GO:0043524; C:GO:0005759; P:GO:0008217; C:GO:0005615; P:GO:0007283; P:GO:0060052; P:GO:0060087;	-	EC:1.15.1.1	-
Caenorhabditis briggsae	calcium atpase	5	F:GO:0005388; C:GO:0016021; P:GO:0006754; F:GO:0005524; P:GO:0006816	-	EC:3.6.3.8	IPR001757; IPR005834; G3DSA:3.40.1110.10 (GENE3D), G3DSA:3.40.50.1000 (GENE3D), PTHR11939:SF76 (PANTHER), SSF56784 (SUPERFAMILY), SSF81660 (SUPERFAMILY)
Pongo abelii	ribosomal protein l36a-like	6	C:GO:0005840; F:GO:0003735; F:GO:0005515; C:GO:0005829; P:GO:0032526; P:GO:0006414	-		IPR000552; IPR011332
Caenorhabditis elegans	rho gtpase activating protein 23	3	C:GO:0005737; F:GO:0005100; P:GO:0007266	-		IPR000198; IPR008936; PTHR23175 (PANTHER), PTHR23175:SF3 (PANTHER)
Caenorhabditis elegans	scavenger receptor	3	F:GO:0005044; F:GO:0005488; C:GO:0016020	-		PTHR19331 (PANTHER), PTHR19331:SF24 (PANTHER)
Loa loa	eukaryotic elongation factor-2 ki-se	8	P:GO:0006468; F:GO:0003746; F:GO:0005509; F:GO:0005524; F:GO:0004686; C:GO:0005829; F:GO:0005516; P:GO:0006414	-	EC:2.7.11.20	IPR004166; IPR011009; PTHR14187 (PANTHER), PTHR14187:SF2 (PANTHER)
	-	0				-

Caenorhabditis briggsae	r--binding motif x-linked 2	9	P:GO:0009792; P:GO:0002119; F:GO:0003729; F:GO:0005515; C:GO:0071011; P:GO:0040007; P:GO:0000398; F:GO:0000166; C:GO:0071013	-		IPR000504; IPR012677; PTHR23139 (PANTHER), PTHR23139:SF8 (PANTHER), SSF54928 (SUPERFAMILY)
Loa loa	serine threonine-protein ki-se tao3	7	F:GO:0004860; P:GO:0046329; F:GO:0004674; C:GO:0005739; P:GO:0046330; F:GO:0000166; P:GO:0046777	-	EC:2.7.11.0	PTHR22986 (PANTHER), PTHR22986:SF27 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-dys-1 protein	7	P:GO:0007271; F:GO:0005515; P:GO:0040017; C:GO:0016010; F:GO:0005277; P:GO:0015870; P:GO:0046716	-		-
Caenorhabditis elegans	egf lag seven-pass g-type receptor 1 (flamingo drosophila)	0		P:GO:0001736; P:GO:0007626; F:GO:0046983; P:GO:0045176; P:GO:0042249; F:GO:0003674; P:GO:0007156; C:GO:0016021; P:GO:0007155; P:GO:0007186; C:GO:0016020; P:GO:0042472; F:GO:0005509; P:GO:0007218; F:GO:0004872; F:GO:0004871; P:GO:0007275; P:GO:0008150; P:GO:0007417; P:GO:0007166; P:GO:0007413; P:GO:0007165; F:GO:0004888; F:GO:0004930; C:GO:0005887; C:GO:0005886; C:GO:0005575		IPR013320; G3DSA:2.10.25.10 (GENE3D)
Brugia malayi	hsp70-interacting protein	0		F:GO:0005488; C:GO:0000151; F:GO:0004842; P:GO:0016567		IPR001440; IPR011990; IPR013026; IPR019734; IPR023114; PTHR22904 (PANTHER), PTHR22904:SF27 (PANTHER), SSF48452 (SUPERFAMILY)
	-	0				-

Angiostrongylus cantonensis	26s proteasome regulatory chain 4	9	C:GO:0000502; C:GO:0005730; P:GO:0051436; P:GO:0051437; P:GO:0031145; F:GO:0005524; F:GO:0016887; F:GO:0005515; C:GO:0005737	-		IPR003593; IPR003959; IPR003960; G3DSA:1.10.8.60 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23073 (PANTHER), PTHR23073:SF9 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	udp-n-acetylglucosamine transporter	5	C:GO:0000139; P:GO:0015780; F:GO:0005338; F:GO:0005351; C:GO:0016021	-		IPR004689; IPR007271; PTHR10231:SF15 (PANTHER), SignalP (SIGNALP), SSF103481 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Loa loa	3-hydroxyisobutyryl-coenzyme a hydrolase	7	P:GO:0009792; F:GO:0005515; P:GO:0040010; P:GO:0009083; F:GO:0016853; F:GO:0003860; C:GO:0005739	-	EC:3.1.2.4	PTHR11941 (PANTHER)
Xenopus (Silurana) tropicalis	pi-plc x domain-containing protein 3	0		P:GO:0006629; F:GO:0016787; P:GO:0023034; P:GO:0016042; F:GO:0003674; P:GO:0007165; F:GO:0008081; C:GO:0005575; F:GO:0004629; F:GO:0004871; P:GO:0008150		IPR017946
Caenorhabditis elegans	abnormal dye filling family member (dyf-14)	1	C:GO:0043232	-		IPR009053; PD936484 (PRODOM)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021		PTHR23294 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	haloacid dehaloge-se-like hydrolase family protein	1	F:GO:0003824	-		G3DSA:3.40.50.1000 (GENE3D), PTHR18901 (PANTHER), SSF56784 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	briggsae cbr--s-30 protein	0		F:GO:0046872; P:GO:0006508; F:GO:0008237; F:GO:0016787; F:GO:0008233; F:GO:0008270; F:GO:0004222		-
Caenorhabditis briggsae	briggsae cbr--s-30 protein	2	F:GO:0046872; F:GO:0008237	-		-

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	aquaporin 8	5	C:GO:0016020; F:GO:0015250; C:GO:0043025; C:GO:0005929; P:GO:0006833	-		IPR000425; PTHR19139:SF25 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	large subunit ribosomal protein 2	9	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; F:GO:0005515; P:GO:0040010; P:GO:0000003; P:GO:0040011; P:GO:0006412	-	EC:3.6.5.3	-
Caenorhabditis briggsae	large subunit ribosomal protein 2	9	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; F:GO:0005515; P:GO:0040010; P:GO:0000003; P:GO:0040011; P:GO:0006412	-	EC:3.6.5.3	IPR002171; IPR008991; IPR014722; IPR014726; IPR022669; IPR022671; PTHR13691:SF4 (PANTHER)
Caenorhabditis briggsae	large subunit ribosomal protein 2	9	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; F:GO:0005515; P:GO:0040010; P:GO:0000003; P:GO:0040011; P:GO:0006412	-	EC:3.6.5.3	IPR002171; IPR008991; IPR014722; IPR014726; IPR022669; IPR022671; PTHR13691:SF4 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	grpe_caeel ame: full= protein mitochondrial flags: precursor	10	P:GO:0040010; F:GO:0000774; P:GO:0006457; P:GO:0030150; F:GO:0051087; P:GO:0002119; C:GO:0005759; P:GO:0006898; F:GO:0042803; P:GO:0009792	-		IPR000740; IPR013805; PTHR21237:SF8 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG18219 [Caenorhabditis briggsae]	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	general transcription factor 3c	0		F:GO:0005515		IPR019136; PTHR13230 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0006364; C:GO:0005575		IPR000238; IPR015946

Caenorhabditis briggsae	tm2 domain-containing protein	0		C:GO:0016021		IPR007829
Loa loa	briggsae cbr-kin-5 protein	9	C:GO:0005929; C:GO:0030425; F:GO:0005515; P:GO:0034606; F:GO:0004672; C:GO:0030424; P:GO:0034608; C:GO:0043025; F:GO:0000166	-		IPR000980; IPR020685; IPR020764; SSF55550 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein R05G6.1 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	phosphorylase b ki-se	3	F:GO:0004339; P:GO:0005977; F:GO:0005516	-	EC:3.2.1.3	IPR008734; IPR011613; PTHR10749:SF2 (PANTHER)
Caenorhabditis elegans	hypothetical protein M60.6 [Caenorhabditis elegans]	1	C:GO:0016021	-		IPR007237; SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein M60.6 [Caenorhabditis elegans]	1	C:GO:0016021	-		SignalP (SIGNALP)
	-	0				IPR005645
	-	0				-
	-	0				-
Caenorhabditis elegans	vinculin	6	F:GO:0005200; P:GO:0007016; C:GO:0030054; F:GO:0005515; P:GO:0007155; C:GO:0015629	-		IPR000633; IPR006077
Caenorhabditis elegans	vinculin	6	F:GO:0005200; P:GO:0007016; C:GO:0030054; F:GO:0005515; P:GO:0007155; C:GO:0015629	-		IPR000633; IPR006077
	-	0				-
	-	0				-
Caenorhabditis briggsae	mitogen-activated protein ki-se ki-se	4	P:GO:0006468; F:GO:0005515; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF34 (PANTHER)
	-	0				-
Caenorhabditis elegans	serine threonine-protein ki-se chk2	9	F:GO:0005488; P:GO:0045132; P:GO:0000077; F:GO:0016301; P:GO:0007281; P:GO:0008630; P:GO:0009792; P:GO:0006919; C:GO:0005634	-		IPR000719; IPR011009; IPR017442; IPR020636; IPR020648; G3DSA:1.10.510.10 (GENE3D)
Glossina morsitans morsitans	protein mo25	2	P:GO:0001700; F:GO:0005488	-		SignalP (SIGNALP)
Caenorhabditis elegans	ribosomal protein s6 polypeptide 1	1	F:GO:0005488	-		IPR007330; G3DSA:1.20.58.280 (GENE3D), PTHR22965 (PANTHER), SSF116846 (SUPERFAMILY)

Homo sapiens	type alpha 2	8	F:GO:0005201; F:GO:0030674; C:GO:0005615; P:GO:0016337; C:GO:0005578; P:GO:0009749; P:GO:0030198; C:GO:0042383	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	multidrug resistance protein family member (mrp-1)	4	F:GO:0042626; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF35 (PANTHER)
Brugia malayi	d- ligase 3	2	P:GO:0006259; F:GO:0005488	-		IPR001660; IPR012308; G3DSA:1.10.3260.10 (GENE3D), PTHR10459 (PANTHER), PTHR10459:SF11 (PANTHER)
Caenorhabditis briggsae	class i chiti-se	8	F:GO:0004383; P:GO:0006032; P:GO:0016998; F:GO:0004672; F:GO:0005524; F:GO:0004568; P:GO:0006468; P:GO:0006182	-	EC:4.6.1.2; EC:3.2.1.14	IPR000726; G3DSA:1.10.530.10 (GENE3D), PTHR22595:SF6 (PANTHER), SSF53955 (SUPERFAMILY)
	-	0				-
Brugia malayi	gpi transamidase subunit pig-u family protein	0		C:GO:0005789; F:GO:0003674; P:GO:0006506; C:GO:0016021; P:GO:0051301; F:GO:0016758		IPR009600
Brugia malayi	gpi transamidase component pig-	0		C:GO:0005789; F:GO:0003674; P:GO:0006506; C:GO:0016021; P:GO:0051301; F:GO:0016758		IPR009600
Caenorhabditis briggsae	gpi inositol deacylase pgap1	5	P:GO:0009987; P:GO:0006810; P:GO:0007275; C:GO:0044464; F:GO:0016787	-		IPR012908; PTHR15495 (PANTHER), PTHR15495:SF2 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	coiled-coil domain-containing protein agap005037	2	F:GO:0005515; P:GO:0008340	-		PTHR22741 (PANTHER), PTHR22741:SF2 (PANTHER)
Caenorhabditis briggsae	probable 28s ribosomal protein mitochondrial	0		C:GO:0005840		IPR007741; IPR012336; PTHR13274 (PANTHER)

synthetic construct	cathepsin d	9	P:GO:0000045; C:GO:0005615; C:GO:0031012; C:GO:0005764; F:GO:0004190; C:GO:0042470; P:GO:0008219; P:GO:0006508; C:GO:0005739	-	EC:3.4.23.0	IPR001461; IPR001969; IPR009007; IPR021109; PTHR13683:SF84 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis elegans	lambda-crystallin homolog	5	F:GO:0070403; F:GO:0050104; P:GO:0008152; C:GO:0005829; F:GO:0042803	-	EC:1.1.1.45	IPR006176; IPR016040; SignalP (SIGNALP), SSF51735 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	briggsae cbr-lgc-22 protein	3	C:GO:0016020; F:GO:0005230; P:GO:0006810	-		IPR006202
	-	0				-
	-	0				-
Caenorhabditis elegans	eb module family protein	0		F:GO:0004867		-
Caenorhabditis elegans	eb module family protein	0		F:GO:0004867		IPR002223; PTHR10083 (PANTHER), PTHR10083:SF36 (PANTHER)
Caenorhabditis elegans	lethal family member (let-413)	19	F:GO:0005515; P:GO:0060561; P:GO:0032863; P:GO:0045930; P:GO:0050918; C:GO:0042734; C:GO:0005913; C:GO:0034750; P:GO:0008283; P:GO:0016337; P:GO:0045108; P:GO:0015031; P:GO:0001921; C:GO:0045211; P:GO:0060603; C:GO:0031252; P:GO:0035089; P:GO:0016477; P:GO:0043065	-		IPR001611; PR00019 (PRINTS), G3DSA:3.80.10.10 (GENE3D), PTHR23155 (PANTHER), PTHR23155:SF30 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)

Ailuropoda melanoleuca	receptor-type tyrosine-protein phosphatase f	22	P:GO:0050775; P:GO:0001960; P:GO:0007185; P:GO:0042059; P:GO:0050803; C:GO:0030426; F:GO:0005001; F:GO:0030971; C:GO:0005792; P:GO:0043525; F:GO:0042301; P:GO:0008285; C:GO:0043025; P:GO:0007156; C:GO:0060076; P:GO:0051387; C:GO:0005768; P:GO:0006470; P:GO:0046627; C:GO:0005887; P:GO:0031345; F:GO:0005158	-		-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-nlp-1 protein	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	leucine zipper-ef-hand containing transmembrane protein 1	8	P:GO:0009792; P:GO:0042407; C:GO:0005743; P:GO:0040018; F:GO:0005515; F:GO:0005509; P:GO:0000003; P:GO:0006898	-		IPR011685; PTHR14009 (PANTHER), PTHR14009:SF1 (PANTHER)
	-	0				-
Pongo abelii	PREDICTED: hypothetical protein LOC100439541 [Pongo abelii]	0				-
Caenorhabditis elegans	hypothetical protein T25F10.3 [Caenorhabditis elegans]	0				-
Stylochus zebra	transposase [Stylochus zebra]	0				-
	-	0				IPR008160; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER)
Caenorhabditis elegans	actin-binding homolog 1b	3	F:GO:0003779; F:GO:0004713; C:GO:0015629	-	EC:2.7.10.0	SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	leucine rich repeat family protein	0		F:GO:0005515		-

Caenorhabditis elegans	cyclin-dependent ki-se 5	17	P:GO:0008340; P:GO:0007049; P:GO:0010468; P:GO:0051932; P:GO:0000003; P:GO:0051301; P:GO:0048489; F:GO:0005524; P:GO:0007269; P:GO:0008045; C:GO:0016533; F:GO:0004693; P:GO:0009792; F:GO:0008083; F:GO:0030332; C:GO:0016020; P:GO:0006468	-	EC:2.7.11.22	IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF110 (PANTHER)
Caenorhabditis elegans	hypothetical protein Y37E11AL.5 [Caenorhabditis elegans]	1	C:GO:0016020	-		IPR000203
Caenorhabditis briggsae	briggsae cbr-wrs-2 protein	7	P:GO:0007031; F:GO:0008270; F:GO:0004830; C:GO:0005778; P:GO:0006436; F:GO:0005524; F:GO:0005515	-	EC:6.1.1.2	-
	-	0				-
Caenorhabditis briggsae	acyl- synthetase long-chain family member 1	7	P:GO:0042221; P:GO:0044255; P:GO:0009792; C:GO:0031090; C:GO:0044446; F:GO:0003824; C:GO:0005739	-		IPR000873; IPR020845; G3DSA:2.30.38.10 (GENE3D), G3DSA:3.40.50.980 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF8 (PANTHER), SSF56801 (SUPERFAMILY)
Caenorhabditis briggsae	variant sh3 domain containing protein	1	F:GO:0008081	-	EC:3.1.4.0	PTHR10336 (PANTHER), PTHR10336:SF22 (PANTHER)
Caenorhabditis elegans	probable sig-l peptidase complex subunit 2	13	F:GO:0008233; C:GO:0005787; P:GO:0006465; C:GO:0016021; P:GO:0000003; P:GO:0018996; C:GO:0005792; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0006898; P:GO:0009792; P:GO:0040015	-		IPR009582; PTHR13085 (PANTHER)

Caenorhabditis elegans	probable sig-l peptidase complex subunit 2	13	F:GO:0008233; C:GO:0005787; P:GO:0006465; C:GO:0016021; P:GO:0000003; P:GO:0018996; C:GO:0005792; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0006898; P:GO:0009792; P:GO:0040015	-		IPR000276; SignalP (SIGNALP)
Caenorhabditis briggsae	hydroxyacid-oxoacid mitochondrial precursor	7	F:GO:0047988; F:GO:0046872; P:GO:0015993; P:GO:0009073; P:GO:0055114; F:GO:0003856; C:GO:0005739	-	EC:1.1.99.24; EC:4.2.3.4	IPR001670; IPR018211; G3DSA:1.20.1090.10 (GENE3D), G3DSA:3.40.50.1970 (GENE3D), PTHR11496 (PANTHER), SSF56796 (SUPERFAMILY)
Caenorhabditis briggsae	hydroxyacid-oxoacid mitochondrial precursor	7	F:GO:0047988; F:GO:0046872; P:GO:0015993; P:GO:0009073; P:GO:0055114; F:GO:0003856; C:GO:0005739	-	EC:1.1.99.24; EC:4.2.3.4	IPR001670; IPR018211; G3DSA:1.20.1090.10 (GENE3D), G3DSA:3.40.50.1970 (GENE3D), PTHR11496 (PANTHER), SSF56796 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-abf-2 protein	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	P:GO:0008104	-		PTHR16166 (PANTHER), PTHR16166:SF25 (PANTHER)
Caenorhabditis elegans	peptidase s9 prolyl oligopeptidase active site domain protein	2	P:GO:0008152; F:GO:0008236	-		-
	-	0				PTHR16675 (PANTHER), PTHR16675:SF53 (PANTHER), SignalP (SIGNALP)
Macaca mulatta	tumor differentially expressed 2-like	1	C:GO:0016021	-		-
	-	0				SignalP (SIGNALP)

Caenorhabditis briggsae	#NAME?	20	P:GO:0008340; P:GO:0015672; P:GO:0035158; P:GO:0008360; P:GO:0051124; P:GO:0035159; P:GO:0019991; P:GO:0009612; P:GO:0006754; F:GO:0005391; P:GO:0001700; C:GO:0005918; P:GO:0007268; C:GO:0005890; P:GO:0009266; C:GO:0005634; F:GO:0005524; P:GO:0050905; P:GO:0001894; P:GO:0008344	-	EC:3.6.3.9	-
Caenorhabditis briggsae	briggsae cbr-vit-6 protein	0		F:GO:0045735; F:GO:0005319; F:GO:0008565; P:GO:0006869; P:GO:0009792; C:GO:0005576; P:GO:0006886; P:GO:0008340; P:GO:0040010		IPR001747; IPR011030; SSF48431 (SUPERFAMILY)
Caenorhabditis elegans	domain containing protein	0		C:GO:0005737; P:GO:0007165; F:GO:0005515; C:GO:0005622		PTHR14130 (PANTHER), PTHR14130:SF1 (PANTHER)
	-	0				-
	-	0				-
Brugia malayi	patched family protein	10	P:GO:0009792; P:GO:0002119; P:GO:0040018; P:GO:0001703; P:GO:0018996; P:GO:0000910; P:GO:0040010; P:GO:0000003; P:GO:0040011; C:GO:0016020	-		IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER), SSF82866 (SUPERFAMILY)
Caenorhabditis elegans	cysteine-rich pdz-binding	5	P:GO:0009792; P:GO:0040007; P:GO:0002119; P:GO:0040011; P:GO:0001703	-		-
	-	0				-
Caenorhabditis elegans	atp-dependent r- helicase ddx18	3	F:GO:0003676; F:GO:0005524; F:GO:0008026	-		IPR000629; IPR011545; IPR014001; IPR014014; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF23 (PANTHER), SSF52540 (SUPERFAMILY)

Homo sapiens	major histocompatibility class f	5	P:GO:0006955; F:GO:0032393; C:GO:0016021; P:GO:0002474; C:GO:0042612	-		-
	-	0				-
						IPR003961; IPR008957; IPR013783; PR00014 (PRINTS), PTHR19900 (PANTHER), PTHR19900:SF7 (PANTHER)
Loa loa	elegans protein partially confirmed by transcript evidence	0				PTHR21512 (PANTHER), PTHR21512:SF6 (PANTHER)
Loa loa	elegans protein partially confirmed by transcript evidence	0				PTHR21512 (PANTHER), PTHR21512:SF6 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0003723; P:GO:0009451; P:GO:0001522; F:GO:0009982		-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	5	P:GO:0002119; P:GO:0018991; P:GO:0040010; P:GO:0006898; P:GO:0008406	-		IPR007146
	-	0				-
Caenorhabditis elegans	mgc64464 protein	1	F:GO:0005515	-		IPR011990; IPR013026; IPR013105; IPR019734; PTHR16056 (PANTHER), SignalP (SIGNALP), SSF48452 (SUPERFAMILY)
Mus musculus	cofilin 1 (non-muscle)	20	P:GO:0009615; P:GO:0006468; P:GO:0007266; P:GO:0001842; C:GO:0030027; P:GO:0001755; C:GO:0005576; C:GO:0005829; P:GO:0006916; F:GO:0003779; P:GO:0030836; P:GO:0030030; P:GO:0045792; P:GO:0051789; P:GO:0043200; P:GO:0030010; C:GO:0016363; C:GO:0030864; P:GO:0006606; P:GO:0000910	-		IPR002108; IPR017904; G3DSA:3.40.20.10 (GENE3D), PTHR11913 (PANTHER), PTHR11913:SF2 (PANTHER), SSF55753 (SUPERFAMILY)
	-	0				-
Chlamydomonas incerta	plus agglutinin	0		F:GO:0005524; F:GO:0003774; C:GO:0016459; C:GO:0019867		SignalP (SIGNALP)
Caenorhabditis elegans	cell growth-regulating nucleolar	2	C:GO:0005730; F:GO:0005515	-		IPR014898; PTHR13100 (PANTHER), PTHR13100:SF6 (PANTHER), SSF57667 (SUPERFAMILY)

Caenorhabditis elegans	nucleolar protein with mif4g domain 1	4	C:GO:0005730; P:GO:0002119; P:GO:0040018; F:GO:0005515	-		IPR003891; PTHR18034 (PANTHER), PTHR18034:SF4 (PANTHER)
Caenorhabditis elegans	nucleolar protein with mif4g domain 1	4	C:GO:0005730; P:GO:0002119; P:GO:0040018; F:GO:0005515	-		IPR003891; PTHR18034 (PANTHER), PTHR18034:SF4 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	amop domain containing protein	1	P:GO:0007160	-		SignalP (SIGNALP)
Caenorhabditis elegans	zip zinc transporter family protein	5	P:GO:0030001; C:GO:0016021; P:GO:0009792; F:GO:0046873; P:GO:0055085	-		IPR003689; PTHR11040 (PANTHER), PTHR11040:SF8 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	propionyl coenzyme a beta polypeptide	6	P:GO:0009062; F:GO:0005515; C:GO:0005759; F:GO:0005524; F:GO:0004658; P:GO:0009063	-	EC:6.4.1.3	IPR000022; IPR011762; IPR011763; G3DSA:3.90.226.10 (GENE3D), PTHR22855 (PANTHER), PTHR22855:SF14 (PANTHER), SSF52096 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	atp-dependent d- helicase q1	7	P:GO:0006310; P:GO:0006281; P:GO:0006260; F:GO:0003677; F:GO:0005524; F:GO:0043140; C:GO:0005634	-		IPR004589; IPR011545; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR13710:SF12 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	colon cancer-associated protein mic1	1	F:GO:0005515	-		IPR009755; PTHR12897 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-

Loa loa	tbp-associated factor 1-like	27	F:GO:0002039; P:GO:0000080; P:GO:0051123; F:GO:0008270; F:GO:0004402; P:GO:0018107; P:GO:0006974; F:GO:0000166; F:GO:0017025; P:GO:0046777; P:GO:0010552; P:GO:0060261; C:GO:0005730; P:GO:0000117; P:GO:0032436; P:GO:0018105; F:GO:0004674; F:GO:0003713; P:GO:0006368; C:GO:0045120; P:GO:0042493; C:GO:0005669; F:GO:0016986; F:GO:0010843; F:GO:0070577; P:GO:0016573; C:GO:0071339	-	EC:2.3.1.48; EC:2.7.11.0	IPR022591; PTHR13900 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-d--2 protein	2	F:GO:0005488; F:GO:0017111	-	EC:3.6.1.15	IPR014808; PTHR10887 (PANTHER), PTHR10887:SF14 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-dsc-4 protein	1	P:GO:0040011	-		PTHR13024 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	endoplasmic reticulum mannosyl-oligosaccharide -alpha-mannosidase	3	C:GO:0016020; F:GO:0004571; F:GO:0005509	-	EC:3.2.1.113	IPR001382; PTHR11742:SF7 (PANTHER), SignalP (SIGNALP)
	-	0				-
Brugia malayi	briggsae cbr-rpy-1 protein	7	C:GO:0005856; C:GO:0045211; P:GO:0007268; C:GO:0030054; F:GO:0033130; P:GO:0019915; F:GO:0008270	-		IPR019568; PTHR10098 (PANTHER), PTHR10098:SF7 (PANTHER)
	-	0				IPR014044; SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	mitochondrial ribosomal protein l11	7	P:GO:0006412; P:GO:0040010; C:GO:0005840; F:GO:0003735; P:GO:0002119; P:GO:0006898; P:GO:0009792	-	EC:3.6.5.3	IPR000911; IPR020783; IPR020784; PD001367 (PRODOM), PTHR11661:SF1 (PANTHER)

Caenorhabditis elegans	39s ribosomal protein mitochondrial	7	P:GO:0006412; C:GO:0005762; P:GO:0040010; F:GO:0003735; P:GO:0002119; P:GO:0006898; P:GO:0009792	-	EC:3.6.5.3	IPR000911; IPR020783; IPR020784; PD001367 (PRODOM), PTHR11661:SF1 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	acylamino-acid-releasing enzyme	1	F:GO:0008236	-		-
Caenorhabditis elegans	protein	8	P:GO:0006412; P:GO:0048731; P:GO:0040010; C:GO:0005840; F:GO:0003735; P:GO:0000003; P:GO:0002119; P:GO:0009792	-	EC:3.6.5.3	IPR000988; PTHR10792:SF1 (PANTHER)
Caenorhabditis elegans	glutamate synthase	10	P:GO:0006537; P:GO:0009792; F:GO:0045181; P:GO:0002119; F:GO:0051536; F:GO:0005506; F:GO:0010181; P:GO:0040010; P:GO:0055114; F:GO:0050660	-		IPR000583; IPR017932; G3DSA:3.60.20.10 (GENE3D), PTHR11938 (PANTHER), PTHR11938:SF1 (PANTHER), SSF56235 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	pim (mammalian oncogene) related ki-se family member (prk-1)	3	F:GO:0004674; F:GO:0005524; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR22984 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	4	C:GO:0016021; F:GO:0008271; P:GO:0008272; P:GO:0055085	-		IPR011547; PTHR11814 (PANTHER), PTHR11814:SF25 (PANTHER), SignalP (SIGNALP)
	-	0				-
Loa loa	elegans protein confirmed by transcript evidence	1	F:GO:0005488	-		IPR001079; IPR008985; IPR013320; PTHR11346:SF29 (PANTHER)
	-	0				IPR005514; G3DSA:2.40.10.10 (GENE3D)
Caenorhabditis elegans	-d-dependent malic mitochondrial	16	P:GO:0060070; P:GO:0000122; F:GO:0003714; F:GO:0004470; F:GO:0016616; P:GO:0006108; C:GO:0005667; F:GO:0046872; P:GO:0030282; F:GO:0051287; P:GO:0045944; F:GO:0003690; P:GO:0055114; P:GO:0048625; P:GO:0045599; C:GO:0005739	-	EC:1.1.1.0	IPR012302; IPR016040; PTHR23406 (PANTHER), PTHR23406:SF2 (PANTHER), SSF51735 (SUPERFAMILY)

	-	0				SignalP (SIGNALP)
	-	0				-
Brugia malayi	briggsae cbr-gmn-1 protein	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	P:GO:0006952; C:GO:0016021	-		IPR004316; IPR018175; SignalP (SIGNALP)
Loa loa	asparagine-linked glycosylation 9 homolog (alpha mannosyltransferase)	1	C:GO:0044464	-		IPR005599
	-	0				IPR022272
Caenorhabditis briggsae	steroid receptor-interacting snf2 domain	5	F:GO:0005524; F:GO:0004872; F:GO:0004386; F:GO:0003677; F:GO:0005515	-		IPR000330; PTHR10799 (PANTHER), PTHR10799:SF51 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	alanine aminotransferase	6	F:GO:0030170; P:GO:0000003; C:GO:0005739; F:GO:0016847; P:GO:0009058; F:GO:0008483	-	EC:4.4.1.14; EC:2.6.1.0	IPR004839; IPR015421; IPR015424; PTHR11751 (PANTHER), PTHR11751:SF29 (PANTHER)
	-	0				-
Brugia malayi	dual oxidase	19	P:GO:0018149; P:GO:0006979; P:GO:0006952; F:GO:0016174; P:GO:0040032; F:GO:0005509; C:GO:0016021; P:GO:0042338; P:GO:0055114; P:GO:0040007; F:GO:0004601; F:GO:0009055; F:GO:0008484; P:GO:0002119; P:GO:0040011; F:GO:0020037; F:GO:0050660; P:GO:0009792; C:GO:0005882	-	EC:1.6.3.1; EC:1.11.1.7; EC:3.1.6.0	IPR002007; IPR010255; PTHR11972 (PANTHER), PTHR11972:SF1 (PANTHER)
Brugia malayi	surfeit locus protein 4	14	P:GO:0040035; P:GO:0009792; P:GO:0002119; C:GO:0012505; C:GO:0005794; P:GO:0032940; C:GO:0031090; P:GO:0040011; P:GO:0019915; P:GO:0040007; C:GO:0005783; C:GO:0044425; C:GO:0044446; P:GO:0002009	-		-
						IPR007110; IPR010939; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF9 (PANTHER), SSF48726 (SUPERFAMILY)

	-	0				-
	-	0				G3DSA:3.15.10.10 (GENE3D), SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-ugt-62 protein	0		F:GO:0016740; F:GO:0030246; C:GO:0016021; F:GO:0016758; F:GO:0016757; P:GO:0005975; P:GO:0030259; P:GO:0040010; P:GO:0008152		-
Loa loa	integrator complex subunit 9	3	F:GO:0005515; P:GO:0016180; C:GO:0032039	-		IPR022712; G3DSA:3.60.15.10 (GENE3D), PTHR11203 (PANTHER), PTHR11203:SF2 (PANTHER), SSF56281 (SUPERFAMILY)
Caenorhabditis elegans	nuclear hormone receptor family member (nhr-105)	2	F:GO:0005515; P:GO:0006350	-		IPR008946
Macaca mulatta	cd63 antigen	11	C:GO:0005765; C:GO:0043234; P:GO:0045807; C:GO:0031088; F:GO:0032403; C:GO:0031902; C:GO:0030658; P:GO:0045785; P:GO:0030855; P:GO:0010633; C:GO:0005887	-		-
Caenorhabditis elegans	trafficking protein particle complex subunit 2	3	P:GO:0006888; C:GO:0005801; P:GO:0033227	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	6	P:GO:0009792; F:GO:0042626; C:GO:0005886; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		IPR003439; IPR003593; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF96 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	P:GO:0019915	-		IPR010291; PTHR23294 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	variable abnormal morphology family member (vab-10)	0				-
	-	0				-
	-	0				-
Loa loa	transcription factor	0		F:GO:0046872; F:GO:0008270; F:GO:0005515; P:GO:0019915; C:GO:0005634; F:GO:0003677		IPR000253; IPR008984; IPR011011; IPR013083
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	hspc171 protein	1	P:GO:0000003	-		IPR008506; PTHR13505:SF3 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	hypothetical protein F58H1.7 [Caenorhabditis elegans]	0				-
	-	0				-

Brugia malayi	mediator of r- polymerase ii transcription subunit 22	12	P:GO:0040010; P:GO:0006357; P:GO:0040035; F:GO:0016455; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0040017; P:GO:0006898; C:GO:0016592; P:GO:0009792; P:GO:0040018	-		IPR009332; PTHR12434:SF2 (PANTHER), PF06179 (PFAM)
Pongo abelii	angiotensin converting enzyme (ec)	8	C:GO:0030863; P:GO:0030032; C:GO:0071203; F:GO:0003779; C:GO:0008290; C:GO:0030027; P:GO:0051693; C:GO:0016020	-		IPR001548; PTHR10514:SF2 (PANTHER)
	-	0				-
Loa loa	membrane-associated ring finger 6	2	F:GO:0046872; C:GO:0044464	-		IPR011016; IPR013083; IPR018957; PTHR13145 (PANTHER), SSF57850 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	phosphoethanolamine n-methyltransferase	9	P:GO:0009792; P:GO:0002119; F:GO:0008757; P:GO:0032940; P:GO:0009877; P:GO:0009312; P:GO:0040017; P:GO:0040010; P:GO:0000003	-		G3DSA:3.40.50.150 (GENE3D), PTHR10108 (PANTHER), PTHR10108:SF3 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	5	C:GO:0016021; P:GO:0040010; F:GO:0004573; P:GO:0009311; P:GO:0040011	-	EC:3.2.1.106	IPR004888; IPR008928; PTHR10412 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	phenylalanyl-tr- beta subunit	7	C:GO:0005625; F:GO:0004826; F:GO:0003723; F:GO:0005524; F:GO:0000287; P:GO:0006432; C:GO:0005829	-	EC:6.1.1.20	G3DSA:3.30.930.10 (GENE3D), PTHR10947 (PANTHER), PS51483 (PROFILE), SSF55681 (SUPERFAMILY)
	-	0				IPR007087; IPR015880; PTHR23224 (PANTHER), PTHR23224:SF222 (PANTHER)
	-	0				-
	-	0				-
	-	0				-

Loa loa	elegans protein partially confirmed by transcript evidence	3	P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF112 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Nippostrongylus brasiliensis	globin	6	F:GO:0020037; C:GO:0005615; C:GO:0005737; F:GO:0005344; P:GO:0015671; F:GO:0019825	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Brugia malayi	s-p-associated protein	7	C:GO:0005829; F:GO:0000149; C:GO:0008021; P:GO:0006887; P:GO:0007269; P:GO:0006886; C:GO:0016020	-		SignalP (SIGNALP)
Drosophila willistoni	viral a-type inclusion	0				-
Caenorhabditis elegans	ubiquitin carboxyl-termi-l hydrolase family protein	1	F:GO:0016787	-		-
	-	0				-
Caenorhabditis elegans	atp-binding domain-containing protein 3	10	P:GO:0006412; C:GO:0005829; P:GO:0034227; P:GO:0048598; P:GO:0048599; P:GO:0007283; P:GO:0040025; P:GO:0002098; F:GO:0000049; P:GO:0006974	-	EC:3.6.5.3	PTHR11807 (PANTHER), PTHR11807:SF3 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	mitochondrial ribosomal protein l28	9	C:GO:0005840; P:GO:0044238; C:GO:0005739; P:GO:0034645; P:GO:0040007; P:GO:0010171; P:GO:0002119; P:GO:0010467; P:GO:0009792	-		PTHR13528 (PANTHER)
Caenorhabditis elegans	electron-transfer-flavoprotein beta polypeptide	4	P:GO:0006119; C:GO:0005875; F:GO:0009055; C:GO:0005811	-		IPR012255; IPR014729; IPR014730; SSF52402 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				IPR003677
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis briggsae	briggsae cbr-ppn-1 protein	3	F:GO:0008233; F:GO:0005515; C:GO:0005576	-		IPR002223; IPR020901; PTHR10083 (PANTHER), PTHR10083:SF18 (PANTHER)

	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER)
Brugia malayi	protein-tyrosine phosphatase containing protein	1	F:GO:0016791	-	EC:3.1.3.0	IPR000242; IPR000387; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis elegans	uncharacterized protein kiaa0174	1	F:GO:0005515	-		IPR005061; PTHR12161 (PANTHER), PTHR12161:SF3 (PANTHER)
	-	0				IPR005828
	-	0				SignalP (SIGNALP)
	-	0				-
						IPR003598; IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF5 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	adenosine deami-se that acts on r- family member (adr-1)	1	P:GO:0032501	-		IPR001159; IPR002466; IPR014720; PTHR10910 (PANTHER), PTHR10910:SF1 (PANTHER), SSF54768 (SUPERFAMILY)
Caenorhabditis elegans	adenosine deami-se that acts on r- family member (adr-1)	1	P:GO:0032501	-		IPR001159; IPR002466; IPR014720; PTHR10910 (PANTHER), PTHR10910:SF1 (PANTHER), SSF54768 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	dph5 homolog	2	P:GO:0017183; F:GO:0004164	-	EC:2.1.1.98	-
Caenorhabditis elegans	dph5 homolog	2	P:GO:0008152; F:GO:0008168	-	EC:2.1.1.0	-
Caenorhabditis elegans	nhl repeat-containing	3	F:GO:0008270; F:GO:0005515; P:GO:0006915	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	acyl-coenzyme a dehydroge-se member 8	5	F:GO:0003995; P:GO:0006629; P:GO:0055114; P:GO:0034641; F:GO:0050660	-	EC:1.3.99.3	IPR006089; IPR006091; IPR006092; IPR009075; IPR009100; IPR013786; PTHR10909 (PANTHER), PTHR10909:SF10 (PANTHER)
Caenorhabditis elegans	acyl-coenzyme a dehydroge-se member 8	5	F:GO:0003995; P:GO:0006629; P:GO:0055114; P:GO:0034641; F:GO:0050660	-	EC:1.3.99.3	IPR006089; IPR006091; IPR006092; IPR009075; IPR009100; IPR013786; PTHR10909 (PANTHER), PTHR10909:SF10 (PANTHER)
Caenorhabditis elegans	beta-lactamase-like protein 2	0		F:GO:0046872; F:GO:0016787		G3DSA:3.60.15.10 (GENE3D), PTHR23131 (PANTHER), SSF56281 (SUPERFAMILY)
	-	0				-
	-	0				-

Brugia malayi	wd-repeat protein	0		F:GO:0008415; F:GO:0016740; F:GO:0004402		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR19856 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Brugia malayi	leucyl-tr- synthetase	5	F:GO:0004823; P:GO:0006429; F:GO:0005515; F:GO:0005524; C:GO:0005829	-	EC:6.1.1.4	G3DSA:3.90.740.10 (GENE3D), PTHR11946 (PANTHER), PTHR11946:SF10 (PANTHER), SSF52374 (SUPERFAMILY)
Loa loa	uncoordi-ted family member (unc-13)	3	P:GO:0046928; C:GO:0005886; C:GO:0045202	-		IPR014770; PTHR10480 (PANTHER)
Caenorhabditis elegans	integrin beta pat-3	6	F:GO:0005178; C:GO:0031252; C:GO:0005925; P:GO:0007155; C:GO:0016021; P:GO:0023052	-		IPR002369; IPR003659; IPR015812; IPR016201; SignalP (SIGNALP)
	-	0				-
	-	0				-
Oryza sativa Japonica Group	ring finger-like	0		C:GO:0005739; C:GO:0016023; C:GO:0016020		-
	-	0				-
Caenorhabditis briggsae	low density lipoprotein receptor-related protein 4	14	P:GO:0009888; P:GO:0051605; C:GO:0016020; P:GO:0065008; F:GO:0016787; P:GO:0030326; P:GO:0048513; P:GO:0051179; P:GO:0003002; P:GO:0030178; P:GO:0030154; P:GO:0007399; N:GO:0071844; F:GO:0005488	-		IPR000033; IPR011042; PTHR10529 (PANTHER), SSF63825 (SUPERFAMILY)
Leishmania infantum JPCM5	viral a-type inclusion protein	1	F:GO:0005488	-		IPR009053; PD936484 (PRODOM)
Caenorhabditis elegans	polarity and osmotic sensitivity defect family member (pod-2)	0		F:GO:0005524; F:GO:0016874; P:GO:0008152; F:GO:0003824; F:GO:0009374; P:GO:0006633; F:GO:0003989		PTHR18866 (PANTHER), PTHR18866:SF6 (PANTHER)
Caenorhabditis elegans	gamma-glutamyltranspeptidase family protein	0		F:GO:0003840		IPR000101; SSF56235 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	huntingtin interacting protein	4	F:GO:0005488; P:GO:0044260; P:GO:0090304; F:GO:0016740	-		IPR001214; IPR006560; G3DSA:2.170.270.10 (GENE3D), PTHR22884 (PANTHER), PTHR22884:SF36 (PANTHER), SSF82199 (SUPERFAMILY)
	-	0				-

Caenorhabditis elegans	subfamily member 21	5	C:GO:0005840; P:GO:0006457; F:GO:0031072; P:GO:0000003; F:GO:0008270	-		IPR001623; IPR015609; IPR018253; PTHR11821:SF10 (PANTHER)
Caenorhabditis elegans	subfamily member 21	6	C:GO:0005840; P:GO:0006457; F:GO:0003676; F:GO:0031072; P:GO:0000003; F:GO:0008270	-		IPR001623; IPR015609; IPR018253; PTHR11821:SF10 (PANTHER)
Brugia malayi	probable atp-dependent r- helicase ddx41	9	F:GO:0046872; P:GO:0006915; F:GO:0004386; F:GO:0003676; F:GO:0005515; P:GO:0007275; C:GO:0005634; F:GO:0000166; P:GO:0006396	-		G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF46 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	hypothetical protein Bm1_54750 [Brugia malayi]	0				-
Brugia malayi	potassium channel tetramerisation domain containing 10	11	P:GO:0043161; F:GO:0005249; C:GO:0005730; C:GO:0031463; P:GO:0006813; C:GO:0008076; F:GO:0004842; P:GO:0016567; F:GO:0005515; P:GO:0034220; C:GO:0005737	-	EC:6.3.2.19	IPR000210; IPR003131; IPR011333; PTHR11145 (PANTHER)
Brugia malayi	tetraspanin 18	1	C:GO:0016020	-		IPR000301; IPR018499; IPR018503; PTHR19282 (PANTHER), PTHR19282:SF34 (PANTHER), SignalP (SIGNALP)
Ailuropoda melanoleuca	lamin a c	13	C:GO:0005626; C:GO:0016363; P:GO:0006998; P:GO:0035105; C:GO:0005638; P:GO:0007517; P:GO:0007283; N:GO:0090343; P:GO:0055015; F:GO:0005515; C:GO:0048471; C:GO:0005635; F:GO:0005198	-		-
	-	0				-
	-	0				-
	-	0				-

Bos taurus	heavy chain non-muscle	43	P:GO:0001525; C:GO:0030863; P:GO:0008360; C:GO:0031594; P:GO:0030048; F:GO:0030898; P:GO:0051295; C:GO:0005913; P:GO:0016337; F:GO:0043531; P:GO:0032796; P:GO:0015031; C:GO:0001772; P:GO:0050900; P:GO:0007229; C:GO:0005829; P:GO:0007520; F:GO:0000146; P:GO:0006509; P:GO:0043534; C:GO:0008305; C:GO:0005819; C:GO:0001726; P:GO:0007132; C:GO:0032154; P:GO:0000904; P:GO:0001768; F:GO:0043495;	-		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	7	C:GO:0005737; P:GO:0040010; P:GO:0055114; P:GO:0006561; P:GO:0006898; F:GO:0004349; F:GO:0004350	-	EC:2.7.2.11; EC:1.2.1.41	IPR001048; PTHR11063 (PANTHER), PTHR11063:SF2 (PANTHER)
	-	0				-
Ostertagia ostertagi	heat shock protein family member (hsp-)	1	P:GO:0009408	-		IPR001436; IPR002068; IPR008978; G3DSA:2.60.40.790 (GENE3D), PTHR11527 (PANTHER), PTHR11527:SF28 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-opt-2 protein	0		P:GO:0006857; F:GO:0015198; C:GO:0016021; C:GO:0016020; F:GO:0005215; P:GO:0006810		PTHR11654 (PANTHER), PTHR11654:SF11 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	ras family protein	9	C:GO:0005737; F:GO:0005525; C:GO:0005886; F:GO:0005515; P:GO:0006913; P:GO:0006886; C:GO:0005634; P:GO:0007264; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-

Loa loa	vacuolar protein sorting-associated	11	F:GO:0000149; C:GO:0008021; P:GO:0000003; P:GO:0018996; P:GO:0006605; P:GO:0002119; P:GO:0016082; P:GO:0006898; P:GO:0034058; P:GO:0006904; P:GO:0007040	-		IPR001619; G3DSA:3.40.50.2060 (GENE3D), PTHR11679:SF3 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	cytosolic regulator pianissimo	0		F:GO:0005488; P:GO:0007165; C:GO:0005622		PTHR13298 (PANTHER), PTHR13298:SF2 (PANTHER)
Caenorhabditis elegans	6-pyruvoyl tetrahydrobiopterin synthase	10	F:GO:0046872; C:GO:0005667; P:GO:0006729; F:GO:0042802; F:GO:0003874; P:GO:0007366; F:GO:0043565; F:GO:0016563; F:GO:0003700; P:GO:0045893	-	EC:4.2.3.12	IPR007115; G3DSA:3.30.479.10 (GENE3D), SSF55620 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	fg-gap repeat family protein	19	P:GO:0007279; F:GO:0005515; P:GO:0040007; C:GO:0016442; F:GO:0004521; P:GO:0033227; P:GO:0051607; F:GO:0035197; P:GO:0035087; P:GO:0030422; C:GO:0005737; P:GO:0035071; P:GO:0007367; C:GO:0070578; P:GO:0002119; P:GO:0045071; P:GO:0035195; P:GO:0070868; P:GO:0035190	-		PTHR13412 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	thap domain containing 4	0		F:GO:0003676		IPR011038; IPR014878; PTHR15854 (PANTHER)

Homo sapiens	-scent polypeptide-associated complex alpha polypeptide	9	P:GO:0006412; F:GO:0003677; F:GO:0017025; C:GO:0005854; P:GO:0044419; F:GO:0003713; P:GO:0015031; C:GO:0005634; P:GO:0045941	-	EC:3.6.5.3	-
Caenorhabditis briggsae	Hypothetical protein CBG12993 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	vacuolar proton pump subunit f	12	F:GO:0046933; P:GO:0015986; P:GO:0040007; P:GO:0000003; P:GO:0018996; P:GO:0002119; F:GO:0046961; P:GO:0040011; P:GO:0006898; P:GO:0060041; P:GO:0009792; C:GO:0033180	-	EC:3.6.3.14	IPR005772; IPR008218; G3DSA:3.40.50.10580 (GENE3D)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	aldehyde dehydroge-se	2	P:GO:0008152; F:GO:0016491	-		IPR012394; IPR015590; IPR016160; IPR016161; IPR016163
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	briggsae cbr-cpg-4 protein	0		P:GO:0040010		SignalP (SIGNALP)
	-	0				-
Brugia malayi	histone acetyltransferase type b catalytic subunit	3	P:GO:0009987; F:GO:0016747; P:GO:0009792	-	EC:2.3.1.0	IPR016181; IPR019467; G3DSA:3.90.360.10 (GENE3D), PTHR12046 (PANTHER)
Brugia malayi	hypothetical protein Bm1_53660 [Brugia malayi]	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	colony stimulating factor 1 receptor	2	F:GO:0016301; P:GO:0048518	-		IPR003599; IPR007110; IPR013106; IPR013783; SignalP (SIGNALP), SSF48726 (SUPERFAMILY)
						IPR003599; IPR003961; IPR008957; IPR013098; IPR013783; PR00014 (PRINTS), PTHR19900 (PANTHER), PTHR19900:SF7 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
Brugia malayi	in family member (ttn-1)	10	P:GO:0014866; F:GO:0004672; P:GO:0016310; F:GO:0008092; C:GO:0031674; P:GO:0048738; P:GO:0009792; P:GO:0050790; C:GO:0044446; C:GO:0005634	-		IPR003598; IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF17 (PANTHER), SSF48726 (SUPERFAMILY)

Caenorhabditis briggsae	isocitrate dehydroge-se	6	F:GO:0051287; P:GO:0055114; F:GO:0000287; P:GO:0006099; F:GO:0004449; C:GO:0005739	-	EC:1.1.1.41	IPR001804; IPR004434; IPR019818; PTHR11835:SF5 (PANTHER), SignalP (SIGNALP), SSF53659 (SUPERFAMILY)
Caenorhabditis elegans	atp-dependent r- helicase an3	15	C:GO:0005875; F:GO:0004004; C:GO:0016442; P:GO:0040007; P:GO:0002168; P:GO:0007286; P:GO:0002119; P:GO:0042006; C:GO:0043186; F:GO:0000166; C:GO:0043025; P:GO:0048477; P:GO:0009792; C:GO:0005811; P:GO:0016246	-		IPR011545; IPR014014; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF56 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	cdk5 regulatory subunit associated protein 3	1	P:GO:0000079	-		IPR008491
Bos taurus	ribosomal protein s14	12	F:GO:0048027; P:GO:0000122; F:GO:0005515; P:GO:0000028; P:GO:0006414; C:GO:0005730; F:GO:0045182; P:GO:0030490; P:GO:0030218; F:GO:0003735; C:GO:0022627; C:GO:0005739	-		IPR001971; IPR018102; PTHR11759:SF1 (PANTHER), SSF53137 (SUPERFAMILY)
Polysphondylium pallidum PN500	choriogenin h	0		P:GO:0006468; F:GO:0003677; C:GO:0005634; F:GO:0003676; F:GO:0005524; F:GO:0046872; P:GO:0006355; F:GO:0004674; P:GO:0006350; F:GO:0004672; F:GO:0005509; F:GO:0003700; F:GO:0000166; F:GO:0005488; C:GO:0012505; C:GO:0005794; P:GO:0045449; F:GO:0008270; F:GO:0005544		-
Saccoglossus kowalevskii	intracister-l a particle-promoted polypeptide-like	0		F:GO:0005515		-

Bombyx mori	endonuclease-reverse transcriptase	1	F:GO:0003824	-		IPR005135; G3DSA:3.60.10.10 (GENE3D), PTHR23227 (PANTHER), PTHR23227:SF14 (PANTHER)
Loa loa	hypothetical protein LOAG_08094 [Loa loa]	0				-
	-	0				-
Xenopus (Silurana) tropicalis	inhibitor of kappa light polypeptide gene enhancer in b- ki-se complex-associated protein	10	P:GO:0006357; C:GO:0005730; C:GO:0016591; F:GO:0008607; C:GO:0008023; F:GO:0003677; F:GO:0005515; F:GO:0016944; C:GO:0005737; P:GO:0006468	-		-
Brugia malayi	1-acylglycerol-3-phosphate o-acyltransferase 9	10	P:GO:0007595; P:GO:0002071; C:GO:0016021; C:GO:0005789; P:GO:0032006; P:GO:0046339; P:GO:0019432; P:GO:0006631; F:GO:0004366; P:GO:0040014	-	EC:2.3.1.15	PTHR23063 (PANTHER), PTHR23063:SF2 (PANTHER)
Rattus norvegicus	histone h3 type 2	4	C:GO:0000786; F:GO:0003677; P:GO:0006334; C:GO:0005634	-		IPR000164; IPR007125; IPR009072
	-	0				-
	-	0				-
Ancylostoma caninum	kunitz-like protease inhibitor precursor	0		P:GO:0008542; P:GO:0007176; C:GO:0048471; P:GO:0048669; F:GO:0005215; P:GO:0007626; P:GO:0051563; C:GO:0045177; P:GO:0006897; C:GO:0016021; P:GO:0040014; C:GO:0016020; P:GO:0051402; P:GO:0045944; F:GO:0016504; P:GO:0008088; P:GO:0008344; P:GO:0006417; C:GO:0005624; P:GO:0050803; F:GO:0004867; P:GO:0006378; F:GO:0042802; P:GO:0007617; C:GO:0031410; C:GO:0051233; F:GO:0005488;		IPR002223; PTHR10083 (PANTHER), PTHR10083:SF39 (PANTHER), SignalP (SIGNALP)

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis elegans	inorganic pyrophosphatase	9	C:GO:0005737; P:GO:0009792; P:GO:0002119; P:GO:0040010; P:GO:0000003; F:GO:0004427; C:GO:0016021; P:GO:0006796; P:GO:0040039	-	EC:3.6.1.1	IPR008162
	-	0				-
Loa loa	novel protein	4	P:GO:0008152; F:GO:0008134; F:GO:0003824; C:GO:0005634	-		G3DSA:3.40.50.980 (GENE3D), PTHR22754 (PANTHER), PTHR22754:SF8 (PANTHER)
Caenorhabditis elegans	dmx-like 1	0		F:GO:0003674; P:GO:0008150		PTHR13950 (PANTHER), PTHR13950:SF1 (PANTHER)
Loa loa	cgmp-dependent 3 -cyclic phosphodiesterase	8	F:GO:0004118; P:GO:0046069; F:GO:0030552; C:GO:0045121; P:GO:0050794; F:GO:0042803; F:GO:0030553; P:GO:0006198	-		IPR003018; G3DSA:3.30.450.40 (GENE3D), PTHR11347 (PANTHER), PTHR11347:SF4 (PANTHER), SSF55781 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	pqq enzyme repeat family protein	12	P:GO:0006468; P:GO:0000003; F:GO:0005515; C:GO:0030176; P:GO:0010467; P:GO:0090304; F:GO:0004521; P:GO:0040017; F:GO:0004674; P:GO:0006987; F:GO:0000287; F:GO:0005524	-	EC:2.7.11.0	IPR011047; IPR018391
Caenorhabditis elegans	lsm4 u6 small nuclear r- associated (cerevisiae)	11	F:GO:0003723; P:GO:0008340; P:GO:0040027; P:GO:0008380; P:GO:0010171; C:GO:0005688; F:GO:0005515; P:GO:0040011; P:GO:0006898; P:GO:0006397; P:GO:0009792	-		IPR001163; IPR006649; IPR010920; G3DSA:2.30.30.100 (GENE3D), PTHR23338 (PANTHER), PTHR23338:SF16 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0004134; P:GO:0006508; P:GO:0005978; P:GO:0005975; F:GO:0003824; F:GO:0043169; P:GO:0009792; F:GO:0004135		-
Loa loa	yh82_caeel ame: full=uncharacterized protein	0		F:GO:0005184; C:GO:0005576		IPR001166; IPR018251
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-tag-293 protein	0				-
Saccoglossus kowalevskii	5 -nucleotidase domain containing 2	0		F:GO:0046872; F:GO:0003674; F:GO:0016787; C:GO:0005575		IPR007087; IPR015880; IPR022755; PTHR20863 (PANTHER), PTHR20863:SF2 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis elegans	zinc finger protein 593	8	P:GO:0009792; P:GO:0002119; F:GO:0003676; C:GO:0005622; P:GO:0040010; P:GO:0000003; P:GO:0006898; F:GO:0008270	-		IPR007087; IPR015880; IPR022755; PTHR20863 (PANTHER), PTHR20863:SF2 (PANTHER), SSF57667 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis briggsae	mitochondrial ribosomal protein s25	1	C:GO:0005840	-		SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein C54D1.7 [Caenorhabditis elegans]	0				-
Pongo abelii	heavy chain non-muscle	44	C:GO:0030863; P:GO:0008360; C:GO:0031594; P:GO:0030048; F:GO:0030898; P:GO:0051295; C:GO:0005913; P:GO:0016337; F:GO:0043531; P:GO:0032796; P:GO:0015031; C:GO:0001772; P:GO:0050900; P:GO:0007229; C:GO:0005829; P:GO:0007520; F:GO:0000146; P:GO:0006509; P:GO:0043534; C:GO:0008305; C:GO:0005819; C:GO:0001726; P:GO:0007132; F:GO:0005391; C:GO:0032154; P:GO:0000904; P:GO:0001768;	-	EC:3.6.3.9	IPR001609; PTHR13140 (PANTHER), PTHR13140:SF23 (PANTHER)
	-	0				SignalP (SIGNALP)

Caenorhabditis briggsae	adipocyte plasma membrane-associated protein	2	C:GO:0044464; F:GO:0003824	-		IPR004141; IPR011042; IPR018119; PTHR10426:SF6 (PANTHER), SignalP (SIGNALP), SSF63829 (SUPERFAMILY)
Loa loa	hypothetical protein LOAG_05120 [Loa loa]	0				IPR001863
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Angiostrongylus cantonensis	thyroglobulin type-1 repeat family protein	1	F:GO:0005509	-		IPR000716; IPR011992; IPR018247; IPR019577; PTHR12036 (PANTHER), PTHR12036:SF1 (PANTHER), SignalP (SIGNALP), SSF47473 (SUPERFAMILY)
Angiostrongylus cantonensis	thyroglobulin type-1 repeat family protein	0		F:GO:0005509		SignalP (SIGNALP)
Caenorhabditis elegans	cap-gly domain-containing protein	1	P:GO:0008340	-		G3DSA:3.80.10.10 (GENE3D), PS51450 (PROFILE)
Angiostrongylus cantonensis	major allergen	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021		IPR010291; PTHR23294 (PANTHER), SignalP (SIGNALP)
Brugia malayi	bromodomain containing protein	1	C:GO:0044424	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR16266 (PANTHER)
Brugia malayi	pleckstrin homology domain interacting protein	4	F:GO:0005515; P:GO:0007169; P:GO:0048522; P:GO:0009725	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR16266 (PANTHER), PTHR16266:SF4 (PANTHER)
Ailuropoda melanoleuca	triosephosphate isomerase 1	11	C:GO:0005829; P:GO:0006633; C:GO:0005625; P:GO:0006098; P:GO:0019682; F:GO:0004807; F:GO:0005515; P:GO:0006096; P:GO:0006094; C:GO:0005634; P:GO:0009790	-	EC:5.3.1.1	-
Danio rerio	atp-binding sub-family a member 1	18	P:GO:0002790; P:GO:0010875; P:GO:0043691; P:GO:0006911; F:GO:0005548; P:GO:0008203; P:GO:0006497; P:GO:0045332; F:GO:0008509; P:GO:0071222; P:GO:0071300; F:GO:0017111; C:GO:0005887; C:GO:0005794; F:GO:0005515; P:GO:0055099; F:GO:0017127; P:GO:0033700	-	EC:3.6.1.15	G3DSA:3.40.50.300 (GENE3D), PTHR19229 (PANTHER), PTHR19229:SF34 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-

Caenorhabditis briggsae	Hypothetical protein CBG20567 [Caenorhabditis briggsae]	0				IPR003659; SignalP (SIGNALP)
Caenorhabditis elegans	e3 ubiquitin-protein ligase huwe1-like	4	C:GO:0005622; F:GO:0016881; F:GO:0005488; P:GO:0006464	-	EC:6.3.2.0	-
Ailuropoda melanoleuca	fibrillarin	11	C:GO:0001651; C:GO:0001652; C:GO:0031428; C:GO:0015030; F:GO:0030515; F:GO:0005515; P:GO:0016074; P:GO:0006364; P:GO:0032259; F:GO:0008168; P:GO:0008033	-	EC:2.1.1.0	-
Brugia malayi	ymp3_caeel ame: full=uncharacterized protein	0				IPR019335
	-	0				-
	-	0				-
Brugia malayi	ago piwi domain protein	0		F:GO:0003676; F:GO:0003743		IPR003165; IPR012337; PTHR22891 (PANTHER)
Caenorhabditis elegans	aar2 protein	1	F:GO:0005515	-		IPR007946
Caenorhabditis elegans	aar2 protein	1	F:GO:0005515	-		IPR007946
	-	0				-
Caenorhabditis elegans	lysocardiolipin acyltransferase 1	4	F:GO:0008415; F:GO:0005515; C:GO:0016021; P:GO:0008152	-		IPR002123; PTHR10983 (PANTHER), PTHR10983:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	lysocardiolipin acyltransferase 1	4	F:GO:0008415; F:GO:0005515; C:GO:0016021; P:GO:0008152	-		IPR002123; PTHR10983 (PANTHER), PTHR10983:SF1 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	transmembrane and coiled-coil domains 7	2	P:GO:0000003; P:GO:0048856	-		IPR011989; IPR016024; PTHR20959 (PANTHER)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG21482 [Caenorhabditis briggsae]	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	6	P:GO:0006680; C:GO:0005886; P:GO:0018991; F:GO:0004348; P:GO:0040011; C:GO:0016021	-	EC:3.2.1.45	IPR006775; IPR008928; PTHR12654 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	helicase conserved c-termi-l domain containing protein	2	F:GO:0005488; F:GO:0016787	-		IPR017871; PTHR11752 (PANTHER), PTHR11752:SF3 (PANTHER)
	-	0				IPR006058
	-	0				-
	-	0				-

Pongo abelii	collagen alpha-2 chain-like	17	P:GO:0042476; F:GO:0030674; P:GO:0070208; P:GO:0043589; P:GO:0008217; F:GO:0042802; C:GO:0005615; F:GO:0046332; P:GO:0001501; F:GO:0048407; C:GO:0005584; P:GO:0030199; P:GO:0007179; F:GO:0005201; P:GO:0001568; P:GO:0007266; C:GO:0005886	-		IPR000885; PTHR10499 (PANTHER), PTHR10499:SF71 (PANTHER), PS51461 (PROFILE)
Aedes aegypti	split isoform c	7	P:GO:0003002; P:GO:0001709; P:GO:0009887; P:GO:0006928; P:GO:0042063; P:GO:0007166; P:GO:0048699	-		IPR010912; IPR016194; G3DSA:2.40.290.10 (GENE3D)
Aedes aegypti	split isoform c	7	P:GO:0003002; P:GO:0001709; P:GO:0009887; P:GO:0006928; P:GO:0042063; P:GO:0007166; P:GO:0048699	-		IPR010912; IPR016194; G3DSA:2.40.290.10 (GENE3D)
Loa loa	protein split ends	3	F:GO:0005488; P:GO:0007275; P:GO:0050789	-		IPR010912; IPR012921; IPR016194; G3DSA:2.40.290.10 (GENE3D)
Aedes aegypti	split isoform c	7	P:GO:0003002; P:GO:0001709; P:GO:0009887; P:GO:0006928; P:GO:0042063; P:GO:0007166; P:GO:0048699	-		IPR010912; IPR012921; IPR016194; G3DSA:2.40.290.10 (GENE3D)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	nudix family protein	0		F:GO:0016787		IPR000086; PTHR12318 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0004672; F:GO:0005524; P:GO:0006468		IPR012877
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0006508; F:GO:0004181; F:GO:0008270		-
Loa loa	kh domain containing protein	3	P:GO:0044238; F:GO:0003676; P:GO:0044237	-		IPR004087; IPR004088; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR11208 (PANTHER), PTHR11208:SF8 (PANTHER), SSF54791 (SUPERFAMILY)
	-	0				-

Trichoplax adhaerens	eukaryotic translation initiation factor 4h	1	F:GO:0005488	-		IPR000504; IPR012677; PTHR23236 (PANTHER), PTHR23236:SF2 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
	-	0				-
Homo sapiens	pancreatic progenitor cell differentiation and proliferation factor	2	P:GO:0007275; P:GO:0030154	-		PD349947 (PRODOM)
Loa loa	peptidylprolyl isomerase -like 3	6	P:GO:0006457; P:GO:0008380; C:GO:0005681; F:GO:0005515; P:GO:0006397; F:GO:0003755	-	EC:5.2.1.8	IPR004394; G3DSA:3.30.460.10 (GENE3D)
Loa loa	calmodulin-like protein	2	P:GO:0009792; F:GO:0005509	-		-
Pan troglodytes	elongation factor mitochondrial precursor	7	F:GO:0003746; C:GO:0005743; F:GO:0005525; F:GO:0005515; C:GO:0042645; P:GO:0006414; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
	-	0				-
Homo sapiens	apolipoprotein a-i binding protein	3	C:GO:0005576; C:GO:0005739; F:GO:0005515	-		IPR004443; G3DSA:3.40.50.10260 (GENE3D), PTHR13232 (PANTHER), PTHR13232:SF8 (PANTHER)
Caenorhabditis briggsae	pin4 protein	9	C:GO:0005730; F:GO:0003681; P:GO:0006457; C:GO:0005759; C:GO:0005819; P:GO:0006364; C:GO:0030684; F:GO:0003755; F:GO:0003690	-	EC:5.2.1.8	-
Caenorhabditis briggsae	type iii restriction res subunit family protein	3	F:GO:0005524; F:GO:0003677; F:GO:0008026	-		IPR004179; PTHR11752 (PANTHER), PTHR11752:SF8 (PANTHER)
Caenorhabditis elegans	peroxisomal membrane protein related family member (pmp-5)	1	C:GO:0044464	-		G3DSA:3.40.50.300 (GENE3D), PTHR11384 (PANTHER), PTHR11384:SF3 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Homo sapiens	prolyl 4- beta polypeptide	12	F:GO:0003756; F:GO:0004656; C:GO:0005793; P:GO:0045454; C:GO:0009986; C:GO:0042470; C:GO:0005792; C:GO:0005788; F:GO:0005515; P:GO:0018401; C:GO:0005576; C:GO:0005886	-	EC:5.3.4.1; EC:1.14.11.2	-

Caenorhabditis briggsae	multiple pdz domain protein	7	P:GO:0042552; C:GO:0005923; P:GO:0023034; C:GO:0016021; C:GO:0045202; P:GO:0007155; F:GO:0005515	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR19964 (PANTHER), PTHR19964:SF10 (PANTHER)
Caenorhabditis briggsae	zinc finger ran-binding domain-containing protein 2	2	C:GO:0005622; F:GO:0008270	-		IPR001876; G3DSA:4.10.1060.10 (GENE3D), PTHR12999 (PANTHER), PTHR12999:SF4 (PANTHER), SSF90209 (SUPERFAMILY)
Caenorhabditis briggsae	prolyl 4-hydroxylase	6	F:GO:0031418; F:GO:0005506; F:GO:0004656; P:GO:0055114; F:GO:0016702; C:GO:0005783	-	EC:1.14.11.2; EC:1.13.11.0	IPR011990; IPR013547; PTHR10869 (PANTHER), PTHR10869:SF13 (PANTHER)
Saccoglossus kowalevskii	ensangp00000010363	0				PTHR22930 (PANTHER)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	6	P:GO:0040010; P:GO:0010171; P:GO:0040011; P:GO:0006898; P:GO:0002009; P:GO:0009792	-		-
Nematostella vectensis	coagulation factor xiii b chain precursor (protein-glutamine gamma-glutamyltransferase b chain) (transglutami-se b chain) (fibrin-stabilizing factor b subunit)	0		F:GO:0005488; P:GO:0007155		IPR000436; IPR016060; PTHR19325 (PANTHER), PTHR19325:SF25 (PANTHER), SignalP (SIGNALP)
	-	0				-
Brugia malayi	cytoplasmic intermediate filament protein	3	P:GO:0048856; P:GO:0007275; P:GO:0040007	-		IPR001664
Caenorhabditis elegans	beta3 protein	12	P:GO:0009792; P:GO:0010171; P:GO:0002119; C:GO:0005794; F:GO:0005515; C:GO:0030117; F:GO:0008565; P:GO:0006886; P:GO:0007040; P:GO:0019915; P:GO:0040007; P:GO:0006897	-		IPR002553; IPR011989; IPR016024; PTHR11134 (PANTHER), PTHR11134:SF1 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-cpg-2 protein	2	P:GO:0032502; P:GO:0032501	-		IPR002557; G3DSA:2.170.140.10 (GENE3D), PTHR11177 (PANTHER), PTHR11177:SF37 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-cpg-2 protein	3	P:GO:0009792; P:GO:0000281; F:GO:0008061	-		IPR002557; G3DSA:2.170.140.10 (GENE3D), PTHR11177 (PANTHER), PTHR11177:SF37 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-cpg-2 protein	2	P:GO:0032502; P:GO:0032501	-		IPR002557; G3DSA:2.170.140.10 (GENE3D), PTHR11177 (PANTHER), PTHR11177:SF37 (PANTHER)
	-	0				-
	-	0				-

Caenorhabditis elegans	coiled-coil domain containing 134-like	0		C:GO:0005576		SignalP (SIGNALP)
Caenorhabditis elegans	coiled-coil domain containing 134-like	0		C:GO:0005576		-
Caenorhabditis briggsae	Hypothetical protein CBG04113 [Caenorhabditis briggsae]	0		F:GO:0031072		-
Chlorobaculum tepidum	AF287482_5Orf122 [Chlorobaculum tepidum]	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	phosphodiesterase cgmp-inhibited	3	F:GO:0046872; P:GO:0007165; F:GO:0004114	-	EC:3.1.4.17	IPR002073; PTHR11347 (PANTHER), PTHR11347:SF28 (PANTHER), SSF109604 (SUPERFAMILY)
Caenorhabditis briggsae	prolyl 4-hydroxylase	2	F:GO:0005488; F:GO:0016491	-		IPR013547; PTHR10869 (PANTHER), PTHR10869:SF13 (PANTHER)
Caenorhabditis elegans	inositol -trisphosphate receptor	5	P:GO:0006816; F:GO:0005220; P:GO:0055085; C:GO:0016021; C:GO:0005783	-		IPR013662; IPR015925; PTHR13715:SF2 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Loa loa	fk506 binding protein 12-rapamycin associated protein 1	41	F:GO:0004674; P:GO:0030838; P:GO:0032868; P:GO:0032314; P:GO:0007584; C:GO:0070438; P:GO:0045727; C:GO:0005625; P:GO:0043610; P:GO:0016049; C:GO:0031931; P:GO:0005979; P:GO:0032095; C:GO:0005942; F:GO:0008144; C:GO:0000139; P:GO:0043200; P:GO:0018107; P:GO:0031529; P:GO:0050731; P:GO:0045859; P:GO:0031998; P:GO:0051496; F:GO:0005524; P:GO:0007281; P:GO:0018105; C:GO:0031932;	-	EC:2.7.11.0	IPR000403; IPR009076; IPR010452; IPR011009; IPR018936; G3DSA:3.30.1010.10 (GENE3D), PTHR11139 (PANTHER), PTHR11139:SF9 (PANTHER)
Caenorhabditis briggsae	solute carrier family member b2	4	P:GO:0006024; P:GO:0051216; P:GO:0001649; C:GO:0016020	-		IPR013657; PTHR10778 (PANTHER), PTHR10778:SF12 (PANTHER), SignalP (SIGNALP), SSF103481 (SUPERFAMILY)
	-	0				-

Pongo abelii	type alpha 1	22	P:GO:0009314; P:GO:0018149; P:GO:0030168; P:GO:0048565; P:GO:0043206; C:GO:0005586; P:GO:0007229; P:GO:0050777; P:GO:0007507; P:GO:0007160; C:GO:0005615; F:GO:0046332; P:GO:0001501; F:GO:0048407; P:GO:0043588; P:GO:0030199; F:GO:0005178; P:GO:0007179; P:GO:0034097; P:GO:0032964; F:GO:0005201; P:GO:0001568	-		IPR008160; PTHR10499 (PANTHER), PTHR10499:SF125 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	guanine nucleotide exchange factor mss4	0		P:GO:0007264; F:GO:0008270; F:GO:0005085		IPR007515; IPR011057; IPR011323; PTHR13276 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Loa loa	briggsae cbr-pqn-85 protein	11	P:GO:0070193; P:GO:0007064; C:GO:0034991; P:GO:0006355; P:GO:0051306; C:GO:0000795; C:GO:0005700; C:GO:0034990; F:GO:0016563; P:GO:0010628; C:GO:0035327	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
Brugia malayi	calponin homology	1	F:GO:0005515	-		IPR001715; PTHR11915 (PANTHER), PTHR11915:SF47 (PANTHER)
Loa loa	selenocysteine lyase	1	F:GO:0016740	-		IPR000192; IPR015421; IPR015424; PTHR11601 (PANTHER)
Caenorhabditis elegans	acyl-coenzyme a dehydroge-se member 8	4	F:GO:0004085; F:GO:0050660; P:GO:0055114; C:GO:0005739	-	EC:1.3.99.2	IPR006090; IPR009075; PTHR10909 (PANTHER), PTHR10909:SF10 (PANTHER)
Caenorhabditis elegans	acyl-coenzyme a dehydroge-se member 8	4	F:GO:0004085; F:GO:0050660; P:GO:0055114; C:GO:0005739	-	EC:1.3.99.2	IPR006090; IPR009075; PTHR10909 (PANTHER), PTHR10909:SF10 (PANTHER)

Caenorhabditis briggsae	dual specificity catalytic domain containing protein	4	F:GO:0004725; P:GO:0006470; P:GO:0008340; F:GO:0008138	-	EC:3.1.3.48	IPR000340; IPR000387; IPR016130; IPR020422; G3DSA:3.90.190.10 (GENE3D), PTHR10159 (PANTHER), PTHR10159:SF21 (PANTHER), SSF52799 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	rala-binding protein 1	2	P:GO:0007264; F:GO:0017160	-		IPR000198; IPR008936; PTHR12783 (PANTHER), PTHR12783:SF1 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-dhs-17 protein	3	F:GO:0016491; P:GO:0055114; F:GO:0005488	-		-
Pongo abelii	guanine nucleotide binding protein (g protein) alpha inhibiting activity polypeptide 2	18	C:GO:0045121; F:GO:0004871; F:GO:0005515; P:GO:0007193; P:GO:0000186; P:GO:0001973; P:GO:0051927; C:GO:0005624; P:GO:0007213; F:GO:0005525; C:GO:0005829; P:GO:0007214; P:GO:0008284; F:GO:0003924; C:GO:0005886; P:GO:0050805; C:GO:0005634; P:GO:0007584	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
	-	0				IPR001810
	-	0				-
	-	0				-
Caenorhabditis briggsae	vesicle-fusing atpase	8	P:GO:0009792; P:GO:0002119; F:GO:0005515; P:GO:0032940; P:GO:0000003; P:GO:0040011; P:GO:0040007; P:GO:0006898	-		G3DSA:1.10.8.60 (GENE3D), PTHR23078 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-ttr-17 protein	0		P:GO:0016539		IPR001534; SignalP (SIGNALP)
Brugia malayi	phosphopantothenoylcysteine decarboxylase	6	P:GO:0002119; F:GO:0005515; P:GO:0040010; P:GO:0000003; P:GO:0006898; F:GO:0003824	-		IPR003382; PTHR14359 (PANTHER), PTHR14359:SF11 (PANTHER)
	-	0				-
Caenorhabditis elegans	isoform a	3	F:GO:0004872; C:GO:0016021; F:GO:0005509	-		IPR002172; PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER)
Brugia malayi	transportin 3	1	F:GO:0005515	-		IPR011989; IPR013598; IPR016024; PTHR12363 (PANTHER), PTHR12363:SF5 (PANTHER)

	-	0				-
	-	0				-
	-	0				-
Loa loa	probable tr- pseudouridine synthase 2	1	P:GO:0016070	-		-
	-	0				-
Haemonchus contortus	glutathione s-transferase	4	P:GO:0008340; P:GO:0040010; F:GO:0005515; F:GO:0016740	-		IPR004045; IPR004046; IPR010987; IPR012335; IPR012336; IPR017933; PTHR11571 (PANTHER), PTHR11571:SF6 (PANTHER)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Callithrix jacchus	vimentin	11	F:GO:0005200; P:GO:0006928; C:GO:0005886; C:GO:0031252; C:GO:0030424; C:GO:0005882; P:GO:0045103; F:GO:0019901; F:GO:0008022; C:GO:0005829; P:GO:0044419	-		IPR001664; IPR016044; IPR018039; G3DSA:1.20.5.170 (GENE3D), PTHR23239:SF1 (PANTHER)
	-	0				-
Homo sapiens	glutathione s-transferase pi	9	C:GO:0005737; P:GO:0007417; F:GO:0004364; P:GO:0006805; F:GO:0005515; F:GO:0008144; P:GO:0006916; C:GO:0005634; F:GO:0043295	-	EC:2.5.1.18	-
Caenorhabditis elegans	novel protein	3	P:GO:0009792; P:GO:0040010; P:GO:0006898	-		IPR016024; PTHR12444 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	general transcription factor polypeptide 62kda	2	P:GO:0008152; F:GO:0016740	-		IPR011993; IPR013876; PTHR12856 (PANTHER), SSF50729 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	low-density lipoprotein receptor	2	C:GO:0016021; F:GO:0005509	-		IPR000033; IPR006210; IPR011042; IPR013032; G3DSA:2.10.25.10 (GENE3D), PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER), SignalP (SIGNALP), SSF57196 (SUPERFAMILY), SSF63825 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	briggsae cbr-eat-3 protein	0		C:GO:0030061; C:GO:0016021; C:GO:0016020; C:GO:0005743; C:GO:0030425; C:GO:0005741; C:GO:0005739; P:GO:0006915; P:GO:0007007; F:GO:0000166; F:GO:0005525; C:GO:0005758; F:GO:0003924; P:GO:0007601; P:GO:0045768		PTHR11566 (PANTHER), PTHR11566:SF8 (PANTHER)
Brugia malayi	surfeit locus protein 4	14	P:GO:0040035; P:GO:0009792; P:GO:0002119; C:GO:0012505; C:GO:0005794; P:GO:0032940; C:GO:0031090; P:GO:0040011; P:GO:0019915; P:GO:0040007; C:GO:0005783; C:GO:0044425; C:GO:0044446; P:GO:0002009	-		SignalP (SIGNALP)
Caenorhabditis briggsae	block of proliferation 1	11	P:GO:0040010; P:GO:0051726; C:GO:0070545; P:GO:0040035; P:GO:0000463; P:GO:0002119; F:GO:0005515; P:GO:0006898; C:GO:0005654; P:GO:0008283; P:GO:0009792	-		IPR012953; PTHR17605 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	peroxisomal biogenesis factor 6	8	C:GO:0005829; P:GO:0016561; F:GO:0042623; F:GO:0008022; F:GO:0032403; C:GO:0005778; P:GO:0050821; F:GO:0005524	-		IPR003593; IPR003959; G3DSA:1.10.8.60 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23077 (PANTHER), PTHR23077:SF2 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-lrs-1 protein	5	F:GO:0004823; P:GO:0006429; F:GO:0005515; F:GO:0005524; C:GO:0005829	-	EC:6.1.1.4	-

Brugia malayi	d- repair protein rev1	7	F:GO:0016779; P:GO:0040010; F:GO:0005488; C:GO:0043231; P:GO:0006898; P:GO:0009792; P:GO:0006974	-	EC:2.7.7.0	IPR001126; IPR017963; G3DSA:3.30.70.270 (GENE3D), PTHR11076:SF13 (PANTHER), SSF56672 (SUPERFAMILY)
Caenorhabditis elegans	deoxyribonuclease ii family protein	0		P:GO:0006259; F:GO:0004531		IPR004947; PTHR10858:SF10 (PANTHER)
	-	0				-
Caenorhabditis briggsae	multidrug-resistance like protein isoform m	3	F:GO:0016887; P:GO:0006810; F:GO:0000166	-		PTHR19242 (PANTHER), PTHR19242:SF31 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	acyl-coa dehydroge-se	6	C:GO:0005759; P:GO:0055114; F:GO:0003995; P:GO:0006631; P:GO:0019915; F:GO:0050660	-	EC:1.3.99.3	IPR006089; IPR006090; IPR006091; IPR009075; IPR009100; PTHR10909 (PANTHER), PTHR10909:SF10 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Loa loa	cyclin g associated ki-se	2	F:GO:0005488; F:GO:0004672	-		IPR001623; PTHR23172 (PANTHER), PTHR23172:SF21 (PANTHER)
Caenorhabditis briggsae	briggsae cbr--s-5 protein	0		F:GO:0046872; P:GO:0006508; F:GO:0008237; F:GO:0016787; F:GO:0008233; F:GO:0008270; F:GO:0004222; P:GO:0007413		IPR001506; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF73 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-smp-2 protein	0		P:GO:0007399; P:GO:0030154; F:GO:0004872; P:GO:0007275; C:GO:0016021; C:GO:0016020		IPR001627; IPR015943
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	P:GO:0008340	-		IPR011701; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR10074 (PANTHER), PTHR10074:SF12 (PANTHER)
	-	0				-
Loa loa	elegans protein partially confirmed by transcript evidence	2	P:GO:0040010; F:GO:0005515	-		-
Loa loa	elegans protein partially confirmed by transcript evidence	2	P:GO:0040010; F:GO:0005515	-		-
Caenorhabditis elegans	briggsae cbr-ced-5 protein	6	P:GO:0043652; F:GO:0032403; F:GO:0030695; F:GO:0019899; P:GO:0040039; F:GO:0017124	-		PTHR23317 (PANTHER), PTHR23317:SF16 (PANTHER)
	-	0				SignalP (SIGNALP)

Brugia malayi	protein-tyrosine phosphatase containing protein	1	F:GO:0016791	-	EC:3.1.3.0	IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF18 (PANTHER), SSF52799 (SUPERFAMILY)
Brugia malayi	serine threonine protein phosphatase pp1-alpha catalytic subunit	4	P:GO:0006470; F:GO:0046872; F:GO:0004722; P:GO:0000003	-		IPR004843; IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF19 (PANTHER), SSF56300 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-unc- protein	0		F:GO:0005488; F:GO:0008270		-
	-	0				SignalP (SIGNALP)
Loa loa	nucleolar protein 10	5	C:GO:0005730; P:GO:0009792; P:GO:0002119; P:GO:0018991; P:GO:0040010	-		PTHR14927 (PANTHER)
Caenorhabditis elegans	d- polymerase theta	3	F:GO:0008026; F:GO:0003676; F:GO:0005524	-		PTHR11752 (PANTHER), PTHR11752:SF3 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG24887 [Caenorhabditis briggsae]	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG06557 [Caenorhabditis briggsae]	0		C:GO:0016020		IPR000494; G3DSA:3.80.20.20 (GENE3D), PTHR21662 (PANTHER), PTHR21662:SF1 (PANTHER), SignalP (SIGNALP), SSF52058 (SUPERFAMILY)
Caenorhabditis briggsae	dedicator of cytokinesis family protein	1	F:GO:0005488	-		IPR010703; PTHR23317 (PANTHER), PTHR23317:SF26 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-nrf-6 protein	5	F:GO:0016747; P:GO:0009792; P:GO:0010171; P:GO:0040017; P:GO:0006898	-	EC:2.3.1.0	PTHR11161 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; C:GO:0016020; F:GO:0016787; F:GO:0003676; F:GO:0003674; F:GO:0003824; C:GO:0005575; P:GO:0008152; F:GO:0046872; P:GO:0008150		IPR002591; IPR017850; PTHR10151 (PANTHER), PTHR10151:SF28 (PANTHER)
	-	0				-
Nippostrongylus brasiliensis	elegans protein partially confirmed by transcript evidence	1	P:GO:0009792	-		IPR003677; PTHR21593 (PANTHER)
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis briggsae	chaperonin containing subunit 6a (zeta 1)	10	P:GO:0040035; P:GO:0009792; P:GO:0002119; C:GO:0005832; P:GO:0051086; F:GO:0005524; P:GO:0008340; P:GO:0040011; F:GO:0051082; P:GO:0040007	-		IPR002194; IPR002423; IPR012722; IPR017998; G3DSA:1.10.560.10 (GENE3D), G3DSA:3.30.260.10 (GENE3D), G3DSA:3.50.7.10 (GENE3D), SSF52029 (SUPERFAMILY), SSF54849 (SUPERFAMILY)
Caenorhabditis elegans	calponin transgelin	2	F:GO:0003779; P:GO:0006939	-		IPR000557; IPR001715; IPR003096; PTHR18959 (PANTHER), PTHR18959:SF3 (PANTHER)
	-	0				-
Brugia malayi	elegans protein partially confirmed by transcript evidence	4	P:GO:0000003; P:GO:0040010; P:GO:0006898; P:GO:0002119	-		-
Caenorhabditis brenneri	f-box protein fbl2	0		F:GO:0016874		G3DSA:3.80.10.10 (GENE3D), PTHR23125 (PANTHER), PTHR23125:SF32 (PANTHER), SSF52047 (SUPERFAMILY)
Caenorhabditis elegans	glucose transporter 1 transcript	3	C:GO:0016020; F:GO:0022891; P:GO:0006810	-		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005488	-		-
Caenorhabditis elegans	deah (asp-glu-ala-his) box polypeptide partial	6	F:GO:0003676; P:GO:0000381; F:GO:0008026; F:GO:0005524; F:GO:0005515; P:GO:0002121	-		-
Caenorhabditis briggsae	atp synthase h+ transporting mitochondrial f1 complex delta subunit	11	F:GO:0046961; P:GO:0000003; P:GO:0040010; F:GO:0046933; C:GO:0005743; P:GO:0042777; C:GO:0045261; P:GO:0009792; P:GO:0002119; C:GO:0005811; F:GO:0005524	-	EC:3.6.3.14	IPR001469; IPR020546; PTHR13822:SF1 (PANTHER)

Brugia malayi	cullin 3	20	P:GO:0008054; P:GO:0007369; P:GO:0008629; P:GO:0035024; C:GO:0005794; P:GO:0007050; P:GO:0008284; F:GO:0004842; F:GO:0031625; P:GO:0016567; P:GO:0001831; C:GO:0005827; P:GO:0000082; P:GO:0043149; P:GO:0000090; F:GO:0030332; C:GO:0005634; P:GO:0016477; C:GO:0031463; P:GO:0000910	-	EC:6.3.2.19	IPR001373; IPR016159; G3DSA:1.20.1310.10 (GENE3D)
Canis familiaris	aminoadipate-semialdehyde dehydroge-se	0		F:GO:0016874; P:GO:0006629; F:GO:0000036; P:GO:0006810; F:GO:0000166; F:GO:0005524; F:GO:0003674; P:GO:0055114; F:GO:0031177; F:GO:0016491; F:GO:0003824; C:GO:0005575; F:GO:0048037; P:GO:0008152; P:GO:0008150; F:GO:0004043		IPR000873; IPR020845; G3DSA:3.40.50.980 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF11 (PANTHER), SSF56801 (SUPERFAMILY)
Caenorhabditis elegans	peptidase family m3 containing protein	6	F:GO:0004222; P:GO:0045449; F:GO:0003702; P:GO:0006367; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	-
Loa loa	wd repeat-containing protein 47	2	F:GO:0016740; F:GO:0005515	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR19863 (PANTHER), PTHR19863:SF2 (PANTHER)
Caenorhabditis briggsae	tyrosine-protein ki-se pr2	8	F:GO:0004674; P:GO:0042059; P:GO:0040027; F:GO:0004713; F:GO:0005524; F:GO:0005515; P:GO:0009792; P:GO:0006468	-	EC:2.7.11.0; EC:2.7.10.0	IPR000719; IPR001245; IPR008266; IPR011009; IPR020685; G3DSA:1.10.510.10 (GENE3D), PTHR23256:SF266 (PANTHER)
Caenorhabditis elegans	alkylation repair homolog 8 (coli)	1	P:GO:0040010	-		-
Caenorhabditis briggsae	briggsae cbr-frl-1 protein	2	P:GO:0030036; F:GO:0003779	-		IPR010472; IPR016024; PTHR23213 (PANTHER), PTHR23213:SF24 (PANTHER)

Ancylostoma caninum	secreted protein asp-2	0		F:GO:0009055; P:GO:0019646; C:GO:0005576		SignalP (SIGNALP)
Caenorhabditis elegans	cdc42p	4	C:GO:0016020; C:GO:0005622; F:GO:0005525; P:GO:0007264	-		IPR001806; IPR013753; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF39 (PANTHER)
Caenorhabditis elegans	yso2_caeel ame: full=uncharacterized protein flags: precursor	0		P:GO:0000003		IPR013568
Caenorhabditis briggsae	n-6 adenine-specific d- methyltransferase 1	1	F:GO:0016740	-		IPR002052; IPR004557; IPR007848; G3DSA:3.40.50.150 (GENE3D), PTHR18895 (PANTHER), PTHR18895:SF8 (PANTHER), SSF53335 (SUPERFAMILY)
Nippostrongylus brasiliensis	keratin-like protein	1	P:GO:0009792	-		IPR003677; PTHR21593 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Callithrix jacchus	chromosome 11 open reading frame isoform cra_a	0		C:GO:0016021; C:GO:0016020		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Hydra magnipapillata	uncharacterized transposase-like protein	0		F:GO:0046872; P:GO:0055114; F:GO:0009055; F:GO:0016491; F:GO:0020037; F:GO:0005506; F:GO:0004497		IPR007087; IPR015880
Brugia malayi	zinc c2h2 type family protein	0		F:GO:0008270; C:GO:0005622		IPR015880
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	F:GO:0003676; F:GO:0000166	-		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	4	P:GO:0007186; C:GO:0016021; C:GO:0005622; F:GO:0008270	-		-
Caenorhabditis elegans	tubulin polymerization-promoting protein family member 2	2	P:GO:0002119; P:GO:0000003	-		-
Caenorhabditis briggsae	dedicator of cytokinesis family protein	1	F:GO:0005488	-		-
Caenorhabditis elegans	programmed cell death 11	8	P:GO:0040010; P:GO:0006396; F:GO:0005488; P:GO:0018991; P:GO:0002119; P:GO:0009792; P:GO:0008406; C:GO:0005634	-		IPR003107; IPR008847; IPR011990; IPR013026; PTHR23270 (PANTHER), SSF48452 (SUPERFAMILY)

Caenorhabditis briggsae	briggsae cbr-cdh-1 protein	0		C:GO:0016021; C:GO:0016020; P:GO:0002119; P:GO:0040011; P:GO:0040010; C:GO:0005886; P:GO:0007156; F:GO:0005509; P:GO:0007155		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	ribosomal protein l7a	2	C:GO:0005840; P:GO:0042254	-		IPR001921; IPR004037; IPR004038; IPR018492; G3DSA:3.30.1330.30 (GENE3D), PTHR23105 (PANTHER), SSF55315 (SUPERFAMILY)
Caenorhabditis elegans	ribosomal protein l7a	2	C:GO:0005840; P:GO:0042254	-		IPR001921; IPR004037; IPR004038; IPR018492; G3DSA:3.30.1330.30 (GENE3D), PTHR23105 (PANTHER), SSF55315 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-
Loa loa	epidermal growth factor receptor	7	P:GO:0006468; F:GO:0004714; F:GO:0005515; F:GO:0004716; F:GO:0005524; C:GO:0016021; P:GO:0007169	-	EC:2.7.10.1	-
Caenorhabditis elegans	hypothetical protein B0041.5 [Caenorhabditis elegans]	3	P:GO:0007411; P:GO:0019915; P:GO:0007413	-		PTHR23051 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	transcription initiation factor tfiib	10	F:GO:0003743; P:GO:0006413; P:GO:0006357; F:GO:0008270; P:GO:0006367; C:GO:0005667; F:GO:0016251; P:GO:0051101; F:GO:0008134; P:GO:0009792	-		SignalP (SIGNALP)
Caenorhabditis briggsae	amp-activated protein ki-se gamma2 subunit-like	8	P:GO:0031323; P:GO:0016310; F:GO:0032559; P:GO:0044238; P:GO:0050790; F:GO:0019887; P:GO:0006950; F:GO:0004679	-		IPR000644; IPR013785; PTHR13780 (PANTHER), SSF54631 (SUPERFAMILY)
	-	0				-

Caenorhabditis elegans	ras- family 12	6	P:GO:0007264; C:GO:0005622; F:GO:0003924; P:GO:0015031; C:GO:0016020; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR013753; IPR020849; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF81 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Loa loa	retinol dehydroge-se 14	5	C:GO:0005783; P:GO:0008152; F:GO:0003824; C:GO:0005739; F:GO:0005488	-		IPR002198; IPR002347; IPR016040; PTHR19410:SF98 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis briggsae	protein	1	P:GO:0040010	-		IPR000449; IPR002833; IPR009060; IPR015940; G3DSA:1.10.8.10 (GENE3D), G3DSA:3.40.1490.10 (GENE3D), PTHR12649 (PANTHER), SSF102462 (SUPERFAMILY)
Caenorhabditis elegans	protein	1	P:GO:0040010	-		IPR000449; IPR002833; IPR009060; IPR015940; G3DSA:1.10.8.10 (GENE3D), G3DSA:3.40.1490.10 (GENE3D), PTHR12649 (PANTHER), SSF102462 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	probable ribosome biogenesis protein nep1	8	C:GO:0005737; C:GO:0005730; P:GO:0009792; P:GO:0002119; F:GO:0003723; P:GO:0000003; P:GO:0006364; P:GO:0042274	-		IPR005304; PTHR12636:SF3 (PANTHER)
Caenorhabditis elegans	hypothetical protein F09G2.1 [Caenorhabditis elegans]	0		F:GO:0005524; F:GO:0004672; F:GO:0004713; P:GO:0006468		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Pongo abelii	ribosomal protein l10a	7	F:GO:0003735; F:GO:0003723; P:GO:0009653; C:GO:0022625; C:GO:0005739; P:GO:0006414; P:GO:0006396	-		IPR002143; IPR016094; PTHR23105 (PANTHER), PTHR23105:SF4 (PANTHER)
	-	0				IPR008139; IPR011001
Brugia malayi	a-phase promoting complex subunit 8 cdc23 family protein	3	P:GO:0009987; P:GO:0048856; P:GO:0007275	-		IPR007192
Caenorhabditis elegans	atp-binding sub-family c (cftr mrp) member 1	5	F:GO:0042626; C:GO:0005886; P:GO:0006810; C:GO:0016021; F:GO:0000166	-		IPR001140; IPR003439; IPR003593; IPR011527; IPR017871; IPR017940; G3DSA:1.20.1560.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF34 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)

Brugia malayi	negative elongation factor b homolog	0		F:GO:0003746; P:GO:0016481; C:GO:0005634		-
	-	0				-
Caenorhabditis briggsae	cat eye syndrome chromosome candidate 5	0		C:GO:0005739; F:GO:0016787; P:GO:0008152; C:GO:0005575		G3DSA:3.40.50.1000 (GENE3D), PTHR14269 (PANTHER), PTHR14269:SF4 (PANTHER), SignalP (SIGNALP), SSF56784 (SUPERFAMILY)
	-	0				-
Nematostella vectensis	low-density lipoprotein	0		P:GO:0006508; F:GO:0004252; F:GO:0005509; F:GO:0004872; F:GO:0016787; C:GO:0016021; F:GO:0003824; C:GO:0016020		IPR002172; PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-brd-1 protein	0		F:GO:0008270; F:GO:0005515; C:GO:0005622		IPR001841; IPR013083; IPR017907; PTHR12590 (PANTHER)
	-	0				-
Loa loa	nurf (nucleosome remodeling factor) complex homolog family member (nurf-1)	12	P:GO:0030097; P:GO:0000003; P:GO:0040010; P:GO:0035076; P:GO:0006727; P:GO:0048813; P:GO:0035073; F:GO:0046872; C:GO:0016589; F:GO:0016922; P:GO:0042766; P:GO:0045893	-		IPR001965; IPR011011; IPR013032; IPR013083; IPR019786; IPR019787; PTHR12321 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-cyn-17 protein	0		F:GO:0003755; P:GO:0006457; F:GO:0016853		IPR002130; IPR015891; PTHR11071 (PANTHER), PTHR11071:SF72 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	phosphoglycerate mutase	0				IPR013078; G3DSA:3.40.50.1240 (GENE3D), PTHR23029 (PANTHER), SSF53254 (SUPERFAMILY)
Caenorhabditis briggsae	ain family member (clp-1)	6	C:GO:0016021; P:GO:0008219; C:GO:0005622; P:GO:0006508; F:GO:0004198; F:GO:0005509	-		IPR001300; IPR022684; PTHR10183 (PANTHER), PTHR10183:SF45 (PANTHER), SSF54001 (SUPERFAMILY)
	-	0				-
	-	0				IPR003582

Homo sapiens	b-cell receptor-associated protein 31	13	P:GO:0016192; C:GO:0005829; P:GO:0006915; C:GO:0000139; F:GO:0004872; P:GO:0007283; P:GO:0006955; F:GO:0005102; C:GO:0033116; P:GO:0007165; P:GO:0006886; C:GO:0005789; C:GO:0005887	-		IPR008417; PTHR12701:SF4 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	mannose- 1	13	F:GO:0005509; P:GO:0006457; C:GO:0016021; F:GO:0005537; C:GO:0005793; F:GO:0042802; C:GO:0044422; C:GO:0005792; P:GO:0006888; F:GO:0051082; C:GO:0005783; C:GO:0005794; P:GO:0007596	-		IPR005052; IPR008985; IPR013320; PTHR12223:SF7 (PANTHER)
Caenorhabditis briggsae	sorting nexin 13	4	C:GO:0016021; P:GO:0007154; F:GO:0035091; F:GO:0005515	-		IPR013937; PTHR22775 (PANTHER), PTHR22775:SF8 (PANTHER)
	-	0				-
Ailuropoda melanoleuca	suppressor of ty 5 homolog (cerevisiae) isoform cra_a	12	P:GO:0032968; P:GO:0007049; P:GO:0045944; P:GO:0045090; F:GO:0019899; P:GO:0000122; F:GO:0008159; F:GO:0008148; F:GO:0046982; C:GO:0005654; P:GO:0006338; P:GO:0010033	-		PTHR11125 (PANTHER)

Pongo abelii	nuclear distribution gene c homolog (nidulans)	10	P:GO:0007097; P:GO:0008283; C:GO:0005794; P:GO:0043434; F:GO:0005515; P:GO:0007275; P:GO:0007067; C:GO:0005634; P:GO:0051301; C:GO:0005874	-		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	fog-3	0				-
	-	0				-
	-	0				-
	-	0				-
Loa loa	a-macroglobulin complement component family protein	1	C:GO:0005576	-		IPR008930; IPR009048; IPR011626; G3DSA:1.50.10.20 (GENE3D), PTHR11412 (PANTHER), PTHR11412:SF30 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	5	F:GO:0008536; P:GO:0006611; C:GO:0005643; F:GO:0005049; C:GO:0005737	-		PTHR12596 (PANTHER), PTHR12596:SF2 (PANTHER)
Caenorhabditis elegans	fh2 domain-containing protein 1	2	F:GO:0005515; P:GO:0040011	-		-
	-	0				-
Loa loa	hypothetical protein LOAG_09870 [Loa loa]	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	r- pseudouridylate synthase domain containing 2	3	F:GO:0009982; F:GO:0003723; P:GO:0001522	-	EC:5.4.99.12	-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
Ancylostoma duodenale	ancylostoma-secreted protein 1 precursor	0		C:GO:0005576		SignalP (SIGNALP)
Ancylostoma ceylanicum	secreted-protein 1 precursor	0		C:GO:0005576		-
Caenorhabditis elegans	uncoordi-ted family member (unc-103)	7	P:GO:0055085; P:GO:0051291; P:GO:0006355; P:GO:0006813; F:GO:0005242; P:GO:0007165; C:GO:0005887	-		IPR005821; G3DSA:1.10.287.70 (GENE3D), PTHR10217 (PANTHER), PTHR10217:SF15 (PANTHER), SignalP (SIGNALP), SSF81324 (SUPERFAMILY)
Ancylostoma caninum	briggsae cbr-vap-1 protein	1	P:GO:0009987	-		IPR001283; IPR014044; IPR018244; PTHR10334:SF11 (PANTHER)
Ancylostoma caninum	secreted protein asp-2	0		F:GO:0009055; P:GO:0019646; P:GO:0006898; C:GO:0005576		IPR001283; IPR014044; IPR018244; PTHR10334:SF11 (PANTHER)

Ancylostoma caninum	secreted protein asp-2	0		F:GO:0009055; P:GO:0019646; P:GO:0006898; C:GO:0005576		IPR001283; IPR014044; IPR018244; PTHR10334:SF11 (PANTHER)
Ancylostoma caninum	secreted protein asp-2	0		F:GO:0009055; P:GO:0019646; P:GO:0006898; C:GO:0005576		IPR001283; IPR014044; IPR018244; PTHR10334:SF11 (PANTHER)
Caenorhabditis elegans	paz piwi domain-containing family member (ppw-1)	0		F:GO:0003676; P:GO:0000003; P:GO:0016246		IPR003100; IPR003165; IPR012337; G3DSA:2.170.260.10 (GENE3D), PTHR22891 (PANTHER), SSF101690 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	fatty acid elongation protein 3	2	P:GO:0040010; C:GO:0016021	-		IPR002076
	-	0				-
	-	0				-
Ancylostoma ceylanicum	metalloprotease 1 precursor	3	F:GO:0004222; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	IPR001506; IPR006026; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
	-	0				IPR001611; PR00019 (PRINTS), G3DSA:3.80.10.10 (GENE3D), PTHR10588 (PANTHER), PTHR10588:SF23 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)
Caenorhabditis elegans	inin family member (atn-1)	32	F:GO:0005178; P:GO:0007629; F:GO:0030375; C:GO:0031143; C:GO:0043197; C:GO:0005884; P:GO:0051289; P:GO:0040010; P:GO:0051017; C:GO:0030175; P:GO:0007016; F:GO:0070080; P:GO:0030035; F:GO:0005509; P:GO:0006936; P:GO:0048041; F:GO:0046983; C:GO:0005730; C:GO:0005829; F:GO:0051370; F:GO:0008307; P:GO:0009792; P:GO:0007067; F:GO:0042802; F:GO:0031432; C:GO:0055120;	-		IPR001589; IPR001715; IPR002017; G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF47 (PANTHER), SSF46966 (SUPERFAMILY)

Strongylocentrotus purpuratus	brevican	1	C:GO:0044464	-		IPR001304; IPR016186; IPR016187; PTHR22801 (PANTHER), PTHR22801:SF9 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
Loa loa	tpr repeat-containing protein	0		F:GO:0005488		IPR001440; IPR011990; IPR013026; IPR019734; IPR023011; SSF48452 (SUPERFAMILY)
Caenorhabditis elegans	alkylated d- repair protein alkb homolog 8	9	C:GO:0005829; P:GO:0040010; F:GO:0003676; F:GO:0016300; F:GO:0005515; F:GO:0000166; P:GO:0030488; C:GO:0005634; P:GO:0006974	-		IPR005123; G3DSA:2.60.120.590 (GENE3D), SSF51197 (SUPERFAMILY)
Loa loa	cell division protein ki-se 5	11	P:GO:0009792; P:GO:0006468; P:GO:0010468; F:GO:0008083; P:GO:0048489; F:GO:0005524; P:GO:0000003; C:GO:0016020; F:GO:0004674; P:GO:0051301; P:GO:0051932	-	EC:2.7.11.0	IPR011009; G3DSA:1.10.510.10 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF110 (PANTHER)
Physcomitrella patens subsp. patens	c- b domain protein	0		F:GO:0016740; F:GO:0008061; F:GO:0016787; P:GO:0006471; C:GO:0005576; F:GO:0005515; C:GO:0005618; F:GO:0030145; P:GO:0006030; P:GO:0007155; F:GO:0005488; F:GO:0003950		-
Brugia malayi	gon-4-like (elegans)	2	C:GO:0005737; C:GO:0005634	-		-
Caenorhabditis elegans	transmembrane protein with metallophosphoesterase domain	2	C:GO:0016021; F:GO:0016787	-		G3DSA:3.60.21.10 (GENE3D), SSF56300 (SUPERFAMILY)
Caenorhabditis elegans	ankyrin repeat and fyve domain containing 1	2	C:GO:0005737; F:GO:0005488	-		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF258 (PANTHER)

Caenorhabditis elegans	cg8844	10	P:GO:0022900; P:GO:0008340; C:GO:0005743; P:GO:0040007; P:GO:0000003; P:GO:0019915; P:GO:0002119; C:GO:0070469; F:GO:0005515; F:GO:0003954	-	EC:1.6.99.3	IPR019377; PTHR13094 (PANTHER)
Caenorhabditis briggsae	enhancer of ksr-1 lethality family member (ekl-6)	2	P:GO:0000003; P:GO:0048856	-		-
	-	0				-
Brugia malayi	protein binding	7	P:GO:0009792; P:GO:0002119; P:GO:0008380; P:GO:0018991; F:GO:0070063; P:GO:0040010; P:GO:0006898	-		IPR001202; G3DSA:2.20.70.10 (GENE3D), PTHR11864 (PANTHER)
Caenorhabditis elegans	ibromatosis homolog family member (nfm-1)	5	C:GO:0005856; P:GO:0009792; C:GO:0005737; F:GO:0008092; C:GO:0019898	-		IPR000299; IPR011993; IPR018980; G3DSA:1.20.5.450 (GENE3D), PTHR23281 (PANTHER), PTHR23281:SF1 (PANTHER), SSF50729 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	C:GO:0016021; P:GO:0006813; F:GO:0005267	-		IPR013099; G3DSA:1.10.287.70 (GENE3D), PTHR11003 (PANTHER), PTHR11003:SF7 (PANTHER), SignalP (SIGNALP), SSF81324 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	transmembrane protein 1	0		F:GO:0005488; P:GO:0016192; C:GO:0016021; P:GO:0006814; C:GO:0005794; F:GO:0015081		-
Monosiga brevicollis MX1	5 -nucleotidase	0		F:GO:0008253; C:GO:0005737; F:GO:0000287; F:GO:0016787		IPR006434; PF05822 (PFAM)
Loa loa	negative elongation factor a homolog	0		F:GO:0003746		SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-hda-4 protein	1	P:GO:0009987	-		-
	-	0				-
Caenorhabditis briggsae	kelch domain-containing protein 10	0		F:GO:0003674; F:GO:0005515; C:GO:0005575		-
	-	0				IPR001849
Caenorhabditis elegans	abnormal cell migration family member (mig-15)	2	F:GO:0005515; F:GO:0004672	-		G3DSA:1.10.510.10 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF83 (PANTHER)
Loa loa	hypothetical protein LOAG_09252 [Loa loa]	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG03410 [Caenorhabditis briggsae]	1	P:GO:0006898	-		PTHR21072 (PANTHER), PTHR21072:SF1 (PANTHER)
	-	0				-

Loa loa	protein ki-se domain containing protein	7	P:GO:0006468; P:GO:0030154; P:GO:0032501; F:GO:0005515; F:GO:0005524; F:GO:0000287; F:GO:0004674	-	EC:2.7.11.0	-
Brugia malayi	developmentally regulated gtp binding protein 2	5	F:GO:0005525; C:GO:0005622; C:GO:0016021; P:GO:0015684; F:GO:0015093	-		-
	-	0				-
Caenorhabditis elegans	proteasome-associated protein ecm29 homolog	2	P:GO:0007067; C:GO:0044424	-		PTHR23346 (PANTHER), PTHR23346:SF2 (PANTHER)
Caenorhabditis briggsae	cysteine expressed	6	F:GO:0030170; F:GO:0004124; F:GO:0005515; P:GO:0006535; F:GO:0016740; C:GO:0005739	-	EC:2.5.1.47	IPR001216; IPR001926; IPR005856; IPR005859; G3DSA:3.40.50.1100 (GENE3D), PTHR10314 (PANTHER), PTHR10314:SF8 (PANTHER)
Caenorhabditis briggsae	vacuolar protein sorting 13d isoform 2	1	P:GO:0008104	-		IPR009543; PTHR16166 (PANTHER), PTHR16166:SF24 (PANTHER)
	-	0				-
Caenorhabditis elegans	argi-se	4	P:GO:0006525; F:GO:0004053; F:GO:0008270; F:GO:0005515	-	EC:3.5.3.1	IPR006035; IPR014033; SSF52768 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Macaca mulatta	eukaryotic initiation factor 4ai	11	F:GO:0003743; C:GO:0016281; C:GO:0005829; F:GO:0003729; P:GO:0045948; P:GO:0031100; F:GO:0008026; P:GO:0006200; F:GO:0000339; F:GO:0005524; F:GO:0005515	-		IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF2 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	pdz domain containing protein	5	P:GO:0009792; P:GO:0040007; P:GO:0040035; F:GO:0005515; P:GO:0002119	-		-
Caenorhabditis elegans	hypothetical protein F46C8.3 [Caenorhabditis elegans]	0				IPR020999
Caenorhabditis elegans	hypothetical protein F46C8.3 [Caenorhabditis elegans]	0				IPR020999
Apis mellifera	zinc finger protein	0		F:GO:0003676; P:GO:0060026; F:GO:0008270; F:GO:0005515; P:GO:0019915; C:GO:0005622		-
	-	0				-

Caenorhabditis elegans	ubiquitin ligase	6	P:GO:0001701; F:GO:0005515; P:GO:0006511; F:GO:0004842; P:GO:0007608; P:GO:0042048	-	EC:6.3.2.19	IPR003126; PTHR21497 (PANTHER), PTHR21497:SF3 (PANTHER)
Caenorhabditis elegans	folylpolyglutamate synthase	3	C:GO:0005737; F:GO:0005488; P:GO:0044237	-		-
Caenorhabditis elegans	elegans fln-2 isoform partially confirmed by transcript evidence	0		F:GO:0003779; P:GO:0009612		IPR001298; IPR013783; IPR014756; IPR017868; PTHR11915 (PANTHER), PTHR11915:SF55 (PANTHER)
Caenorhabditis elegans	filamin abp280 repeat family protein	0		F:GO:0003779		IPR001298; IPR013783; IPR014756; IPR017868; PTHR11915 (PANTHER), PTHR11915:SF55 (PANTHER)
	-	0				-
	-	0				-
Homo sapiens	apolipoprotein e	69	P:GO:0007186; P:GO:0010468; P:GO:0050728; F:GO:0042803; C:GO:0031232; C:GO:0034364; C:GO:0042627; P:GO:0006707; F:GO:0016209; P:GO:0007010; P:GO:0019934; F:GO:0008201; P:GO:0010875; P:GO:0007263; P:GO:0043691; C:GO:0034363; F:GO:0005543; P:GO:0051651; P:GO:0010544; F:GO:0046911; P:GO:0042311; P:GO:0046907; P:GO:0002021; P:GO:0045471; P:GO:0034375; F:GO:0001540; P:GO:0006874;	-		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021		PTHR23294 (PANTHER), SignalP (SIGNALP)
Brugia malayi	trypsin family protein	0		P:GO:0006508; F:GO:0004252; F:GO:0003824		IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR19355 (PANTHER), PTHR19355:SF82 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	P:GO:0040011	-		IPR000535; IPR008962; PTHR22947 (PANTHER)
	-	0				-
Caenorhabditis briggsae	zinc finger ccch-type containing 10	3	F:GO:0008270; F:GO:0003676; P:GO:0002009	-		IPR000571; G3DSA:4.10.1000.10 (GENE3D), PTHR12675 (PANTHER), SSF90229 (SUPERFAMILY)

Caenorhabditis elegans	zinc finger ccch-type containing 10	2	P:GO:0002009; F:GO:0005488	-		IPR000571; G3DSA:4.10.1000.10 (GENE3D), PTHR12675 (PANTHER), SSF90229 (SUPERFAMILY)
Caenorhabditis briggsae	dead (asp-glu-ala-asp) box polypeptide 10	7	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0008026; F:GO:0003676; P:GO:0040010; F:GO:0005524	-		IPR000629; IPR001650; IPR011545; IPR014001; IPR014014; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF24 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	briggsae cbr-larp-2 protein	0				-
	-	0				-
Caenorhabditis elegans	apyrase family member (apy-1)	5	C:GO:0016021; P:GO:0008340; P:GO:0040010; F:GO:0016462; F:GO:0005515	-		IPR009283
	-	0				IPR003961; IPR013783
	-	0				-
	-	0				-
Caenorhabditis elegans	numb-associated ki-se	4	P:GO:0009792; F:GO:0016301; P:GO:0008340; C:GO:0016020	-		-
Caenorhabditis elegans	numb-associated ki-se	4	P:GO:0009792; F:GO:0016301; P:GO:0008340; C:GO:0016020	-		-
Caenorhabditis elegans	numb-associated ki-se	4	P:GO:0009792; F:GO:0016301; P:GO:0008340; C:GO:0016020	-		-
Homo sapiens	mitochondrial inner membrane protein oxa1l	10	P:GO:0033615; C:GO:0043234; C:GO:0005746; P:GO:0055114; P:GO:0032780; P:GO:0009060; P:GO:0032981; P:GO:0051354; C:GO:0032592; P:GO:0051205	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Ancylostoma caninum	mater-l embryonic leucine zipper ki-se	5	C:GO:0005737; P:GO:0006468; F:GO:0005515; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR011009; IPR015739; IPR017442; IPR020636; G3DSA:3.30.200.20 (GENE3D)

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	7	P:GO:0040010; F:GO:0015078; C:GO:0000276; P:GO:0015986; P:GO:0000003; P:GO:0002119; P:GO:0009792	-		-
Caenorhabditis briggsae	acyl- dehydroge-se	8	P:GO:0006468; F:GO:0004713; P:GO:0055114; F:GO:0016787; F:GO:0005524; F:GO:0003995; F:GO:0050660; P:GO:0006508	-	EC:2.7.10.0; EC:1.3.99.3	-
Mus musculus	heterogeneous nuclear ribonucleoprotein a1	14	C:GO:0005681; F:GO:0003727; C:GO:0005730; P:GO:0000380; P:GO:0006405; C:GO:0030530; F:GO:0005515; P:GO:0051170; F:GO:0000166; F:GO:0003697; P:GO:0044419; C:GO:0005654; C:GO:0005737; P:GO:0051028	-		IPR000504; IPR012677; IPR021662; PTHR10432 (PANTHER), PTHR10432:SF13 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	presenilin rhomboid-like	3	F:GO:0008233; C:GO:0016020; C:GO:0005739	-		IPR002610; IPR022764; G3DSA:1.20.1540.10 (GENE3D), SSF144091 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis elegans	mus (drosophila mutagen sensitive) related family member (mus-81)	0		F:GO:0016740; F:GO:0008168; P:GO:0006259; C:GO:0005634; F:GO:0003677; F:GO:0018024; P:GO:0006281; F:GO:0003824; P:GO:0019725; F:GO:0005515; P:GO:0040010; F:GO:0004518		-
Caenorhabditis elegans	related to yeast vacuolar protein sorting factor family member (vps-34)	7	F:GO:0005488; F:GO:0004672; C:GO:0005942; P:GO:0046854; F:GO:0016303; P:GO:0048015; P:GO:0006468	-	EC:2.7.1.137	IPR001263; IPR015433; IPR016024; PTHR10048:SF7 (PANTHER)
	-	0				-
	-	0				IPR008728; PTHR12896 (PANTHER)
Trichostrongylus vitrinus	serine or cysteine protease inhibitor	2	F:GO:0005515; C:GO:0005634	-		IPR000215; G3DSA:2.30.39.10 (GENE3D), PTHR11461:SF25 (PANTHER)

Harpegnathos saltator	protein trs85-like protein	0				PTHR12975 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	ring finger protein 157	9	P:GO:0009987; P:GO:0040010; P:GO:0008340; F:GO:0046872; P:GO:0040035; P:GO:0018996; P:GO:0010171; P:GO:0040011; C:GO:0044424	-		PTHR22996 (PANTHER)
	-	0				-
Loa loa	lanthionine synthetase c-like protein	0		F:GO:0003824		-
Loa loa	splicing arginine serine-rich 15	2	P:GO:0009792; C:GO:0005634	-		IPR000504; IPR012677; PTHR14124 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	uroca-se domain containing 1	2	P:GO:0006548; F:GO:0016153	-	EC:4.2.1.49	IPR000193
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-ncx-3 protein	0		P:GO:0006816; C:GO:0016021; P:GO:0007154; C:GO:0016020; P:GO:0055085; F:GO:0005432		PTHR11878 (PANTHER), PTHR11878:SF2 (PANTHER)
Caenorhabditis briggsae	zinc finger c-x8-c-x5-c-x3-h type	3	F:GO:0003676; F:GO:0008270; F:GO:0005515	-		IPR000571; G3DSA:4.10.1000.10 (GENE3D), PTHR14493 (PANTHER), PTHR14493:SF1 (PANTHER), SSF90229 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein T05A12.3 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	membrane protein	0		F:GO:0003674; P:GO:0008150		IPR019410; G3DSA:3.40.50.150 (GENE3D), PTHR23109 (PANTHER), SSF53335 (SUPERFAMILY)
Caenorhabditis elegans	family with sequence similarity member a	0		F:GO:0003674; P:GO:0008150		IPR019410; G3DSA:3.40.50.150 (GENE3D), PTHR23109 (PANTHER), SSF53335 (SUPERFAMILY)
Caenorhabditis briggsae	family c2 u-ssigned peptidase (c02 family)	6	C:GO:0016021; P:GO:0008219; C:GO:0005622; P:GO:0006508; F:GO:0004198; F:GO:0005509	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-

Caenorhabditis briggsae	low-density lipoprotein receptor-related protein 2	30	P:GO:0042953; P:GO:0010165; P:GO:0010951; P:GO:0006898; C:GO:0031526; P:GO:0046879; P:GO:0031100; P:GO:0033280; C:GO:0005624; P:GO:0032526; P:GO:0006766; P:GO:0007568; P:GO:0008283; C:GO:0005615; F:GO:0005509; C:GO:0016021; P:GO:0030900; P:GO:0020028; C:GO:0005794; F:GO:0030492; C:GO:0005905; C:GO:0030139; P:GO:0016197; P:GO:0042493; C:GO:0005768; P:GO:0045056; F:GO:0004872; C:GO:0005783;	-		IPR000033; IPR011042; PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER), SSF63825 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-asp-6 protein	4	P:GO:0008219; F:GO:0005515; P:GO:0040011; F:GO:0008233	-		IPR001461; IPR009007; IPR021109; PTHR13683:SF53 (PANTHER)
	-	0				-
Angiostrongylus cantonensis	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
Brugia malayi	aspartyl aminopeptidase	6	C:GO:0005737; F:GO:0005515; F:GO:0004177; P:GO:0006508; F:GO:0008270; F:GO:0008237	-	EC:3.4.11.0	IPR001948; G3DSA:2.30.250.10 (GENE3D), G3DSA:3.40.630.10 (GENE3D), SSF53187 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-rpy-1 protein	7	C:GO:0005856; C:GO:0045211; P:GO:0007268; C:GO:0030054; F:GO:0033130; P:GO:0019915; F:GO:0008270	-		IPR019568; PTHR10098 (PANTHER), PTHR10098:SF7 (PANTHER)
Caenorhabditis briggsae	mediator of r- polymerase ii subunit 8 homolog	8	P:GO:0040010; P:GO:0000003; P:GO:0010171; P:GO:0002119; P:GO:0002009; P:GO:0009792; P:GO:0040018; P:GO:0006350	-		-
Macaca mulatta	upf0587 protein c1orf123 homolog	0		F:GO:0003674; F:GO:0000166; C:GO:0005575		-

Caenorhabditis elegans	trehalose 6-phosphate synthase	3	P:GO:0034608; F:GO:0016740; P:GO:0005992	-		G3DSA:3.40.50.2000 (GENE3D), SSF53756 (SUPERFAMILY)
Macaca mulatta	ciliary rootlet coiled- rootletin	4	P:GO:0009987; C:GO:0005856; C:GO:0044446; C:GO:0005737	-		IPR007240; PD936484 (PRODOM)
	-	0				-
Pongo abelii	cd9 antigen	9	P:GO:0030168; P:GO:0030913; P:GO:0008285; P:GO:0007155; F:GO:0005515; P:GO:0007342; P:GO:0006928; C:GO:0031092; C:GO:0005887	-		SignalP (SIGNALP)
Caenorhabditis elegans	uncoordi-ted family member (unc-79)	0		F:GO:0008270		PTHR21696 (PANTHER)
Ostreococcus lucimarinus CCE9901	protein ki-se domain containing protein	4	P:GO:0002119; F:GO:0016301; P:GO:0040010; P:GO:0040011	-		IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
Caenorhabditis elegans	aphorin related family member (smp-1)	11	P:GO:0031987; P:GO:0007416; P:GO:0001964; C:GO:0016021; P:GO:0048854; F:GO:0004872; F:GO:0005515; P:GO:0008039; P:GO:0016199; P:GO:0048813; C:GO:0005886	-		IPR001627; IPR015943; PTHR11036 (PANTHER), PTHR11036:SF29 (PANTHER), SignalP (SIGNALP)
	-	0				-
Dictyostelium discoideum AX4	mutt domain	0		C:GO:0005634; F:GO:0016787; C:GO:0005739; C:GO:0005737; F:GO:0003674; F:GO:0000210; C:GO:0005575; P:GO:0008152; P:GO:0008150		IPR000086; IPR003293; IPR015797; IPR020084; IPR020476; PTHR13994 (PANTHER), PS51462 (PROFILE)

Caenorhabditis elegans	sodium-calcium exchanger	19	P:GO:0002026; P:GO:0055085; F:GO:0005432; C:GO:0005901; P:GO:0051924; F:GO:0015081; P:GO:0000003; P:GO:0002028; F:GO:0015085; P:GO:0007204; P:GO:0060401; F:GO:0005515; C:GO:0042383; P:GO:0007154; P:GO:0009792; P:GO:0006936; P:GO:0006950; P:GO:0010033; C:GO:0005887	-		IPR004836; PTHR11878 (PANTHER), PTHR11878:SF4 (PANTHER)
Drosophila grimshawi	dtdp-glucose 4-6-dehydratase	3	P:GO:0044237; F:GO:0048040; F:GO:0050662	-	EC:4.1.1.35	G3DSA:3.90.25.10 (GENE3D), PTHR10366 (PANTHER), PTHR10366:SF35 (PANTHER), SSF51735 (SUPERFAMILY)
Homo sapiens	cytochrome c oxidase subunit via polypeptide 1	3	C:GO:0005751; F:GO:0004129; P:GO:0006091	-	EC:1.9.3.1	IPR001349; SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	hypothetical protein F54A3.1 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	bro1 domain-containing protein brox	0		C:GO:0016020; P:GO:0008150		IPR004328; G3DSA:1.25.40.280 (GENE3D), PTHR23032 (PANTHER)
Ostertagia ostertagi	calcium activated nucleotidase isoform cra_b	9	F:GO:0004871; P:GO:0043123; F:GO:0017110; C:GO:0044446; C:GO:0044425; C:GO:0031090; C:GO:0012505; C:GO:0005783; P:GO:0009191	-	EC:3.6.1.6	IPR009283
Ostertagia ostertagi	calcium activated nucleotidase isoform cra_b	9	F:GO:0004871; P:GO:0043123; F:GO:0017110; C:GO:0044446; C:GO:0044425; C:GO:0031090; C:GO:0012505; C:GO:0005783; P:GO:0009191	-	EC:3.6.1.6	IPR009283
Brugia malayi	hypothetical protein Bm1_46970 [Brugia malayi]	0				-
Dictyocaulus viviparus	briggsae cbr-ccg-1 protein	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG12763 [Caenorhabditis briggsae]	0				-

Loa loa	pre-mr- splicing factor atp-dependent r- helicase	7	F:GO:0004004; F:GO:0003676; F:GO:0005515; C:GO:0071011; F:GO:0005524; P:GO:0000398; C:GO:0071013	-		IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR18934 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG03940 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)
Angiostrongylus cantonensis	c2 domain containing protein	1	P:GO:0009792	-		IPR000008; IPR008973; G3DSA:2.60.40.150 (GENE3D), PTHR10024 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	brix domain-containing protein 1	0		F:GO:0005515		IPR007109; PTHR12728 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-dcr-1 protein	19	C:GO:0005793; P:GO:0001525; F:GO:0004525; P:GO:0030324; P:GO:0030423; F:GO:0005515; F:GO:0000166; C:GO:0030426; P:GO:0035116; C:GO:0016442; P:GO:0030422; P:GO:0019827; F:GO:0004386; C:GO:0030425; C:GO:0030424; P:GO:0048754; P:GO:0031054; F:GO:0003725; P:GO:0055013	-	EC:3.1.26.3	IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR14950 (PANTHER), PTHR14950:SF3 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	fatty acid synthase	20	F:GO:0008144; C:GO:0005829; P:GO:0006633; F:GO:0004319; F:GO:0008270; C:GO:0005625; C:GO:0005739; P:GO:0055114; P:GO:0006084; F:GO:0000036; F:GO:0004314; F:GO:0004320; F:GO:0019171; F:GO:0070402; F:GO:0004316; F:GO:0004315; F:GO:0042803; C:GO:0042587; C:GO:0005794; F:GO:0004313	-	EC:1.3.1.10; EC:2.3.1.39; EC:3.1.2.14; EC:1.1.1.100; EC:2.3.1.41; EC:2.3.1.38	IPR000794; IPR001227; IPR014030; IPR014031; IPR014043; IPR016035; IPR016036; IPR016038; IPR016039; IPR018201; G3DSA:3.30.70.250 (GENE3D), PTHR11712:SF5 (PANTHER)

Oscheius tipulae	deformed	7	F:GO:0030528; F:GO:0003700; F:GO:0043565; P:GO:0007275; F:GO:0016787; C:GO:0005634; P:GO:0006355	-		IPR000047; IPR001356; IPR009057; IPR012287; IPR017970; IPR020479; PTHR19418 (PANTHER), PTHR19418:SF166 (PANTHER)
Caenorhabditis briggsae	major facilitator superfamily protein	2	C:GO:0016023; C:GO:0016020	-		IPR008509; IPR016196; G3DSA:1.20.1250.20 (GENE3D)
Onchocerca volvulus	abc transporter family protein	3	F:GO:0016887; P:GO:0006810; C:GO:0016020	-		IPR001140; IPR011527; IPR017940; G3DSA:1.20.1560.10 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF96 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	cut-like 1	6	F:GO:0030528; P:GO:0006810; F:GO:0005488; P:GO:0006357; C:GO:0016020; C:GO:0005794	-		PTHR14043 (PANTHER), PTHR14043:SF3 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	5	P:GO:0009792; P:GO:0002119; P:GO:0006810; P:GO:0040010; P:GO:0000003	-		IPR011701; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR10074 (PANTHER), PTHR10074:SF22 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Brugia malayi	sig-l-induced proliferation-associated protein 1	16	C:GO:0043234; P:GO:0030308; F:GO:0046582; C:GO:0030133; F:GO:0008022; P:GO:0007010; P:GO:0007162; P:GO:0042631; P:GO:0051056; C:GO:0012505; C:GO:0048471; P:GO:0050790; P:GO:0045786; P:GO:0008283; C:GO:0016020; C:GO:0005634	-		IPR000331; PTHR15711 (PANTHER), SSF111347 (SUPERFAMILY)
Nicotiana tabacum	conserved protein	2	C:GO:0005739; C:GO:0009507	-		-
Caenorhabditis elegans	cell death abnormality family member (ced-7)	1	P:GO:0009987	-		PTHR19229 (PANTHER), PTHR19229:SF18 (PANTHER), SignalP (SIGNALP)
	-	0				-
Brugia malayi	zinc c2h2 type family protein	0		F:GO:0008270; C:GO:0005622		IPR015880
	-	0				-

Branchiostoma floridae	tetraspanin 97e	1	C:GO:0016020	-		IPR000301; IPR018499; PTHR19282 (PANTHER), PTHR19282:SF4 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	class member 2	2	F:GO:0004553; F:GO:0005488	-	EC:3.2.1.0	IPR011013; IPR011682; G3DSA:2.70.98.30 (GENE3D), PTHR11607 (PANTHER), PTHR11607:SF4 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				PTHR12187 (PANTHER), PTHR12187:SF2 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein D1043.1 [Caenorhabditis elegans]	0		F:GO:0005488		PTHR13322 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0042626; F:GO:0005215; C:GO:0016021; P:GO:0006810; F:GO:0000166; F:GO:0017111; F:GO:0005524; F:GO:0016887; P:GO:0055085		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	P:GO:0009792; P:GO:0000003	-		-
Caenorhabditis elegans	probable -dh-ubiquinone oxidoreductase 13 kda-a precursor	1	F:GO:0016491	-		PTHR13156 (PANTHER)
	-	0				-
Caenorhabditis elegans	lin-7 homolog b	9	C:GO:0016323; P:GO:0007269; C:GO:0005923; C:GO:0019717; C:GO:0045211; P:GO:0006887; C:GO:0014069; F:GO:0030165; P:GO:0015031	-		IPR001478; IPR004172; IPR014775; G3DSA:2.30.42.10 (GENE3D), PTHR14063 (PANTHER), PTHR14063:SF2 (PANTHER), SSF101288 (SUPERFAMILY)
Ascaris lumbricoides	intermediate filament protein	10	C:GO:0005737; P:GO:0010171; P:GO:0002119; P:GO:0018996; F:GO:0005515; C:GO:0005882; P:GO:0040010; P:GO:0040011; P:GO:0006898; F:GO:0005198	-		-
Caenorhabditis elegans	thioredoxin family protein	1	P:GO:0006974	-		IPR008979; IPR010400; G3DSA:2.60.120.470 (GENE3D)
	-	0				-
Caenorhabditis elegans	briggsae cbr-rpm-1 protein	4	P:GO:0030071; F:GO:0005515; F:GO:0008270; C:GO:0005680	-		PTHR12846 (PANTHER), PTHR12846:SF2 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	transmembrane protein 67	11	C:GO:0005815; C:GO:0044463; C:GO:0005929; F:GO:0005515; C:GO:0044425; C:GO:0031090; C:GO:0012505; P:GO:0009653; C:GO:0005783; C:GO:0005886; N:GO:0071842	-		IPR019170
Caenorhabditis briggsae	chromosome 14 open reading frame 153	1	P:GO:0008629	-		IPR018796
	-	0				-
Loa loa	gtp binding protein 5	6	F:GO:0005515; C:GO:0016021; P:GO:0015684; F:GO:0015093; C:GO:0005739; F:GO:0000166	-		IPR002917; IPR006073; IPR014100; G3DSA:3.40.50.300 (GENE3D), PTHR11702 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG06862 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	Hypothetical protein CBG06862 [Caenorhabditis briggsae]	0				-
	-	0				-
	-	0				-
	-	0				-
Loa loa	elegans protein confirmed by transcript evidence	0		P:GO:0000003; P:GO:0040035; P:GO:0002009		-
Brugia malayi	hd phosphohydrolase family protein	0		P:GO:0009058; F:GO:0016779; F:GO:0016787; F:GO:0003824		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	briggsae cbr-dep-1 protein	3	P:GO:0040026; P:GO:0040027; F:GO:0016787	-		-
Caenorhabditis briggsae	amiloride-sensitive sodium channel family protein	2	P:GO:0006810; P:GO:0007413	-		IPR001873; G3DSA:2.60.470.10 (GENE3D), PTHR11690:SF11 (PANTHER)
Callithrix jacchus	PREDICTED: hypothetical protein LOC100405620, partial [Callithrix jacchus]	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	5	C:GO:0005615; P:GO:0008152; F:GO:0005515; F:GO:0004866; F:GO:0016740	-		IPR001917; IPR002890; IPR011625; PTHR11412 (PANTHER), PTHR11412:SF4 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	5	C:GO:0005615; P:GO:0008152; F:GO:0005515; F:GO:0004866; F:GO:0016740	-		IPR001917; IPR002890; IPR011625; PTHR11412 (PANTHER), PTHR11412:SF4 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	5	C:GO:0005615; P:GO:0008152; F:GO:0005515; F:GO:0004866; F:GO:0016740	-		IPR001917; IPR002890; IPR011625; PTHR11412 (PANTHER), PTHR11412:SF4 (PANTHER)

Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	5	C:GO:0005615; P:GO:0008152; F:GO:0005515; F:GO:0004866; F:GO:0016740	-		IPR001917; IPR002890; IPR011625; PTHR11412 (PANTHER), PTHR11412:SF4 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	5	F:GO:0004428; P:GO:0046854; P:GO:0000003; P:GO:0008219; P:GO:0048015	-		SignalP (SIGNALP)
Caenorhabditis elegans	dedicator of cytokinesis 3	7	F:GO:0005083; P:GO:0043652; C:GO:0005886; F:GO:0032403; F:GO:0019899; P:GO:0040039; F:GO:0017124	-		PTHR23317 (PANTHER), PTHR23317:SF16 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR008574
Caenorhabditis briggsae	deah (asp-glu-ala-his) box polypeptide 37	10	P:GO:0040010; P:GO:0008340; F:GO:0003676; F:GO:0008026; P:GO:0000003; F:GO:0005524; P:GO:0002119; P:GO:0006898; P:GO:0009792; P:GO:0016246	-		IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR18934 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				
	-	0				
Physcomitrella patens subsp. patens	histidine-rich protein 2	0		F:GO:0005524; C:GO:0016021; F:GO:0042626; P:GO:0055085; P:GO:0006810		SignalP (SIGNALP)
Physcomitrella patens subsp. patens	histidine-rich protein 2	0		F:GO:0005524; C:GO:0016021; F:GO:0042626; P:GO:0055085; P:GO:0006810		SignalP (SIGNALP)
Physcomitrella patens subsp. patens	predicted protein [Physcomitrella patens subsp. patens]	0				SignalP (SIGNALP)
Physcomitrella patens subsp. patens	predicted protein [Physcomitrella patens subsp. patens]	0				SignalP (SIGNALP)
Physcomitrella patens subsp. patens	predicted protein [Physcomitrella patens subsp. patens]	0				SignalP (SIGNALP)
Physcomitrella patens subsp. patens	predicted protein [Physcomitrella patens subsp. patens]	0				SignalP (SIGNALP)
Caenorhabditis elegans	teneurin family member (ten-1)	0		C:GO:0016020		PTHR11219 (PANTHER), PTHR11219:SF4 (PANTHER)
Caenorhabditis briggsae	teneurin family member (ten-1)	1	P:GO:0048749	-		-
Caenorhabditis briggsae	teneurin family member (ten-1)	1	P:GO:0048749	-		-
Saccoglossus kowalevskii	d-se domain containing 3	2	C:GO:0005739; F:GO:0004518	-		IPR001130; IPR015992; IPR018228; G3DSA:3.20.20.140 (GENE3D), SSF51556 (SUPERFAMILY)

Caenorhabditis elegans	hat family dimerisation domain containing protein	0		F:GO:0003676; F:GO:0046983		SignalP (SIGNALP)
Caenorhabditis elegans	hat family dimerisation domain containing protein	0		F:GO:0003676; F:GO:0046983		SignalP (SIGNALP)
	-	0				-
Loa loa	fibronectin type iii domain containing protein	2	C:GO:0043231; C:GO:0044444	-		IPR003961; IPR008957; IPR013783; PR00014 (PRINTS), PTHR19900 (PANTHER), PTHR19900:SF3 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Loa loa	ferredoxin 1	11	P:GO:0006694; F:GO:0009055; F:GO:0005506; P:GO:0055114; F:GO:0051537; F:GO:0019899; P:GO:0050790; F:GO:0008022; C:GO:0005739; F:GO:0042803; P:GO:0006091	-		IPR001041; IPR012675; PTHR23426 (PANTHER), PTHR23426:SF1 (PANTHER)
Brugia malayi	histone 1	4	C:GO:0000786; F:GO:0003677; P:GO:0006334; C:GO:0005634	-		SignalP (SIGNALP)
	-	0				-
Brugia malayi	elegans protein partially confirmed by transcript evidence	8	P:GO:0002119; P:GO:0006468; F:GO:0005515; P:GO:0040010; F:GO:0005524; P:GO:0040011; P:GO:0019915; F:GO:0004674	-	EC:2.7.11.0	-
Brugia malayi	casein ki-se	5	P:GO:0006468; P:GO:0040010; F:GO:0005524; P:GO:0019915; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
Caenorhabditis briggsae	nucleolar protein 6	0		C:GO:0005694; C:GO:0000794; F:GO:0003723; P:GO:0006364; P:GO:0008150; C:GO:0005634; C:GO:0005730		IPR005554
Caenorhabditis briggsae	briggsae cbr-hyl-1 protein	1	C:GO:0016020	-		IPR006634; PTHR12560 (PANTHER), SignalP (SIGNALP)

Loa loa	elegans protein confirmed by transcript evidence	0		C:GO:0016021; P:GO:0010171; C:GO:0016020; P:GO:0006814; P:GO:0006898; P:GO:0006813; P:GO:0006811; P:GO:0006810; P:GO:0000003; P:GO:0009792; P:GO:0002119; P:GO:0040018; P:GO:0006754; F:GO:0005391; P:GO:0040011; P:GO:0040010; P:GO:0040007		IPR000402; SignalP (SIGNALP)
Loa loa	pyruvate dehydroge-se beta	8	P:GO:0008340; F:GO:0005515; P:GO:0006974; F:GO:0008168; P:GO:0043414; P:GO:0045449; C:GO:0044451; P:GO:0016568	-	EC:2.1.1.0	IPR001214; IPR001965; IPR011011; IPR013083; IPR017956; IPR019786; IPR019787; G3DSA:2.170.270.10 (GENE3D), PTHR16286 (PANTHER), SSF82199 (SUPERFAMILY)
Caenorhabditis elegans	heat shock factor binding protein 1	9	P:GO:0019064; C:GO:0005856; F:GO:0046789; P:GO:0000122; F:GO:0003714; C:GO:0019031; P:GO:0006936; P:GO:0006950; C:GO:0005634	-		-
Caenorhabditis elegans	cysteine-rich venom	1	F:GO:0005515	-		IPR002919; IPR013032; G3DSA:2.10.25.10 (GENE3D), PTHR23259 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis sp. PS1010	hypothetical protein Csp3_JD07.001 [Caenorhabditis sp. PS1010]	0				-
	-	0				-
Homo sapiens	phospholipase d3	7	C:GO:0005789; C:GO:0005624; P:GO:0016042; F:GO:0005515; F:GO:0070290; F:GO:0004630; C:GO:0016021	-	EC:3.1.4.4	IPR001736; IPR013582; G3DSA:3.30.870.10 (GENE3D), PTHR10185 (PANTHER), SSF56024 (SUPERFAMILY)

Caenorhabditis elegans	unc-5 homolog b	0		C:GO:0009986; C:GO:0016021; P:GO:0006915; F:GO:0003674; P:GO:0007275; P:GO:0007165; C:GO:0005575; F:GO:0004872; F:GO:0005515; P:GO:0008150		PTHR12582 (PANTHER), PTHR12582:SF2 (PANTHER)
	-	0				-
Caenorhabditis elegans	d--directed r- polymerase i subunit rpa2	9	F:GO:0003899; P:GO:0040007; P:GO:0040035; F:GO:0003677; P:GO:0002119; F:GO:0032549; P:GO:0009792; P:GO:0006350; C:GO:0005634	-	EC:2.7.7.6	IPR007120; IPR007121; IPR015712; G3DSA:2.40.270.10 (GENE3D), G3DSA:3.90.1100.10 (GENE3D), PTHR20856:SF5 (PANTHER), SSF64484 (SUPERFAMILY)
Caenorhabditis elegans	probable r--binding protein 19	2	C:GO:0005730; F:GO:0003676	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF63 (PANTHER), SSF54928 (SUPERFAMILY)
Angiostrongylus cantonensis	elegans protein confirmed by transcript evidence	0				-
	-	0				SignalP (SIGNALP)
	-	0				IPR000626; G3DSA:3.10.20.90 (GENE3D)
Brugia malayi	hypothetical protein Bm1_35525 [Brugia malayi]	0				-
Caenorhabditis briggsae	solute carrier family member 27	6	F:GO:0005488; C:GO:0005743; P:GO:0055085; C:GO:0016021; P:GO:0006091; F:GO:0005215	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	cathepsin l-like cysteine protei-se	5	P:GO:0048102; C:GO:0045169; C:GO:0016021; F:GO:0004197; P:GO:0006508	-	EC:3.4.22.0	IPR000169; IPR000668; IPR013128; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF26 (PANTHER), SignalP (SIGNALP), SSF54001 (SUPERFAMILY)
Caenorhabditis elegans	endothelin-converting enzyme	1	F:GO:0008237	-		IPR000718; IPR008753; G3DSA:1.10.1380.10 (GENE3D), PTHR11733:SF24 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	kinesin family member 1b	10	F:GO:0003777; C:GO:0030659; P:GO:0007274; C:GO:0005875; C:GO:0005874; F:GO:0019894; P:GO:0007270; F:GO:0005524; F:GO:0016887; P:GO:0008089	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-

	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-unc-45 protein	1	F:GO:0005488	-		PTHR22904 (PANTHER), PTHR22904:SF28 (PANTHER), PF11701 (PFAM), SignalP (SIGNALP)
Caenorhabditis elegans	o-linked c transferase	0		C:GO:0005634		-
Caenorhabditis elegans	fmrf-like peptide family member (flp-22)	1	P:GO:0007218	-		IPR002544; PTHR20986 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	transmembrane protein 57	0		C:GO:0016021		IPR019130; PTHR13289 (PANTHER), SignalP (SIGNALP)
	-	0				IPR008160; PTHR10499 (PANTHER), PTHR10499:SF104 (PANTHER)
	-	0				-
	-	0				PTHR22743 (PANTHER), PTHR22743:SF10 (PANTHER)
Caenorhabditis brenneri	polymerase iii (d- directed) polypeptide b	6	P:GO:0009304; F:GO:0003899; F:GO:0003677; P:GO:0031017; F:GO:0032549; P:GO:0048565	-	EC:2.7.7.6	IPR007642; SSF64484 (SUPERFAMILY)
Caenorhabditis briggsae	peroxisomal -trans-enoyl- isomerase	5	F:GO:0005488; C:GO:0005777; P:GO:0006635; F:GO:0016863; C:GO:0005739	-	EC:5.3.3.0	IPR000582; IPR001753; IPR014352; G3DSA:3.90.226.10 (GENE3D), PTHR11941 (PANTHER), SSF52096 (SUPERFAMILY)
Caenorhabditis briggsae	peroxisomal -trans-enoyl- isomerase	5	F:GO:0005488; C:GO:0005777; P:GO:0006635; F:GO:0016863; C:GO:0005739	-	EC:5.3.3.0	IPR000582; IPR001753; IPR014352; G3DSA:3.90.226.10 (GENE3D), PTHR11941 (PANTHER), SSF52096 (SUPERFAMILY)
	-	0				-
Heliconius melpomene	endonuclease-reverse transcriptase -e01	0		F:GO:0003723; P:GO:0006278; F:GO:0004519; F:GO:0003964		IPR000477

	macrophage migration inhibitory factor	44	P:GO:0006954; P:GO:0033138; P:GO:0048146; P:GO:0007506; P:GO:0007530; P:GO:0090238; P:GO:0070374; P:GO:0001546; P:GO:0031666; P:GO:0043030; P:GO:0043406; F:GO:0008083; C:GO:0005615; P:GO:0007569; P:GO:0061081; F:GO:0005160; P:GO:0071157; P:GO:0043518; P:GO:0050731; P:GO:0030890; P:GO:0045087; P:GO:0001516; F:GO:0005125; P:GO:0032269; C:GO:0005737; P:GO:0010629;	-	EC:5.3.3.12; EC:5.3.2.1	-
	-	0				SignalP (SIGNALP)
Brugia malayi	beta like 1	1	F:GO:0042802	-		IPR013180; PTHR14978 (PANTHER)
Caenorhabditis briggsae	solute carrier family 37 (glycerol-3-phosphate transporter) member 3	2	P:GO:0055085; C:GO:0016021	-		SignalP (SIGNALP)
Caenorhabditis elegans	4-coumarate:coenzyme a ligase 3	1	F:GO:0003824	-		IPR000873; G3DSA:2.30.38.10 (GENE3D), G3DSA:3.40.50.980 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF43 (PANTHER), SSF56801 (SUPERFAMILY)
Caenorhabditis briggsae	calpain 5	8	P:GO:0042004; P:GO:0060014; C:GO:0005622; P:GO:0001553; F:GO:0004198; P:GO:0019099; P:GO:0006508; C:GO:0016020	-		-
Caenorhabditis briggsae	calpain 5	8	P:GO:0042004; P:GO:0060014; C:GO:0005622; P:GO:0001553; F:GO:0004198; P:GO:0019099; P:GO:0006508; C:GO:0016020	-		IPR022682; IPR022683; IPR022684; G3DSA:2.60.120.380 (GENE3D), PTHR10183 (PANTHER), PTHR10183:SF32 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis elegans	photosystem i assembly	0		P:GO:0008152; F:GO:0003824; C:GO:0005575		IPR005137; PTHR21381:SF4 (PANTHER)
Caenorhabditis elegans	hypothetical protein F23H11.2 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	P:GO:0040011	-		SignalP (SIGNALP)
	-	0				-
Ancylostoma ceylanicum	kunitz type serine protease inhibitor	2	F:GO:0004867; F:GO:0008233	-		IPR002223; PTHR10083 (PANTHER), PTHR10083:SF39 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	Hypothetical protein F49D11.10 [Caenorhabditis elegans]	0				IPR011042
Ancylostoma ceylanicum	secreted protein 5 precursor	0		P:GO:0008340; C:GO:0005576		IPR014044; SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	alkylation repair homolog 6-like isoform 1	2	F:GO:0010302; C:GO:0044424	-		-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	4	F:GO:0016491; F:GO:0005515; P:GO:0040010; P:GO:0008152	-		IPR002198; IPR016040; PTHR19410:SF76 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	alpha- -mannosyl-glycoprotein 2-beta-n-acetylglucosaminyltransferase	3	C:GO:0000139; F:GO:0003827; P:GO:0006487	-	EC:2.4.1.101	IPR004139; G3DSA:3.90.550.10 (GENE3D), SignalP (SIGNALP)
Caenorhabditis sp. PS1010	elegans protein confirmed by transcript evidence	0				PTHR14167 (PANTHER), PTHR14167:SF2 (PANTHER)
Caenorhabditis elegans	2-acylglycerol o-acyltransferase 1	5	P:GO:0006071; C:GO:0005789; P:GO:0008610; C:GO:0016021; F:GO:0003846	-	EC:2.3.1.22	IPR007130
	-	0				-
Homo sapiens	lipolysis stimulated lipoprotein receptor	11	P:GO:0009790; C:GO:0005730; F:GO:0004872; C:GO:0034362; C:GO:0005794; C:GO:0005886; C:GO:0042627; P:GO:0001889; C:GO:0016021; P:GO:0019216; C:GO:0034361	-		-
Apis mellifera	zinc c2h2 type family protein	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		-
Caenorhabditis briggsae	activating sig-l cointegrator 1 complex subunit 3	3	F:GO:0005524; F:GO:0003677; F:GO:0008026	-		IPR011545; G3DSA:3.40.50.300 (GENE3D), PTHR11752 (PANTHER), PTHR11752:SF8 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)

Caenorhabditis briggsae	bone morphogenetic protein	9	C:GO:0005576; F:GO:0004222; P:GO:0007275; C:GO:0005622; P:GO:0006508; P:GO:0030154; F:GO:0005509; F:GO:0008270; F:GO:0016874	-	EC:3.4.24.0	IPR001506; IPR006026; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF70 (PANTHER), SSF55486 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	organic cation transporter family member (oct-2)	4	P:GO:0019915; C:GO:0016021; P:GO:0055085; F:GO:0005215	-		PTHR11600 (PANTHER), PTHR11600:SF44 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	multidrug resistance protein family member (mrp-1)	4	F:GO:0042626; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		IPR001140; IPR011527; IPR017940; IPR018062; G3DSA:1.20.1560.10 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF35 (PANTHER), SignalP (SIGNALP)
	-	0				-
Brugia malayi	cpb-3	6	P:GO:0009987; F:GO:0003723; C:GO:0045202; F:GO:0000166; C:GO:0044424; C:GO:0016020	-		IPR000504; IPR012677; PTHR12566 (PANTHER), SSF54928 (SUPERFAMILY)
Brugia malayi	cpb-3	6	P:GO:0009987; F:GO:0003723; C:GO:0045202; F:GO:0000166; C:GO:0044424; C:GO:0016020	-		IPR000504; IPR012677; PTHR12566 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein Y48G9A.3 [Caenorhabditis elegans]	1	P:GO:0000003	-		-
	-	0				-
Caenorhabditis briggsae	u6 snr--associated sm-like protein lsm7	5	F:GO:0003676; P:GO:0008340; C:GO:0030529; P:GO:0040007; P:GO:0002119	-		-
Caenorhabditis briggsae	briggsae cbr-tmd-2 protein	4	C:GO:0045169; C:GO:0005856; P:GO:0000003; F:GO:0005523	-		IPR004934; G3DSA:3.80.10.10 (GENE3D), PTHR10901:SF4 (PANTHER), SSF52047 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-zig-5 protein	0				IPR007110; IPR013783
Brugia malayi	laminin alpha chain	0		C:GO:0005606; F:GO:0005102; C:GO:0005604; P:GO:0045995; C:GO:0005578; P:GO:0030155; C:GO:0031012; P:GO:0030334; P:GO:0007155		-

Brugia malayi	transcription elongation factor spt6-like	2	P:GO:0044260; P:GO:0090304	-		IPR000980; IPR003029; IPR012340; IPR016027; IPR022967; PTHR10145 (PANTHER), PTHR10145:SF1 (PANTHER), SSF55550 (SUPERFAMILY)
Caenorhabditis elegans	schip1 protein	0		F:GO:0004553; C:GO:0042597; F:GO:0003674; P:GO:0008150; C:GO:0005575		IPR015649
Monodelphis domestica	ribosomal protein s21	5	F:GO:0003735; F:GO:0047485; C:GO:0022627; F:GO:0043022; P:GO:0006414	-		IPR001931; IPR018279
	-	0				-
Caenorhabditis briggsae	mitochondrial carrier protein	9	P:GO:0055085; P:GO:0015868; F:GO:0005488; C:GO:0016021; C:GO:0005743; F:GO:0000295; P:GO:0009792; P:GO:0040018; P:GO:0051503	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF34 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	btb poz domain-containing protein 8	0		F:GO:0005515		IPR000210; IPR011333; IPR013069; IPR013089; PTHR23230:SF179 (PANTHER)
	-	0				-
Caenorhabditis elegans	hypothetical protein F20D6.11 [Caenorhabditis elegans]	2	C:GO:0005739; P:GO:0042981	-		G3DSA:3.50.50.60 (GENE3D), PTHR22912 (PANTHER), PTHR22912:SF7 (PANTHER)
	-	0				-
Caenorhabditis elegans	upf0493 protein kiaa1632-like	1	P:GO:0040017	-		-
Brugia malayi	ubiquitin carboxyl-termi-l hydrolase 16	5	P:GO:0016568; F:GO:0008234; P:GO:0044267; P:GO:0045449; F:GO:0005515	-		IPR001394; IPR018200; PTHR10420 (PANTHER), PTHR10420:SF52 (PANTHER), SSF54001 (SUPERFAMILY)
Brugia malayi	ubiquitin carboxyl-termi-l hydrolase 16	5	P:GO:0016568; F:GO:0008234; P:GO:0044267; P:GO:0045449; F:GO:0005515	-		IPR001394; IPR018200; PTHR10420 (PANTHER), PTHR10420:SF52 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein Y55D5A.4 [Caenorhabditis elegans]	0				-
Loa loa	amine oxidase (flavin containing) domain 1	6	P:GO:0016568; P:GO:0019219; F:GO:0032453; F:GO:0046872; P:GO:0032501; P:GO:0006306	-		-

Caenorhabditis elegans	dead (asp-glu-ala-asp) box polypeptide 58	8	F:GO:0017111; F:GO:0008270; F:GO:0003676; P:GO:0032728; P:GO:0032727; P:GO:0045087; F:GO:0005515; P:GO:0002230	-	EC:3.6.1.15	G3DSA:3.40.50.300 (GENE3D), PTHR14074 (PANTHER)
Caenorhabditis briggsae	dead (asp-glu-ala-asp) box polypeptide 58	7	F:GO:0008270; P:GO:0032728; P:GO:0032727; P:GO:0045087; F:GO:0005515; P:GO:0002230; F:GO:0016787	-		IPR006935; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR14074 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	integrator complex subunit isoform cra_a	3	F:GO:0005515; P:GO:0016180; C:GO:0032039	-		PTHR13322 (PANTHER)
Caenorhabditis briggsae	hiv tat specific factor 1	2	P:GO:0040011; P:GO:0010171	-		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	u3 small nucleolar homolog a	7	P:GO:0040010; P:GO:0040035; P:GO:0019915; P:GO:0002119; F:GO:0005515; P:GO:0006898; C:GO:0044424	-		IPR006709; PTHR14150:SF12 (PANTHER)
Caenorhabditis elegans	u3 small nucleolar homolog a	7	P:GO:0040010; P:GO:0040035; P:GO:0019915; P:GO:0002119; F:GO:0005515; P:GO:0006898; C:GO:0044424	-		IPR006709; PTHR14150:SF12 (PANTHER)
	-	0				PR01217 (PRINTS)
Caenorhabditis elegans	ceramide glucosyl transferase family member (cgt-3)	1	F:GO:0016740	-		G3DSA:3.90.550.10 (GENE3D), PTHR12726 (PANTHER), SSF53448 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-clk-2 protein	7	P:GO:0009411; P:GO:0008340; P:GO:0010165; P:GO:0000723; P:GO:0000003; P:GO:0000077; C:GO:0005737	-		SignalP (SIGNALP)

Caenorhabditis elegans	small nuclear ribonucleoprotein sm d3	11	C:GO:0030532; P:GO:0007417; F:GO:0003676; C:GO:0071011; P:GO:0007517; P:GO:0007052; P:GO:0048542; P:GO:0007422; P:GO:0000398; C:GO:0071013; P:GO:0030182	-		IPR001163; IPR006649; IPR010920; G3DSA:2.30.30.100 (GENE3D), PTHR23338 (PANTHER), PTHR23338:SF17 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Teladorsagia circumcincta	class 3 lipase protein	2	F:GO:0004806; P:GO:0006629	-	EC:3.1.1.3	-
	-	0				-
Caenorhabditis elegans	cell line derived transforming sequence-like	5	F:GO:0005085; C:GO:0005886; P:GO:0008624; C:GO:0005829; C:GO:0005739	-		PTHR22826 (PANTHER), PTHR22826:SF3 (PANTHER)
	-	0				-
Caenorhabditis briggsae	f-box only protein isoform cra_a	3	F:GO:0005515; P:GO:0043161; C:GO:0044424	-		IPR007397; IPR008979; G3DSA:2.60.120.260 (GENE3D)
Loa loa	dual oxidase	18	P:GO:0018149; P:GO:0006979; P:GO:0006952; F:GO:0016174; P:GO:0040032; F:GO:0005509; C:GO:0016021; P:GO:0042338; P:GO:0055114; P:GO:0040007; F:GO:0004601; F:GO:0009055; P:GO:0002119; P:GO:0040011; F:GO:0020037; F:GO:0050660; P:GO:0009792; C:GO:0005882	-	EC:1.6.3.1; EC:1.11.1.7	IPR002007; IPR010255; PTHR11475 (PANTHER)
Caenorhabditis elegans	acyl-coenzyme a short branched chain	11	P:GO:0009792; P:GO:0006637; P:GO:0006952; F:GO:0009055; F:GO:0005515; C:GO:0005759; F:GO:0016937; P:GO:0055114; P:GO:0008340; P:GO:0006631; F:GO:0050660	-		IPR006089; IPR006090; IPR006091; IPR006092; IPR009075; IPR009100; IPR013786; PTHR10909 (PANTHER), PTHR10909:SF10 (PANTHER), SignalP (SIGNALP)

Caenorhabditis elegans	subfamily member 19	10	P:GO:0009792; P:GO:0002119; C:GO:0005743; F:GO:0031072; P:GO:0055085; P:GO:0000003; C:GO:0016021; P:GO:0040007; P:GO:0006898; P:GO:0015031	-		IPR001623; PTHR12763 (PANTHER), PTHR12763:SF7 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	solute carrier family 41 member 1	3	C:GO:0016021; F:GO:0008324; P:GO:0006812	-		IPR006667; PTHR16228 (PANTHER)
Caenorhabditis elegans	thump domain containing 3	0		F:GO:0003723; F:GO:0008168; F:GO:0003674; F:GO:0016740; P:GO:0008152; P:GO:0008150; F:GO:0005515; C:GO:0005575		IPR000241; IPR004114; G3DSA:3.40.50.150 (GENE3D), PTHR10108 (PANTHER), PTHR10108:SF26 (PANTHER), SSF143437 (SUPERFAMILY), SSF53335 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
	complement component q b chain	7	C:GO:0005602; P:GO:0045087; P:GO:0007568; P:GO:0051384; P:GO:0006958; P:GO:0007420; F:GO:0042803	-		IPR001073; IPR008983; PTHR10499 (PANTHER), PTHR10499:SF34 (PANTHER)
Caenorhabditis elegans	4-nitrophenylphosphatase	2	P:GO:0008152; F:GO:0016791	-	EC:3.1.3.0	G3DSA:3.40.50.1000 (GENE3D), PTHR19288 (PANTHER), PTHR19288:SF11 (PANTHER), SSF56784 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	hypothetical protein Y37E11AL.5 [Caenorhabditis elegans]	0		P:GO:0007218; F:GO:0005509; P:GO:0007156; C:GO:0016021; C:GO:0016020; C:GO:0005886		-
	-	0				-
Brugia malayi	excision repair cross-complementing rodent repair complementation group 8	3	P:GO:0044238; P:GO:0044260; P:GO:0006950	-		-
Brugia malayi	ribonuclease p protein subunit p29	7	P:GO:0040010; P:GO:0006396; F:GO:0005488; P:GO:0040035; C:GO:0030529; F:GO:0016787; C:GO:0005634	-		IPR002730; PTHR13348 (PANTHER)

Loa loa	low-density lipoprotein receptor repeat class b containing protein	6	C:GO:0005615; P:GO:0019538; F:GO:0005515; P:GO:0045860; F:GO:0003824; C:GO:0016020	-		IPR002172; PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER)
Brugia malayi	wd repeat domain 39	3	C:GO:0005856; P:GO:0016226; F:GO:0005488	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR19920 (PANTHER)
Loa loa	e3 ubiquitin-protein ligase bre1a	0		F:GO:0031625; P:GO:0000209; P:GO:0006511; P:GO:0006468; C:GO:0005634; C:GO:0005694; F:GO:0005524; F:GO:0002039; F:GO:0046872; P:GO:0016568; F:GO:0016301; P:GO:0006664; F:GO:0004674; F:GO:0016874; C:GO:0000151; F:GO:0004672; F:GO:0004842; P:GO:0010390; P:GO:0030336; F:GO:0042393; F:GO:0000166; P:GO:0045941; P:GO:0032583; F:GO:0003713; C:GO:0005730; P:GO:0033523; F:GO:0008270;		PTHR23163 (PANTHER)

Loa loa	e3 ubiquitin-protein ligase bre1a	0		F:GO:0031625; P:GO:0000209; P:GO:0006511; P:GO:0006468; C:GO:0005634; C:GO:0005694; F:GO:0005524; F:GO:0002039; F:GO:0046872; P:GO:0016568; F:GO:0016301; P:GO:0006664; F:GO:0004674; F:GO:0016874; C:GO:0000151; F:GO:0004672; F:GO:0004842; P:GO:0010390; P:GO:0030336; F:GO:0042393; F:GO:0000166; P:GO:0045941; P:GO:0032583; F:GO:0003713; C:GO:0005730; P:GO:0033523; F:GO:0008270;		PTHR23163 (PANTHER)
Ectocarpus siliculosus	r- helicase	2	F:GO:0004386; F:GO:0000166	-		G3DSA:3.40.50.300 (GENE3D), PTHR18934 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Brugia malayi	d- damage-binding protein 1	9	C:GO:0005737; C:GO:0031464; C:GO:0031465; P:GO:0009793; F:GO:0005515; P:GO:0043161; F:GO:0003684; P:GO:0006974; C:GO:0005634	-		PTHR10644 (PANTHER), PTHR10644:SF3 (PANTHER)
Caenorhabditis elegans	briggsae cbr-unc-84 protein	5	P:GO:0090292; C:GO:0031965; C:GO:0034993; P:GO:0090286; F:GO:0005515	-		IPR012919; PTHR12911 (PANTHER), PTHR12911:SF7 (PANTHER), PS51469 (PROFILE)

Caenorhabditis elegans	s-phase ki-se-associated protein 1	16	P:GO:0008340; C:GO:0005654; P:GO:0016246; F:GO:0005515; P:GO:0051437; P:GO:0040010; P:GO:0006898; P:GO:0040011; C:GO:0005829; C:GO:0019005; P:GO:0009792; P:GO:0002009; F:GO:0004842; P:GO:0002119; P:GO:0031146; P:GO:0040035	-	EC:6.3.2.19	IPR001232; IPR011333; IPR016072; IPR016073; IPR016897; PTHR11165:SF21 (PANTHER)
Caenorhabditis elegans	ariadne ubiquitin-conjugating enzyme e2 binding protein	6	C:GO:0005737; F:GO:0016566; F:GO:0005515; F:GO:0004842; F:GO:0008270; P:GO:0016481	-	EC:6.3.2.19	PTHR11685 (PANTHER), PTHR11685:SF16 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis elegans	ariadne ubiquitin-conjugating enzyme e2 binding protein	4	C:GO:0005737; F:GO:0005515; F:GO:0004842; F:GO:0008270	-	EC:6.3.2.19	-
	-	0				-
	-	0				-
	-	0				-
Cyanothece sp. PCC 7425	transposase of insertion sequence isrm10-1	0				-
	-	0				-
Loa loa	set binding factor 2	4	P:GO:0016311; P:GO:0007283; F:GO:0016791; C:GO:0044464	-	EC:3.1.3.0	IPR001194; IPR005112; PTHR10807 (PANTHER), PTHR10807:SF1 (PANTHER)
Loa loa	calpain 7	1	F:GO:0016787	-		IPR007330; G3DSA:1.20.58.280 (GENE3D), PTHR23074 (PANTHER), PTHR23074:SF3 (PANTHER), SSF116846 (SUPERFAMILY)
Loa loa	calpain 7	3	P:GO:0019915; C:GO:0005622; F:GO:0008234	-		IPR001300; IPR007330; IPR022682; IPR022684; G3DSA:1.20.58.280 (GENE3D), G3DSA:2.60.120.380 (GENE3D), G3DSA:3.90.70.10 (GENE3D), PTHR10183 (PANTHER), PTHR10183:SF22 (PANTHER), SSF116846 (SUPERFAMILY), SSF54001 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein Y47G6A.29 [Caenorhabditis elegans]	0				-
Mus musculus	polo-like ki-se 3	1	F:GO:0005488	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0005524; C:GO:0005856; F:GO:0000166; F:GO:0003774; C:GO:0016459		IPR000299; IPR019748

Brugia malayi	hypothetical kda protein in chromosome	0		F:GO:0005515		-
	-	0				-
Caenorhabditis elegans	hypothetical protein F39B1.1 [Caenorhabditis elegans]	0		F:GO:0016740; P:GO:0007154; F:GO:0004428; F:GO:0016303; P:GO:0046854; F:GO:0016301; P:GO:0019915; P:GO:0002119; P:GO:0048015; C:GO:0005942; F:GO:0005515; F:GO:0035091; F:GO:0016773; F:GO:0005488		-
	-	0				-
Brugia malayi	glucose phosphate dehydroge-se	4	P:GO:0006006; F:GO:0004345; P:GO:0055114; F:GO:0005488	-	EC:1.1.1.49	IPR001282; IPR019796; IPR022674; IPR022675; G3DSA:3.30.360.10 (GENE3D), SSF55347 (SUPERFAMILY)
Caenorhabditis elegans	rrs1 protein	7	P:GO:0009792; P:GO:0002119; P:GO:0042254; P:GO:0040010; P:GO:0000003; P:GO:0040019; C:GO:0005634	-		IPR007023
Caenorhabditis elegans	rrs1 protein	7	P:GO:0009792; P:GO:0002119; P:GO:0042254; P:GO:0040010; P:GO:0000003; P:GO:0040019; C:GO:0005634	-		IPR007023
Caenorhabditis elegans	phosphatidylinositol glycan anchor class a	6	P:GO:0045132; C:GO:0016021; P:GO:0016254; F:GO:0005515; C:GO:0005789; F:GO:0016757	-		IPR013234; PTHR12526 (PANTHER), PTHR12526:SF37 (PANTHER), SSF53756 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	leucine rich repeat family protein	0		F:GO:0003674; P:GO:0008150		G3DSA:3.80.10.10 (GENE3D), PTHR13824 (PANTHER), PTHR13824:SF6 (PANTHER), SSF52047 (SUPERFAMILY)
Caenorhabditis briggsae	brain tumor protein	3	F:GO:0008270; C:GO:0005622; F:GO:0005515	-		IPR001258; IPR011042; IPR013017; PTHR13712 (PANTHER), PTHR13712:SF6 (PANTHER), SSF101898 (SUPERFAMILY)
Caenorhabditis elegans	rab6 interacting protein 1	1	F:GO:0005515	-		IPR004012; SSF140741 (SUPERFAMILY)
Caenorhabditis elegans	denn madd domain containing 5a	1	F:GO:0005515	-		IPR004012; SSF140741 (SUPERFAMILY)

Brugia malayi	bromodomain containing protein	13	P:GO:0006367; F:GO:0005515; F:GO:0008270; F:GO:0016251; F:GO:0003743; F:GO:0016563; P:GO:0000117; P:GO:0051726; F:GO:0043565; C:GO:0005669; P:GO:0045944; F:GO:0035174; P:GO:0016573	-		IPR022591; PTHR13900 (PANTHER)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	isoform b	4	F:GO:0004794; P:GO:0008152; F:GO:0030170; F:GO:0016597	-	EC:4.3.1.19	IPR001926; G3DSA:3.40.50.1100 (GENE3D), PTHR10314 (PANTHER), PTHR10314:SF17 (PANTHER)
Caenorhabditis elegans	regulator of g protein sig-ling family member (rgs-7)	3	F:GO:0004871; P:GO:0007165; C:GO:0044424	-		IPR000342; IPR016137; G3DSA:1.10.167.10 (GENE3D), G3DSA:1.10.196.10 (GENE3D), PTHR10845 (PANTHER), PTHR10845:SF30 (PANTHER)
	-	0				-
Caenorhabditis elegans	tr--dihydrouridine synthase 3-like	6	F:GO:0003676; P:GO:0055114; F:GO:0050660; F:GO:0008270; F:GO:0017150; P:GO:0008033	-		IPR001269; IPR013785; IPR018517; PTHR11082:SF8 (PANTHER), SSF51395 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	lipase family protein	2	F:GO:0016787; P:GO:0006629	-		IPR002921; G3DSA:3.40.50.1820 (GENE3D), SSF53474 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0003676		IPR012337
Caenorhabditis elegans	temporarily assigned gene -me family member (tag-234)	0		P:GO:0000003; P:GO:0040011; P:GO:0019915		G3DSA:2.10.60.10 (GENE3D)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0040011; P:GO:0006898; C:GO:0005576		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	2	C:GO:0030054; C:GO:0015629	-		PD968187 (PRODOM)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				G3DSA:2.30.30.100 (GENE3D)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Brugia malayi	elegans protein partially confirmed by transcript evidence	0		F:GO:0003674; P:GO:0008150		-
Caenorhabditis elegans	acid alpha partial	5	F:GO:0004553; C:GO:0005773; C:GO:0009505; P:GO:0008152; C:GO:0048046	-	EC:3.2.1.0	IPR000322; PTHR22762:SF10 (PANTHER), SSF51011 (SUPERFAMILY)

Caenorhabditis elegans	low quality protein: uncharacterized mfs-type transporter c19orf28-like	2	P:GO:0055085; C:GO:0016021	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	briggsae cbr-nlp-15 protein	0		F:GO:0005179; P:GO:0007218; C:GO:0016020; F:GO:0005184; P:GO:0055085; C:GO:0005576; P:GO:0006810		-
	-	0				-
Populus trichocarpa	duf814 family protein	8	F:GO:0008131; F:GO:0005507; F:GO:0003676; P:GO:0009793; F:GO:0048038; P:GO:0009308; P:GO:0055114; F:GO:0008270	-	EC:1.4.3.4; EC:1.4.3.6	PTHR15239 (PANTHER)
Caenorhabditis elegans	aspartyl aminopeptidase	4	F:GO:0008233; C:GO:0005622; F:GO:0005515; P:GO:0006518	-		IPR001948; G3DSA:3.40.630.10 (GENE3D), SSF53187 (SUPERFAMILY)
Brugia malayi	briggsae cbr-lgc-26 protein	7	C:GO:0030659; C:GO:0016021; F:GO:0005230; F:GO:0004872; P:GO:0006811; C:GO:0045211; P:GO:0030100	-		IPR006201; IPR006202; PTHR18945:SF42 (PANTHER)
Caenorhabditis elegans	cyclin-dependent ki-se inhibitor 1c (kip2)	6	P:GO:0050789; P:GO:0007049; P:GO:0048856; P:GO:0040007; P:GO:0007275; P:GO:0022414	-		IPR003175; G3DSA:4.10.365.10 (GENE3D), PTHR10265:SF6 (PANTHER)
	-	0				-
Caenorhabditis briggsae	g protein-coupled receptor 177	4	P:GO:0023033; C:GO:0031410; F:GO:0005515; P:GO:0007275	-		IPR009551; SignalP (SIGNALP)
Caenorhabditis briggsae	g protein-coupled receptor 177	4	P:GO:0023033; C:GO:0031410; F:GO:0005515; P:GO:0007275	-		IPR009551; SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	general transcription factor 3c polypeptide 1	0		F:GO:0003709; P:GO:0006350; C:GO:0000127; C:GO:0030529; F:GO:0005515; F:GO:0003677; C:GO:0005634		-

Caenorhabditis elegans	apical junction molecule family member (ajm-1)	7	P:GO:0009792; C:GO:0043296; P:GO:0045216; F:GO:0005488; C:GO:0005913; P:GO:0040010; P:GO:0040011	-		IPR002893; PTHR21517 (PANTHER), SSF144232 (SUPERFAMILY)
Caenorhabditis briggsae	apical junction molecule family member (ajm-1)	7	P:GO:0009792; C:GO:0043296; F:GO:0005488; P:GO:0045216; C:GO:0005913; P:GO:0040010; P:GO:0040011	-		IPR002893; PTHR21517 (PANTHER), SSF144232 (SUPERFAMILY)
Caenorhabditis sp. PS1010	cadherin domain containing protein	1	P:GO:0007409	-		IPR002126; IPR015919; PTHR10596 (PANTHER)
Pediculus humanus corporis	kruppel-like factor 2	11	F:GO:0030528; P:GO:0032715; F:GO:0008270; F:GO:0043565; P:GO:0030218; P:GO:0035188; F:GO:0005515; F:GO:0003700; P:GO:0045893; P:GO:0048785; C:GO:0005634	-		IPR007087; IPR013087; IPR015880; PTHR23223 (PANTHER), PTHR23223:SF23 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis elegans	protein	3	F:GO:0008026; P:GO:0010569; F:GO:0000166	-		PTHR11472 (PANTHER), PTHR11472:SF4 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	ensangg00000009686 protein	0		F:GO:0003723; F:GO:0003725; F:GO:0005515; C:GO:0005622		-
Caenorhabditis elegans	isoform a	0		F:GO:0004984; F:GO:0005549; P:GO:0007608; C:GO:0016020		IPR019176; PTHR21780 (PANTHER)
Caenorhabditis elegans	isoform a	0		F:GO:0004984; F:GO:0005549; P:GO:0007608; C:GO:0016020		IPR019176; PTHR21780 (PANTHER)
Caenorhabditis briggsae	r--binding protein 27	4	P:GO:0010171; F:GO:0003676; P:GO:0040010; C:GO:0044424	-		G3DSA:1.20.1390.10 (GENE3D)
Caenorhabditis briggsae	briggsae cbr-lin-33 protein	0		P:GO:0008219		-
	-	0				-
Caenorhabditis briggsae	ylm4_caeel ame: full=uncharacterized protein	4	P:GO:0009792; P:GO:0040010; F:GO:0005515; P:GO:0002119	-		PTHR12899 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG13570 [Caenorhabditis briggsae]	3	P:GO:0018991; P:GO:0040035; P:GO:0006898	-		-

	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	uncoordi-ted family member (unc-103)	0		F:GO:0005249; C:GO:0016021; C:GO:0016020; P:GO:0006813; P:GO:0055085; P:GO:0006811; F:GO:0005216; P:GO:0006810		-
	-	0				PS51257 (PROFILE)
	-	0				-
Brugia malayi	protein ki-se domain containing protein	5	P:GO:0006468; F:GO:0005515; P:GO:0016246; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017441; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF32 (PANTHER)
	-	0				-
Caenorhabditis briggsae	chaperonin containing subunit 5	14	C:GO:0005815; P:GO:0009615; P:GO:0040010; P:GO:0008340; P:GO:0006457; C:GO:0005730; C:GO:0005832; P:GO:0040035; F:GO:0005524; P:GO:0002119; P:GO:0040011; P:GO:0006898; F:GO:0051082; P:GO:0009792	-		IPR002194; IPR002423; IPR012718; IPR017998; G3DSA:1.10.560.10 (GENE3D), G3DSA:3.30.260.10 (GENE3D), G3DSA:3.50.7.10 (GENE3D), SSF52029 (SUPERFAMILY), SSF54849 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	hypothetical protein C24A3.2 [Caenorhabditis elegans]	1	F:GO:0005515	-		SignalP (SIGNALP)
Caenorhabditis elegans	ryanodine receptor	8	F:GO:0004872; P:GO:0006629; F:GO:0005219; P:GO:0006816; P:GO:0006874; P:GO:0055085; F:GO:0005509; C:GO:0016021	-		IPR002048; IPR011992; IPR015925; IPR018247; IPR018248; IPR018249; PTHR13715:SF11 (PANTHER), SSF47473 (SUPERFAMILY)
Loa loa	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	ga18470	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		-
Caenorhabditis briggsae	briggsae cbr-dct-5 protein	0		C:GO:0016021; C:GO:0016020		PD031729 (PRODOM)
	-	0				-
	-	0				-

Caenorhabditis briggsae	ubiquinol-cytochrome c reductase binding protein	13	P:GO:0040010; P:GO:0008340; F:GO:0008121; C:GO:0005743; P:GO:0055114; P:GO:0045333; P:GO:0000003; P:GO:0010171; P:GO:0002119; C:GO:0070469; P:GO:0006119; P:GO:0009792; P:GO:0040018	-	EC:1.10.2.2	IPR003197
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein F28B4.3 [Caenorhabditis elegans]	1	P:GO:0040010	-		-
Pongo abelii	ornithine decarboxylase antizyme 1	4	P:GO:0006596; F:GO:0008073; P:GO:0050790; F:GO:0005515	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	fibroblast growth factor receptor 1	13	P:GO:0043589; F:GO:0000166; P:GO:0042664; C:GO:0016021; P:GO:0048916; P:GO:0060249; P:GO:0031101; P:GO:0048738; F:GO:0005007; P:GO:0009953; P:GO:0035121; P:GO:0008543; P:GO:0001889	-		IPR000719; IPR001245; IPR011009; IPR017441; IPR020685; IPR020725; G3DSA:3.30.200.20 (GENE3D)
	-	0				-
Phytophthora infestans T30-4	microtubule -associated protein eb1	0		F:GO:0008017		-
	-	0				-
Caenorhabditis elegans	hypothetical protein T20G5.14 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				-
	-	0				-
Pediculus humanus corporis	probable histone acetyltransferase myst1	7	F:GO:0004402; P:GO:0030099; P:GO:0016481; P:GO:0045893; P:GO:0043984; F:GO:0008134; C:GO:0071339	-	EC:2.3.1.48	IPR016181; IPR016197; G3DSA:2.30.30.270 (GENE3D), PTHR10615 (PANTHER), PTHR10615:SF34 (PANTHER), PF11717 (PFAM)
Caenorhabditis briggsae	briggsae cbr-hmr-1 protein	3	F:GO:0005515; P:GO:0009987; P:GO:0023052	-		IPR002126; IPR015919; IPR020894; PTHR10596 (PANTHER), PTHR10596:SF114 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	F:GO:0016787	-		IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF9 (PANTHER), SSF56300 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-

Loa loa	zinc c2h2 type family protein	0		F:GO:0046872; P:GO:0000003; F:GO:0003676; F:GO:0008270; P:GO:0009792; C:GO:0005634; C:GO:0005622		IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), SignalP (SIGNALP), SSF57667 (SUPERFAMILY)
Loa loa	zinc c2h2 type family protein	0		F:GO:0046872; P:GO:0000003; F:GO:0003676; F:GO:0008270; P:GO:0009792; C:GO:0005634; C:GO:0005622		IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis elegans	methylmalonyl- mutase	4	F:GO:0046872; F:GO:0004494; P:GO:0008152; F:GO:0031419	-	EC:5.4.99.2	IPR006158; IPR006159; PTHR23408 (PANTHER), PTHR23408:SF1 (PANTHER)
Caenorhabditis briggsae	lethal essential for life l2efl	2	P:GO:0009408; F:GO:0005515	-		IPR001436; IPR002068; IPR008978; G3DSA:2.60.40.790 (GENE3D), PTHR11527 (PANTHER), PTHR11527:SF23 (PANTHER)
Caenorhabditis briggsae	lethal essential for life l2efl	2	P:GO:0009408; F:GO:0005515	-		IPR001436; IPR002068; IPR008978; G3DSA:2.60.40.790 (GENE3D), PTHR11527 (PANTHER), PTHR11527:SF23 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	fanconi anemia complementation group d2 isoform	0				-
Loa loa	fanconi anemia complementation group d2 isoform	0				SignalP (SIGNALP)

Brugia malayi	mh1 domain containing protein	40	F:GO:0003700; P:GO:0045892; F:GO:0042803; P:GO:0032909; P:GO:0001701; P:GO:0072133; F:GO:0070411; P:GO:0007498; P:GO:0060391; P:GO:0042177; P:GO:0010862; C:GO:0005829; P:GO:0030511; P:GO:0032525; P:GO:0072134; P:GO:0010718; P:GO:0001666; P:GO:0060395; P:GO:0030509; P:GO:0045944; F:GO:0010843; P:GO:0001702; P:GO:0007492; C:GO:0032444; P:GO:0048859; F:GO:0030616; P:GO:0051098; F:GO:0016563;	-		IPR003619; IPR013019; IPR013790; IPR015288; PTHR13703:SF12 (PANTHER)
	-	0				-
Caenorhabditis briggsae	uhrf1 binding protein 1	0		F:GO:0003674; C:GO:0005575		PTHR22774 (PANTHER), PTHR22774:SF5 (PANTHER)
Caenorhabditis elegans	tr--dihydrouridine synthase 2	6	F:GO:0003725; C:GO:0005622; P:GO:0055114; F:GO:0050660; F:GO:0017150; P:GO:0008033	-		IPR001269; IPR013785; IPR018517; PTHR11082:SF4 (PANTHER)
Caenorhabditis elegans	hypothetical protein C15F1.2 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0005488	-		IPR017853; PTHR23208 (PANTHER), PTHR23208:SF13 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0005488	-		IPR017853; PTHR23208 (PANTHER), PTHR23208:SF13 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	u58758_13 transcription elongation regulator homolog protein isoform partially confirmed by transcript evidence	7	P:GO:0040035; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0016246; P:GO:0040011; P:GO:0040007	-		IPR002713
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	-dh-cytochrome b5 reductase 2	9	F:GO:0004128; P:GO:0009792; P:GO:0002119; P:GO:0032940; P:GO:0040010; P:GO:0055114; C:GO:0016021; P:GO:0006898; P:GO:0016126	-	EC:1.6.2.2	IPR001433; IPR001709; IPR001834; IPR008333; IPR017927; IPR017938; G3DSA:2.40.30.10 (GENE3D), G3DSA:3.40.50.80 (GENE3D), PTHR19370 (PANTHER), PTHR19370:SF4 (PANTHER), SSF52343 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-pes-9 protein	4	F:GO:0008237; F:GO:0016805; P:GO:0006508; F:GO:0005515	-	EC:3.4.13.0	IPR002933; IPR011650; G3DSA:3.30.70.360 (GENE3D), G3DSA:3.40.630.10 (GENE3D), PTHR11014 (PANTHER), PTHR11014:SF15 (PANTHER), SSF53187 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG01593 [Caenorhabditis briggsae]	4	P:GO:0007186; C:GO:0016021; P:GO:0007165; F:GO:0004930	-		-
Caenorhabditis briggsae	protein vac14 homolog	4	F:GO:0005515; C:GO:0043231; C:GO:0044444; C:GO:0016020	-		IPR021841; PTHR16023 (PANTHER)
	-	0				-
Macaca mulatta	milk fat globule-egf factor 8 isoform cra_b	17	P:GO:0001525; P:GO:0006910; F:GO:0008429; C:GO:0009897; P:GO:0043627; P:GO:0050766; C:GO:0005615; P:GO:0006911; P:GO:0007155; F:GO:0005178; F:GO:0001786; C:GO:0031012; P:GO:0044419; P:GO:0008284; C:GO:0005737; C:GO:0019897; P:GO:0007338	-		SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-nlp-42 protein	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	P:GO:0040010	-		IPR002656; PTHR11161 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-hyl-1 protein	6	P:GO:0019216; P:GO:0044249; P:GO:0008610; P:GO:0009889; P:GO:0044255; C:GO:0016020	-		IPR006634; PTHR12560 (PANTHER)

Caenorhabditis elegans	longevity assurance factor 1	7	C:GO:0016021; P:GO:0006641; P:GO:0032933; P:GO:0050995; P:GO:0046513; P:GO:0046889; C:GO:0005886	-		-
Brugia malayi	non-structural mainte-nce of chromosomes element 1 homolog	0		F:GO:0046872; P:GO:0006281; F:GO:0008270; P:GO:0006310; P:GO:0023034; P:GO:0009792; F:GO:0005515; C:GO:0005634		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG12142 [Caenorhabditis briggsae]	6	C:GO:0016021; P:GO:0009792; P:GO:0040010; P:GO:0055085; F:GO:0005215; P:GO:0002119	-		-
Caenorhabditis elegans	hog (hedgehog-like family) family member (wrt-5)	1	F:GO:0005515	-		PTHR11889 (PANTHER), PTHR11889:SF12 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-nsy-4 protein	1	C:GO:0016021	-		IPR006187; IPR010761; SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	glycogen synthase	7	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0005978; F:GO:0005515; F:GO:0004373; P:GO:0040011	-	EC:2.4.1.11	IPR008631; SignalP (SIGNALP)
Brugia malayi	cleavage stimulation factor subunit 3 isoform 2	2	P:GO:0006397; C:GO:0005634	-		IPR003107; PTHR19980 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	protein transport protein sec16b	1	F:GO:0005515	-		PTHR13402 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0019915; P:GO:0040018; P:GO:0040011	-		IPR000615; IPR021134; SignalP (SIGNALP)
Brugia malayi	protein phosphatase 1 regulatory inhibitor subunit	8	P:GO:0040035; P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040018; P:GO:0040010; P:GO:0008340; P:GO:0006898	-		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF165 (PANTHER)
Brugia malayi	helix-turn- psq domain containing protein	0		P:GO:0019915; F:GO:0003677		-
Caenorhabditis briggsae	phosphatidylinositol n-acetylglucosaminyltransferase	4	F:GO:0016757; P:GO:0006506; C:GO:0016021; P:GO:0045132	-		PTHR12526 (PANTHER), PTHR12526:SF37 (PANTHER)

Caenorhabditis elegans	organic cation transporter	0		C:GO:0016021; C:GO:0016020; P:GO:0055085; F:GO:0005215; P:GO:0006810		PTHR11600 (PANTHER), PTHR11600:SF35 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	(poly glutamine tract) toxicity enhancer family member (pqe-1)	0		F:GO:0003676; F:GO:0004527; C:GO:0005622		-
	-	0				-
Caenorhabditis elegans	yhb8_caeel ame: full=uncharacterized protein flags: precursor	0				-
	-	0				-
	-	0				-
Pan troglodytes	zinc finger ccch-type containing 13	0		F:GO:0003676; F:GO:0046872; F:GO:0008270		-
Caenorhabditis elegans	quinine non-avoider family member (qui-1)	0				-
Brugia malayi	topoisomerase iii alpha	6	C:GO:0043229; P:GO:0071103; P:GO:0007276; P:GO:0007126; P:GO:0006259; F:GO:0003916	-		IPR000380; IPR013497; IPR013826
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	shc (src homology domain c-termi-l) adaptor homolog family member (shc-2)	0		F:GO:0005515		PTHR12583 (PANTHER), PTHR12583:SF5 (PANTHER)
	-	0				-
Caenorhabditis elegans	isoform cra_a	12	P:GO:0009987; C:GO:0005764; C:GO:0005903; C:GO:0044459; F:GO:0004872; C:GO:0030139; C:GO:0044437; F:GO:0005515; C:GO:0031090; C:GO:0012505; P:GO:0008152; P:GO:0015031	-		IPR000859; PTHR22991 (PANTHER)
	-	0				-
Ascaris suum	thymidylate synthase	9	F:GO:0004799; P:GO:0055114; P:GO:0000003; P:GO:0006545; F:GO:0004146; P:GO:0010171; P:GO:0006231; P:GO:0009792; F:GO:0050661	-	EC:2.1.1.45; EC:1.5.1.3	IPR000398

Caenorhabditis elegans	acetoacetyl- synthetase	19	P:GO:0071394; C:GO:0005829; P:GO:0014074; P:GO:0006629; P:GO:0042594; P:GO:0010243; P:GO:0050872; P:GO:0045471; P:GO:0001889; P:GO:0007584; P:GO:0071333; P:GO:0060612; P:GO:0071397; F:GO:0000166; P:GO:0034201; P:GO:0042493; F:GO:0047760; P:GO:0032024; F:GO:0030729	-	EC:6.2.1.2; EC:6.2.1.16	IPR000873; PTHR11968 (PANTHER), PTHR11968:SF40 (PANTHER), SSF56801 (SUPERFAMILY)
Caenorhabditis elegans	high density lipoprotein binding protein	12	P:GO:0040010; F:GO:0003723; P:GO:0018991; P:GO:0040035; F:GO:0008289; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0040017; P:GO:0009792; C:GO:0005737; C:GO:0005886	-		IPR004087; IPR004088; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR10627 (PANTHER), PTHR10627:SF9 (PANTHER), SSF54791 (SUPERFAMILY)
Caenorhabditis elegans	d-glucuronyl c5-epimerase	6	P:GO:0009950; C:GO:0005794; P:GO:0015012; F:GO:0047464; C:GO:0016020; P:GO:0030210	-	EC:5.1.3.17	IPR010598; PTHR13174 (PANTHER)
	-	0				-
Caenorhabditis elegans	novel protein containing 10 heat domains	3	C:GO:0043231; C:GO:0044444; P:GO:0007067	-		IPR011989
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		C:GO:0016021; P:GO:0055085		G3DSA:1.20.1250.20 (GENE3D), PTHR11662 (PANTHER), PTHR11662:SF11 (PANTHER)
	-	0				-
Caenorhabditis briggsae	general transcription factor polypeptide alpha 220kda	0		F:GO:0003709; P:GO:0006350; P:GO:0045449; C:GO:0030529; C:GO:0000127; F:GO:0005515; C:GO:0005634; F:GO:0003677		PTHR15180 (PANTHER)
	-	0				-
Loa loa	hypothetical protein LOAG_02637 [Loa loa]	0				-
	-	0				-

	-	0				-
	-	0				-
Caenorhabditis briggsae	protein	2	P:GO:0008152; F:GO:0003824	-		PTHR11968 (PANTHER), PTHR11968:SF8 (PANTHER)
Caenorhabditis elegans	clc-type chloride channel family member (clh-2)	5	P:GO:0009792; C:GO:0005886; P:GO:0006810; P:GO:0000003; F:GO:0005216	-		IPR000644; IPR001807; IPR013785; IPR014743; PTHR11689:SF5 (PANTHER), SSF54631 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	patched homolog 1	7	P:GO:0009792; P:GO:0002119; P:GO:0040018; P:GO:0018996; P:GO:0000003; P:GO:0040011; C:GO:0016021	-		-
Loa loa	vav 3 oncogene	17	P:GO:0043087; P:GO:0006909; F:GO:0005154; P:GO:0030032; P:GO:0030217; P:GO:0006955; P:GO:0006906; P:GO:0007229; P:GO:0048468; C:GO:0005829; P:GO:0007264; P:GO:0043552; P:GO:0006915; P:GO:0045785; F:GO:0030676; C:GO:0005886; P:GO:0016477	-		IPR001715; IPR003096; PTHR22826 (PANTHER), PTHR22826:SF53 (PANTHER)
Callithrix jacchus	poly binding protein 2	11	P:GO:0043161; F:GO:0003723; P:GO:0050687; F:GO:0031625; P:GO:0016071; P:GO:0008380; P:GO:0045087; F:GO:0003677; C:GO:0030529; C:GO:0005737; C:GO:0005634	-		IPR004087; IPR004088; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR10288 (PANTHER), PTHR10288:SF48 (PANTHER), SSF54791 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	vacuolar protein sorting-associated protein 28 homolog	2	P:GO:0015031; C:GO:0005768	-		IPR007143; IPR017898; IPR017899; SSF140111 (SUPERFAMILY), SSF140427 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	4	P:GO:0006633; F:GO:0004768; P:GO:0055114; C:GO:0016021	-	EC:1.14.19.1	SignalP (SIGNALP)
Loa loa	heat domain-containing	0		F:GO:0005488		SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	4	P:GO:0009792; P:GO:0000003; P:GO:0040010; P:GO:0002119	-		IPR007087; IPR015880
	-	0				-
Loa loa	mitogen-activated protein ki-se ki-se ki-se ki-se 3	7	P:GO:0006468; F:GO:0005083; F:GO:0005515; P:GO:0007254; F:GO:0005524; P:GO:0050790; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017441; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF75 (PANTHER)
Brugia malayi	protein set-	1	F:GO:0016740	-		IPR000504; IPR012677; SSF54928 (SUPERFAMILY)
Pristionchus pacificus	briggsae cbr-tra-1 protein	8	C:GO:0005737; P:GO:0007283; F:GO:0003676; P:GO:0019101; P:GO:0019099; F:GO:0008022; C:GO:0005634; F:GO:0008270	-		IPR007087; IPR013087; IPR015880; PTHR19818 (PANTHER), PTHR19818:SF17 (PANTHER)
Loa loa	i lweq domain containing protein	0		F:GO:0003779; F:GO:0005198; P:GO:0007155; C:GO:0015629		-
Caenorhabditis elegans	alter-tive splicing type 3	0		F:GO:0003674; P:GO:0008150		IPR004882; PTHR12375:SF17 (PANTHER)
Caenorhabditis elegans	viral a-type inclusion protein	1	F:GO:0005515	-		PD936484 (PRODOM)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	3	C:GO:0016021; F:GO:0005272; P:GO:0006814	-		IPR001873; SignalP (SIGNALP)
Caenorhabditis elegans	nicotinic acetylcholine receptor alpha subunit 63b	7	P:GO:0009792; P:GO:0002119; C:GO:0005887; F:GO:0005230; P:GO:0006810; P:GO:0040007; C:GO:0045202	-		IPR002394; IPR006201; IPR006202; IPR018000; PTHR18945:SF62 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-sinh-1 protein	0				-
Caenorhabditis briggsae	briggsae cbr-sinh-1 protein	0				-
	-	0				-
Callithrix jacchus	ribophorin i	7	C:GO:0030867; F:GO:0005515; C:GO:0042470; C:GO:0008250; C:GO:0016021; F:GO:0004579; P:GO:0018279	-	EC:2.4.1.119	SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-scp-1 protein	2	P:GO:0009792; C:GO:0016021	-		-

Caenorhabditis briggsae	Hypothetical protein CBG13933 [Caenorhabditis briggsae]	0		F:GO:0046872; P:GO:0040010; P:GO:0006898; F:GO:0008270; F:GO:0005515		-
	-	0				-
	-	0				-
	-	0				PTHR11003 (PANTHER), PTHR11003:SF9 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	cyclin l2	8	P:GO:0009792; P:GO:0002119; P:GO:0006350; P:GO:0000003; P:GO:0008340; P:GO:0040011; P:GO:0040007; C:GO:0005634	-		IPR006670; IPR006671; IPR011028; IPR013763; IPR015429; IPR015431
Loa loa	ubiquitin protein ligase	0		P:GO:0000003; F:GO:0016874; F:GO:0016881; P:GO:0006464; C:GO:0005622		IPR000048
Caenorhabditis elegans	hed family member (ptc-3)	6	P:GO:0009792; P:GO:0002119; P:GO:0040018; P:GO:0018996; P:GO:0000003; P:GO:0040011	-		PTHR10796 (PANTHER), PTHR10796:SF34 (PANTHER)
Ostertagia ostertagi	metalloprotease iii	3	F:GO:0004222; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	-
	-	0				SignalP (SIGNALP)
	-	0				-
Brugia malayi	phospholipase active site motif family protein	0		F:GO:0016780; P:GO:0008152; P:GO:0008654; F:GO:0003824		PTHR12586 (PANTHER)
Caenorhabditis elegans	ef hand family protein	0		F:GO:0005509		IPR018247; IPR018249
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-hex-4 protein	0		F:GO:0004553; P:GO:0005975; F:GO:0043169; F:GO:0003824		IPR013781; IPR015883
	-	0				-
Loa loa	ww domain containing protein	0		F:GO:0005515		IPR002713; PTHR11864 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	5	P:GO:0007156; C:GO:0005886; P:GO:0007411; F:GO:0050839; P:GO:0016338	-		IPR000782; PTHR10900 (PANTHER), PTHR10900:SF10 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-

Caenorhabditis elegans	briggsae cbr-unc-40 protein	0		F:GO:0016787; P:GO:0006468; P:GO:0048010; F:GO:0004725; F:GO:0016162; F:GO:0005524; F:GO:0004721; C:GO:0016021; C:GO:0016020; P:GO:0007155; F:GO:0016798; F:GO:0004872; P:GO:0008152; F:GO:0005021; F:GO:0016791; P:GO:0006470; P:GO:0016311; P:GO:0016358; C:GO:0005887; F:GO:0005515; F:GO:0016740; F:GO:0050254		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Homo sapiens	lysosomal alpha-glucosidase precursor	18	F:GO:0032450; P:GO:0007626; P:GO:0005980; P:GO:0055010; P:GO:0043181; P:GO:0060048; P:GO:0007040; P:GO:0000023; C:GO:0005765; P:GO:0050884; P:GO:0005985; F:GO:0005529; P:GO:0046716; P:GO:0050885; P:GO:0002026; C:GO:0005625; P:GO:0002086; P:GO:0043587	-		-
	-	0				-
Caenorhabditis briggsae	c6orf153 protein	5	P:GO:0009792; P:GO:0000003; P:GO:0040007; P:GO:0006898; P:GO:0002119	-		IPR009292
Caenorhabditis briggsae	loc496075 protein	0				IPR003226
	-	0				-

Caenorhabditis briggsae	fer (fps fes related) tyrosine ki-se	12	P:GO:0040010; F:GO:0017137; P:GO:0023034; P:GO:0000003; F:GO:0004713; F:GO:0045296; F:GO:0045295; F:GO:0003779; F:GO:0000166; F:GO:0019901; C:GO:0005737; P:GO:0006468	-	EC:2.7.10.0	IPR000719; IPR001245; IPR008266; IPR011009; IPR020685; IPR020764; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
	-	0				PF05804 (PFAM)
	-	0				-
Caenorhabditis elegans	tetratricopeptide repeat domain 17	3	P:GO:0040010; P:GO:0040017; F:GO:0005488	-		PTHR16091 (PANTHER)
	-	0				SignalP (SIGNALP)
Loa loa	uncharacterized protein kiaa0329 kiaa0297	0		F:GO:0005488; F:GO:0004512; P:GO:0008152; P:GO:0008654; F:GO:0003824; P:GO:0006021		IPR001680; IPR011046; IPR015943; PTHR23287 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	hypothetical protein Bm1_40770 [Brugia malayi]	0				-
	-	0				-
Homo sapiens	cytochrome c oxidase subunit iv	7	P:GO:0007584; F:GO:0005515; C:GO:0005751; C:GO:0016021; C:GO:0005634; F:GO:0004129; P:GO:0006091	-	EC:1.9.3.1	-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	polymerase iii (d- directed) polypeptide 39 kda	2	F:GO:0005488; P:GO:0000003	-		IPR007832
Caenorhabditis elegans	tr- (5-methylaminomethyl-2-thiouridylate)-methyltransferase	4	P:GO:0008033; P:GO:0006529; C:GO:0005737; F:GO:0008168	-	EC:2.1.1.0	IPR004506; IPR014729; SSF52402 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-ego-1 protein	1	F:GO:0005515	-		-
Loa loa	amp-binding enzyme family protein	1	F:GO:0005488	-		IPR000873; G3DSA:3.40.50.980 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF11 (PANTHER), SignalP (SIGNALP), SSF56801 (SUPERFAMILY)

Callithrix jacchus	poly binding protein 2	11	P:GO:0043161; F:GO:0003723; P:GO:0050687; F:GO:0031625; P:GO:0016071; P:GO:0008380; P:GO:0045087; F:GO:0003677; C:GO:0030529; C:GO:0005737; C:GO:0005634	-		PTHR10288 (PANTHER), PTHR10288:SF48 (PANTHER)
Callithrix jacchus	glutamine synthetase	10	C:GO:0005829; P:GO:0009749; C:GO:0005739; F:GO:0004351; F:GO:0042802; P:GO:0006542; F:GO:0005524; F:GO:0004356; P:GO:0008283; C:GO:0005794	-	EC:4.1.1.15; EC:6.3.1.2	SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	fh1 fh2 domain-containing protein 3	3	P:GO:0030036; C:GO:0044424; F:GO:0003779	-		IPR015425; PTHR23213 (PANTHER), PTHR23213:SF3 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	membrane calcium atpase family member (mca-1)	5	F:GO:0005388; C:GO:0016021; P:GO:0006754; F:GO:0005524; P:GO:0006816	-	EC:3.6.3.8	SignalP (SIGNALP)
	-	0				-
Strongylocentrotus purpuratus	atp-binding cassette protein c4-like	2	P:GO:0006810; C:GO:0016020	-		IPR001140; IPR011527; IPR017940; G3DSA:1.20.1560.10 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF97 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	P:GO:0008104	-		IPR009543; PTHR16166 (PANTHER), PTHR16166:SF25 (PANTHER)
	-	0				-
	-	0				PTHR10827 (PANTHER), PTHR10827:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	uhrf1-binding protein 1-like	0				PTHR22774 (PANTHER), PTHR22774:SF5 (PANTHER)
Caenorhabditis briggsae	atp-dependent clp protease atp-binding subunit clpx	8	P:GO:0006457; P:GO:0006355; C:GO:0005743; F:GO:0051082; F:GO:0016887; F:GO:0008233; F:GO:0008134; F:GO:0005524	-		-

Caenorhabditis briggsae	atp-dependent clp protease atp-binding subunit clpx	8	P:GO:0006457; P:GO:0006355; C:GO:0005743; F:GO:0051082; F:GO:0016887; F:GO:0008233; F:GO:0008134; F:GO:0005524	-		IPR003593; IPR004487; IPR013093; IPR019489; G3DSA:1.10.8.60 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR11262 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	g elongation mitochondrial 2	2	F:GO:0005488; P:GO:0032543	-		IPR000640; IPR004161; IPR005517; IPR009000; IPR009022; IPR014721; IPR020568; G3DSA:2.40.30.10 (GENE3D), G3DSA:3.30.70.870 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF13 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	F:GO:0005044; F:GO:0005488; C:GO:0016020	-		-
	-	0				-
	-	0				-
Camponotus floridanus	cutc copper transporter homolog	7	C:GO:0005737; F:GO:0042802; P:GO:0006825; P:GO:0051262; F:GO:0005507; P:GO:0055070; C:GO:0005634	-		IPR005627
Caenorhabditis briggsae	af303259_1 2o16	0				-
Caenorhabditis briggsae	af303259_1 2o16	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	kiaa2021 protein	2	P:GO:0009792; P:GO:0000003	-		IPR001313; IPR011989; IPR016024
Caenorhabditis elegans	stromal cell derived factor 4	6	P:GO:0050896; P:GO:0032502; P:GO:0017156; F:GO:0005515; C:GO:0043231; C:GO:0044444	-		IPR002048; IPR011992; IPR018247; IPR018249; PTHR10827 (PANTHER), PTHR10827:SF13 (PANTHER), SSF47473 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	death-associated protein ki-se 1	8	F:GO:0005516; P:GO:0007243; F:GO:0004672; F:GO:0016491; F:GO:0005524; C:GO:0015629; P:GO:0008624; P:GO:0006468	-		SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	P:GO:0019915; P:GO:0008152; F:GO:0016740	-		IPR002213; PTHR11926:SF3 (PANTHER), SignalP (SIGNALP), SSF53756 (SUPERFAMILY)

Caenorhabditis elegans	cgmp-dependent protein ki-se foraging	4	P:GO:0006468; F:GO:0005524; P:GO:0000003; F:GO:0004674	-	EC:2.7.11.0	-
Loa loa	mitogen-activated protein-binding protein-interacting protein	3	C:GO:0005768; F:GO:0005515; C:GO:0016020	-		IPR004942; G3DSA:3.30.450.30 (GENE3D), PTHR13323 (PANTHER), SSF103196 (SUPERFAMILY)
	-	0				-
Ailuropoda melanoleuca	myosin regulatory light chain 12b	7	P:GO:0006936; F:GO:0005515; C:GO:0016459; C:GO:0045177; F:GO:0005509; F:GO:0003774; P:GO:0008152	-		IPR011992; IPR018249; PTHR23049 (PANTHER), PTHR23049:SF6 (PANTHER), SSF47473 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	eukaryotic translation initiation factor x-chromosomal	9	F:GO:0003743; P:GO:0040010; F:GO:0003723; P:GO:0045948; P:GO:0000003; P:GO:0040011; P:GO:0006898; P:GO:0009792; P:GO:0040018	-		IPR001253; IPR006196; IPR012340; IPR016027; IPR018104
	-	0				-
Caenorhabditis elegans	briggsae cbr-btf-1 protein	1	F:GO:0005488	-		-
Loa loa	chitin deacetylase 1	2	P:GO:0005975; F:GO:0016810	-		IPR002509; IPR011330
Caenorhabditis briggsae	Hypothetical protein CBG01490 [Caenorhabditis briggsae]	0		F:GO:0008312; F:GO:0030942; C:GO:0005786; P:GO:0006614; C:GO:0048500; F:GO:0005515; P:GO:0045900		SignalP (SIGNALP)

Branchiostoma floridae	glycosyl hydrolase family catalytic domain containing protein	27	P:GO:0001501; C:GO:0001669; P:GO:0006689; P:GO:0007605; P:GO:0007626; C:GO:0016020; P:GO:0006874; P:GO:0007040; P:GO:0031323; F:GO:0016231; P:GO:0044267; C:GO:0005764; P:GO:0006044; P:GO:0008049; F:GO:0046982; P:GO:0019915; F:GO:0005529; P:GO:0030203; F:GO:0043169; P:GO:0050885; P:GO:0048477; F:GO:0042803; P:GO:0042552; P:GO:0009313; P:GO:0008654; P:GO:0007341; C:GO:0005625	-		IPR001540; IPR013781
Loa loa	hypothetical protein LOAG_05551 [Loa loa]	0				-
Caenorhabditis briggsae	briggsae cbr-cpg-4 protein	0		P:GO:0040010		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	dy-min	3	F:GO:0003924; F:GO:0005515; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000375; IPR001401; IPR001849; IPR003130; IPR011993; IPR019762; IPR020850; IPR022812; G3DSA:3.40.50.300 (GENE3D), PTHR11566 (PANTHER), PTHR11566:SF12 (PANTHER), SSF50729 (SUPERFAMILY), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	major intrinsic protein	9	C:GO:0016323; P:GO:0045087; P:GO:0006833; P:GO:0000003; P:GO:0008340; P:GO:0050829; C:GO:0016021; F:GO:0015250; P:GO:0015793	-		IPR000425; IPR022357; PTHR19139:SF11 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	splicing factor subunit 2	7	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0018996; F:GO:0005515; P:GO:0040011; P:GO:0040007	-		-

Caenorhabditis elegans	succinyl-coa synthetase beta chain	7	F:GO:0004776; P:GO:0009792; C:GO:0005811; C:GO:0045244; F:GO:0005524; P:GO:0006099; F:GO:0004775	-	EC:6.2.1.4; EC:6.2.1.5	IPR005809; IPR005811; IPR013816; IPR016102; IPR017866; SSF56059 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	hydroxysteroid dehydroge-se	2	P:GO:0009792; P:GO:0000003	-		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Loa loa	briggsae cbr-cln- protein	0		C:GO:0005886; P:GO:0006672; P:GO:0043086; P:GO:0001575; P:GO:0006898; P:GO:0006865; C:GO:0016021; P:GO:0008150; C:GO:0016020; P:GO:0007042; P:GO:0007040; P:GO:0042133; C:GO:0005783; C:GO:0008021; P:GO:0000046; P:GO:0008340; P:GO:0016242; C:GO:0005624; P:GO:0046662; C:GO:0030176; P:GO:0001508; P:GO:0015809; F:GO:0048306; C:GO:0000139; P:GO:0016044; P:GO:0043524; P:GO:0008306;		IPR003492; SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	ab-hydrolase associated lipase region family protein	1	P:GO:0006629	-		IPR000073; IPR006693; G3DSA:3.40.50.1820 (GENE3D), PTHR11005 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	ab-hydrolase associated lipase region family protein	1	P:GO:0006629	-		IPR000073; IPR006693; G3DSA:3.40.50.1820 (GENE3D), PTHR11005 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	P:GO:0006629	-		IPR000073; IPR006693; G3DSA:3.40.50.1820 (GENE3D), PTHR11005 (PANTHER), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	ab-hydrolase associated lipase region family protein	1	P:GO:0006629	-		IPR000073; IPR006693; G3DSA:3.40.50.1820 (GENE3D), PTHR11005 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)

Caenorhabditis elegans	ab-hydrolase associated lipase region family protein	1	P:GO:0006629	-		IPR000073; IPR006693; G3DSA:3.40.50.1820 (GENE3D), PTHR11005 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	ab-hydrolase associated lipase region family protein	1	P:GO:0006629	-		IPR000073; IPR006693; G3DSA:3.40.50.1820 (GENE3D), PTHR11005 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-wht-2 protein	4	C:GO:0016021; F:GO:0016887; F:GO:0005524; P:GO:0010171	-		IPR003439; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR19241 (PANTHER), PTHR19241:SF30 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	hypothetical protein C09F12.3 [Caenorhabditis elegans]	0		C:GO:0016021; P:GO:0007186		G3DSA:1.20.1070.10 (GENE3D), PTHR22751 (PANTHER), PTHR22751:SF8 (PANTHER), SSF81321 (SUPERFAMILY)
Caenorhabditis elegans	bola-like protein 3-like	1	F:GO:0005515	-		IPR002634; PTHR12735:SF2 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0006898; P:GO:0002119; P:GO:0040007		-
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
Loa loa	sumo1 sentrin specific peptidase 6	0		C:GO:0005634; F:GO:0003676; F:GO:0008270; F:GO:0003674; C:GO:0005575; F:GO:0008234; F:GO:0008233; P:GO:0006508; P:GO:0008150		IPR003653; PTHR12438 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis briggsae	von willebrand factor type egf and pentraxin domain-containing protein 1-like	0		F:GO:0003674; F:GO:0005488; F:GO:0005509; C:GO:0016021; C:GO:0016020; P:GO:0008150; C:GO:0005575		-
Caenorhabditis elegans	dap (death associated protein ki-se) like ki-se family member (dlk-1)	15	P:GO:0018105; C:GO:0005829; P:GO:0007254; F:GO:0004674; F:GO:0046872; P:GO:0016572; P:GO:0018107; C:GO:0033267; C:GO:0005624; F:GO:0000166; F:GO:0019901; C:GO:0030426; F:GO:0042803; P:GO:0046777; C:GO:0005886	-	EC:2.7.11.0	IPR000719; IPR001245; IPR011009; G3DSA:1.10.510.10 (GENE3D), PTHR23257 (PANTHER), PTHR23257:SF85 (PANTHER)

Brugia malayi	coiled-coil domain-containing protein 76	0		F:GO:0008168; F:GO:0016455; P:GO:0045449; C:GO:0016592		IPR007871; PTHR12998 (PANTHER)
Caenorhabditis briggsae	hypothetical kda protein in chromosome	3	P:GO:0040007; P:GO:0006898; P:GO:0002119	-		-
	-	0				-
Caenorhabditis elegans	er degradation mannosidase alpha-like 3	4	F:GO:0004569; P:GO:0006516; C:GO:0044464; P:GO:0043161	-	EC:3.2.1.130	IPR001382; IPR003137; G3DSA:3.50.30.30 (GENE3D), PTHR11742:SF8 (PANTHER), SSF52025 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis briggsae	exosome complex exonuclease rrp44	7	F:GO:0003723; F:GO:0005515; F:GO:0016219; P:GO:0006364; C:GO:0000178; F:GO:0008859; C:GO:0005634	-	EC:3.1.13.1	-
	-	0				-
Danio rerio	gap-pol poly	1	F:GO:0005488	-		IPR000477; G3DSA:3.30.70.270 (GENE3D), PTHR10178 (PANTHER), PTHR10178:SF14 (PANTHER), SSF56672 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	per1-like family protein	1	F:GO:0005515	-		IPR007217
	-	0				-
	-	0				-
Caenorhabditis briggsae	mitotic control protein dis3	0		F:GO:0003723; F:GO:0004540; C:GO:0005652; P:GO:0006397; C:GO:0000177; C:GO:0000176; F:GO:0000175; C:GO:0005634		PTHR23355 (PANTHER), PTHR23355:SF13 (PANTHER)
Caenorhabditis elegans	briggsae cbr-spp-5 protein	0				IPR008138; IPR008139; IPR011001; PTHR21579 (PANTHER), PTHR21579:SF6 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Loa loa	type iii restriction res subunit family protein	0		F:GO:0003676; F:GO:0004386; F:GO:0005524; F:GO:0000166; F:GO:0016787; F:GO:0017111; F:GO:0008026		-
Caenorhabditis elegans	leucine-zipper-containing transcription factor lzf	2	P:GO:0040010; P:GO:0006974	-		IPR019386
	-	0				-

Homo sapiens	complement component 3	16	F:GO:0048037; P:GO:0006957; F:GO:0005102; P:GO:0010951; P:GO:0050766; P:GO:0045766; C:GO:0005615; P:GO:0001798; P:GO:0007596; P:GO:0007165; P:GO:0010575; P:GO:0006935; P:GO:0007186; P:GO:0006958; F:GO:0004866; P:GO:0001970	-		IPR001134; IPR008993; IPR018933; PTHR11412 (PANTHER), PTHR11412:SF14 (PANTHER)
Caenorhabditis elegans	adp atp translocase	11	P:GO:0040010; P:GO:0008340; P:GO:0040002; P:GO:0040035; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0006898; P:GO:0002009; P:GO:0009792; C:GO:0016020	-		IPR001993; IPR002067; IPR002113; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF35 (PANTHER)
Caenorhabditis elegans	tryptophan oxyge-se	8	P:GO:0040010; P:GO:0019441; P:GO:0055114; F:GO:0042802; P:GO:0006508; F:GO:0004197; F:GO:0004833; F:GO:0020037	-	EC:3.4.22.0; EC:1.13.11.11	IPR004981; SSF140959 (SUPERFAMILY)
Caenorhabditis briggsae	cystathionine beta-synthase	17	P:GO:0043506; P:GO:0019448; P:GO:0051593; F:GO:0020037; P:GO:0043418; C:GO:0005730; C:GO:0005829; P:GO:0070814; F:GO:0031625; F:GO:0030170; P:GO:0006565; P:GO:0019344; F:GO:0004122; F:GO:0042803; C:GO:0005625; P:GO:0001958; P:GO:0019346	-	EC:4.2.1.22	IPR001926; G3DSA:3.40.50.1100 (GENE3D), PTHR10314 (PANTHER), PTHR10314:SF8 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	armadillo beta-catenin-like repeat family protein	1	F:GO:0005515	-		-
Caenorhabditis elegans	dehydroge-se reductase sdr family member 4	2	F:GO:0016491; P:GO:0008152	-		IPR002198; IPR002347; IPR010916; IPR016040; PTHR19410:SF65 (PANTHER), SSF51735 (SUPERFAMILY)

	-	0				SignalP (SIGNALP)
Brugia malayi	serine threonine-protein phosphatase 2a regulatory subunit b	24	F:GO:0051721; P:GO:0008340; P:GO:0000003; F:GO:0005102; C:GO:0034704; C:GO:0000159; P:GO:0040010; P:GO:0035307; F:GO:0016853; C:GO:0005737; F:GO:0046982; P:GO:0032516; P:GO:0032515; P:GO:0009792; P:GO:0002119; F:GO:0008601; F:GO:0016887; F:GO:0042803; C:GO:0005625; C:GO:0005634; F:GO:0005524; P:GO:0035308; F:GO:0008160; P:GO:0043065	-		IPR004327; SSF140984 (SUPERFAMILY)
Loa loa	hypothetical protein LOAG_03154 [Loa loa]	0		F:GO:0005509; P:GO:0007155		IPR003410
	-	0				-
Caenorhabditis elegans	folliculin isoform 1	0				-
Loa loa	mediator of r- polymerase ii transcription subunit 31	5	P:GO:0009792; C:GO:0016592; P:GO:0045449; F:GO:0016455; P:GO:0000003	-		-
Loa loa	mediator of r- polymerase ii transcription subunit 31	5	P:GO:0009792; C:GO:0016592; P:GO:0045449; F:GO:0016455; P:GO:0000003	-		-
Loa loa	amop domain containing protein	0		P:GO:0007160; C:GO:0016021		PTHR13802 (PANTHER), PTHR13802:SF2 (PANTHER)
Caenorhabditis elegans	nfkb inhibitor interacting ras-like 2	4	F:GO:0005525; C:GO:0005622; P:GO:0007264; P:GO:0015031	-		IPR001806; IPR005225; IPR013684; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF275 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	nfkb inhibitor interacting ras-like 2	4	F:GO:0005525; C:GO:0005622; P:GO:0007264; P:GO:0015031	-		IPR001806; IPR005225; IPR013684; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF275 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	calpain 5	6	P:GO:0042004; C:GO:0005622; F:GO:0004198; P:GO:0019099; P:GO:0006508; C:GO:0016020	-		-
	-	0				-

	-	0				-
Pongo abelii	low quality protein: guanine nucleotide-binding protein subunit beta-2-like 1-like	10	C:GO:0005737; F:GO:0004872; P:GO:0008104; P:GO:0023034; P:GO:0007205; C:GO:0005886; F:GO:0005102; F:GO:0019903; C:GO:0043025; F:GO:0005080	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR19868 (PANTHER)
Loa loa	interferon regulatory factor 2 binding protein 2	3	P:GO:0045449; F:GO:0005515; C:GO:0005634	-		-
Loa loa	membrane-associated guanylate ki-se	1	F:GO:0005515	-		IPR001452; G3DSA:2.30.30.40 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23122 (PANTHER), PTHR23122:SF4 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Brugia malayi	bicaudal c homolog 1-like	0		F:GO:0003723; P:GO:0007275; F:GO:0005515		IPR004087; G3DSA:3.30.1370.10 (GENE3D), PTHR10627 (PANTHER), PTHR10627:SF1 (PANTHER), SSF54791 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	thyroid hormone receptor interactor 4	2	F:GO:0030528; P:GO:0040024	-		IPR009349; PTHR12963 (PANTHER)
Caenorhabditis elegans	thyroid hormone receptor interactor 4	2	F:GO:0030528; P:GO:0040024	-		IPR009349; PTHR12963 (PANTHER)
Caenorhabditis briggsae	tyrosine-protein ki-se transmembrane receptor ror	4	F:GO:0004872; F:GO:0004713; C:GO:0016020; F:GO:0000166	-	EC:2.7.10.0	IPR000719; IPR001245; IPR008266; IPR011009; IPR020685; IPR020742; G3DSA:1.10.510.10 (GENE3D)
Angiostrongylus cantonensis	protein ki-se domain containing protein	4	P:GO:0006468; F:GO:0005524; P:GO:0000003; F:GO:0004674	-	EC:2.7.11.0	IPR011009; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
Caenorhabditis briggsae	serine threonine ki-se 38 like	7	C:GO:0005737; P:GO:0006468; F:GO:0046872; P:GO:0007399; F:GO:0005524; C:GO:0005634; F:GO:0004674	-	EC:2.7.11.0	PTHR22985 (PANTHER), PTHR22985:SF33 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Loa loa	sig-l recognition particle receptor alpha subunit	1	F:GO:0005488	-		IPR007222; IPR011012; PTHR11564 (PANTHER), PTHR11564:SF1 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-

Loa loa	tho complex 2	7	P:GO:0045132; P:GO:0000003; P:GO:0040007; P:GO:0010171; F:GO:0005515; P:GO:0002119; P:GO:0040011	-		IPR021726; PTHR21597 (PANTHER)
	-	0				-
Caenorhabditis elegans	translocase of outer mitochondrial membrane 22 homolog	5	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040010; P:GO:0006898	-		IPR005683; PD033325 (PRODOM), PTHR12504 (PANTHER)
	-	0				-
Caenorhabditis elegans	trehalase family protein	3	C:GO:0016021; P:GO:0005991; F:GO:0004555	-	EC:3.2.1.28	IPR001661; PTHR23403:SF1 (PANTHER)
	-	0				-
	-	0				IPR003006
	-	0				-
Caenorhabditis remanei	apa-2	13	C:GO:0005829; F:GO:0008565; P:GO:0040010; P:GO:0048268; F:GO:0008022; P:GO:0000003; F:GO:0008289; P:GO:0050690; C:GO:0030122; P:GO:0040011; P:GO:0006898; P:GO:0006886; P:GO:0009792	-		IPR002553; IPR011989; PTHR22780 (PANTHER), PTHR22780:SF4 (PANTHER)
Caenorhabditis elegans	dap (death associated protein ki-se) like ki-se family member (dlk-1)	1	F:GO:0005515	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	14	C:GO:0030054; F:GO:0015464; P:GO:0007274; P:GO:0008340; P:GO:0043050; P:GO:0006811; P:GO:0007271; P:GO:0048609; C:GO:0042995; C:GO:0045203; C:GO:0045211; P:GO:0040011; F:GO:0004889; C:GO:0005892	-		IPR006029; IPR006201; G3DSA:1.20.120.370 (GENE3D), PTHR18945:SF57 (PANTHER)

Caenorhabditis elegans	suppressor with morphological effect on genitalia family member (smg-1)	0		F:GO:0016740; F:GO:0004674; F:GO:0000166; C:GO:0005737; F:GO:0005524; F:GO:0016301; P:GO:0000184; F:GO:0016773; F:GO:0046872; F:GO:0005488		-
Ixodes scapularis	conserved hypothetical protein [Ixodes scapularis]	0				IPR019180
	-	0				-
Caenorhabditis briggsae	briggsae cbr-smgl-1 protein	0				SignalP (SIGNALP)
Loa loa	twik (kcnk-like) family of potassium alpha subunit 39a	1	F:GO:0005216	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hexoki-se family protein	4	P:GO:0060361; F:GO:0005524; P:GO:0006096; F:GO:0004396	-	EC:2.7.1.1	IPR001312; IPR022673; G3DSA:3.40.367.20 (GENE3D), SSF53067 (SUPERFAMILY)
Pan troglodytes	cytochrome c oxidase subunit viic	4	C:GO:0005743; C:GO:0016021; F:GO:0004129; P:GO:0006091	-	EC:1.9.3.1	IPR004202; G3DSA:4.10.49.10 (GENE3D), SSF81427 (SUPERFAMILY)
	-	0				-
Brugia malayi	death-associated protein ki-se 1	8	F:GO:0005516; P:GO:0007243; F:GO:0004674; P:GO:0006916; F:GO:0005524; P:GO:0008624; C:GO:0005737; P:GO:0006468	-	EC:2.7.11.0	-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Loa loa	epidermal growth factor receptor	1	F:GO:0016740	-		IPR006212; IPR009030; IPR020685; IPR020688; G3DSA:2.10.220.10 (GENE3D)
	-	0				-
Homo sapiens	gamma-inducible protein 30	7	F:GO:0015036; P:GO:0019886; C:GO:0005764; P:GO:0048147; P:GO:0055114; P:GO:0050821; C:GO:0005576	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	major facilitator superfamily protein	2	P:GO:0006810; C:GO:0016020	-		IPR016196; G3DSA:1.20.1250.20 (GENE3D), PTHR11600 (PANTHER), PTHR11600:SF35 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0006508; F:GO:0016491; F:GO:0004190; C:GO:0016021		-

Caenorhabditis elegans	luc7-like protein 3	6	P:GO:0008380; F:GO:0003729; P:GO:0006915; F:GO:0005515; P:GO:0006950; C:GO:0005634	-		IPR004882; PTHR12375:SF17 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Apis mellifera	ubl carboxyl-termi-l	0		P:GO:0090231; P:GO:0016579; F:GO:0004221; P:GO:0007067; C:GO:0005634; F:GO:0016787; P:GO:0051301; F:GO:0008270; P:GO:0006511; F:GO:0008234; F:GO:0004843; P:GO:0051322; F:GO:0008233; P:GO:0060564; F:GO:0046872; P:GO:0007049		IPR001394; IPR018200; PTHR10420 (PANTHER), PTHR10420:SF58 (PANTHER), SSF54001 (SUPERFAMILY)
Ornithorhynchus anatinus	ribosomal protein l23	7	C:GO:0005829; C:GO:0005730; F:GO:0003735; P:GO:0006414; F:GO:0005515; P:GO:0006610; C:GO:0022626	-		IPR000218; IPR019972; PTHR11761:SF4 (PANTHER)
	-	0				-
Caenorhabditis elegans	variable abnormal morphology family member (vab-10)	0				-
Caenorhabditis elegans	c-type lectin family member (clec-90)	0				SignalP (SIGNALP)
Caenorhabditis elegans	c-type lectin family member (clec-90)	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR021859; PTHR16148 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	yp69_caeel ame: full=uncharacterized protein	0				-
	-	0				-
	-	0				-
	-	0				IPR018254
Brugia malayi	ribonucleases p mrp protein subunit pop1 containing protein	1	P:GO:0006396	-		IPR009723; PTHR22731 (PANTHER)
	-	0				-

Brugia malayi	protein ki-se family member (kin-20)	10	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0006468; P:GO:0040018; P:GO:0040010; F:GO:0005524; P:GO:0000003; P:GO:0040011; F:GO:0004674	-	EC:2.7.11.0	IPR011009; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF18 (PANTHER)
Brugia malayi	probable atp-dependent r- helicase ddx41-like	11	F:GO:0003723; C:GO:0005681; F:GO:0008270; P:GO:0006915; F:GO:0008026; P:GO:0006200; P:GO:0008380; F:GO:0005524; F:GO:0005515; P:GO:0007275; P:GO:0006397	-		IPR000629; IPR001650; IPR011545; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF46 (PANTHER), SSF52540 (SUPERFAMILY)
Harpegnathos saltator	zinc finger protein	0		F:GO:0003676; F:GO:0046983; F:GO:0003677		IPR008906; IPR012337
	-	0				-
Cyathostomum cf. pateratum HM-2009	gut-associated larval antigen-1	0				IPR003677; PTHR21593 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	glycerophosphoryl diester phosphodiesterase	2	F:GO:0008081; P:GO:0040010	-	EC:3.1.4.0	IPR004129; IPR017946
	-	0				-
	-	0				-
Thermotogales bacterium mesG1.Ag.4.2	chromosome segregation protein smc	0				-
Pongo abelii	ornithine decarboxylase	7	P:GO:0006596; P:GO:0008284; F:GO:0004586; P:GO:0001822; F:GO:0005515; C:GO:0005829; P:GO:0009615	-	EC:4.1.1.17	SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	abnormal spindle-like microcephaly-associated protein	1	F:GO:0005515	-		-
Caenorhabditis elegans	dynein heavy chain	11	F:GO:0003777; C:GO:0005829; P:GO:0006810; C:GO:0030286; C:GO:0005874; P:GO:0006200; F:GO:0005524; P:GO:0007018; F:GO:0016887; F:GO:0005515; C:GO:0005794	-		PD936484 (PRODOM), G3DSA:3.40.50.300 (GENE3D), PTHR10676 (PANTHER), PTHR10676:SF28 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-

Caenorhabditis briggsae	briggsae cbr-gck-4 protein	13	P:GO:0040010; P:GO:0000910; F:GO:0042802; F:GO:0005524; P:GO:0010171; P:GO:0032879; P:GO:0002119; P:GO:0040011; P:GO:0046777; P:GO:0010800; P:GO:0008283; C:GO:0005737; F:GO:0042801	-		IPR000719; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF67 (PANTHER)
Canis familiaris	phosphoribosyl transferase domain containing 1	0		P:GO:0009116; C:GO:0005737; P:GO:0006166; F:GO:0004422		-
	-	0				-
Brugia malayi	leucine rich repeat family protein	0		F:GO:0005515		IPR001611; G3DSA:3.80.10.10 (GENE3D), PTHR11375 (PANTHER), PS51450 (PROFILE), SSF52047 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	phosphorylase b ki-se	4	F:GO:0016301; F:GO:0004339; P:GO:0005977; F:GO:0005516	-	EC:3.2.1.3	IPR008734; IPR008928; IPR011613; PTHR10749:SF2 (PANTHER)
Loa loa	d- repair protein rad4 containing protein	1	P:GO:0006974	-		IPR004583; IPR018325; SSF54001 (SUPERFAMILY)
Caenorhabditis briggsae	r- (guanine-9-) methyltransferase domain containing 2	0				IPR007356; IPR016009; PTHR13563:SF6 (PANTHER)
Loa loa	gtpase activating protein and vps9 domains 1	0		F:GO:0005096; P:GO:0051056; P:GO:0007165; C:GO:0005622		-
	-	0				-
Pan troglodytes	t- immune regulator 1	8	F:GO:0015078; C:GO:0033177; C:GO:0005739; P:GO:0015986; P:GO:0006968; C:GO:0016324; P:GO:0008284; C:GO:0005887	-		-
Saccharomyces cerevisiae RM11-1a	proteoglycan 4	0		F:GO:0016787; C:GO:0016021; C:GO:0016020; F:GO:0008195		-
	-	0				-
	-	0				-
	-	0				-

Homo sapiens	proteasome (macropain) beta 10	9	P:GO:0051436; P:GO:0051437; F:GO:0004298; P:GO:0031145; P:GO:0006959; P:GO:0044419; C:GO:0005737; C:GO:0005839; C:GO:0005634	-	EC:3.4.25.0	IPR001353; G3DSA:3.60.20.10 (GENE3D), PTHR11599 (PANTHER), PTHR11599:SF1 (PANTHER), PS51476 (PROFILE), SSF56235 (SUPERFAMILY)
	-	0				IPR006578
Caenorhabditis elegans	- h exchanger family member (nhx-9)	6	P:GO:0009792; F:GO:0015385; P:GO:0055085; P:GO:0006885; C:GO:0016021; P:GO:0006814	-		IPR006153
	-	0				-
	-	0				-
Brugia malayi	nuclear hormone receptor family member (nhr-23)	3	F:GO:0004872; F:GO:0005488; P:GO:0006350	-		IPR000536; IPR001723; IPR008946; PTHR11865 (PANTHER), PTHR11865:SF176 (PANTHER)
	-	0				-
Aedes aegypti	bone morphogenetic protein receptor type	0		F:GO:0004675; P:GO:0007178; C:GO:0016020; F:GO:0004672; F:GO:0005024; P:GO:0006468; F:GO:0000166; F:GO:0005524; F:GO:0004872; F:GO:0004702		IPR000472; G3DSA:2.10.60.10 (GENE3D)
Brugia malayi	hypothetical protein [Brugia malayi]	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	eph receptor a2	0		P:GO:0048013; P:GO:0006468; P:GO:0048320; P:GO:0045765; P:GO:0030182; P:GO:0006915; F:GO:0005524; F:GO:0016301; C:GO:0016021; C:GO:0016020; F:GO:0004672; P:GO:0001570; F:GO:0004872; P:GO:0007169; F:GO:0000166; P:GO:0001525; P:GO:0007165; P:GO:0021915; P:GO:0043535; P:GO:0060035; F:GO:0005003; P:GO:0014028; F:GO:0004714; C:GO:0005887; F:GO:0005515; F:GO:0004713;		IPR001245; IPR011009; IPR020685; IPR020725
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0004601; F:GO:0004867; F:GO:0004447; P:GO:0030326; C:GO:0016021; P:GO:0007186; C:GO:0016020; P:GO:0009653; P:GO:0007218; F:GO:0005509; F:GO:0004872; F:GO:0004871; P:GO:0008218; P:GO:0007166; F:GO:0005488; P:GO:0007165; F:GO:0004888; F:GO:0004930; P:GO:0007160; P:GO:0055114; C:GO:0005578; C:GO:0005886; C:GO:0005576; F:GO:0016491; P:GO:0018298; F:GO:0005201		-
Caenorhabditis elegans	yms5_caeel ame: full=uncharacterized protein flags: precursor	0		P:GO:0007160; C:GO:0016021		IPR001846

	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0032012; C:GO:0005622; F:GO:0005086	-		-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis elegans	type alpha 1	2	F:GO:0005509; F:GO:0003824	-		IPR002035; G3DSA:3.40.50.410 (GENE3D), PTHR22992 (PANTHER), PTHR22992:SF9 (PANTHER), SSF53300 (SUPERFAMILY)
Xenopus (Silurana) tropicalis	heat shock cog-te 71 kda	2	F:GO:0005524; P:GO:0006950	-		IPR001023; IPR013126; G3DSA:2.60.34.10 (GENE3D), PTHR19375:SF1 (PANTHER), SSF100920 (SUPERFAMILY)
	-	0				-
Brugia malayi	endonuclease iii-like protein 1	5	P:GO:0006284; F:GO:0004519; F:GO:0003677; C:GO:0043231; F:GO:0051539	-		IPR003265; IPR011257; G3DSA:1.10.340.30 (GENE3D), PTHR10359 (PANTHER), PTHR10359:SF2 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Brugia malayi	chk1 checkpoint-like protein	0				-
Caenorhabditis briggsae	ubiquitin protein ligase e3 component n-recognin 2	5	F:GO:0005488; P:GO:0044267; F:GO:0016874; P:GO:0030163; C:GO:0044424	-		PTHR21497 (PANTHER), PTHR21497:SF6 (PANTHER)
	-	0				-
	-	0				-
Bombyx mori	endonuclease-reverse transcriptase	1	F:GO:0003824	-		-
	-	0				-
Caenorhabditis briggsae	calpain 5	6	P:GO:0042004; C:GO:0005622; F:GO:0004198; P:GO:0019099; P:GO:0006508; C:GO:0016020	-		IPR000169; IPR001300; IPR022684; PTHR10183 (PANTHER), PTHR10183:SF32 (PANTHER), SSF54001 (SUPERFAMILY)
Loa loa	2700029m09rik protein	0		F:GO:0003674; P:GO:0008150; C:GO:0005575		IPR019361; PTHR13386 (PANTHER)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG09473 [Caenorhabditis briggsae]	0		F:GO:0005509; P:GO:0007156; P:GO:0007155; C:GO:0016021; C:GO:0016020; C:GO:0005886		-
Caenorhabditis briggsae	tbc (tre-2 bub2 cdc16) domain family member (tbc-19)	0		P:GO:0032313; C:GO:0005622; F:GO:0005097		-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG11154 [Caenorhabditis briggsae]	0				-

Caenorhabditis elegans	yo93_caeel ame: full=uncharacterized protein	0		P:GO:0000003; P:GO:0040011; P:GO:0040010; P:GO:0006898; P:GO:0002119; P:GO:0009792; P:GO:0040018		-
	-	0				-
Brugia malayi	elegans protein confirmed by transcript evidence	0		P:GO:0000003; F:GO:0005488		IPR011990; PTHR12830 (PANTHER), PTHR12830:SF8 (PANTHER), SSF48452 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	intesti-l acid phosphatase protein partially confirmed by transcript evidence	0		C:GO:0016021; F:GO:0016787; C:GO:0016020; F:GO:0003993		IPR000560; G3DSA:3.40.50.1240 (GENE3D), PTHR11567 (PANTHER), PTHR11567:SF13 (PANTHER), SSF53254 (SUPERFAMILY)
Homo sapiens	immunoglobulin heavy chain variable region	0				IPR003596; IPR013106; IPR013783; PTHR23266 (PANTHER), PTHR23266:SF7 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	chromosome 20 open reading frame 54	0		P:GO:0032218; F:GO:0032217; P:GO:0034605; F:GO:0004872; C:GO:0016020; P:GO:0007605; C:GO:0005887; F:GO:0005515		-
Caenorhabditis elegans	phosphorylase b ki-se	3	F:GO:0004339; P:GO:0005977; F:GO:0005516	-	EC:3.2.1.3	-
Drosophila ananassae	GF18021 [Drosophila a--ssae]	0				IPR019955; G3DSA:3.10.20.90 (GENE3D), SSF54236 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG10792 [Caenorhabditis briggsae]	0		P:GO:0008152; F:GO:0003824		IPR004245; PTHR10974:SF5 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0006260; P:GO:0006281; F:GO:0003910; F:GO:0008270; P:GO:0006310		IPR019406
	-	0				-
Loa loa	breast cancer antiestrogen resistance 3	0		P:GO:0007264; F:GO:0005515; F:GO:0005085; C:GO:0005622		-
	-	0				-
Bacillus cereus AH1273	lpxtg-motif cell wall anchor domain protein	0		F:GO:0005488; C:GO:0009986		-
	-	0				-
	-	0				-
Caenorhabditis elegans	abc transporter family member (abt-2)	0				PTHR19229 (PANTHER), PTHR19229:SF25 (PANTHER)

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	6	F:GO:0004181; P:GO:0040003; P:GO:0007476; P:GO:0006911; P:GO:0007431; C:GO:0016020	-	EC:3.4.17.0	IPR004316; IPR018179
Homo sapiens	AF269289_1unknown [Homo sapiens]	8	P:GO:0060761; P:GO:0009887; P:GO:0032091; P:GO:0010553; F:GO:0003714; P:GO:0090090; P:GO:0070555; C:GO:0005634	-		SignalP (SIGNALP)
Homo sapiens	calreticulin	56	F:GO:0051087; P:GO:0045665; F:GO:0005506; F:GO:0051082; P:GO:0008284; C:GO:0016529; F:GO:0031625; C:GO:0005625; F:GO:0042562; F:GO:0044183; C:GO:0005829; F:GO:0001849; P:GO:0030866; F:GO:0005178; F:GO:0003729; C:GO:0005788; C:GO:0005615; P:GO:0007283; P:GO:0033144; C:GO:0005844; C:GO:0005792; P:GO:0042981; P:GO:0017148; P:GO:0033574; P:GO:0045740; P:GO:0002502; P:GO:0006611;	-		IPR001580; IPR008985; IPR009169; IPR013320; IPR018124
	-	0				SignalP (SIGNALP)
	-	0				-
Loa loa	chromosome condensation protein c-termi-l region containing protein	0		F:GO:0005488		IPR011989
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	multiple pdz domain protein family member (mpz-1)	3	C:GO:0016021; C:GO:0048471; F:GO:0005515	-		-
Caenorhabditis elegans	pleckstrin and sec7 domain containing 4	5	F:GO:0005086; P:GO:0032012; C:GO:0005622; C:GO:0005886; F:GO:0005515	-		IPR000904; G3DSA:1.10.1000.11 (GENE3D), PTHR10663 (PANTHER), PTHR10663:SF3 (PANTHER)
	-	0				-

Caenorhabditis briggsae	copine domain atypical protein isoform partially confirmed by transcript evidence	0				IPR005479
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	atp-binding sub-family a member 3	7	F:GO:0042626; C:GO:0005624; P:GO:0042493; C:GO:0005886; P:GO:0006810; C:GO:0042599; F:GO:0000166	-		IPR003439; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR19229 (PANTHER), PTHR19229:SF25 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	clathrin coat assembly protein ap-1	6	C:GO:0030135; P:GO:0016183; C:GO:0030131; P:GO:0007269; F:GO:0005515; P:GO:0006886	-		IPR001392; IPR008968; G3DSA:2.60.40.1170 (GENE3D), PTHR11998 (PANTHER), PTHR11998:SF11 (PANTHER)
Caenorhabditis elegans	clathrin coat assembly protein ap-1	6	C:GO:0030135; P:GO:0016183; C:GO:0030131; P:GO:0007269; F:GO:0005515; P:GO:0006886	-		IPR001392; IPR008968; IPR018240; G3DSA:2.60.40.1170 (GENE3D), PTHR11998 (PANTHER), PTHR11998:SF11 (PANTHER)
	-	0				-
Caenorhabditis elegans	uncoordi-ted family member (unc-22)	6	C:GO:0030018; P:GO:0006468; F:GO:0008307; P:GO:0007498; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR003599; IPR013098; IPR013783; PTHR19900 (PANTHER), PTHR19900:SF7 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	carbohydrate thermoresistant glucoki-se family	3	F:GO:0005488; F:GO:0016301; P:GO:0044238	-		IPR000623; G3DSA:3.40.50.300 (GENE3D), SSF52540 (SUPERFAMILY)
	-	0				G3DSA:3.40.50.1240 (GENE3D)
Caenorhabditis elegans	aspartyl glutamyl-tr-(asn gln) amidotransferase subunit	0		P:GO:0006450; F:GO:0016740		IPR003837; PTHR15004 (PANTHER), SSF141000 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-

Caenorhabditis elegans	briggsae cbr-nmy-1 protein	20	F:GO:0005516; F:GO:0008307; F:GO:0043531; F:GO:0000146; P:GO:0008360; P:GO:0048739; C:GO:0030016; C:GO:0030496; P:GO:0048251; F:GO:0051015; P:GO:0000281; C:GO:0001725; F:GO:0005524; C:GO:0032154; C:GO:0005938; P:GO:0006939; F:GO:0030898; P:GO:0030048; P:GO:0030241; C:GO:0032982	-		IPR001609; PTHR13140 (PANTHER), PTHR13140:SF23 (PANTHER), SSF52540 (SUPERFAMILY)
Homo sapiens	prosaposin	19	P:GO:0055085; F:GO:0008047; P:GO:0043065; P:GO:0006687; P:GO:0045161; C:GO:0016021; C:GO:0005743; C:GO:0043202; C:GO:0005615; F:GO:0008289; P:GO:0006869; F:GO:0005515; P:GO:0009966; P:GO:0007585; F:GO:0005319; C:GO:0005578; F:GO:0005529; P:GO:0006919; C:GO:0005794	-		IPR003119; IPR007856; IPR008138; IPR008139; IPR008373; IPR011001; PTHR11480 (PANTHER), PTHR11480:SF3 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	phosphoinositide 3-ki-se regulatory subunit 4	4	F:GO:0005515; F:GO:0016740; P:GO:0019915; C:GO:0005829	-		IPR011989
	-	0				-
Caenorhabditis elegans	dehydroge-se reductase sdr family member 4	4	F:GO:0008667; P:GO:0009239; P:GO:0055114; F:GO:0005488	-	EC:1.3.1.28	IPR002198; IPR002347; IPR016040; PTHR19410:SF67 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Camponotus floridanus	uncharacterized transposase-like protein	0		F:GO:0046872; P:GO:0055114; F:GO:0009055; F:GO:0016491; F:GO:0020037; F:GO:0005506; F:GO:0004497		-

Caenorhabditis elegans	tetratricopeptide repeat protein 35	7	F:GO:0005515; P:GO:0040017; P:GO:0040010; P:GO:0000003; P:GO:0006898; C:GO:0005783; C:GO:0005739	-		IPR011990; IPR013026; PTHR12760 (PANTHER), SSF48452 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	hypothetical protein Bm1_31385 [Brugia malayi]	0		F:GO:0005515		-
Homo sapiens	NM-4 [Homo sapiens]	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	acetyl-coenzyme a carboxylase alpha	3	F:GO:0016874; P:GO:0008152; F:GO:0000166	-		IPR005482; IPR011053; IPR011054; IPR011764; IPR013816; G3DSA:2.40.50.100 (GENE3D), PTHR18866 (PANTHER), PTHR18866:SF6 (PANTHER)
Caenorhabditis briggsae	mitochondrial thiamine pyrophosphate carrier	7	P:GO:0009792; F:GO:0005488; C:GO:0005743; P:GO:0040018; P:GO:0055085; C:GO:0016021; F:GO:0005215	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF34 (PANTHER)
	-	0				-
Caenorhabditis elegans	hif (hypoxia inducible factor) homolog family member (hif-1)	2	P:GO:0006350; P:GO:0050794	-		G3DSA:3.30.450.20 (GENE3D), PTHR23043 (PANTHER), PTHR23043:SF7 (PANTHER), SignalP (SIGNALP)
Loa loa	novel protein containing six wd40 domains at c-terminus	3	F:GO:0005515; P:GO:0050794; C:GO:0044464	-		IPR001680; IPR004083; IPR011046; IPR015943; IPR017986; IPR019782; PTHR12848:SF2 (PANTHER)
Caenorhabditis elegans	cation transporting atpase protein isoform partially confirmed by transcript evidence	5	C:GO:0016021; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0006812	-		IPR000150; IPR000695; IPR001757; G3DSA:3.40.50.1000 (GENE3D), PTHR11939:SF54 (PANTHER), SSF56784 (SUPERFAMILY)
Caenorhabditis elegans	cation transporting atpase protein isoform partially confirmed by transcript evidence	5	C:GO:0016021; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0006812	-		IPR000150; IPR000695; IPR001757; G3DSA:3.40.50.1000 (GENE3D), PTHR11939:SF54 (PANTHER), SSF56784 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	protein phosphatase regulatory subunit 11	0		F:GO:0004864; P:GO:0008152; F:GO:0003824; C:GO:0005625; F:GO:0005515		IPR011107
	-	0				-
	-	0				-

Caenorhabditis briggsae	briggsae cbr-pus-1 protein	0		F:GO:0003723; P:GO:0009451; F:GO:0009982		SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-pus-1 protein	0		F:GO:0003723; P:GO:0009451; F:GO:0009982		-
Caenorhabditis briggsae	briggsae cbr-pus-1 protein	0		F:GO:0003723; P:GO:0009451; F:GO:0009982		-
Caligus clemensi	transcription elongation factor b polypeptide 1	5	F:GO:0003746; P:GO:0006511; C:GO:0008023; F:GO:0005515; P:GO:0048813	-		-
Caenorhabditis elegans	tetratricopeptide repeat protein 4	7	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0040018; P:GO:0040010; P:GO:0040011; P:GO:0006898	-		PTHR22904 (PANTHER), PTHR22904:SF16 (PANTHER)
Caenorhabditis elegans	briggsae cbr-chs-1 protein	4	P:GO:0009792; P:GO:0000003; C:GO:0005887; P:GO:0040010	-		-
Brugia malayi	rwd domain containing protein	0		F:GO:0046872; F:GO:0008270; F:GO:0005515		-
Caenorhabditis elegans	spermine spermidine synthase family protein	2	F:GO:0016740; F:GO:0005515	-		PTHR12176 (PANTHER)
Brugia malayi	hypothetical protein [Brugia malayi]	0				-
Caenorhabditis briggsae	Hypothetical protein CBG04176 [Caenorhabditis briggsae]	0				IPR019128
Brugia malayi	kinetochore-associated protein 1 (rough deal homolog)	4	P:GO:0000278; C:GO:0005856; P:GO:0022402; C:GO:0044446	-		-
	-	0				-
Caenorhabditis briggsae	amidophosphoribosyltransferase	10	P:GO:0007595; P:GO:0031100; P:GO:0032869; P:GO:0006164; C:GO:0005625; P:GO:0009116; P:GO:0060135; P:GO:0051289; F:GO:0004044; P:GO:0009113	-	EC:2.4.2.14	IPR000583; IPR000836; IPR005854; IPR017932; G3DSA:3.40.50.2020 (GENE3D), G3DSA:3.60.20.10 (GENE3D), SSF53271 (SUPERFAMILY), SSF56235 (SUPERFAMILY)
Brugia malayi	metallo-beta-lactamase superfamily protein	0		F:GO:0046872; F:GO:0003674; P:GO:0008152; F:GO:0016787; P:GO:0008150; C:GO:0005575		IPR001279; G3DSA:3.60.15.10 (GENE3D), PTHR23200 (PANTHER), PTHR23200:SF10 (PANTHER), SSF56281 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	gex interacting protein family member (gei-3)	0		C:GO:0005634		-
	-	0				-

	-	0				-
Haemonchus contortus	glutamate dehydroge-se	22	C:GO:0009331; P:GO:0007629; F:GO:0004353; P:GO:0046168; P:GO:0040010; C:GO:0005759; P:GO:0006127; P:GO:0046693; C:GO:0005576; F:GO:0050660; P:GO:0006006; F:GO:0051287; F:GO:0004344; P:GO:0008364; P:GO:0009060; F:GO:0004367; P:GO:0006116; F:GO:0004352; P:GO:0006641; F:GO:0042803; C:GO:0005811; P:GO:0019551	-	EC:1.4.1.3; EC:1.1.99.10; EC:1.1.1.8; EC:1.4.1.2	IPR006095; IPR006096; IPR006097; IPR014362; IPR016040; G3DSA:3.40.192.10 (GENE3D), PTHR11606 (PANTHER), SSF51735 (SUPERFAMILY), SSF53223 (SUPERFAMILY)
	-	0				-
Caenorhabditis brenneri	syntaxin-18	8	P:GO:0002119; F:GO:0005515; P:GO:0006810; P:GO:0040010; P:GO:0000003; P:GO:0040011; P:GO:0009987; C:GO:0016021	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	P:GO:0007411; P:GO:0007413	-		IPR001841; IPR013083; PTHR21578 (PANTHER)
Ostertagia ostertagi	fatty acid and retinol-binding protein 1	4	C:GO:0005576; F:GO:0005504; F:GO:0005515; F:GO:0019841	-		IPR008632; SignalP (SIGNALP)
Ostertagia ostertagi	fatty acid and retinol-binding protein 1	4	C:GO:0005576; F:GO:0005504; F:GO:0005515; F:GO:0019841	-		IPR008632

Brugia malayi	protein phosphatase catalytic gamma isoform	23	P:GO:0046822; C:GO:0043197; P:GO:0007275; C:GO:0016607; F:GO:0019901; P:GO:0007084; C:GO:0005624; C:GO:0000777; P:GO:0051301; P:GO:0005977; C:GO:0005730; C:GO:0005829; C:GO:0005741; F:GO:0046872; P:GO:0007067; F:GO:0042802; P:GO:0007126; C:GO:0070688; P:GO:0006470; C:GO:0005625; P:GO:0016568; C:GO:0045202; F:GO:0004722	-		IPR004843; IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF19 (PANTHER), SSF56300 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-bam-2 protein	1	C:GO:0005887	-		-
	-	0				IPR000436
Loa loa	pre-mr--splicing factor 18	3	F:GO:0019870; C:GO:0044428; P:GO:0006396	-		IPR004098; IPR014906; PTHR13007 (PANTHER), PTHR13007:SF7 (PANTHER)
Caenorhabditis elegans	ead transcription factor family member (fkh-7)	6	F:GO:0003700; F:GO:0043565; P:GO:0000003; C:GO:0005634; F:GO:0008270; P:GO:0006355	-		IPR001766; IPR011991; IPR018122; SSF46785 (SUPERFAMILY)
	-	0				IPR000477
Caenorhabditis elegans	phospholipase b	1	F:GO:0016787	-		IPR001087; IPR013830; IPR013831; PTHR21325 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	major facilitator superfamily protein	4	P:GO:0019915; C:GO:0016021; P:GO:0055085; F:GO:0005215	-		IPR011701; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11662 (PANTHER), PTHR11662:SF21 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG22271 [Caenorhabditis briggsae]	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	solute carrier family member 1	2	C:GO:0016020; P:GO:0006865	-		IPR006047; IPR013781; IPR017853; G3DSA:3.90.400.10 (GENE3D), PTHR10357 (PANTHER), PTHR10357:SF11 (PANTHER)
Caenorhabditis elegans	solute carrier family member 1	2	C:GO:0016020; P:GO:0006865	-		IPR013032

Brugia malayi	bloom syndrome protein	26	P:GO:0000085; P:GO:0031572; C:GO:0000781; F:GO:0002039; P:GO:0045910; P:GO:0045941; P:GO:0010165; C:GO:0016605; P:GO:0000724; P:GO:0051276; P:GO:0031297; C:GO:0005737; P:GO:0000079; C:GO:0005730; P:GO:0046631; P:GO:0051259; P:GO:0051782; F:GO:0000739; P:GO:0048478; F:GO:0051880; C:GO:0000800; C:GO:0016363; F:GO:0004003; F:GO:0000405; F:GO:0005524; F:GO:0009378	-		IPR004589; IPR011545; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR13710:SF14 (PANTHER), SSF52540 (SUPERFAMILY)
Callithrix jacchus	ergic and golgi 3	6	C:GO:0005789; C:GO:0005794; F:GO:0005515; P:GO:0016192; C:GO:0016021; C:GO:0033116	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-ugt-25 protein	0		F:GO:0016740; F:GO:0030246; C:GO:0016021; F:GO:0003700; C:GO:0005634; F:GO:0016758; F:GO:0016757; P:GO:0005975; P:GO:0030259; P:GO:0006355; P:GO:0008152; P:GO:0045449		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	sphingomyelin phosphodiesterase	4	P:GO:0046513; F:GO:0004767; C:GO:0005576; P:GO:0006685	-	EC:3.1.4.12	-
Caenorhabditis briggsae	briggsae cbr-ncl-1 protein	2	F:GO:0005515; F:GO:0046872	-		-
	-	0				IPR002870
	-	0				-

Caenorhabditis elegans	dsh homolog 3	21	C:GO:0031410; P:GO:0051641; N:GO:2000026; C:GO:0043005; P:GO:0016055; P:GO:0042325; P:GO:0043009; P:GO:0044238; P:GO:0044260; P:GO:0002009; P:GO:0007409; P:GO:0023060; P:GO:0050877; P:GO:0050808; F:GO:0042802; C:GO:0000267; P:GO:0065008; P:GO:0007154; P:GO:0006928; P:GO:0048598; P:GO:0009887	-		IPR000591; IPR001478; IPR011991; IPR015506; G3DSA:2.30.42.10 (GENE3D), PTHR10878:SF1 (PANTHER), SSF46785 (SUPERFAMILY)
Caenorhabditis briggsae	rnp-1 like r--binding protein	3	F:GO:0003676; P:GO:0009792; F:GO:0000166	-		-
Homo sapiens	isoform cra_b	10	F:GO:0008270; C:GO:0005739; F:GO:0030145; P:GO:0006355; P:GO:0010815; F:GO:0003677; P:GO:0006508; F:GO:0070006; F:GO:0042803; C:GO:0005634	-		PTHR14360 (PANTHER), PTHR14360:SF2 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Homo sapiens	PREDICTED: hypothetical protein XP_002343485 [Homo sapiens]	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis briggsae	tetratricopeptide repeat domain 17	2	P:GO:0040010; P:GO:0040017	-		-
Loa loa	stat d- binding domain containing protein	0		P:GO:0006355; F:GO:0005509; F:GO:0004871; P:GO:0045449; P:GO:0007165; F:GO:0005515; F:GO:0003700; C:GO:0005634		-
Aedes aegypti	ubiquitin-conjugating enzyme e2-230k	0		P:GO:0051246; P:GO:0043687; F:GO:0019787		IPR000608; IPR016135; PTHR11621 (PANTHER), PTHR11621:SF13 (PANTHER)
Caenorhabditis briggsae	rho gtpase activating protein family member (rga-4)	0		P:GO:0007165; C:GO:0005622		IPR000198; IPR008936; PTHR15670 (PANTHER)
	-	0				-

Caenorhabditis elegans	ankyrin repeat domain protein	2	F:GO:0005488; F:GO:0003824	-		IPR002110; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER), PTHR18958:SF241 (PANTHER)
Caenorhabditis elegans	scy1 protein ki-se	3	P:GO:0006468; F:GO:0005524; F:GO:0004672	-		-
	-	0				-
Caenorhabditis elegans	argo-ute protein group	1	P:GO:0000003	-		IPR003100; G3DSA:2.170.260.10 (GENE3D), PTHR22891 (PANTHER), SSF101690 (SUPERFAMILY)
Caenorhabditis elegans	argo-ute protein group	1	P:GO:0000003	-		IPR003100; G3DSA:2.170.260.10 (GENE3D), PTHR22891 (PANTHER), SSF101690 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	rho gtpase activating protein 29	3	F:GO:0046872; P:GO:0007165; C:GO:0005622	-		PTHR15228 (PANTHER), PTHR15228:SF7 (PANTHER)
Caenorhabditis elegans	3 exoribonuclease domain 2 containing protein	0		F:GO:0003723; P:GO:0006402; C:GO:0005739; F:GO:0004654; P:GO:0006396; F:GO:0000175		IPR003029; IPR012162; IPR012340; IPR015847; IPR016027; SSF54791 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	d--repair protein complementing xp-g cells	7	P:GO:0009411; P:GO:0006289; F:GO:0004519; F:GO:0003677; F:GO:0005515; C:GO:0005654; P:GO:0009792	-		IPR001044; IPR006084; IPR006085; G3DSA:3.40.50.1010 (GENE3D), SSF88723 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0000003; C:GO:0005856; F:GO:0005198; C:GO:0044297; C:GO:0031143; P:GO:0019915; P:GO:0040018		SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	3	C:GO:0034703; F:GO:0005261; P:GO:0055080	-		-
	-	0				-
Angiostrongylus cantonensis	col-184	0		C:GO:0016021; F:GO:0042302		IPR008160; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-vha-5 protein	5	F:GO:0015078; F:GO:0005516; C:GO:0033177; P:GO:0015986; C:GO:0045202	-		IPR002490; PTHR11629:SF1 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-

Caenorhabditis elegans	solute carrier family 15 (h+ peptide transporter) member 2	9	C:GO:0005887; F:GO:0042936; C:GO:0005624; F:GO:0042895; P:GO:0006855; F:GO:0015334; F:GO:0005515; P:GO:0042938; P:GO:0042891	-		IPR000109; IPR016196; IPR018456; PTHR11654 (PANTHER), PTHR11654:SF12 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				G3DSA:3.10.20.90 (GENE3D)
Caenorhabditis briggsae	g-patch domain containing protein	3	P:GO:0019915; P:GO:0010171; P:GO:0002119	-		-
Caenorhabditis elegans	lethal family member (let-2)	3	C:GO:0005587; F:GO:0030020; P:GO:0016043	-		IPR008160; PTHR10499 (PANTHER), PTHR10499:SF114 (PANTHER)
	-	0				-
Caenorhabditis elegans	downstream of receptor ki-se	13	P:GO:0007265; P:GO:0008360; P:GO:0007613; P:GO:0008355; P:GO:0045500; P:GO:0007015; P:GO:0001700; P:GO:0008293; P:GO:0008595; F:GO:0005070; C:GO:0005886; F:GO:0005118; P:GO:0007476	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	heparan sulfate 3-o-sulfotransferase isoform cra_a	2	P:GO:0019915; F:GO:0016740	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0008107; P:GO:0005975; C:GO:0016021; C:GO:0016020		IPR002516; PTHR22898 (PANTHER)
	-	0				-
Brugia malayi	moz sas family protein	0		F:GO:0046872; P:GO:0045449; F:GO:0008270; F:GO:0016747; F:GO:0005515; C:GO:0005634		IPR001965; IPR013083

Caenorhabditis briggsae	moz sas family protein	0		C:GO:0000792; C:GO:0000791; C:GO:0005634; F:GO:0003677; F:GO:0003676; P:GO:0048477; F:GO:0046872; F:GO:0030528; P:GO:0016458; F:GO:0003682; P:GO:0045449; F:GO:0016747; C:GO:0005700; P:GO:0045893; P:GO:0045892; F:GO:0008270; C:GO:0005622; F:GO:0005515		IPR001965; IPR011011; IPR013083; IPR017956; IPR019786
	-	0				SignalP (SIGNALP)
Pongo abelii	lamin a c	13	C:GO:0005626; C:GO:0016363; P:GO:0006998; P:GO:0035105; C:GO:0005638; P:GO:0007517; P:GO:0007283; N:GO:0090343; P:GO:0055015; F:GO:0005515; C:GO:0048471; C:GO:0005635; F:GO:0005198	-		IPR001322; IPR001664; G3DSA:2.60.40.1260 (GENE3D), PTHR23239:SF12 (PANTHER), SSF74853 (SUPERFAMILY)
Ajellomyces capsulatus H143	calmodulin-binding coil-coil protein	0		P:GO:0055114; F:GO:0016491; F:GO:0032440; F:GO:0003774; C:GO:0016459		-
Caenorhabditis elegans	tyrosine-protein ki-se pr2	9	F:GO:0004674; P:GO:0035071; P:GO:0042059; P:GO:0040027; F:GO:0005524; F:GO:0005515; F:GO:0004715; P:GO:0009792; P:GO:0006468	-	EC:2.7.11.0; EC:2.7.10.2	IPR000719; IPR001245; IPR011009; IPR020685; G3DSA:1.10.510.10 (GENE3D), PTHR23256:SF266 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG01593 [Caenorhabditis briggsae]	3	C:GO:0016020; P:GO:0023052; F:GO:0004872	-		-

Homo sapiens	enolase 1	14	P:GO:0009615; C:GO:0000015; P:GO:0000122; F:GO:0003714; F:GO:0004252; C:GO:0031430; F:GO:0004634; P:GO:0006096; F:GO:0003677; P:GO:0030308; F:GO:0000287; F:GO:0003700; C:GO:0005886; C:GO:0005634	-	EC:3.4.21.0; EC:4.2.1.11	IPR000941; IPR001354; IPR020809; IPR020810; G3DSA:3.20.20.120 (GENE3D), SSF51604 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	rhomboid family 1	7	F:GO:0008233; C:GO:0012505; C:GO:0005794; C:GO:0031090; C:GO:0016021; C:GO:0005783; C:GO:0044446	-		IPR002610; IPR022764; G3DSA:1.20.1540.10 (GENE3D), SSF144091 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	yqk3_caeel ame: full=uncharacterized protein	2	P:GO:0000003; P:GO:0006898	-		IPR007356; PTHR13563:SF4 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	programmed cell death 8	5	P:GO:0045454; F:GO:0050660; C:GO:0005737; P:GO:0055114; F:GO:0016491	-		IPR004099; IPR016156; G3DSA:3.50.50.60 (GENE3D), PTHR22912 (PANTHER), PTHR22912:SF32 (PANTHER)
Ostertagia ostertagi	hypothetical protein jmo23 [Ostertagia ostertagi]	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	amin (actin binding protein) alpha family member (fl--1)	0		F:GO:0003676; F:GO:0000166		PTHR11915 (PANTHER), PTHR11915:SF55 (PANTHER)
Caenorhabditis elegans	procollagen- -oxoglutarate 5-dioxyge-se 3	7	P:GO:0008045; F:GO:0031418; F:GO:0005506; P:GO:0055114; F:GO:0016702; F:GO:0008475; C:GO:0005783	-	EC:1.13.11.0; EC:1.14.11.4	IPR008266
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	4	P:GO:0040035; P:GO:0018991; P:GO:0008340; P:GO:0002009	-		IPR002259; PTHR10332:SF6 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	F:GO:0030170; P:GO:0006520; F:GO:0016829	-		IPR001597; IPR015421; IPR015424; PTHR10289 (PANTHER)

Caenorhabditis briggsae	26s protease regulatory subunit 7	15	F:GO:0008233; P:GO:0008340; C:GO:0000502; P:GO:0051436; P:GO:0051437; P:GO:0000003; P:GO:0031145; F:GO:0005524; P:GO:0002119; F:GO:0016887; F:GO:0005515; P:GO:0044419; P:GO:0009792; C:GO:0005737; C:GO:0005634	-		-
	-	0				-
Caenorhabditis elegans	briggsae cbr-set-14 protein	0		F:GO:0046872; F:GO:0008270		-
	-	0				-
Caenorhabditis elegans	neuron -vigator 3	0		F:GO:0005216; F:GO:0005244; C:GO:0016021; F:GO:0005272; P:GO:0006814; P:GO:0006811; P:GO:0006810; F:GO:0000166; F:GO:0017111; F:GO:0005524; P:GO:0034765; C:GO:0031012; F:GO:0008201; P:GO:0007049; P:GO:0034220		IPR001715; PTHR12784 (PANTHER), PTHR12784:SF1 (PANTHER)
Caenorhabditis briggsae	uncoordi-ted family member (unc-2)	0				-
Hydra magnipapillata	sumo ligase	0		P:GO:0048589; P:GO:0001701; C:GO:0005634; P:GO:0007296; F:GO:0046872; F:GO:0016874; P:GO:0001570; P:GO:0003007; P:GO:0048844; P:GO:0008150; P:GO:0048146; P:GO:0045944; C:GO:0005737; P:GO:0045449; P:GO:0007569; C:GO:0016607; F:GO:0008270; F:GO:0005515; C:GO:0005575		-

synthetic construct	cytochrome c oxidase subunit viib	6	P:GO:0034220; P:GO:0015992; C:GO:0016021; P:GO:0008152; F:GO:0004129; C:GO:0005746	-	EC:1.9.3.1	IPR008433; G3DSA:4.10.51.10 (GENE3D), SSF81423 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Zea mays	protein	0				-
Sorghum bicolor	hypothetical protein SORBIDRAFT_01g024221 [Sorghum bicolor]	0				-
Sorghum bicolor	hypothetical protein SORBIDRAFT_01g024221 [Sorghum bicolor]	0				-
Zea mays	protein	0				-
Pisum sativum	senescence-associated protein	0				
Pisum sativum	senescence-associated protein	0				-
Caenorhabditis briggsae	senescence-associated protein	0				
Tetrahymena thermophila	senescence-associated protein	0				-
Tetrahymena thermophila	senescence-associated protein	0				-
Tetrahymena thermophila	senescence-associated protein	0				-
Tetrahymena thermophila	senescence-associated protein	0				-
Caenorhabditis briggsae	Hypothetical protein CBG11901 [Caenorhabditis briggsae]	0				
Tetrahymena thermophila	senescence-associated protein	0				-
Tetrahymena thermophila	senescence-associated protein	0				-
Ancylostoma caninum	surface-associated antigen 1	0				PD031131 (PRODOM), SignalP (SIGNALP)
Caenorhabditis elegans	a-ki-se-anchor-protein 84	3	F:GO:0003723; P:GO:0009792; P:GO:0008340	-		IPR002999; IPR004087; IPR004088; IPR008191; IPR018111; IPR018351; G3DSA:2.30.30.140 (GENE3D), G3DSA:3.30.1370.10 (GENE3D), PTHR12727 (PANTHER), SSF54791 (SUPERFAMILY), SSF63748 (SUPERFAMILY)
Caenorhabditis elegans	a-ki-se-anchor-protein 84	3	F:GO:0003723; P:GO:0009792; P:GO:0008340	-		IPR002999; IPR004087; IPR004088; IPR008191; IPR018111; IPR018351; G3DSA:2.30.30.140 (GENE3D), G3DSA:3.30.1370.10 (GENE3D), PTHR12727 (PANTHER), SignalP (SIGNALP), SSF54791 (SUPERFAMILY), SSF63748 (SUPERFAMILY)
Caenorhabditis elegans	a-ki-se-anchor-protein 84	3	F:GO:0003723; P:GO:0009792; P:GO:0008340	-		IPR002999; IPR004087; IPR004088; IPR008191; IPR018111; IPR018351; G3DSA:2.30.30.140 (GENE3D), G3DSA:3.30.1370.10 (GENE3D), PTHR12727 (PANTHER), SSF54791 (SUPERFAMILY), SSF63748 (SUPERFAMILY)
Caenorhabditis brenneri	ubr4 protein	2	F:GO:0005488; C:GO:0044464	-		PTHR21725 (PANTHER)
	-	0				-
Caenorhabditis elegans	subfamily member 5	2	F:GO:0046872; P:GO:0000003	-		IPR007087; IPR015609; IPR015880; IPR022755; PTHR11821:SF10 (PANTHER), SSF57667 (SUPERFAMILY)

Caenorhabditis elegans	isoform a	2	C:GO:0016021; F:GO:0005509	-		IPR000033; IPR000152; IPR001881; IPR011042; IPR013032; IPR013091; IPR018097; G3DSA:2.10.25.10 (GENE3D), PTHR10529 (PANTHER), SSF57196 (SUPERFAMILY), SSF63825 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	human a1 homolog family member (hrp-1)	0		F:GO:0003676; F:GO:0000166; C:GO:0030529		IPR000504; IPR012677; PTHR10432 (PANTHER), SignalP (SIGNALP), SSF54928 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				IPR013090
Taeniopygia guttata	u5 small nuclear ribonucleoprotein 40 kda protein	4	P:GO:0008380; F:GO:0005515; C:GO:0044428; C:GO:0030529	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	briggsae cbr-vps- protein	1	F:GO:0005515	-		IPR001619; PTHR11679:SF1 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Canis familiaris	alpha 1c	7	P:GO:0007018; F:GO:0005525; F:GO:0005515; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000217; IPR002452; IPR003008; IPR008280; IPR018316; IPR023123; PTHR11588:SF11 (PANTHER)
Canis familiaris	alpha 1c	7	P:GO:0007018; F:GO:0005525; F:GO:0005515; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000217; IPR002452; IPR003008; IPR008280; IPR018316; IPR023123; PTHR11588:SF11 (PANTHER)
	-	0				-

Loa loa	rap ran-gap family protein	23	P:GO:0032956; C:GO:0043005; P:GO:0043491; P:GO:0007169; C:GO:0043234; P:GO:0035467; P:GO:0044087; P:GO:0021987; C:GO:0005829; C:GO:0045121; C:GO:0043231; P:GO:0006469; P:GO:0045184; P:GO:0006897; P:GO:0042221; P:GO:0009968; N:GO:0071844; P:GO:0008285; P:GO:0014065; P:GO:0051259; F:GO:0046983; F:GO:0005096; C:GO:0005624	-		IPR018515; SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr--s-5 protein	0		F:GO:0046872; P:GO:0006508; F:GO:0008237; F:GO:0016787; F:GO:0008233; F:GO:0004222; F:GO:0008270; P:GO:0007413		G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF73 (PANTHER)
Callithrix jacchus	transmembrane emp24 protein transport domain containing 9	4	C:GO:0016021; C:GO:0005789; C:GO:0005793; P:GO:0006810	-		-
Loa loa	phosphoesterase pa-phosphatase related	1	C:GO:0016020	-		IPR000326; IPR016118; PTHR14969 (PANTHER), PTHR14969:SF3 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	nop14 nucleolar protein homolog	3	P:GO:0009792; P:GO:0002119; P:GO:0006898	-		SignalP (SIGNALP)
Caenorhabditis brenneri	arv1 homolog (cerevisiae)	1	P:GO:0009792	-		IPR007290
	-	0				-
Taeniopygia guttata	an1-type zinc finger protein 1	0		F:GO:0046872; F:GO:0003674; P:GO:0008150; F:GO:0008270; C:GO:0005575		IPR000058; PTHR14677 (PANTHER), PTHR14677:SF3 (PANTHER), SSF118310 (SUPERFAMILY)
Brugia malayi	nematode astacin protease protein 30	3	F:GO:0004222; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	-
	-	0				-

	-	0				-
Caenorhabditis briggsae	briggsae cbr-sfxn-2 protein	4	F:GO:0008324; P:GO:0055085; P:GO:0006812; C:GO:0016020	-		IPR004686; PTHR11153:SF7 (PANTHER)
Caenorhabditis elegans	eif4e binding protein	5	P:GO:0006629; P:GO:0040010; P:GO:0000003; P:GO:0006898; C:GO:0042995	-		PTHR13237 (PANTHER), PTHR13237:SF3 (PANTHER)
Brugia malayi	lim domain containing protein	0		F:GO:0046872; F:GO:0008270		-
	-	0				-
Pongo abelii	adp-ribosylation-like factor 6 interacting protein 4	2	C:GO:0005634; P:GO:0008380	-		-
	-	0				-
Caenorhabditis elegans	nucleolar atpase	5	P:GO:0009792; P:GO:0040007; P:GO:0040035; P:GO:0002119; P:GO:0040011	-		-
Homo sapiens	-dh dehydroge-se	6	P:GO:0006814; F:GO:0008137; C:GO:0005747; P:GO:0006120; F:GO:0005515; C:GO:0005759	-	EC:1.6.5.3	PTHR12126 (PANTHER), PTHR12126:SF1 (PANTHER)
	-	0				-
Caenorhabditis briggsae	d- polymerase zeta catalytic subunit	0		P:GO:0010224; F:GO:0016740; F:GO:0003677; P:GO:0006260; F:GO:0003676; F:GO:0000166; F:GO:0003887; P:GO:0006281; F:GO:0016779; C:GO:0016035; P:GO:0009411; P:GO:0006139		IPR012337; PTHR10322 (PANTHER), PTHR10322:SF5 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	trio and f-actin binding protein	2	F:GO:0019899; C:GO:0044424	-		-
Caenorhabditis elegans	teneurin family member (ten-1)	0				-
Loa loa	melibiase family protein	1	F:GO:0016787	-		IPR002241; IPR013785; IPR017853; PTHR11452 (PANTHER)
Caenorhabditis elegans	briggsae cbr-opt-2 protein	0		P:GO:0006857; F:GO:0015198; C:GO:0016021; C:GO:0016020; F:GO:0005215; P:GO:0006810		SignalP (SIGNALP)
	-	0				IPR016186; IPR016187
	-	0				-

Caenorhabditis briggsae	flightless i homolog	5	C:GO:0005730; P:GO:0006936; F:GO:0003779; P:GO:0007275; C:GO:0005813	-		IPR007122; IPR007123; G3DSA:3.40.20.10 (GENE3D), PTHR11977:SF6 (PANTHER), SSF55753 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	myosin heavy chain	4	F:GO:0003779; C:GO:0016459; F:GO:0005524; F:GO:0003774	-		IPR002928
	-	0				-
	-	0				-
Caenorhabditis elegans	biotin protein ligase family member (bpl-1)	0				-
Caenorhabditis elegans	biotin protein ligase family member (bpl-1)	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	10	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040002; P:GO:0040011; C:GO:0005576; P:GO:0019915; P:GO:0040007; P:GO:0006898; F:GO:0042302	-		IPR002486; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER), SignalP (SIGNALP)
Xenopus laevis	lim domain only 4	11	P:GO:0045665; P:GO:0007369; F:GO:0008270; F:GO:0003712; P:GO:0007498; P:GO:0030900; C:GO:0005667; P:GO:0001843; P:GO:0031076; F:GO:0003700; P:GO:0045944	-		-
Caenorhabditis briggsae	mitochondrial carrier protein	6	F:GO:0005488; C:GO:0005743; F:GO:0015226; P:GO:0055085; C:GO:0016021; P:GO:0019915	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF75 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-ing-3 protein	2	F:GO:0005515; F:GO:0046872	-		PTHR10333 (PANTHER), PTHR10333:SF12 (PANTHER)
Caenorhabditis briggsae	transmembrane amino acid transporter protein	4	P:GO:0019915; C:GO:0016020; P:GO:0040010; P:GO:0040011	-		IPR013057; PTHR22950 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				IPR006849
Tribolium castaneum	cg31751 cg31751-pa	0		F:GO:0016301; C:GO:0005737; F:GO:0016740		IPR002575; IPR011009; G3DSA:3.90.1200.10 (GENE3D)
	-	0				-

Caenorhabditis briggsae	cation transporting atpase protein isoform partially confirmed by transcript evidence	6	P:GO:0046034; P:GO:0006811; F:GO:0016820; F:GO:0016887; F:GO:0000166; C:GO:0016020	-	EC:3.6.3.0	IPR001757; IPR004014; IPR008250; G3DSA:2.70.150.10 (GENE3D), PTHR11939:SF54 (PANTHER), PF12409 (PFAM), SSF81653 (SUPERFAMILY), SSF81665 (SUPERFAMILY)
Caenorhabditis briggsae	cation-transporting atpase	2	F:GO:0016820; F:GO:0016887	-	EC:3.6.3.0	IPR001757; IPR004014; IPR008250; G3DSA:2.70.150.10 (GENE3D), PTHR11939:SF54 (PANTHER), PF12409 (PFAM), SSF81653 (SUPERFAMILY), SSF81665 (SUPERFAMILY)
Caenorhabditis briggsae	ophagy (yeast atg homolog) family member (atg-2)	0				PTHR13190 (PANTHER), PTHR13190:SF2 (PANTHER)
Caenorhabditis elegans	hypothetical protein F23F1.9 [Caenorhabditis elegans]	4	P:GO:0040035; P:GO:0002119; P:GO:0040007; P:GO:0006898	-		IPR009668
Caenorhabditis elegans	d--directed r- polymerase ii largest subunit	6	F:GO:0003899; F:GO:0003677; P:GO:0006350; F:GO:0032549; C:GO:0005634; F:GO:0008270	-	EC:2.7.7.6	IPR007081; IPR015700; PTHR19376 (PANTHER), SSF64484 (SUPERFAMILY)
Caenorhabditis briggsae	variable abnormal morphology family member (vab-10)	0		F:GO:0005509; P:GO:0007050; F:GO:0003779		PTHR11915 (PANTHER), PTHR11915:SF49 (PANTHER), SSF75399 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	4	C:GO:0016021; P:GO:0008340; F:GO:0005337; P:GO:0006810	-		IPR002259; PTHR10332:SF6 (PANTHER)
Caenorhabditis elegans	briggsae cbr-cdt-1 protein	9	C:GO:0005737; P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0006260; P:GO:0001703; P:GO:0040011; P:GO:0040007; C:GO:0005634	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	solute carrier family member 1	0		C:GO:0016021; C:GO:0016020; F:GO:0008324; P:GO:0006812; P:GO:0006811; P:GO:0006810; F:GO:0003674; C:GO:0005575; P:GO:0008150; C:GO:0005886; P:GO:0034220		PTHR16228 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	mitochondrial ribosomal protein s23	5	P:GO:0009792; P:GO:0002119; P:GO:0018991; P:GO:0040010; P:GO:0006898	-		IPR019520; PF10484 (PFAM)
	-	0				-
Loa loa	nucleolar r--associated protein alpha	0				SignalP (SIGNALP)
Caenorhabditis briggsae	carnitine o-acyltransferase	1	F:GO:0016740	-		IPR000542; PTHR22589:SF8 (PANTHER), SSF52777 (SUPERFAMILY)
	-	0				IPR014044
Caenorhabditis elegans	ophagy (yeast atg homolog) family member (atg-2)	0				-
	-	0				-
Caenorhabditis briggsae	cytochrome c oxidase copper chaperone	4	C:GO:0005758; P:GO:0006825; F:GO:0008047; F:GO:0016531	-		IPR007745; IPR009069
Brugia malayi	myosin heavy nonmuscle or smooth muscle	4	F:GO:0003779; C:GO:0016459; F:GO:0005524; F:GO:0003774	-		IPR001609; PTHR13140 (PANTHER), PTHR13140:SF23 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				IPR000436; IPR016060; SignalP (SIGNALP)
Loa loa	elegans protein partially confirmed by transcript evidence	3	P:GO:0009792; P:GO:0000003; P:GO:0040010	-		PTHR13847 (PANTHER), PTHR13847:SF12 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	tfiih complex helicase	5	F:GO:0003677; F:GO:0004003; F:GO:0005524; P:GO:0006289; C:GO:0005634	-		IPR001945; IPR002464; IPR010614; IPR010643; IPR014013; PTHR11472 (PANTHER), PTHR11472:SF1 (PANTHER)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG05033 [Caenorhabditis briggsae]	0		P:GO:0008152; F:GO:0016787		-
	-	0				SignalP (SIGNALP)
Loa loa	general transcription factor polypeptide 62kda	0		P:GO:0006367; F:GO:0016251; F:GO:0016740; P:GO:0008152; C:GO:0005675; P:GO:0008150; C:GO:0005575		PTHR12856 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	2	P:GO:0006629; F:GO:0004806	-	EC:3.1.1.3	-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-

Brugia malayi	atp-dependent d- helicase q5	4	F:GO:0004386; C:GO:0005634; F:GO:0000166; P:GO:0006281	-		IPR001650; IPR004589; G3DSA:3.40.50.300 (GENE3D), PTHR13710:SF6 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-rcq-5 protein	5	F:GO:0005525; F:GO:0017116; P:GO:0006974; F:GO:0003924; P:GO:0045930	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR002464; IPR004589; IPR011545; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR13710:SF6 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-rcq-5 protein	5	F:GO:0005525; F:GO:0017116; P:GO:0006974; F:GO:0003924; P:GO:0045930	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR002464; IPR004589; IPR011545; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR13710:SF6 (PANTHER), SSF52540 (SUPERFAMILY)
Brugia malayi	atp-dependent d- helicase q5	4	F:GO:0004386; C:GO:0005634; F:GO:0000166; P:GO:0006281	-		IPR001650; IPR004589; G3DSA:3.40.50.300 (GENE3D), PTHR13710:SF6 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	general transcription factor iih subunit 2	17	P:GO:0006367; P:GO:0000718; F:GO:0008094; P:GO:0002031; F:GO:0008270; P:GO:0040010; P:GO:0040011; F:GO:0047485; P:GO:0009411; C:GO:0005675; P:GO:0009792; P:GO:0006368; F:GO:0008135; P:GO:0002119; P:GO:0045449; P:GO:0010171; F:GO:0008353	-	EC:2.7.11.23	IPR002035; IPR007198; PTHR12695 (PANTHER), PTHR12695:SF2 (PANTHER), SSF53300 (SUPERFAMILY)
Brugia malayi	ubiquitin conjugation factor e4	0		F:GO:0034450; C:GO:0000151; F:GO:0004842; F:GO:0005515; P:GO:0016567; P:GO:0006511		IPR019474; PTHR13931 (PANTHER), PTHR13931:SF2 (PANTHER)
Brugia malayi	wd-repeat protein 26	0		F:GO:0003674; C:GO:0005737		-
	-	0				-
Caenorhabditis elegans	williams-beuren syndrome chromosome region 16 protein	0		C:GO:0005739		IPR000408; IPR009091; PTHR22870 (PANTHER), PTHR22870:SF11 (PANTHER)
Drosophila virilis	low-density lipoprotein	0		C:GO:0005905; F:GO:0005509; F:GO:0004872; C:GO:0016021; F:GO:0005041; C:GO:0016020; P:GO:0006897		IPR006210; IPR011042; G3DSA:2.10.25.10 (GENE3D), PTHR10529 (PANTHER), PTHR10529:SF6 (PANTHER), SSF75011 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-rbc-1 protein	2	P:GO:0009987; P:GO:0050789	-		PTHR13950 (PANTHER), PTHR13950:SF1 (PANTHER)
	-	0				-

Brugia malayi	structural mainte-nce of chromosomes protein 4	4	P:GO:0007076; F:GO:0005524; C:GO:0005694; F:GO:0046982	-		IPR003395; G3DSA:3.40.50.300 (GENE3D), PTHR18937 (PANTHER), PTHR18937:SF13 (PANTHER), SSF52540 (SUPERFAMILY)
Bombyx mori	endonuclease-reverse transcriptase	2	F:GO:0003676; F:GO:0016740	-		-
Brugia malayi	briggsae cbr-sgcb-1 protein	0		C:GO:0016012; C:GO:0016021; P:GO:0007010		SignalP (SIGNALP)
Pan troglodytes	transcription factor ap-2 beta (activating enhancer binding protein 2 beta)	7	P:GO:0045817; F:GO:0043565; P:GO:0007399; F:GO:0046983; F:GO:0003700; F:GO:0003713; C:GO:0005634	-		IPR004979; IPR013854; PTHR10812:SF6 (PANTHER)
Loa loa	guanine nucleotide-binding protein g alpha subunit	7	F:GO:0004871; P:GO:0007213; F:GO:0005515; P:GO:0007193; P:GO:0008283; F:GO:0016787; F:GO:0005525	-		IPR001019; IPR001408; IPR011025; IPR016059; G3DSA:3.40.50.300 (GENE3D), PTHR10218:SF71 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein T16G12.9 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	vacuolar protein sorting 35	3	F:GO:0005515; C:GO:0044444; C:GO:0016020	-		IPR005378; SignalP (SIGNALP)
	-	0				-
	-	0				-
Hydra magnipapillata	acyl-coenzyme a dehydroge-se member 10	0		P:GO:0055114; F:GO:0016491; F:GO:0003995; P:GO:0008152; F:GO:0016787; F:GO:0003824; F:GO:0016627; F:GO:0050660		PTHR10909 (PANTHER), PTHR10909:SF6 (PANTHER)
Caenorhabditis elegans	briggsae cbr-sulp-6 protein	0		C:GO:0016021; C:GO:0016020; P:GO:0055085; P:GO:0006810; F:GO:0005215		PTHR11814 (PANTHER), PTHR11814:SF10 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	trrap-like (transcription transformation domain-associated protein) family member (trr-1)	5	P:GO:0016570; F:GO:0005515; P:GO:0050794; C:GO:0000123; P:GO:0006350	-		IPR011989; IPR016024
Caenorhabditis briggsae	briggsae cbr-ptb-1 protein	0		F:GO:0003676; F:GO:0003723; F:GO:0000166; P:GO:0006397; F:GO:0005515; C:GO:0005634		-
	-	0				-

Callithrix jacchus	proteasome (macropain) 26s 4	11	F:GO:0008233; C:GO:0000502; C:GO:0005739; P:GO:0051436; P:GO:0051437; P:GO:0031145; F:GO:0005524; F:GO:0016887; F:GO:0005515; P:GO:0001824; C:GO:0005634	-		IPR003959; IPR003960; G3DSA:3.40.50.300 (GENE3D), PTHR23073 (PANTHER), PTHR23073:SF8 (PANTHER), SSF52540 (SUPERFAMILY)
Brugia malayi	elegans protein partially confirmed by transcript evidence	0		F:GO:0005515		-
Loa loa	ring finger protein isoform cra_a	0		F:GO:0016874; C:GO:0005634; P:GO:0000003; F:GO:0008270; P:GO:0002119; F:GO:0019787; F:GO:0005515; P:GO:0040010; F:GO:0046872; P:GO:0006350; P:GO:0040007; P:GO:0045449		IPR001841; IPR002867; IPR006575; IPR016135; IPR017907; PTHR11685 (PANTHER), PTHR11685:SF7 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis briggsae	patched family protein	5	P:GO:0018996; C:GO:0016021; P:GO:0040018; F:GO:0008158; P:GO:0040011	-		IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR011021; PTHR11188 (PANTHER), PTHR11188:SF11 (PANTHER)
Bombyx mori	endonuclease-reverse transcriptase	0		F:GO:0003723; C:GO:0005737; P:GO:0006278; F:GO:0004519; C:GO:0005634; F:GO:0003964		IPR005135; PTHR23227 (PANTHER), PTHR23227:SF14 (PANTHER)
Caenorhabditis elegans	atp-dependent d- helicase	7	F:GO:0043140; P:GO:0006260; F:GO:0003676; C:GO:0005622; F:GO:0005524; P:GO:0006310; P:GO:0006281	-		IPR004589; IPR011545; G3DSA:3.40.50.300 (GENE3D), PTHR13710:SF16 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	alanyl-tr- synthetase	6	P:GO:0006412; F:GO:0003676; F:GO:0032555; F:GO:0004812; P:GO:0043039; C:GO:0005737	-	EC:3.6.5.3	IPR018164; IPR018165; G3DSA:3.30.930.10 (GENE3D), PTHR11777 (PANTHER), SSF55681 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)

Caenorhabditis briggsae	uncoordi-ted family member (unc-52)	4	P:GO:0048705; P:GO:0009888; P:GO:0030239; C:GO:0005578	-		IPR000034; IPR000742; IPR002049; IPR002172; IPR003006; IPR003598; IPR003599; IPR007110; IPR013032; IPR013098; IPR013783; IPR018031; G3DSA:2.10.25.10 (GENE3D), G3DSA:2.170.300.10 (GENE3D), PTHR10574 (PANTHER), PTHR10574:SF20 (PANTHER), SSF48726 (SUPERFAMILY), SSF57196 (SUPERFAMILY)
Caenorhabditis briggsae	rh50 glycoprotein	9	P:GO:0009792; P:GO:0015670; C:GO:0005887; P:GO:0055085; F:GO:0051739; P:GO:0015696; P:GO:0006873; F:GO:0008519; F:GO:0030506	-		-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-wrn-1 protein	2	P:GO:0044237; F:GO:0016787	-		IPR002121; IPR010997
Ancylostoma caninum	secreted protein 4 precursor	0		C:GO:0005576		IPR001283; IPR014044; PTHR10334:SF2 (PANTHER)
Ancylostoma ceylanicum	secreted protein 5 precursor	0		C:GO:0005576		IPR001283; IPR014044; PTHR10334:SF2 (PANTHER)
	-	0				IPR001283; IPR014044; PTHR10334:SF2 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	C:GO:0034703; F:GO:0005261; P:GO:0055080	-		-
Caenorhabditis briggsae	briggsae cbr-vps- protein	0		P:GO:0006904; P:GO:0016192; F:GO:0005515		-
Loa loa	laterally symmetric (defective in lateral asymmetry) family member (lsy-2)	6	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0005488; P:GO:0040010; P:GO:0040011	-		IPR007087; IPR015880
Loa loa	laterally symmetric (defective in lateral asymmetry) family member (lsy-2)	6	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0005488; P:GO:0040010; P:GO:0040011	-		IPR007087; IPR015880
Loa loa	elegans protein confirmed by transcript evidence	1	P:GO:0019915	-		-

Brugia malayi	zinc finger ccch-type containing 12a	0		C:GO:0005634; F:GO:0016787; P:GO:0006915; F:GO:0003676; C:GO:0005737; F:GO:0008270; P:GO:0001525; P:GO:0007275; P:GO:0030154; F:GO:0046872; F:GO:0004519		-
Caenorhabditis elegans	thymidylate ki-se	7	C:GO:0005739; P:GO:0009221; P:GO:0040007; P:GO:0002119; F:GO:0016301; C:GO:0005654; P:GO:0009792	-		IPR018094; IPR018095; G3DSA:3.40.50.300 (GENE3D), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0016301; F:GO:0005524; F:GO:0004672; F:GO:0000166; P:GO:0006468; F:GO:0004674		IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF12 (PANTHER)
						IPR008160; PTHR10499 (PANTHER), PTHR10499:SF114 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG08700 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)
Camponotus floridanus	protein ki-se	0		F:GO:0016301; F:GO:0004672; F:GO:0005524; F:GO:0016740; F:GO:0000166; P:GO:0006468; F:GO:0004709; F:GO:0004674		IPR000719; IPR011009; IPR017441; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR22986 (PANTHER)
Caenorhabditis elegans	hypothetical protein T07D1.3 [Caenorhabditis elegans]	0		P:GO:0055114; F:GO:0016491; C:GO:0016021		SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-

Caenorhabditis elegans	mre11 meiotic recombi-tion 11 homolog a	21	C:GO:0000781; P:GO:0033674; C:GO:0005654; P:GO:0032508; P:GO:0007131; F:GO:0008022; P:GO:0007507; C:GO:0030870; F:GO:0004527; P:GO:0006302; C:GO:0005730; F:GO:0003677; P:GO:0000723; F:GO:0004520; P:GO:0031954; C:GO:0000794; C:GO:0000790; C:GO:0048471; F:GO:0004003; P:GO:0007062; P:GO:0032876	-		IPR003701; IPR004843; IPR007281; G3DSA:3.60.21.10 (GENE3D), SSF56300 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	briggsae cbr-ugt-60 protein	4	P:GO:0005975; P:GO:0030259; F:GO:0030246; F:GO:0016758	-	EC:2.4.1.0	SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	sodium hydrogen exchanger 3	6	P:GO:0009792; F:GO:0015385; P:GO:0055085; P:GO:0006885; C:GO:0016021; P:GO:0006814	-		SignalP (SIGNALP)
Loa loa	sepiapterin reductase	5	F:GO:0004757; P:GO:0006729; P:GO:0006519; P:GO:0044106; P:GO:0010033	-	EC:1.1.1.153	IPR002198; IPR002347; IPR016040; PTHR19410:SF116 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	atp synthase mitochondrial f1 complex assembly factor	0		P:GO:0043461; F:GO:0005515; C:GO:0005575		IPR011419; G3DSA:1.10.3580.10 (GENE3D), PTHR21013:SF9 (PANTHER), SignalP (SIGNALP)
	-	0				-

Caenorhabditis briggsae	briggsae cbr-tax-6 protein	19	P:GO:0043029; P:GO:0030217; P:GO:0001975; F:GO:0004723; C:GO:0005626; P:GO:0007507; P:GO:0010468; F:GO:0046982; F:GO:0046872; P:GO:0034097; C:GO:0043234; P:GO:0001915; C:GO:0030424; P:GO:0046716; P:GO:0006470; F:GO:0019855; F:GO:0005516; C:GO:0005625; C:GO:0043204	-		-
	-	0				-
Brugia malayi	zinc c2h2 type family protein	7	P:GO:0040010; F:GO:0003676; F:GO:0046872; P:GO:0045449; P:GO:0000003; F:GO:0005515; P:GO:0009792	-		IPR007087; IPR013087; IPR015880; PTHR23224 (PANTHER), PTHR23224:SF30 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0004222; F:GO:0016787; F:GO:0008270; F:GO:0008237; C:GO:0031012; F:GO:0008233; P:GO:0006508; P:GO:0008152; F:GO:0046872		IPR001818; G3DSA:3.40.390.10 (GENE3D), PTHR10201 (PANTHER), PTHR10201:SF5 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG22251 [Caenorhabditis briggsae]	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	rr- methyltransferase mitochondrial precursor	1	C:GO:0009536	-		IPR001537; IPR013123; G3DSA:3.30.1330.30 (GENE3D), G3DSA:3.40.1280.10 (GENE3D), PTHR12029 (PANTHER), PTHR12029:SF7 (PANTHER), SSF55315 (SUPERFAMILY), SSF75217 (SUPERFAMILY)
Caenorhabditis elegans	tr- rr- methyltransferase	2	F:GO:0016740; C:GO:0009536	-		IPR013123; G3DSA:3.30.1330.30 (GENE3D), PTHR12029 (PANTHER), PTHR12029:SF7 (PANTHER), SSF55315 (SUPERFAMILY)

Ailuropoda melanoleuca	beta	20	C:GO:0042612; P:GO:0019882; P:GO:0042267; C:GO:0045298; P:GO:0006928; F:GO:0005525; F:GO:0042288; C:GO:0016021; P:GO:0006184; P:GO:0051225; C:GO:0005829; C:GO:0005874; P:GO:0051258; P:GO:0007067; F:GO:0042277; F:GO:0032403; F:GO:0003924; P:GO:0007018; F:GO:0005200; P:GO:0030182	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000217; IPR003008; PTHR11588:SF11 (PANTHER)
	-	0				-
	-	0				-
Brugia malayi	zinc c2h2 type family protein	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		IPR007087; IPR013087; IPR015880
	-	0				-
Caenorhabditis elegans	cox15 cytochrome c oxidase assembly protein	6	F:GO:0004129; C:GO:0005746; P:GO:0006784; P:GO:0007585; P:GO:0008535; P:GO:0006123	-	EC:1.9.3.1	IPR003780; PTHR23289 (PANTHER)
Caenorhabditis elegans	serine threonine ki-se 38	10	P:GO:0007243; F:GO:0004674; F:GO:0031435; P:GO:0043407; F:GO:0005524; P:GO:0007399; F:GO:0000287; C:GO:0070688; C:GO:0005737; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22985 (PANTHER), PTHR22985:SF33 (PANTHER)
Caenorhabditis elegans	geranylgeranyl transferase type-2 subunit alpha	11	F:GO:0004663; P:GO:0009792; P:GO:0002119; F:GO:0005488; P:GO:0018346; P:GO:0018344; P:GO:0040010; P:GO:0008340; P:GO:0040011; P:GO:0008219; P:GO:0002009	-	EC:2.5.1.60	IPR002088; IPR008940; PTHR11129 (PANTHER), PTHR11129:SF2 (PANTHER), SSF48439 (SUPERFAMILY)

Caenorhabditis elegans	geranylgeranyl transferase type-2 subunit alpha	11	F:GO:0004663; P:GO:0009792; P:GO:0002119; F:GO:0005488; P:GO:0018346; P:GO:0018344; P:GO:0040010; P:GO:0008340; P:GO:0040011; P:GO:0008219; P:GO:0002009	-	EC:2.5.1.60	IPR002088; IPR008940; PTHR11129 (PANTHER), PTHR11129:SF2 (PANTHER), SSF48439 (SUPERFAMILY)
Caenorhabditis elegans	thrombospondin type 1 domain containing protein	0		F:GO:0005044; F:GO:0030247; C:GO:0031012; C:GO:0005576; P:GO:0006955		IPR000884; G3DSA:2.20.100.10 (GENE3D)
Caenorhabditis elegans	lysine-specific demethylase 2b	12	P:GO:0016568; F:GO:0051864; F:GO:0008270; C:GO:0005730; F:GO:0019843; P:GO:0055114; P:GO:0045449; P:GO:0000003; F:GO:0016702; F:GO:0003677; F:GO:0005515; P:GO:0006974	-	EC:1.14.11.27; EC:1.13.11.0	PTHR23123 (PANTHER)
Caenorhabditis elegans	ring finger protein 40	1	F:GO:0005488	-		PTHR23163 (PANTHER)
	-	0				SignalP (SIGNALP)
Aspergillus clavatus NRRL 1	sulfur metabolism regulator	0		F:GO:0016301; P:GO:0008150; F:GO:0005515; C:GO:0005575; P:GO:0006511		IPR001232; IPR011333; IPR016072; IPR016073; PTHR11165:SF21 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	9	P:GO:0010171; P:GO:0002119; P:GO:0040002; P:GO:0040011; C:GO:0016021; C:GO:0005576; P:GO:0019915; P:GO:0006898; F:GO:0042302	-		SignalP (SIGNALP)
Caenorhabditis elegans	inosine triphosphate pyrophosphatase	2	F:GO:0047429; P:GO:0008152	-	EC:3.6.1.19	IPR002637; G3DSA:3.90.950.10 (GENE3D), PTHR11067:SF7 (PANTHER), SSF52972 (SUPERFAMILY)
	-	0				-
Brugia malayi	amme syndrome candidate gene 1 protein homolog	0		P:GO:0008150; C:GO:0005575		IPR002733; G3DSA:3.30.1490.150 (GENE3D), G3DSA:3.30.700.20 (GENE3D), PTHR13016 (PANTHER), SignalP (SIGNALP), SSF143447 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	yo30_caebr ame: full=gilt-like protein cbg03282 flags: precursor	0		C:GO:0005576		-

Caenorhabditis elegans	endo-b-n-acetylglucosaminidase family member (eng-1)	5	P:GO:0009056; F:GO:0016874; F:GO:0005488; F:GO:0016787; P:GO:0044238	-		IPR005201
	-	0				-
Caenorhabditis briggsae	d- repair protein rad50	1	P:GO:0007126	-		IPR007517; IPR013134; PD968187 (PRODOM), PTHR18867 (PANTHER), PTHR18867:SF11 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Canis familiaris	eukaryotic translation elongation factor 1 gamma	6	F:GO:0003746; C:GO:0005853; F:GO:0005515; C:GO:0005829; P:GO:0009615; P:GO:0006414	-		IPR001662; PTHR11260 (PANTHER), PTHR11260:SF4 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-cln- protein	41	[illegible] C:GO:0043005; P:GO:0043086; C:GO:0005802; P:GO:0006457; C:GO:0005776; C:GO:0000139; P:GO:0001508; C:GO:0030176; P:GO:0006898; C:GO:0005624; C:GO:0005764; P:GO:0016242; P:GO:0008306; C:GO:0005770; P:GO:0043524; P:GO:0051480; P:GO:0046662; P:GO:0007042; P:GO:0045861; P:GO:0016485; P:GO:0009792; P:GO:0006681; P:GO:0042133; P:GO:0006520; C:GO:0005795; C:GO:0005769; F:GO:0051082;	-		IPR003492; IPR016196; SignalP (SIGNALP)
Loa loa	fgfr1 oncogene partner 2	1	F:GO:0005515	-		IPR008555
	-	0				-
Rattus norvegicus	isoform cra_a	0				-
	-	0				IPR010916
	-	0				-
	-	0				-
Caenorhabditis elegans	riken cd- c330023m02 gene	1	F:GO:0005515	-		PTHR22767 (PANTHER), PTHR22767:SF3 (PANTHER)
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	cullin 5	10	C:GO:0005829; P:GO:0006511; F:GO:0031625; C:GO:0005624; C:GO:0031466; F:GO:0004842; P:GO:0006970; F:GO:0016931; P:GO:0051480; C:GO:0005634	-	EC:6.3.2.19	IPR011991; IPR019559; PTHR11932 (PANTHER), PTHR11932:SF16 (PANTHER), SSF46785 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis elegans	rapamycin-insensitive companion of mtor	9	P:GO:0080090; P:GO:0051056; P:GO:0035468; C:GO:0044424; P:GO:0032956; P:GO:0009967; P:GO:0042325; P:GO:0051896; F:GO:0005488	-		IPR011989; IPR016024; PTHR13298 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	poly-a polymerase family member (pap-1)	0		P:GO:0010171; C:GO:0005634; P:GO:0000003; F:GO:0003723; P:GO:0002119; P:GO:0009792; P:GO:0002009; P:GO:0043631; P:GO:0040011; P:GO:0040010; P:GO:0006350; P:GO:0040007; P:GO:0040035; F:GO:0004652		IPR007012
Caenorhabditis briggsae	methionine synthase reductase	5	F:GO:0016491; P:GO:0000003; P:GO:0006520; F:GO:0050662; F:GO:0000166	-		IPR003097; IPR017938; IPR023173; PTHR19384 (PANTHER), PTHR19384:SF11 (PANTHER)
Caenorhabditis elegans	nuclear receptor nhr-1	7	F:GO:0003700; F:GO:0043565; F:GO:0003707; P:GO:0019915; C:GO:0005634; F:GO:0008270; P:GO:0006355	-		IPR000536; IPR008946; PTHR11865 (PANTHER), PTHR11865:SF218 (PANTHER)
Brugia malayi	nematode cuticle collagen n-termi-l domain containing protein	3	F:GO:0042302; P:GO:0040011; P:GO:0010171	-		IPR002486; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER), SignalP (SIGNALP)

Homo sapiens	calreticulin	56	F:GO:0051087; P:GO:0045665; F:GO:0005506; F:GO:0051082; P:GO:0008284; C:GO:0016529; F:GO:0031625; C:GO:0005625; F:GO:0042562; F:GO:0044183; C:GO:0005829; F:GO:0001849; P:GO:0030866; F:GO:0005178; F:GO:0003729; C:GO:0005788; C:GO:0005615; P:GO:0007283; P:GO:0033144; C:GO:0005844; C:GO:0005792; P:GO:0042981; P:GO:0017148; P:GO:0033574; P:GO:0045740; P:GO:0002502; P:GO:0006611;	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG08295 [Caenorhabditis briggsae]	0				IPR017871
Caenorhabditis elegans	vacuolar protein sorting 13d	0		P:GO:0008104		PTHR16166 (PANTHER), PTHR16166:SF24 (PANTHER)
	-	0				-
Onchocerca volvulus	thioredoxin	0		P:GO:0045454; F:GO:0016491; F:GO:0016209		IPR012335; IPR012336; PTHR13871 (PANTHER), PTHR13871:SF5 (PANTHER)
	-	0				SignalP (SIGNALP)
Leishmania major strain Friedlin	proteophosphoglycan 5	0				-
Leishmania major strain Friedlin	proteophosphoglycan 5	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis briggsae	briggsae cbr-edc-3 protein	1	F:GO:0005515	-		IPR019050
Caenorhabditis elegans	phospholipase c gamma	1	F:GO:0008081	-	EC:3.1.4.0	IPR011993; PTHR10336 (PANTHER), PTHR10336:SF22 (PANTHER)
Caenorhabditis elegans	amp-binding enzyme family protein	11	P:GO:0006633; F:GO:0005488; C:GO:0043231; P:GO:0007420; P:GO:0007584; C:GO:0044446; C:GO:0044444; C:GO:0031090; P:GO:0014070; F:GO:0004467; F:GO:0003987	-	EC:6.2.1.3; EC:6.2.1.1	-

Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	7	P:GO:0009792; C:GO:0032040; P:GO:0040010; P:GO:0000003; P:GO:0006364; P:GO:0006898; P:GO:0045132	-		-
	-	0				-
Loa loa	uracil-d- glycosylase	2	P:GO:0006281; F:GO:0016799	-	EC:3.2.2.0	IPR002043; IPR005122; IPR018085
Loa loa	uracil-d- glycosylase	2	P:GO:0006281; F:GO:0016799	-	EC:3.2.2.0	IPR002043; IPR005122; IPR018085
	-	0				-
Loa loa	elegans protein partially confirmed by transcript evidence	6	P:GO:0007160; C:GO:0031012; P:GO:0008218; F:GO:0005509; P:GO:0018298; C:GO:0016020	-		IPR000152; IPR006210; IPR006605; IPR009017; IPR013032
	-	0				-
Caenorhabditis elegans	briggsae cbr-ttr-6 protein	0				IPR001534
	-	0				-
Caenorhabditis briggsae	tyrosyl-tr- synthetase	6	P:GO:0000003; F:GO:0000166; F:GO:0004812; P:GO:0006418; P:GO:0009792; C:GO:0044424	-		IPR002305; IPR015624; G3DSA:1.10.240.10 (GENE3D), PTHR11946 (PANTHER), SSF52374 (SUPERFAMILY)
Caenorhabditis elegans	uncoordi-ted family member (unc-52)	12	P:GO:0048704; P:GO:0002062; P:GO:0007420; P:GO:0030239; C:GO:0005605; P:GO:0007155; F:GO:0005515; P:GO:0001958; P:GO:0048738; P:GO:0008104; P:GO:0030198; P:GO:0060351	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	ribosomal protein s6 polypeptide 1-like	2	F:GO:0005488; P:GO:0009987	-		IPR011009; G3DSA:3.30.200.20 (GENE3D), PTHR22985 (PANTHER)
Caenorhabditis elegans	tumor susceptibility gene 101	11	P:GO:0046755; P:GO:0045926; F:GO:0048306; C:GO:0005730; P:GO:0048513; C:GO:0005770; F:GO:0031625; C:GO:0005769; P:GO:0050794; C:GO:0005886; P:GO:0043162	-		IPR008883; IPR016135; IPR017916; PTHR23306 (PANTHER), PTHR23306:SF4 (PANTHER), PS51322 (PROFILE), SSF140111 (SUPERFAMILY)
Caenorhabditis elegans	chromosome 9 open reading frame 41	0				-

Ailuropoda melanoleuca	eukaryotic translation initiation factor 3 subunit k	8	C:GO:0005852; F:GO:0003723; F:GO:0005515; P:GO:0045948; F:GO:0003743; C:GO:0005634; C:GO:0005829; F:GO:0043022	-		IPR005062; IPR009374; IPR016020; IPR016024
Caenorhabditis elegans	protein phosphatase catalytic alpha isoform	25	P:GO:0046822; P:GO:0005981; P:GO:0030324; P:GO:0000003; C:GO:0043197; F:GO:0043021; P:GO:0051301; C:GO:0005730; C:GO:0005829; C:GO:0005741; F:GO:0046872; P:GO:0009792; P:GO:0007067; F:GO:0042802; P:GO:0005979; P:GO:0007126; P:GO:0002119; P:GO:0048754; C:GO:0070688; P:GO:0006470; P:GO:0016568; C:GO:0043204; F:GO:0008599; F:GO:0004722; C:GO:0042587	-		IPR004843; IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF19 (PANTHER), SignalP (SIGNALP), SSF56300 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	3	C:GO:0034703; F:GO:0005261; P:GO:0055080	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
Brugia malayi	briggsae cbr-let-413 protein	15	C:GO:0044456; P:GO:0009653; C:GO:0005911; F:GO:0005515; P:GO:0007163; P:GO:0023051; P:GO:0031323; P:GO:0040011; P:GO:0045108; P:GO:0015031; C:GO:0005737; P:GO:0006915; P:GO:0048522; P:GO:0030154; C:GO:0005912	-		IPR001611; IPR003591; PR00019 (PRINTS), G3DSA:3.80.10.10 (GENE3D), PTHR23155 (PANTHER), PTHR23155:SF29 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)
	-	0				-
	-	0				-

Caenorhabditis briggsae	briggsae cbr-ssl-1 protein	26	P:GO:0030097; C:GO:0000785; P:GO:0000381; P:GO:0035207; F:GO:0005515; F:GO:0017111; P:GO:0016458; P:GO:0040010; P:GO:0035222; P:GO:0048813; P:GO:0040011; C:GO:0005701; P:GO:0007517; P:GO:0045747; P:GO:0007400; C:GO:0005730; P:GO:0007391; P:GO:0006350; P:GO:0008105; F:GO:0003677; P:GO:0002119; P:GO:0048749; P:GO:0048477; P:GO:0007476; P:GO:0040035; P:GO:0006325	-	EC:3.6.1.15	IPR000330; IPR006562; IPR014001; IPR014012; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10799 (PANTHER), PTHR10799:SF75 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	ribosomal protein l16 containing protein	8	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; F:GO:0005515; P:GO:0040010; P:GO:0006412; F:GO:0019843	-	EC:3.6.5.3	-
	-	0				-
Caenorhabditis briggsae	temporarily assigned gene -me family member (tag-308)	0				-
Caenorhabditis elegans	nucleoside diphosphate-linked moiety x motif 19	0		C:GO:0005777; F:GO:0046872; C:GO:0005739; P:GO:0006911; F:GO:0016787		IPR000086; IPR015797; PTHR12318 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	enoyl- hydratase	1	F:GO:0003824	-		IPR001753; G3DSA:3.90.226.10 (GENE3D), PTHR11941 (PANTHER), SSF52096 (SUPERFAMILY)
Caenorhabditis elegans	ophagy (yeast atg homolog) family member (atg-2)	0				IPR005522; PTHR13190 (PANTHER), PTHR13190:SF2 (PANTHER)
	-	0				-
Caenorhabditis briggsae	ferm domain-containing	1	C:GO:0044464	-		IPR000299; IPR011993; IPR014352; IPR018979; IPR018980; IPR019748; IPR019749; IPR019750; G3DSA:3.10.20.90 (GENE3D), PTHR23280 (PANTHER), SSF50729 (SUPERFAMILY), SSF54236 (SUPERFAMILY)

Caenorhabditis briggsae	ferm domain-containing	1	C:GO:0044464	-		IPR000299; IPR011993; IPR014352; IPR018979; IPR018980; IPR019748; IPR019749; IPR019750; G3DSA:3.10.20.90 (GENE3D), PTHR23280 (PANTHER), SSF50729 (SUPERFAMILY), SSF54236 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	briggsae cbr-rhy-1 protein	0		C:GO:0016021; F:GO:0016747		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	5	P:GO:0009792; P:GO:0002119; F:GO:0004553; F:GO:0005515; P:GO:0040007	-	EC:3.2.1.0	SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-mbr-1 protein	14	C:GO:0005700; P:GO:0007613; P:GO:0006919; P:GO:0008628; P:GO:0035072; P:GO:0035069; P:GO:0006911; P:GO:0019915; F:GO:0043565; P:GO:0006914; F:GO:0003700; P:GO:0045893; F:GO:0042803; C:GO:0005634	-		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0000003; P:GO:0040035; P:GO:0006898; P:GO:0009792		-
Brugia malayi	fanci (fanconi anemia complex component i) homolog family member (fnci-1)	0				-
Caenorhabditis elegans	ched related family member (ptr-23)	7	P:GO:0018996; C:GO:0016021; P:GO:0008340; P:GO:0000003; P:GO:0040025; F:GO:0008158; P:GO:0040011	-		-
	-	0				-
Brugia malayi	elegans protein confirmed by transcript evidence	7	P:GO:0008340; P:GO:0040007; P:GO:0010171; F:GO:0005488; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		-
Caenorhabditis elegans	tomosyn sy-ptic protein family member (tom-1)	3	P:GO:0006887; F:GO:0017075; C:GO:0005892	-		PTHR10241 (PANTHER), PTHR10241:SF7 (PANTHER)
Caenorhabditis elegans	ral guanine nucleotide dissociation stimulator-like 1	5	F:GO:0005085; P:GO:0051056; C:GO:0005622; F:GO:0005515; P:GO:0040010	-		IPR000651; IPR001895; IPR008937; IPR019804; G3DSA:1.20.870.10 (GENE3D), PTHR23113:SF29 (PANTHER)

	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	P:GO:0040010	-		IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF12 (PANTHER)
Harpegnathos saltator	histone	17	P:GO:0040010; C:GO:0000786; P:GO:0008340; P:GO:0009725; P:GO:0008360; P:GO:0007420; F:GO:0003677; C:GO:0005700; P:GO:0010171; P:GO:0007155; P:GO:0002119; F:GO:0005515; P:GO:0006334; P:GO:0009792; P:GO:0007140; C:GO:0005634; P:GO:0006974	-		IPR010916
Callithrix jacchus	transmembrane protein 147	2	F:GO:0005515; C:GO:0016021	-		IPR019164; PTHR12869 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	tbc1 domain member 10b	3	F:GO:0005097; C:GO:0005622; P:GO:0032313	-		IPR000195; PTHR22957 (PANTHER), PTHR22957:SF49 (PANTHER)
Homo sapiens	eukaryotic translation initiation factor 4 gamma 1 isoform 6	8	C:GO:0016281; F:GO:0003723; F:GO:0005515; P:GO:0006446; F:GO:0003743; P:GO:0016070; C:GO:0005829; P:GO:0044419	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG18919 [Caenorhabditis briggsae]	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	probable exonuclease mut-7 homolog	2	F:GO:0016787; F:GO:0005515	-		-
	-	0				-
Ancylostoma ceylanicum	metalloprotease 1 precursor	1	F:GO:0008233	-		IPR001506; IPR006026; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)

Caenorhabditis briggsae	-+ k+ alpha 1 polypeptide	23	P:GO:0006940; F:GO:0005515; P:GO:0002087; P:GO:0008542; P:GO:0045822; C:GO:0005792; P:GO:0040011; C:GO:0016021; P:GO:0019229; P:GO:0051481; C:GO:0005737; F:GO:0046872; P:GO:0006754; C:GO:0042383; P:GO:0045988; F:GO:0005391; P:GO:0001504; P:GO:0006813; P:GO:0002026; F:GO:0005524; P:GO:0008217; P:GO:0006814; P:GO:0008344	-	EC:3.6.3.9	IPR000695; IPR001757; IPR013200; G3DSA:1.20.1110.10 (GENE3D), PTHR11939:SF100 (PANTHER), SSF56784 (SUPERFAMILY)
Bacillus thuringiensis serovar kurstaki str. T03a001	collagen triple helix repeat domain protein	0				-
Homo sapiens	sy-ptotagmin viii	7	P:GO:0007340; C:GO:0001669; C:GO:0005886; C:GO:0008021; C:GO:0016021; F:GO:0048306; F:GO:0005215	-		IPR000008; IPR008973; G3DSA:2.60.40.150 (GENE3D), PTHR10024 (PANTHER), PTHR10024:SF6 (PANTHER)
Loa loa	negative elongation factor c d	0		F:GO:0003746; P:GO:0016481; C:GO:0005634		IPR006942
Caenorhabditis briggsae	d- repair exonuclease	23	C:GO:0000781; P:GO:0033674; F:GO:0030145; C:GO:0005654; P:GO:0032508; P:GO:0007131; F:GO:0008022; P:GO:0007507; C:GO:0030870; F:GO:0004527; P:GO:0006302; C:GO:0005730; F:GO:0003677; P:GO:0000723; P:GO:0031954; F:GO:0004519; C:GO:0000794; C:GO:0000790; C:GO:0048471; F:GO:0004003; P:GO:0007062; P:GO:0032876; F:GO:0004722	-		-

Caenorhabditis briggsae	lymphocyte antigen 75	0		F:GO:0005488; F:GO:0005529		IPR001304; IPR016186; IPR016187; IPR018378; PTHR22801 (PANTHER)
Caenorhabditis elegans	uroca-se domain containing 1	2	P:GO:0006548; F:GO:0016153	-	EC:4.2.1.49	IPR000193; SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG05629 [Caenorhabditis briggsae]	0				-
Haemonchus contortus	gata transcription factor	4	F:GO:0003700; F:GO:0043565; F:GO:0008270; P:GO:0006355	-		-
	-	0				-
	-	0				IPR015155
	-	0				IPR000436; IPR016060; SignalP (SIGNALP)
Caenorhabditis elegans	tetraspanin 5	1	C:GO:0016021	-		IPR000301; IPR008952; IPR018499; PTHR19282 (PANTHER), PTHR19282:SF57 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	acid phosphatase family protein confirmed by transcript evidence	0		F:GO:0003993		G3DSA:3.40.50.1240 (GENE3D), PTHR11567 (PANTHER), PTHR11567:SF28 (PANTHER)
Caenorhabditis elegans	rr- methylase family	3	P:GO:0009987; F:GO:0005488; F:GO:0008168	-	EC:2.1.1.0	IPR001537; G3DSA:3.40.1280.10 (GENE3D), PTHR12029 (PANTHER), PTHR12029:SF11 (PANTHER), SSF75217 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Macaca mulatta	class member 1	8	C:GO:0005625; F:GO:0004559; C:GO:0005764; P:GO:0006013; P:GO:0006517; F:GO:0008270; P:GO:0007611; F:GO:0005537	-	EC:3.2.1.24	IPR011013; IPR011682; G3DSA:2.70.98.30 (GENE3D), PTHR11607 (PANTHER), PTHR11607:SF3 (PANTHER)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG18497 [Caenorhabditis briggsae]	0				-
	-	0				SignalP (SIGNALP)
Loa loa	eukaryotic translation initiation factor 3	1	F:GO:0003676	-		IPR003100; G3DSA:2.170.260.10 (GENE3D), PTHR22891 (PANTHER), SSF101690 (SUPERFAMILY)
	-	0				-
Loa loa	g protein-coupled receptor 89	9	P:GO:0034765; C:GO:0032580; F:GO:0004871; C:GO:0016021; P:GO:0051452; C:GO:0030660; P:GO:0043123; F:GO:0008308; P:GO:0015031	-		IPR015672; PF12430 (PFAM), SignalP (SIGNALP)
Caenorhabditis elegans	activator of basal transcription 1	5	P:GO:0040007; P:GO:0040035; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		-
	-	0				-

Pongo abelii	hla-b associated transcript 2	3	C:GO:0005634; F:GO:0005515; C:GO:0005737	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0008270; C:GO:0005622		IPR007087; IPR013032; IPR015880
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0008270; C:GO:0005622		IPR007087; IPR013032; IPR015880
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	P:GO:0009792	-		-
Caenorhabditis briggsae	tafazzin	30	P:GO:0060271; P:GO:0030097; P:GO:0001933; P:GO:0008284; P:GO:0042407; P:GO:0060048; P:GO:0060390; P:GO:0035329; P:GO:0035414; P:GO:0048738; F:GO:0047184; F:GO:0003714; P:GO:0010718; P:GO:0032049; F:GO:0003713; P:GO:0045944; P:GO:0001649; P:GO:0042775; P:GO:0006469; C:GO:0005739; C:GO:0005667; P:GO:0000122; P:GO:0045599; P:GO:0090090; P:GO:0032835; P:GO:0032981; C:GO:0005730;	-	EC:2.3.1.23	IPR000872; IPR002123; G3DSA:3.40.1130.10 (GENE3D), SignalP (SIGNALP), SSF69593 (SUPERFAMILY)

Caenorhabditis briggsae	tafazzin	30	P:GO:0060271; P:GO:0030097; P:GO:0001933; P:GO:0008284; P:GO:0042407; P:GO:0060048; P:GO:0060390; P:GO:0035329; P:GO:0035414; P:GO:0048738; F:GO:0047184; F:GO:0003714; P:GO:0010718; P:GO:0032049; F:GO:0003713; P:GO:0045944; P:GO:0001649; P:GO:0042775; P:GO:0006469; C:GO:0005739; C:GO:0005667; P:GO:0000122; P:GO:0045599; P:GO:0090090; P:GO:0032835; P:GO:0032981; C:GO:0005730;	-	EC:2.3.1.23	IPR000872; IPR002123; G3DSA:3.40.1130.10 (GENE3D), SignalP (SIGNALP), SSF69593 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Loa loa	germ cell-less homolog 1	3	P:GO:0009987; F:GO:0042802; C:GO:0044428	-		PTHR23231 (PANTHER), PTHR23231:SF2 (PANTHER)
Brugia malayi	trehalase	5	F:GO:0004135; P:GO:0009792; P:GO:0005978; P:GO:0005991; F:GO:0004555	-	EC:3.2.1.33; EC:3.2.1.28	IPR001661; IPR008928; PTHR23403:SF1 (PANTHER)
	-	0				-
Caenorhabditis briggsae	c2 domain containing protein	2	F:GO:0046872; C:GO:0016021	-		PTHR21119 (PANTHER), PTHR21119:SF1 (PANTHER)
Caenorhabditis elegans	hypothetical protein F40E3.5 [Caenorhabditis elegans]	0		F:GO:0016787; F:GO:0004721		IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF4 (PANTHER), SSF56300 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	acid ceramidase	0		P:GO:0006629; C:GO:0005764; F:GO:0016787; F:GO:0003824; P:GO:0006672; F:GO:0017040		-
Caenorhabditis briggsae	syntaxin 12	1	C:GO:0044464	-		-
Caenorhabditis briggsae	glycosyl group 2 family protein	4	C:GO:0016021; C:GO:0005794; F:GO:0016757; F:GO:0005529	-		-

Homo sapiens	atp h+ mitochondrial f0 subunit b1	6	F:GO:0015078; C:GO:0000276; P:GO:0042776; F:GO:0016887; F:GO:0005515; C:GO:0005759	-		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		C:GO:0005739		IPR008381
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	4	P:GO:0000003; P:GO:0040010; P:GO:0006898; P:GO:0002119	-		-
Caenorhabditis elegans	viral a-type inclusion protein repeat containing protein	0				-
Loa loa	mitochondrial protein 18 kda	1	C:GO:0016020	-		IPR001765; IPR019560
Caenorhabditis briggsae	Hypothetical protein CBG23277 [Caenorhabditis briggsae]	0		P:GO:0009058; F:GO:0016847; F:GO:0003824; F:GO:0030170; F:GO:0016769		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-rig-4 protein	0		P:GO:0046533; P:GO:0007155; C:GO:0016021; P:GO:0042675; C:GO:0016020; C:GO:0005887		IPR003598; IPR003599; IPR003961; IPR007110; IPR008957; IPR013098; IPR013783; PTHR10489 (PANTHER), PTHR10489:SF57 (PANTHER), SignalP (SIGNALP), SSF48726 (SUPERFAMILY)
	-	0				-
	-	0				IPR006578
Brugia malayi	hed family member (ptc-3)	0		C:GO:0016021; C:GO:0016020; P:GO:0000003; P:GO:0040018; P:GO:0002119; P:GO:0009792; F:GO:0008158; P:GO:0040011; P:GO:0040007; P:GO:0018996		PD019290 (PRODOM)
	-	0				-
Caenorhabditis elegans	glucose-6-phosphate dehydroge-se	4	P:GO:0006006; F:GO:0004345; P:GO:0055114; F:GO:0005488	-	EC:1.1.1.49	IPR016040; IPR022674; SSF51735 (SUPERFAMILY)
	-	0				-
Loa loa	proteasome regulatory non-atpase-like protein	5	C:GO:0005875; C:GO:0008541; P:GO:0006508; F:GO:0005488; F:GO:0004175	-		IPR000717; IPR011991; PTHR10678 (PANTHER), PTHR10678:SF2 (PANTHER), SSF46785 (SUPERFAMILY)
	-	0				PTHR13712 (PANTHER), PTHR13712:SF63 (PANTHER)

Pristionchus pacificus	armadillo beta-catenin-like repeat family protein	0		C:GO:0016020; C:GO:0005634; C:GO:0030054; C:GO:0005737; P:GO:0001708; P:GO:0007275; P:GO:0006350; P:GO:0016055; P:GO:0045449; F:GO:0005488		PTHR23315 (PANTHER), PTHR23315:SF3 (PANTHER)
	-	0				-
	-	0				-
						-
Loa loa	2 -phosphodiesterase 12	1	F:GO:0016787	-		IPR005135; PTHR12121 (PANTHER), PTHR12121:SF12 (PANTHER)
	-	0				-
	-	0				-
Angiostrongylus cantonensis	transcription regulator	1	F:GO:0030528	-		SignalP (SIGNALP)
Caenorhabditis briggsae	nitrogen permease regulator-like 3	0		F:GO:0003674; C:GO:0005575		IPR005365; SignalP (SIGNALP)
Caenorhabditis sp. PS1010	serine threonine-protein ki-se	1	F:GO:0005488	-		-
	-	0				-
	-	0				-
Loa loa	myosin xviiia	4	P:GO:0009987; C:GO:0005730; F:GO:0042802; C:GO:0005794	-		IPR001609; PTHR13140 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	beclin 1	15	P:GO:0035121; P:GO:0012501; P:GO:0040010; P:GO:0008340; P:GO:0009267; P:GO:0040024; P:GO:0040027; P:GO:0040035; C:GO:0031410; P:GO:0040011; P:GO:0030163; P:GO:0009792; P:GO:0040018; P:GO:0006914; C:GO:0005634	-		-
Caenorhabditis briggsae	osta1_caeel ame: full=organic solute transporter alpha-like protein	4	C:GO:0016021; P:GO:0009792; P:GO:0006810; F:GO:0005215	-		IPR005178; PTHR23423:SF3 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	multidrug resistance protein family member (mrp-1)	4	P:GO:0009987; P:GO:0006810; F:GO:0042626; C:GO:0005887	-		SignalP (SIGNALP)

Nematostella vectensis	endonuclease-reverse transcriptase	0		F:GO:0003723; F:GO:0004527; P:GO:0006278; F:GO:0004519; F:GO:0003964		PTHR23227 (PANTHER), PTHR23227:SF14 (PANTHER)
Heliconius melpomene	endonuclease-reverse transcriptase	1	F:GO:0005488	-		IPR000477; IPR015706; PTHR19446:SF100 (PANTHER)
Caenorhabditis briggsae	cationic amino acid transporter	5	P:GO:0019915; C:GO:0016021; F:GO:0015171; C:GO:0005886; P:GO:0003333	-		IPR002293; IPR004841; PTHR11785:SF74 (PANTHER), SignalP (SIGNALP)
Homo sapiens	hCG2041804 [Homo sapiens]	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	brox_caeel ame: full=bro1 domain-containing protein brox homolog	0				PTHR23032 (PANTHER)
Caenorhabditis elegans	pecanex-like protein 1	2	C:GO:0016021; P:GO:0040011	-		PTHR12372 (PANTHER)
Caenorhabditis briggsae	pecanex-like protein 1	1	P:GO:0040011	-		-
Caenorhabditis elegans	pecanex-like protein 1	2	C:GO:0016020; P:GO:0040011	-		-
	-	0				-
Caenorhabditis elegans	placental protein 11 related	6	F:GO:0003723; P:GO:0044238; P:GO:0044260; F:GO:0046872; F:GO:0004521; C:GO:0005634	-		IPR018998; PTHR12439 (PANTHER), SSF142877 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	6	P:GO:0009056; P:GO:0018991; F:GO:0004553; P:GO:0006665; P:GO:0040011; C:GO:0016020	-	EC:3.2.1.0	PTHR12654 (PANTHER), PF12215 (PFAM)
Caenorhabditis elegans	plasmid mainte-nce protein containing protein	0		P:GO:0006506; F:GO:0016740; F:GO:0005529; C:GO:0031227; F:GO:0016757		IPR005599; SignalP (SIGNALP)
	-	0				-
Loa loa	elegans protein confirmed by transcript evidence	0		P:GO:0006952; F:GO:0016787; F:GO:0004415; P:GO:0005975; P:GO:0008152; F:GO:0016798; F:GO:0003824; C:GO:0005576		IPR013785; IPR017853; IPR018155
Caenorhabditis briggsae	briggsae cbr-pme-5 protein	0				IPR002110; IPR020683; PTHR18958 (PANTHER)
	-	0				-
Caenorhabditis elegans	proteasome component	1	P:GO:0007067	-		-
	-	0				-

Loa loa	bone morphogenic protein 6	23	N:GO:0061138; P:GO:0031325; P:GO:0007178; P:GO:0048699; P:GO:0042325; P:GO:0035295; P:GO:0010941; P:GO:0001822; P:GO:0001654; P:GO:0045597; P:GO:0040007; P:GO:0010646; P:GO:0048646; P:GO:0035466; F:GO:0005515; N:GO:2000027; P:GO:0048523; P:GO:0022612; P:GO:0045449; P:GO:0051093; P:GO:0048598; P:GO:0010604; P:GO:0060284	-		IPR001839; IPR002405; IPR015615; IPR017948; G3DSA:2.10.90.10 (GENE3D), SSF57501 (SUPERFAMILY)
Angiostrongylus cantonensis	galectin protein 140	0		F:GO:0042302		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	phosphatase and actin regulator 1	1	F:GO:0005488	-		IPR004018; PTHR12751 (PANTHER), PTHR12751:SF3 (PANTHER)
Caenorhabditis elegans	myosin light chain	4	P:GO:0009792; C:GO:0016459; F:GO:0032036; P:GO:0000003	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	sorting nexin-2	5	P:GO:0009792; P:GO:0007126; P:GO:0018991; F:GO:0005515; P:GO:0006810	-		IPR015404; PTHR10555 (PANTHER), PTHR10555:SF28 (PANTHER)
Caenorhabditis briggsae	eri1 exoribonuclease 3 isoform 1	3	F:GO:0016787; F:GO:0005515; C:GO:0005886	-		IPR012337; IPR013520; G3DSA:3.30.420.10 (GENE3D), PTHR23044 (PANTHER), PTHR23044:SF8 (PANTHER)
Ostertagia ostertagi	translatio-lly controlled tumor protein	8	C:GO:0005737; P:GO:0009792; P:GO:0002119; F:GO:0005515; P:GO:0000003; P:GO:0040011; P:GO:0040007; P:GO:0006898	-		-
	-	0				SignalP (SIGNALP)

Ostertagia ostertagi	translatio-lly controlled tumor protein	8	P:GO:0009792; C:GO:0005737; P:GO:0000003; P:GO:0040007; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		IPR001790; IPR011057; IPR011323; IPR018105
Ostertagia ostertagi	translatio-lly controlled tumor protein	8	P:GO:0009792; C:GO:0005737; P:GO:0000003; P:GO:0040007; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		-
Caenorhabditis briggsae	60s acidic ribosomal protein p0	6	C:GO:0005840; F:GO:0003735; F:GO:0005515; P:GO:0042254; F:GO:0003906; P:GO:0006414	-	EC:4.2.99.18	IPR001790; PTHR21141 (PANTHER), PTHR21141:SF3 (PANTHER)
Caenorhabditis elegans	hypothetical protein C25H3.11 [Caenorhabditis elegans]	0		P:GO:0008104		-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021		PTHR23294 (PANTHER), SignalP (SIGNALP)
Macaca mulatta	secreted cysteine-rich	8	F:GO:0050840; P:GO:0042127; C:GO:0031093; F:GO:0005518; P:GO:0071363; P:GO:0001503; F:GO:0005509; C:GO:0005604	-		-
	-	0				-
Caenorhabditis briggsae	udp-xylose and udp-n-acetylglucosamine transporter	8	C:GO:0000139; F:GO:0005464; P:GO:0015790; P:GO:0055085; P:GO:0015788; F:GO:0005351; C:GO:0016021; F:GO:0005462	-		IPR013657; PTHR10778 (PANTHER), PTHR10778:SF4 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	udp-xylose and udp-n-acetylglucosamine transporter	8	C:GO:0000139; F:GO:0005464; P:GO:0015790; P:GO:0055085; P:GO:0015788; F:GO:0005351; C:GO:0016021; F:GO:0005462	-		IPR013657; PTHR10778 (PANTHER), PTHR10778:SF4 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	arginyl-tr- synthetase	3	F:GO:0004812; P:GO:0006418; F:GO:0000166	-		IPR001278; IPR014729; IPR015945; SSF52374 (SUPERFAMILY)
Caenorhabditis elegans	coiled-coil domain containing 132	0		F:GO:0003674; P:GO:0008150		IPR019515; PTHR13258 (PANTHER)

Caenorhabditis elegans	briggsae cbr-ugt-62 protein	3	P:GO:0044238; P:GO:0040010; F:GO:0016757	-		IPR002213
Caenorhabditis briggsae	low-density lipoprotein	2	C:GO:0016021; F:GO:0005509	-		IPR000033; IPR002172; IPR006210; IPR011042; G3DSA:2.10.25.10 (GENE3D), PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER), SSF57196 (SUPERFAMILY), SSF63825 (SUPERFAMILY)
Nasonia vitripennis	tk fer protein ki-se	0		F:GO:0019901; P:GO:0006468; C:GO:0005634; F:GO:0017137; F:GO:0005524; F:GO:0016301; P:GO:0007155; P:GO:0018108; F:GO:0004674; F:GO:0008092; F:GO:0045296; F:GO:0004672; F:GO:0045295; F:GO:0050839; F:GO:0000166; P:GO:0046777; C:GO:0005737; F:GO:0003779; P:GO:0007165; F:GO:0030145; F:GO:0000287; F:GO:0004715; F:GO:0005515; F:GO:0004713; F:GO:0016740; C:GO:0005575; P:GO:0006935		IPR000719; IPR000980; IPR001245; IPR011009; IPR020685; G3DSA:1.10.510.10 (GENE3D), SSF55550 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0005515		-
	-	0				-
Loa loa	rdd family protein	0		F:GO:0003674; C:GO:0005575		IPR010432; PTHR13659 (PANTHER)
	-	0				-
	-	0				-
						IPR003961; IPR008957; IPR013783; PR00014 (PRINTS), PTHR19900 (PANTHER), PTHR19900:SF7 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	type i inositol- -trisphosphate 5-phosphatase	3	P:GO:0046855; F:GO:0004445; F:GO:0005515	-	EC:3.1.3.56	G3DSA:3.60.10.10 (GENE3D), PTHR12997 (PANTHER), PTHR12997:SF3 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-

Caenorhabditis briggsae	integrin alpha-ps2	11	P:GO:0009792; F:GO:0004872; P:GO:0002119; P:GO:0007229; P:GO:0018991; P:GO:0032940; P:GO:0007155; P:GO:0040007; P:GO:0006898; P:GO:0040039; C:GO:0008305	-		G3DSA:2.130.10.130 (GENE3D), PTHR23220 (PANTHER), PTHR23220:SF11 (PANTHER), SSF69318 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-fut-1 protein	3	F:GO:0016757; C:GO:0005794; C:GO:0016020	-		IPR001503; PTHR11929:SF8 (PANTHER)
Caenorhabditis elegans	b-box zinc finger family protein	1	F:GO:0046872	-		-
Loa loa	hypothetical protein LOAG_11558 [Loa loa]	0				-
Caenorhabditis elegans	phosphoserine aminotransferase 1	3	F:GO:0030170; F:GO:0004648; P:GO:0006564	-	EC:2.6.1.52	IPR000192; IPR015421; IPR015424; PTHR21152 (PANTHER), PTHR21152:SF1 (PANTHER)
	-	0				-
Caenorhabditis elegans	pan domain containing protein	0				-
Caenorhabditis briggsae	nuclear autoantigenic sperm protein	0		C:GO:0005694; F:GO:0005488; P:GO:0007275; P:GO:0040011; P:GO:0008150; F:GO:0005515; C:GO:0005634; C:GO:0005575		-
Caenorhabditis briggsae	nuclear autoantigenic sperm protein	0		C:GO:0005694; F:GO:0005488; P:GO:0007275; P:GO:0040011; P:GO:0008150; F:GO:0005515; C:GO:0005634; C:GO:0005575		IPR011990; IPR019544; IPR019734; PTHR15081 (PANTHER), PTHR15081:SF4 (PANTHER), SSF48452 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	P:GO:0040011; F:GO:0005488	-		PTHR15081 (PANTHER), PTHR15081:SF3 (PANTHER)
Caenorhabditis briggsae	nuclear autoantigenic sperm protein	0		C:GO:0005694; F:GO:0005488; P:GO:0007275; P:GO:0040011; P:GO:0008150; C:GO:0005634; C:GO:0005575		-
Caenorhabditis briggsae	nuclear autoantigenic sperm protein	0		C:GO:0005694; F:GO:0005488; P:GO:0007275; P:GO:0040011; P:GO:0008150; F:GO:0005515; C:GO:0005634; C:GO:0005575		IPR011990; IPR019544; IPR019734; PTHR15081 (PANTHER), PTHR15081:SF4 (PANTHER), SSF48452 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	P:GO:0040011; F:GO:0005488	-		PTHR15081 (PANTHER), PTHR15081:SF3 (PANTHER)

Caenorhabditis elegans	nuclear autoantigenic sperm	2	P:GO:0040011; F:GO:0005488	-		PTHR15081 (PANTHER), PTHR15081:SF4 (PANTHER)
Caenorhabditis briggsae	nuclear autoantigenic sperm protein	0		C:GO:0005694; F:GO:0005488; P:GO:0007275; P:GO:0040011; P:GO:0008150; F:GO:0005515; C:GO:0005634; C:GO:0005575		-
Caenorhabditis briggsae	citron (rho- serine threonine ki-se 21)	11	P:GO:0000278; C:GO:0043231; F:GO:0016740; P:GO:0048468; C:GO:0005737; P:GO:0006996; P:GO:0009792; P:GO:0050794; P:GO:0022403; F:GO:0005488; P:GO:0030182	-		IPR001180; PTHR12894 (PANTHER), PTHR12894:SF10 (PANTHER), PS50219 (PROFILE)
Caenorhabditis elegans	ryanodine receptor homologue	11	P:GO:0055085; P:GO:0006629; C:GO:0005875; F:GO:0005509; C:GO:0016021; F:GO:0004872; P:GO:0006874; P:GO:0006816; C:GO:0005789; F:GO:0005219; P:GO:0006936	-		-
Caenorhabditis briggsae	Hypothetical protein CBG15114 [Caenorhabditis briggsae]	0		P:GO:0045454; F:GO:0009055; F:GO:0015035		IPR002109; IPR012335; IPR012336
Caenorhabditis briggsae	pyruvate ki-se	8	P:GO:0009792; F:GO:0004743; F:GO:0016830; P:GO:0006725; F:GO:0005515; F:GO:0030955; F:GO:0000287; P:GO:0006096	-	EC:2.7.1.40	IPR001697; IPR015793; IPR015794; IPR015813

Caenorhabditis elegans	carbamoyl-phosphate synthetase aspartate and dihydroorotase	25	C:GO:0005654; P:GO:0006541; F:GO:0070335; F:GO:0004070; P:GO:0018107; P:GO:0023034; C:GO:0044430; P:GO:0046777; C:GO:0015629; P:GO:0006309; P:GO:0006928; F:GO:0004672; P:GO:0006936; C:GO:0005829; F:GO:0004537; F:GO:0004151; F:GO:0005523; P:GO:0030263; C:GO:0016363; P:GO:0006207; F:GO:0004088; F:GO:0019899; C:GO:0005886; F:GO:0005524; P:GO:0006221	-	EC:2.1.3.2; EC:3.5.2.3; EC:6.3.5.5	G3DSA:3.20.20.140 (GENE3D), PTHR11647 (PANTHER), PTHR11647:SF2 (PANTHER), SSF51556 (SUPERFAMILY)
Caenorhabditis briggsae	amino acid permease family protein	4	P:GO:0019915; C:GO:0016020; P:GO:0006865; P:GO:0055085	-		IPR002293; IPR004841; IPR015606; SignalP (SIGNALP)
Caenorhabditis elegans	ribosomal r- processing 12 homolog (cerevisiae)	2	C:GO:0044464; F:GO:0005488	-		PTHR21576 (PANTHER), PTHR21576:SF2 (PANTHER)
Caenorhabditis briggsae	beige beach domain containing protein	2	F:GO:0008270; C:GO:0005622	-		-
	-	0				-
Harpegnathos saltator	cytochrome p450	6	F:GO:0009055; F:GO:0004497; F:GO:0020037; P:GO:0055114; C:GO:0016020; C:GO:0005783	-		IPR001128; IPR002403; IPR017972
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR017970; IPR018625; SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-cct-1 protein	14	P:GO:0040010; C:GO:0005753; C:GO:0005875; F:GO:0008553; P:GO:0006457; P:GO:0040035; P:GO:0007052; P:GO:0006911; F:GO:0005524; P:GO:0002119; P:GO:0040039; P:GO:0006898; F:GO:0051082; P:GO:0009792	-	EC:3.6.3.6	IPR002194; IPR002423; IPR012715; IPR017998; G3DSA:1.10.560.10 (GENE3D), G3DSA:3.30.260.10 (GENE3D), G3DSA:3.50.7.10 (GENE3D), SSF52029 (SUPERFAMILY), SSF54849 (SUPERFAMILY)
	-	0				-

Caenorhabditis elegans	uncoordi-ted family member (unc-44)	0		F:GO:0005509; P:GO:0007156; P:GO:0007155; C:GO:0016021; C:GO:0016020; F:GO:0005515; C:GO:0005886		-
Caenorhabditis elegans	prkca-binding protein	21	F:GO:0005080; P:GO:0015844; P:GO:0006468; F:GO:0005102; C:GO:0030666; F:GO:0008022; P:GO:0007205; C:GO:0042734; P:GO:0006605; C:GO:0005794; P:GO:0043045; P:GO:0023060; P:GO:0043046; P:GO:0006890; C:GO:0048471; F:GO:0016887; P:GO:0051260; P:GO:0045161; C:GO:0005886; P:GO:0043113; C:GO:0005739	-		IPR010504; PTHR12141 (PANTHER), PTHR12141:SF2 (PANTHER), SSF103657 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	egf-like domain containing protein	0		F:GO:0005509		IPR011038
	-	0				-
	-	0				-
Caenorhabditis briggsae	loc446287 protein	2	P:GO:0055114; F:GO:0003995	-	EC:1.3.99.3	IPR006091; IPR009100
Caenorhabditis briggsae	Hypothetical protein CBG16936 [Caenorhabditis briggsae]	0				IPR000436; IPR016060; PTHR19325 (PANTHER), PTHR19325:SF25 (PANTHER)
	-	0				-
Loa loa	hypothetical protein LOAG_02167 [Loa loa]	0				IPR013924
Caenorhabditis elegans	slo-2	6	C:GO:0016020; P:GO:0006813; P:GO:0008152; F:GO:0003824; F:GO:0015269; F:GO:0005488	-		PTHR10027 (PANTHER), PTHR10027:SF6 (PANTHER)
	-	0				-

Pongo abelii	filamin a	28	F:GO:0004871; C:GO:0005802; P:GO:0043433; P:GO:0034394; C:GO:0015629; P:GO:0050821; P:GO:0051220; C:GO:0005576; C:GO:0005829; F:GO:0001948; P:GO:0051764; P:GO:0043123; F:GO:0051015; F:GO:0048365; P:GO:0045022; P:GO:0007195; F:GO:0042803; F:GO:0034989; P:GO:0031532; F:GO:0034988; C:GO:0005886; F:GO:0008134; P:GO:0042177; C:GO:0005634; P:GO:0042993; C:GO:0005938;	-		IPR013783; IPR014756; IPR017868; PTHR11915 (PANTHER), PTHR11915:SF24 (PANTHER)
Caenorhabditis briggsae	wd repeat domain 11	0				IPR011046; IPR015943
Caenorhabditis elegans	cell adhesion molecule	8	F:GO:0030506; P:GO:0007417; P:GO:0007409; P:GO:0045162; P:GO:0048513; N:GO:0071842; P:GO:0090066; C:GO:0044459	-		IPR003961; IPR008957; IPR013783; PTHR10489 (PANTHER), PTHR10489:SF39 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein Y47G6A.29 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	sodium calcium	11	P:GO:0055085; F:GO:0005432; F:GO:0031072; P:GO:0008016; P:GO:0045214; C:GO:0016021; P:GO:0000003; P:GO:0006874; P:GO:0006816; P:GO:0007154; P:GO:0009792	-		IPR004837; PTHR11878 (PANTHER), PTHR11878:SF4 (PANTHER)

Caenorhabditis elegans	briggsae cbr-ncx-3 protein	14	P:GO:0006814; F:GO:0005432; F:GO:0005516; C:GO:0005739; C:GO:0005874; P:GO:0071320; C:GO:0043197; P:GO:0060402; P:GO:0021537; C:GO:0043025; C:GO:0042383; P:GO:0007154; P:GO:0034220; C:GO:0005887	-		IPR004837; PTHR11878 (PANTHER), PTHR11878:SF2 (PANTHER), SignalP (SIGNALP)
Ixodes scapularis	protein-tyrosine non-receptor type nt5	7	C:GO:0005737; F:GO:0004725; C:GO:0005856; F:GO:0004872; C:GO:0019898; F:GO:0008092; P:GO:0006470	-	EC:3.1.3.48	-
Caenorhabditis elegans	transcription factor protein	11	F:GO:0030528; P:GO:0034976; F:GO:0010843; C:GO:0016021; P:GO:0002062; P:GO:0006355; F:GO:0046983; F:GO:0003700; P:GO:0006986; C:GO:0005789; C:GO:0005634	-		IPR004827; IPR008917; IPR011616; G3DSA:1.20.5.170 (GENE3D), PTHR22952 (PANTHER), PTHR22952:SF7 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F08F3.1 [Caenorhabditis elegans]	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	chromosome 14 open reading frame 133	4	C:GO:0005768; F:GO:0005515; P:GO:0046907; P:GO:0015031	-		IPR019177; PTHR13364 (PANTHER)
Caenorhabditis briggsae	citrate lyase beta like	4	F:GO:0046872; F:GO:0008815; P:GO:0006725; C:GO:0009346	-	EC:4.1.3.6	IPR005000; IPR011206; IPR015813
Pongo abelii	ribosomal protein l18a	5	F:GO:0003735; F:GO:0003723; F:GO:0005515; C:GO:0022625; P:GO:0006414	-		-
Brugia malayi	arp1 actin-related protein 1 homolog centractin alpha	6	C:GO:0005815; C:GO:0005869; F:GO:0005515; P:GO:0016192; F:GO:0005524; C:GO:0005829	-		IPR004000; G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), PTHR11937:SF46 (PANTHER), SSF53067 (SUPERFAMILY)

Pongo abelii	protein phosphatase catalytic alpha isoform	20	P:GO:0005981; P:GO:0030324; C:GO:0043197; F:GO:0005515; P:GO:0007143; F:GO:0043021; P:GO:0051301; C:GO:0000164; C:GO:0005730; C:GO:0005829; F:GO:0046872; P:GO:0005979; P:GO:0006417; P:GO:0048754; C:GO:0070688; P:GO:0006470; C:GO:0043204; F:GO:0008599; F:GO:0004722; C:GO:0042587	-		-
	-	0				-
Loa loa	exostoses 2	1	F:GO:0016757	-		SignalP (SIGNALP)
Caenorhabditis briggsae	ypp3_caeel ame: full=uncharacterized serine carboxypeptidase flags: precursor	0		P:GO:0006508; F:GO:0004185		IPR001563; G3DSA:3.40.50.1820 (GENE3D), PTHR11802:SF9 (PANTHER)
Caenorhabditis elegans	solute carrier family member b3	3	C:GO:0000139; C:GO:0016021; P:GO:0055085	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG02118 [Caenorhabditis briggsae]	0				-
	-	0				-
	-	0				IPR002052
	-	0				-
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0		F:GO:0003725; C:GO:0005622		-
Caenorhabditis briggsae	beta-lactamase family protein	0				IPR001466; IPR012338; G3DSA:3.40.710.10 (GENE3D), PTHR10566 (PANTHER), PTHR10566:SF6 (PANTHER)
Caenorhabditis elegans	epithelial fusion failure family member (eff-1)	0				-
	-	0				-
Caenorhabditis elegans	low-density lipoprotein receptor related family member (lrp-1)	3	F:GO:0004872; C:GO:0016021; F:GO:0005509	-		-
Caenorhabditis elegans	Hypothetical protein T15B7.1 [Caenorhabditis elegans]	0		F:GO:0005102; C:GO:0005615; P:GO:0007165; P:GO:0009792		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0000003; P:GO:0018996; P:GO:0002119; P:GO:0009792; P:GO:0040007		-

Caenorhabditis briggsae	tr--dihydrouridine synthase 1-like	4	F:GO:0050660; P:GO:0055114; F:GO:0017150; P:GO:0008033	-		IPR001269; PTHR11082:SF5 (PANTHER)
Caenorhabditis briggsae	nuclear receptor nhr-114	8	F:GO:0042802; F:GO:0003700; F:GO:0043565; F:GO:0003707; P:GO:0019915; C:GO:0005634; F:GO:0008270; P:GO:0006355	-		IPR008946; PTHR11865 (PANTHER), PTHR11865:SF218 (PANTHER)
Caenorhabditis elegans	protocadherin 11 x-linked	4	P:GO:0002119; P:GO:0040010; P:GO:0040011; C:GO:0016020	-		IPR002126; IPR015919; IPR020894; PTHR10596 (PANTHER), PTHR10596:SF74 (PANTHER)
Caenorhabditis elegans	rab6ip1-like protein	0				IPR004012; SSF140741 (SUPERFAMILY)
Caenorhabditis briggsae	udp-glucose ceramide glucosyltransferase-like 1	5	F:GO:0003980; P:GO:0051084; P:GO:0006486; F:GO:0051082; C:GO:0005783	-		IPR009448
Caenorhabditis briggsae	lung seven transmembrane receptor family protein	0		F:GO:0004872; C:GO:0016021		-
Caenorhabditis briggsae	ral	14	P:GO:0008340; P:GO:0046329; P:GO:0007391; P:GO:0007264; C:GO:0005622; P:GO:0006913; P:GO:0045087; F:GO:0004767; P:GO:0007298; F:GO:0005515; F:GO:0003924; P:GO:0006886; F:GO:0005525; C:GO:0005886	-	EC:3.1.4.12; EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	SignalP (SIGNALP)
Caenorhabditis briggsae	d-2-like helicase	11	P:GO:0045740; F:GO:0016890; P:GO:0006284; C:GO:0005760; P:GO:0006264; P:GO:0043137; F:GO:0017108; F:GO:0016887; F:GO:0000166; F:GO:0004386; C:GO:0005654	-	EC:3.1.25.0	-
Trichostrongylus vitrinus	serine or cysteine protease inhibitor	5	F:GO:0008233; F:GO:0004867; F:GO:0005515; P:GO:0007275; C:GO:0005634	-		IPR000215; G3DSA:3.30.497.10 (GENE3D), PTHR11461:SF25 (PANTHER)

Trichostrongylus vitrinus	serine or cysteine protease inhibitor	5	F:GO:0008233; F:GO:0004867; F:GO:0005515; P:GO:0007275; C:GO:0005634	-		IPR000215; G3DSA:3.30.497.10 (GENE3D), PTHR11461:SF25 (PANTHER)
	-	0				-
Caenorhabditis briggsae	splicing factor 3a subunit 3 (spliceosome-associated protein 61) (sap 61)	14	P:GO:0051533; F:GO:0008270; F:GO:0003676; C:GO:0071011; C:GO:0005686; P:GO:0040035; P:GO:0009566; P:GO:0018996; P:GO:0007052; P:GO:0010171; F:GO:0005515; P:GO:0000398; P:GO:0040039; C:GO:0071013	-		IPR000690; IPR015880; PTHR12786 (PANTHER), PTHR12786:SF2 (PANTHER), PF11931 (PFAM)
	-	0				-
Caenorhabditis elegans	briggsae cbr-ced-5 protein	7	F:GO:0005083; P:GO:0043652; C:GO:0005886; F:GO:0032403; F:GO:0019899; P:GO:0040039; F:GO:0017124	-		PTHR23317 (PANTHER), PTHR23317:SF16 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	sp1070 cg9138-pa	2	C:GO:0016021; F:GO:0005509	-		IPR000436; IPR016060
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	P:GO:0019915	-		-
Caenorhabditis elegans	brain protein 16	0		F:GO:0003674; F:GO:0005488; P:GO:0008150; C:GO:0005575		IPR007205; IPR007206
Caenorhabditis elegans	inositol polyphosphate-5- 40kda	1	F:GO:0004437	-		IPR000300; IPR005135; G3DSA:3.60.10.10 (GENE3D), PTHR12997 (PANTHER), PTHR12997:SF2 (PANTHER)
Caenorhabditis elegans	iron-responsive element-binding protein 1	6	P:GO:0006879; F:GO:0005515; F:GO:0051539; F:GO:0003994; P:GO:0008152; C:GO:0005829	-	EC:4.2.1.3	-
	-	0				-
Brugia malayi	high mobility group family	0		F:GO:0003677; C:GO:0005634		IPR000910; IPR009071; PTHR10270 (PANTHER), PTHR10270:SF31 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis remanei	elegans protein confirmed by transcript evidence	0		P:GO:0007218; C:GO:0016021		SignalP (SIGNALP)

Caenorhabditis elegans	r- pseudouridylate synthase domain-containing protein 2-like	4	P:GO:0009451; F:GO:0003723; F:GO:0005515; F:GO:0009982	-	EC:5.4.99.12	IPR006145; IPR006224; IPR020103; PTHR10436 (PANTHER)
Caenorhabditis elegans	glutaredoxin family protein	2	C:GO:0043231; P:GO:0040010	-		IPR002109; IPR011767; IPR012335; IPR012336; IPR014025; PTHR10168 (PANTHER), PTHR10168:SF19 (PANTHER)
Caenorhabditis briggsae	chromosome 20 open reading frame 54	7	P:GO:0009792; C:GO:0005887; F:GO:0005515; P:GO:0034605; P:GO:0032218; F:GO:0032217; P:GO:0006898	-		IPR009357; SignalP (SIGNALP)
	-	0				IPR000307; PTHR12919:SF1 (PANTHER)
	-	0				-
Brugia malayi	protein ki-se domain containing protein	3	P:GO:0040022; F:GO:0016301; P:GO:0051729	-		IPR000719; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER), SignalP (SIGNALP)
Brugia malayi	protein ki-se domain containing protein	3	P:GO:0040022; F:GO:0016301; P:GO:0051729	-		IPR000719; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	iron only hydroge-se large c-termi-l domain containing protein	2	F:GO:0005488; P:GO:0044249	-		IPR004108; IPR009016; G3DSA:3.40.950.10 (GENE3D), PTHR11615 (PANTHER), PTHR11615:SF31 (PANTHER)
Caenorhabditis elegans	ipase c family member (plc-3)	0				-
Caenorhabditis elegans	5 - cytosolic iii	5	F:GO:0008253; P:GO:0055086; F:GO:0008665; F:GO:0005488; C:GO:0005783	-	EC:3.1.3.5	IPR006434; PF05822 (PFAM)
Caenorhabditis briggsae	briggsae cbr-gei-9 protein	4	P:GO:0009792; P:GO:0040010; P:GO:0000003; P:GO:0006898	-		-
	-	0				-
Danio rerio	eorge syndrome critical region gene 8	5	P:GO:0031053; F:GO:0003725; F:GO:0005515; C:GO:0005737; C:GO:0005634	-		-
Caenorhabditis elegans	transcription termi-tion	2	P:GO:0006264; P:GO:0006390	-		IPR003690; PTHR13068 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG07646 [Caenorhabditis briggsae]	0				PTHR10984 (PANTHER), PTHR10984:SF1 (PANTHER)

Caenorhabditis briggsae	briggsae cbr-evl-14 protein	3	F:GO:0005488; P:GO:0008283; P:GO:0007049	-		PTHR12663 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-evl-14 protein	3	F:GO:0005488; P:GO:0008283; P:GO:0007049	-		PTHR12663 (PANTHER)
Caenorhabditis elegans	tip41-like protein	1	P:GO:0018991	-		IPR007303; PTHR21021 (PANTHER), PTHR21021:SF16 (PANTHER)
	-	0				-
Loa loa	cyclin g associated ki-se	6	P:GO:0006468; F:GO:0031072; C:GO:0044464; F:GO:0005524; F:GO:0004674; F:GO:0030332	-	EC:2.7.11.0	IPR001623; PTHR23172 (PANTHER), PTHR23172:SF19 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-eor-1 protein	1	F:GO:0005515	-		-
Caenorhabditis briggsae	uncoordi-ted family member (unc-52)	2	P:GO:0030239; C:GO:0005578	-		IPR003598; IPR007110; IPR013098; IPR013783; PTHR10574 (PANTHER), PTHR10574:SF20 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	hypothetical protein K11C4.2 [Caenorhabditis elegans]	0		C:GO:0016021		-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0008270; C:GO:0005622		-
Caenorhabditis elegans	major facilitator superfamily protein	1	P:GO:0019915	-		PTHR11662 (PANTHER), PTHR11662:SF21 (PANTHER)
	-	0				-
Apis mellifera	coagulation factor x	2	F:GO:0008233; F:GO:0005488	-		IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR19355 (PANTHER), PTHR19355:SF82 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	protein tyrosine receptor isoform cra_a	16	P:GO:0006470; P:GO:0040037; P:GO:0040010; P:GO:0018991; P:GO:0040002; F:GO:0004872; P:GO:0046627; F:GO:0004725; P:GO:0010171; P:GO:0002119; P:GO:0040017; F:GO:0042803; P:GO:0002009; C:GO:0005737; C:GO:0005886; P:GO:0007185	-	EC:3.1.3.48	IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF43 (PANTHER), SSF52799 (SUPERFAMILY)
	-	0				-

Caenorhabditis elegans	hypothetical protein F25G6.9 [Caenorhabditis elegans]	0		F:GO:0008312; F:GO:0030942; C:GO:0005786; P:GO:0006614; C:GO:0048500; F:GO:0005515; P:GO:0045900		-
Caenorhabditis elegans	sorting nexin 6	6	P:GO:0030512; P:GO:0016481; F:GO:0042803; F:GO:0035091; C:GO:0005737; P:GO:0015031	-		IPR001683; PTHR10555 (PANTHER), PTHR10555:SF4 (PANTHER)
						-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Ajellomyces dermatitidis ER-3	hypothetical protein BDCG_03388 [Ajellomyces dermatitidis ER-3]	0				-
Loa loa	ring finger protein	1	F:GO:0005488	-		IPR001841; IPR013083; IPR017907; IPR018957; PTHR10825 (PANTHER), PTHR10825:SF17 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein Y71H2AM.15 [Caenorhabditis elegans]	2	F:GO:0005515; P:GO:0008340	-		-
Caenorhabditis elegans	hypothetical protein ZK154.4 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	acetyl-coenzyme a carboxylase alpha	8	P:GO:0008610; F:GO:0016874; P:GO:0042592; P:GO:0042221; P:GO:0032501; F:GO:0000166; C:GO:0005811; P:GO:0044237	-		IPR016185; PTHR18866 (PANTHER), PTHR18866:SF6 (PANTHER)
Ixodes scapularis	protein tyrosine	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	amidase domain containing	1	F:GO:0003824	-		IPR000120; PTHR11895:SF5 (PANTHER)
Loa loa	hypothetical protein LOAG_06054 [Loa loa]	2	P:GO:0007186; C:GO:0016021	-		-
	-	0				-
Caenorhabditis sp. PS1010	briggsae cbr-aph-2 protein	0		F:GO:0016874; P:GO:0006418; C:GO:0016021; F:GO:0000166; C:GO:0005737; P:GO:0006412; F:GO:0005524; F:GO:0004818; P:GO:0016485; F:GO:0004812; F:GO:0016876; P:GO:0006424; P:GO:0043039		-
Caenorhabditis elegans	p40	0				-

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	3	C:GO:0016020; F:GO:0005216; P:GO:0006811	-		IPR013099; G3DSA:1.10.287.70 (GENE3D), PTHR11003 (PANTHER), PTHR11003:SF7 (PANTHER), SSF81324 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	zinc finger protein	14	P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0035152; P:GO:0006915; P:GO:0040018; F:GO:0003676; P:GO:0040010; P:GO:0008340; P:GO:0040011; P:GO:0019915; C:GO:0005634; F:GO:0008270; P:GO:0002009	-		IPR007087; IPR013087; IPR015880; PTHR23228 (PANTHER), PTHR23228:SF41 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis elegans	ubiquitin protein ligase	4	C:GO:0005622; F:GO:0016881; F:GO:0005515; P:GO:0006464	-	EC:6.3.2.0	IPR000569; IPR001202; G3DSA:2.20.70.10 (GENE3D), PTHR11254 (PANTHER), PTHR11254:SF65 (PANTHER)
Caenorhabditis elegans	ubiquitin protein ligase	4	C:GO:0005622; F:GO:0016881; F:GO:0005515; P:GO:0006464	-	EC:6.3.2.0	IPR000008; IPR000569; IPR001202; IPR008973; IPR018029; G3DSA:2.20.70.10 (GENE3D), G3DSA:2.60.40.150 (GENE3D), PTHR11254 (PANTHER), PTHR11254:SF65 (PANTHER)
	-	0				-
	-	0				IPR001394; PTHR10420 (PANTHER), PTHR10420:SF40 (PANTHER), SSF54001 (SUPERFAMILY)
Angiostrongylus cantonensis	somatostatin receptor	1	F:GO:0004872	-		IPR000276; IPR017452; G3DSA:1.20.1070.10 (GENE3D), PTHR22751 (PANTHER), PTHR22751:SF8 (PANTHER), SignalP (SIGNALP), SSF81321 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	sh3-domain grb2-like endophilin b2	8	C:GO:0005737; C:GO:0005730; P:GO:0009792; P:GO:0007126; P:GO:0046847; P:GO:0007165; F:GO:0017124; F:GO:0008093	-		-
	-	0				-
Caenorhabditis briggsae	f37c4_caeel ame: full=protein	1	F:GO:0005515	-		-
	-	0				-
Caenorhabditis elegans	lethal k05819-like	0		F:GO:0015662; C:GO:0016020; P:GO:0006754; P:GO:0006812		PTHR13219 (PANTHER)

Caenorhabditis briggsae	udp- c: n-acetylgalactosaminyltransferase	9	P:GO:0018243; C:GO:0032580; C:GO:0016021; F:GO:0030145; P:GO:0018242; F:GO:0004653; C:GO:0048471; C:GO:0005576; F:GO:0005529	-	EC:2.4.1.41	IPR001173; G3DSA:3.90.550.10 (GENE3D), PTHR11675 (PANTHER), SSF53448 (SUPERFAMILY)
Caenorhabditis elegans	d-k protein	14	P:GO:0051603; P:GO:0030512; P:GO:0021680; P:GO:0021589; C:GO:0005788; P:GO:0031398; F:GO:0043022; P:GO:0006983; C:GO:0005576; C:GO:0009986; P:GO:0006987; P:GO:0040019; F:GO:0051787; F:GO:0005524	-		IPR019651; SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein F55A12.2 [Caenorhabditis elegans]	1	P:GO:0040010	-		-
	-	0				-
Caenorhabditis elegans	hed family member (ptc-3)	6	P:GO:0009792; P:GO:0002119; P:GO:0040018; P:GO:0018996; P:GO:0000003; P:GO:0040011	-		-
Caenorhabditis elegans	lipase maturation factor 2	1	C:GO:0044464	-		SignalP (SIGNALP)
Haemonchus contortus	uncoordi-ted family member (unc-49)	6	F:GO:0004890; C:GO:0045211; C:GO:0030054; F:GO:0005230; P:GO:0006811; C:GO:0016021	-		IPR006201; IPR006202; IPR018000; PTHR18945:SF95 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				PS51257 (PROFILE), SignalP (SIGNALP)
Caenorhabditis elegans	nurf (nucleosome remodeling factor) complex homolog family member (nurf-1)	2	P:GO:0000003; P:GO:0040010	-		-
Caenorhabditis elegans	nucleolar protein 120kda	12	P:GO:0040010; F:GO:0003723; P:GO:0008340; P:GO:0006364; P:GO:0000003; P:GO:0002119; F:GO:0005515; F:GO:0008757; P:GO:0040039; P:GO:0009792; P:GO:0040015; P:GO:0040019	-		IPR001678; IPR011023; IPR018314; G3DSA:3.40.50.150 (GENE3D), PTHR22807 (PANTHER), PTHR22807:SF11 (PANTHER), SSF53335 (SUPERFAMILY)

Caenorhabditis elegans	briggsae cbr-acr-6 protein	3	P:GO:0009792; P:GO:0002119; P:GO:0040007	-		-
Caenorhabditis elegans	type iii restriction res subunit family protein	2	F:GO:0017111; F:GO:0005488	-	EC:3.6.1.15	-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	yqk4_caeel ame: full=uncharacterized protein flags: precursor	0				-
Caenorhabditis briggsae	male sterility protein	3	P:GO:0008152; F:GO:0016491; F:GO:0005515	-		IPR004262; PTHR11011 (PANTHER), PTHR11011:SF8 (PANTHER)
Caenorhabditis elegans	briggsae cbr-tag-97 protein	0		P:GO:0006355; F:GO:0043565; F:GO:0003677; C:GO:0005634; F:GO:0003700		IPR003118
Brugia malayi	hypothetical protein [Brugia malayi]	0				IPR009378
	-	0				-
	-	0				-
Caenorhabditis elegans	c-type lectin 1	1	P:GO:0009792	-		IPR001304; IPR002181; IPR002353; IPR014716; IPR016186; IPR016187; PTHR22801 (PANTHER), PTHR22801:SF9 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	methylmalonyl coenzyme a mutase	7	F:GO:0046872; F:GO:0004494; F:GO:0031419; C:GO:0005759; P:GO:0009791; P:GO:0008152; F:GO:0047548	-	EC:5.4.99.2; EC:5.4.99.4	IPR006098; IPR006099; IPR006158; IPR006159; IPR014348; IPR016176; PTHR23408 (PANTHER), PTHR23408:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	methylmalonyl coenzyme a mutase	7	F:GO:0046872; F:GO:0004494; F:GO:0031419; C:GO:0005759; P:GO:0009791; P:GO:0008152; F:GO:0047548	-	EC:5.4.99.2; EC:5.4.99.4	IPR006098; IPR006099; IPR014348; IPR016176; PTHR23408 (PANTHER), PTHR23408:SF1 (PANTHER)
Caenorhabditis elegans	methylmalonyl coenzyme a mutase	6	F:GO:0046872; F:GO:0004494; F:GO:0031419; C:GO:0005759; P:GO:0009791; P:GO:0008152	-	EC:5.4.99.2	IPR006098; IPR006099; IPR006158; IPR006159; IPR014348; IPR016176; PTHR23408 (PANTHER), PTHR23408:SF1 (PANTHER)
Caenorhabditis elegans	methylmalonyl coenzyme a mutase	6	F:GO:0046872; F:GO:0004494; F:GO:0031419; C:GO:0005759; P:GO:0009791; P:GO:0008152	-	EC:5.4.99.2	IPR006098; IPR006099; IPR006158; IPR006159; IPR014348; IPR016176; PTHR23408 (PANTHER), PTHR23408:SF1 (PANTHER)
Caenorhabditis elegans	methylmalonyl coenzyme a mutase	7	F:GO:0046872; F:GO:0004494; F:GO:0031419; C:GO:0005759; P:GO:0009791; P:GO:0008152; F:GO:0047548	-	EC:5.4.99.2; EC:5.4.99.4	IPR006098; IPR006099; IPR006158; IPR006159; IPR014348; IPR016176; PTHR23408 (PANTHER), PTHR23408:SF1 (PANTHER)

Caenorhabditis elegans	ain family member (clp-1)	6	C:GO:0016021; P:GO:0008219; C:GO:0005622; P:GO:0006508; F:GO:0004198; F:GO:0005509	-		IPR022682; IPR022683; G3DSA:2.60.120.380 (GENE3D), PTHR10183 (PANTHER), PTHR10183:SF45 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	n-acylethanolamine-hydrolyzing acid amidase	0		P:GO:0006629; C:GO:0005764; F:GO:0003674; C:GO:0005737; F:GO:0016787; P:GO:0008150		-
	-	0				-
Caenorhabditis elegans	carboxypeptidase d	5	F:GO:0004181; P:GO:0006508; F:GO:0008270; P:GO:0006911; P:GO:0007476	-	EC:3.4.17.0	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11532 (PANTHER), PTHR11532:SF2 (PANTHER), SSF53187 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Loa loa	cell division cycle related family member (cdc-)	17	F:GO:0070011; P:GO:0008103; F:GO:0005515; P:GO:0042052; P:GO:0007317; P:GO:0007029; P:GO:0007030; P:GO:0016320; C:GO:0045169; P:GO:0008104; C:GO:0000502; C:GO:0005875; P:GO:0006508; F:GO:0016887; C:GO:0005783; C:GO:0005811; F:GO:0005524	-		IPR015415; G3DSA:1.10.8.60 (GENE3D), PTHR23077 (PANTHER), PTHR23077:SF18 (PANTHER)
Loa loa	clathrin coat assembly protein ap-1	6	P:GO:0016183; P:GO:0007269; P:GO:0040025; F:GO:0005515; P:GO:0006886; C:GO:0030121	-		-
Cooperia oncophora	latrophilin-like protein 2	6	P:GO:0007218; C:GO:0016021; P:GO:0007165; C:GO:0005886; F:GO:0005529; F:GO:0004930	-		IPR000203; PTHR12011 (PANTHER), PTHR12011:SF56 (PANTHER)
Caenorhabditis elegans	yl54_caeel ame: full=uncharacterized protein	0				-

Phoca largha	lactate dehydroge-se b	5	F:GO:0005488; F:GO:0004459; P:GO:0055114; P:GO:0006096; C:GO:0005739	-	EC:1.1.1.27	IPR015955; IPR018177; IPR022383; PTHR11540 (PANTHER), PTHR11540:SF3 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	15	P:GO:0007605; P:GO:0007588; F:GO:0008553; P:GO:0006885; C:GO:0031526; P:GO:0015991; C:GO:0016021; P:GO:0001503; F:GO:0051117; P:GO:0015986; C:GO:0016471; C:GO:0005768; P:GO:0040013; C:GO:0033177; C:GO:0016324	-	EC:3.6.3.6	IPR002490; PTHR11629:SF23 (PANTHER)
	-	0				-
Caenorhabditis elegans	cytoskeleton-associated protein 5	1	F:GO:0005515	-		IPR010916; IPR011989; PTHR12609 (PANTHER)
Caenorhabditis briggsae	d- repair endonuclease xpf	7	P:GO:0006310; P:GO:0033683; F:GO:0004520; P:GO:0007127; P:GO:0009792; C:GO:0000109; F:GO:0043566	-		IPR011335; IPR020819; PTHR10150 (PANTHER)
Caenorhabditis briggsae	proton-coupled amino acid transporter 1	4	C:GO:0005886; F:GO:0015171; P:GO:0006865; C:GO:0016021	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	der1-like domain member 2	7	P:GO:0030433; C:GO:0030176; F:GO:0005515; P:GO:0030968; P:GO:0030970; P:GO:0030307; P:GO:0008284	-		-
Caenorhabditis elegans	der1-like domain member 2	7	P:GO:0030433; C:GO:0030176; F:GO:0005515; P:GO:0030968; P:GO:0030970; P:GO:0030307; P:GO:0008284	-		IPR007599; SignalP (SIGNALP)
Caenorhabditis elegans	der1-like domain member 2	7	P:GO:0030433; C:GO:0030176; F:GO:0005515; P:GO:0030968; P:GO:0030970; P:GO:0030307; P:GO:0008284	-		IPR007599; SignalP (SIGNALP)
	-	0				-
	-	0				-

	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Nematostella vectensis	kiaa1033 protein	1	C:GO:0071203	-		-
Sinorhizobium medicae WSM419	tr- modification gtpase	10	C:GO:0005737; P:GO:0006259; F:GO:0046872; F:GO:0008094; F:GO:0005525; F:GO:0003677; P:GO:0006400; F:GO:0005524; P:GO:0007264; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Caenorhabditis briggsae	briggsae cbr-rbc-2 protein	0				IPR015943; IPR017986; IPR019782; PTHR22847 (PANTHER), PTHR22847:SF4 (PANTHER)
Caenorhabditis briggsae	chondroitin polymerizing factor	8	P:GO:0000910; F:GO:0016758; P:GO:0040035; P:GO:0006898; P:GO:0048871; P:GO:0009792; C:GO:0016020; C:GO:0005794	-	EC:2.4.1.0	IPR008428
Loa loa	akt-interacting protein	10	C:GO:0070695; C:GO:0030897; P:GO:0001934; P:GO:0008333; P:GO:0032092; F:GO:0005515; P:GO:0045022; P:GO:0007032; P:GO:0007040; C:GO:0005886	-		IPR000608; IPR016135; PTHR11621 (PANTHER), PTHR11621:SF7 (PANTHER)
	-	0				-
Caenorhabditis elegans	yx7o_caeel ame: full=uncharacterized protein flags: precursor	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		C:GO:0016021		-
Caenorhabditis elegans	protease-associated domain-containing protein of 21	0		F:GO:0008233; P:GO:0007521; C:GO:0005576		IPR003137; G3DSA:3.50.30.30 (GENE3D), PTHR22702 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-

Caenorhabditis elegans	can cell migration defective family member (cam-1)	16	P:GO:0016477; P:GO:0007411; C:GO:0030424; C:GO:0032809; F:GO:0004674; C:GO:0030425; P:GO:0005975; P:GO:0040035; P:GO:0007169; F:GO:0005524; C:GO:0031594; F:GO:0005515; F:GO:0004714; C:GO:0005887; P:GO:0006468; P:GO:0045200	-	EC:2.7.11.0; EC:2.7.10.1	-
Caenorhabditis elegans	enhancer of mr--decapping protein 3	0		F:GO:0003674; C:GO:0005737; C:GO:0000932; P:GO:0008150; F:GO:0005515; C:GO:0005575		IPR021024
Caenorhabditis elegans	28s ribosomal protein s5	9	P:GO:0006412; P:GO:0040010; F:GO:0003723; C:GO:0005840; C:GO:0005739; F:GO:0003735; P:GO:0002119; P:GO:0006898; P:GO:0009792	-	EC:3.6.5.3	IPR000851; IPR013810; IPR014720; IPR018192; PTHR13718:SF3 (PANTHER), SSF54768 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
						-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR021010; SSF141739 (SUPERFAMILY)
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG11345 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	briggsae cbr-pqn-20 protein	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-pqn-20 protein	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-pqn-20 protein	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-pqn-20 protein	0				SignalP (SIGNALP)
Caenorhabditis elegans	in family member (ttn-1)	4	P:GO:0009987; F:GO:0005488; F:GO:0004674; P:GO:0009792	-	EC:2.7.11.0	IPR003598; IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)

Pongo abelii	filamin alpha (actin binding protein 280)	28	F:GO:0004871; C:GO:0005802; P:GO:0043433; P:GO:0034394; C:GO:0015629; P:GO:0050821; P:GO:0051220; C:GO:0005576; C:GO:0005829; F:GO:0001948; P:GO:0051764; P:GO:0043123; F:GO:0051015; F:GO:0048365; P:GO:0045022; P:GO:0007195; F:GO:0042803; F:GO:0034989; P:GO:0031532; F:GO:0034988; C:GO:0005886; F:GO:0008134; P:GO:0042177; C:GO:0005634; P:GO:0042993; C:GO:0005938; P:GO:0043113	-		-
Caenorhabditis elegans	ankyrin repeat domain-containing protein 13c	1	C:GO:0005783	-		IPR021832; PTHR12447 (PANTHER)
	-	0				SignalP (SIGNALP)
Ancylostoma ceylanicum	metalloprotease 1 precursor	1	F:GO:0008233	-		IPR000859; PTHR10127 (PANTHER), PTHR10127:SF60 (PANTHER)
Caenorhabditis briggsae	wu:fc51g12 protein	9	F:GO:0008017; P:GO:0000910; P:GO:0045132; C:GO:0000922; P:GO:0090307; C:GO:0005813; P:GO:0051299; P:GO:0009792; F:GO:0008574	-	EC:3.6.4.4	IPR001752; PTHR16012 (PANTHER), PTHR16012:SF82 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	erin family member (cdh-6)	2	C:GO:0016020; P:GO:0007155	-		-

Loa loa	lethal family member (let-413)	24	F:GO:0005515; P:GO:0060561; P:GO:0032863; P:GO:0045930; P:GO:0050918; C:GO:0042734; C:GO:0005913; C:GO:0034750; P:GO:0008283; P:GO:0016337; C:GO:0016323; P:GO:0045108; P:GO:0015031; P:GO:0016080; P:GO:0001921; C:GO:0045211; P:GO:0060603; C:GO:0031252; P:GO:0008105; P:GO:0035089; P:GO:0016331; P:GO:0043615; P:GO:0043065; P:GO:0048488	-		IPR001611; PR00019 (PRINTS), G3DSA:3.80.10.10 (GENE3D), PTHR23155 (PANTHER), PTHR23155:SF30 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	briggsae cbr-igcm-1 protein	0		C:GO:0016020		PTHR11640 (PANTHER), PTHR11640:SF2 (PANTHER)
Caenorhabditis briggsae	ras protein	0		F:GO:0005525; F:GO:0003924; P:GO:0007264; F:GO:0000166; C:GO:0016020; P:GO:0007165; C:GO:0005886; C:GO:0005622		IPR001806; IPR013753; IPR020849; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF126 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	multiple pdz domain protein family member (mpz-1)	7	P:GO:0042552; C:GO:0044456; C:GO:0005923; C:GO:0016021; F:GO:0008022; P:GO:0007155; C:GO:0042995	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR19964 (PANTHER), PTHR19964:SF5 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	9	P:GO:0009792; F:GO:0016491; P:GO:0040018; P:GO:0019373; F:GO:0005506; P:GO:0040017; P:GO:0040010; P:GO:0000003; P:GO:0008340	-		IPR001128; PTHR19383:SF176 (PANTHER)
	-	0				-

Caenorhabditis elegans	r- polymerase i polypeptide b	9	F:GO:0003899; P:GO:0040007; P:GO:0040035; P:GO:0002119; F:GO:0005515; F:GO:0032549; C:GO:0005654; P:GO:0009792; P:GO:0006350	-	EC:2.7.7.6	SSF64484 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Loa loa	protein ki-se domain containing protein	0		F:GO:0016301; F:GO:0004672; F:GO:0005524; F:GO:0000166; P:GO:0006468; F:GO:0004674		-
Caenorhabditis briggsae	tetratricopeptide repeat protein 7a	0		F:GO:0005488		IPR011990; IPR013026; PTHR23083 (PANTHER), SSF48452 (SUPERFAMILY)
Brugia malayi	calcium atpase	5	F:GO:0005388; C:GO:0016021; P:GO:0006754; F:GO:0005524; P:GO:0006816	-	EC:3.6.3.8	IPR001757; G3DSA:1.20.1110.10 (GENE3D), PTHR11939:SF76 (PANTHER), SSF56784 (SUPERFAMILY)
Homo sapiens	complement c1r subcomponent precursor	6	F:GO:0004252; P:GO:0045087; F:GO:0005509; P:GO:0006958; C:GO:0005576; P:GO:0006508	-	EC:3.4.21.0	-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	briggsae cbr-asm-1 protein	4	P:GO:0046513; F:GO:0004767; C:GO:0005576; P:GO:0006685	-	EC:3.1.4.12	-
Caenorhabditis briggsae	ptk2 protein tyrosine ki-se 2	4	P:GO:0009987; F:GO:0004672; F:GO:0000166; C:GO:0044464	-		IPR001245; IPR011009; IPR017441; IPR020685; G3DSA:3.30.200.20 (GENE3D), PTHR23256:SF267 (PANTHER)
Ostertagia ostertagi	excretory secretory antigen	1	F:GO:0019841	-		-
Caenorhabditis elegans	uncoordi-ted family member (unc-89)	0				IPR013783; PTHR19897 (PANTHER), PTHR19897:SF5 (PANTHER)
Caenorhabditis briggsae	membrane bound o-acyl mboat protein isoform partially confirmed by transcript evidence	2	C:GO:0016021; P:GO:0010171	-		IPR004299; PTHR13906 (PANTHER), PTHR13906:SF2 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Homo sapiens	transmembrane protein 176b	4	C:GO:0031965; P:GO:0030154; P:GO:0009887; C:GO:0016021	-		-
	-	0				SignalP (SIGNALP)
Loa loa	lethal family member (let-23)	2	F:GO:0005488; F:GO:0004672	-		-

Macaca mulatta	elongation factor 2	7	C:GO:0005737; F:GO:0003746; F:GO:0005525; F:GO:0005515; C:GO:0030529; P:GO:0006414; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000795; G3DSA:3.40.50.300 (GENE3D), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein F35H10.10 [Caenorhabditis elegans]	4	P:GO:0007186; C:GO:0016021; P:GO:0007165; F:GO:0004930	-		IPR017978; PTHR11336 (PANTHER), PTHR11336:SF8 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	uncoordi-ted family member (unc-26)	7	P:GO:0046549; F:GO:0003676; P:GO:0006796; P:GO:0007268; P:GO:0050808; P:GO:0006897; F:GO:0004437	-		IPR002013; PTHR11200 (PANTHER), PTHR11200:SF10 (PANTHER)
Caenorhabditis briggsae	6-phosphofructo-2- isoform a	7	F:GO:0003873; P:GO:0007420; F:GO:0004331; F:GO:0005524; F:GO:0005515; P:GO:0006110; P:GO:0006003	-	EC:2.7.1.105; EC:3.1.3.46	IPR001345; IPR003094; IPR013078; IPR013079; G3DSA:3.40.50.1240 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR10606:SF11 (PANTHER), SSF52540 (SUPERFAMILY), SSF53254 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	protein tyrosine receptor q	5	P:GO:0009987; P:GO:0040027; F:GO:0016791; P:GO:0040026; C:GO:0016020	-	EC:3.1.3.0	IPR003961; IPR008957; IPR013783; PTHR19900 (PANTHER), PTHR19900:SF7 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				IPR000210; IPR011333; IPR013069
Caenorhabditis briggsae	peroxisomal carnitine o-octanoyltransferase	4	F:GO:0008415; C:GO:0005777; P:GO:0006810; P:GO:0042221	-		IPR000542; PTHR22589:SF9 (PANTHER), SSF52777 (SUPERFAMILY)
Caenorhabditis briggsae	calcium-binding protein p22	12	P:GO:0045056; P:GO:0002119; F:GO:0015459; P:GO:0019722; P:GO:0017156; P:GO:0040010; F:GO:0005509; P:GO:0000003; P:GO:0040011; P:GO:0006813; C:GO:0005829; P:GO:0007264	-		IPR002048; IPR011992; IPR018247; IPR018248; IPR018249; PTHR23056 (PANTHER), PTHR23056:SF4 (PANTHER), SSF47473 (SUPERFAMILY)
Ambystoma tigrinum virus	unknown [Ambystoma tigrinum virus]	0		P:GO:0006353; F:GO:0003715		IPR017956
Caenorhabditis elegans	variable abnormal morphology family member (vab-19)	0				-

Loa loa	variable abnormal morphology family member (vab-10)	0				G3DSA:3.90.1290.10 (GENE3D), SSF75399 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-nhx-2 protein	16	P:GO:0006814; P:GO:0001101; P:GO:0045768; P:GO:0007243; F:GO:0015385; C:GO:0016021; P:GO:0010447; C:GO:0005624; C:GO:0045121; P:GO:0014070; F:GO:0008134; C:GO:0016323; P:GO:0034220; P:GO:0009792; P:GO:0006885; P:GO:0015992	-		IPR004709; IPR006153; IPR018407; IPR018422; SignalP (SIGNALP)
Monodelphis domestica	ubiquitin specific peptidase 3	8	P:GO:0000278; F:GO:0004221; P:GO:0006281; F:GO:0042393; C:GO:0000790; P:GO:0016578; P:GO:0031647; F:GO:0004843	-	EC:3.1.2.15	IPR001394; IPR018200; PTHR10420 (PANTHER), PTHR10420:SF58 (PANTHER), SignalP (SIGNALP), SSF54001 (SUPERFAMILY)
Trichoplax adhaerens	ubiquitin specific peptidase 3	1	F:GO:0016787	-		IPR001394; IPR018200; PTHR10420 (PANTHER), PTHR10420:SF58 (PANTHER), SSF54001 (SUPERFAMILY)
	-	0				-
	-	0				-
Loa loa	phosphatidylinositol glycan anchor class u	2	P:GO:0034394; F:GO:0003923	-		IPR009600; SignalP (SIGNALP)
Caenorhabditis briggsae	phosphatidylinositol glycan anchor class u	2	P:GO:0034394; F:GO:0003923	-		IPR009600; SignalP (SIGNALP)
	-	0				-
Loa loa	polymerase ii (d- directed) polypeptide	10	F:GO:0003899; F:GO:0030275; F:GO:0004672; P:GO:0006367; P:GO:0008380; C:GO:0005665; F:GO:0003677; F:GO:0046983; P:GO:0006368; C:GO:0005666	-	EC:2.7.7.6	IPR008193; IPR009025; IPR011261; G3DSA:3.30.1360.10 (GENE3D), PTHR13946 (PANTHER), PTHR13946:SF16 (PANTHER)

Caenorhabditis briggsae	alpha 1	20	P:GO:0001764; P:GO:0048514; P:GO:0030155; P:GO:0060441; P:GO:0060445; P:GO:0045198; C:GO:0005608; P:GO:0045995; C:GO:0005606; P:GO:0002011; F:GO:0043208; C:GO:0005615; P:GO:0030334; F:GO:0005102; P:GO:0008045; P:GO:0030903; F:GO:0005201; P:GO:0031290; P:GO:0007166; P:GO:0007634	-		SignalP (SIGNALP)
Caenorhabditis elegans	fk506-binding protein family member (fkb-5)	4	P:GO:0006457; P:GO:0040010; P:GO:0008340; F:GO:0003755	-	EC:5.2.1.8	IPR001179; G3DSA:3.10.50.40 (GENE3D), PTHR10516:SF9 (PANTHER), SignalP (SIGNALP), SSF54534 (SUPERFAMILY)
Haemonchus contortus	ornithine decarboxylase 1	7	P:GO:0009615; C:GO:0005829; P:GO:0009446; F:GO:0005515; P:GO:0048513; P:GO:0008284; F:GO:0004586	-	EC:4.1.1.17	-
Ailuropoda melanoleuca	triosephosphate isomerase 1	11	C:GO:0005829; P:GO:0006633; C:GO:0005625; P:GO:0006098; P:GO:0019682; F:GO:0004807; F:GO:0005515; P:GO:0006096; P:GO:0006094; C:GO:0005634; P:GO:0009790	-	EC:5.3.1.1	-
Bos taurus	upf0608 protein c19orf42 homolog	1	C:GO:0016020	-		-
Brugia malayi	polyubiquitin precursor	5	C:GO:0005737; P:GO:0000003; P:GO:0040007; C:GO:0005634; P:GO:0002119	-		IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), PTHR10666:SF9 (PANTHER), SSF54236 (SUPERFAMILY)
Brugia malayi	polyubiquitin precursor	5	C:GO:0005737; P:GO:0000003; P:GO:0040007; C:GO:0005634; P:GO:0002119	-		IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), PTHR10666:SF9 (PANTHER), SSF54236 (SUPERFAMILY)
Brugia malayi	polyubiquitin precursor	5	C:GO:0005737; P:GO:0000003; P:GO:0040007; C:GO:0005634; P:GO:0002119	-		IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), PTHR10666:SF9 (PANTHER), SSF54236 (SUPERFAMILY)

Brugia malayi	polyubiquitin precursor	5	C:GO:0005737; P:GO:0000003; P:GO:0040007; C:GO:0005634; P:GO:0002119	-		-
Brugia malayi	polyubiquitin precursor	5	C:GO:0005737; P:GO:0000003; P:GO:0040007; C:GO:0005634; P:GO:0002119	-		IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), PTHR10666:SF9 (PANTHER), SSF54236 (SUPERFAMILY)
Brugia malayi	polyubiquitin precursor	5	C:GO:0005737; P:GO:0000003; P:GO:0040007; C:GO:0005634; P:GO:0002119	-		IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), PTHR10666:SF9 (PANTHER), SSF54236 (SUPERFAMILY)
Brugia malayi	polyubiquitin precursor	5	C:GO:0005737; P:GO:0000003; P:GO:0040007; C:GO:0005634; P:GO:0002119	-		IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), PTHR10666:SF9 (PANTHER), SSF54236 (SUPERFAMILY)
Brugia malayi	polyubiquitin precursor	5	C:GO:0005737; P:GO:0000003; P:GO:0040007; C:GO:0005634; P:GO:0002119	-		IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), PTHR10666:SF9 (PANTHER), SSF54236 (SUPERFAMILY)
Brugia malayi	polyubiquitin precursor	5	C:GO:0005737; P:GO:0000003; P:GO:0040007; C:GO:0005634; P:GO:0002119	-		IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), PTHR10666:SF9 (PANTHER), SSF54236 (SUPERFAMILY)
Loa loa	polyubiquitin precursor	5	C:GO:0005737; P:GO:0000003; P:GO:0040007; C:GO:0005634; P:GO:0002119	-		
Caenorhabditis briggsae	abnormal go-d development family member (gon-2)	6	P:GO:0007067; P:GO:0055085; P:GO:0006811; C:GO:0016021; P:GO:0008406; F:GO:0005216	-		PTHR13800 (PANTHER), SignalP (SIGNALP)
	-	0				-

Pongo abelii	collagen alpha-2 chain precursor	17	P:GO:0042476; F:GO:0030674; P:GO:0070208; P:GO:0043589; P:GO:0008217; F:GO:0042802; C:GO:0005615; F:GO:0046332; P:GO:0001501; F:GO:0048407; C:GO:0005584; P:GO:0030199; P:GO:0007179; F:GO:0005201; P:GO:0001568; P:GO:0007266; C:GO:0005886	-		SignalP (SIGNALP)
Brugia malayi	mkiaa0297 protein	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG06123 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	Hypothetical protein CBG06123 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	2	P:GO:0055085; C:GO:0016021	-		-
	-	0				-
Dictyocaulus viviparus	putative protein [Dictyocaulus viviparus]	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR001534
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	follicle stimulating hormone receptor	11	F:GO:0004963; P:GO:0006952; P:GO:0040010; C:GO:0016021; P:GO:0007186; P:GO:0000003; C:GO:0009986; F:GO:0005515; P:GO:0007165; P:GO:0009792; C:GO:0005886	-		PTHR23154 (PANTHER), PTHR23154:SF24 (PANTHER)
	-	0				-
Caenorhabditis briggsae	metallo-beta-lactamase superfamily protein	1	F:GO:0016787	-		G3DSA:3.60.15.10 (GENE3D), PTHR12553 (PANTHER), PTHR12553:SF3 (PANTHER), SSF56281 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-unc- protein	0		F:GO:0005488; F:GO:0008270		PTHR21696 (PANTHER)
Loa loa	AIDA-1b [Loa loa]	0				-
Ixodes scapularis	vacuolar multi-drug resistance abc transporter	6	F:GO:0042626; P:GO:0055085; P:GO:0055114; F:GO:0005524; C:GO:0016021; F:GO:0032440	-	EC:1.3.1.74	-
	-	0				-

Caenorhabditis elegans	uncoordi-ted family member (unc-73)	10	C:GO:0043005; F:GO:0005515; P:GO:0023034; P:GO:0007409; F:GO:0016740; P:GO:0016192; C:GO:0043025; C:GO:0048471; P:GO:0050773; F:GO:0005085	-		IPR000219; IPR001849; IPR011993; PTHR22826 (PANTHER), PTHR22826:SF39 (PANTHER), SSF50729 (SUPERFAMILY)
Caenorhabditis elegans	d- replication licensing factor mcm3	14	F:GO:0016851; P:GO:0006268; P:GO:0000910; P:GO:0015995; C:GO:0042555; P:GO:0040035; F:GO:0003677; F:GO:0005524; C:GO:0000785; F:GO:0016887; F:GO:0005515; P:GO:0030174; P:GO:0009792; F:GO:0003682	-	EC:6.6.1.1	IPR001208; IPR003593; IPR008046; IPR018525; G3DSA:3.40.50.300 (GENE3D), PTHR11630 (PANTHER), PTHR11630:SF46 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	heat repeat containing 1	4	P:GO:0009792; P:GO:0002119; P:GO:0040010; P:GO:0040011	-		IPR016024; IPR022125; PTHR13457 (PANTHER)
	-	0				-
Caenorhabditis briggsae	30s ribosomal protein s12	7	P:GO:0009792; P:GO:0002119; F:GO:0003735; C:GO:0015935; P:GO:0000003; P:GO:0040007; P:GO:0006412	-	EC:3.6.5.3	IPR005679; IPR006032; IPR012340; IPR016027
Caenorhabditis briggsae	briggsae cbr-gei-11 protein	0		P:GO:0045449; C:GO:0005634; F:GO:0003677		-
	-	0				-
Caenorhabditis briggsae	large ala glu-rich protein	0				PTHR18947 (PANTHER), PTHR18947:SF4 (PANTHER)
Caenorhabditis elegans	hypothetical protein F31A3.5 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Pongo abelii	type alpha 2	8	F:GO:0005201; F:GO:0030674; C:GO:0005615; P:GO:0016337; C:GO:0005578; P:GO:0009749; P:GO:0030198; C:GO:0042383	-		-
Caenorhabditis briggsae	egg laying defective family member (egl-8)	5	P:GO:0006629; F:GO:0005488; F:GO:0004629; C:GO:0044464; P:GO:0023052	-		IPR011992; IPR015359; PTHR10336 (PANTHER), PTHR10336:SF8 (PANTHER), SSF47473 (SUPERFAMILY)

	-	0				-
Caenorhabditis elegans	inositol -trisphosphate receptor	26	F:GO:0035091; P:GO:0051291; C:GO:0005654; F:GO:0005515; P:GO:0050913; C:GO:0005640; P:GO:0050916; P:GO:0007204; C:GO:0005792; F:GO:0070679; P:GO:0051592; C:GO:0031095; C:GO:0043209; C:GO:0005730; C:GO:0043025; F:GO:0000822; P:GO:0007165; P:GO:0007186; P:GO:0070588; P:GO:0050917; P:GO:0051260; C:GO:0005783; F:GO:0043533; C:GO:0005887; F:GO:0015085; F:GO:0005220	-		IPR015925; PTHR13715:SF2 (PANTHER)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG19004 [Caenorhabditis briggsae]	2	F:GO:0005524; F:GO:0003824	-		-
Caenorhabditis briggsae	briggsae cbr-lin-13 protein	0		F:GO:0003674; P:GO:0040027; F:GO:0008270; C:GO:0005634; C:GO:0005622		IPR007087; IPR015880; SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-lin-13 protein	0		F:GO:0003674; P:GO:0040027; F:GO:0008270; C:GO:0005634; C:GO:0005622		IPR007087; IPR015880; SignalP (SIGNALP)
Chthoniobacter flavus Ellin428	thymidylate ki-se	6	P:GO:0007283; P:GO:0030154; F:GO:0016301; F:GO:0005515; P:GO:0007275; C:GO:0005576	-		IPR004879; PTHR12145 (PANTHER)
Caenorhabditis briggsae	actin interacting protein 2	2	F:GO:0050660; F:GO:0016491	-		IPR006094; IPR016166; IPR016167; IPR016168; PTHR11748 (PANTHER), PTHR11748:SF7 (PANTHER)
	-	0				-
Brugia malayi	clathrin coat assembly protein	7	F:GO:0009982; F:GO:0030515; F:GO:0005515; C:GO:0031429; P:GO:0016192; P:GO:0006886; C:GO:0030131	-	EC:5.4.99.12	IPR008968; G3DSA:2.60.40.1170 (GENE3D), PTHR11998 (PANTHER), PTHR11998:SF4 (PANTHER)
	-	0				-

	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-jtr-1 protein	0		C:GO:0016021		-
Caenorhabditis briggsae	prominin-like protein	0		C:GO:0016021		-
Loa loa	cullin family protein	7	P:GO:0006306; F:GO:0031625; F:GO:0003677; C:GO:0031461; P:GO:0006511; F:GO:0008270; F:GO:0008168	-	EC:2.1.1.0	-
Caenorhabditis briggsae	alpha neutral c	7	F:GO:0004558; P:GO:0005975; P:GO:0009792; F:GO:0030246; P:GO:0040007; F:GO:0005515; P:GO:0002119	-	EC:3.2.1.20	IPR000322; IPR017853; PTHR22762:SF7 (PANTHER), SSF51011 (SUPERFAMILY)
	-	0				-
	-	0				-
Haemonchus contortus	hemicentin 1	5	F:GO:0008270; F:GO:0004222; P:GO:0006508; P:GO:0009792; C:GO:0016020	-	EC:3.4.24.0	-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Brugia malayi	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	mitogen-activated protein ki-se ki-se ki-se 5	7	F:GO:0008656; P:GO:0007257; F:GO:0005524; F:GO:0000287; F:GO:0004709; P:GO:0008624; F:GO:0042803	-	EC:2.7.11.25	PTHR22986 (PANTHER), PTHR22986:SF54 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0003674; F:GO:0016740; F:GO:0016905; C:GO:0005575		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR22841 (PANTHER), PTHR22841:SF1 (PANTHER)
Caenorhabditis briggsae	alanyl-tr- synthetase	2	F:GO:0005488; C:GO:0005739	-		IPR012947; IPR018163; PTHR11777 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
Brugia malayi	lin-52 homolog	0		F:GO:0003674; P:GO:0008150; C:GO:0005575		IPR018737
Brugia malayi	lmbr1-like conserved region family protein	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Haemonchus contortus	cuticular collagen	5	C:GO:0016021; P:GO:0010171; F:GO:0042302; P:GO:0040010; P:GO:0040011	-		-

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				IPR004988; SignalP (SIGNALP)
Branchiostoma floridae	atp-binding sub-family a member 2	10	P:GO:0006810; C:GO:0043231; P:GO:0044238; P:GO:0042221; C:GO:0044446; F:GO:0016887; C:GO:0044425; C:GO:0044444; F:GO:0000166; P:GO:0050794	-		PTHR19229 (PANTHER), PTHR19229:SF33 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	four domain-type voltage-gated ion channel alpha-1 subunit	5	C:GO:0016021; F:GO:0005272; F:GO:0005244; P:GO:0006811; P:GO:0055085	-		PTHR10037 (PANTHER), PTHR10037:SF60 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
						IPR007110; IPR013098; IPR013783; PTHR19900 (PANTHER), PTHR19900:SF1 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	non-erythrocytic 1	12	P:GO:0007184; C:GO:0005829; F:GO:0005516; C:GO:0043234; C:GO:0005730; F:GO:0032403; C:GO:0008091; F:GO:0003779; P:GO:0007182; C:GO:0032437; F:GO:0005200; C:GO:0005886	-		IPR001589; IPR001715; PTHR11915 (PANTHER), PTHR11915:SF48 (PANTHER)
Mycobacterium abscessus ATCC 19977	possible nf-180	0		P:GO:0000226; P:GO:0031133; C:GO:0005883; C:GO:0005882; P:GO:0060052; C:GO:0030424; P:GO:0008088; P:GO:0045110; F:GO:0005515; C:GO:0031594; C:GO:0012505; F:GO:0005199; F:GO:0005198		-
	-	0				-
Caenorhabditis briggsae	unc-50 homolog (elegans)	2	C:GO:0043231; C:GO:0016020	-		IPR007881; PTHR12841:SF5 (PANTHER)
	-	0				-
	-	0				-

Andrena erigeniae	mariner transposase	0		F:GO:0046872; P:GO:0015074; F:GO:0016787; F:GO:0004519; P:GO:0006310; F:GO:0004518; F:GO:0003677; C:GO:0005634		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0016888		-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein C09F12.3 [Caenorhabditis elegans]	2	P:GO:0007186; C:GO:0016021	-		IPR000276; G3DSA:1.20.1070.10 (GENE3D)
	-	0				IPR001810
Caenorhabditis briggsae	zinc finger protein 563	1	F:GO:0005488	-		IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)
	-	0				-
Strongylocentrotus purpuratus	kinesin-like protein kif15	0		P:GO:0007018; C:GO:0005819; C:GO:0005874; F:GO:0000166; C:GO:0005737; F:GO:0005524; F:GO:0003777; F:GO:0003774; C:GO:0005856		PTHR18956 (PANTHER), PTHR18956:SF2 (PANTHER)
Ancylostoma ceylanicum	secreted protein 5 precursor	0		P:GO:0006898; C:GO:0005576		IPR014044
	-	0				-
Ailuropoda melanoleuca	polyadenylate-binding protein 1	9	P:GO:0006378; P:GO:0008380; P:GO:0048255; C:GO:0005681; F:GO:0008494; F:GO:0008022; C:GO:0005829; F:GO:0000166; F:GO:0008143	-		-
	-	0				-
Caenorhabditis elegans	transthyretin-related family domain protein confirmed by transcript evidence	0				IPR001534
Caenorhabditis elegans	Hypothetical protein ZK1127.13 [Caenorhabditis elegans]	0				-

Brugia malayi	profilin	25	P:GO:0007411; P:GO:0048133; P:GO:0007296; P:GO:0008286; P:GO:0035159; P:GO:0040018; C:GO:0015629; P:GO:0007568; P:GO:0035193; P:GO:0032507; C:GO:0005737; F:GO:0003779; P:GO:0007420; P:GO:0007285; P:GO:0007015; P:GO:0060250; P:GO:0042594; P:GO:0007295; F:GO:0005159; P:GO:0007488; P:GO:0007300; P:GO:0030717; N:GO:0071844; P:GO:0046620; P:GO:0000910	-		IPR002097; IPR005455; G3DSA:3.30.450.30 (GENE3D)
Haemonchus contortus	microsomal aminopeptidase	3	C:GO:0016020; F:GO:0046872; F:GO:0070011	-		IPR001930; PTHR11533:SF29 (PANTHER)
Haemonchus contortus	microsomal aminopeptidase	5	C:GO:0016021; F:GO:0008237; P:GO:0006508; F:GO:0008270; F:GO:0004177	-	EC:3.4.11.0	IPR001930; PTHR11533:SF29 (PANTHER)
Pongo abelii	cytoplasmic dynein 1 heavy chain 1-like	12	F:GO:0003777; C:GO:0005829; P:GO:0006810; C:GO:0005874; F:GO:0042623; P:GO:0006200; P:GO:0007052; C:GO:0005868; F:GO:0005524; P:GO:0007018; F:GO:0005515; C:GO:0005794	-		IPR004273; PTHR10676 (PANTHER), PTHR10676:SF28 (PANTHER)
	-	0				-
Caenorhabditis elegans	musashi homolog 2	4	C:GO:0005737; C:GO:0005844; F:GO:0000166; F:GO:0008266	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF17 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	musashi homolog 2	4	C:GO:0005737; C:GO:0005844; F:GO:0000166; F:GO:0008266	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-rde-1 protein	0		F:GO:0003676		-
Caenorhabditis elegans	hypothetical protein F42G8.5 [Caenorhabditis elegans]	0				-

Caenorhabditis elegans	briggsae cbr-itx-1 protein	0				-
	-	0				-
Caenorhabditis elegans	nuclear vcp-like	2	F:GO:0016887; F:GO:0005524	-		-
Caenorhabditis briggsae	mboat family protein	3	P:GO:0008354; C:GO:0016020; P:GO:0007291	-		IPR004299; PTHR13906 (PANTHER), PTHR13906:SF4 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG01142 [Caenorhabditis briggsae]	0				IPR000494; G3DSA:3.80.20.20 (GENE3D), PTHR21662 (PANTHER), SSF52058 (SUPERFAMILY)
	-	0				-
Loa loa	protein tyrosine receptor d	5	F:GO:0004725; P:GO:0007391; C:GO:0005912; P:GO:0007399; P:GO:0006470	-	EC:3.1.3.48	-
	-	0				-
	-	0				-
Caenorhabditis elegans	pdz domain containing protein	1	P:GO:0007275	-		IPR001478; G3DSA:2.30.42.10 (GENE3D)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	P:GO:0007186; C:GO:0016021	-		IPR007087; IPR017452; IPR019427; G3DSA:1.20.1070.10 (GENE3D), PTHR22751 (PANTHER), PTHR22751:SF12 (PANTHER), SignalP (SIGNALP), SSF81321 (SUPERFAMILY)
Caenorhabditis briggsae	chromosome 19 open reading frame isoform cra_a	2	P:GO:0055085; C:GO:0016021	-		IPR016196; G3DSA:1.20.1250.20 (GENE3D)
Brugia malayi	xap-5 protein	6	P:GO:0009792; P:GO:0002119; P:GO:0008340; P:GO:0040011; P:GO:0040007; C:GO:0005634	-		IPR007005
	-	0				-
	-	0				-
Brugia malayi	related to yeast vacuolar protein sorting factor family member (vps-18)	0		F:GO:0008270; F:GO:0005515		PTHR23323 (PANTHER), PTHR23323:SF25 (PANTHER)
	-	0				-
Caenorhabditis elegans	negative effector of r- polymerase iii	1	P:GO:0040010	-		IPR015257
	-	0				-
Caenorhabditis briggsae	pap 25a associated domain containing protein	1	F:GO:0005515	-		G3DSA:3.30.460.10 (GENE3D), PTHR12271 (PANTHER), PTHR12271:SF14 (PANTHER), SSF81301 (SUPERFAMILY), SSF81631 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	6	P:GO:0005975; P:GO:0030259; C:GO:0016021; F:GO:0030246; F:GO:0016758; P:GO:0040010	-	EC:2.4.1.0	IPR002213; G3DSA:3.40.50.2000 (GENE3D), PTHR11926:SF3 (PANTHER), SSF53756 (SUPERFAMILY)
Caenorhabditis elegans	tlc domain containing 1	0		F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150		IPR006634

Caenorhabditis briggsae	slowpoke potassium channel family member (slo-2)	6	F:GO:0005488; F:GO:0015269; P:GO:0006813; P:GO:0008152; C:GO:0016020; F:GO:0003824	-		PTHR10027 (PANTHER), PTHR10027:SF6 (PANTHER)
Caenorhabditis elegans	amp-binding enzyme family protein	3	P:GO:0008152; C:GO:0016020; F:GO:0003824	-		IPR000873; G3DSA:3.40.50.980 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF15 (PANTHER), SSF56801 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein T05B11.1 [Caenorhabditis elegans]	0				-
Ciona intestinalis	novel protein	0		F:GO:0020037; F:GO:0005506; F:GO:0009055; P:GO:0000003; P:GO:0055114; F:GO:0016491; P:GO:0040039; P:GO:0040011; F:GO:0046872; F:GO:0004497		-
Caenorhabditis elegans	sy-ptotagmin i	6	P:GO:0016079; F:GO:0005509; F:GO:0000149; P:GO:0045955; C:GO:0030285; F:GO:0005215	-		IPR000008; IPR001565; IPR008973; IPR018029; IPR020477; G3DSA:2.60.40.150 (GENE3D), PTHR10024 (PANTHER), PTHR10024:SF40 (PANTHER)
Loa loa	leucine rich repeat family protein	0		C:GO:0016021; F:GO:0005515		IPR001611; G3DSA:3.80.10.10 (GENE3D), PTHR23154 (PANTHER), PTHR23154:SF127 (PANTHER), SSF52058 (SUPERFAMILY)
Caenorhabditis elegans	s-adenosylhomocysteine hydrolase	15	P:GO:0055114; P:GO:0000003; F:GO:0004013; P:GO:0032940; P:GO:0006730; F:GO:0004455; P:GO:0008652; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0006898; P:GO:0009792; P:GO:0040015; F:GO:0048037	-	EC:3.3.1.1; EC:1.1.1.86	IPR000043; IPR015878; IPR020082; G3DSA:3.40.50.1480 (GENE3D), SSF51735 (SUPERFAMILY), SSF52283 (SUPERFAMILY)

Caenorhabditis elegans	s-adenosylhomocysteine hydrolase	15	P:GO:0055114; P:GO:0000003; F:GO:0004013; P:GO:0032940; P:GO:0006730; F:GO:0004455; P:GO:0008652; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0006898; P:GO:0009792; P:GO:0040015; F:GO:0048037	-	EC:3.3.1.1; EC:1.1.1.86	IPR000043; IPR015878; IPR020082; G3DSA:3.40.50.1480 (GENE3D), SSF51735 (SUPERFAMILY), SSF52283 (SUPERFAMILY)
Ciona intestinalis	chromosome 10 open reading frame 119	0		F:GO:0003674; P:GO:0008150; C:GO:0005575		IPR019140; PTHR13489 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	h transporter (pgp related) family member (haf-9)	6	F:GO:0015197; F:GO:0042626; P:GO:0015833; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		G3DSA:1.20.1560.10 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF82 (PANTHER)
	-	0				-
Caenorhabditis elegans	angiomotin isoform 2	1	F:GO:0005515	-		IPR009114; PTHR14826:SF2 (PANTHER)
Callithrix jacchus	glutamine synthetase	10	C:GO:0005829; P:GO:0009749; C:GO:0005739; F:GO:0004351; F:GO:0042802; P:GO:0006542; F:GO:0005524; F:GO:0004356; P:GO:0008283; C:GO:0005794	-	EC:4.1.1.15; EC:6.3.1.2	IPR008146; IPR014746; PTHR20852 (PANTHER), PTHR20852:SF14 (PANTHER), SSF55931 (SUPERFAMILY)
Caenorhabditis briggsae	u729_caebr ame: full=upf0729 protein cbg02799	0				-
Ancylostoma ceylanicum	metalloprotease 1 precursor	2	F:GO:0046872; F:GO:0008237	-		IPR001506; IPR006026; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
Ancylostoma ceylanicum	metalloprotease 1 precursor	1	F:GO:0008233	-		IPR001506; IPR006026; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		C:GO:0016021; F:GO:0042302		IPR002486; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)

Loa loa	tir (toll and interleukin 1 receptor) domain protein family member (tir-1)	5	P:GO:0007165; P:GO:0045087; C:GO:0031224; F:GO:0042802; F:GO:0004888	-		IPR011989; PTHR22998 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	C:GO:0005856	-		IPR011990; PTHR16056 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	C:GO:0005856	-		IPR011990; PTHR16056 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				IPR017849
	-	0				SignalP (SIGNALP)
Mus musculus	ribosomal protein s8	4	F:GO:0003735; F:GO:0005515; C:GO:0022627; P:GO:0006414	-		IPR001047; IPR018283; IPR022309; PTHR10394 (PANTHER), PTHR10394:SF1 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0016539		IPR001534
	-	0				-
Caenorhabditis elegans	amp-activated ki-se family member (aak-2)	4	F:GO:0004683; P:GO:0006468; F:GO:0005515; F:GO:0005524	-	EC:2.7.11.17	IPR000719; IPR011009; IPR015741; IPR017441; IPR017442; IPR020636; G3DSA:3.30.200.20 (GENE3D)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0005515		PTHR18958 (PANTHER), PTHR18958:SF116 (PANTHER)
Caenorhabditis elegans	homolog of hedgehog ransferase family member (hhat-2)	0				-
	-	0				-
Harpegnathos saltator	histone-lysine n-methyltransferase setmar	2	P:GO:0006313; F:GO:0004803	-		SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-alh-8 protein	7	F:GO:0004491; F:GO:0018478; P:GO:0055114; F:GO:0000062; P:GO:0019859; P:GO:0006573; C:GO:0005739	-	EC:1.2.1.27; EC:1.2.1.18	-
Loa loa	homeodomain interacting protein ki-se family member (hpk-1)	5	P:GO:0006468; F:GO:0003677; F:GO:0005524; P:GO:0008340; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017441; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF117 (PANTHER)
	-	0				SignalP (SIGNALP)

Pongo abelii	decorin	16	P:GO:0042060; F:GO:0047485; P:GO:0001890; C:GO:0005615; P:GO:0009887; F:GO:0050840; P:GO:0007519; F:GO:0005518; P:GO:0007568; F:GO:0005539; P:GO:0001822; C:GO:0005578; P:GO:0019800; P:GO:0032496; P:GO:0030198; P:GO:0009612	-		PTHR23154 (PANTHER), PTHR23154:SF71 (PANTHER)
	-	0				-
Eptatretus burgeri	protein tyrosine receptor f	22	P:GO:0050775; P:GO:0001960; P:GO:0007185; P:GO:0042059; P:GO:0050803; C:GO:0030426; F:GO:0005001; F:GO:0030971; C:GO:0005792; P:GO:0043525; F:GO:0042301; P:GO:0008285; C:GO:0043025; P:GO:0007156; C:GO:0060076; P:GO:0051387; C:GO:0005768; P:GO:0006470; P:GO:0046627; C:GO:0005887; P:GO:0031345; F:GO:0005158	-		IPR000242; IPR000387; IPR016130; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SignalP (SIGNALP), SSF52799 (SUPERFAMILY)
Caenorhabditis elegans	hydroxymethylglutaryl- lyase	5	C:GO:0005875; C:GO:0005759; P:GO:0006551; F:GO:0004419; F:GO:0016740	-	EC:4.1.3.4	-
	-	0				-
Caenorhabditis elegans	hypothetical protein C17G10.7 [Caenorhabditis elegans]	1	P:GO:0019915	-		SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	F:GO:0004437; P:GO:0008299; C:GO:0016021	-		IPR000760; IPR020550; G3DSA:3.40.190.80 (GENE3D), PTHR20854:SF8 (PANTHER), SSF56655 (SUPERFAMILY)

Caenorhabditis elegans	solute carrier family 30 (zinc transporter) member 5	11	F:GO:0005385; P:GO:0055085; P:GO:0006824; P:GO:0006829; P:GO:0006882; C:GO:0016021; C:GO:0005624; C:GO:0030667; C:GO:0016324; P:GO:0010043; C:GO:0005794	-		IPR002524; G3DSA:1.20.1510.10 (GENE3D), SignalP (SIGNALP)
Caenorhabditis briggsae	acyl- synthetase short-chain family member 2	10	P:GO:0019542; P:GO:0006085; C:GO:0005829; P:GO:0019413; P:GO:0008610; C:GO:0005730; P:GO:0019915; F:GO:0005515; F:GO:0016208; F:GO:0003987	-	EC:6.2.1.1	IPR000873; IPR011904; IPR020845; G3DSA:2.30.38.10 (GENE3D), G3DSA:3.30.300.30 (GENE3D), G3DSA:3.40.50.980 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF42 (PANTHER), PF11930 (PFAM), SSF56801 (SUPERFAMILY)
	-	0				-
Aedes aegypti	multiple ankyrin repeats single kh domain protein	0		F:GO:0003723		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF281 (PANTHER)
Caenorhabditis elegans	glutaminyl-peptide cyclotransferase	6	P:GO:0019915; C:GO:0005576; C:GO:0016021; F:GO:0016603; P:GO:0006508; F:GO:0008233	-	EC:2.3.2.5	IPR007484; G3DSA:3.40.630.10 (GENE3D), PTHR12283 (PANTHER), SSF53187 (SUPERFAMILY)
Caenorhabditis elegans	r- polymerase ii subunit a c-termi-l domain phosphatase	3	F:GO:0004721; C:GO:0005634; C:GO:0005700	-	EC:3.1.3.16	IPR004274; G3DSA:3.40.50.1000 (GENE3D), PTHR23081 (PANTHER), SSF56784 (SUPERFAMILY)
Homo sapiens	atp h+ mitochondrial f1 epsilon subunit	7	F:GO:0046961; C:GO:0005759; P:GO:0006172; F:GO:0046933; P:GO:0042776; C:GO:0000275; P:GO:0006200	-	EC:3.6.3.14	-
Nematostella vectensis	phosphatidylinositol-specific phospholipase x domain containing 3	0		P:GO:0006629; F:GO:0016787; P:GO:0023034; P:GO:0016042; F:GO:0003674; P:GO:0007165; F:GO:0008081; C:GO:0005575; F:GO:0004629; F:GO:0005515; F:GO:0004871; P:GO:0008150		IPR017946
	-	0				-

Homo sapiens	cytochrome c oxidase subunit via polypeptide 1	5	P:GO:0034220; C:GO:0005751; P:GO:0015992; F:GO:0004129; P:GO:0006091	-	EC:1.9.3.1	SignalP (SIGNALP)
Caenorhabditis briggsae	oligopeptide transporter	3	F:GO:0015198; C:GO:0016021; P:GO:0006857	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	hypothetical protein Y41D4B.11 [Caenorhabditis elegans]	0		P:GO:0000003; P:GO:0040035; P:GO:0006898; P:GO:0018991		-
Caenorhabditis elegans	briggsae cbr-apt-10 protein	4	F:GO:0005515; P:GO:0006886; C:GO:0030131; P:GO:0006897	-		IPR008968; IPR012320; G3DSA:2.60.40.1170 (GENE3D), PTHR11998 (PANTHER), PTHR11998:SF1 (PANTHER)
Caenorhabditis briggsae	sc blase (phospholipid scramblase) family member (scrm-1)	1	F:GO:0005515	-		-
Caenorhabditis elegans	briggsae cbr-rod-1 protein	0		C:GO:0000940; P:GO:0000070; C:GO:0005819; C:GO:0005694; C:GO:0005634; P:GO:0007067; C:GO:0000776; P:GO:0007094; C:GO:0005737; P:GO:0051301; F:GO:0003674; C:GO:0005575; C:GO:0005828; P:GO:0007049; P:GO:0008150; C:GO:0005856		-
Caenorhabditis elegans	briggsae cbr-sinh-1 protein	0		F:GO:0003824; C:GO:0016020		-
Caenorhabditis elegans	briggsae cbr-tag-208 protein	4	C:GO:0005737; C:GO:0043232; F:GO:0005515; F:GO:0005198	-		IPR001452; G3DSA:2.30.30.40 (GENE3D), PTHR10661 (PANTHER), PTHR10661:SF3 (PANTHER)
	-	0				-
Caenorhabditis elegans	laminin alpha chain	3	P:GO:0009987; C:GO:0005578; P:GO:0050789	-		-
Loa loa	peripheral plasma membrane protein cask	5	P:GO:0006468; F:GO:0005515; F:GO:0004713; F:GO:0005524; F:GO:0004674	-	EC:2.7.10.0; EC:2.7.11.0	-
Angiostrongylus cantonensis	elegans protein confirmed by transcript evidence	1	F:GO:0005488	-		SSF57850 (SUPERFAMILY)
Loa loa	briggsae cbr-crn-2 protein	1	F:GO:0016888	-	EC:3.1.21.0	-
Loa loa	ring finger protein 20	0		F:GO:0046872; F:GO:0008270; F:GO:0005515		PTHR23163 (PANTHER)
Loa loa	ring finger protein 20	0		F:GO:0046872; F:GO:0008270; F:GO:0005515		PTHR23163 (PANTHER)
Caenorhabditis elegans	bat2 n-terminus family protein	0				IPR009738; PTHR14038 (PANTHER)

Caenorhabditis briggsae	von hippel-lindau disease tumor	5	P:GO:0002119; P:GO:0007411; P:GO:0006950; P:GO:0040010; P:GO:0000003	-		IPR022772; PD035809 (PRODOM), G3DSA:2.60.40.780 (GENE3D), SSF49468 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein Y18H1A.9 [Caenorhabditis elegans]	0		P:GO:0006508; F:GO:0004181; F:GO:0008270		IPR003146; IPR009020; G3DSA:3.30.70.340 (GENE3D), PTHR11705 (PANTHER), PTHR11705:SF12 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-mog-4 protein	4	F:GO:0003676; F:GO:0005524; F:GO:0005515; F:GO:0008026	-		IPR007502; PTHR18934 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	mitochondrial carrier protein	6	P:GO:0009792; C:GO:0005743; P:GO:0040018; P:GO:0055085; C:GO:0016021; F:GO:0005215	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D)
Brugia malayi	carbonic anhydrase	0		F:GO:0046872; P:GO:0006730; F:GO:0008270; F:GO:0004089		IPR001148; IPR018338; IPR018340; SignalP (SIGNALP)
Brugia malayi	arid4a protein	2	C:GO:0005622; F:GO:0005488	-		PTHR13964 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	nuclear cap-binding protein subunit 1	2	F:GO:0005488; P:GO:0006397	-		IPR003890; IPR016021; IPR016024; PTHR12412 (PANTHER), PTHR12412:SF2 (PANTHER)
Caenorhabditis elegans	utp21 specific wd40 associated domain containing protein	0		C:GO:0032040; P:GO:0006364		IPR001680; IPR007319; IPR015943; IPR017986; IPR019781; IPR019782; PTHR22847 (PANTHER), SSF101908 (SUPERFAMILY)
	-	0				-

Pongo abelii	type alpha 1	31	P:GO:0060351; P:GO:0001957; P:GO:0071363; P:GO:0007605; P:GO:0034505; P:GO:0042542; P:GO:0001649; P:GO:0009612; P:GO:0001568; P:GO:0060325; F:GO:0005201; C:GO:0005615; P:GO:0048706; P:GO:0015031; F:GO:0048407; C:GO:0005737; P:GO:0043434; P:GO:0071300; P:GO:0007601; P:GO:0010812; C:GO:0005584; F:GO:0042802; P:GO:0060346; P:GO:0032964; P:GO:0030199; P:GO:0051591; P:GO:0031960;	-		IPR001007; PTHR10499 (PANTHER), PTHR10499:SF46 (PANTHER), SignalP (SIGNALP), SSF57603 (SUPERFAMILY)
	-	0				-
	-	0				-
Loa loa	replication factor c subunit 2	14	F:GO:0016851; P:GO:0006260; P:GO:0015995; P:GO:0006200; P:GO:0000003; F:GO:0003689; P:GO:0006297; F:GO:0005524; F:GO:0005515; P:GO:0040011; P:GO:0015979; C:GO:0005654; P:GO:0009792; C:GO:0005663	-	EC:6.6.1.1	IPR003593; IPR003959; IPR008921; IPR013748; G3DSA:1.10.8.60 (GENE3D), G3DSA:1.20.272.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR11669 (PANTHER), SSF52540 (SUPERFAMILY)
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	1	P:GO:0019915	-		-
Caenorhabditis briggsae	Hypothetical protein CBG07553 [Caenorhabditis briggsae]	0				IPR010916
	-	0				-
Caenorhabditis briggsae	vacuolar protein sorting 13a isoform cra_a	2	P:GO:0008104; F:GO:0005515	-		PTHR16166 (PANTHER), PTHR16166:SF25 (PANTHER)
Caenorhabditis elegans	adamts-9 precursor (a disintegrin and metalloprotei-se with thrombospondin motifs 9) (adam-ts 9) (adam-ts9)	5	F:GO:0004222; P:GO:0006508; F:GO:0008270; C:GO:0005578; P:GO:0048070	-	EC:3.4.24.0	IPR012314; PTHR13723 (PANTHER), PTHR13723:SF33 (PANTHER)

Brugia malayi	rad50 family protein	8	P:GO:0050896; P:GO:0040010; P:GO:0045132; P:GO:0006915; P:GO:0000003; C:GO:0044464; P:GO:0009792; F:GO:0003824	-		G3DSA:3.40.50.300 (GENE3D), PTHR18867 (PANTHER), PTHR18867:SF11 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	3 -5 exonuclease family protein	9	P:GO:0006139; F:GO:0003676; C:GO:0005622; F:GO:0005515; P:GO:0018996; F:GO:0008408; P:GO:0000003; P:GO:0040011; P:GO:0002009	-		-
	-	0				SignalP (SIGNALP)
Brugia malayi	mitochondrial ribosomal protein l28	7	P:GO:0009792; P:GO:0010171; P:GO:0002119; C:GO:0044444; C:GO:0043229; P:GO:0040007; C:GO:0030529	-		PTHR13528 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0008643; C:GO:0016021; P:GO:0055085; F:GO:0005215; P:GO:0006810		IPR005828; IPR016196; G3DSA:1.20.1250.20 (GENE3D), PTHR11600 (PANTHER), PTHR11600:SF97 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	riken cd- 2410127l17	0		F:GO:0003674; P:GO:0008150		IPR012901
Caenorhabditis briggsae	Hypothetical protein CBG01544 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	olfactory ing defective family member (olrn-1)	0				-
	-	0				-
	-	0				-
	-	0				IPR001878
	-	0				-
	-	0				-
Caenorhabditis elegans	patched family protein	5	P:GO:0018996; C:GO:0016021; P:GO:0040018; F:GO:0008158; P:GO:0040011	-		IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER), SSF82866 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	microfibrillar-associated protein 1	8	P:GO:0040010; P:GO:0040035; P:GO:0018996; P:GO:0002119; P:GO:0006898; P:GO:0009792; P:GO:0001703; P:GO:0016246	-		SignalP (SIGNALP)

Nippostrongylus brasiliensis	heat shock protein family member (hsp-)	1	P:GO:0009408	-		IPR001436; IPR002068; IPR008978; G3DSA:2.60.40.790 (GENE3D), PTHR11527 (PANTHER), PTHR11527:SF28 (PANTHER)
Ostertagia ostertagi	heat shock protein family member (hsp-)	1	P:GO:0009408	-		IPR001436; IPR002068; PTHR11527 (PANTHER), PTHR11527:SF28 (PANTHER)
Ancylostoma ceylanicum	kunitz-type protease inhibitor-like protein	0		F:GO:0004222; F:GO:0008270; P:GO:0007275; C:GO:0005578; F:GO:0008237; C:GO:0031012; C:GO:0005576; F:GO:0030414; F:GO:0008233; F:GO:0004867		IPR002223; IPR020901; PTHR10083 (PANTHER), PTHR10083:SF39 (PANTHER), SignalP (SIGNALP)
Ancylostoma ceylanicum	kunitz-type protease inhibitor-like protein	0		F:GO:0004222; F:GO:0008270; P:GO:0007275; C:GO:0005578; F:GO:0008237; C:GO:0031012; C:GO:0005576; F:GO:0030414; F:GO:0008233; F:GO:0004867		IPR002223; IPR020901; PTHR10083 (PANTHER), PTHR10083:SF39 (PANTHER), SignalP (SIGNALP)
Ancylostoma ceylanicum	kunitz-type protease inhibitor-like protein	0		F:GO:0004222; F:GO:0008270; P:GO:0007275; C:GO:0005578; F:GO:0008237; C:GO:0031012; C:GO:0005576; F:GO:0030414; F:GO:0008233; F:GO:0004867		-
Ancylostoma ceylanicum	kunitz-type protease inhibitor-like protein	0		F:GO:0004222; F:GO:0008270; P:GO:0007275; C:GO:0005578; F:GO:0008237; C:GO:0031012; C:GO:0005576; F:GO:0030414; F:GO:0008233; F:GO:0004867		-
Ancylostoma ceylanicum	kunitz-type protease inhibitor-like protein	0		F:GO:0004222; F:GO:0008270; P:GO:0007275; C:GO:0005578; F:GO:0008237; C:GO:0031012; C:GO:0005576; F:GO:0030414; F:GO:0008233; F:GO:0004867		-

Ancylostoma ceylanicum	kunitz-type protease inhibitor-like protein	0		F:GO:0004222; F:GO:0008270; P:GO:0007275; C:GO:0005578; F:GO:0008237; C:GO:0031012; C:GO:0005576; F:GO:0030414; F:GO:0008233; F:GO:0004867		-
Caenorhabditis briggsae	briggsae cbr-eat-18 protein	0				-
Caenorhabditis briggsae	Hypothetical protein CBG04563 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)
Ixodes scapularis	riken cd- 2700097o09	0		F:GO:0000062; F:GO:0008176; P:GO:0008150; F:GO:0018024; P:GO:0009792		-
Caenorhabditis elegans	laminin alpha chain	3	P:GO:0007155; P:GO:0050794; C:GO:0005604	-		IPR001791; IPR008985; IPR012680; IPR013320
Caenorhabditis briggsae	kiaa1688 protein	4	C:GO:0005856; P:GO:0007165; C:GO:0005634; F:GO:0005515	-		IPR001202; G3DSA:2.20.70.10 (GENE3D), PTHR23177 (PANTHER), PTHR23177:SF1 (PANTHER)
Callithrix jacchus	ig lambda-chain (v-d-j) precursor	3	C:GO:0005576; F:GO:0003823; P:GO:0006955	-		IPR013783; PTHR23267 (PANTHER), PTHR23267:SF14 (PANTHER), SignalP (SIGNALP)
Loa loa	hypothetical protein LOAG_02385 [Loa loa]	0				-
	-	0				-
Caenorhabditis briggsae	sorbs2 protein	2	P:GO:0023034; C:GO:0044464	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	abnormal axis family member (ttx-7)	0		P:GO:0016311; F:GO:0004437		IPR000760; G3DSA:3.40.190.80 (GENE3D), PTHR20854:SF4 (PANTHER)
Caenorhabditis briggsae	u3 small nucleolar ribonucleoprotein protein imp4	10	P:GO:0009792; F:GO:0004812; P:GO:0002119; F:GO:0003676; F:GO:0005524; P:GO:0000003; P:GO:0040007; P:GO:0006898; C:GO:0030529; P:GO:0006412	-	EC:3.6.5.3	IPR004154; IPR007109; G3DSA:3.40.50.10480 (GENE3D), PTHR22734 (PANTHER)
	-	0				-
	-	0				IPR015880
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-

Loa loa	erin family member (cdh-6)	0		P:GO:0007218; F:GO:0005509; P:GO:0007156; F:GO:0004930; P:GO:0007155; C:GO:0016021; C:GO:0016020; C:GO:0005886		-
Angiostrongylus cantonensis	col-19	6	P:GO:0009792; C:GO:0060107; F:GO:0042302; F:GO:0005515; C:GO:0060111; P:GO:0040002	-		IPR002486; IPR008160; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	activating sig-l cointegrator 1 complex subunit 3	3	F:GO:0005524; F:GO:0003677; F:GO:0008026	-		IPR011545; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR11752 (PANTHER), PTHR11752:SF8 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0005524; P:GO:0006468		IPR011009; IPR012877; G3DSA:3.90.1200.10 (GENE3D)
Brugia malayi	ys03_caeel ame: full=uncharacterized protein	5	P:GO:0048856; F:GO:0003677; P:GO:0007275; P:GO:0000003; C:GO:0005634	-		IPR000910
	-	0				-
Caenorhabditis briggsae	briggsae cbr-sulp-8 protein	3	C:GO:0016020; P:GO:0006810; F:GO:0005215	-		IPR002645; PTHR11814 (PANTHER), PTHR11814:SF10 (PANTHER)
Brugia malayi	riken cd- 2700097o09	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Ornithorhynchus anatinus	protocadherin 19	0				IPR002126; IPR015919; PTHR10596 (PANTHER), PTHR10596:SF77 (PANTHER)
Loa loa	sig-l recognition particle receptor subunit beta	6	C:GO:0043231; F:GO:0005515; P:GO:0006898; P:GO:0009792; C:GO:0005737; C:GO:0016020	-		IPR019009; G3DSA:3.40.50.300 (GENE3D), PTHR19326 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
Loa loa	bcl2-associated athanogene 2	3	F:GO:0005515; P:GO:0040002; P:GO:0040011	-		PTHR12334 (PANTHER), SignalP (SIGNALP)
Loa loa	bcl2-associated athanogene 2	3	F:GO:0005515; P:GO:0040002; P:GO:0040011	-		PTHR12334 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	interleukin-1 receptor-associated ki-se 1	5	P:GO:0006468; F:GO:0005515; F:GO:0005524; P:GO:0007165; F:GO:0004674	-	EC:2.7.11.0	-
Loa loa	small family member (sma-9)	1	F:GO:0005515	-		IPR007087; IPR015880

	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	low-density lipoprotein receptor-related protein 2	3	F:GO:0004872; F:GO:0005509; C:GO:0016021	-		IPR006210; G3DSA:2.10.25.10 (GENE3D), PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER)
Caenorhabditis elegans	sec14l1 protein	5	C:GO:0016020; C:GO:0005794; F:GO:0005488; P:GO:0006810; F:GO:0005215	-		IPR001071; IPR001251; IPR008273; IPR011074; G3DSA:1.10.8.20 (GENE3D), PTHR23324 (PANTHER), PTHR23324:SF8 (PANTHER)
	-	0				-
Pan troglodytes	PREDICTED: hypothetical protein [Pan troglodytes]	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0032313; C:GO:0005622; F:GO:0005097		-
Haemonchus contortus	heat shock protein family member (hsp-)	0		P:GO:0006950; P:GO:0009408		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-dnj-9 protein	1	F:GO:0031072	-		IPR001623; IPR015609; IPR018253; PTHR11821:SF82 (PANTHER)
Caenorhabditis briggsae	isoprenylcysteine carboxyl methyltransferase	5	P:GO:0044281; P:GO:0008104; F:GO:0003880; C:GO:0005783; P:GO:0006464	-		IPR007269; PTHR12714 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				IPR002110; IPR020683
Caenorhabditis elegans	ccr4-not transcription subunit 3	10	C:GO:0005737; P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0030528; P:GO:0045449; F:GO:0005515; P:GO:0008340; P:GO:0040007; C:GO:0005634	-		IPR007207; PTHR23326 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	cadmium-inducible lysosomal protein cdr-5	3	P:GO:0002119; P:GO:0040007; P:GO:0040002	-		PTHR12289 (PANTHER), PTHR12289:SF17 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Loa loa	otu domain-containing protein 6b	0		P:GO:0008150; F:GO:0008233; C:GO:0005575		IPR003323; PTHR12419 (PANTHER), SSF54001 (SUPERFAMILY)
	-	0				-
	-	0				-

Caenorhabditis elegans	mitogen-activated protein ki-se ki-se 1	38	P:GO:0004674; P:GO:0034111; P:GO:0032402; C:GO:0033267; P:GO:0060711; F:GO:0004728; C:GO:0005625; F:GO:0004708; P:GO:0032968; P:GO:0051384; C:GO:0005829; C:GO:0032839; P:GO:0003056; P:GO:0006979; P:GO:0045597; P:GO:0032320; P:GO:0006935; C:GO:0005886; C:GO:0043204; C:GO:0048471; P:GO:0030216; C:GO:0005794; P:GO:0048812; P:GO:0007050; F:GO:0005524; P:GO:0030335; P:GO:0048313; P:GO:0008285;	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017441; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF46 (PANTHER)
Caenorhabditis elegans	coenzyme q4 homolog	1	C:GO:0005739	-		IPR007715; PTHR12922 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-aex-3 protein	7	P:GO:0007618; P:GO:0030421; P:GO:0018991; C:GO:0005623; F:GO:0017112; P:GO:0007268; P:GO:0050794	-		IPR001194; IPR005112; PTHR13008 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	farnesyl diphosphate synthase	6	P:GO:0009792; P:GO:0002119; F:GO:0004337; F:GO:0004161; P:GO:0040007; P:GO:0045337	-	EC:2.5.1.10; EC:2.5.1.1	IPR000092; IPR008949; PTHR11525 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	integrin alpha-ps1	1	C:GO:0016021	-		IPR000413; IPR013517; IPR013519; IPR013649; IPR018184; G3DSA:2.130.10.130 (GENE3D), G3DSA:2.60.40.1510 (GENE3D), G3DSA:2.60.40.1530 (GENE3D), PTHR23220 (PANTHER), PTHR23220:SF11 (PANTHER), PS51470 (PROFILE), SSF69179 (SUPERFAMILY), SSF69318 (SUPERFAMILY)

Caenorhabditis briggsae	integrin alpha-ps1	1	C:GO:0016021	-		IPR000413; IPR013517; IPR013519; IPR013649; IPR018184; G3DSA:2.130.10.130 (GENE3D), G3DSA:2.60.40.1510 (GENE3D), G3DSA:2.60.40.1530 (GENE3D), PTHR23220 (PANTHER), PTHR23220:SF11 (PANTHER), PS51470 (PROFILE), SSF69179 (SUPERFAMILY), SSF69318 (SUPERFAMILY)
Ciona intestinalis	secreted lectin homolog -1	0		F:GO:0005488; P:GO:0007155; F:GO:0005529		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG22233 [Caenorhabditis briggsae]	3	P:GO:0007411; P:GO:0019915; P:GO:0007413	-		PTHR23051 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	sushi domain containing	2	C:GO:0016021; P:GO:0007160	-		IPR001846; PTHR13802 (PANTHER), PTHR13802:SF1 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	tryptophanyl-tr- synthetase	8	C:GO:0005625; P:GO:0008285; F:GO:0005515; F:GO:0000166; F:GO:0004812; P:GO:0006418; P:GO:0045765; C:GO:0005737	-		-
Caenorhabditis elegans	transmembrane protein 170a	0		F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150; C:GO:0005575		-
Caenorhabditis briggsae	calcium atpase	7	F:GO:0005388; C:GO:0016021; P:GO:0006754; F:GO:0005524; P:GO:0006816; C:GO:0005737; P:GO:0030182	-	EC:3.6.3.8	-
Loa loa	headcase protein	0				-
Caenorhabditis briggsae	hmg coenzyme asynthase	10	P:GO:0009792; P:GO:0010171; P:GO:0002119; F:GO:0004421; P:GO:0018996; P:GO:0040010; P:GO:0000003; P:GO:0040011; P:GO:0008152; P:GO:0006898	-	EC:2.3.3.10	IPR000590; IPR013528; IPR013746; IPR016038; IPR016039; PTHR11877 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)

Caenorhabditis briggsae	ylx3_caeel ame: full=uncharacterized protein	6	C:GO:0016021; P:GO:0009792; P:GO:0040010; P:GO:0055085; F:GO:0005215; P:GO:0002119	-		PTHR11600 (PANTHER), PTHR11600:SF28 (PANTHER)
Loa loa	mynd finger family protein	1	F:GO:0046872	-		PTHR12197 (PANTHER), PTHR12197:SF9 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	short-chain dehydroge-se reductase sdr	0		P:GO:0006633; F:GO:0051287; P:GO:0042619; F:GO:0018454; F:GO:0016787; C:GO:0005737; P:GO:0055114; F:GO:0004316; F:GO:0016491; F:GO:0003824; P:GO:0008152; F:GO:0005488		SignalP (SIGNALP)
Homo sapiens	alpha-2-macroglobulin precursor	12	F:GO:0004867; F:GO:0043120; F:GO:0019966; P:GO:0001869; P:GO:0007584; C:GO:0005615; C:GO:0031093; F:GO:0019959; F:GO:0019899; P:GO:0010037; P:GO:0051384; P:GO:0006953	-		IPR011625
Loa loa	hypothetical protein LOAG_05911 [Loa loa]	0				-
Brugia malayi	anion exchange protein	7	C:GO:0005887; F:GO:0005452; F:GO:0008510; P:GO:0055085; P:GO:0006885; P:GO:0015701; P:GO:0006814	-		IPR003020; IPR011531; PTHR11453:SF9 (PANTHER), SignalP (SIGNALP)

Ancylostoma caninum	c-type lectin family member (clec-266)	0		F:GO:0001874; P:GO:0050766; F:GO:0001872; F:GO:0005529; P:GO:0016337; P:GO:0008037; P:GO:0032760; F:GO:0003674; F:GO:0030247; C:GO:0016021; P:GO:0006911; C:GO:0016020; P:GO:0006910; P:GO:0002238; F:GO:0030169; F:GO:0008329; F:GO:0004872; P:GO:0008150; P:GO:0006955; F:GO:0005488; P:GO:0007165; C:GO:0009897; P:GO:0001879; P:GO:0001878; C:GO:0005575; F:GO:0001846; P:GO:0002752		SignalP (SIGNALP)
Ancylostoma caninum	collectin sub-family member 12	0		F:GO:0030169; F:GO:0008329; C:GO:0016021; C:GO:0016020; F:GO:0005529; F:GO:0003674; P:GO:0006910; P:GO:0007165; C:GO:0005575; F:GO:0004872; F:GO:0046872; P:GO:0008150; P:GO:0006955; F:GO:0005488		SignalP (SIGNALP)

Ancylostoma caninum	c-type lectin family member (clec-266)	0		F:GO:0001874; P:GO:0050766; F:GO:0001872; F:GO:0005529; P:GO:0016337; P:GO:0008037; P:GO:0032760; F:GO:0003674; F:GO:0030247; C:GO:0016021; P:GO:0006911; C:GO:0016020; P:GO:0006910; P:GO:0002238; F:GO:0030169; F:GO:0008329; F:GO:0004872; P:GO:0008150; P:GO:0006955; F:GO:0005488; P:GO:0007165; C:GO:0009897; P:GO:0001879; P:GO:0001878; C:GO:0005575; F:GO:0001846; P:GO:0002752		SignalP (SIGNALP)
	-	0				-
Brugia malayi	hypothetical protein Bm1_17960 [Brugia malayi]	0				-
Caenorhabditis briggsae	briggsae cbr-msh-5 protein	0		F:GO:0005524; P:GO:0007131; F:GO:0005515; P:GO:0006298; F:GO:0030983; C:GO:0005634		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-lad-2 protein	0				-
Capsicum annuum	aromatic amino acid	0		P:GO:0006519; F:GO:0004058; F:GO:0003824; P:GO:0019752; F:GO:0016831; F:GO:0016829; F:GO:0030170		IPR002129; IPR015422; IPR015424; PTHR11999:SF11 (PANTHER)
Caenorhabditis briggsae	patched family protein	5	P:GO:0018996; C:GO:0016021; P:GO:0040018; F:GO:0008158; P:GO:0040011	-		-
	-	0				-
Caenorhabditis elegans	d- polymerase eta	6	P:GO:0006301; F:GO:0003684; F:GO:0003887; P:GO:0006290; F:GO:0000166; C:GO:0005634	-	EC:2.7.7.7	IPR001126; IPR017963; G3DSA:3.30.70.270 (GENE3D), PTHR11076:SF11 (PANTHER), SSF56672 (SUPERFAMILY)

Caenorhabditis elegans	phospholipase d3	3	P:GO:0008152; C:GO:0044425; F:GO:0003824	-		IPR013582; PTHR10185 (PANTHER), SSF56024 (SUPERFAMILY)
Brugia malayi	valyl-tr- synthetase	5	F:GO:0005515; P:GO:0006418; C:GO:0005829; F:GO:0004832; F:GO:0000166	-	EC:6.1.1.9	IPR001412; IPR002300; IPR002303; IPR014729; PTHR11946 (PANTHER), SSF52374 (SUPERFAMILY)
	-	0				-
Ciona intestinalis	mitogen-activated protein ki-se ki-se 5	7	F:GO:0004672; P:GO:0000165; P:GO:0007507; P:GO:0048522; F:GO:0005515; F:GO:0000166; C:GO:0005819	-		IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF45 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	copine domain atypical protein isoform partially confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	n-acetyllactosamine synthase	0		C:GO:0016021; P:GO:0005975; F:GO:0016757		SignalP (SIGNALP)
Ailuropoda melanoleuca	capping protein (actin filament) gelsolin-like	10	C:GO:0031965; C:GO:0005730; P:GO:0051016; P:GO:0007076; P:GO:0051301; C:GO:0042470; C:GO:0000796; F:GO:0003779; C:GO:0008290; P:GO:0030031	-		IPR007122; IPR007123; G3DSA:3.40.20.10 (GENE3D), PTHR11977:SF13 (PANTHER), SSF55753 (SUPERFAMILY)
Caenorhabditis elegans	nmd3 homolog	4	C:GO:0005737; C:GO:0005634; F:GO:0043023; P:GO:0000055	-		IPR007064; PTHR12746 (PANTHER)
Caenorhabditis briggsae	cysteine mitochondrial	10	C:GO:0005829; P:GO:0006777; P:GO:0018283; P:GO:0006461; F:GO:0031071; C:GO:0005759; F:GO:0042803; F:GO:0030170; C:GO:0005634; P:GO:0006534	-	EC:2.8.1.7	IPR000192; IPR015421; IPR015422; IPR015424; PTHR11601 (PANTHER)

Caenorhabditis briggsae	cysteine mitochondrial	10	C:GO:0005829; P:GO:0006777; P:GO:0018283; P:GO:0006461; F:GO:0031071; C:GO:0005759; F:GO:0042803; F:GO:0030170; C:GO:0005634; P:GO:0006534	-	EC:2.8.1.7	IPR000192; IPR015421; IPR015422; IPR015424; PTHR11601 (PANTHER)
Haemonchus contortus	peptidase c13 family protein	0		P:GO:0000003; P:GO:0006508; P:GO:0009792; F:GO:0004197; C:GO:0005575		IPR001096; PTHR12000:SF3 (PANTHER)
Haemonchus contortus	peptidase c13 family protein	0		P:GO:0000003; P:GO:0006508; P:GO:0009792; F:GO:0004197		IPR001096; PTHR12000:SF3 (PANTHER)
Haemonchus contortus	cysteine mitochondrial	12	C:GO:0005829; P:GO:0006777; P:GO:0018283; P:GO:0000003; P:GO:0006461; F:GO:0031071; C:GO:0005759; F:GO:0042803; P:GO:0009792; F:GO:0030170; C:GO:0005634; P:GO:0006534	-	EC:2.8.1.7	IPR001096; PTHR12000:SF4 (PANTHER), SignalP (SIGNALP)
Haemonchus contortus	cysteine mitochondrial	12	C:GO:0005829; P:GO:0006777; P:GO:0018283; P:GO:0000003; P:GO:0006461; F:GO:0031071; C:GO:0005759; F:GO:0042803; P:GO:0009792; F:GO:0030170; C:GO:0005634; P:GO:0006534	-	EC:2.8.1.7	IPR001096; PTHR12000:SF4 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	C:GO:0016021; F:GO:0005261; P:GO:0015672	-		-
Caenorhabditis elegans	r- helicase	0		F:GO:0004386; F:GO:0003723; P:GO:0006139; C:GO:0005737; P:GO:0006281; P:GO:0006974; F:GO:0016788; P:GO:0006310		IPR003029; IPR012340; IPR016027; IPR022967; IPR023097; PTHR10724 (PANTHER)
Caenorhabditis elegans	class v family	1	F:GO:0003824	-		IPR000192; IPR015421; IPR015424

Brugia malayi	probable nucleolar gtp-binding protein	13	P:GO:0008156; P:GO:0030336; F:GO:0005515; P:GO:0050821; F:GO:0005525; P:GO:0000079; P:GO:0008285; P:GO:0022408; P:GO:0031397; C:GO:0048471; F:GO:0003924; P:GO:0033342; C:GO:0005634	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR012973; PTHR11702 (PANTHER), PTHR11702:SF4 (PANTHER)
	-	0				SignalP (SIGNALP)
Brugia malayi	patched family protein	2	F:GO:0008158; C:GO:0016021	-		-
Caenorhabditis elegans	Hypothetical protein Y17G7B.23a [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	Hypothetical protein Y17G7B.23a [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	egf-like domain containing protein	0				IPR006210; IPR013032
Caenorhabditis briggsae	polymerase (d- directed) epsilon	8	F:GO:0005488; P:GO:0006259; P:GO:0040035; F:GO:0016740; P:GO:0040011; P:GO:0006997; P:GO:0002009; P:GO:0009792	-		PTHR10670 (PANTHER)
Caenorhabditis briggsae	uncoordi-ted family member (unc-89)	0		F:GO:0004672; F:GO:0005524; F:GO:0005089; P:GO:0006468; P:GO:0035023; F:GO:0004674; C:GO:0005622		IPR011009; G3DSA:1.10.510.10 (GENE3D)
Caenorhabditis elegans	cytochrome b5-like heme steroid binding domain containing protein	0		F:GO:0020037; C:GO:0016021; C:GO:0005576		IPR001199; PTHR10281 (PANTHER), PTHR10281:SF4 (PANTHER), SignalP (SIGNALP)
Loa loa	solute carrier family member e1	1	C:GO:0016020	-		IPR000620; PTHR11132 (PANTHER), SSF103481 (SUPERFAMILY)
Caenorhabditis elegans	rho gtpase activating protein 29	3	F:GO:0046872; P:GO:0007165; C:GO:0005622	-		PTHR15228 (PANTHER), PTHR15228:SF7 (PANTHER)
	-	0				-
Caenorhabditis elegans	gpi ethanolamine phosphate transferase 2	0		P:GO:0008152; C:GO:0016021; F:GO:0003824; F:GO:0008484		PTHR23072 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	ankyrin repeat-containing protein	0				-
Caenorhabditis elegans	briggsae cbr-uvt-3 protein	0		F:GO:0005524; P:GO:0015937; F:GO:0004594		PTHR12280 (PANTHER), PTHR12280:SF3 (PANTHER)
	-	0				-

Lethenteron japonicum	transcription factor ap-2	15	P:GO:0050935; C:GO:0030135; P:GO:0006355; P:GO:0051216; P:GO:0030902; P:GO:0014036; P:GO:0014032; P:GO:0030318; P:GO:0008104; P:GO:0006897; P:GO:0048522; P:GO:0007480; C:GO:0005886; F:GO:0005488; P:GO:0030182	-		IPR004979; IPR013854; PTHR10812:SF4 (PANTHER)
Loa loa	smad1 5 protein	22	P:GO:0006468; P:GO:0030901; F:GO:0005515; P:GO:0042592; P:GO:0001657; P:GO:0010552; P:GO:0030902; C:GO:0005737; P:GO:0061036; P:GO:0008285; C:GO:0005667; F:GO:0003702; P:GO:0042493; P:GO:0006954; P:GO:0007276; F:GO:0003700; P:GO:0002051; P:GO:0001710; P:GO:0071407; P:GO:0045669; P:GO:0030509; P:GO:0000165	-		IPR001132; IPR008984; IPR013790; IPR017855; PTHR13703:SF19 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-sep-1 protein	0		P:GO:0006508; F:GO:0008233; F:GO:0005515; C:GO:0005634		-
	-	0				-

Pongo abelii	filamin a	28	F:GO:0004871; C:GO:0005802; P:GO:0043433; P:GO:0034394; C:GO:0015629; P:GO:0050821; P:GO:0051220; C:GO:0005576; C:GO:0005829; F:GO:0001948; P:GO:0051764; P:GO:0043123; F:GO:0051015; F:GO:0048365; P:GO:0045022; P:GO:0007195; F:GO:0042803; F:GO:0034989; P:GO:0031532; F:GO:0034988; C:GO:0005886; F:GO:0008134; P:GO:0042177; C:GO:0005634; P:GO:0042993; C:GO:0005938; P:GO:0043113	-		IPR001298; IPR013783; IPR014756; IPR017868; PTHR11915 (PANTHER), PTHR11915:SF24 (PANTHER)
Caenorhabditis elegans	metallophosphoesterase domain containing 1	0		F:GO:0003674; F:GO:0016787; P:GO:0008150; C:GO:0005575		IPR004843; G3DSA:3.60.21.10 (GENE3D), PTHR12905 (PANTHER), SignalP (SIGNALP), SSF56300 (SUPERFAMILY)
Caenorhabditis elegans	class b secretin-like g-protein coupled receptor	3	P:GO:0007166; C:GO:0016020; F:GO:0004930	-		IPR003287; IPR017983; PTHR12011 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0008152; F:GO:0003824		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	F:GO:0004725; P:GO:0006470; F:GO:0008138	-	EC:3.1.3.48	SignalP (SIGNALP)
	-	0				-
Macaca fascicularis	-dh dehydroge-se	5	P:GO:0006120; P:GO:0007605; F:GO:0008137; P:GO:0006810; C:GO:0005747	-	EC:1.6.5.3	PTHR12868 (PANTHER)
Caenorhabditis elegans	inner membrane mitochondrial	2	C:GO:0005743; C:GO:0016021	-		IPR019133; PTHR15415 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	in family member (ttn-1)	1	P:GO:0009792	-		-
Caenorhabditis briggsae	r- polymerase ii subunit a c-termi-l domain phosphatase	1	C:GO:0005622	-		IPR001357; G3DSA:3.40.50.10190 (GENE3D), PTHR23081 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-

	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F59E12.11 [Caenorhabditis elegans]	0		P:GO:0002119; F:GO:0005515; P:GO:0040007		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				IPR021629
Caenorhabditis elegans	phd finger protein 8	1	F:GO:0005488	-		IPR003347; IPR013129; PTHR23123 (PANTHER), SSF51197 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	r- dependent r- polymerase family protein	1	F:GO:0005515	-		IPR007855
Caenorhabditis briggsae	briggsae cbr-ncx-3 protein	3	P:GO:0006810; P:GO:0009987; C:GO:0016020	-		IPR004836; PTHR11878 (PANTHER), PTHR11878:SF2 (PANTHER)
Caenorhabditis elegans	bromodomain containing protein	10	F:GO:0030528; P:GO:0000117; F:GO:0008270; P:GO:0006352; P:GO:0045944; F:GO:0035174; F:GO:0043565; F:GO:0005515; P:GO:0016573; C:GO:0005669	-		PTHR13900 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		C:GO:0005737		IPR010504; PTHR12141 (PANTHER), PTHR12141:SF1 (PANTHER), SSF103657 (SUPERFAMILY)
Caenorhabditis briggsae	quinone oxidoreductase	8	F:GO:0003960; F:GO:0003730; F:GO:0070402; P:GO:0042178; P:GO:0007601; C:GO:0005829; F:GO:0070404; P:GO:0051289	-	EC:1.6.5.5	IPR002085; IPR011032; IPR013149; IPR016040; G3DSA:3.90.180.10 (GENE3D), PTHR11695:SF30 (PANTHER), SSF51735 (SUPERFAMILY)

Loa loa	member ras oncogene family	25	P:GO:0006895; C:GO:0042599; C:GO:0005829; P:GO:0045176; C:GO:0005764; C:GO:0042175; P:GO:0007264; F:GO:0001948; P:GO:0032880; C:GO:0005795; P:GO:0006913; C:GO:0005624; F:GO:0019003; P:GO:0007589; C:GO:0005770; C:GO:0005769; P:GO:0007269; C:GO:0005791; C:GO:0030140; F:GO:0003924; C:GO:0048471; C:GO:0016324; P:GO:0006886; C:GO:0005634; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001806; IPR003579; IPR005225; IPR013753; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF248 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	te-scin xb	0		F:GO:0005044; C:GO:0016020		-
Ciona intestinalis	amine oxidase	3	C:GO:0005739; P:GO:0008152; C:GO:0016020	-		IPR001613; IPR002937; G3DSA:3.50.50.60 (GENE3D), PTHR10742 (PANTHER), PTHR10742:SF5 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				IPR013753; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF278 (PANTHER), SSF52540 (SUPERFAMILY)
Tribolium castaneum	ankyrin repeat protein	0		C:GO:0000785; P:GO:0007517; F:GO:0003682; C:GO:0005634; F:GO:0003677; P:GO:0006306; F:GO:0000166; F:GO:0005524; P:GO:0006333; F:GO:0016887; P:GO:0006936; C:GO:0031674; F:GO:0008307; F:GO:0005198		IPR002110; IPR006034; IPR020683; PTHR11707:SF3 (PANTHER), SignalP (SIGNALP)

Tribolium castaneum	ankyrin repeat protein	0		C:GO:0000785; P:GO:0007517; F:GO:0003682; C:GO:0005634; F:GO:0003677; P:GO:0006306; F:GO:0000166; F:GO:0005524; P:GO:0006333; F:GO:0016887; P:GO:0006936; C:GO:0031674; F:GO:0008307; F:GO:0005198		IPR002110; IPR006034; IPR020683; PTHR11707:SF3 (PANTHER), SignalP (SIGNALP)
Brugia malayi	lim domain containing protein	4	F:GO:0008270; P:GO:0008152; F:GO:0016491; F:GO:0009055	-		IPR003953; G3DSA:3.50.50.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF45 (PANTHER), SSF51905 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	d- polymerase theta	6	F:GO:0003684; P:GO:0006259; F:GO:0016740; F:GO:0000166; F:GO:0004386; C:GO:0005654	-		G3DSA:3.40.50.300 (GENE3D), PTHR11752 (PANTHER), PTHR11752:SF3 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0030259; F:GO:0016740; F:GO:0030246; P:GO:0008152; P:GO:0005975; C:GO:0016021; F:GO:0016758; F:GO:0016757		IPR002213; PTHR11926:SF3 (PANTHER)
Caenorhabditis elegans	briggsae cbr-frm-7 protein	0		F:GO:0005488; C:GO:0005856		-
Pan troglodytes	actin related protein 2 3 complex subunit 1b	6	C:GO:0005737; F:GO:0005200; C:GO:0005885; P:GO:0030833; P:GO:0006928; F:GO:0003779	-		IPR015943; PTHR10709 (PANTHER), PTHR10709:SF10 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	cdk5 regulatory subunit associated protein 3	2	F:GO:0005515; P:GO:0000079	-		IPR008491
	-	0				-
Caenorhabditis elegans	briggsae cbr-tag-68 protein	5	F:GO:0003700; F:GO:0005515; C:GO:0005667; P:GO:0006355; P:GO:0007179	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein Y23H5B.4 [Caenorhabditis elegans]	0				-
	-	0				-

Caenorhabditis briggsae	fatty acid amide hydrolase	8	P:GO:0009062; F:GO:0017064; F:GO:0016788; F:GO:0005543; C:GO:0031090; F:GO:0004040; C:GO:0044425; F:GO:0042803	-	EC:3.5.1.4	IPR000120; IPR015830; IPR020556; PTHR11895:SF4 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	cg13690	2	F:GO:0004519; F:GO:0003676	-		IPR001352; IPR012337; IPR023160; G3DSA:3.30.420.10 (GENE3D)
Caenorhabditis elegans	briggsae cbr-rnh-2 protein	2	F:GO:0004519; F:GO:0003676	-		IPR001352; IPR012337; IPR023160; G3DSA:3.30.420.10 (GENE3D)
	-	0				-
Callithrix jacchus	ribosomal protein s15	0		F:GO:0003723; F:GO:0003677; C:GO:0005634; C:GO:0030529; P:GO:0042274; F:GO:0003735; C:GO:0015935; P:GO:0009790; P:GO:0006414; C:GO:0022627; P:GO:0006412; P:GO:0000028; P:GO:0006364; C:GO:0005840; P:GO:0000056; C:GO:0005829; C:GO:0005654; C:GO:0005622; F:GO:0005515		-
	-	0				-
Caenorhabditis briggsae	yo22_caeel ame: full=uncharacterized protein	2	P:GO:0040011; P:GO:0040018	-		-
Physarum polycephalum	cytosolic glycoprotein fp21	13	P:GO:0040010; P:GO:0006511; P:GO:0008340; F:GO:0016874; P:GO:0040035; P:GO:0002119; F:GO:0005515; P:GO:0040011; F:GO:0016301; P:GO:0006898; P:GO:0002009; P:GO:0009792; P:GO:0016246	-		SignalP (SIGNALP)
	-	0				-
Brugia malayi	titin	1	P:GO:0009792	-		IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF13 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-

Pongo abelii	activating transcription factor 4 (tax-responsive enhancer element b67)	14	P:GO:0034976; P:GO:0045944; P:GO:0007214; C:GO:0005667; F:GO:0008022; C:GO:0032590; P:GO:0006520; F:GO:0043565; F:GO:0016563; F:GO:0046983; F:GO:0003700; P:GO:0006094; F:GO:0003704; C:GO:0005737	-		-
Caenorhabditis briggsae	cg2222-pa	4	P:GO:0040035; P:GO:0010171; P:GO:0040011; P:GO:0006898	-		IPR010492
	-	0				-
	-	0				-
Caenorhabditis briggsae	glycosyl hydrolases family 31 protein	3	F:GO:0004558; P:GO:0005975; F:GO:0030246	-	EC:3.2.1.20	IPR000322; IPR017853; PTHR22762:SF10 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F18E9.3 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	laminin alpha chain	7	C:GO:0005606; P:GO:0030334; P:GO:0045995; P:GO:0007517; P:GO:0030155; F:GO:0005102; F:GO:0005198	-		IPR002049; IPR013032; G3DSA:2.10.25.10 (GENE3D), PTHR10574 (PANTHER), PTHR10574:SF38 (PANTHER), SSF57196 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	sp1070 cg9138-pa	3	P:GO:0035152; C:GO:0016324; F:GO:0005488	-		IPR009030; IPR011641; G3DSA:2.10.220.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF72 (PANTHER)
Brugia malayi	protein ki-se domain containing protein	5	P:GO:0001700; P:GO:0006468; F:GO:0004713; F:GO:0005524; F:GO:0004674	-	EC:2.7.10.0; EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR23257 (PANTHER), PTHR23257:SF95 (PANTHER)
	-	0				-
	-	0				IPR007222
	-	0				-
Tribolium castaneum	rwd domain-containing protein 4a	0		F:GO:0004872		IPR006575; IPR016135; PTHR21275 (PANTHER)
Tribolium castaneum	rwd domain-containing protein 4a	0		F:GO:0004872		IPR006575; IPR016135; PTHR21275 (PANTHER)
Caenorhabditis briggsae	-dh oxidase	1	F:GO:0003824	-		IPR013785; PTHR22893 (PANTHER), PTHR22893:SF6 (PANTHER)
Caenorhabditis elegans	hypothetical protein Y54E10A.11 [Caenorhabditis elegans]	0		F:GO:0008270		SignalP (SIGNALP)
Drosophila mojavensis	tbc1 domain family member 30-like	3	F:GO:0005097; C:GO:0005622; P:GO:0032313	-		-

Caenorhabditis briggsae	cop9 sig-losome complex subunit 2	10	P:GO:0000910; P:GO:0018991; F:GO:0004871; C:GO:0005730; C:GO:0008180; F:GO:0005515; P:GO:0007165; P:GO:0009792; C:GO:0005737; P:GO:0006366	-		PTHR10678 (PANTHER), PTHR10678:SF3 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-ssq-2 protein	0		F:GO:0008061; P:GO:0006030; C:GO:0005576		-
Caenorhabditis elegans	cmc1 protein	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Saccoglossus kowalevskii	udp- c:beta- -n-acetylgalactosaminyltransferase 1	0		F:GO:0016740; C:GO:0016021; C:GO:0016020; F:GO:0047273; C:GO:0000139; F:GO:0008378; F:GO:0016757; P:GO:0009312; C:GO:0005794; F:GO:0047915; F:GO:0008499; P:GO:0006486		-
Loa loa	elegans protein partially confirmed by transcript evidence	3	P:GO:0006541; F:GO:0004359; F:GO:0005515	-	EC:3.5.1.2	IPR012338; IPR015868; PTHR12544:SF3 (PANTHER)
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				SignalP (SIGNALP)
Caenorhabditis elegans	laminin alpha chain	3	P:GO:0007155; P:GO:0050794; C:GO:0005604	-		-
Caenorhabditis elegans	uncoordi-ted family member (unc-5)	0		F:GO:0004872; P:GO:0007165; F:GO:0005515		PTHR12582 (PANTHER), PTHR12582:SF2 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	polypyrimidine tract binding protein	14	P:GO:0007219; P:GO:0008103; F:GO:0005515; P:GO:0008586; F:GO:0000166; F:GO:0000900; F:GO:0003730; C:GO:0005737; P:GO:0000398; P:GO:0008587; P:GO:0007319; F:GO:0008187; C:GO:0005634; C:GO:0030529	-		-
	-	0				-
Caenorhabditis elegans	cuticular collagen	3	C:GO:0016021; P:GO:0010171; F:GO:0005515	-		-

Caenorhabditis elegans	isoform cra_a	2	F:GO:0005488; P:GO:0006350	-		IPR007087; IPR013087; IPR015880; PTHR23224 (PANTHER), PTHR23224:SF446 (PANTHER), SSF57667 (SUPERFAMILY)
Loa loa	hypothetical protein LOAG_02820 [Loa loa]	1	F:GO:0004175	-		SignalP (SIGNALP)
Caenorhabditis elegans	transmembrane protein 195	0		F:GO:0005506; P:GO:0006633; C:GO:0016021; F:GO:0050479; C:GO:0016020; F:GO:0003674; P:GO:0046485; P:GO:0055114; F:GO:0016491; C:GO:0005575; P:GO:0006643; C:GO:0005783; P:GO:0008150		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Loa loa	msp-domain protein 1 variant	0		C:GO:0005856; F:GO:0005198		IPR000535; IPR008962; PTHR22947 (PANTHER)
Caenorhabditis elegans	nuclear migration protein nudc	0				PTHR12356 (PANTHER), PTHR12356:SF3 (PANTHER)
Caenorhabditis briggsae	glia maturation factor beta	9	P:GO:0006468; F:GO:0008047; F:GO:0008083; F:GO:0004871; F:GO:0004860; C:GO:0005622; F:GO:0003779; P:GO:0007399; P:GO:0007165	-		IPR002108; IPR011171; G3DSA:3.40.20.10 (GENE3D), SignalP (SIGNALP), SSF55753 (SUPERFAMILY)
Caenorhabditis briggsae	temporarily assigned gene -me family member (tag-308)	0				-
	-	0				-
Caenorhabditis elegans	zinc finger protein	0		F:GO:0008270; C:GO:0005622		IPR007087; IPR015880

Saccoglossus kowalevskii	plectin isoform 1hij	0		F:GO:0005200; P:GO:0030855; C:GO:0009925; C:GO:0009986; C:GO:0043292; F:GO:0003674; C:GO:0042383; C:GO:0016020; F:GO:0008092; C:GO:0005618; C:GO:0048471; F:GO:0047485; P:GO:0007584; P:GO:0031581; C:GO:0005737; F:GO:0003779; C:GO:0005626; C:GO:0005829; C:GO:0005622; C:GO:0005856; P:GO:0007565; C:GO:0016324; C:GO:0005575		-
	-	0				-
Haemonchus contortus	elegans protein partially confirmed by transcript evidence	7	P:GO:0018996; P:GO:0008340; F:GO:0004867; P:GO:0040002; P:GO:0002119; P:GO:0040011; F:GO:0008233	-		-
Haemonchus contortus	elegans protein partially confirmed by transcript evidence	7	P:GO:0018996; P:GO:0008340; F:GO:0004867; P:GO:0040002; P:GO:0002119; P:GO:0040011; F:GO:0008233	-		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	P:GO:0006810; P:GO:0042221	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Ancylostoma caninum	-dh dehydroge-se subunit i	4	C:GO:0016021; P:GO:0055114; C:GO:0005739; F:GO:0008137	-	EC:1.6.5.3	IPR001694; SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-

Caenorhabditis briggsae	gamma-glutamyltransferase 7	2	F:GO:0016746; C:GO:0016020	-		-
	-	0				-
Caenorhabditis elegans	nucleoside diphosphate ki-se b	29	C:GO:0030027; F:GO:0005515; P:GO:0002762; P:GO:0007155; P:GO:0040007; F:GO:0004550; P:GO:0006898; P:GO:0006241; P:GO:0006355; P:GO:0030819; C:GO:0005882; F:GO:0046872; P:GO:0006165; C:GO:0001726; P:GO:0009792; F:GO:0003677; P:GO:0045618; P:GO:0006183; P:GO:0002119; P:GO:0006228; P:GO:0050679; F:GO:0003700; C:GO:0048471; C:GO:0005886; C:GO:0005634; F:GO:0005524; P:GO:0043066; P:GO:0040035;	-	EC:2.7.4.6	IPR001564; IPR023005; SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-exc-5 protein	4	F:GO:0005089; C:GO:0005622; P:GO:0035023; F:GO:0008270	-		IPR001849; IPR011993; PTHR12673 (PANTHER), PTHR12673:SF8 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0006810; F:GO:0015116; C:GO:0016021	-		IPR011547; IPR018045; PTHR11814 (PANTHER), PTHR11814:SF25 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-unc-84 protein	1	F:GO:0005515	-		IPR012919; PTHR12911 (PANTHER), PTHR12911:SF7 (PANTHER), PS51469 (PROFILE)
	-	0				-
Caenorhabditis elegans	ap-2 complex subunit alpha-2	13	C:GO:0005829; F:GO:0008565; P:GO:0040010; P:GO:0048268; F:GO:0008022; P:GO:0000003; P:GO:0050690; C:GO:0030122; P:GO:0040011; P:GO:0006898; P:GO:0006886; C:GO:0030141; P:GO:0009792	-		IPR008152; IPR009028; IPR013038; IPR013041; PTHR22780 (PANTHER), PTHR22780:SF4 (PANTHER)
	-	0				-

Caenorhabditis elegans	transmembrane anterior posterior transformation protein 1 homolog	5	F:GO:0016520; P:GO:0048706; P:GO:0001701; C:GO:0016021; P:GO:0009791	-		IPR008010
Caenorhabditis elegans	pleckstrin homology domain family g (with ef domain) member 1	3	F:GO:0005089; C:GO:0005622; P:GO:0035023	-		IPR000219; IPR001849; IPR011993; PTHR22826 (PANTHER), PTHR22826:SF50 (PANTHER), SSF50729 (SUPERFAMILY)
Caenorhabditis briggsae	ser thr protein phosphatase	0		F:GO:0048037; F:GO:0016787; F:GO:0004724; F:GO:0004721		IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF4 (PANTHER), SSF56300 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein C01B7.5 [Caenorhabditis elegans]	1	F:GO:0005515	-		-
Caenorhabditis briggsae	ubiquitin protein ligase e3 component n-recognin 3	5	P:GO:0009790; F:GO:0016874; F:GO:0005488; P:GO:0044267; P:GO:0007610	-		PTHR21497 (PANTHER), PTHR21497:SF3 (PANTHER)
	-	0				-
	-	0				IPR016186
	-	0				IPR003006
	-	0				-
Homo sapiens	PREDICTED: hypothetical protein XP_002342418 [Homo sapiens]	0				-
Loa loa	trithorax protein ash2	5	P:GO:0040035; F:GO:0046872; P:GO:0040027; F:GO:0005515; P:GO:0040007	-		IPR001965; IPR011011; IPR013083; IPR019786
Caenorhabditis elegans	alg12_caeel ame: full=probable dolichyl-p-man:man c -pp-dolichyl-alpha- -mannosyltransferase ame: full=asparagine-linked glycosylation protein 12 homolog ame: full=mannosyltransferase alg12 homolog	4	C:GO:0031224; P:GO:0006488; F:GO:0000009; C:GO:0005783	-		IPR005599; SignalP (SIGNALP)
Caenorhabditis briggsae	u3 small nucleolar homolog a	8	P:GO:0040010; P:GO:0040035; P:GO:0007283; P:GO:0019915; P:GO:0002119; F:GO:0005515; P:GO:0006898; C:GO:0044424	-		IPR006709; PTHR14150:SF12 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Loa loa	gex interacting protein family member (gei-17)	5	P:GO:0009987; F:GO:0005488; C:GO:0044446; P:GO:0048513; C:GO:0005634	-		IPR003034; IPR004181; G3DSA:1.10.720.30 (GENE3D), PTHR10782 (PANTHER), PS51466 (PROFILE), SSF68906 (SUPERFAMILY)
Brugia malayi	transportin 1	7	C:GO:0005737; F:GO:0005515; P:GO:0000060; F:GO:0008565; F:GO:0008139; C:GO:0005634; P:GO:0044419	-		IPR011989; IPR016024; PTHR10527 (PANTHER), PTHR10527:SF3 (PANTHER)

Caenorhabditis elegans	uncoordi-ted family member (unc-115)	3	P:GO:0007010; F:GO:0003779; F:GO:0008270	-		IPR003128; IPR007122
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG09330 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG19874 [Caenorhabditis briggsae]	5	P:GO:0002119; P:GO:0040010; P:GO:0000003; P:GO:0006898; F:GO:0003824	-		IPR002738; IPR016195; G3DSA:3.20.20.140 (GENE3D)
	-	0				PTHR12547 (PANTHER), PTHR12547:SF17 (PANTHER)
	-	0				-
Caenorhabditis elegans	abnormal cell lineage family member (lin-7)	1	C:GO:0005622	-		IPR001684; SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	xanthine dehydroge-se	10	P:GO:0008340; F:GO:0051537; P:GO:0055114; F:GO:0009055; F:GO:0004855; F:GO:0004854; F:GO:0043546; F:GO:0050660; P:GO:0009115; F:GO:0005506	-	EC:1.17.3.2; EC:1.17.1.4	-
Caenorhabditis briggsae	related to yeast vacuolar protein sorting factor family member (vps-34)	4	P:GO:0009987; F:GO:0005488; F:GO:0016773; F:GO:0016301	-	EC:2.7.1.0	IPR002420; IPR008973; IPR015433; G3DSA:2.60.40.150 (GENE3D), PTHR10048:SF7 (PANTHER)
	-	0				-
Teladorsagia circumcincta	fmrfamide-related peptide flp-18 precursor	2	C:GO:0005576; P:GO:0007218	-		IPR002544; PTHR20986 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	riboki-se	2	P:GO:0044262; F:GO:0016301	-		IPR002139; IPR011611; G3DSA:3.40.1190.20 (GENE3D), PTHR10584 (PANTHER), PTHR10584:SF29 (PANTHER), SSF53613 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	methyltransferase type 11	4	P:GO:0044238; P:GO:0043412; F:GO:0008168; P:GO:0044260	-	EC:2.1.1.0	-
	-	0				-

Brugia malayi	ran-binding protein 7	0		P:GO:0006325; P:GO:0008283; P:GO:0016318; C:GO:0048471; P:GO:0007173; P:GO:0051276; P:GO:0045465; P:GO:0031936; P:GO:0035311; F:GO:0004674; F:GO:0004672; F:GO:0008536; P:GO:0042675; F:GO:0008565; P:GO:0007169; P:GO:0006606; F:GO:0035175; F:GO:0005524; P:GO:0043524; P:GO:0006886; F:GO:0005488; C:GO:0005938; P:GO:0006468; P:GO:0048749; C:GO:0005643; P:GO:0008586; C:GO:0016456;		-
Caenorhabditis elegans	chondroitin sulfate synthase 1	2	F:GO:0016758; C:GO:0032580	-	EC:2.4.1.0	IPR008428; G3DSA:3.90.550.10 (GENE3D), SignalP (SIGNALP), SSF53448 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	ypt5_caeel ame: full=uncharacterized protein	0		P:GO:0000003		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-flp-15 protein	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	solute carrier family 39 (zinc transporter) member 9	4	C:GO:0016020; P:GO:0006829; F:GO:0005385; P:GO:0055085	-		IPR003689; PTHR16133 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	atp-citrate synthase	11	P:GO:0015936; C:GO:0005829; F:GO:0003878; C:GO:0009346; P:GO:0006200; F:GO:0008815; P:GO:0044262; F:GO:0004775; F:GO:0005524; F:GO:0005515; P:GO:0006101	-	EC:2.3.3.8; EC:4.1.3.6; EC:6.2.1.5	IPR002020; IPR003781; IPR005810; IPR005811; IPR013650; IPR013816; IPR014608; IPR016040; IPR016102; IPR016141; IPR016142; IPR016143; IPR017440; IPR017866; PTHR23118 (PANTHER), SSF51735 (SUPERFAMILY), SSF56059 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-

Caenorhabditis briggsae	probable e3 ubiquitin-protein ligase mycbp2	4	P:GO:0030071; F:GO:0005515; F:GO:0008270; C:GO:0005680	-		IPR004939; IPR008979; G3DSA:2.60.120.260 (GENE3D), PTHR12846 (PANTHER), PTHR12846:SF2 (PANTHER)
Loa loa	protein ki-se domain containing protein	0		F:GO:0016301; F:GO:0004672; F:GO:0005524; P:GO:0006468		IPR000276; IPR011009; G3DSA:3.30.200.20 (GENE3D)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	C:GO:0005578	-		-
Caenorhabditis briggsae	briggsae cbr-snt-5 protein	3	C:GO:0016021; C:GO:0008021; P:GO:0006810	-		IPR008973; G3DSA:2.60.40.150 (GENE3D), PTHR10024 (PANTHER), PTHR10024:SF41 (PANTHER)
Caenorhabditis elegans	ywq1_caeel ame: full=uncharacterized protein	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	filamin abp280 repeat family protein	8	P:GO:0009792; P:GO:0010171; C:GO:0005840; F:GO:0003735; F:GO:0003779; P:GO:0007126; P:GO:0000003; P:GO:0006412	-	EC:3.6.5.3	IPR001298; IPR013783; IPR014756; IPR017868; PTHR11915 (PANTHER), PTHR11915:SF24 (PANTHER)
Caenorhabditis elegans	nicoti-mide nucleotide adenylyltransferase 3	8	C:GO:0005739; P:GO:0009435; F:GO:0004515; P:GO:0000003; P:GO:0019915; F:GO:0000309; P:GO:0043526; P:GO:0009792	-	EC:2.7.7.18; EC:2.7.7.1	IPR004820; IPR005248; IPR014729; SSF52374 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-alh-11 protein	0		P:GO:0055114; F:GO:0016491; P:GO:0008152		G3DSA:2.30.30.330 (GENE3D), PF05708 (PFAM)
Homo sapiens	-dh dehydroge-se	5	P:GO:0006120; F:GO:0008137; P:GO:0006810; C:GO:0005747; C:GO:0016021	-	EC:1.6.5.3	SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	akt pkb serine threonine ki-se	62	F:GO:0043325; P:GO:0006954; P:GO:0007186; F:GO:0004674; P:GO:0030334; P:GO:0060709; P:GO:0042640; P:GO:0046329; P:GO:0043491; P:GO:0090004; P:GO:0045429; C:GO:0005625; P:GO:0032094; P:GO:0034405; P:GO:0001893; P:GO:0031999; P:GO:0043053; P:GO:0046326; P:GO:0010765; C:GO:0030027; C:GO:0005829; P:GO:0016567; P:GO:0006924; P:GO:0045884; C:GO:0005654; P:GO:0045725; P:GO:0040010;	-	EC:2.7.11.0	IPR000719; IPR011009; IPR015744; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR22985 (PANTHER)
Brugia malayi	ankyrin unc44	4	P:GO:0044260; F:GO:0004672; P:GO:0044238; F:GO:0000166	-		IPR002110; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER), PTHR18958:SF302 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	trans-sialidase	1	C:GO:0044464	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	ferm domain (-ezrin-radixin-moesin) family member (frm-1)	1	F:GO:0005515	-		-
Caenorhabditis elegans	udp- ransferase family member (ugt-29)	3	P:GO:0019915; P:GO:0008152; F:GO:0016740	-		SignalP (SIGNALP)
	-	0				-
Ancylostoma duodenale	secreted protein asp-2	0		P:GO:0040011; C:GO:0005576		IPR001283; IPR014044; PTHR10334:SF11 (PANTHER)
Brugia malayi	r- polymerase domain 1 family protein	6	F:GO:0003899; F:GO:0003677; P:GO:0006350; F:GO:0032549; C:GO:0005634; F:GO:0008270	-	EC:2.7.7.6	IPR007081; IPR015700; PTHR19376 (PANTHER), SSF64484 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis elegans	eukaryotic translation initiation factor 2	11	C:GO:0005845; F:GO:0000340; P:GO:0035279; C:GO:0016442; F:GO:0070551; P:GO:0035278; C:GO:0035068; F:GO:0005515; F:GO:0035197; P:GO:0045947; P:GO:0031054	-		IPR003165; IPR012337; PTHR22891 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-prk-2 protein	3	F:GO:0004674; F:GO:0005524; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22984 (PANTHER)
Caenorhabditis briggsae	nuclear receptor binding protein	8	P:GO:0007254; F:GO:0004674; F:GO:0005524; C:GO:0012505; C:GO:0048471; F:GO:0042803; C:GO:0005634; P:GO:0006468	-	EC:2.7.11.0	IPR001245; IPR011009; G3DSA:3.30.200.20 (GENE3D), PTHR13902 (PANTHER), PTHR13902:SF9 (PANTHER)
Brugia malayi	rhomboid family protein	0		F:GO:0004252; F:GO:0005509; C:GO:0016021; C:GO:0016020; F:GO:0008233; P:GO:0007165		IPR002610; IPR011992; IPR018249; IPR022764; G3DSA:1.20.1540.10 (GENE3D), SSF144091 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-ncx-3 protein	0		P:GO:0006816; C:GO:0016021; P:GO:0007154; C:GO:0016020; P:GO:0055085; F:GO:0005432		IPR003644; PTHR11878 (PANTHER), PTHR11878:SF2 (PANTHER), SSF141072 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	tumor suppressor candidate 4	0		C:GO:0005789; F:GO:0004672; P:GO:0006506; C:GO:0016021; P:GO:0008150; F:GO:0005515; P:GO:0033673; C:GO:0005575		IPR009348
Caenorhabditis elegans	neutral endopeptidase	3	C:GO:0016021; F:GO:0004222; P:GO:0006508	-	EC:3.4.24.0	IPR000718; IPR008753; G3DSA:1.10.1380.10 (GENE3D), PTHR11733:SF20 (PANTHER)
Ailuropoda melanoleuca	u2 snrnp auxiliary factor small subunit variant 1	7	F:GO:0050733; C:GO:0015030; C:GO:0005681; F:GO:0003723; F:GO:0008270; P:GO:0000398; F:GO:0000166	-		IPR000504; IPR009145; IPR012677; SSF54928 (SUPERFAMILY)
	-	0				-
Strongylocentrotus purpuratus	mflj00229 protein	0		F:GO:0003674; P:GO:0008150		IPR012860; SignalP (SIGNALP)

Strongylocentrotus purpuratus	mflj00229 protein	0		F:GO:0003674; P:GO:0008150		IPR012860; SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG12581 [Caenorhabditis briggsae]	1	F:GO:0005515	-		IPR001715
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-gtl-2 protein	1	P:GO:0006810	-		PTHR13800 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	7	P:GO:0007160; F:GO:0005518; C:GO:0031012; P:GO:0008218; F:GO:0005509; P:GO:0018298; C:GO:0016020	-		IPR000033; IPR011042; PTHR10529 (PANTHER), PTHR10529:SF4 (PANTHER), SSF63825 (SUPERFAMILY)
Caenorhabditis elegans	lobulin-like cell adhesion molecule family member (igcm-3)	1	P:GO:0019915	-		-
Loa loa	elegans protein partially confirmed by transcript evidence	0				-
Haemonchus contortus	zinc metallopeptidase	0		P:GO:0006508; F:GO:0008237; F:GO:0004222		-
Caenorhabditis elegans	phosphatidylinositol glycan anchor class b	12	P:GO:0040010; P:GO:0008340; P:GO:0044267; P:GO:0034645; P:GO:0000003; P:GO:0010171; P:GO:0002119; C:GO:0044425; P:GO:0040011; P:GO:0009792; F:GO:0016757; C:GO:0005783	-		IPR005599; SignalP (SIGNALP)
Mus musculus	eukaryotic translation initiation factor 5a	23	P:GO:0006406; F:GO:0003746; P:GO:0007568; F:GO:0047485; P:GO:0006611; C:GO:0005789; F:GO:0003743; P:GO:0006452; F:GO:0043022; C:GO:0005829; C:GO:0005643; C:GO:0030425; P:GO:0008284; P:GO:0008612; C:GO:0043025; P:GO:0006917; F:GO:0017070; C:GO:0005642; P:GO:0055085; P:GO:0045905; P:GO:0051149; P:GO:0045901; P:GO:0043066	-		IPR001884; IPR005824; IPR008991; IPR014722; PTHR11673:SF2 (PANTHER)
	-	0				SignalP (SIGNALP)

	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0008270; F:GO:0005515		-
	-	0				-
Caenorhabditis briggsae	nipped-b homolog	31	P:GO:0007605; F:GO:0042826; P:GO:0034613; P:GO:0003151; P:GO:0006974; F:GO:0008022; C:GO:0032116; P:GO:0040018; F:GO:0070087; P:GO:0060325; F:GO:0047485; P:GO:0071481; P:GO:0061010; P:GO:0034088; P:GO:0045444; P:GO:0050890; P:GO:0031065; P:GO:0007420; P:GO:0010553; P:GO:0048703; P:GO:0048592; P:GO:0035261; P:GO:0045995; P:GO:0045778; P:GO:0042471; P:GO:0042634; P:GO:0061038;	-		-
Caenorhabditis briggsae	tr- (5-methylaminomethyl-2-thiouridylate)-methyltransferase	6	C:GO:0005737; F:GO:0004808; P:GO:0006529; P:GO:0006400; F:GO:0005524; F:GO:0000049	-	EC:2.1.1.61	-
	-	0				-
	-	0				-
Loa loa	protein ki-se domain containing protein	0		F:GO:0016301; F:GO:0004672; F:GO:0005524; F:GO:0000166; P:GO:0006468; F:GO:0004674		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Loa loa	prefoldin subunit 4	3	P:GO:0006457; C:GO:0016272; F:GO:0051082	-		IPR002777; PTHR21100 (PANTHER), PTHR21100:SF3 (PANTHER)
Brugia malayi	Alpha-catulin [Brugia malayi]	0		F:GO:0005198; P:GO:0007155; C:GO:0015629		-
Ailuropoda melanoleuca	ribosomal protein s26	6	F:GO:0003729; F:GO:0003735; P:GO:0006414; C:GO:0022627; P:GO:0033119; F:GO:0005515	-		IPR000892

	-	0				-
	-	0				-
Acyrthosiphon pisum	ffa-1 protein	3	P:GO:0006259; F:GO:0046872; F:GO:0008026	-		IPR004589; IPR011545; IPR014021; G3DSA:3.40.50.300 (GENE3D), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	histone h1 like family member (hil-1)	0		C:GO:0005694; C:GO:0000786; P:GO:0006334; F:GO:0003677; C:GO:0005634		IPR005818; IPR005819; IPR011991; PTHR11467 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-sbp-1 protein	0		P:GO:0045449; F:GO:0030528; F:GO:0005515; C:GO:0005634		-
Caenorhabditis elegans	udp-glucose glycoprotein:glucosyltransferase	3	F:GO:0003980; P:GO:0006486; C:GO:0005783	-		IPR002495; IPR009448; G3DSA:3.90.550.10 (GENE3D), SSF53448 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	protein ki-se domain containing protein	5	P:GO:0007283; P:GO:0006468; F:GO:0004672; F:GO:0005524; P:GO:0040011	-		IPR011009; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
Caenorhabditis elegans	kiaa1018 protein	2	F:GO:0005515; P:GO:0006281	-		-
Caenorhabditis elegans	large subunit ribosomal protein 30	3	C:GO:0005840; F:GO:0003735; P:GO:0006412	-	EC:3.6.5.3	IPR000231; IPR004038; IPR022991; G3DSA:3.30.1330.30 (GENE3D), PTHR11449:SF1 (PANTHER), SSF55315 (SUPERFAMILY)
	-	0				-
Brugia malayi	protein furry homolog-like	1	F:GO:0005515	-		PTHR12295 (PANTHER), PTHR12295:SF6 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				IPR000436; IPR016060; SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	clathrin coat assembly protein ap-1	5	P:GO:0016192; P:GO:0040025; F:GO:0005515; P:GO:0006886; C:GO:0030121	-		IPR011012; G3DSA:3.30.450.60 (GENE3D), PTHR11998 (PANTHER), PTHR11998:SF11 (PANTHER)
Caenorhabditis elegans	r- binding protein	2	F:GO:0000166; F:GO:0003729	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF41 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	methyltransferase domain containing 2	6	F:GO:0004483; F:GO:0005488; P:GO:0080009; C:GO:0005622; P:GO:0006370; P:GO:0000003	-	EC:2.1.1.57	IPR002877; G3DSA:3.40.50.150 (GENE3D), PTHR16121 (PANTHER), SSF53335 (SUPERFAMILY)

Caenorhabditis elegans	solute carrier family 17 (anion sugar transporter) member 5	8	C:GO:0016023; C:GO:0005886; P:GO:0055085; C:GO:0005765; C:GO:0016021; F:GO:0015136; F:GO:0015293; P:GO:0015739	-		IPR011701; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11662 (PANTHER), PTHR11662:SF30 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0000003; P:GO:0006350; P:GO:0045449; F:GO:0005515; F:GO:0003677; C:GO:0005634		IPR000679; IPR000949; IPR001005; IPR009057
	-	0				-
	-	0				-
Caenorhabditis elegans	wh2 motif family protein	0				-
Caenorhabditis briggsae	nicotinic acetylcholine receptor non-alpha subunit	6	F:GO:0004872; C:GO:0045211; C:GO:0030054; P:GO:0006811; C:GO:0016021; F:GO:0004889	-		IPR006029; IPR006201; G3DSA:1.20.120.370 (GENE3D), PTHR18945:SF72 (PANTHER), SignalP (SIGNALP)
Angiostrongylus cantonensis	briggsae cbr-mdt-6 protein	13	P:GO:0006357; P:GO:0040007; P:GO:0040027; P:GO:0040035; P:GO:0007283; F:GO:0016455; P:GO:0007281; C:GO:0016592; F:GO:0003713; P:GO:0048477; P:GO:0009792; P:GO:0008406; C:GO:0005737	-		-
Loa loa	importin 8	0		F:GO:0042626; P:GO:0015031; F:GO:0008536; F:GO:0008565; C:GO:0005634; P:GO:0006810; C:GO:0005737; P:GO:0007165; P:GO:0006886; F:GO:0008262; F:GO:0005515; C:GO:0005887; P:GO:0008283; F:GO:0005488		PTHR10997 (PANTHER), PTHR10997:SF18 (PANTHER)

Caenorhabditis briggsae	polymerase iii (d- directed) polypeptide 155kda	9	F:GO:0003899; P:GO:0009615; F:GO:0008270; P:GO:0032728; P:GO:0045087; F:GO:0003677; F:GO:0032549; P:GO:0006351; C:GO:0005666	-	EC:2.7.7.6	IPR007083; IPR015700; PTHR19376 (PANTHER), SSF64484 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	in family member (-b-1)	1	F:GO:0005515	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR16154 (PANTHER), PTHR16154:SF3 (PANTHER)
	-	0				G3DSA:3.40.50.300 (GENE3D), SSF52540 (SUPERFAMILY)
Brugia malayi	grip domain containing protein	0				-
Caenorhabditis elegans	fatty acid thase family member (fasn-1)	0				-
Caenorhabditis briggsae	protein ki-se c alpha binding protein	1	F:GO:0005515	-		IPR001478; IPR010504; G3DSA:2.30.42.10 (GENE3D), PTHR12141 (PANTHER), PTHR12141:SF2 (PANTHER)
	-	0				SignalP (SIGNALP)
Apis mellifera	wd repeat domain 19	0		F:GO:0005488; C:GO:0019861		-
Caenorhabditis briggsae	glutathione peroxidase	2	F:GO:0004601; C:GO:0005739	-	EC:1.11.1.7	IPR000889; IPR012335; IPR012336; SignalP (SIGNALP)
Caenorhabditis briggsae	glutathione peroxidase	2	F:GO:0004601; C:GO:0005739	-	EC:1.11.1.7	SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	sulfate transporter	4	P:GO:0006810; P:GO:0009987; C:GO:0044425; F:GO:0005215	-		IPR011547; PTHR11814 (PANTHER), PTHR11814:SF25 (PANTHER)
Loa loa	hypothetical protein LOAG_07566 [Loa loa]	0		F:GO:0005488		-
Caenorhabditis briggsae	component of oligomeric golgi complex 8	1	C:GO:0005794	-		IPR007255; IPR016159
Caenorhabditis briggsae	briggsae cbr-prg-1 protein	4	P:GO:0009987; F:GO:0003676; F:GO:0005515; C:GO:0044424	-		IPR003100; G3DSA:2.170.260.10 (GENE3D), PTHR22892 (PANTHER), SSF101690 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	metalloprotei-se inhibitor 2 precursor	3	F:GO:0005515; F:GO:0008191; C:GO:0005578	-		IPR001134; IPR001820; IPR008993; G3DSA:2.40.50.120 (GENE3D), PTHR11844:SF1 (PANTHER), SignalP (SIGNALP)
Loa loa	trehalase family protein	5	P:GO:0009792; P:GO:0002119; P:GO:0005991; P:GO:0040007; F:GO:0004555	-	EC:3.2.1.28	IPR001661; IPR018232; PTHR23403:SF1 (PANTHER)
	-	0				-

Caenorhabditis elegans	platelet-activating factor acetylhydrolase	1	P:GO:0006629	-		IPR005065; G3DSA:3.40.50.1820 (GENE3D), PF03403 (PFAM), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein F46F11.9 [Caenorhabditis elegans]	5	P:GO:0045927; P:GO:0032501; P:GO:0009653; P:GO:0000003; P:GO:0040011	-		SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	F:GO:0004872; F:GO:0005515; P:GO:0006350	-		-
	-	0				-
	-	0				IPR000436; IPR016060
Caenorhabditis briggsae	1 protein	3	F:GO:0005488; P:GO:0032501; P:GO:0032502	-		IPR000884; PR01705 (PRINTS), G3DSA:2.20.100.10 (GENE3D), PTHR22906 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	map kinse-erk ki-se	7	C:GO:0005625; F:GO:0004708; P:GO:0006468; F:GO:0005515; C:GO:0005938; F:GO:0005524; C:GO:0005829	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR008574; SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	p38 map ki-se family member (pmk-2)	5	C:GO:0005737; F:GO:0005515; P:GO:0006950; P:GO:0007243; F:GO:0008339	-		-
	-	0				-
Branchiostoma floridae	kiaa0979 protein	5	C:GO:0000785; F:GO:0042802; P:GO:0008285; C:GO:0005634; P:GO:0007064	-		PTHR12663 (PANTHER)
Ancylostoma caninum	metalloprotease 1 precursor	5	P:GO:0019915; F:GO:0004222; P:GO:0000003; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	IPR001506; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)

Cyanothece sp. ATCC 51142	viral a-type inclusion protein repeat protein	0		C:GO:0001931; C:GO:0005826; P:GO:0000212; C:GO:0005886; F:GO:0000146; P:GO:0043534; P:GO:0001768; F:GO:0043531; F:GO:0016887; P:GO:0050900; P:GO:0001701; P:GO:0000910; P:GO:0007520; C:GO:0005913; F:GO:0051015; C:GO:0005622; P:GO:0006928; F:GO:0043495; C:GO:0031252; C:GO:0005819; P:GO:0007132; F:GO:0042803; F:GO:0005524; P:GO:0030048; P:GO:0016337; P:GO:0006509; P:GO:0015031;		-
Caenorhabditis elegans	sulfite alpha subunit	5	F:GO:0005488; F:GO:0016491; P:GO:0044237; P:GO:0055114; P:GO:0000003	-		IPR015702; G3DSA:3.40.50.80 (GENE3D), PTHR19384 (PANTHER), SSF52343 (SUPERFAMILY)
Caenorhabditis elegans	cartilage associated protein	1	F:GO:0005488	-		PTHR13986 (PANTHER), PTHR13986:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	ester hydrolase c11orf54 homolog	1	F:GO:0005488	-		IPR015021; SSF117856 (SUPERFAMILY)
Caenorhabditis briggsae	cg9119 cg9119-pa	0		F:GO:0016788; F:GO:0008270; C:GO:0005634		IPR015021; SSF117856 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-cdh-1 protein	4	P:GO:0002119; P:GO:0040010; P:GO:0040011; C:GO:0016020	-		IPR002126; IPR015919; PTHR10596 (PANTHER), PTHR10596:SF77 (PANTHER)
	-	0				-
Hydra magnipapillata	tyrosyl-d- phodphodiesterase 1	0				G3DSA:3.30.870.20 (GENE3D), SSF56024 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	protein serine threonine ki-se	0		F:GO:0016740; F:GO:0004674; F:GO:0004672; F:GO:0016787; P:GO:0006468; F:GO:0000166; F:GO:0005524; F:GO:0016301; F:GO:0004709		-

Caenorhabditis briggsae	u5 small nuclear ribonucleoprotein 200 kda helicase	9	P:GO:0018991; C:GO:0005681; F:GO:0008026; P:GO:0040007; P:GO:0008380; F:GO:0003677; F:GO:0005524; P:GO:0002119; P:GO:0009792	-		-
Caenorhabditis elegans	uncoordi-ted family member (unc-52)	4	P:GO:0001525; P:GO:0030239; P:GO:0007519; C:GO:0005578	-		IPR003598; IPR007110; IPR013098; IPR013783; PTHR10489 (PANTHER), PTHR10489:SF27 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
	-	0				-
Ostertagia ostertagi	sxc2 protein	0				IPR003582
Brugia malayi	ancient conserved domain protein	0		P:GO:0040010		G3DSA:3.10.580.10 (GENE3D), PTHR12064 (PANTHER)
Ailuropoda melanoleuca	smt3 suppressor of mif two 3 homolog 2 (cerevisiae)	8	P:GO:0016925; F:GO:0031625; F:GO:0016564; P:GO:0034613; P:GO:0032436; F:GO:0019789; P:GO:0016481; C:GO:0005634	-		IPR019955; IPR022617; G3DSA:3.10.20.90 (GENE3D), PTHR10562 (PANTHER), SSF54236 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	nonsense-mediated mr- decay protein	0				PTHR15696 (PANTHER), SSF48452 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-ugt-58 protein	1	F:GO:0016757	-		IPR002213; SignalP (SIGNALP), SSF53756 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-npp-14 protein	0				IPR015943; PTHR23193 (PANTHER), PTHR23193:SF1 (PANTHER)
Homo sapiens	alpha-2-macroglobulin precursor	12	F:GO:0004867; F:GO:0043120; F:GO:0019966; P:GO:0001869; P:GO:0007584; C:GO:0005615; C:GO:0031093; F:GO:0019959; F:GO:0019899; P:GO:0010037; P:GO:0051384; P:GO:0006953	-		IPR009048; PTHR11412 (PANTHER), PTHR11412:SF36 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
synthetic construct	keratin 8	6	P:GO:0007010; C:GO:0005737; P:GO:0044419; F:GO:0005198; F:GO:0005515; C:GO:0045095	-		IPR001664; IPR003054; IPR016044
	-	0				-

Caenorhabditis elegans	ylr106cp-like protein	0		C:GO:0005634; F:GO:0000166; F:GO:0008134; F:GO:0017111; F:GO:0005524; F:GO:0016887; P:GO:0006355; C:GO:0005622; P:GO:0043254		PTHR22908 (PANTHER), PTHR22908:SF13 (PANTHER)
Caenorhabditis elegans	exportin 4	0		F:GO:0005488; C:GO:0005737; P:GO:0008150; F:GO:0005515; C:GO:0005575; C:GO:0005634; P:GO:0006810; P:GO:0015031		IPR018039
	-	0				-
Pan troglodytes	lysyl hydroxylase isoform 5	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				IPR001664; PTHR23239:SF13 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	kh domain containing protein	10	P:GO:0021905; F:GO:0003723; P:GO:0051216; P:GO:0007420; P:GO:0014036; P:GO:0048812; P:GO:0045947; P:GO:0048755; C:GO:0005737; C:GO:0005634	-		IPR004087; IPR004088; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR10603 (PANTHER), PTHR10603:SF3 (PANTHER), SSF54791 (SUPERFAMILY)
Brugia malayi	kh domain containing protein	10	P:GO:0021905; F:GO:0003723; P:GO:0051216; P:GO:0007420; P:GO:0014036; P:GO:0048812; P:GO:0045947; P:GO:0048755; C:GO:0005737; C:GO:0005634	-		IPR004087; IPR004088; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR10603 (PANTHER), PTHR10603:SF3 (PANTHER), SSF54791 (SUPERFAMILY)

Brugia malayi	kh domain containing protein	10	P:GO:0021905; F:GO:0003723; P:GO:0051216; P:GO:0007420; P:GO:0014036; P:GO:0048812; P:GO:0045947; P:GO:0048755; C:GO:0005737; C:GO:0005634	-		IPR004087; IPR004088; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR10603 (PANTHER), PTHR10603:SF3 (PANTHER), SSF54791 (SUPERFAMILY)
Macaca mulatta	ribosomal protein s3a	9	P:GO:0006413; F:GO:0003723; P:GO:0006917; C:GO:0005730; F:GO:0003735; P:GO:0006414; C:GO:0022627; P:GO:0030154; F:GO:0005515	-		-
Caenorhabditis elegans	protein tapt1-like protein	1	P:GO:0009792	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	p- protein	12	C:GO:0005960; F:GO:0004375; F:GO:0016829; P:GO:0019464; C:GO:0005739; P:GO:0055114; C:GO:0009941; F:GO:0005524; F:GO:0005515; P:GO:0046686; F:GO:0030170; C:GO:0048046	-	EC:1.4.4.2	IPR005829; IPR015424; IPR020580; IPR020581
Caenorhabditis elegans	briggsae cbr-unc-68 protein	8	F:GO:0004872; P:GO:0006629; F:GO:0005219; P:GO:0006816; P:GO:0006874; P:GO:0055085; F:GO:0005509; C:GO:0016021	-		-
Caenorhabditis elegans	aquaporin 3	3	P:GO:0055085; C:GO:0016021; F:GO:0005215	-		IPR000425; PTHR19139:SF11 (PANTHER)
Brugia malayi	ap-2 complex subunit mu-1	9	P:GO:0016192; C:GO:0005829; F:GO:0008289; C:GO:0005778; P:GO:0050690; C:GO:0030122; F:GO:0005515; F:GO:0005215; P:GO:0006886	-		-
	-	0				-
	-	0				-

Taeniopygia guttata	cytochrome b5 reductase 3	10	F:GO:0004128; C:GO:0016021; P:GO:0055114; C:GO:0005741; P:GO:0006636; P:GO:0030497; F:GO:0050660; C:GO:0005789; P:GO:0006695; P:GO:0017144	-	EC:1.6.2.2	-
Loa loa	protein-l-isoaspartate o-methyltransferase domain-containing protein 1	0		P:GO:0006479; F:GO:0016740; P:GO:0032259; F:GO:0008168; F:GO:0004719; C:GO:0005737; F:GO:0003674; P:GO:0006464; P:GO:0008150		IPR000682; G3DSA:3.40.50.150 (GENE3D), SSF53335 (SUPERFAMILY)
Haemonchus contortus	latrophilin-like protein 2	6	P:GO:0007218; C:GO:0016021; P:GO:0007165; C:GO:0005886; F:GO:0005529; F:GO:0004930	-		IPR020003; IPR022624
Caenorhabditis briggsae	briggsae cbr-ooc-3 protein	0				-
Caenorhabditis briggsae	briggsae cbr-ooc-3 protein	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	sex-determining protein fem-1	3	P:GO:0051438; F:GO:0005515; F:GO:0004842	-	EC:6.3.2.19	PTHR18958 (PANTHER), PTHR18958:SF131 (PANTHER)
	-	0				-
Caenorhabditis elegans	riken cd- c030006k11 gene	1	C:GO:0005739	-		-
Caenorhabditis elegans	yqy2_caeel ame: full=uncharacterized protein	0		F:GO:0004872; F:GO:0004871; F:GO:0004930; C:GO:0016021; P:GO:0008152; F:GO:0008080; P:GO:0007165; P:GO:0007186		IPR000182; IPR016181
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0005488		-
Caenorhabditis elegans	alpha- -mannosyl-glycoprotein 2-beta-n-acetylglucosaminyltransferase-like	6	C:GO:0005624; C:GO:0044431; P:GO:0006487; F:GO:0008375; C:GO:0016020; P:GO:0009311	-		IPR007754; IPR018130; SignalP (SIGNALP), SSF53448 (SUPERFAMILY)
Caenorhabditis elegans	alpha- -mannosyl-glycoprotein 2-beta-n-acetylglucosaminyltransferase-like	6	C:GO:0005624; C:GO:0044431; P:GO:0006487; F:GO:0008375; C:GO:0016020; P:GO:0009311	-		IPR007754; IPR018130; SignalP (SIGNALP), SSF53448 (SUPERFAMILY)

Caenorhabditis elegans	cleavage and polyadenylation specific factor 3-like	5	C:GO:0005737; P:GO:0043484; F:GO:0016787; P:GO:0016180; C:GO:0032039	-		IPR001279; G3DSA:3.60.15.10 (GENE3D), PTHR11203 (PANTHER), PTHR11203:SF8 (PANTHER), SSF56281 (SUPERFAMILY)
Caenorhabditis elegans	inositol -trisphosphate receptor	4	F:GO:0004872; F:GO:0005262; P:GO:0006811; C:GO:0016020	-		IPR015925; PTHR13715:SF2 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	3	P:GO:0044238; P:GO:0019915; F:GO:0016757	-		IPR002213; G3DSA:3.40.50.2000 (GENE3D), PTHR11926:SF3 (PANTHER), SSF53756 (SUPERFAMILY)
Bos taurus	cold shock domain-containing protein e1	6	F:GO:0003723; C:GO:0005743; P:GO:0006355; P:GO:0008584; F:GO:0003677; F:GO:0005515	-		IPR002059; PTHR12913 (PANTHER)
	-	0				SignalP (SIGNALP)
Loa loa	zinc transporter zip13	0		C:GO:0016021; C:GO:0016020; P:GO:0030001; P:GO:0006811; P:GO:0006810; P:GO:0006829; F:GO:0046873; P:GO:0055085; F:GO:0005385		-
Caenorhabditis elegans	heat1_caeel ame: full=heat repeat-containing protein 1 homolog ame: full=target of erk ki-se protein 1	4	P:GO:0009792; P:GO:0040010; P:GO:0002119; P:GO:0040011	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	t-cell activation ase activating protein	6	F:GO:0005096; P:GO:0009792; P:GO:0000003; P:GO:0007165; C:GO:0005622; P:GO:0040010	-		IPR000198; IPR008936; PTHR23179 (PANTHER), PTHR23179:SF1 (PANTHER)
Caenorhabditis briggsae	mitochondrial inner membrane protein	1	C:GO:0016021	-		IPR019133; PTHR15415 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	sperm autoantigenic protein 17	1	P:GO:0009987	-		IPR000048; IPR003117; G3DSA:1.20.890.10 (GENE3D)
Pan troglodytes	proteasome (macropain) activator subunit 1 (pa28 alpha)	9	P:GO:0010950; P:GO:0019884; P:GO:0051436; P:GO:0051437; C:GO:0008537; P:GO:0031145; F:GO:0005515; N:GO:0061133; C:GO:0005737	-		IPR003186; IPR009077; PTHR10660:SF5 (PANTHER)
Loa loa	hypothetical protein LOAG_04165 [Loa loa]	0				-

Caenorhabditis briggsae	glutamine-dependent -d(+) synthetase	3	F:GO:0016874; F:GO:0005488; P:GO:0006807	-		PTHR23090 (PANTHER), PTHR23090:SF1 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	scp(small c-termi-l domain phosphatase)-like phosphatase family member (scpl-1)	1	F:GO:0016791	-	EC:3.1.3.0	IPR004274; IPR011948; G3DSA:3.40.50.1000 (GENE3D), PTHR12210 (PANTHER), PTHR12210:SF12 (PANTHER), SSF56784 (SUPERFAMILY)
	-	0				IPR006849
Caenorhabditis elegans	membrane calcium atpase family member (mca-1)	10	P:GO:0048840; F:GO:0005388; F:GO:0005516; P:GO:0060119; P:GO:0006754; F:GO:0005524; P:GO:0048919; P:GO:0006816; F:GO:0000287; C:GO:0005887	-	EC:3.6.3.8	IPR001757; IPR006068; IPR013200; G3DSA:1.20.1110.10 (GENE3D), PTHR11939:SF75 (PANTHER), SSF56784 (SUPERFAMILY), SSF81665 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	briggsae cbr-fozi-1 protein	4	P:GO:0030036; F:GO:0003779; C:GO:0005622; F:GO:0008270	-		IPR015880
Caenorhabditis elegans	cub domain containing protein	11	P:GO:0001885; F:GO:0046872; P:GO:0035162; P:GO:0035124; P:GO:0006508; F:GO:0008237; F:GO:0005515; P:GO:0048264; P:GO:0030513; P:GO:0001568; P:GO:0001707	-		IPR000859; PTHR10127 (PANTHER), PTHR10127:SF70 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	gut-associated larval antigen-1	0		C:GO:0005882; P:GO:0009792		-
Caenorhabditis briggsae	ffr_caeel ame: full=protein fat-free homolog	1	F:GO:0005515	-		IPR014812; PTHR15954 (PANTHER)
Caenorhabditis elegans	d- polymerase zeta catalytic subunit	7	F:GO:0003887; P:GO:0006260; C:GO:0016035; P:GO:0019985; F:GO:0003677; F:GO:0008408; F:GO:0000166	-	EC:2.7.7.7	IPR006134; PTHR10322 (PANTHER), PTHR10322:SF5 (PANTHER), SSF56672 (SUPERFAMILY)

Caenorhabditis elegans	low-density lipoprotein receptor-related protein 2-like	2	P:GO:0050794; C:GO:0044464	-		IPR000033; IPR000152; IPR000742; IPR001881; IPR002172; IPR006210; IPR011042; IPR013032; IPR018097; G3DSA:2.10.25.10 (GENE3D), PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER), SignalP (SIGNALP), SSF57196 (SUPERFAMILY), SSF63825 (SUPERFAMILY)
Caenorhabditis elegans	low-density lipoprotein receptor-related protein 2-like	2	P:GO:0050794; C:GO:0044464	-		IPR000033; IPR000152; IPR000742; IPR001881; IPR002172; IPR006210; IPR011042; IPR013032; IPR018097; G3DSA:2.10.25.10 (GENE3D), PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER), SignalP (SIGNALP), SSF57196 (SUPERFAMILY), SSF63825 (SUPERFAMILY)
Caenorhabditis briggsae	mitochondrial import inner membrane translocase subunit tim23	6	F:GO:0008565; C:GO:0005739; P:GO:0040035; P:GO:0009792; P:GO:0015031; C:GO:0016020	-		IPR003397; PTHR15371 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR001534
	-	0				-
Caenorhabditis elegans	gamma-glutamyltranspeptidase family protein	0		F:GO:0003840; C:GO:0016021		IPR000101
	-	0				-
	-	0				-
Apis mellifera	stretchin-mlck cg18255- isoform a	0				-
Apis mellifera	stretchin-mlck cg18255- isoform a	0		P:GO:0015031; C:GO:0016021; C:GO:0016020; F:GO:0030348; C:GO:0031201; P:GO:0043312; P:GO:0006904; P:GO:0043304; C:GO:0005829; C:GO:0042582; P:GO:0016192; C:GO:0042581; C:GO:0005886; C:GO:0070820		-
Ancylostoma caninum	secreted protein 4 precursor	0		C:GO:0005576		IPR014044
	-	0				-
Caenorhabditis elegans	l1p family of ribosomal proteins containing protein	10	P:GO:0006412; P:GO:0040010; F:GO:0003723; P:GO:0006396; C:GO:0005840; P:GO:0008340; F:GO:0003735; P:GO:0002119; P:GO:0006898; P:GO:0009792	-	EC:3.6.5.3	PTHR23105 (PANTHER), PTHR23105:SF8 (PANTHER)

Caenorhabditis elegans	ubiquitin carboxyl-termi-l hydrolase family protein	1	F:GO:0016787	-		-
synthetic construct	cellular retinoic acid binding protein 2	12	F:GO:0001972; P:GO:0006810; P:GO:0035115; F:GO:0019841; P:GO:0006355; P:GO:0008544; P:GO:0042573; P:GO:0007165; F:GO:0005215; F:GO:0016918; C:GO:0005737; C:GO:0005634	-		IPR000463; IPR000566; IPR011038; IPR012674
	-	0				-
	-	0				-
Rattus norvegicus	poly binding protein 1	12	P:GO:0043161; F:GO:0003723; F:GO:0008494; P:GO:0050687; F:GO:0031625; P:GO:0008380; P:GO:0045087; F:GO:0003697; C:GO:0030529; P:GO:0006397; C:GO:0005737; C:GO:0005634	-		SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-tag-97 protein	0		P:GO:0006355; F:GO:0043565; C:GO:0005634; F:GO:0003700		-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-unc-71 protein	3	F:GO:0004222; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Brugia malayi	r-se3 domain containing protein	8	F:GO:0004525; F:GO:0003723; P:GO:0000910; P:GO:0031053; P:GO:0007052; P:GO:0019953; P:GO:0009792; C:GO:0005634	-	EC:3.1.26.3	IPR000999; PTHR11207 (PANTHER), SignalP (SIGNALP)
Hydra magnipapillata	hat family dimerisation domain containing protein	0		C:GO:0009536; F:GO:0005515		-
Caenorhabditis elegans	cg32635 cg32635-pa	0		F:GO:0005488		-
Caenorhabditis elegans	cg32635 cg32635-pa	0		F:GO:0005488; F:GO:0004872; C:GO:0016021; C:GO:0016020		-

Loa loa	isoform c	3	P:GO:0035152; C:GO:0016324; F:GO:0005112	-		IPR000152; IPR000742; IPR001881; IPR006209; IPR006210; IPR013032; IPR018097; PR00010 (PRINTS), G3DSA:2.10.25.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF245 (PANTHER), SSF57196 (SUPERFAMILY)
	-	0				-
Loa loa	dock7 protein	0		F:GO:0005525; F:GO:0008168; F:GO:0051020; F:GO:0005488; F:GO:0004872; P:GO:0032259; F:GO:0005085		IPR021816; PTHR23317 (PANTHER), PTHR23317:SF27 (PANTHER)
						IPR008160; PTHR10499 (PANTHER), PTHR10499:SF114 (PANTHER)
Caenorhabditis elegans	acid phosphatase family protein confirmed by transcript evidence	1	F:GO:0003993	-	EC:3.1.3.2	IPR000560; G3DSA:3.40.50.1240 (GENE3D), PTHR11567 (PANTHER), PTHR11567:SF28 (PANTHER), SignalP (SIGNALP), SSF53254 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	a-phase promoting complex subunit 1	1	F:GO:0005515	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	phosphatidylinositol 4-ki-se	3	P:GO:0000003; P:GO:0008219; F:GO:0016740	-		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-inft-1 protein	0		F:GO:0003779; P:GO:0040011; P:GO:0016043; F:GO:0005515; P:GO:0030036		IPR001759
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Brugia malayi	hypothetical protein Bm1_07015 [Brugia malayi]	0				-
Caenorhabditis elegans	udp-sugar transporter ust74c (fringe connection protein)	2	P:GO:0008643; C:GO:0016021	-		PTHR11132 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)

synthetic construct	apolipoprotein c-i	23	P:GO:0010873; C:GO:0042627; P:GO:0033344; C:GO:0034361; P:GO:0008203; C:GO:0034364; P:GO:0034379; P:GO:0042157; F:GO:0031210; P:GO:0010900; P:GO:0048261; P:GO:0034375; F:GO:0005504; P:GO:0051005; P:GO:0033700; P:GO:0006641; C:GO:0005783; P:GO:0045717; F:GO:0004859; P:GO:0034382; P:GO:0032375; P:GO:0010916; F:GO:0060228	-		IPR006781; SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	mgc83251 protein	0		F:GO:0005488		-
Cyathostominae sp. JM-2007a	temporarily assigned gene -me family member (tag-273)	2	F:GO:0008270; P:GO:0000003	-		-
Brugia malayi	hypothetical protein Bm1_48510 [Brugia malayi]	0				PTHR13587 (PANTHER), PTHR13587:SF1 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Loa loa	arp1 actin-related protein 1 homolog centractin alpha	6	C:GO:0005815; C:GO:0005869; F:GO:0005515; P:GO:0016192; F:GO:0005524; C:GO:0005829	-		SignalP (SIGNALP)
Caenorhabditis briggsae	hypothetical transporter	4	P:GO:0055085; P:GO:0040011; C:GO:0016021; P:GO:0007413	-		-
	-	0				-
Caenorhabditis briggsae	mr- turnover protein 4 homolog	2	C:GO:0005840; P:GO:0042254	-		-
	-	0				-
Caenorhabditis elegans	cnksr family member 3	1	P:GO:0040026	-		IPR001478; IPR001660; IPR010993; IPR013761; IPR017874; IPR021129; G3DSA:2.30.42.10 (GENE3D), PTHR12844 (PANTHER)
Caenorhabditis elegans	nucleolar complex-associated protein	1	C:GO:0005730	-		SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0006508; F:GO:0008236; F:GO:0016787		-
Strongylocentrotus purpuratus	ensangp00000010363	0				-
	-	0				-

	-	0				SignalP (SIGNALP)
Loa loa	phosphatidylinositol 3- and 4-ki-se family protein	0		F:GO:0016301; F:GO:0005524; F:GO:0005488; F:GO:0016740; F:GO:0000166; F:GO:0016773; F:GO:0004674		-
Caenorhabditis elegans	tetratricopeptide repeat protein 27	1	F:GO:0005515	-		IPR011990; IPR013026; PTHR16193 (PANTHER), SSF48452 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	dihydroorotate dehydroge-se	3	F:GO:0004152; P:GO:0034404; P:GO:0046483	-	EC:1.3.99.11	IPR012135; IPR013785
Caenorhabditis elegans	isoform b	2	P:GO:0008152; F:GO:0016791	-	EC:3.1.3.0	-
Caenorhabditis elegans	vhs domain containing protein	0		P:GO:0006886; C:GO:0005622		IPR002014; IPR004152; IPR008942; IPR018205; G3DSA:1.20.58.160 (GENE3D), PTHR13856 (PANTHER), PTHR13856:SF30 (PANTHER), SSF89009 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	polarity and osmotic sensitivity defect family member (pod-2)	0		F:GO:0005524; F:GO:0016874; P:GO:0008152; F:GO:0003824; F:GO:0009374; P:GO:0006633; F:GO:0003989		G3DSA:3.90.226.10 (GENE3D), PTHR18866 (PANTHER), PTHR18866:SF6 (PANTHER), SSF52096 (SUPERFAMILY)
Caenorhabditis briggsae	-dh oxidase	2	F:GO:0003824; P:GO:0043581	-		IPR001155; IPR013785; PTHR22893 (PANTHER), PTHR22893:SF6 (PANTHER), SSF51395 (SUPERFAMILY)
	-	0				-
Angiostrongylus cantonensis	elegans protein confirmed by transcript evidence	16	P:GO:0006468; P:GO:0007595; P:GO:0040018; P:GO:0007409; P:GO:0010033; P:GO:0021983; F:GO:0046983; C:GO:0005667; F:GO:0046872; P:GO:0046887; P:GO:0008361; F:GO:0043565; P:GO:0007165; P:GO:0042493; F:GO:0003700; P:GO:0045944	-		IPR001630; IPR004827; IPR011616; G3DSA:1.20.5.170 (GENE3D), PTHR22952 (PANTHER), PTHR22952:SF11 (PANTHER)
Caenorhabditis briggsae	beta-lactamase family protein	0				IPR001466; IPR012338; G3DSA:3.40.710.10 (GENE3D), PTHR10566 (PANTHER), PTHR10566:SF6 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0008236; C:GO:0016021; C:GO:0016020		IPR002469; G3DSA:2.140.10.30 (GENE3D)
	-	0				-

Trichostrongylus vitrinus	serine or cysteine protease inhibitor	5	P:GO:0008380; F:GO:0005515; C:GO:0005634; F:GO:0003824; P:GO:0008406	-		IPR000215; G3DSA:2.30.39.10 (GENE3D), G3DSA:3.30.497.10 (GENE3D), PTHR11461:SF25 (PANTHER)
Loa loa	high incidence of males (increased x chromosome loss) family member (him-4)	0		P:GO:0007399; F:GO:0005488; F:GO:0005509; P:GO:0007155; C:GO:0031225; F:GO:0005515; C:GO:0005886		IPR007110; IPR013098; IPR013783; PTHR10489 (PANTHER), PTHR10489:SF27 (PANTHER), SSF48726 (SUPERFAMILY)
Homo sapiens	anti-hiv-1 immunoglobulin heavy chain gamma-1 precursor	7	P:GO:0006955; F:GO:0003823; C:GO:0005576; C:GO:0005624; C:GO:0016021; F:GO:0005515; C:GO:0005886	-		IPR003006; IPR003596; IPR003597; IPR007110; IPR013106; IPR013783; PTHR23266 (PANTHER), PTHR23266:SF4 (PANTHER), SignalP (SIGNALP), SSF48726 (SUPERFAMILY)
Homo sapiens	igh@ protein	7	P:GO:0006955; F:GO:0003823; C:GO:0005576; C:GO:0005624; C:GO:0016021; F:GO:0005515; C:GO:0005886	-		IPR003006; IPR003597; IPR007110; IPR013106; IPR013783; PTHR23266 (PANTHER), PTHR23266:SF4 (PANTHER), SSF48726 (SUPERFAMILY)
Rattus sp.	immunoglobulin heavy chain	7	P:GO:0006955; F:GO:0003823; C:GO:0005576; C:GO:0005624; C:GO:0016021; F:GO:0005515; C:GO:0005886	-		IPR003006; IPR003597; IPR007110; IPR013783; PTHR23266 (PANTHER), PTHR23266:SF4 (PANTHER), SSF48726 (SUPERFAMILY)
Homo sapiens	anti-rabies sojb immunoglobulin heavy chain	6	P:GO:0006955; F:GO:0003823; C:GO:0005576; C:GO:0005624; C:GO:0016021; C:GO:0005886	-		IPR003006; IPR003597; IPR007110; IPR013106; IPR013783; PTHR23266 (PANTHER), PTHR23266:SF4 (PANTHER), SSF48726 (SUPERFAMILY)
synthetic construct	b chain crystal structure of a human type iii fc gamma receptor in complex with an fc fragment of igg1	7	P:GO:0006955; F:GO:0003823; C:GO:0005576; C:GO:0005624; C:GO:0016021; F:GO:0005515; C:GO:0005886	-		IPR003006; IPR003597; IPR007110; IPR013783; PTHR23266 (PANTHER), PTHR23266:SF4 (PANTHER), SSF48726 (SUPERFAMILY)
Homo sapiens	igh@ protein	7	P:GO:0006955; F:GO:0003823; C:GO:0005576; C:GO:0005624; C:GO:0016021; F:GO:0005515; C:GO:0005886	-		IPR003006; IPR003597; IPR007110; IPR013106; IPR013783; PTHR23266 (PANTHER), PTHR23266:SF4 (PANTHER), SSF48726 (SUPERFAMILY)
Homo sapiens	immunoglobulin heavy chain variable region	0				
Homo sapiens	immunoglobulin heavy chain variable region	0				

Homo sapiens	igh@ protein	7	P:GO:0006955; F:GO:0003823; C:GO:0005576; C:GO:0005624; C:GO:0016021; F:GO:0005515; C:GO:0005886	-		IPR003006; IPR003597; IPR007110; IPR013106; IPR013783; PTHR23266 (PANTHER), PTHR23266:SF4 (PANTHER), SSF48726 (SUPERFAMILY)
Homo sapiens	anti-hiv-1 gp120 immunoglobulin heavy chain	7	P:GO:0006955; F:GO:0003823; C:GO:0005576; C:GO:0005624; C:GO:0016021; F:GO:0005515; C:GO:0005886	-		IPR003006; IPR003597; IPR007110; IPR013106; IPR013783; PTHR23266 (PANTHER), PTHR23266:SF4 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	charged multivesicular body protein 2a	2	P:GO:0015031; P:GO:0009792	-		IPR005024; PTHR10476 (PANTHER), PTHR10476:SF4 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	entric chromosome binding protein family member (hcp-6)	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	spermidine synthase	7	P:GO:0006468; F:GO:0004715; P:GO:0008295; F:GO:0005515; F:GO:0004766; F:GO:0005524; C:GO:0005829	-	EC:2.7.10.2; EC:2.5.1.16	IPR001045; G3DSA:2.30.140.10 (GENE3D), G3DSA:3.40.50.150 (GENE3D), PTHR11558:SF11 (PANTHER), SSF53335 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	beta- -galactosyltransferase	4	P:GO:0045747; P:GO:0009636; P:GO:0075015; F:GO:0008376	-		IPR003859; G3DSA:3.90.550.10 (GENE3D), PTHR19300:SF7 (PANTHER), SignalP (SIGNALP), SSF53448 (SUPERFAMILY)
Caenorhabditis elegans	multidrug resistance protein family member (mrp-1)	6	F:GO:0042626; C:GO:0044459; P:GO:0055085; F:GO:0005524; F:GO:0008514; C:GO:0016021	-		IPR011527; IPR017940; G3DSA:1.20.1560.10 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF35 (PANTHER), SignalP (SIGNALP)
Macaca mulatta	complement factor b	6	F:GO:0004252; P:GO:0006957; C:GO:0005886; F:GO:0001848; C:GO:0005576; P:GO:0006508	-	EC:3.4.21.0	PTHR19325 (PANTHER), PTHR19325:SF22 (PANTHER)
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	6	F:GO:0003899; P:GO:0040010; P:GO:0000003; P:GO:0007413; P:GO:0006898; P:GO:0006350	-	EC:2.7.7.6	IPR002092; G3DSA:1.10.150.20 (GENE3D), G3DSA:1.10.287.280 (GENE3D), G3DSA:3.30.70.370 (GENE3D), SSF56672 (SUPERFAMILY)

Caenorhabditis briggsae	briggsae cbr-ncx-3 protein	0		P:GO:0006816; C:GO:0016021; P:GO:0007154; C:GO:0016020; P:GO:0055085; F:GO:0005432		PTHR11878 (PANTHER), PTHR11878:SF2 (PANTHER)
Caenorhabditis elegans	solute carrier family member b1	8	P:GO:0009792; C:GO:0005792; C:GO:0005622; P:GO:0006810; P:GO:0040010; P:GO:0000003; C:GO:0044425; F:GO:0005459	-		IPR013657; PTHR10778 (PANTHER), PTHR10778:SF10 (PANTHER), SignalP (SIGNALP), SSF103481 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-cdh-1 protein	0		C:GO:0016021; C:GO:0016020; P:GO:0002119; P:GO:0040011; P:GO:0040010; C:GO:0005886; P:GO:0007156; F:GO:0005509; P:GO:0007155		IPR002126; IPR015919
	-	0				-
	-	0				-
Caenorhabditis elegans	forkhead protein forkhead protein domain	28	P:GO:0007423; P:GO:0009888; P:GO:0007495; F:GO:0031624; P:GO:0006309; P:GO:0007389; F:GO:0003704; F:GO:0043028; F:GO:0016563; C:GO:0005667; P:GO:0030111; F:GO:0003705; P:GO:0006917; P:GO:0009790; P:GO:0010551; P:GO:0009887; F:GO:0030331; P:GO:0051090; P:GO:0016481; P:GO:0045944; F:GO:0003690; P:GO:0007399; F:GO:0008301; F:GO:0010843; P:GO:0043280; P:GO:0030166; F:GO:0008134	-		IPR001766; IPR011991; IPR018122; SSF46785 (SUPERFAMILY)
Ixodes scapularis	xylitol dehydroge-se	5	F:GO:0003939; P:GO:0005975; P:GO:0055114; F:GO:0046526; F:GO:0008270	-	EC:1.1.1.14; EC:1.1.1.9	IPR002085; IPR002328; IPR011032; IPR013154; G3DSA:3.90.180.10 (GENE3D), PTHR11695:SF38 (PANTHER)

Caenorhabditis briggsae	polypeptide n-acetylgalactosaminyltransferase 13	4	F:GO:0004653; C:GO:0005794; P:GO:0006493; C:GO:0016020	-	EC:2.4.1.41	IPR001173; G3DSA:3.90.550.10 (GENE3D), PTHR11675 (PANTHER), SSF53448 (SUPERFAMILY)
Caenorhabditis elegans	hcp beta-lactamase-like protein cg13865	4	P:GO:0043161; F:GO:0003684; P:GO:0006289; C:GO:0005634	-		IPR006597; IPR011990; PTHR13891 (PANTHER), SSF81901 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	2	P:GO:0006810; C:GO:0016020	-		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	apical junction molecule family member (ajm-1)	8	P:GO:0009792; C:GO:0043296; F:GO:0046872; P:GO:0045216; F:GO:0008092; C:GO:0005913; P:GO:0040010; P:GO:0040011	-		IPR001092
	-	0				-
Brugia malayi	#NAME?	3	P:GO:0009451; F:GO:0003824; F:GO:0051539	-		IPR002792; IPR005839; G3DSA:3.80.30.20 (GENE3D)
	-	0				-
Caenorhabditis briggsae	transport protein sec61 subunit beta	5	P:GO:0030970; P:GO:0000060; P:GO:0000003; P:GO:0030433; F:GO:0048408	-		IPR005609; PTHR13509 (PANTHER)
Caenorhabditis elegans	glycoside hydrolase family 25 protein	4	F:GO:0005515; P:GO:0008340; P:GO:0008152; F:GO:0003824	-		IPR013781; IPR017853; PTHR23208 (PANTHER), PTHR23208:SF13 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	2-hydroxyacyl- lyase 1	3	F:GO:0030976; F:GO:0000287; F:GO:0003824	-		IPR011766; G3DSA:3.40.50.970 (GENE3D), PTHR18968 (PANTHER), PTHR18968:SF6 (PANTHER), SSF52518 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	isoform a	3	C:GO:0005737; P:GO:0042325; F:GO:0005515	-		IPR008025; PTHR16188:SF2 (PANTHER)
Caenorhabditis elegans	hypothetical protein Y72A10A.1 [Caenorhabditis elegans]	0				IPR001810; IPR022364; G3DSA:3.80.10.10 (GENE3D), SignalP (SIGNALP)
Caenorhabditis elegans	serpentine class ab (class a-like) family member (srab-14)	3	C:GO:0016021; P:GO:0007606; F:GO:0004888	-		-

Caenorhabditis briggsae	nfx1-type zinc finger-containing protein 1	0		F:GO:0008168; F:GO:0003700; C:GO:0005634; F:GO:0003676; F:GO:0003964; F:GO:0008270; F:GO:0003723; P:GO:0006278; P:GO:0006355; P:GO:0006508		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	3	P:GO:0040015; P:GO:0040010; P:GO:0040011	-		IPR000859; IPR001304; IPR016186; IPR016187; PTHR22991 (PANTHER)
	-	0				-
Caenorhabditis briggsae	rho-associated protein ki-se 1	5	F:GO:0005488; P:GO:0023052; F:GO:0016740; P:GO:0050794; C:GO:0005737	-		IPR000961; IPR001849; IPR002219; IPR011993; PD936484 (PRODOM), G3DSA:3.30.60.20 (GENE3D), PTHR22988 (PANTHER), SSF50729 (SUPERFAMILY), SSF57889 (SUPERFAMILY)
Loa loa	elegans protein partially confirmed by transcript evidence	0		P:GO:0000003; P:GO:0040011; P:GO:0009792; P:GO:0002119; P:GO:0040007; F:GO:0005515		-
Caenorhabditis briggsae	gcc2 and gcc3 family protein	5	P:GO:0035152; C:GO:0016324; F:GO:0005515; F:GO:0005509; C:GO:0016021	-		IPR000742; IPR006210; IPR011641; IPR013032; G3DSA:2.10.25.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF226 (PANTHER), SSF57196 (SUPERFAMILY)
	-	0				-
	-	0				-
Loa loa	asparagine synthetase domain containing 1	1	P:GO:0006520	-		-
Caenorhabditis elegans	mitogen-activated protein ki-se ki-se ki-se 15	4	P:GO:0006468; F:GO:0005515; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR001245; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF54 (PANTHER)
Caenorhabditis elegans	carbonic anhydrase	4	P:GO:0044237; F:GO:0008270; F:GO:0004089; P:GO:0015976	-	EC:4.2.1.1	IPR001765; PTHR11002:SF1 (PANTHER)
	-	0				-
Caenorhabditis briggsae	alanine-glyoxylate aminotransferase	2	F:GO:0030170; F:GO:0008483	-	EC:2.6.1.0	IPR005814; IPR015421; PTHR11986:SF23 (PANTHER)
	-	0				-
Caenorhabditis elegans	seryl-tr- synthetase	6	F:GO:0005515; F:GO:0005524; C:GO:0005829; P:GO:0006434; C:GO:0005739; F:GO:0004828	-	EC:6.1.1.11	-

Homo sapiens	major histocompatibility class dp alpha 1	9	C:GO:0005789; C:GO:0005887; C:GO:0042613; C:GO:0005794; P:GO:0002504; C:GO:0005765; F:GO:0032395; C:GO:0010008; P:GO:0006955	-		SignalP (SIGNALP)
Caenorhabditis elegans	potential gamma-butyrobetaine hydroxylase	3	F:GO:0005488; F:GO:0016491; P:GO:0008152	-		IPR003819; IPR012776; G3DSA:3.60.130.10 (GENE3D), PTHR10696 (PANTHER), SSF51197 (SUPERFAMILY)
Caenorhabditis elegans	ap-3 complex subunit beta-2	12	P:GO:0009792; P:GO:0010171; P:GO:0002119; C:GO:0005794; F:GO:0005515; C:GO:0030117; F:GO:0008565; P:GO:0006886; P:GO:0007040; P:GO:0019915; P:GO:0040007; P:GO:0006897	-		IPR002553; IPR011989; IPR016024; PTHR11134 (PANTHER), PTHR11134:SF2 (PANTHER)
Ancylostoma caninum	metalloprotease 1 precursor	3	F:GO:0046872; P:GO:0000003; F:GO:0008237	-		IPR001506; IPR013032; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER)
Caenorhabditis elegans	exosome complex exonuclease rrp45	8	P:GO:0009792; P:GO:0002119; F:GO:0000175; F:GO:0003723; P:GO:0040010; P:GO:0000003; F:GO:0016779; P:GO:0006396	-	EC:2.7.7.0	-
	ankyrin repeat protein	0		F:GO:0004672; F:GO:0005524; F:GO:0000062; F:GO:0005488; F:GO:0000166; P:GO:0006468; F:GO:0004674		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF241 (PANTHER)
	-	0				-
	-	0				-
	-	0				IPR016059
Brugia malayi	grip and coiled-coil domain-containing protein 1	0		C:GO:0005737; C:GO:0016020; C:GO:0000139; C:GO:0005794; F:GO:0005515		-
Brugia malayi	d--damage inducible protein 2	0		P:GO:0006508; F:GO:0004190; C:GO:0005575		IPR000449; IPR009007; IPR009060; IPR015940; IPR019103; IPR021109; G3DSA:1.10.8.10 (GENE3D), PTHR12917 (PANTHER), PTHR12917:SF1 (PANTHER)

Caenorhabditis elegans	brefeldin a-inhibited guanine nucleotide-exchange protein 2-like	11	C:GO:0005829; P:GO:0040010; F:GO:0005488; C:GO:0000139; P:GO:0032012; P:GO:0000003; F:GO:0005085; P:GO:0002119; P:GO:0040011; P:GO:0006898; P:GO:0009792	-		IPR000904; G3DSA:1.10.220.20 (GENE3D), PTHR10663 (PANTHER), PTHR10663:SF1 (PANTHER)
	-	0				-
Caenorhabditis briggsae	s1 r- binding domain containing protein	3	P:GO:0022414; P:GO:0007275; P:GO:0040007	-		-
Caenorhabditis briggsae	yrn9_caeel ame: full=uncharacterized protein	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	9	P:GO:0009792; F:GO:0046872; F:GO:0016491; P:GO:0040018; P:GO:0040017; P:GO:0040010; P:GO:0000003; P:GO:0008340; P:GO:0008152	-		IPR001128; PTHR19383:SF176 (PANTHER), SignalP (SIGNALP)
	-	0				-
Ancylostoma caninum	secreted protein asp-2	0		C:GO:0005576		IPR001283; IPR014044; SignalP (SIGNALP)
	-	0				-
Dictyocaulus viviparus	elegans protein confirmed by transcript evidence	2	P:GO:0009792; F:GO:0005509	-		IPR002048; IPR011992; IPR018247; IPR018248; IPR018249; PTHR23050 (PANTHER), PTHR23050:SF10 (PANTHER), SSF47473 (SUPERFAMILY)
Homo sapiens	major histocompatibility class dp alpha 1	9	C:GO:0005789; C:GO:0005887; C:GO:0042613; C:GO:0005794; P:GO:0002504; C:GO:0005765; F:GO:0032395; C:GO:0010008; P:GO:0006955	-		SignalP (SIGNALP)
	-	0				-
Loa loa	rhotekin-like isoform 2	3	F:GO:0017049; P:GO:0007165; F:GO:0005095	-		-
	-	0				IPR008610
Caenorhabditis elegans	type iii restriction res subunit family protein	5	P:GO:0006259; C:GO:0017117; F:GO:0003677; F:GO:0005524; F:GO:0017116	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-

Loa loa	cohesin subunit sa-	28	F:GO:0005515; P:GO:0006412; P:GO:0016045; P:GO:0007141; C:GO:0005576; C:GO:0005730; P:GO:0007286; F:GO:0003677; C:GO:0005875; F:GO:0003735; P:GO:0045449; P:GO:0032494; P:GO:0008592; P:GO:0007379; C:GO:0005811; F:GO:0032500; P:GO:0006965; F:GO:0016019; C:GO:0005887; P:GO:0045087; C:GO:0035327; C:GO:0000922; C:GO:0005721; P:GO:0006260; C:GO:0008278; C:GO:0000780; C:GO:0022627;	-	EC:3.6.5.3	IPR020839; PTHR11199 (PANTHER)
Loa loa	cohesin subunit sa-	28	F:GO:0005515; P:GO:0006412; P:GO:0016045; P:GO:0007141; C:GO:0005576; C:GO:0005730; P:GO:0007286; F:GO:0003677; C:GO:0005875; F:GO:0003735; P:GO:0045449; P:GO:0032494; P:GO:0008592; P:GO:0007379; C:GO:0005811; F:GO:0032500; P:GO:0006965; F:GO:0016019; C:GO:0005887; P:GO:0045087; C:GO:0035327; C:GO:0000922; C:GO:0005721; P:GO:0006260; C:GO:0008278; C:GO:0000780; C:GO:0022627	-	EC:3.6.5.3	IPR020839; PTHR11199 (PANTHER)
Loa loa	ankyrin repeat and sterile alpha motif domain containing partial	0				IPR006020; IPR011993; PTHR18958 (PANTHER), PTHR18958:SF212 (PANTHER), SSF50729 (SUPERFAMILY)

Caenorhabditis elegans	d--binding protein smubp-2	0		F:GO:0008168; F:GO:0003700; C:GO:0005634; F:GO:0003677; F:GO:0003676; F:GO:0000166; F:GO:0017111; F:GO:0008270; F:GO:0005524; P:GO:0006355; P:GO:0006508; C:GO:0005622; F:GO:0046872		PTHR10887 (PANTHER), PTHR10887:SF10 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG20927 [Caenorhabditis briggsae]	0		F:GO:0046872; F:GO:0008270; C:GO:0005622		-
Caenorhabditis briggsae	Hypothetical protein CBG20927 [Caenorhabditis briggsae]	0		F:GO:0046872; F:GO:0008270; C:GO:0005622		-
Caenorhabditis elegans	ectopic membrane ruffles in embryo protein 1	4	F:GO:0005524; F:GO:0008641; F:GO:0016881; P:GO:0045116	-	EC:6.3.2.0	IPR000594; IPR009036; IPR016040; PTHR10953 (PANTHER), PTHR10953:SF6 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG21486 [Caenorhabditis briggsae]	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	actin related protein 2 3 subunit 5-like	11	P:GO:0043652; C:GO:0005856; P:GO:0016331; P:GO:0010631; P:GO:0040007; P:GO:0000003; P:GO:0034314; P:GO:0002119; F:GO:0005515; P:GO:0009792; C:GO:0005737	-		-
Loa loa	d- mismatch repair protein containing protein	1	F:GO:0005515	-		IPR002099; IPR003594; IPR011186
Macaca mulatta	keratin 8	6	P:GO:0007010; C:GO:0005737; P:GO:0044419; F:GO:0005198; F:GO:0005515; C:GO:0045095	-		-
Caenorhabditis briggsae	uncoordi-ted family member (unc-89)	0		F:GO:0004672; F:GO:0005524; F:GO:0005089; P:GO:0006468; P:GO:0035023; F:GO:0004674; C:GO:0005622		IPR003961; IPR008957; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF5 (PANTHER)
Caenorhabditis briggsae	glutamate decarboxylase	3	F:GO:0030170; P:GO:0019752; F:GO:0016831	-	EC:4.1.1.0	IPR002129; IPR015421; SignalP (SIGNALP)

	-	0				-
Caenorhabditis briggsae	vacuolar protein sorting-associated protein	1	P:GO:0008104	-		IPR009543; IPR015412; PTHR16166 (PANTHER), PTHR16166:SF25 (PANTHER)
Caenorhabditis briggsae	vacuolar protein sorting-associated protein	1	P:GO:0008104	-		IPR009543; IPR015412; PTHR16166 (PANTHER), PTHR16166:SF25 (PANTHER)
Caenorhabditis briggsae	vacuolar protein sorting-associated protein	1	P:GO:0008104	-		IPR009543; IPR015412; PTHR16166 (PANTHER), PTHR16166:SF25 (PANTHER)
	-	0				-
						IPR008160; PTHR10499 (PANTHER), PTHR10499:SF131 (PANTHER)
Ancylostoma ceylanicum	tissue factor pathway inhibitor	4	F:GO:0030414; C:GO:0005615; C:GO:0005886; P:GO:0007598	-		IPR002223; IPR020901; PTHR10083 (PANTHER), PTHR10083:SF39 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	hypothetical protein Y66H1A.5 [Caenorhabditis elegans]	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		PTHR15092 (PANTHER), PTHR15092:SF2 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	4	C:GO:0005576; F:GO:0008061; F:GO:0005515; P:GO:0006030	-		PTHR11201 (PANTHER), PTHR11201:SF241 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-cpg-2 protein	4	P:GO:0009792; P:GO:0000281; P:GO:0030703; F:GO:0008061	-		-
Caenorhabditis briggsae	tr- nucleotidyl cca- 1	4	P:GO:0002119; P:GO:0008340; P:GO:0040007; P:GO:0006898	-		SSF81891 (SUPERFAMILY)
Caenorhabditis elegans	ipase c family member (plc-1)	9	F:GO:0005085; P:GO:0006629; F:GO:0004871; C:GO:0005622; F:GO:0004435; P:GO:0040010; F:GO:0005509; P:GO:0009566; P:GO:0007264	-	EC:3.1.4.11	IPR000159; PTHR10336 (PANTHER), PTHR10336:SF6 (PANTHER), SignalP (SIGNALP), SSF54236 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein Y48G9A.11 [Caenorhabditis elegans]	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		-
Caenorhabditis elegans	atp-binding sub-family a member 4	2	F:GO:0017111; F:GO:0000166	-	EC:3.6.1.15	PTHR19229 (PANTHER), PTHR19229:SF20 (PANTHER)
	-	0				-
	-	0				-

Caenorhabditis elegans	xylosyltransferase i	8	C:GO:0043231; P:GO:0030166; C:GO:0044444; P:GO:0070555; P:GO:0034605; P:GO:0048681; F:GO:0016757; C:GO:0016020	-		IPR003406; PTHR19297:SF1 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	F:GO:0005515; P:GO:0000003	-		IPR018617; SignalP (SIGNALP)
Caenorhabditis elegans	patched family protein	2	F:GO:0008158; C:GO:0016021	-		-
Caenorhabditis elegans	transmembrane protein 195	6	P:GO:0006643; F:GO:0005506; P:GO:0046485; C:GO:0016020; F:GO:0050479; C:GO:0005783	-	EC:1.14.16.5	IPR006694; PTHR21624 (PANTHER)
Caenorhabditis elegans	protein ki-se domain containing protein	3	F:GO:0004672; P:GO:0040010; F:GO:0000166	-		-
Caenorhabditis elegans	n-acetyltransferase -t13	0		C:GO:0005737; F:GO:0008415; F:GO:0016740; P:GO:0008152; F:GO:0008080; F:GO:0008999; F:GO:0005515		IPR000182; IPR016181; PTHR23091 (PANTHER), PTHR23091:SF2 (PANTHER)
Caenorhabditis elegans	n-acetyltransferase -t13	0		C:GO:0005737; F:GO:0008415; F:GO:0016740; P:GO:0008152; F:GO:0008080; F:GO:0008999; F:GO:0005515		IPR000182; IPR016181; PTHR23091 (PANTHER), PTHR23091:SF2 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-asp-6 protein	4	P:GO:0008219; F:GO:0005515; P:GO:0040011; F:GO:0008233	-		IPR001461; IPR001969; IPR009007; IPR021109; PTHR13683:SF53 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	cytochrome b-c1 complex subunit 9	1	P:GO:0009792	-		IPR008027; SignalP (SIGNALP)
Caenorhabditis briggsae	mcsc-pending-prov protein	5	C:GO:0005743; P:GO:0055085; F:GO:0005509; C:GO:0016021; F:GO:0005215	-		IPR001993; IPR002048; IPR002067; IPR002167; IPR011992; IPR018108; IPR018247; IPR018249; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF34 (PANTHER), SSF47473 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-lev-8 protein	6	F:GO:0004872; C:GO:0045211; C:GO:0030054; P:GO:0006811; C:GO:0016021; F:GO:0004889	-		-
	-	0				-

Caenorhabditis briggsae	aspartate mitochondrial	19	P:GO:0006107; P:GO:0015908; P:GO:0006533; C:GO:0043234; P:GO:0019551; P:GO:0006532; F:GO:0004069; C:GO:0005743; P:GO:0045471; F:GO:0005543; C:GO:0009986; F:GO:0019899; P:GO:0019550; C:GO:0005759; F:GO:0016597; F:GO:0042803; F:GO:0030170; C:GO:0005886; C:GO:0043204	-	EC:2.6.1.1	IPR000796; IPR004838; IPR004839; IPR015421; IPR015424
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Drosophila grimshawi	restin (reed-steinberg cell-expressed intermediate filament-associated protein)	8	F:GO:0008017; C:GO:0005875; C:GO:0005794; C:GO:0045169; F:GO:0003779; C:GO:0005938; P:GO:0007349; C:GO:0005876	-		PTHR18916 (PANTHER), PTHR18916:SF4 (PANTHER)
Caenorhabditis elegans	cingulin	0		C:GO:0005923; C:GO:0030054; F:GO:0003779; C:GO:0016459; F:GO:0003774; C:GO:0019861; F:GO:0005515; P:GO:0008150; P:GO:0001539		-
Teladorsagia circumcincta	l3b25 precusor	0				-
Caenorhabditis elegans	hypothetical protein C18B12.6 [Caenorhabditis elegans]	0				PTHR10984 (PANTHER), PTHR10984:SF1 (PANTHER)
	-	0				SignalP (SIGNALP)
Macaca mulatta	chromosome 1 open reading frame 43	3	F:GO:0016491; C:GO:0016021; F:GO:0050662	-		IPR010876
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	P:GO:0006810	-		IPR001898; PTHR10283 (PANTHER), PTHR10283:SF15 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				IPR000436; SignalP (SIGNALP)
	-	0				IPR000436; SignalP (SIGNALP)
	-	0				IPR000436; SignalP (SIGNALP)

Brugia malayi	nuclear receptor subfamily 2 group c member 2-like	7	C:GO:0031981; F:GO:0046872; P:GO:0006355; F:GO:0003677; F:GO:0004879; F:GO:0005515; C:GO:0005737	-		IPR000536; IPR008946; PTHR11865 (PANTHER), PTHR11865:SF147 (PANTHER)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG18218 [Caenorhabditis briggsae]	0		P:GO:0006898; F:GO:0003677; F:GO:0003887; P:GO:0000003; P:GO:0002119; P:GO:0009792; P:GO:0040010; P:GO:0006350; P:GO:0040035		-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	P:GO:0009792; C:GO:0016021; P:GO:0000003; P:GO:0040011	-		-
Homo sapiens	decorin	16	P:GO:0042060; F:GO:0047485; P:GO:0001890; C:GO:0005615; P:GO:0009887; F:GO:0050840; P:GO:0007519; F:GO:0005518; P:GO:0007568; F:GO:0005539; P:GO:0001822; C:GO:0005578; P:GO:0019800; P:GO:0032496; P:GO:0030198; P:GO:0009612	-		-
	-	0				IPR003677
	-	0				IPR003677
Caenorhabditis briggsae	briggsae cbr-ptr-3 protein	0		C:GO:0016021; C:GO:0016020; F:GO:0008158		IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER)
Caenorhabditis briggsae	phosphogluco-te mutase	11	C:GO:0005829; P:GO:0019388; P:GO:0006874; P:GO:0019255; P:GO:0060361; P:GO:0006011; F:GO:0004619; F:GO:0000287; P:GO:0005992; F:GO:0004614; P:GO:0005978	-	EC:5.4.2.1; EC:5.4.2.2	IPR005844; IPR016055; PTHR22573 (PANTHER), PTHR22573:SF5 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)

Loa loa	hed family member (ptc-3)	8	P:GO:0009792; F:GO:0004872; P:GO:0002119; P:GO:0040018; P:GO:0018996; P:GO:0000003; P:GO:0040011; C:GO:0016021	-		PTHR10796 (PANTHER), PTHR10796:SF34 (PANTHER)
Caenorhabditis elegans	beta 1	6	P:GO:0019388; C:GO:0005625; C:GO:0005764; F:GO:0005515; F:GO:0016936; F:GO:0004565	-	EC:3.2.1.23	IPR001944; IPR013781; IPR017853; IPR019801; PTHR23421:SF2 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	clathrin coat assembly protein ap-1	9	P:GO:0006892; C:GO:0005794; P:GO:0016044; F:GO:0005515; P:GO:0006886; C:GO:0005829; C:GO:0030131; C:GO:0030665; P:GO:0044419	-		IPR011012; G3DSA:3.30.450.60 (GENE3D), PTHR11998 (PANTHER), PTHR11998:SF11 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0005509; C:GO:0016021		PTHR12294 (PANTHER), PTHR12294:SF1 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	major facilitator superfamily protein	5	C:GO:0016021; P:GO:0000003; P:GO:0040007; P:GO:0055085; P:GO:0002119	-		PTHR11360 (PANTHER), PTHR11360:SF15 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	protein yipf5 (yip1 family member 5)	3	F:GO:0050660; C:GO:0016021; F:GO:0016491	-		IPR006977; PTHR21236 (PANTHER), PTHR21236:SF2 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0005488	-		IPR002919; IPR013032; G3DSA:2.10.25.10 (GENE3D)
Branchiostoma floridae	transmembrane protein 77	0		F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150; C:GO:0005575		IPR019402; PTHR21324 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	briggsae cbr-gex-2 protein	9	P:GO:0006915; P:GO:0016337; P:GO:0016477; C:GO:0019717; C:GO:0030054; F:GO:0005515; P:GO:0010172; C:GO:0045202; C:GO:0048471	-		IPR008081

	-	0				-
Caenorhabditis elegans	set (trithorax polycomb) domain containing family member (set-18)	1	F:GO:0005515	-		PTHR12197 (PANTHER), PTHR12197:SF9 (PANTHER)
Caenorhabditis elegans	serine threonine-protein phosphatase 4 catalytic subunit	13	P:GO:0001525; P:GO:0007126; P:GO:0018991; F:GO:0004704; F:GO:0046872; P:GO:0040007; P:GO:0007052; C:GO:0005813; F:GO:0004722; P:GO:0002119; F:GO:0005515; P:GO:0009792; C:GO:0005634	-		IPR004843; IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF22 (PANTHER), SSF56300 (SUPERFAMILY)
Caenorhabditis elegans	riboki-se	4	P:GO:0005975; F:GO:0016301; P:GO:0044281; P:GO:0044237	-		IPR002139; IPR011611; G3DSA:3.40.1190.20 (GENE3D), PTHR10584 (PANTHER), PTHR10584:SF29 (PANTHER), SSF53613 (SUPERFAMILY)
	-	0				-
Brugia malayi	mortality factor 4-like protein 1	0		F:GO:0003682; C:GO:0000785; P:GO:0006333; C:GO:0005634		IPR000953; IPR008676; IPR016197; G3DSA:2.30.30.270 (GENE3D), PF11717 (PFAM)
	-	0				-
Tribolium castaneum	transmembrane protein 14c	1	C:GO:0005739	-		IPR005349
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	taf5 r- polymerase tata box binding protein -associated 100kda	12	F:GO:0016986; P:GO:0006367; C:GO:0005730; F:GO:0010843; C:GO:0033276; F:GO:0046983; C:GO:0015629; P:GO:0006368; F:GO:0003700; F:GO:0004402; C:GO:0005669; C:GO:0005737	-	EC:2.3.1.48	IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR19879 (PANTHER)
	-	0				-
Caenorhabditis elegans	laminin alpha chain	12	P:GO:0030155; C:GO:0005608; P:GO:0045995; C:GO:0005606; C:GO:0005615; P:GO:0030334; F:GO:0005102; N:GO:0061138; P:GO:0030154; P:GO:0048513; F:GO:0005201; P:GO:0007166	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis briggsae	chromatin assembly factor 1 subunit a	1	P:GO:0009987	-		IPR022043; PTHR15272 (PANTHER)
Caenorhabditis elegans	myosin light polypeptide 5 regulatory	2	P:GO:0055085; C:GO:0016021	-		-
Caenorhabditis briggsae	eb module family protein	2	F:GO:0016810; P:GO:0005975	-		IPR006149
	-	0				-
Caenorhabditis elegans	intraflagellar transport protein 140	0		F:GO:0003674; F:GO:0005488; P:GO:0008150; C:GO:0005575		-
	-	0				-
	-	0				-
	-	0				-
Loa loa	wgr domain containing protein	6	P:GO:0044260; C:GO:0031981; P:GO:0090304; F:GO:0016740; F:GO:0005515; P:GO:0006974	-		IPR001510; PTHR15447 (PANTHER), SSF57716 (SUPERFAMILY)
	-	0				-
	-	0				-
Angiostrongylus cantonensis	exostosin family protein	5	C:GO:0016021; P:GO:0005975; P:GO:0009059; F:GO:0003824; P:GO:0044237	-		IPR004263; PTHR11062 (PANTHER), PTHR11062:SF6 (PANTHER)
Angiostrongylus cantonensis	exostosin family protein	5	C:GO:0016021; P:GO:0005975; P:GO:0009059; F:GO:0003824; P:GO:0044237	-		IPR012506; SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	cell division cycle 2-like 2 (pitslre proteins)	10	P:GO:0006915; F:GO:0004674; P:GO:0050684; P:GO:0006355; P:GO:0001558; F:GO:0005524; F:GO:0005515; P:GO:0007067; C:GO:0005634; P:GO:0006468	-	EC:2.7.11.0	IPR011009; IPR017442; IPR020636; IPR020648; G3DSA:1.10.510.10 (GENE3D)
	-	0				IPR010916
Caenorhabditis briggsae	Hypothetical protein CBG19878 [Caenorhabditis briggsae]	0		F:GO:0008289		-
Loa loa	polymerase (d- directed) delta regulatory subunit	6	P:GO:0040010; P:GO:0006259; P:GO:0040035; P:GO:0040011; P:GO:0009792; C:GO:0005634	-		IPR007185; PTHR10416 (PANTHER)
Ipomoea batatas	retrotransposon polyprotein	3	P:GO:0006259; F:GO:0003676; F:GO:0003824	-		PTHR10178 (PANTHER), PTHR10178:SF14 (PANTHER), SSF56672 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-dys-1 protein	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				IPR019392; PTHR21508 (PANTHER)
	-	0				-

Hyposoter didymator virus	af479654_1thr-ser protein	0		F:GO:0008061; P:GO:0006030; C:GO:0005576		-
Hyposoter didymator virus	af479654_1thr-ser protein	0		F:GO:0008061; P:GO:0006030; C:GO:0005576		-
Caenorhabditis elegans	atp-dependent r- helicase dhx8	2	F:GO:0016787; F:GO:0005488	-		IPR007502; PTHR18934 (PANTHER)
	-	0				IPR017907
Caenorhabditis elegans	transmembrane protein 38a	3	C:GO:0016021; F:GO:0005261; P:GO:0015672	-		IPR007866; PTHR12454:SF2 (PANTHER)
	-	0				-
Caenorhabditis elegans	iq calmodulin-binding motif domain protein	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	rod-like dye-filling defective family member (rdy-2)	3	C:GO:0016021; P:GO:0006468; F:GO:0005524	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR001534; SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG16791 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	Hypothetical protein CBG16791 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein T07C12.12 [Caenorhabditis elegans]	0				IPR013894; PTHR14790 (PANTHER), PTHR14790:SF2 (PANTHER)
Caenorhabditis briggsae	voltage gated chloride channel family protein	6	P:GO:0009792; F:GO:0005247; P:GO:0055085; P:GO:0000003; C:GO:0016021; P:GO:0006821	-		IPR001807; PTHR11689:SF5 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Botryotinia fuckeliana B05.10	predicted protein [Botryotinia fuckelia- B05.10]	0				-
Caenorhabditis elegans	nop seven associated protein 1	0		P:GO:0000003; P:GO:0040035; P:GO:0002119; P:GO:0040007		-
Caenorhabditis briggsae	uso1 p115 like vesicle tethering head region containing protein	12	F:GO:0008565; C:GO:0000139; P:GO:0048280; C:GO:0005795; F:GO:0042802; P:GO:0032940; P:GO:0019915; P:GO:0007030; P:GO:0040039; P:GO:0006898; P:GO:0006886; C:GO:0005783	-		IPR011989; IPR016024; PTHR10013 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG09842 [Caenorhabditis briggsae]	2	F:GO:0005515; F:GO:0016787	-		IPR002018; G3DSA:3.40.50.1820 (GENE3D), PTHR11559:SF21 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
	-	0				-
	-	0				PR01217 (PRINTS)

Caenorhabditis elegans	cyclin b3	0		C:GO:0005634		IPR004367; IPR006670; IPR006671; IPR011028; IPR013763; IPR014400; IPR015452; PTHR10177 (PANTHER)
Caenorhabditis elegans	cyclin b3	0		C:GO:0005634		IPR004367; IPR006670; IPR006671; IPR011028; IPR013763; IPR014400; IPR015452; PTHR10177 (PANTHER)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG07076 [Caenorhabditis briggsae]	4	P:GO:0019915; P:GO:0009792; P:GO:0040010; P:GO:0040035	-		-
Caenorhabditis elegans	briggsae cbr-ttll-5 protein	1	F:GO:0016874	-		IPR004344; PTHR12241:SF8 (PANTHER), SSF56059 (SUPERFAMILY)
Loa loa	hypothetical protein LOAG_09502 [Loa loa]	0		P:GO:0040010		IPR011991
Brugia malayi	homeobox domain containing protein	12	F:GO:0030528; P:GO:0040010; F:GO:0008270; P:GO:0006355; P:GO:0040035; F:GO:0043565; P:GO:0002119; F:GO:0003700; P:GO:0040011; P:GO:0006898; P:GO:0002009; C:GO:0005634	-		IPR001356; IPR009057; IPR012287; PTHR18973 (PANTHER), PTHR18973:SF19 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Loa loa	multiple pdz domain protein family member (mpz-1)	2	F:GO:0005515; C:GO:0016021	-		-
	-	0				-
Caenorhabditis elegans	endonuclease-reverse transcriptase	0		F:GO:0003723; P:GO:0006278; P:GO:0045449; F:GO:0030528; F:GO:0004519; F:GO:0003964		IPR005135; G3DSA:3.60.10.10 (GENE3D), PTHR23227 (PANTHER), PTHR23227:SF14 (PANTHER), SignalP (SIGNALP)
Neisseria elongata subsp. glycolytica ATCC 29315	hypothetical protein NEIELOOT_01783 [Neisseria elongata subsp. glycolytica ATCC 29315]	0				-
	-	0				-
Camponotus floridanus	endonuclease-reverse transcriptase	0		F:GO:0003723; P:GO:0006278; P:GO:0045449; F:GO:0030528; F:GO:0004519; F:GO:0003964		IPR005135; G3DSA:3.60.10.10 (GENE3D)
	-	0				-
	-	0				-

Homo sapiens	isoform cra_a	23	F:GO:0050291; P:GO:0048511; F:GO:0008270; P:GO:0007275; F:GO:0047058; P:GO:0006357; P:GO:0046677; P:GO:0010243; F:GO:0047057; P:GO:0046513; C:GO:0005792; P:GO:0030193; C:GO:0016021; C:GO:0005789; F:GO:0046983; P:GO:0014070; F:GO:0003702; F:GO:0043565; P:GO:0050820; F:GO:0003700; P:GO:0055114; P:GO:0042373; C:GO:0005634	-	EC:2.3.1.24; EC:1.1.4.2; EC:1.1.4.1	PTHR12138 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0008270		-
Brugia malayi	set binding factor 2	2	F:GO:0005515; C:GO:0016020	-		IPR001194; IPR005113; PTHR10807 (PANTHER), PTHR10807:SF1 (PANTHER)
Caenorhabditis briggsae	patched family protein	4	P:GO:0040018; P:GO:0018996; P:GO:0007275; P:GO:0040011	-		IPR000731; IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-mex-3 protein	3	F:GO:0008270; F:GO:0005515; F:GO:0003723	-		IPR004087; IPR004088; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR23285 (PANTHER), SSF54791 (SUPERFAMILY)
Caenorhabditis elegans	paps (adenosine 3 -phosphate 5 -phosphosulfate) transporter family member (pst-1)	2	P:GO:0055085; C:GO:0016021	-		-
Caenorhabditis elegans	sex determining protein mog-3	4	P:GO:0040019; P:GO:0009792; P:GO:0010171; P:GO:0040010	-		IPR022209

	fibronectin 1	18	P:GO:0042060; P:GO:0018149; P:GO:0016477; P:GO:0001525; P:GO:0008360; C:GO:0005793; C:GO:0005604; P:GO:0007044; P:GO:0007160; C:GO:0031093; P:GO:0034446; F:GO:0005518; C:GO:0005577; C:GO:0016324; F:GO:0008201; F:GO:0005201; F:GO:0016504; P:GO:0006953	-		IPR000562; IPR013806; PR00013 (PRINTS), G3DSA:2.10.10.10 (GENE3D), PTHR22918 (PANTHER)
	-	0				PTHR22898 (PANTHER)
	-	0				-
Ciona intestinalis	zinc finger protein	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		IPR007087; IPR015880
Caenorhabditis briggsae	b-box zinc finger family protein	4	C:GO:0043229; F:GO:0005488; P:GO:0048667; P:GO:0050794	-		PTHR12846 (PANTHER), PTHR12846:SF2 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-tre-2 protein	5	P:GO:0009792; P:GO:0002119; F:GO:0016798; P:GO:0008152; P:GO:0040007	-		IPR001661; PTHR23403:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	quinone oxidoreductase	6	F:GO:0003960; C:GO:0005625; F:GO:0003730; F:GO:0050661; P:GO:0055114; F:GO:0008270	-	EC:1.6.5.5	IPR002085; IPR011032; IPR013154; G3DSA:3.90.180.10 (GENE3D), PTHR11695:SF30 (PANTHER)
	-	0				-
Caenorhabditis elegans	monocarboxylate transporter	3	P:GO:0000003; P:GO:0040007; P:GO:0002119	-		IPR011701; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11360 (PANTHER), PTHR11360:SF15 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	adam metallopeptidase with thrombospondin type 1 9	4	F:GO:0004222; C:GO:0005578; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	IPR012314
Caenorhabditis briggsae	Hypothetical protein CBG15659 [Caenorhabditis briggsae]	4	P:GO:0002119; P:GO:0009792; P:GO:0000003; P:GO:0040007	-		PTHR15892 (PANTHER)
Caenorhabditis elegans	adipokinetic hormone receptor	1	F:GO:0004930	-		-

Caenorhabditis briggsae	vesicular glutamate transporter	2	P:GO:0055085; C:GO:0016021	-		IPR011701; IPR016196; G3DSA:1.20.1250.20 (GENE3D), PTHR11662 (PANTHER), PTHR11662:SF29 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	lysophospholipid acyltransferase 7	1	F:GO:0016740	-		IPR004299; PTHR13906 (PANTHER), PTHR13906:SF5 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Homo sapiens	hCG1990620 [Homo sapiens]	0				-
Brugia malayi	d- pantothe-te metabolism flavoprotein	10	P:GO:0046843; P:GO:0007303; P:GO:0055091; P:GO:0007297; P:GO:0070328; P:GO:0007476; P:GO:0030036; P:GO:0022416; P:GO:0030713; P:GO:0030708	-		IPR007085; PTHR12290 (PANTHER), PTHR12290:SF2 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
Brugia malayi	protein ki-se domain containing protein	0		F:GO:0016301; F:GO:0004672; F:GO:0005524; F:GO:0000166; P:GO:0006468; F:GO:0004674		-
Caenorhabditis elegans	zinc finger protein	0		F:GO:0008270; C:GO:0005622		IPR007087; IPR015880
Macaca mulatta	protein disulfide isomerase family member 6	8	P:GO:0006457; C:GO:0005788; C:GO:0005793; C:GO:0005886; P:GO:0045454; F:GO:0005515; C:GO:0042470; F:GO:0003756	-	EC:5.3.4.1	-
Brugia malayi	furry homolog	1	F:GO:0005515	-		PTHR12295 (PANTHER), PTHR12295:SF6 (PANTHER)
	-	0				-

Caenorhabditis briggsae	briggsae cbr-pri-1 protein	0		F:GO:0016740; F:GO:0003896; P:GO:0000910; P:GO:0006260; P:GO:0000003; P:GO:0051301; C:GO:0005658; P:GO:0002119; P:GO:0009792; P:GO:0002009; P:GO:0040007; P:GO:0040035; P:GO:0006269; F:GO:0003899		-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Angiostrongylus cantonensis	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	set (trithorax polycomb) domain containing family member (set-2)	3	F:GO:0005488; F:GO:0016740; C:GO:0044451	-		IPR015722; G3DSA:2.170.270.10 (GENE3D), PTHR22884 (PANTHER), PF11764 (PFAM)
Caenorhabditis elegans	heparan sulfate 2-o-sulfotransferase 1	6	P:GO:0060676; C:GO:0016021; C:GO:0000139; P:GO:0015014; F:GO:0004394; P:GO:0030202	-		IPR005331; IPR007734; PTHR12129:SF3 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				IPR000731; IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	tyrosine-protein ki-se transmembrane receptor	4	P:GO:0006468; F:GO:0005524; F:GO:0004672; F:GO:0005515	-		IPR001245; IPR020685; G3DSA:1.10.510.10 (GENE3D), PTHR23256:SF274 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	probable e3 ubiquitin-protein ligase mycbp2	1	F:GO:0005488	-		PTHR12846 (PANTHER), PTHR12846:SF2 (PANTHER)
Caenorhabditis elegans	acyl- thioesterase ii	2	P:GO:0019915; F:GO:0016787	-		IPR003703; G3DSA:3.10.129.10 (GENE3D), PTHR11066:SF3 (PANTHER), SSF54637 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein F34D10.9 [Caenorhabditis elegans]	0		P:GO:0006270		-
Caenorhabditis elegans	sy-ptotagmin x	6	P:GO:0050803; P:GO:0006950; C:GO:0008021; P:GO:0006810; C:GO:0016021; F:GO:0005215	-		IPR000008; IPR008973; IPR018029; G3DSA:2.60.40.150 (GENE3D), PTHR10024 (PANTHER), PTHR10024:SF41 (PANTHER)

Caenorhabditis elegans	unc-13 homolog b (elegans)	0		F:GO:0001566; P:GO:0016082; C:GO:0016020; C:GO:0045202; P:GO:0023034; C:GO:0030054; C:GO:0005794; P:GO:0006887; C:GO:0005575; P:GO:0007268; F:GO:0046872; C:GO:0005886		PTHR10480 (PANTHER)
Caenorhabditis elegans	dead (asp-glu-ala-asp) box polypeptide 58	1	F:GO:0005488	-		SignalP (SIGNALP)
Caenorhabditis elegans	yqy2_caeel ame: full=uncharacterized protein	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical tyrosi-se-like protein in chromosome	4	F:GO:0005515; F:GO:0046872; P:GO:0008152; F:GO:0016491	-		-
	-	0				-
Caenorhabditis elegans	g protein beta subunit-like	9	P:GO:0032314; F:GO:0005515; P:GO:0040018; C:GO:0005829; P:GO:0019915; P:GO:0032008; P:GO:0050731; P:GO:0002119; P:GO:0030838	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR19842 (PANTHER)
Steinernema feltiae	glycogen synthase	7	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0005978; F:GO:0005515; F:GO:0004373; P:GO:0040011	-	EC:2.4.1.11	IPR008631; SSF53756 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG14642 [Caenorhabditis briggsae]	0		F:GO:0008168; F:GO:0016740; P:GO:0008152; C:GO:0016021; F:GO:0003824		IPR001045; G3DSA:3.40.50.150 (GENE3D), PTHR12176 (PANTHER), SSF53335 (SUPERFAMILY)
	-	0				IPR002013; PTHR11200 (PANTHER), PTHR11200:SF11 (PANTHER)
Haemonchus contortus	elegans protein confirmed by transcript evidence	5	F:GO:0015078; C:GO:0033177; C:GO:0016021; P:GO:0015986; P:GO:0040013	-		IPR002490; PTHR11629:SF23 (PANTHER), SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	short chain dehydroge-se reductase family member 5	5	P:GO:0009239; P:GO:0055114; C:GO:0016021; F:GO:0008667; F:GO:0050662	-	EC:1.3.1.28	IPR002198; IPR002347; IPR016040; PTHR19410:SF36 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis briggsae	egf-like domain containing protein	1	P:GO:0032502	-		IPR000742; IPR006210; IPR013032; G3DSA:2.170.300.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF238 (PANTHER), SignalP (SIGNALP), SSF57196 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-dhs-29 protein	5	P:GO:0006694; C:GO:0016021; P:GO:0055114; F:GO:0005488; F:GO:0003854	-	EC:1.1.1.145	SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	isoform a	1	P:GO:0000003	-		IPR000408; IPR009091; PTHR22870 (PANTHER), PTHR22870:SF28 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-dct-9 protein	1	P:GO:0009792	-		IPR000535; IPR008962
	-	0				-
Caenorhabditis elegans	ryanodine receptor	16	F:GO:0005515; F:GO:0005219; P:GO:0032026; P:GO:0006816; C:GO:0019717; P:GO:0051592; F:GO:0005509; C:GO:0016021; P:GO:0051480; P:GO:0006629; C:GO:0043234; P:GO:0042493; C:GO:0030018; P:GO:0055085; F:GO:0004872; P:GO:0007584	-		IPR005821; IPR009460; IPR015925; PTHR13715:SF11 (PANTHER)
Caenorhabditis briggsae	like protein	0		F:GO:0016779; F:GO:0016740		IPR002876; G3DSA:3.30.70.980 (GENE3D)
	-	0				-
Caenorhabditis elegans	olfactomedin-like domain containing protein	0		P:GO:0000003		IPR003112; PTHR23192 (PANTHER), PTHR23192:SF6 (PANTHER)
	-	0				-
	-	0				IPR013783
	-	0				-
Caenorhabditis elegans	novel protein vertebrate large homolog 5	1	F:GO:0005515	-		IPR001452; IPR001478; IPR008144; G3DSA:2.30.30.40 (GENE3D), G3DSA:2.30.42.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR13865 (PANTHER), PTHR13865:SF5 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				IPR001412; SignalP (SIGNALP)
	-	0				-
	-	0				-

Caenorhabditis briggsae	organic cation transporter protein	7	P:GO:0009792; P:GO:0002119; P:GO:0006915; P:GO:0006810; P:GO:0040007; C:GO:0016020; F:GO:0005215	-		IPR005828; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11600 (PANTHER), PTHR11600:SF42 (PANTHER)
Argas monolakensis	mitochondrial associated endoribonuclease mar1-isochorismatase superfamily	0		C:GO:0005739; P:GO:0008152; F:GO:0003824; F:GO:0005515; F:GO:0042802		IPR000868; PTHR14119 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-sfxn- protein	0		F:GO:0008324; C:GO:0016021; C:GO:0016020; P:GO:0055085; P:GO:0006812		IPR004686; PTHR11153:SF9 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG13916 [Caenorhabditis briggsae]	0				-
Ostertagia ostertagi	metalloprotease 1 precursor	2	F:GO:0046872; F:GO:0008237	-		-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR001534; SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR001534; SignalP (SIGNALP)
Caenorhabditis briggsae	tbc1 domain member 10a	5	F:GO:0005097; C:GO:0005622; F:GO:0030165; P:GO:0032313; C:GO:0005902	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	beta lysosomal	3	P:GO:0005975; F:GO:0004553; F:GO:0043169	-	EC:3.2.1.0	-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	2	F:GO:0016791; C:GO:0005737	-	EC:3.1.3.0	IPR000242; IPR000387; IPR016130; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis briggsae	phosphoinositide-3- delta polypeptide	6	P:GO:0009987; P:GO:0050789; P:GO:0040024; P:GO:0007568; F:GO:0016301; P:GO:0007610	-		IPR001263; IPR002420; IPR008973; IPR015433; IPR016024; G3DSA:2.60.40.150 (GENE3D), PTHR10048:SF14 (PANTHER)

Aedes aegypti	fringe	0		P:GO:0007451; F:GO:0016757; P:GO:0007450; P:GO:0008593; P:GO:0006493; P:GO:0048477; F:GO:0008375; P:GO:0007293; C:GO:0016021; C:GO:0016020; F:GO:0033829; P:GO:0007389; C:GO:0005783; P:GO:0048190; P:GO:0001745; P:GO:0035286; P:GO:0007219; P:GO:0045747; P:GO:0045746; P:GO:0035111; P:GO:0007476; P:GO:0008587; C:GO:0005795; C:GO:0005794; P:GO:0048749; F:GO:0008194; C:GO:0030173;		IPR003378; PTHR10811 (PANTHER), PTHR10811:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	ryanodine receptor	8	F:GO:0004872; P:GO:0006629; F:GO:0005219; P:GO:0006816; P:GO:0006874; P:GO:0055085; F:GO:0005509; C:GO:0016021	-		IPR015925; PTHR13715:SF11 (PANTHER), SignalP (SIGNALP)
Loa loa	zinc finger protein	2	F:GO:0008270; C:GO:0005622	-		-
Caenorhabditis elegans	hypothetical protein T06D8.1 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
Caenorhabditis briggsae	prion-like-(q n-rich)-domain-bearing protein family member (pqn-22)	1	P:GO:0009792	-		-
	-	0				-
Brugia malayi	ctr copper transporter family protein	0		C:GO:0016021; F:GO:0005375; P:GO:0006825		IPR007274; PTHR12483:SF4 (PANTHER)
	-	0				SignalP (SIGNALP)
Loa loa	yqp1_caeel ame: full=uncharacterized protein	0				SignalP (SIGNALP)

Homo sapiens	adp-ribosylation factor 1	17	F:GO:0005057; C:GO:0000139; F:GO:0005515; F:GO:0008270; F:GO:0005525; P:GO:0015031; C:GO:0005829; P:GO:0060872; P:GO:0032312; P:GO:0006892; P:GO:0006890; C:GO:0048471; F:GO:0003924; C:GO:0005886; P:GO:0048205; F:GO:0008060; C:GO:0030017	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
	-	0				-
	-	0				-
Caenorhabditis elegans	homogentisate -dioxyge-se	5	F:GO:0042802; F:GO:0004411; P:GO:0055114; P:GO:0006559; P:GO:0006570	-	EC:1.13.11.5	IPR005708; IPR011051
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	C:GO:0044464	-		IPR000276; IPR017452; G3DSA:1.20.1070.10 (GENE3D), PTHR22751 (PANTHER), PTHR22751:SF8 (PANTHER), SignalP (SIGNALP), SSF81321 (SUPERFAMILY)
Loa loa	polymerase iii (d- directed) polypeptide b	9	F:GO:0003899; P:GO:0009615; P:GO:0032728; P:GO:0045089; F:GO:0046872; F:GO:0003677; F:GO:0032549; P:GO:0006350; C:GO:0005634	-	EC:2.7.7.6	-
	-	0				-
	-	0				-
Loa loa	piwi domain containing protein	0		F:GO:0003676		IPR003165; PTHR22891 (PANTHER)
Caenorhabditis briggsae	serine or cysteine protease inhibitor	13	P:GO:0033986; P:GO:0046687; F:GO:0030414; P:GO:0006954; P:GO:0034014; C:GO:0005615; F:GO:0005515; P:GO:0014070; P:GO:0034097; P:GO:0010288; P:GO:0032355; P:GO:0032496; C:GO:0005634	-		IPR000215; G3DSA:2.30.39.10 (GENE3D), G3DSA:3.30.497.10 (GENE3D), PTHR11461:SF25 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	t family of potassium channels family member (twk-39)	0		F:GO:0005216		-

Caenorhabditis elegans	briggsae cbr-ile-2 protein	0		C:GO:0016021; C:GO:0016020; P:GO:0048881; P:GO:0009792; P:GO:0018991		IPR005052; IPR008985; IPR013320; PTHR12223:SF6 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-cdt-1 protein	9	C:GO:0005737; P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0006260; P:GO:0001703; P:GO:0040011; P:GO:0040007; C:GO:0005634	-		IPR014939; SSF46785 (SUPERFAMILY)
Homo sapiens	achain the structure of ca2+ sensor (case-12)	22	P:GO:0060316; C:GO:0005654; P:GO:0010880; F:GO:0031996; F:GO:0031997; P:GO:0060315; P:GO:0051592; P:GO:0018298; F:GO:0005509; P:GO:0006936; P:GO:0032465; P:GO:0006091; C:GO:0005576; C:GO:0005829; F:GO:0019904; C:GO:0005813; F:GO:0031432; P:GO:0007186; C:GO:0005876; C:GO:0005886; C:GO:0000922; P:GO:0008218	-		IPR002048; IPR011992; IPR018247; IPR018248; IPR018249; PTHR23050 (PANTHER), PTHR23050:SF20 (PANTHER), SSF47473 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-such-1 protein	0		P:GO:0000003; F:GO:0005488		-
	-	0				-
Plasmodium falciparum 3D7	zinc finger c-x8-c-x5-c-x3-h	0		F:GO:0003676; F:GO:0046872; C:GO:0020011; F:GO:0008270		-
	-	0				-
Caenorhabditis elegans	3-phosphoserine phosphatase	4	F:GO:0000287; C:GO:0009507; F:GO:0004647; P:GO:0006564	-	EC:3.1.3.3	IPR023190; PTHR10000 (PANTHER), SSF56784 (SUPERFAMILY)
	-	0				IPR008160; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER)
Ovis aries	ribosomal protein l34	6	F:GO:0003735; F:GO:0003723; F:GO:0005515; C:GO:0022625; C:GO:0005739; P:GO:0006414	-		SignalP (SIGNALP)
	-	0				-

	-	0				-
	-	0				-
Caenorhabditis elegans	annexin a7	15	P:GO:0065008; P:GO:0007109; C:GO:0042582; F:GO:0005509; P:GO:0006909; C:GO:0030496; F:GO:0005544; F:GO:0048155; C:GO:0042581; F:GO:0048306; C:GO:0005819; C:GO:0045335; C:GO:0005635; C:GO:0005654; P:GO:0051592	-		IPR001464; IPR018252; IPR018502; PTHR10502:SF13 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0006629; F:GO:0016787; F:GO:0004806		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Homo sapiens	peptidylprolyl isomerase b (cyclophilin b)	7	P:GO:0006457; C:GO:0005788; C:GO:0042470; P:GO:0051169; F:GO:0042277; F:GO:0051082; F:GO:0003755	-	EC:5.2.1.8	IPR002130; IPR015891; IPR020892; PTHR11071 (PANTHER), PTHR11071:SF63 (PANTHER)
Caenorhabditis elegans	ubr1_caeel ame: full=e3 ubiquitin-protein ligase ubr-1 ame: full=n-recognin-1 ame: full=ubiquitin-protein ligase e3-alpha	0				-
Drosophila yakuba	GE23539 [Drosophila yakuba]	0		F:GO:0003676; F:GO:0000166; F:GO:0003682; C:GO:0030529; C:GO:0000785; P:GO:0006333; F:GO:0003677; C:GO:0005634		-
Caenorhabditis briggsae	nidogen 2	6	F:GO:0005518; C:GO:0031012; P:GO:0044237; P:GO:0007155; P:GO:0040010; C:GO:0016020	-		IPR000152; IPR000742; IPR001881; IPR013032; IPR013091; IPR018097; G3DSA:2.10.25.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF84 (PANTHER), SSF57196 (SUPERFAMILY)
Caenorhabditis elegans	phosphate transporter family protein	5	P:GO:0006810; P:GO:0040027; P:GO:0040035; P:GO:0009792; C:GO:0016020	-		IPR001204; PTHR11101:SF12 (PANTHER), PS51257 (PROFILE), SignalP (SIGNALP)

Caenorhabditis elegans	phosphate transporter family protein	6	P:GO:0009987; P:GO:0006810; P:GO:0040027; P:GO:0040035; C:GO:0044425; P:GO:0009792	-		IPR001204; PTHR11101:SF12 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	fyve zinc finger family protein	0		F:GO:0046872; F:GO:0008270; C:GO:0005622		IPR000306; IPR007087; IPR011011; IPR013083; IPR015880; IPR017455; PTHR13510 (PANTHER), PTHR13510:SF10 (PANTHER)
	-	0				-
Caenorhabditis elegans	n-acetyltransferase 10	8	P:GO:0009792; P:GO:0008152; F:GO:0008080; P:GO:0040007; P:GO:0040035; F:GO:0005515; P:GO:0002119; P:GO:0040011	-		IPR013562; PTHR10925 (PANTHER), PTHR10925:SF5 (PANTHER)
Ancylostoma duodenale	ancylostoma-secreted protein 1 precursor	0		C:GO:0005576		IPR014044
Caenorhabditis briggsae	copine domain atypical protein isoform partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	von willebrand factor type egf and pentraxin domain containing 1	2	P:GO:0040010; F:GO:0005509	-		SignalP (SIGNALP)
Brugia malayi	hypothetical protein Bm1_04595 [Brugia malayi]	0		F:GO:0003676		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	possible integral membrane efflux protein	7	P:GO:0009792; P:GO:0002119; P:GO:0055085; P:GO:0040010; P:GO:0000003; P:GO:0042221; C:GO:0016021	-		PTHR10074 (PANTHER), PTHR10074:SF22 (PANTHER), SignalP (SIGNALP)
Brugia malayi	replication factor a 73 kda subunit	1	F:GO:0005515	-		IPR012340; IPR013955; IPR016027; PTHR23273 (PANTHER)
	-	0				-
Brugia malayi	low-density lipoprotein receptor	3	C:GO:0016021; F:GO:0004872; F:GO:0005509	-		IPR011042; PTHR10529 (PANTHER), SSF101898 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	5	P:GO:0018996; P:GO:0009792; P:GO:0040017; P:GO:0040007; P:GO:0002119	-		-
	-	0				-

Caenorhabditis elegans	protein ki-se domain containing protein	0		F:GO:0016740; C:GO:0019028; F:GO:0004674; P:GO:0018108; F:GO:0004672; P:GO:0006468; F:GO:0000166; F:GO:0004715; F:GO:0005524; F:GO:0016301; F:GO:0004713; C:GO:0019012; P:GO:0016032; F:GO:0005515; F:GO:0005198		-
Caenorhabditis elegans	voltage-gated calcium channel beta subunit	2	P:GO:0006816; F:GO:0005245	-		IPR000584; IPR001452; IPR008144; G3DSA:2.30.30.40 (GENE3D), G3DSA:3.40.50.300 (GENE3D), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	ras-related protein rap-1b precursor	9	C:GO:0005911; F:GO:0005525; P:GO:0008283; F:GO:0005515; C:GO:0005829; P:GO:0060026; P:GO:0007264; F:GO:0019003; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Ancylostoma caninum	dual specificity mitogen-activated protein ki-se ki-se 4	15	P:GO:0007257; P:GO:0043525; F:GO:0004713; C:GO:0005829; F:GO:0004674; C:GO:0032839; P:GO:0001934; P:GO:0048263; F:GO:0008545; C:GO:0033267; P:GO:0045740; C:GO:0005634; F:GO:0005524; F:GO:0031435; C:GO:0043204	-	EC:2.7.10.0; EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF38 (PANTHER)
Caenorhabditis briggsae	phosphatidylinositol 4-ki-se	7	P:GO:0008219; P:GO:0046854; P:GO:0000003; C:GO:0030660; F:GO:0004430; F:GO:0005515; P:GO:0048015	-	EC:2.7.1.67	IPR000403; IPR001263; IPR011009; IPR015433; IPR016024; IPR018936; G3DSA:3.30.1010.10 (GENE3D), PTHR10048:SF15 (PANTHER)
Caenorhabditis elegans	dap (death associated protein ki-se) like ki-se family member (dlk-1)	1	F:GO:0005515	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	C:GO:0016021	-		-
	-	0				-
	-	0				-

Gallus gallus	chromosome 14 open reading frame 102	1	F:GO:0005488	-		IPR013633; PTHR13471 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	3	F:GO:0051537; F:GO:0046872; F:GO:0009055	-		-
Caenorhabditis briggsae	loc100135354 protein	4	C:GO:0005764; P:GO:0006810; P:GO:0040010; C:GO:0016020	-		PTHR13146 (PANTHER), SignalP (SIGNALP)
	-	0				-
Brugia malayi	guanine nucleotide exchange factor for ras-like gtpases n-termi-l motif family protein	3	C:GO:0005622; F:GO:0030234; P:GO:0007264	-		IPR000651; IPR008937; PTHR23113:SF22 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-kgb-1 protein	3	F:GO:0005515; F:GO:0004674; F:GO:0000166	-	EC:2.7.11.0	PTHR11295 (PANTHER), PTHR11295:SF62 (PANTHER)
Caenorhabditis elegans	endoplasmic reticulum metallopeptidase 1	5	P:GO:0001541; F:GO:0008233; P:GO:0040011; C:GO:0005783; C:GO:0044425	-		IPR007484; G3DSA:3.40.630.10 (GENE3D), PTHR12147 (PANTHER), SSF53187 (SUPERFAMILY)
	-	0				-
Caenorhabditis sp. PS1010	galactose ki-se	6	P:GO:0006810; P:GO:0006012; P:GO:0046835; F:GO:0000166; F:GO:0004335; C:GO:0005737	-	EC:2.7.1.6	-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Brugia malayi	origin recognition complex subunit 5	0		P:GO:0006260; C:GO:0000808; C:GO:0005634		-
Brugia malayi	#NAME?	0		F:GO:0016813; C:GO:0005737; F:GO:0016403; F:GO:0016787		G3DSA:3.75.10.10 (GENE3D), PTHR12737 (PANTHER), PTHR12737:SF4 (PANTHER)
	-	0				-
	-	0				-
Pan troglodytes	cytochrome c oxidase subunit iv isoform 1	7	P:GO:0007584; F:GO:0005515; C:GO:0005751; C:GO:0016021; C:GO:0005634; F:GO:0004129; P:GO:0006091	-	EC:1.9.3.1	IPR004203; PTHR10707 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-ztf-4 protein	1	F:GO:0005515	-		PTHR13968 (PANTHER), PTHR13968:SF1 (PANTHER)

	-	0				IPR002223; PTHR10083 (PANTHER), PTHR10083:SF39 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	proline oxidase	2	P:GO:0009064; P:GO:0042331	-		-
Caenorhabditis briggsae	acetyl-coenzyme a acyltransferase 2	3	P:GO:0006695; C:GO:0005739; F:GO:0003988	-	EC:2.3.1.16	IPR002155; IPR016038; IPR016039; IPR020610; IPR020613; IPR020615; IPR020616; IPR020617; PTHR18919:SF10 (PANTHER)
Caenorhabditis briggsae	acetyl-coenzyme a acyltransferase 2	3	P:GO:0006695; C:GO:0005739; F:GO:0003988	-	EC:2.3.1.16	IPR002155; IPR016038; IPR016039; IPR020610; IPR020613; IPR020615; IPR020616; IPR020617; PTHR18919:SF10 (PANTHER)
Caenorhabditis briggsae	calcitonin gene-related peptide-receptor component protein	5	F:GO:0003899; F:GO:0005488; P:GO:0006383; F:GO:0004930; C:GO:0009360	-	EC:2.7.7.6	IPR005574; IPR006590; IPR010997; PTHR15561 (PANTHER)
Caenorhabditis elegans	pan domain containing protein	0				IPR003014
	-	0				-
Homo sapiens	AF370417_1PP13850 [Homo sapiens]	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Ancylostoma ceylanicum	secreted protein 5 precursor	0		P:GO:0006898; C:GO:0005576		-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0004888; C:GO:0016021; F:GO:0003676; F:GO:0004930; F:GO:0008270; F:GO:0003674; C:GO:0005575; C:GO:0005622; P:GO:0007606; P:GO:0008150		IPR000344; SignalP (SIGNALP)
Danio rerio	host cell factor 1	9	C:GO:0071339; P:GO:0006013; P:GO:0043254; P:GO:0045449; F:GO:0042802; F:GO:0004476; F:GO:0008080; C:GO:0070688; C:GO:0005737	-	EC:5.3.1.8	PTHR23244 (PANTHER), PTHR23244:SF36 (PANTHER)
Caenorhabditis briggsae	low-density lipoprotein receptor domain class a containing protein	1	P:GO:0019915	-		IPR002172; PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER)
Caenorhabditis briggsae	low-density lipoprotein receptor domain class a containing protein	1	P:GO:0019915	-		IPR002172; PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER)
Caenorhabditis briggsae	low-density lipoprotein receptor domain class a containing protein	1	P:GO:0019915	-		IPR002172; PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-arr-1 protein	5	P:GO:0007600; P:GO:0007165; P:GO:0045746; P:GO:0007610; P:GO:0040010	-		IPR000698; IPR011021; IPR011022; IPR014752; IPR014753; IPR014756; IPR017864; PTHR11792:SF5 (PANTHER)

Caenorhabditis elegans	briggsae cbr-opt-2 protein	3	P:GO:0006857; C:GO:0005887; F:GO:0005427	-		-
	-	0				-
Caenorhabditis elegans	alpha- -mannosyltransferase	6	P:GO:0009792; P:GO:0002119; C:GO:0005811; P:GO:0040015; P:GO:0040010; F:GO:0016740	-		PTHR12526 (PANTHER), PTHR12526:SF22 (PANTHER), SignalP (SIGNALP), SSF53756 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	calcium dependent protein ki-se	7	C:GO:0005737; C:GO:0005856; C:GO:0005886; F:GO:0005515; F:GO:0004672; P:GO:0009987; F:GO:0000166	-		IPR000719; IPR011009; IPR017441; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR11042 (PANTHER), PTHR11042:SF4 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Adineta vaga	transposase [Adineta vaga]	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	esterase d	2	C:GO:0016023; F:GO:0018738	-	EC:3.1.2.12	IPR000801; IPR014186; G3DSA:3.40.50.1820 (GENE3D), SSF53474 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Mus musculus	ran binding protein 9	9	F:GO:0008565; C:GO:0005875; F:GO:0008536; F:GO:0042393; P:GO:0006606; C:GO:0005813; P:GO:0006461; P:GO:0007020; C:GO:0005634	-		IPR001870; IPR003877; IPR008985; IPR018355; PTHR12864 (PANTHER), PTHR12864:SF1 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-spas-1 protein	12	P:GO:0051013; F:GO:0008017; P:GO:0031117; P:GO:0001578; C:GO:0015630; P:GO:0034214; P:GO:0051260; F:GO:0005524; F:GO:0008568; C:GO:0048471; C:GO:0044430; C:GO:0016020	-	EC:3.6.4.3	-

NADP, mitochondrial isoform 3	isocitrate dehydroge-se	9	F:GO:0051287; F:GO:0004450; P:GO:0006103; P:GO:0055114; F:GO:0000287; P:GO:0006099; P:GO:0006102; C:GO:0005739; P:GO:0006097	-	EC:1.1.1.42	IPR001804; IPR004790; SSF53659 (SUPERFAMILY)
Loa loa	haloacid dehaloge-se-like hydrolase family protein	0		P:GO:0008152; F:GO:0016787; F:GO:0003824		G3DSA:3.40.50.1000 (GENE3D)
Caenorhabditis elegans	f-box and wd-40 domain protein	20	P:GO:0030512; P:GO:0008355; P:GO:0030708; P:GO:0030162; P:GO:0045849; F:GO:0051219; P:GO:0046843; P:GO:0030713; C:GO:0005737; C:GO:0019005; P:GO:0008285; P:GO:0045475; P:GO:0007088; P:GO:0030178; F:GO:0004842; P:GO:0008588; P:GO:0030720; P:GO:0030727; P:GO:0007298; P:GO:0045879	-	EC:6.3.2.19	IPR001680; IPR001810; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; IPR022364; G3DSA:1.20.1280.50 (GENE3D), PTHR22844 (PANTHER), PTHR22844:SF10 (PANTHER)

Caenorhabditis elegans	heavy polypeptide non- isoform cra_a	37	P:GO:0007411; P:GO:0001764; P:GO:0007097; P:GO:0006930; C:GO:0043197; P:GO:0008360; P:GO:0021680; C:GO:0031594; C:GO:0030426; P:GO:0030048; P:GO:0055015; F:GO:0030898; P:GO:0021592; P:GO:0055003; P:GO:0001778; P:GO:0008283; F:GO:0043531; P:GO:0006887; F:GO:0000146; C:GO:0005819; P:GO:0060041; C:GO:0043025; C:GO:0032154; P:GO:0021670; C:GO:0030424; P:GO:0000281; C:GO:0030496; P:GO:0050885;	-		SignalP (SIGNALP)
	-	0				-
Pongo abelii	myosin regulatory light chain mrcl2	0				SignalP (SIGNALP)
Strongylocentrotus purpuratus	zinc finger partial	0		C:GO:0005618; C:GO:0016021; F:GO:0016787; C:GO:0016020; F:GO:0004222; F:GO:0008233; F:GO:0008270; C:GO:0005576		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	F:GO:0003951; P:GO:0008152; F:GO:0005515	-	EC:2.7.1.23	-
	-	0				-
	-	0				-
Loa loa	hypothetical protein LOAG_07599 [Loa loa]	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	ankyrin repeats- partial	1	C:GO:0016021	-		-
	-	0				-

Caenorhabditis briggsae	briggsae cbr-cyn-4 protein	9	P:GO:0006457; P:GO:0040022; F:GO:0005515; P:GO:0000209; C:GO:0005796; F:GO:0004842; C:GO:0005634; F:GO:0003755; C:GO:0000151	-	EC:6.3.2.19; EC:5.2.1.8	IPR002130; IPR015891; PTHR11071 (PANTHER), PTHR11071:SF42 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	hemopexin family protein	0		F:GO:0004222; F:GO:0016787; F:GO:0008270; F:GO:0008237; C:GO:0031012; F:GO:0008233; P:GO:0006508; P:GO:0008152; F:GO:0046872		PTHR10201 (PANTHER), PTHR10201:SF5 (PANTHER)
	-	0				-
Caenorhabditis elegans	ras family protein	12	P:GO:0050774; P:GO:0032402; C:GO:0043231; P:GO:0009306; P:GO:0007015; P:GO:0008360; P:GO:0007264; P:GO:0007155; P:GO:0006888; F:GO:0003924; C:GO:0005811; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Caenorhabditis elegans	alpha beta hydrolase	0		F:GO:0016787		IPR000463; G3DSA:3.40.50.1820 (GENE3D), SSF53474 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	nucleolar complex protein 2 homolog	10	P:GO:0000003; P:GO:0016246; F:GO:0005515; P:GO:0040007; P:GO:0006898; P:GO:0019915; P:GO:0009792; P:GO:0002119; P:GO:0051729; C:GO:0005634	-		IPR005343; PTHR12687:SF4 (PANTHER)
Loa loa	briggsae cbr-tag-76 protein	1	F:GO:0003676	-		-
Caenorhabditis briggsae	tubulin folding cofactor e-like protein family member (coel-1)	0		F:GO:0005515		G3DSA:3.80.10.10 (GENE3D), PTHR15140 (PANTHER), SSF52058 (SUPERFAMILY)
Caenorhabditis briggsae	esterase d	1	F:GO:0016788	-		-
Caenorhabditis elegans	cub domain containing protein	0		F:GO:0004872; F:GO:0016787		IPR000859
Caenorhabditis elegans	parasitic stage specific protein 1	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				IPR003582; PTHR21724 (PANTHER)

Caenorhabditis briggsae	atp-binding sub-family a member 3	9	P:GO:0012501; C:GO:0042599; P:GO:0043652; C:GO:0016021; F:GO:0042626; C:GO:0005624; F:GO:0005524; P:GO:0042493; C:GO:0005886	-		G3DSA:3.40.50.300 (GENE3D), PTHR19229 (PANTHER), PTHR19229:SF18 (PANTHER), SSF52540 (SUPERFAMILY)
Haemonchus contortus	syntaxin binding protein-	1	P:GO:0006904	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR001534
Caenorhabditis elegans	histone deacetylase 6	0		C:GO:0048471; C:GO:0000118; P:GO:0006350; P:GO:0090035; P:GO:0006515; C:GO:0005881; P:GO:0010870; P:GO:0051789; P:GO:0051788; P:GO:0006511; P:GO:0016568; P:GO:0043242; P:GO:0043241; P:GO:0009967; F:GO:0042903; P:GO:0006476; P:GO:0000209; F:GO:0016787; C:GO:0031252; P:GO:0010033; P:GO:0070301; F:GO:0051879; F:GO:0008270; F:GO:0043014; P:GO:0070848; C:GO:0005875; P:GO:0070846;		-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	scp-like extracellular protein	1	C:GO:0005576	-		IPR001283; IPR014044; PTHR10334:SF8 (PANTHER)
Caenorhabditis elegans	acyl-coenzyme a dehydroge-se member 9	7	P:GO:0009792; F:GO:0016491; P:GO:0040010; P:GO:0055114; P:GO:0000003; P:GO:0006898; F:GO:0050660	-		PTHR10909 (PANTHER), PTHR10909:SF9 (PANTHER)
Caenorhabditis elegans	protein ki-se domain containing protein	4	P:GO:0006468; F:GO:0005524; P:GO:0040011; F:GO:0004674	-	EC:2.7.11.0	PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
Caenorhabditis elegans	nematode cuticle collagen n-termi-l domain containing protein	0		C:GO:0016021; F:GO:0042302		IPR008160; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER)

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	9	C:GO:0016023; C:GO:0005886; P:GO:0010053; P:GO:0040010; F:GO:0004558; P:GO:0040011; C:GO:0016021; C:GO:0005783; P:GO:0009311	-	EC:3.2.1.20	IPR004888; PTHR10412 (PANTHER)
	-	0				IPR011547; PTHR11814 (PANTHER), PTHR11814:SF25 (PANTHER)
Caenorhabditis elegans	ubiquitin carboxyl-termi-l hydrolase family protein	5	C:GO:0043231; F:GO:0008234; P:GO:0044267; C:GO:0044444; C:GO:0016020	-		IPR001394; IPR018200; PTHR10420 (PANTHER), PTHR10420:SF62 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis elegans	set domain containing 3	0		F:GO:0003674		IPR015353; G3DSA:3.90.1410.10 (GENE3D), PTHR13271 (PANTHER), SSF82199 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	dead h box polypeptide rig-i	7	F:GO:0043021; F:GO:0004386; F:GO:0003677; C:GO:0005622; F:GO:0005515; F:GO:0005524; F:GO:0008270	-		IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR14074 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
Teladorsagia circumcincta	fmrf-like peptide family member (flp-11)	1	P:GO:0007218	-		-
Caenorhabditis briggsae	abnormal go-d development family member (gon-2)	4	P:GO:0007067; P:GO:0006810; C:GO:0016020; P:GO:0008406	-		PTHR13800 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	nuc173 domain-containing protein	0		F:GO:0005488; P:GO:0008150		IPR012978; PTHR21576 (PANTHER), PTHR21576:SF2 (PANTHER)
	-	0				IPR001879
Callithrix jacchus	ribosomal protein l4	5	F:GO:0003735; F:GO:0003723; F:GO:0005515; C:GO:0022625; P:GO:0006414	-		IPR002136; IPR013000; G3DSA:3.40.1370.10 (GENE3D), PTHR19431 (PANTHER)

Chlorocebus aethiops	heavy polypeptide non-muscle	44	P:GO:0001525; C:GO:0030863; P:GO:0008360; C:GO:0031594; P:GO:0030048; F:GO:0030898; P:GO:0051295; C:GO:0005913; P:GO:0016337; F:GO:0043531; P:GO:0032796; P:GO:0015031; C:GO:0001772; P:GO:0050900; P:GO:0007229; C:GO:0005829; P:GO:0007520; F:GO:0000146; P:GO:0006509; P:GO:0043534; C:GO:0008305; C:GO:0005819; C:GO:0001726; P:GO:0007132; F:GO:0005391; C:GO:0032154; P:GO:0000904; P:GO:0001768;	-	EC:3.6.3.9	IPR002928
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	solute carrier family 25 member 5	10	P:GO:0055085; P:GO:0060547; C:GO:0016021; C:GO:0005743; C:GO:0005741; F:GO:0005471; P:GO:0015867; F:GO:0005515; P:GO:0015866; P:GO:0051935	-		-
	-	0				-
Caenorhabditis elegans	fatty acid desaturase family protein	9	P:GO:0007283; P:GO:0006633; F:GO:0004768; F:GO:0042284; C:GO:0005886; F:GO:0005515; P:GO:0055114; C:GO:0016021; C:GO:0005739	-	EC:1.14.19.1	IPR005804; IPR013866; PTHR12879 (PANTHER)
Caenorhabditis elegans	glucose transporter	3	C:GO:0016020; F:GO:0022891; P:GO:0006810	-		IPR003663; IPR005828; IPR005829; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11600 (PANTHER), PTHR11600:SF107 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis briggsae	briggsae cbr-ltd-1 protein	1	F:GO:0008270	-		IPR002931
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	erin family member (cdh-6)	0		P:GO:0007218; F:GO:0005509; P:GO:0007156; F:GO:0004930; P:GO:0007155; C:GO:0016021; C:GO:0016020; C:GO:0005886		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	nitric oxide synthase-interacting protein	4	P:GO:0051001; C:GO:0005829; C:GO:0005634; F:GO:0005515	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	kiaa0999 protein	5	P:GO:0006468; F:GO:0005515; F:GO:0005524; F:GO:0000287; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22971 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-ada-2 protein	8	P:GO:0009792; P:GO:0010171; P:GO:0040027; P:GO:0040010; P:GO:0000003; P:GO:0008340; P:GO:0040011; P:GO:0006898	-		PTHR12374 (PANTHER)
	-	0				IPR018610
	-	0				-
	-	0				-
Caenorhabditis elegans	protein disulfide isomerase family member 4	5	C:GO:0005788; P:GO:0045454; F:GO:0005515; F:GO:0003756; P:GO:0009306	-	EC:5.3.4.1	IPR005746; IPR005788; IPR012335; IPR012336; IPR013766; IPR017936; IPR017937; PTHR18929 (PANTHER), SignalP (SIGNALP)
	-	0				PR01217 (PRINTS)
Teladorsagia circumcincta	soluble calcium-activated nucleotidase 1	5	P:GO:0040010; P:GO:0008340; F:GO:0005515; F:GO:0016462; C:GO:0005789	-		-
Teladorsagia circumcincta	soluble calcium-activated nucleotidase 1	5	P:GO:0040010; P:GO:0008340; F:GO:0005515; F:GO:0016462; C:GO:0005789	-		SignalP (SIGNALP)

Teladorsagia circumcincta	soluble calcium-activated nucleotidase 1	4	F:GO:0016787; P:GO:0008340; P:GO:0040010; F:GO:0005515	-		IPR009283
Teladorsagia circumcincta	calcium activated nucleotidase 1	5	P:GO:0040010; P:GO:0008340; F:GO:0005515; F:GO:0016462; C:GO:0005789	-		-
Teladorsagia circumcincta	calcium activated nucleotidase isoform cra_b	6	P:GO:0040010; P:GO:0008340; F:GO:0017110; F:GO:0005515; C:GO:0005789; P:GO:0009191	-	EC:3.6.1.6	-
Teladorsagia circumcincta	calcium activated nucleotidase 1	5	P:GO:0040010; P:GO:0008340; F:GO:0005515; F:GO:0016462; C:GO:0005789	-		-
Callithrix jacchus	calcium-regulated heat stable protein 1	5	F:GO:0019902; P:GO:0019722; F:GO:0003677; C:GO:0005829; P:GO:0006355	-		-
Caenorhabditis briggsae	uncharacterized transposase-like protein	0		F:GO:0046872; P:GO:0055114; F:GO:0009055; F:GO:0016491; F:GO:0020037; F:GO:0005506; F:GO:0004497		-
	-	0				-
Caenorhabditis briggsae	major facilitator superfamily protein	1	P:GO:0055085	-		-
	-	0				-
Caenorhabditis briggsae	protein ki-se domain containing protein	7	P:GO:0006468; P:GO:0040018; F:GO:0005515; F:GO:0004713; P:GO:0040010; F:GO:0005524; P:GO:0000003	-	EC:2.7.10.0	IPR000719; IPR001245; IPR011009; IPR020685; IPR020764; G3DSA:1.10.510.10 (GENE3D)
Caenorhabditis briggsae	serine threonine phosphatase	3	P:GO:0019915; P:GO:0000003; F:GO:0004721	-	EC:3.1.3.16	IPR006186; G3DSA:3.60.21.10 (GENE3D), SSF56300 (SUPERFAMILY)

Kocuria rhizophila DC2201	subfamily member 6	0		P:GO:0006950; P:GO:0060710; C:GO:0005634; F:GO:0003677; P:GO:0045892; C:GO:0005737; C:GO:0048471; F:GO:0031072; C:GO:0005575; P:GO:0043154; P:GO:0045109; F:GO:0016564; F:GO:0051087; F:GO:0005515; P:GO:0006457; P:GO:0008150; F:GO:0051082		IPR001623; IPR015609; PTHR11821:SF66 (PANTHER)
Caenorhabditis elegans	glutami-se	6	F:GO:0004359; P:GO:0007268; P:GO:0006543; P:GO:0002087; P:GO:0007610; C:GO:0005739	-	EC:3.5.1.2	-
	-	0				-
Caenorhabditis briggsae	ribosomal protein l3	10	P:GO:0040010; F:GO:0003723; C:GO:0005730; F:GO:0003735; P:GO:0000003; P:GO:0006414; P:GO:0002119; F:GO:0005515; P:GO:0009792; C:GO:0022625	-		-
Brugia malayi	calcium alpha subunit family member (cca-1)	7	P:GO:0051899; P:GO:0045760; P:GO:0043051; P:GO:0006816; P:GO:0055085; C:GO:0005891; F:GO:0008332	-		IPR005445; IPR005821; PTHR10037 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	rab family member (rab-3)	9	P:GO:0016192; P:GO:0048790; P:GO:0007264; C:GO:0008021; F:GO:0004767; F:GO:0003924; C:GO:0048786; P:GO:0015031; F:GO:0005525	-	EC:3.1.4.12; EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001806; IPR013753; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF304 (PANTHER), SSF52540 (SUPERFAMILY)

Loa loa	protein-tyrosine phosphatase	11	P:GO:0006470; P:GO:0007417; C:GO:0030424; F:GO:0004871; P:GO:0040027; F:GO:0004725; P:GO:0040026; P:GO:0008045; P:GO:0007424; C:GO:0045177; C:GO:0016020	-	EC:3.1.3.48	IPR000242; IPR000387; IPR016130; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF75 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis briggsae	cell division protein ki-se 5	25	C:GO:0030424; P:GO:0007049; F:GO:0043125; C:GO:0030425; F:GO:0008353; P:GO:0010468; P:GO:0051932; P:GO:0031175; P:GO:0043525; P:GO:0000003; P:GO:0051301; F:GO:0005176; P:GO:0048489; F:GO:0005524; F:GO:0030549; C:GO:0031594; F:GO:0050321; C:GO:0043025; C:GO:0030426; F:GO:0004693; P:GO:0009792; C:GO:0005737; C:GO:0016020; C:GO:0005634; P:GO:0006468	-	EC:2.7.11.23; EC:2.7.11.26; EC:2.7.11.22	IPR000719; IPR011009; IPR017441; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF110 (PANTHER)
Caenorhabditis elegans	briggsae cbr-smgl-1 protein	0				-
	-	0				-
Caenorhabditis briggsae	protein-tyrosine phosphatase containing protein	3	P:GO:0016311; F:GO:0004721; P:GO:0009792	-	EC:3.1.3.16	-
	-	0				-
	-	0				-
	-	0				-
Loa loa	briggsae cbr-dpy-22 protein	10	P:GO:0040010; P:GO:0018991; P:GO:0045449; P:GO:0040035; P:GO:0010171; P:GO:0040026; P:GO:0040011; P:GO:0009792; P:GO:0040018; C:GO:0005634	-		-
Brugia malayi	hypothetical protein Bm1_05665 [Brugia malayi]	0				SignalP (SIGNALP)
Caenorhabditis elegans	disks large-associated protein 1	0		P:GO:0007267; P:GO:0019915		IPR005026; PTHR12353 (PANTHER), PTHR12353:SF5 (PANTHER)

Caenorhabditis briggsae	disks large-associated protein 1	0		P:GO:0006508; P:GO:0007267; F:GO:0008237; P:GO:0007480; P:GO:0008152; F:GO:0016787; F:GO:0005515; P:GO:0019915		IPR005026; PTHR12353 (PANTHER), PTHR12353:SF5 (PANTHER)
Caenorhabditis elegans	disks large-associated protein 1	0		P:GO:0007267; P:GO:0019915		IPR005026; PTHR12353 (PANTHER), PTHR12353:SF5 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Turnip ringspot virus	polyprotein	3	P:GO:0044238; P:GO:0043170; F:GO:0016787	-		IPR001205; SSF56672 (SUPERFAMILY)
	-	0				-
Loa loa	briggsae cbr-dnc-2 protein	5	F:GO:0042802; C:GO:0005856; P:GO:0007017; P:GO:0006996; P:GO:0000279	-		-
Caenorhabditis briggsae	Hypothetical protein CBG01435 [Caenorhabditis briggsae]	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis briggsae	malate dehydroge-se	4	P:GO:0018991; P:GO:0008152; F:GO:0016491; P:GO:0040011	-		IPR003767; G3DSA:1.10.1530.10 (GENE3D), G3DSA:3.30.1370.60 (GENE3D), SignalP (SIGNALP)
Caenorhabditis briggsae	c family member (clr-1)	11	P:GO:0006470; P:GO:0040037; P:GO:0040010; P:GO:0018991; P:GO:0040002; P:GO:0010171; P:GO:0002119; P:GO:0040017; F:GO:0005001; P:GO:0002009; C:GO:0005886	-		IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF43 (PANTHER), SSF52799 (SUPERFAMILY)
	-	0				-
Apis mellifera	dopa decarboxylase	1	F:GO:0016831	-	EC:4.1.1.0	IPR002129; IPR015421; IPR015424; PTHR11999:SF11 (PANTHER)
	-	0				-
Brugia malayi	notch-like transmembrane receptor	0		P:GO:0007219; P:GO:0030154; F:GO:0004872; P:GO:0007275; C:GO:0016021; C:GO:0016020		IPR010660; IPR011656; PR01983 (PRINTS)
Caenorhabditis briggsae	briggsae cbr-ego-1 protein	0		F:GO:0003968; P:GO:0009792; F:GO:0005515		IPR007855
	-	0				-
Caenorhabditis elegans	immune- lectin-like receptor 3	1	P:GO:0040010	-		IPR001304; IPR016186; IPR016187; PTHR22802 (PANTHER), PTHR22802:SF6 (PANTHER)

Pongo abelii	marcks-like 1	4	P:GO:0008284; F:GO:0005516; P:GO:0016192; C:GO:0005886	-		IPR002101
Caenorhabditis briggsae	sodium calcium	16	P:GO:0002026; P:GO:0055085; C:GO:0030315; F:GO:0005432; F:GO:0031072; F:GO:0005516; P:GO:0045214; C:GO:0016021; C:GO:0005901; P:GO:0051924; P:GO:0000003; P:GO:0002028; C:GO:0005624; P:GO:0007204; P:GO:0007154; P:GO:0009792	-		IPR004836; IPR004837; PTHR11878 (PANTHER), PTHR11878:SF4 (PANTHER)
Caenorhabditis elegans	pdcd (mammalian cell death protein) homolog family member (pdcd-2)	8	C:GO:0005737; P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0040010; C:GO:0016021; P:GO:0006898; F:GO:0008270	-		IPR019013; SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		IPR002919; IPR013032; G3DSA:2.10.25.10 (GENE3D), PTHR23259 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0003723; P:GO:0009451; P:GO:0001522; F:GO:0009982		-
Caenorhabditis elegans	cdk5 regulatory subunit associated protein 1	7	P:GO:0045736; P:GO:0009451; F:GO:0051536; P:GO:0009058; F:GO:0016874; P:GO:0007399; F:GO:0019901	-		IPR002792; IPR005839; G3DSA:3.80.30.20 (GENE3D)
Caenorhabditis elegans	hypothetical protein T12D8.9 [Caenorhabditis elegans]	0				-
Macaca mulatta	serpin peptidase clade h (heat shock protein 47) member (collagen binding protein 1)	9	C:GO:0005788; C:GO:0005793; F:GO:0004867; F:GO:0005518; P:GO:0032964; P:GO:0030199; P:GO:0006986; F:GO:0051082; P:GO:0051604	-		IPR000215; G3DSA:2.30.39.10 (GENE3D), G3DSA:3.30.497.10 (GENE3D), PTHR11461:SF27 (PANTHER)
Caenorhabditis elegans	developmentally-regulated gtp-binding protein 2	5	F:GO:0005525; C:GO:0005622; C:GO:0016021; P:GO:0015684; F:GO:0015093	-		IPR004095; IPR012676; PTHR11702 (PANTHER), PTHR11702:SF7 (PANTHER)

Caenorhabditis briggsae	mitochondrial ornithine transporter 1	5	P:GO:0000066; F:GO:0000064; P:GO:0006520; P:GO:0000050; C:GO:0016020	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF53 (PANTHER)
Loa loa	upf0505 protein c16orf62-like protein	0		F:GO:0003674; P:GO:0008150		PTHR13673 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	clathrin-like protein	7	F:GO:0009982; F:GO:0030515; F:GO:0005515; C:GO:0031429; P:GO:0016192; P:GO:0006886; C:GO:0030131	-	EC:5.4.99.12	IPR001392; IPR008968; IPR011012; IPR018240; IPR022775; G3DSA:2.60.40.1170 (GENE3D), G3DSA:3.30.450.60 (GENE3D), PTHR11998 (PANTHER), PTHR11998:SF4 (PANTHER)
Tomato ringspot virus	r--dependent r- polymerase	1	F:GO:0016787	-		IPR001205; IPR007094; G3DSA:3.30.70.270 (GENE3D), SSF56672 (SUPERFAMILY)
Caenorhabditis elegans	ubiquitin specific protease 48	2	F:GO:0016787; C:GO:0044464	-		IPR001394; IPR018200; PTHR10420 (PANTHER), PTHR10420:SF45 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis elegans	peptidase family m3 containing protein	6	F:GO:0004222; P:GO:0045449; F:GO:0003702; P:GO:0006367; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	SignalP (SIGNALP)
	-	0				-
	-	0				-
Pan troglodytes	guanine nucleotide-binding protein g g g subunit gamma-5-like	0				-
	-	0				-
Caenorhabditis elegans	dnl-type zinc finger protein	3	P:GO:0000003; C:GO:0005739; P:GO:0010171	-		-
	-	0				-
	-	0				-
Loa loa	eukaryotic translation initiation factor 2 subunit 2	11	F:GO:0046872; P:GO:0006413; F:GO:0003723; F:GO:0005515; P:GO:0055085; C:GO:0005850; F:GO:0003743; C:GO:0016021; C:GO:0005829; F:GO:0015293; P:GO:0006814	-		IPR002735; IPR016189; IPR016190; G3DSA:3.30.30.50 (GENE3D), PTHR23001 (PANTHER)
Loa loa	mitogen-activated protein ki-se ki-se ki-se 2	1	F:GO:0016301	-		IPR000719; IPR011009; IPR015748; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22986 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				IPR018486
	-	0				-

Caenorhabditis elegans	briggsae cbr-npp-12 protein	3	C:GO:0005643; F:GO:0046983; P:GO:0006810	-		PTHR23019 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	erv1 alr family protein	4	P:GO:0045454; P:GO:0055114; F:GO:0016972; C:GO:0044464	-	EC:1.8.3.2	IPR006863; IPR017905; PTHR22897 (PANTHER), PTHR22897:SF4 (PANTHER)
Caenorhabditis briggsae	proteasome regulatory non-atpase-like protein	0		F:GO:0005488; C:GO:0000502		PTHR10678 (PANTHER), PTHR10678:SF2 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	ribosomal protein l23a-like	14	P:GO:0006412; P:GO:0040010; C:GO:0005840; P:GO:0051726; P:GO:0040002; F:GO:0019843; F:GO:0003735; P:GO:0040035; P:GO:0002119; F:GO:0000166; P:GO:0006898; P:GO:0009792; P:GO:0040018; P:GO:0016246	-	EC:3.6.5.3	SignalP (SIGNALP)
Brugia malayi	ribosomal protein l23a-like	14	P:GO:0006412; P:GO:0040010; C:GO:0005840; P:GO:0051726; P:GO:0040002; F:GO:0019843; F:GO:0003735; P:GO:0040035; P:GO:0002119; F:GO:0000166; P:GO:0006898; P:GO:0009792; P:GO:0040018; P:GO:0016246	-	EC:3.6.5.3	-
Brugia malayi	ribosomal protein l23a-like	14	P:GO:0006412; P:GO:0040010; C:GO:0005840; P:GO:0051726; P:GO:0040002; F:GO:0019843; F:GO:0003735; P:GO:0040035; P:GO:0002119; F:GO:0000166; P:GO:0006898; P:GO:0009792; P:GO:0040018; P:GO:0016246	-	EC:3.6.5.3	-

Brugia malayi	ribosomal protein l23a-like	14	P:GO:0006412; P:GO:0040010; C:GO:0005840; P:GO:0051726; P:GO:0040002; F:GO:0019843; F:GO:0003735; P:GO:0040035; P:GO:0002119; F:GO:0000166; P:GO:0006898; P:GO:0009792; P:GO:0040018; P:GO:0016246	-	EC:3.6.5.3	SignalP (SIGNALP)
Brugia malayi	ribosomal protein l23a-like	14	P:GO:0006412; P:GO:0040010; C:GO:0005840; P:GO:0051726; P:GO:0040002; F:GO:0019843; F:GO:0003735; P:GO:0040035; P:GO:0002119; F:GO:0000166; P:GO:0006898; P:GO:0009792; P:GO:0040018; P:GO:0016246	-	EC:3.6.5.3	-
Loa loa	ras-related protein rab-	3	P:GO:0015031; F:GO:0005525; P:GO:0007264	-		-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-fer-1 protein	0		C:GO:0016021		PTHR12546 (PANTHER), PTHR12546:SF5 (PANTHER)
Brugia malayi	rho guanine nucleotide exchange factor 7	8	C:GO:0005829; P:GO:0007264; P:GO:0043615; F:GO:0005085; C:GO:0005925; F:GO:0005515; C:GO:0030426; P:GO:0008624	-		PTHR22826 (PANTHER), PTHR22826:SF18 (PANTHER)
	-	0				IPR000875
Caenorhabditis elegans	bile acid beta-glucosidase	7	P:GO:0016142; P:GO:0006680; C:GO:0005886; P:GO:0008206; F:GO:0004348; C:GO:0016021; F:GO:0008422	-	EC:3.2.1.45; EC:3.2.1.21	IPR006775; PTHR12654 (PANTHER)
Caenorhabditis briggsae	db module family protein	0				PTHR21679 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	cg10671 cg10671-pa	1	P:GO:0000003	-		IPR019388; PTHR23129 (PANTHER), SignalP (SIGNALP)

Ancylostoma ceylanicum	cysteine protei-se	7	P:GO:0009792; P:GO:0002119; F:GO:0008233; F:GO:0005515; P:GO:0040011; P:GO:0040007; P:GO:0006898	-		IPR000169; IPR000668; IPR013128; IPR015643; G3DSA:3.90.70.10 (GENE3D), SignalP (SIGNALP), SSF54001 (SUPERFAMILY)
Ancylostoma ceylanicum	cysteine protei-se	7	P:GO:0009792; P:GO:0002119; F:GO:0008233; F:GO:0005515; P:GO:0040011; P:GO:0040007; P:GO:0006898	-		IPR000169; IPR000668; IPR013128; IPR015643; G3DSA:3.90.70.10 (GENE3D), SignalP (SIGNALP), SSF54001 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG15709 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	briggsae cbr-jph-1 protein	0				-
	-	0				-
	-	0				IPR009311; SignalP (SIGNALP)
Homo sapiens	coatomer protein subunit epsilon	8	C:GO:0030126; C:GO:0005829; P:GO:0006890; P:GO:0006891; F:GO:0005515; P:GO:0048205; F:GO:0005198; P:GO:0015031	-		IPR006822
Brugia malayi	short-chain dehydroge-se reductase sdr	5	C:GO:0016021; P:GO:0055114; F:GO:0016491; P:GO:0006508; F:GO:0005515	-		IPR002198; IPR016040; PTHR19410:SF38 (PANTHER), SSF51735 (SUPERFAMILY)
Loa loa	hypothetical protein LOAG_04062 [Loa loa]	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-atm-1 protein	2	C:GO:0000785; F:GO:0016740	-		IPR003152
	-	0				-
	-	0				-
Homo sapiens	filamin beta (actin binding protein 278) isoform cra_a	11	C:GO:0030018; P:GO:0030154; P:GO:0007517; P:GO:0007016; F:GO:0003779; C:GO:0005886; C:GO:0005938; P:GO:0007165; C:GO:0016021; C:GO:0015629; P:GO:0030036	-		-
Caenorhabditis elegans	histone deacetylase	8	P:GO:0016568; P:GO:0006476; P:GO:0006355; F:GO:0033558; F:GO:0016564; F:GO:0019899; C:GO:0005654; P:GO:0014003	-		IPR000286; PTHR10625:SF23 (PANTHER), SSF52768 (SUPERFAMILY)

Strongylocentrotus purpuratus	aldehyde dehydroge-se 1 member b1	4	P:GO:0005975; C:GO:0005759; F:GO:0004029; P:GO:0055114	-	EC:1.2.1.3	IPR015590; IPR016161; IPR016162; PTHR11699:SF46 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein F17H10.1 [Caenorhabditis elegans]	1	P:GO:0009792	-		-
Caenorhabditis briggsae	nucleoside diphosphate-linked moiety x motif 13	0		F:GO:0046872; C:GO:0005739; F:GO:0003674; P:GO:0008152; F:GO:0016787; P:GO:0008150		-
	-	0				-
Loa loa	porcupine homolog	0		F:GO:0008415; F:GO:0016740; P:GO:0007275; C:GO:0016021; C:GO:0016020; P:GO:0008150; P:GO:0016055; P:GO:0007367		IPR004299; PTHR13906 (PANTHER), PTHR13906:SF1 (PANTHER)
Caenorhabditis briggsae	protein of hypothetical function duf28	0				-
Ancylostoma caninum	secreted protein asp-2	0		F:GO:0009055; P:GO:0019646; P:GO:0019915; C:GO:0005576		IPR001283; IPR002413; IPR014044; PTHR10334:SF11 (PANTHER)
Loa loa	groucho protein	7	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0001703; P:GO:0000003; P:GO:0040011; P:GO:0040007	-		IPR005617
Loa loa	groucho tle n-termi-l q-rich domain containing protein	0		P:GO:0010171; C:GO:0005634; P:GO:0000003; P:GO:0009792; P:GO:0002119; P:GO:0009790; P:GO:0001703; P:GO:0040011; P:GO:0007369; P:GO:0040007; P:GO:0045449		IPR005617
Loa loa	groucho tle n-termi-l q-rich domain containing protein	0		P:GO:0010171; C:GO:0005634; P:GO:0000003; P:GO:0009792; P:GO:0002119; P:GO:0009790; P:GO:0001703; P:GO:0040011; P:GO:0007369; P:GO:0040007; P:GO:0045449		IPR005617

Caenorhabditis elegans	briggsae cbr-gck-4 protein	10	P:GO:0040010; P:GO:0000910; F:GO:0005524; P:GO:0010171; P:GO:0032879; P:GO:0002119; P:GO:0040011; P:GO:0010800; P:GO:0008283; F:GO:0042801	-		IPR000719; IPR001245; IPR011009; G3DSA:1.10.510.10 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF67 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	aspartyl-tr- synthetase	5	F:GO:0003676; C:GO:0005739; P:GO:0006422; F:GO:0005524; F:GO:0004815	-	EC:6.1.1.12	SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0005515		-
Brugia malayi	zinc knuckle family protein	2	F:GO:0008270; F:GO:0003676	-		-
Equus caballus	bub1 budding uninhibited by benzimidazoles 1 homolog	0		P:GO:0051983; P:GO:0051301; P:GO:0007067; P:GO:0006468; C:GO:0005634; P:GO:0007094; P:GO:0007063; C:GO:0005694; P:GO:0007093; F:GO:0005524; P:GO:0006915; C:GO:0000777; C:GO:0000776; C:GO:0000775; F:GO:0016301; P:GO:0007049; F:GO:0004674; F:GO:0004672; P:GO:0009790; P:GO:0071173; C:GO:0005816; P:GO:0044419; F:GO:0000166; P:GO:0007059; C:GO:0000780; F:GO:0016740; F:GO:0005515		IPR015661
Caenorhabditis elegans	related to yeast vacuolar protein sorting factor family member (vps-34)	3	F:GO:0004428; F:GO:0016773; P:GO:0009987	-	EC:2.7.1.0	IPR001263; IPR015433; IPR016024; PTHR10048:SF7 (PANTHER)

Caenorhabditis elegans	briggsae cbr-srf-3 protein	5	P:GO:0015785; P:GO:0015788; C:GO:0030173; F:GO:0005462; F:GO:0005459	-		-
Giardia lamblia P15	Hypothetical protein GLP15_3736 [Giardia lamblia P15]	0		P:GO:0045449; F:GO:0003677		IPR009057; IPR011991
	-	0				-
Caenorhabditis briggsae	af303255_1 guanylate-binding protein	11	P:GO:0007029; C:GO:0016021; P:GO:0051260; P:GO:0000003; F:GO:0042802; C:GO:0005792; P:GO:0007409; F:GO:0003924; C:GO:0044431; C:GO:0005789; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR003191; PTHR10751 (PANTHER), PTHR10751:SF3 (PANTHER)
	-	0				-
	-	0				-
	-	0				IPR014044; SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	protein ki-se family member (kin-32)	0		F:GO:0016740; F:GO:0004674; F:GO:0004672; C:GO:0005925; F:GO:0000166; P:GO:0006468; P:GO:0007172; F:GO:0005524; F:GO:0016301; F:GO:0004713; F:GO:0005515; F:GO:0004871; C:GO:0005856		SignalP (SIGNALP)
Caenorhabditis elegans	focal adhesion ki-se	4	P:GO:0009987; F:GO:0004713; F:GO:0000166; C:GO:0044464	-	EC:2.7.10.0	-
Caenorhabditis briggsae	d- polymerase theta	3	F:GO:0008026; F:GO:0003677; F:GO:0005524	-		G3DSA:3.40.50.300 (GENE3D), PTHR11752 (PANTHER), PTHR11752:SF3 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				PTHR12309 (PANTHER), PTHR12309:SF4 (PANTHER)
	-	0				-
Caenorhabditis elegans	pantothe-te ki-se 4	0		F:GO:0016301; F:GO:0005524; P:GO:0015937; C:GO:0005737; F:GO:0016740; F:GO:0000166; F:GO:0004594		IPR011602; PTHR12280 (PANTHER), PTHR12280:SF3 (PANTHER)

Caenorhabditis briggsae	briggsae cbr-dyb-1 protein	12	F:GO:0008092; F:GO:0005277; P:GO:0015870; C:GO:0016014; F:GO:0008270; F:GO:0005509; C:GO:0045202; P:GO:0007271; P:GO:0007529; P:GO:0046716; P:GO:0040017; C:GO:0005737	-		-
Loa loa	hypothetical protein LOAG_02637 [Loa loa]	0				-
Caenorhabditis briggsae	Hypothetical protein CBG00463 [Caenorhabditis briggsae]	0		F:GO:0008270; C:GO:0005622		IPR015880
synthetic construct	protein ki-se chk2	0		P:GO:0000003; P:GO:0006468; C:GO:0005634; P:GO:0042770; F:GO:0005524; F:GO:0046872; P:GO:0007126; F:GO:0016301; P:GO:0006974; P:GO:0007049; F:GO:0004674; P:GO:0009792; P:GO:0000077; P:GO:0010332; F:GO:0004672; F:GO:0000166; P:GO:0008630; C:GO:0000781; C:GO:0016605; P:GO:0045132; F:GO:0005515; F:GO:0016740; C:GO:0005575		IPR000253; IPR008984
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-tag-83 protein	0				IPR014020; G3DSA:2.60.40.1110 (GENE3D)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-lad-2 protein	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F43D9.1 [Caenorhabditis elegans]	2	F:GO:0008158; C:GO:0016020	-		IPR003392; PTHR10796 (PANTHER), PTHR10796:SF13 (PANTHER)

Caenorhabditis briggsae	briggsae cbr-mys-1 protein	15	P:GO:0000003; P:GO:0045941; F:GO:0005515; P:GO:0040027; P:GO:0040010; P:GO:0006898; P:GO:0006355; F:GO:0016740; C:GO:0005737; P:GO:0009792; P:GO:0002009; C:GO:0043234; P:GO:0010171; C:GO:0044451; P:GO:0016568	-		IPR016197; G3DSA:2.30.30.270 (GENE3D), PTHR10615 (PANTHER), PTHR10615:SF30 (PANTHER), PF11717 (PFAM)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	probable tr- (uracil-o -)-methyltransferase-like	0		F:GO:0016740; P:GO:0032259; F:GO:0008168; P:GO:0008033; F:GO:0003676; C:GO:0005737; F:GO:0008270; F:GO:0003674; C:GO:0005575; P:GO:0008150		IPR000571; PTHR21210 (PANTHER)
	-	0				IPR000276; SignalP (SIGNALP)
Brugia malayi	zinc c2h2 type family protein	0		F:GO:0003676; F:GO:0046872; F:GO:0008270; F:GO:0005515; C:GO:0005622		IPR011333
Loa loa	hypothetical protein LOAG_09500 [Loa loa]	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	high incidence of males (increased x chromosome loss) family member (him-4)	0		F:GO:0005509		IPR013783; PTHR19897 (PANTHER), PTHR19897:SF8 (PANTHER)
	-	0				-
Loa loa	melibiase family protein	7	C:GO:0000785; F:GO:0004553; P:GO:0005975; F:GO:0043169; P:GO:0006333; F:GO:0003682; C:GO:0005634	-	EC:3.2.1.0	IPR002241; IPR013785; IPR017853; PTHR11452 (PANTHER)
	-	0				-

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	16	P:GO:0042221; P:GO:0007605; C:GO:0030659; F:GO:0005515; P:GO:0016458; P:GO:0008016; F:GO:0005251; P:GO:0006936; P:GO:0046676; C:GO:0042383; P:GO:0051899; C:GO:0008076; P:GO:0055085; F:GO:0015271; P:GO:0006813; P:GO:0006349	-		IPR013821; IPR015575; PTHR11537 (PANTHER)
Oryctolagus cuniculus	prohibitin	20	C:GO:0005654; C:GO:0031315; F:GO:0005515; C:GO:0030061; P:GO:0031100; P:GO:0045471; P:GO:0016575; F:GO:0016563; P:GO:0008285; P:GO:0034097; P:GO:0043434; P:GO:0001552; P:GO:0007165; P:GO:0042493; P:GO:0016481; P:GO:0006950; C:GO:0005887; P:GO:0043066; P:GO:0006260; F:GO:0016564	-		IPR000163
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis elegans	protein	1	P:GO:0040010	-		IPR000742; IPR006210; IPR013032; IPR013111; G3DSA:2.170.300.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF58 (PANTHER), SSF57196 (SUPERFAMILY)
Caenorhabditis elegans	protein	1	P:GO:0040010	-		IPR000742; IPR006210; IPR013032; IPR013111; G3DSA:2.170.300.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF58 (PANTHER), SSF57196 (SUPERFAMILY)
Caenorhabditis briggsae	transmembrane amino acid transporter protein	2	C:GO:0016021; F:GO:0015171	-		IPR013057; PTHR22950 (PANTHER), PTHR22950:SF5 (PANTHER), SignalP (SIGNALP)

Caenorhabditis briggsae	downstream of receptor ki-se	14	P:GO:0007265; P:GO:0007613; P:GO:0007015; P:GO:0008360; F:GO:0005070; P:GO:0008595; P:GO:0007476; F:GO:0004872; F:GO:0005118; P:GO:0001700; P:GO:0045500; P:GO:0008293; P:GO:0008355; C:GO:0005886	-		IPR001452; G3DSA:2.30.30.40 (GENE3D), PTHR22820 (PANTHER), PTHR22820:SF13 (PANTHER)
Caenorhabditis elegans	cathepsin l-like cysteine protei-se	1	F:GO:0008234	-		IPR000169; IPR000668; IPR013128; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF36 (PANTHER), SSF54001 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis briggsae	staphylococcal nuclease domain-containing protein 1	7	C:GO:0043231; F:GO:0016788; F:GO:0003676; C:GO:0016442; C:GO:0044444; F:GO:0003713; P:GO:0016246	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	intraflagellar transport protein 140	1	F:GO:0005488	-		PTHR15722 (PANTHER), PTHR15722:SF7 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	4	P:GO:0007186; C:GO:0016021; C:GO:0005622; F:GO:0008270	-		IPR019427; G3DSA:1.20.1070.10 (GENE3D), PTHR22751 (PANTHER), PTHR22751:SF8 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	C:GO:0030054; F:GO:0000166	-		-
Caenorhabditis elegans	inositol triphosphate receptor family member (itr-1)	17	F:GO:0035091; F:GO:0005515; F:GO:0005262; C:GO:0016529; F:GO:0008095; C:GO:0005637; C:GO:0005792; P:GO:0006816; P:GO:0050882; P:GO:0009791; C:GO:0005955; C:GO:0005789; P:GO:0032469; C:GO:0005730; P:GO:0001666; C:GO:0014069; P:GO:0055085	-		IPR000699; IPR003608; IPR015925; G3DSA:1.25.10.30 (GENE3D), G3DSA:2.80.10.50 (GENE3D), PTHR13715:SF2 (PANTHER), SSF100909 (SUPERFAMILY)

Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	4	P:GO:0007186; C:GO:0016021; P:GO:0007165; F:GO:0004930	-		PTHR19264 (PANTHER), PTHR19264:SF33 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG06763 [Caenorhabditis briggsae]	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	h+ lysosomal v1 subunit a	14	F:GO:0046961; P:GO:0000003; P:GO:0040010; P:GO:0006898; C:GO:0033180; F:GO:0046933; P:GO:0040011; C:GO:0005829; P:GO:0009792; P:GO:0015986; P:GO:0002119; C:GO:0005887; F:GO:0005524; C:GO:0005739	-	EC:3.6.3.14	-
	-	0				-
Caenorhabditis elegans	sodium- and chloride-dependent creatine transporter 1	8	P:GO:0055085; P:GO:0006814; P:GO:0015881; F:GO:0005309; F:GO:0015220; P:GO:0006836; P:GO:0006936; C:GO:0005887	-		IPR000175; PTHR11616:SF20 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR001810; G3DSA:1.20.1280.50 (GENE3D)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	src-associated protein saw	0		P:GO:0006364; C:GO:0005730		IPR018983; PTHR19924 (PANTHER), PTHR19924:SF2 (PANTHER)
Caenorhabditis elegans	src-associated protein saw	0		P:GO:0006364; C:GO:0005730		IPR018983; PTHR19924 (PANTHER), PTHR19924:SF2 (PANTHER)
Brugia malayi	beta -galactosyltransferase-like	4	F:GO:0016757; C:GO:0044444; P:GO:0009987; C:GO:0044425	-		IPR003378; PTHR10811 (PANTHER), PTHR10811:SF2 (PANTHER)
Caenorhabditis elegans	conserved oligomeric golgi component family member (cogc-4)	5	P:GO:0048213; P:GO:0007030; P:GO:0006890; F:GO:0005515; C:GO:0017119	-		IPR013167; PTHR10483 (PANTHER), PTHR10483:SF7 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	glycosylation related family member (gly-9)	4	F:GO:0004653; C:GO:0005794; P:GO:0009312; C:GO:0016020	-	EC:2.4.1.41	-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG17315 [Caenorhabditis briggsae]	0		F:GO:0005488		-
	-	0				SignalP (SIGNALP)

Caenorhabditis briggsae	briggsae cbr-fkb-3 protein	4	P:GO:0006457; P:GO:0008340; F:GO:0003755; P:GO:0040010	-	EC:5.2.1.8	-
Caenorhabditis elegans	tbc1 domain member 2b	3	F:GO:0005097; C:GO:0005622; P:GO:0032313	-		IPR000195; G3DSA:1.10.8.270 (GENE3D), PTHR22957 (PANTHER), PTHR22957:SF52 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-ced-5 protein	8	C:GO:0005737; F:GO:0005083; P:GO:0043652; C:GO:0005886; F:GO:0032403; F:GO:0019899; P:GO:0040039; F:GO:0017124	-		PTHR23317 (PANTHER), PTHR23317:SF16 (PANTHER)
	-	0				-
Brugia malayi	eukaryotic translation initiation factor 4e	8	F:GO:0003743; P:GO:0006413; C:GO:0016281; F:GO:0003723; C:GO:0005845; P:GO:0048522; P:GO:0009792; F:GO:0031370	-		IPR001040; IPR019770
	-	0				-
Caenorhabditis elegans	dual specificity phosphatase 19	6	P:GO:0006470; F:GO:0008579; P:GO:0000188; F:GO:0005515; F:GO:0008330; C:GO:0005737	-		IPR020417; G3DSA:3.90.190.10 (GENE3D), PTHR10159 (PANTHER), PTHR10159:SF32 (PANTHER), SSF52799 (SUPERFAMILY)
	-	0				-
Brugia malayi	patatin-like phospholipase family protein	1	P:GO:0008152	-		-
Caenorhabditis briggsae	copine family protein	0				IPR010734; PTHR10857 (PANTHER)
Caenorhabditis elegans	tryptophanyl-tr- synthetase	3	F:GO:0004812; P:GO:0006418; F:GO:0000166	-		IPR002306; G3DSA:1.10.240.10 (GENE3D), SSF52374 (SUPERFAMILY)
	-	0				-
	-	0				-
Apis mellifera	dopa decarboxylase	1	F:GO:0016829	-		IPR002129; IPR015421; IPR015424
Caenorhabditis elegans	subfamily m12a u-ssigned peptidase (m12 family)	2	F:GO:0046872; F:GO:0008233	-		IPR000859; PTHR10127 (PANTHER), PTHR10127:SF70 (PANTHER)
Caenorhabditis elegans	n-acetylglucosamine ki-se	5	C:GO:0005625; F:GO:0009384; F:GO:0005515; P:GO:0006044; F:GO:0045127	-	EC:2.7.1.60; EC:2.7.1.59	-
Brugia malayi	gtp-ase activating protein for arf containing protein	0		F:GO:0008060; P:GO:0032312; F:GO:0008270		IPR022018
	-	0				-

Caenorhabditis briggsae	briggsae cbr-daf-12 protein	0		F:GO:0043565; F:GO:0003700; F:GO:0003677; C:GO:0005634; F:GO:0004879; F:GO:0008270; P:GO:0006355; F:GO:0004872; F:GO:0046872; P:GO:0006350; F:GO:0003707; P:GO:0045449		-
Caenorhabditis briggsae	abnormal cell migration family member (mig-10)	1	F:GO:0005515	-		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Brugia malayi	tm2 domain-containing protein 2 precursor	0		F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150; C:GO:0005575		-
	-	0				-
	-	0				-
Trichoplax adhaerens	2-oxoglutarate carrier	5	F:GO:0005488; C:GO:0005743; P:GO:0055085; C:GO:0016021; F:GO:0005215	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF78 (PANTHER)
Caenorhabditis elegans	ribosomal protein l18	9	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; P:GO:0018996; P:GO:0000003; P:GO:0040007; P:GO:0006898; P:GO:0006412	-	EC:3.6.5.3	IPR000039; IPR021131; IPR021132; G3DSA:3.100.10.10 (GENE3D)
Caenorhabditis elegans	ribosomal protein l18	9	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; P:GO:0018996; P:GO:0000003; P:GO:0040007; P:GO:0006898; P:GO:0006412	-	EC:3.6.5.3	IPR000039; IPR021131; IPR021132; G3DSA:3.100.10.10 (GENE3D)
	-	0				-
Caenorhabditis elegans	eps (human endocytosis) related family member (eps-8)	2	F:GO:0005515; F:GO:0004872	-		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0016311; F:GO:0016791; P:GO:0006470; F:GO:0016787; F:GO:0008138; F:GO:0004725; F:GO:0004721		IPR000242; IPR000387; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SignalP (SIGNALP), SSF52799 (SUPERFAMILY)
Loa loa	egl-1 suppressor uptake defective raf enhancer family member (eor-2)	0		F:GO:0003677		-

Caenorhabditis briggsae	peptidase dimerisation domain containing protein	1	F:GO:0016787	-		IPR011650; G3DSA:3.30.70.360 (GENE3D)
Angiostrongylus cantonensis	cuticular collagen	3	P:GO:0010171; F:GO:0042302; F:GO:0005515	-		IPR002486; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	acyl-coenzyme a oxidase pristanoyl	2	F:GO:0016627; P:GO:0008152	-		IPR002655; IPR009075; IPR012258; PTHR10909 (PANTHER)
Branchiostoma floridae	sam domain and hd domain-containing protein 1	0		P:GO:0000003; F:GO:0016787; F:GO:0003824; P:GO:0045088; P:GO:0051607; C:GO:0005634		G3DSA:1.10.3210.10 (GENE3D), PTHR11373 (PANTHER), PTHR11373:SF9 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	C:GO:0005737; P:GO:0006546; F:GO:0016491; F:GO:0004047	-	EC:2.1.2.10	PTHR13847 (PANTHER), PTHR13847:SF16 (PANTHER)
Caenorhabditis elegans	sushi domain containing	2	C:GO:0016021; P:GO:0007160	-		-
Brugia malayi	n terminus of rad21 rec8 like protein	4	C:GO:0043234; C:GO:0000228; C:GO:0000775; P:GO:0007067	-		IPR006910; PTHR12585 (PANTHER), PTHR12585:SF5 (PANTHER)
Homo sapiens	complement component r subcomponent	6	F:GO:0004252; P:GO:0045087; F:GO:0005509; P:GO:0006958; C:GO:0005576; P:GO:0006508	-	EC:3.4.21.0	IPR000152; IPR001881; IPR013091; IPR018097; G3DSA:2.10.25.10 (GENE3D), PTHR19355 (PANTHER), PTHR19355:SF12 (PANTHER), SSF57196 (SUPERFAMILY)
Ancylostoma ceylanicum	venom-allergen-like protein family member (vap-1)	0		P:GO:0040011; P:GO:0006898; C:GO:0005576		IPR001283; IPR014044
	-	0				-
Caenorhabditis elegans	methyltransferase-like protein 5	1	F:GO:0005515	-		IPR002052; IPR007848; G3DSA:3.40.50.150 (GENE3D), PTHR23290 (PANTHER), SignalP (SIGNALP), SSF53335 (SUPERFAMILY)
	-	0				IPR016187
Caenorhabditis briggsae	patched family protein	5	P:GO:0018996; C:GO:0016021; P:GO:0040018; F:GO:0008158; P:GO:0040011	-		-
Caenorhabditis briggsae	alcohol dehydroge-se	3	F:GO:0008270; P:GO:0055114; F:GO:0016491	-		IPR002085; IPR011032; PTHR11695:SF5 (PANTHER)
	-	0				-
Caenorhabditis elegans	low-density lipoprotein receptor-related protein 2	3	C:GO:0016021; F:GO:0004872; F:GO:0005509	-		IPR011042; PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER), SSF63825 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein M05D6.2 [Caenorhabditis elegans]	0				IPR008862; PTHR12832:SF6 (PANTHER)
	-	0				-

Loa loa	loc495188 protein	0		F:GO:0003684; P:GO:0006289; F:GO:0003677; F:GO:0008534; C:GO:0005737; P:GO:0006281; F:GO:0016491; F:GO:0003824; P:GO:0017000; F:GO:0016853; P:GO:0006457; F:GO:0005488		-
Loa loa	loc495188 protein	0		F:GO:0003684; P:GO:0006289; F:GO:0003677; F:GO:0008534; C:GO:0005737; P:GO:0006281; F:GO:0016491; F:GO:0003824; P:GO:0017000; F:GO:0016853; P:GO:0006457; F:GO:0005488		-
	-	0				SignalP (SIGNALP)
Homo sapiens	immunoglobulin heavy chain variable region	0				IPR013783; PTHR23266 (PANTHER), PTHR23266:SF9 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-ddr-2 protein	4	F:GO:0005488; F:GO:0004672; P:GO:0040010; P:GO:0009987	-		IPR000421; IPR008979; IPR020685; IPR020742; G3DSA:2.60.120.260 (GENE3D)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	cleavage and polyadenylation specificity factor	1	F:GO:0016787	-		IPR001279; G3DSA:3.60.15.10 (GENE3D), PTHR11203 (PANTHER), PTHR11203:SF11 (PANTHER), SSF56281 (SUPERFAMILY)
	-	0				-

Strongylocentrotus purpuratus	h4 histone protein	19	C:GO:0005654; F:GO:0005515; P:GO:0040010; P:GO:0006898; P:GO:0040011; C:GO:0000786; P:GO:0019915; P:GO:0009792; P:GO:0045653; F:GO:0043565; P:GO:0002119; P:GO:0010171; P:GO:0006352; F:GO:0016986; P:GO:0006334; P:GO:0006952; P:GO:0048015; P:GO:0040035; P:GO:0032940	-		IPR001951; IPR007125; IPR009072
Strongylocentrotus purpuratus	h4 histone protein	19	C:GO:0005654; F:GO:0005515; P:GO:0040010; P:GO:0006898; P:GO:0040011; C:GO:0000786; P:GO:0019915; P:GO:0009792; P:GO:0045653; F:GO:0043565; P:GO:0002119; P:GO:0010171; P:GO:0006352; F:GO:0016986; P:GO:0006334; P:GO:0006952; P:GO:0048015; P:GO:0040035; P:GO:0032940	-		IPR001951; IPR007125; IPR009072; IPR019809
	-	0				SignalP (SIGNALP)
Pan troglodytes	lysosomal multispanning membrane protein 5	3	C:GO:0005887; C:GO:0005765; P:GO:0006810	-		IPR004687; IPR018397; SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-csn-3 protein	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				SignalP (SIGNALP)
Homo sapiens	pyruvate muscle	9	F:GO:0004743; F:GO:0005515; F:GO:0030955; F:GO:0005524; F:GO:0000287; P:GO:0006096; P:GO:0012501; C:GO:0005634; C:GO:0005829	-	EC:2.7.1.40	-

Caenorhabditis elegans	protein ki-se family member (kin-25)	0		F:GO:0016740; F:GO:0004674; F:GO:0004672; F:GO:0000166; P:GO:0006468; P:GO:0000003; F:GO:0004715; F:GO:0005524; F:GO:0016301; F:GO:0004713; F:GO:0005515; F:GO:0000287; C:GO:0005886		-
Caenorhabditis elegans	myosin heavy chain	34	P:GO:0046664; P:GO:0045200; C:GO:0016461; P:GO:0035159; P:GO:0031036; P:GO:0035072; P:GO:0007443; P:GO:0007395; P:GO:0045214; P:GO:0035017; P:GO:0007297; C:GO:0031672; P:GO:0046663; F:GO:0003779; F:GO:0000146; P:GO:0001736; F:GO:0008307; F:GO:0032027; P:GO:0008258; P:GO:0051259; P:GO:0016203; C:GO:0032154; C:GO:0045179; P:GO:0045184; C:GO:0005863; P:GO:0035317; P:GO:0007427;	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	cdp-alcohol phosphatidyltransferase family protein	3	C:GO:0016020; F:GO:0016780; P:GO:0008654	-	EC:2.7.8.0	PTHR10414 (PANTHER), PTHR10414:SF4 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Brugia malayi	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0019915		IPR000615; IPR021134
	-	0				-

Macaca mulatta	nucleoside diphosphate ki-se b	24	C:GO:0030027; F:GO:0005515; P:GO:0002762; P:GO:0007155; F:GO:0004550; P:GO:0006241; P:GO:0006355; P:GO:0030819; C:GO:0005882; F:GO:0046872; P:GO:0006165; C:GO:0001726; P:GO:0045618; F:GO:0003677; P:GO:0006183; P:GO:0006228; P:GO:0050679; F:GO:0003700; C:GO:0048471; C:GO:0005886; C:GO:0005634; F:GO:0005524; P:GO:0043066; C:GO:0005739	-	EC:2.7.4.6	IPR001564; IPR023005
	-	0				-
Caenorhabditis elegans	tripartite motif-containing 9	11	P:GO:0008340; F:GO:0008270; P:GO:0043161; C:GO:0030425; F:GO:0004842; C:GO:0005856; P:GO:0045955; C:GO:0008021; F:GO:0042803; N:GO:0035544; P:GO:0016079	-	EC:6.3.2.19	IPR000315; IPR001870; IPR003649; IPR003877; IPR003961; IPR008957; IPR008985; IPR013783; IPR017903; G3DSA:4.10.45.10 (GENE3D), PTHR13712 (PANTHER), PTHR13712:SF62 (PANTHER), SSF57845 (SUPERFAMILY)
Caenorhabditis elegans	tripartite motif-containing 9	11	P:GO:0008340; F:GO:0008270; P:GO:0043161; C:GO:0030425; F:GO:0004842; C:GO:0005856; P:GO:0045955; C:GO:0008021; F:GO:0042803; N:GO:0035544; P:GO:0016079	-	EC:6.3.2.19	IPR000315; IPR001870; IPR003649; IPR003877; IPR003961; IPR008957; IPR008985; IPR013783; IPR017903; G3DSA:4.10.45.10 (GENE3D), PTHR13712 (PANTHER), PTHR13712:SF62 (PANTHER), SSF57845 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	intraflagellar transport 140 homolog	0		F:GO:0003674; F:GO:0005488; P:GO:0008150; C:GO:0005575		-
	-	0				-

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	11	F:GO:0003678; P:GO:0040010; P:GO:0032508; P:GO:0000003; F:GO:0003677; F:GO:0005524; P:GO:0002119; C:GO:0005759; P:GO:0006898; P:GO:0009792; C:GO:0005634	-		PTHR12131 (PANTHER)
Caenorhabditis elegans	hypothetical protein R12A1.3 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-oct-2 protein	3	P:GO:0019915; C:GO:0016020; P:GO:0006810	-		PTHR11600 (PANTHER), PTHR11600:SF44 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-inx- protein	5	P:GO:0040035; C:GO:0005921; P:GO:0040010; P:GO:0040011; P:GO:0002009	-		IPR000990
	-	0				-
Caenorhabditis briggsae	amino acid transporter family member (aat-9)	2	C:GO:0009986; P:GO:0006810	-		IPR002293; PTHR11785:SF76 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	P:GO:0007275	-		IPR003961; IPR008957; IPR013783; PTHR19143 (PANTHER), PTHR19143:SF3 (PANTHER)
	-	0				-
Caenorhabditis elegans	cell adhesion	8	P:GO:0009792; P:GO:0002119; P:GO:0018996; F:GO:0005515; P:GO:0000003; P:GO:0008340; P:GO:0040011; P:GO:0006898	-		IPR003961; IPR008957; IPR013783; PR00014 (PRINTS), PTHR10489 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis briggsae	cytoplasmic intermediate filament protein	12	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0018996; F:GO:0005515; P:GO:0040002; C:GO:0005882; P:GO:0008340; P:GO:0040011; P:GO:0040007; P:GO:0006898; F:GO:0005198	-		-
Caenorhabditis briggsae	viral a-type inclusion	1	F:GO:0005515	-		PD936484 (PRODOM)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis sp. PS1010	uncoordi-ted family member (unc-73)	2	P:GO:0009987; C:GO:0005622	-		IPR000219; PTHR22826 (PANTHER), PTHR22826:SF39 (PANTHER)
Brugia malayi	integrator complex subunit 1	2	P:GO:0009790; P:GO:0009653	-		PTHR21224 (PANTHER)

Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0016226; P:GO:0040010; P:GO:0006898; P:GO:0009792; P:GO:0002119; P:GO:0040007; F:GO:0051536		-
	-	0				-
Ailuropoda melanoleuca	proteasome (macropain) alpha 7	9	P:GO:0051436; P:GO:0051437; F:GO:0042802; F:GO:0004298; P:GO:0031145; C:GO:0019773; P:GO:0044419; C:GO:0005737; C:GO:0005634	-	EC:3.4.25.0	IPR001353; G3DSA:3.60.20.10 (GENE3D), PTHR11599 (PANTHER), PTHR11599:SF15 (PANTHER), PS51475 (PROFILE), SSF56235 (SUPERFAMILY)
Caenorhabditis elegans	vacuolar protein sorting-associated protein 13d-like	0		P:GO:0008104		-
Tetrahymena thermophila	zinc dhhc-type containing 16	1	F:GO:0046872	-		SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	40s ribosomal protein s10	2	C:GO:0005840; F:GO:0005515	-		IPR005326; PTHR12146 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	invadolysin cg3953-pa	6	P:GO:0007155; P:GO:0007049; P:GO:0006508; C:GO:0016020; F:GO:0008270; F:GO:0008237	-		IPR001577; G3DSA:2.30.34.10 (GENE3D), SSF55486 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	yl54_caeel ame: full=uncharacterized protein	0				-
Loa loa	spfh domain member 1	5	C:GO:0005789; F:GO:0042578; F:GO:0005515; C:GO:0016021; P:GO:0030433	-		-
	-	0				IPR012574
Angiostrongylus cantonensis	tumor endothelial marker 7	0		F:GO:0004872; P:GO:0007275; C:GO:0016021; C:GO:0016020		-
Caenorhabditis elegans	plexin domain containing 2	0		F:GO:0004872; P:GO:0007275; C:GO:0016021; C:GO:0016020		-

Caenorhabditis elegans	briggsae cbr-tin-13 protein	5	F:GO:0015450; C:GO:0005744; F:GO:0046872; P:GO:0045039; C:GO:0042719	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	organic cation carnitine	0		P:GO:0055114; F:GO:0016491; C:GO:0016021; C:GO:0016020; F:GO:0032440; P:GO:0055085; F:GO:0005215; P:GO:0006810		PTHR11600 (PANTHER), PTHR11600:SF28 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	deah (asp-glu-ala-his) box polypeptide 35	6	P:GO:0008380; F:GO:0008026; F:GO:0003676; C:GO:0005681; P:GO:0006397; F:GO:0005524	-		G3DSA:3.40.50.300 (GENE3D), PTHR18934 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Brugia malayi	mitochondrial glutamate carrier protein	6	F:GO:0005488; C:GO:0005743; P:GO:0055085; C:GO:0016021; P:GO:0019915; F:GO:0005215	-		IPR001993; IPR002067; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF75 (PANTHER)
Caenorhabditis briggsae	cadherin domain containing protein	4	P:GO:0007155; P:GO:0007186; C:GO:0016020; F:GO:0004888	-		-
Caenorhabditis elegans	phosphatidylinositol 4-ki-se alpha	6	F:GO:0005488; P:GO:0008219; P:GO:0030384; P:GO:0000003; P:GO:0007165; F:GO:0004428	-		-
Caenorhabditis elegans	phosphatidylinositol 4- alpha	6	P:GO:0008219; P:GO:0030384; P:GO:0000003; F:GO:0005515; P:GO:0007165; F:GO:0004428	-		-
Caenorhabditis elegans	atp-dependent helicase	6	F:GO:0008026; C:GO:0005622; F:GO:0003723; P:GO:0006200; F:GO:0005524; F:GO:0008270	-		IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR18934 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	folliculin	0		F:GO:0003674; C:GO:0005737; P:GO:0008150; F:GO:0005515		IPR021713
Caenorhabditis elegans	briggsae cbr-asp-6 protein	2	P:GO:0008219; F:GO:0005515	-		IPR001461; IPR009007; IPR021109; PTHR13683:SF53 (PANTHER)
	-	0				-

Caenorhabditis briggsae	r- binding identical	8	C:GO:0005730; P:GO:0006378; P:GO:0009792; P:GO:0008380; F:GO:0003676; F:GO:0005515; P:GO:0006379; F:GO:0000166	-		-
Caenorhabditis briggsae	r- binding identical	8	C:GO:0005730; P:GO:0006378; P:GO:0009792; P:GO:0008380; F:GO:0003676; F:GO:0005515; P:GO:0006379; F:GO:0000166	-		-
	-	0				-
Caenorhabditis briggsae	class type	7	C:GO:0016021; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0015914; F:GO:0000287; F:GO:0004012	-	EC:3.6.3.1	IPR001757; G3DSA:3.40.1110.10 (GENE3D), PTHR11939:SF19 (PANTHER), SSF81660 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	endonuclease exonuclease phosphatase family protein	1	F:GO:0003824	-		G3DSA:3.60.10.10 (GENE3D)
Caenorhabditis elegans	metabotropic gaba-b receptor subtype 2	6	P:GO:0007186; C:GO:0016021; P:GO:0007165; F:GO:0004965; C:GO:0005886; F:GO:0004930	-		IPR017978; IPR017979; PTHR10519 (PANTHER), PTHR10519:SF2 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Homo sapiens	vimentin	12	F:GO:0005200; P:GO:0006928; C:GO:0005886; C:GO:0031252; C:GO:0030424; C:GO:0016363; C:GO:0045098; P:GO:0045103; F:GO:0019901; F:GO:0008022; C:GO:0005829; P:GO:0044419	-		SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Danio rerio	novel protein human major facilitator superfamily domain containing 5 (zgc:91807)	0		C:GO:0016020; P:GO:0006810		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	activating sig-l cointegrator 1 complex subunit 3	3	F:GO:0003676; F:GO:0004386; F:GO:0000166	-		PTHR11752 (PANTHER), PTHR11752:SF8 (PANTHER)
	-	0				-

Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0030259; F:GO:0016740; F:GO:0030246; P:GO:0008152; P:GO:0005975; C:GO:0016021; F:GO:0016758; F:GO:0016757		IPR002213; G3DSA:3.40.50.2000 (GENE3D), PTHR11926:SF3 (PANTHER), SSF53756 (SUPERFAMILY)
Ailuropoda melanoleuca	suppressor of ty 5 homolog (cerevisiae) isoform cra_a	12	P:GO:0032968; P:GO:0007049; P:GO:0045944; P:GO:0045090; F:GO:0019899; P:GO:0000122; F:GO:0008159; F:GO:0008148; F:GO:0046982; C:GO:0005654; P:GO:0006338; P:GO:0010033	-		-
Caenorhabditis briggsae	immunoglobulin i-set domain containing protein	0		F:GO:0005509; F:GO:0003824		-
Caenorhabditis briggsae	peptidylprolyl isomerase domain and wd repeat containing 1	2	P:GO:0006457; F:GO:0003755	-	EC:5.2.1.8	IPR001680; IPR002130; IPR011046; IPR015891; IPR015943; IPR019781; IPR020892; PTHR11071 (PANTHER), PTHR11071:SF40 (PANTHER)
Caenorhabditis elegans	dhhc zinc finger domain containing protein	1	F:GO:0008270	-		IPR001594; PTHR22883 (PANTHER)
						IPR003961; IPR008957; IPR013783; PR00014 (PRINTS), PTHR19900 (PANTHER), PTHR19900:SF7 (PANTHER)
Branchiostoma floridae	isocitrate dehydroge-se	12	P:GO:0006979; F:GO:0051287; F:GO:0004450; P:GO:0006103; P:GO:0006749; P:GO:0055114; F:GO:0000287; P:GO:0008340; C:GO:0005829; P:GO:0006102; C:GO:0005739; F:GO:0042803	-	EC:1.1.1.42	IPR004790
Caenorhabditis elegans	msp domain with glu- and lys-rich c-term domain	0		C:GO:0005856; F:GO:0005198		IPR000535; IPR008962; PTHR10809 (PANTHER)
	-	0				-
Caenorhabditis briggsae	carboxyl transferase domain containing protein	9	C:GO:0005625; P:GO:0006633; P:GO:0006084; F:GO:0005524; F:GO:0016740; F:GO:0004075; C:GO:0005739; F:GO:0009374; F:GO:0003989	-	EC:6.3.4.14; EC:6.4.1.2	IPR005479; IPR013816; PTHR18866 (PANTHER), PTHR18866:SF6 (PANTHER), SSF56059 (SUPERFAMILY)
Caenorhabditis elegans	placental protein 11 related	2	F:GO:0004521; F:GO:0003723	-		PTHR12439 (PANTHER), SSF142877 (SUPERFAMILY)

Pan troglodytes	subfamily member 1 isoform 1	0				-
Caenorhabditis elegans	hypothetical protein F55E10.7 [Caenorhabditis elegans]	0		C:GO:0016021; P:GO:0007186		PTHR19264 (PANTHER), PTHR19264:SF33 (PANTHER)
Ailuropoda melanoleuca	elongation factor 2	8	F:GO:0003746; P:GO:0006414; P:GO:0006184; F:GO:0005515; F:GO:0003924; C:GO:0030529; C:GO:0005737; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0008152; F:GO:0005515; F:GO:0016757	-		IPR002213; G3DSA:3.40.50.2000 (GENE3D), SSF53756 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR021010; SSF141739 (SUPERFAMILY)
	-	0				-
	-	0				-
Loa loa	ubiquitin protein ligase e3 component n-recognin 2	1	F:GO:0005488	-		IPR003126; IPR003769; IPR014719; PTHR21497 (PANTHER), PTHR21497:SF6 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	briggsae cbr-exos-2 protein	0				SignalP (SIGNALP)
	-	0				-
Brugia malayi	domain containing protein	0		P:GO:0007165; C:GO:0005622		-
Brugia malayi	domain containing protein	0		P:GO:0007165; C:GO:0005622		-
Brugia malayi	domain containing protein	0		P:GO:0007165; C:GO:0005622		-
Brugia malayi	domain containing protein	0		P:GO:0007165; C:GO:0005622		-
	-	0				-
Loa loa	krev interaction trapped protein 1	0		F:GO:0005083; F:GO:0005488; C:GO:0005856; C:GO:0016020; F:GO:0005515		IPR002110; IPR020683; PTHR13283 (PANTHER), PTHR13283:SF2 (PANTHER)
	-	0				-
Caenorhabditis elegans	g in family member (glb-18)	3	F:GO:0020037; P:GO:0015671; F:GO:0019825	-		-
	-	0				IPR019473

Caenorhabditis briggsae	nitrilase 2	15	P:GO:0009684; P:GO:0051410; F:GO:0047558; F:GO:0080061; P:GO:0000003; P:GO:0009617; P:GO:0019499; P:GO:0019762; P:GO:0009970; C:GO:0009507; P:GO:0046686; F:GO:0047427; F:GO:0080109; C:GO:0005886; C:GO:0048046	-	EC:4.2.1.65; EC:3.5.5.4	IPR003010; PTHR23088 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; F:GO:0016787; F:GO:0003676; F:GO:0004528; F:GO:0003824; C:GO:0005575; F:GO:0005044; P:GO:0008152; F:GO:0046872; P:GO:0006955		IPR002591; IPR017849; IPR017850; PTHR10151 (PANTHER), PTHR10151:SF28 (PANTHER)
	-	0				IPR017956
Brugia malayi	integrin beta 1 binding protein 1	0		P:GO:0016477; P:GO:0007229; C:GO:0016020; C:GO:0030027; C:GO:0005737; P:GO:0030155; P:GO:0007243; F:GO:0005178; F:GO:0005515; C:GO:0001726; P:GO:0007160; C:GO:0005829		IPR011993; IPR019517
Loa loa	dis3 mitotic control homolog (cerevisiae)-like 2	1	F:GO:0004518	-		IPR001900; PTHR23355 (PANTHER), PTHR23355:SF10 (PANTHER)
Loa loa	dis3 mitotic control homolog (cerevisiae)-like 2	1	F:GO:0016787	-		IPR001900; PTHR23355 (PANTHER), PTHR23355:SF10 (PANTHER)
Brugia malayi	rnb-like protein	0		F:GO:0003723; F:GO:0004540		-
Loa loa	dis3 mitotic control homolog (cerevisiae)-like 2	1	F:GO:0004518	-		IPR001900; PTHR23355 (PANTHER), PTHR23355:SF10 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	F:GO:0015250; C:GO:0043025; C:GO:0005929; P:GO:0006833	-		IPR000425; SignalP (SIGNALP)
Caenorhabditis elegans	tao ki-se 1	6	C:GO:0043231; F:GO:0004674; F:GO:0000166; F:GO:0030295; F:GO:0019901; P:GO:0006468	-	EC:2.7.11.0	-
	-	0				-

Caenorhabditis elegans	inositol-requiring 1 alpha-like	15	P:GO:0000003; F:GO:0005515; C:GO:0030176; C:GO:0005637; P:GO:0010467; P:GO:0046777; P:GO:0090304; F:GO:0004521; P:GO:0040017; P:GO:0007050; F:GO:0004674; P:GO:0006987; P:GO:0006917; F:GO:0000287; F:GO:0005524	-	EC:2.7.11.0	IPR011047; SignalP (SIGNALP)
Monosiga brevicollis MX1	tr- aspartic acid methyltransferase 1	0		P:GO:0006306; F:GO:0008168; F:GO:0016740; C:GO:0005575; F:GO:0003677		IPR001525; G3DSA:3.40.50.150 (GENE3D), PTHR10629:SF8 (PANTHER), SSF53335 (SUPERFAMILY)
	-	0				-
Loa loa	serine threonine protein ki-se	2	F:GO:0016301; P:GO:0000003	-		IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER), SignalP (SIGNALP)
Brugia malayi	hypothetical protein Bm1_45555 [Brugia malayi]	0				-
Caenorhabditis elegans	briggsae cbr-lov-1 protein	6	C:GO:0016020; P:GO:0007218; P:GO:0034608; P:GO:0034606; C:GO:0005929; F:GO:0005515	-		SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-acy-2 protein	9	C:GO:0016021; F:GO:0004016; P:GO:0007188; P:GO:0009190; P:GO:0002119; F:GO:0000166; P:GO:0040011; P:GO:0040015; C:GO:0005886	-	EC:4.6.1.1	IPR001054; PTHR11920 (PANTHER), PTHR11920:SF12 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis elegans	h transporter (pgp related) family member (haf-9)	6	F:GO:0015197; F:GO:0042626; P:GO:0015833; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		-

Caenorhabditis briggsae	phospholipase beta 4	8	C:GO:0005829; F:GO:0004629; C:GO:0030425; C:GO:0005792; F:GO:0005515; C:GO:0014069; C:GO:0005634; C:GO:0005790	-		PTHR10336 (PANTHER), PTHR10336:SF8 (PANTHER)
	-	0				IPR010916
Caenorhabditis elegans	mitochondrial ribosomal protein l13	5	P:GO:0009792; C:GO:0005840; F:GO:0003735; P:GO:0006412; C:GO:0005739	-	EC:3.6.5.3	IPR005822; IPR005823
Loa loa	smc6 structural mainte-nce of chromosomes 6-like 1 isoform cra_a	2	P:GO:0009792; C:GO:0005622	-		G3DSA:3.40.50.300 (GENE3D), PTHR19306 (PANTHER), PTHR19306:SF2 (PANTHER), SSF52540 (SUPERFAMILY)
Branchiostoma floridae	histone deacetylase 1	45	P:GO:0021766; P:GO:0010870; P:GO:0010552; P:GO:0016055; P:GO:0008284; F:GO:0016566; P:GO:0070933; P:GO:0070932; P:GO:0050769; C:GO:0005829; C:GO:0016581; C:GO:0000792; P:GO:0043524; P:GO:0001889; P:GO:0048709; P:GO:0006916; P:GO:0048565; F:GO:0003714; P:GO:0007492; P:GO:0043922; P:GO:0030182; F:GO:0032403; F:GO:0042802; F:GO:0016563; F:GO:0003677; F:GO:0003682;	-		IPR000286; IPR003084; SSF52768 (SUPERFAMILY)

Branchiostoma floridae	histone deacetylase 1	33	P:GO:0007492; F:GO:0004407; F:GO:0003714; P:GO:0070932; F:GO:0042826; P:GO:0021766; P:GO:0010552; C:GO:0016581; P:GO:0070933; P:GO:0045786; P:GO:0010832; F:GO:0016563; C:GO:0005829; P:GO:0043922; P:GO:0008285; P:GO:0006916; P:GO:0043524; P:GO:0008284; C:GO:0043025; P:GO:0010553; F:GO:0042802; F:GO:0003677; C:GO:0016580; C:GO:0000792; P:GO:0006338; P:GO:0042493; F:GO:0003700;	-		IPR000286; IPR003084; SSF52768 (SUPERFAMILY)
Branchiostoma floridae	histone deacetylase 1	45	P:GO:0021766; P:GO:0010870; P:GO:0010552; P:GO:0016055; P:GO:0008284; F:GO:0016566; P:GO:0070933; P:GO:0070932; P:GO:0050769; C:GO:0005829; C:GO:0016581; C:GO:0000792; P:GO:0043524; P:GO:0001889; P:GO:0048709; P:GO:0006916; P:GO:0048565; F:GO:0003714; P:GO:0007492; P:GO:0043922; P:GO:0030182; F:GO:0032403; F:GO:0042802; F:GO:0016563; F:GO:0003677; F:GO:0003682; P:GO:0021903;	-		IPR000286; IPR003084; SSF52768 (SUPERFAMILY)

Branchiostoma floridae	histone deacetylase 1	33	P:GO:0007492; F:GO:0004407; F:GO:0003714; P:GO:0070932; F:GO:0042826; P:GO:0021766; P:GO:0010552; C:GO:0016581; P:GO:0070933; P:GO:0045786; P:GO:0010832; F:GO:0016563; C:GO:0005829; P:GO:0043922; P:GO:0008285; P:GO:0006916; P:GO:0043524; P:GO:0008284; C:GO:0043025; P:GO:0010553; F:GO:0042802; F:GO:0003677; C:GO:0016580; C:GO:0000792; P:GO:0006338; P:GO:0042493; F:GO:0003700;	-			IPR000286; IPR003084; SSF52768 (SUPERFAMILY)
Branchiostoma floridae	histone deacetylase 1	33	P:GO:0007492; F:GO:0004407; F:GO:0003714; P:GO:0070932; F:GO:0042826; P:GO:0021766; P:GO:0010552; C:GO:0016581; P:GO:0070933; P:GO:0045786; P:GO:0010832; F:GO:0016563; C:GO:0005829; P:GO:0043922; P:GO:0008285; P:GO:0006916; P:GO:0043524; P:GO:0008284; C:GO:0043025; P:GO:0010553; F:GO:0042802; F:GO:0003677; C:GO:0016580; C:GO:0000792; P:GO:0006338; P:GO:0042493;	-			IPR000286; IPR003084; SSF52768 (SUPERFAMILY)

Branchiostoma floridae	histone deacetylase 1	33	P:GO:0007492; F:GO:0004407; F:GO:0003714; P:GO:0070932; F:GO:0042826; P:GO:0021766; P:GO:0010552; C:GO:0016581; P:GO:0070933; P:GO:0045786; P:GO:0010832; F:GO:0016563; C:GO:0005829; P:GO:0043922; P:GO:0008285; P:GO:0006916; P:GO:0043524; P:GO:0008284; C:GO:0043025; P:GO:0010553; F:GO:0042802; F:GO:0003677; C:GO:0016580; C:GO:0000792; P:GO:0006338; P:GO:0042493; F:GO:0003700;	-		IPR000286; IPR003084; SSF52768 (SUPERFAMILY)
Branchiostoma floridae	histone deacetylase 1	33	P:GO:0007492; F:GO:0004407; F:GO:0003714; P:GO:0070932; F:GO:0042826; P:GO:0021766; P:GO:0010552; C:GO:0016581; P:GO:0070933; P:GO:0045786; P:GO:0010832; F:GO:0016563; C:GO:0005829; P:GO:0043922; P:GO:0008285; P:GO:0006916; P:GO:0043524; P:GO:0008284; C:GO:0043025; P:GO:0010553; F:GO:0042802; F:GO:0003677; C:GO:0016580; C:GO:0000792; P:GO:0006338; P:GO:0042493; F:GO:0003700;	-		IPR000286; IPR003084; SSF52768 (SUPERFAMILY)

Branchiostoma floridae	histone deacetylase 1	33	P:GO:0007492; F:GO:0004407; F:GO:0003714; P:GO:0070932; F:GO:0042826; P:GO:0021766; P:GO:0010552; C:GO:0016581; P:GO:0070933; P:GO:0045786; P:GO:0010832; F:GO:0016563; C:GO:0005829; P:GO:0043922; P:GO:0008285; P:GO:0006916; P:GO:0043524; P:GO:0008284; C:GO:0043025; P:GO:0010553; F:GO:0042802; F:GO:0003677; C:GO:0016580; C:GO:0000792; P:GO:0006338; P:GO:0042493; F:GO:0003700;	-		IPR000286; IPR003084; SSF52768 (SUPERFAMILY)
Branchiostoma floridae	histone deacetylase 1	33	P:GO:0007492; F:GO:0004407; F:GO:0003714; P:GO:0070932; F:GO:0042826; P:GO:0021766; P:GO:0010552; C:GO:0016581; P:GO:0070933; P:GO:0045786; P:GO:0010832; F:GO:0016563; C:GO:0005829; P:GO:0043922; P:GO:0008285; P:GO:0006916; P:GO:0043524; P:GO:0008284; C:GO:0043025; P:GO:0010553; F:GO:0042802; F:GO:0003677; C:GO:0016580; C:GO:0000792; P:GO:0006338; P:GO:0042493; F:GO:0003700;	-		IPR000286; IPR003084; SSF52768 (SUPERFAMILY)

Branchiostoma floridae	histone deacetylase 1	33	P:GO:0007492; F:GO:0004407; F:GO:0003714; P:GO:0070932; F:GO:0042826; P:GO:0021766; P:GO:0010552; C:GO:0016581; P:GO:0070933; P:GO:0045786; P:GO:0010832; F:GO:0016563; C:GO:0005829; P:GO:0043922; P:GO:0008285; P:GO:0006916; P:GO:0043524; P:GO:0008284; C:GO:0043025; P:GO:0010553; F:GO:0042802; F:GO:0003677; C:GO:0016580; C:GO:0000792; P:GO:0006338; P:GO:0042493; F:GO:0003700;	-		IPR000286; IPR003084; SSF52768 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	nucleolar containing protein	10	C:GO:0005829; P:GO:0040010; C:GO:0005730; P:GO:0006364; C:GO:0030688; P:GO:0000003; P:GO:0002119; F:GO:0005515; P:GO:0006898; P:GO:0009792	-		IPR010301
Caenorhabditis briggsae	skiv2l partial	1	F:GO:0016787	-		PTHR11752 (PANTHER), PTHR11752:SF2 (PANTHER)
Caenorhabditis briggsae	skiv2l partial	1	F:GO:0016787	-		PTHR11752 (PANTHER), PTHR11752:SF2 (PANTHER)
Caenorhabditis briggsae	skiv2l partial	1	F:GO:0016787	-		PTHR11752 (PANTHER), PTHR11752:SF2 (PANTHER)
Loa loa	fem-1 homolog a (elegans)	1	F:GO:0005515	-		-
Brugia malayi	beta lysosomal	5	C:GO:0005625; F:GO:0004567; C:GO:0005764; P:GO:0006516; F:GO:0005537	-	EC:3.2.1.25	PTHR10066 (PANTHER), PTHR10066:SF12 (PANTHER)
	-	0				-
Angiostrongylus cantonensis	gamma-butyrobetaine dioxyge-se	5	F:GO:0005506; P:GO:0055114; F:GO:0016702; F:GO:0008336; P:GO:0045329	-	EC:1.13.11.0 ; EC:1.14.11.1	IPR003819; G3DSA:3.60.130.10 (GENE3D), PTHR10696 (PANTHER), PTHR10696:SF3 (PANTHER), SSF51197 (SUPERFAMILY)
Brugia malayi	protein ki-se domain containing protein	0		F:GO:0016301		-

Caenorhabditis elegans	d- polymerase epsilon subunit 2	2	P:GO:0006259; F:GO:0016740	-		IPR007185; PTHR12708 (PANTHER), PF12213 (PFAM)
Caenorhabditis elegans	trm44_caeel ame: full=probable tr- (uracil-o -)-methyltransferase	0		F:GO:0003676; F:GO:0008168; C:GO:0005737; P:GO:0008033; F:GO:0016740; F:GO:0008270		-
Angiostrongylus cantonensis	gametocyte specific factor 1	0		F:GO:0046872; C:GO:0005737		IPR007917; IPR022776
Caenorhabditis elegans	nucleolar mif4g domain-containing protein 1	2	P:GO:0040018; P:GO:0002119	-		PTHR18034 (PANTHER), PTHR18034:SF4 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				IPR018307; SignalP (SIGNALP)
Caenorhabditis elegans	lethal family member (let-805)	8	P:GO:0018996; P:GO:0009792; P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		IPR003961; IPR008957; IPR013783; PTHR19143 (PANTHER), PTHR19143:SF2 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	homolog subfamily c member 8	1	F:GO:0031072	-		PTHR15606 (PANTHER), PTHR15606:SF1 (PANTHER)
	-	0				SignalP (SIGNALP)
Loa loa	sjchgc03786 protein	0				IPR018801; SignalP (SIGNALP)
Angiostrongylus cantonensis	myosin vi	20	P:GO:0051046; C:GO:0016461; C:GO:0031941; C:GO:0031965; C:GO:0005794; P:GO:0006886; C:GO:0005829; C:GO:0001726; F:GO:0032559; F:GO:0003774; P:GO:0006897; F:GO:0051015; P:GO:0030330; C:GO:0016591; P:GO:0045944; C:GO:0048471; C:GO:0005886; F:GO:0005516; P:GO:0042491; C:GO:0045334	-		PTHR13140 (PANTHER), PTHR13140:SF26 (PANTHER)
	-	0				-
	-	0				-

Caenorhabditis briggsae	serum response factor	35	P:GO:0001829; P:GO:0010735; P:GO:0000003; P:GO:0030336; P:GO:0030431; P:GO:0048589; P:GO:0045597; P:GO:0040010; P:GO:0090009; P:GO:0060261; P:GO:0030155; P:GO:0007430; F:GO:0003704; P:GO:0007616; C:GO:0005737; C:GO:0005730; P:GO:0001947; P:GO:0008285; P:GO:0034097; P:GO:0045987; P:GO:0007475; P:GO:0007015; P:GO:0046716; P:GO:0002119; P:GO:0035154; F:GO:0003700;	-		IPR002100; PTHR11945 (PANTHER), PTHR11945:SF32 (PANTHER)
	-	0				IPR003195
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	briggsae cbr-klf-1 protein	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		-
Caenorhabditis briggsae	fanci (fanconi anemia complex component i) homolog family member (fnci-1)	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	acid sphingomyeli-se-like phosphodiesterase 3b-like	0		F:GO:0004767; P:GO:0008152; C:GO:0005615; P:GO:0006685; F:GO:0016787; F:GO:0000166; F:GO:0016798; C:GO:0005576		IPR004843; G3DSA:3.60.21.10 (GENE3D), PTHR10340 (PANTHER), PTHR10340:SF14 (PANTHER), SignalP (SIGNALP), SSF56300 (SUPERFAMILY)
Brugia malayi	hypothetical protein Bm1_57350 [Brugia malayi]	0				-
Brugia malayi	hypothetical protein Bm1_57350 [Brugia malayi]	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG12007 [Caenorhabditis briggsae]	0				G3DSA:3.90.226.10 (GENE3D), SSF52096 (SUPERFAMILY)
Brugia malayi	beta like 1	5	C:GO:0005730; F:GO:0042802; P:GO:0006917; P:GO:0016445; F:GO:0019899	-		PTHR14978 (PANTHER)

Caenorhabditis elegans	c-type lectin family member (clec-266)	0		F:GO:0030169; F:GO:0008329; C:GO:0016021; C:GO:0016020; F:GO:0005529; F:GO:0003674; P:GO:0006910; P:GO:0007165; C:GO:0005575; F:GO:0004872; P:GO:0008150; P:GO:0006955; F:GO:0005488		IPR001304; IPR016186; IPR016187
	-	0				-
	-	0				-
Caenorhabditis elegans	tetratricopeptide repeat domain 17	2	P:GO:0040010; P:GO:0040017	-		IPR011990; IPR019734; PTHR16091 (PANTHER), SSF48452 (SUPERFAMILY)
Caenorhabditis briggsae	zinc finger protein	1	F:GO:0005488	-		IPR001841; IPR013083; IPR017907; SSF57850 (SUPERFAMILY)
Caenorhabditis briggsae	low-density lipoprotein receptor-related protein 2	3	C:GO:0016021; F:GO:0004872; F:GO:0005509	-		IPR006210; PTHR10529 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-unc-115 protein	3	P:GO:0007010; F:GO:0003779; F:GO:0008270	-		-
Salmo salar	lipopolysaccharide-induced tumor necrosis factor-alpha factor homolog	4	P:GO:0009987; C:GO:0043229; F:GO:0005515; C:GO:0005737	-		IPR006629; PTHR23292 (PANTHER)
Loa loa	fragile site-associated protein	0		F:GO:0005488; F:GO:0003779; P:GO:0016043; P:GO:0030036		-
Caenorhabditis briggsae	yp69_caeel ame: full=uncharacterized protein	0				SignalP (SIGNALP)
Caenorhabditis elegans	ccr4-not transcription complex	0				-
Caenorhabditis elegans	cd63 antigen	3	P:GO:0030001; F:GO:0046872; C:GO:0016021	-		IPR000301; IPR008952; IPR018499; PTHR19282 (PANTHER), PTHR19282:SF12 (PANTHER), SignalP (SIGNALP)
Brugia malayi	ubx domain containing protein	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG03566 [Caenorhabditis briggsae]	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-dct-18 protein	0				-
	-	0				SignalP (SIGNALP)
Strongylocentrotus purpuratus	ensangp00000010363	0				IPR006912; PTHR22930 (PANTHER)
	-	0				-
Caenorhabditis briggsae	cytochrome p450 family protein	3	P:GO:0008152; F:GO:0016491; F:GO:0005506	-		IPR001128; PTHR19383:SF165 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	briggsae cbr-cul-5 protein	4	F:GO:0004872; F:GO:0031625; C:GO:0031461; P:GO:0006511	-		IPR001373; IPR016158; G3DSA:1.20.1310.10 (GENE3D), PTHR11932 (PANTHER), PTHR11932:SF7 (PANTHER)

	-	0				-
Caenorhabditis elegans	polymerase (d- directed) gamma	12	P:GO:0030421; P:GO:0008340; C:GO:0005743; F:GO:0003887; C:GO:0005760; C:GO:0042645; P:GO:0006264; F:GO:0003677; F:GO:0002020; P:GO:0006287; F:GO:0004527; P:GO:0008406	-	EC:2.7.7.7	IPR001098; IPR002297; SignalP (SIGNALP), SSF56672 (SUPERFAMILY)
Caenorhabditis elegans	carnitine palmitoyl transferase family member (cpt-6)	0				-
	-	0				IPR001810; G3DSA:1.20.1280.50 (GENE3D), SignalP (SIGNALP)
Caenorhabditis elegans	xyluloki-se homolog	2	F:GO:0016773; P:GO:0005975	-	EC:2.7.1.0	-
Caenorhabditis briggsae	rab gdp-dissociation inhibitor	11	P:GO:0016192; C:GO:0005875; P:GO:0008340; P:GO:0043087; P:GO:0008219; C:GO:0008021; P:GO:0000003; P:GO:0007269; P:GO:0009792; F:GO:0005093; P:GO:0015031	-		IPR000806; IPR002005; IPR018203; G3DSA:3.30.519.10 (GENE3D), G3DSA:3.50.50.60 (GENE3D), SSF51905 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	mothers against dpp protein	5	F:GO:0003700; F:GO:0005515; C:GO:0005667; P:GO:0006355; P:GO:0007179	-		IPR003619; IPR013019; IPR013790; PTHR13703:SF19 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0003676; P:GO:0006508; F:GO:0008168; F:GO:0008270		G3DSA:3.40.50.300 (GENE3D), PTHR10887 (PANTHER), PTHR10887:SF10 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	alcohol dehydroge-se	3	F:GO:0008270; P:GO:0055114; F:GO:0016491	-		IPR002085; IPR013149; IPR016040; PTHR11695:SF38 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	spermine spermidine synthase family protein	2	F:GO:0016740; F:GO:0005515	-		IPR013216; G3DSA:3.40.50.150 (GENE3D), PTHR12176 (PANTHER), SSF53335 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-aex-3 protein	11	P:GO:0016192; P:GO:0007618; P:GO:0030421; P:GO:0018991; C:GO:0016021; P:GO:0051726; P:GO:0042981; C:GO:0008021; F:GO:0017112; P:GO:0007269; P:GO:0000187	-		-

Caenorhabditis elegans	rab gtpase activating protein 1-like	6	F:GO:0005097; P:GO:0032880; C:GO:0005769; P:GO:0032313; C:GO:0005794; C:GO:0005634	-		IPR022164; PTHR22957 (PANTHER), PTHR22957:SF4 (PANTHER)
	-	0				-
Caenorhabditis elegans	mgc83645 protein	0		F:GO:0005525; F:GO:0000166; C:GO:0005622		IPR002917; IPR006073; G3DSA:3.40.50.300 (GENE3D), PTHR11649 (PANTHER), PTHR11649:SF9 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	subfamily member 5 gamma	4	P:GO:0006457; C:GO:0016020; F:GO:0051082; F:GO:0031072	-		IPR001623; IPR015609; IPR018253; PTHR11821:SF22 (PANTHER)
Caenorhabditis elegans	subfamily member 5 gamma	4	P:GO:0006457; C:GO:0016020; F:GO:0051082; F:GO:0031072	-		IPR001623; IPR015609; IPR018253; PTHR11821:SF22 (PANTHER)
Loa loa	tissue specific transplantation antigen p35b	5	P:GO:0019835; F:GO:0050662; P:GO:0051246; F:GO:0019787; P:GO:0043687	-		IPR001509; G3DSA:3.90.25.10 (GENE3D), PTHR10366 (PANTHER), PTHR10366:SF25 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	u533_caeel ame: full=upf0533 protein	0		F:GO:0005515		IPR010378; PTHR13134:SF2 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Ixodes scapularis	phospholipase d3	3	P:GO:0008152; C:GO:0016021; F:GO:0003824	-		IPR001736; G3DSA:3.30.870.10 (GENE3D), PTHR10185 (PANTHER), SSF56024 (SUPERFAMILY)
Caenorhabditis briggsae	tight junction protein	0		F:GO:0005515		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR19964 (PANTHER)
Caenorhabditis elegans	rab gtpase activating protein 1	3	C:GO:0015630; C:GO:0044444; C:GO:0044430	-		IPR006020; IPR011993; PTHR22957 (PANTHER), PTHR22957:SF4 (PANTHER), SSF50729 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	aspartyl-tr- synthetase	5	C:GO:0005737; F:GO:0003676; P:GO:0006422; F:GO:0005524; F:GO:0004815	-	EC:6.1.1.12	IPR002312; IPR004364; IPR004365; IPR006195; IPR012340; IPR016027; IPR018150; G3DSA:3.30.930.10 (GENE3D), PTHR22594:SF6 (PANTHER), SSF55681 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical tyrosi-se-like protein in chromosome	4	F:GO:0005515; F:GO:0046872; P:GO:0008152; F:GO:0016491	-		SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				IPR012435
	-	0				-
	-	0				-
Caenorhabditis briggsae	gfr receptor alpha 4	0				-
	-	0				-
Loa loa	lim domain containing protein	1	F:GO:0005488	-		-
Brugia malayi	hypothetical protein Bm1_52770 [Brugia malayi]	0				-

Caenorhabditis briggsae	Hypothetical protein CBG01718 [Caenorhabditis briggsae]	2	P:GO:0009792; P:GO:0006898	-			-
	-	0					-
Caenorhabditis elegans	uridine phosphorylase	1	F:GO:0003824	-			IPR000845; IPR010059; IPR018017; G3DSA:3.40.50.1580 (GENE3D), SSF53167 (SUPERFAMILY)
Caenorhabditis briggsae	protein ki-se domain containing protein	2	F:GO:0004672; F:GO:0000166	-			IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
	-	0					-
Pongo abelii	c-x-c chemokine receptor 4	38	P:GO:0009615; P:GO:0001764; P:GO:0008354; C:GO:0016023; C:GO:0030426; P:GO:0008038; P:GO:0001667; F:GO:0015026; P:GO:0060048; P:GO:0007204; P:GO:0030334; P:GO:0050920; F:GO:0016493; P:GO:0043067; F:GO:0016494; C:GO:0016021; P:GO:0051924; F:GO:0043130; P:GO:0022029; C:GO:0009986; C:GO:0031252; F:GO:0003779; F:GO:0032027; P:GO:0008045; F:GO:0031625; P:GO:0001666; P:GO:0006915;	-			SignalP (SIGNALP)
	-	0					SignalP (SIGNALP)
	-	0					-
	-	0					-
Loa loa	palmitoyltransferase zdhhc17	7	F:GO:0019706; F:GO:0004871; P:GO:0042953; F:GO:0015095; C:GO:0030660; P:GO:0043123; F:GO:0005515	-			IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF301 (PANTHER)
Caenorhabditis briggsae	leukocyte cell-derived chemotaxin 2	0					-
Caenorhabditis elegans	motor axon guidance family member (max-2)	6	P:GO:0007411; P:GO:0008340; F:GO:0004674; F:GO:0005524; F:GO:0017048; P:GO:0006468	-		EC:2.7.11.0	IPR000095; IPR000719; IPR008271; IPR011009; IPR015750; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), G3DSA:3.90.810.10 (GENE3D), PTHR22986 (PANTHER)

Pongo abelii	spermidine spermine n1-acetyltransferase	21	P:GO:0015804; F:GO:0008271; P:GO:0006814; C:GO:0005625; C:GO:0016021; F:GO:0019531; F:GO:0004145; P:GO:0008272; F:GO:0015175; F:GO:0005283; F:GO:0019809; P:GO:0046208; P:GO:0006821; F:GO:0005515; P:GO:0042127; F:GO:0015179; P:GO:0034220; P:GO:0019532; C:GO:0005737; C:GO:0005886; F:GO:0015108	-	EC:2.3.1.57	IPR016181; PTHR10545 (PANTHER), PTHR10545:SF5 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	novel protein vertebrate ptprf interacting binding protein 1 (liprin beta 1)	0		F:GO:0008907; P:GO:0015074; F:GO:0003677		IPR001660; IPR010993; IPR013761; IPR021129; PTHR12587 (PANTHER), PTHR12587:SF1 (PANTHER)
Caenorhabditis elegans	tiny fragments locus 9c	1	F:GO:0016740	-		-
Medicago truncatula	r--directed d- polymerase (reverse transcriptase)	0		F:GO:0003723; P:GO:0006278; F:GO:0004519; F:GO:0003964		-
	-	0				-
	-	0				-
Loa loa	rhomboid family protein	4	C:GO:0016021; P:GO:0007165; F:GO:0005509; F:GO:0004252	-	EC:3.4.21.0	IPR002610; IPR022764; G3DSA:1.20.1540.10 (GENE3D), SSF144091 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-tre-1 protein	6	P:GO:0009792; F:GO:0004135; P:GO:0005978; P:GO:0005991; C:GO:0044464; F:GO:0004555	-	EC:3.2.1.33; EC:3.2.1.28	IPR001661; PTHR23403:SF1 (PANTHER)
Brugia malayi	hypothetical protein Bm1_05520 [Brugia malayi]	0				-
Caenorhabditis elegans	briggsae cbr-opt-3 protein	3	C:GO:0016020; P:GO:0006810; F:GO:0005215	-		PTHR11654 (PANTHER), PTHR11654:SF12 (PANTHER)

Homo sapiens	matrix metallopeptidase 9 (gelati-se 92kda 92kda type iv collage-se)	12	P:GO:0043065; F:GO:0008270; C:GO:0005615; P:GO:0001501; F:GO:0004222; P:GO:0006508; F:GO:0005518; P:GO:0030225; P:GO:0051549; C:GO:0005578; P:GO:0030574; P:GO:0030198	-	EC:3.4.24.0	-
	-	0				-
Brugia malayi	hypothetical protein Bm1_13445 [Brugia malayi]	0		P:GO:0008152; F:GO:0016787		IPR002018; G3DSA:3.40.50.1820 (GENE3D), PTHR11559:SF30 (PANTHER)
Brugia malayi	hypothetical protein Bm1_19440 [Brugia malayi]	0				PF09808 (PFAM)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	nucleolar complex associated 4 homolog (cerevisiae)	9	P:GO:0040010; P:GO:0000003; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0006898; P:GO:0009792; P:GO:0040018; C:GO:0005634	-		IPR005612; PTHR12455 (PANTHER)
						IPR003599; IPR007110; IPR010939; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF9 (PANTHER), SSF48726 (SUPERFAMILY)

Caenorhabditis elegans	protein arginine n-methyltransferase	0		F:GO:0016277; F:GO:0035243; C:GO:0005634; P:GO:0030154; F:GO:0035241; P:GO:0018216; P:GO:0043046; P:GO:0016568; P:GO:0000387; F:GO:0008469; P:GO:0034969; P:GO:0006479; F:GO:0042393; C:GO:0005737; F:GO:0008276; F:GO:0043021; P:GO:0043393; P:GO:0045449; F:GO:0008757; F:GO:0008168; P:GO:0016571; C:GO:0005829; P:GO:0006349; F:GO:0044020; F:GO:0016740; C:GO:0005575		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	prefoldin subunit 5	9	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0006457; P:GO:0035046; P:GO:0040010; P:GO:0040011; F:GO:0051082; C:GO:0016272	-		IPR004127; IPR009053; IPR011599; PTHR12674 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0003676; P:GO:0000003		IPR003100; G3DSA:2.170.260.10 (GENE3D), PTHR22891 (PANTHER), SSF101690 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	uncharacterized transposase-like protein	0		F:GO:0046872; P:GO:0055114; F:GO:0009055; F:GO:0016491; F:GO:0020037; F:GO:0005506; F:GO:0004497		-

Caenorhabditis elegans	stan	18	P:GO:0016358; P:GO:0042067; P:GO:0016055; P:GO:0007218; P:GO:0065008; P:GO:0007409; F:GO:0004930; P:GO:0007389; F:GO:0005509; C:GO:0016021; P:GO:0007154; P:GO:0007156; P:GO:0023060; P:GO:0050794; P:GO:0051128; P:GO:0051960; C:GO:0044459; P:GO:0048056	-		IPR002126; IPR015919; IPR020894; PTHR10596 (PANTHER)
Caenorhabditis briggsae	tr- isopentenyltransferase 1	2	F:GO:0005488; C:GO:0043231	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	zinc fyve domain containing 16	8	P:GO:0046008; P:GO:0007343; P:GO:0007143; C:GO:0005769; P:GO:0007616; F:GO:0005515; P:GO:0035039; P:GO:0008355	-		IPR022557; PTHR22835 (PANTHER), PTHR22835:SF12 (PANTHER)
Caenorhabditis elegans	bile acid beta-	4	P:GO:0006680; C:GO:0005886; F:GO:0004348; C:GO:0016021	-	EC:3.2.1.45	PTHR12654 (PANTHER), PF12215 (PFAM)
	-	0				-
	-	0				-
Ixodes scapularis	alcohol dehydroge-se domain protein	7	P:GO:0051164; C:GO:0000267; P:GO:0019405; P:GO:0055114; F:GO:0003939; P:GO:0006060; F:GO:0008270	-	EC:1.1.1.14	IPR002085; IPR002328; IPR011032; IPR013154; G3DSA:3.90.180.10 (GENE3D), PTHR11695:SF38 (PANTHER)
Caenorhabditis elegans	and ph domain containing 6	4	F:GO:0005089; C:GO:0005622; P:GO:0035023; F:GO:0008270	-		IPR000219; PTHR12673 (PANTHER), PTHR12673:SF8 (PANTHER)
Caenorhabditis elegans	deah (asp-glu-ala-his) box polypeptide 37	10	P:GO:0040010; P:GO:0008340; P:GO:0000003; P:GO:0002119; F:GO:0005515; F:GO:0000166; F:GO:0004386; P:GO:0006898; P:GO:0009792; P:GO:0016246	-		IPR007502; PTHR18934 (PANTHER), SSF52540 (SUPERFAMILY)
Loa loa	hypothetical protein LOAG_06715 [Loa loa]	0				-

	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	fibronectin type iii domain containing protein	0				-
Caenorhabditis briggsae	nuclear hormone receptor family protein isoform confirmed by transcript evidence	6	F:GO:0003700; F:GO:0043565; F:GO:0003707; C:GO:0005634; F:GO:0008270; P:GO:0006355	-		-
Caenorhabditis briggsae	Hypothetical protein CBG10437 [Caenorhabditis briggsae]	1	P:GO:0008152	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	xanthine dehydroge-se	5	F:GO:0004031; F:GO:0009055; F:GO:0030151; P:GO:0000003; P:GO:0008152	-	EC:1.2.3.1	IPR008274; PTHR11908 (PANTHER), PTHR11908:SF6 (PANTHER)
Caenorhabditis elegans	hypothetical protein F07F6.8 [Caenorhabditis elegans]	0		P:GO:0006869; F:GO:0008289; C:GO:0016021; C:GO:0005576; F:GO:0005515; P:GO:0042157		IPR008405
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	4	C:GO:0045211; P:GO:0007420; C:GO:0014069; F:GO:0017124	-		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF173 (PANTHER)
Caenorhabditis elegans	briggsae cbr-ins-17 protein	5	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0018996; P:GO:0040010	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis briggsae	histone deacetylase 10	8	F:GO:0004407; P:GO:0016575; C:GO:0000118; P:GO:0000122; F:GO:0016566; C:GO:0005737; P:GO:0014003; F:GO:0042826	-		IPR000286; PTHR10625:SF23 (PANTHER), SSF52768 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0004872; C:GO:0016021; C:GO:0016020; P:GO:0016998; F:GO:0005515		IPR006214; PTHR23291:SF14 (PANTHER)
	-	0				SignalP (SIGNALP)
Homo sapiens	un-med protein product [Homo sapiens]	5	C:GO:0016021; P:GO:0045087; P:GO:0009615; F:GO:0005515; C:GO:0005886	-		-
Caenorhabditis briggsae	briggsae cbr-acl-5 protein	0		F:GO:0008415; C:GO:0016021; P:GO:0008152		SignalP (SIGNALP)

	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Pan troglodytes	p antigen member 2b	0				IPR001664; IPR003054
	-	0				-
Caenorhabditis elegans	potassium-transporting atpase alpha chain 1	9	P:GO:0010155; P:GO:0045851; P:GO:0046034; F:GO:0000166; F:GO:0046982; N:GO:0071805; F:GO:0008900; P:GO:0042493; C:GO:0005887	-	EC:3.6.3.10	IPR001757; IPR018303; G3DSA:3.40.1110.10 (GENE3D), PTHR11939:SF100 (PANTHER), SSF81660 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	y box protein 1	14	F:GO:0002039; F:GO:0003697; C:GO:0071204; C:GO:0030425; P:GO:0008284; P:GO:0006396; F:GO:0043565; P:GO:0046627; P:GO:0045944; C:GO:0048471; P:GO:0016071; P:GO:0043066; P:GO:0001701; F:GO:0003729	-		IPR002059; IPR011129; IPR012340; IPR016027; IPR019844; PTHR11544 (PANTHER), PTHR11544:SF8 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR001466; IPR012338; G3DSA:3.40.710.10 (GENE3D), PTHR10566 (PANTHER), PTHR10566:SF6 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-kgb-1 protein	4	F:GO:0004707; P:GO:0006468; F:GO:0005515; F:GO:0005524	-	EC:2.7.11.24	IPR000719; IPR011009; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF62 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Loa loa	hypothetical protein LOAG_07284 [Loa loa]	0				IPR013256; PTHR22691 (PANTHER), PTHR22691:SF7 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	egf-like domain containing protein	0		F:GO:0005509		-

Caenorhabditis briggsae	acid phosphatase family protein confirmed by transcript evidence	0		F:GO:0003993		IPR000560; G3DSA:3.40.50.1240 (GENE3D), PTHR11567 (PANTHER), PTHR11567:SF28 (PANTHER), SignalP (SIGNALP)
	-	0				-
Tribolium castaneum	pol protein	1	F:GO:0005488	-		IPR001584; IPR012337; G3DSA:3.30.420.10 (GENE3D), PTHR10178 (PANTHER), PTHR10178:SF14 (PANTHER)
	-	0				-
Caenorhabditis elegans	calmodulin	38	P:GO:0051533; P:GO:0007052; P:GO:0043277; P:GO:0007268; P:GO:0016060; F:GO:0070855; P:GO:0051726; P:GO:0008049; P:GO:0051383; P:GO:0016061; P:GO:0016062; P:GO:0016477; P:GO:0042981; P:GO:0040010; C:GO:0031476; C:GO:0030424; P:GO:0006898; C:GO:0005886; C:GO:0005737; P:GO:0051296; F:GO:0004683; C:GO:0000922; P:GO:0009792; P:GO:0006468; C:GO:0048786; C:GO:0005875; F:GO:0005524;	-	EC:2.7.11.17	-
Caenorhabditis briggsae	odd oz protein	0		P:GO:0007366; P:GO:0048058; P:GO:0008360; P:GO:0022416; P:GO:0001745; C:GO:0016020; P:GO:0045467; C:GO:0005578; P:GO:0042051; C:GO:0005887; P:GO:0007155		IPR000742; IPR013032
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Loa loa	protein-tyrosine phosphatase containing protein	0		P:GO:0016311; F:GO:0016791; P:GO:0006470; F:GO:0016787; F:GO:0004725; F:GO:0004721		IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)

	-	0				-
Caenorhabditis elegans	patched family protein	13	P:GO:0009792; P:GO:0002119; F:GO:0008158; P:GO:0040018; P:GO:0001703; P:GO:0018996; P:GO:0000910; P:GO:0006810; P:GO:0040010; P:GO:0000003; P:GO:0040011; C:GO:0016021; F:GO:0005215	-		-
	-	0				-
Caenorhabditis briggsae	solute carrier family 6 (neurotransmitter betaine gaba) member 12	3	F:GO:0015370; P:GO:0006865; C:GO:0016021	-		IPR000175; PTHR11616:SF16 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	adenylate ki-se 1	7	F:GO:0004017; P:GO:0046034; P:GO:0009165; F:GO:0005524; F:GO:0005515; C:GO:0005737; C:GO:0005634	-	EC:2.7.4.3	-
Caenorhabditis elegans	propionyl- carboxylase beta mitochondrial precursor	9	F:GO:0004658; F:GO:0003989; P:GO:0006633; C:GO:0009317; C:GO:0005739; P:GO:0009062; F:GO:0005515; F:GO:0000166; P:GO:0009063	-	EC:6.4.1.3; EC:6.4.1.2	IPR000022; IPR011762; IPR011763; G3DSA:3.90.226.10 (GENE3D), PTHR22855 (PANTHER), PTHR22855:SF14 (PANTHER), SSF52096 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				IPR012315
Loa loa	glycosyl transferase	1	F:GO:0016740	-		IPR001296; PTHR13036 (PANTHER), SSF53756 (SUPERFAMILY)
Caenorhabditis elegans	r- termi-l phosphate cyclase-like 1	3	C:GO:0005730; P:GO:0006364; F:GO:0003963	-	EC:6.5.1.4	IPR000228; IPR013792
	-	0				-
	-	0				-
Mus musculus	mCG51545 [Mus musculus]	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	nuclear r- export factor 1	3	F:GO:0005488; P:GO:0006406; C:GO:0005634	-		G3DSA:3.80.10.10 (GENE3D), PTHR10662 (PANTHER), PTHR10662:SF21 (PANTHER), PF09162 (PFAM), PS51450 (PROFILE), SSF52058 (SUPERFAMILY), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	l-threonine dehydroge-se	5	P:GO:0009058; P:GO:0044237; F:GO:0016616; F:GO:0050662; P:GO:0044238	-	EC:1.1.1.0	SignalP (SIGNALP)

Macaca mulatta	sentrin-specific protease 3-like isoform 3	11	F:GO:0003743; C:GO:0016281; C:GO:0005829; F:GO:0003729; P:GO:0045948; P:GO:0031100; F:GO:0008026; P:GO:0006200; F:GO:0000339; F:GO:0005524; F:GO:0005515	-		IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF2 (PANTHER), SSF52540 (SUPERFAMILY)
Brugia malayi	lim domain containing protein	0		F:GO:0005488; F:GO:0016491; P:GO:0008152; F:GO:0003824; F:GO:0008270		-
Camponotus floridanus	uncharacterized transposase-like protein	0		F:GO:0046872; P:GO:0055114; F:GO:0009055; F:GO:0016491; F:GO:0020037; F:GO:0005506; F:GO:0004497		-
Drosophila ananassae	dehydroge-se reductase (sdr family) member 13	0		P:GO:0055114; F:GO:0005488; F:GO:0016491; P:GO:0008152; F:GO:0003824; C:GO:0005576		IPR002198; IPR016040; PTHR19410:SF98 (PANTHER)
	-	0				PTHR12064 (PANTHER)
	-	0				-
Caenorhabditis briggsae	dipeptidyl anminopeptidase	1	F:GO:0008236	-		IPR001375; G3DSA:3.40.50.1820 (GENE3D), PTHR11731 (PANTHER), PTHR11731:SF7 (PANTHER), SSF53474 (SUPERFAMILY)
Caenorhabditis briggsae	amop domain containing protein	1	P:GO:0007160	-		PTHR13802 (PANTHER), PTHR13802:SF2 (PANTHER)
Caenorhabditis elegans	riken cd- 6330409n04 gene variant 1	0		F:GO:0003674; P:GO:0008150		IPR001870; IPR003877; IPR008985; PTHR20951 (PANTHER)
Caenorhabditis briggsae	acetoacetyl- thiolase	9	C:GO:0005875; P:GO:0006633; C:GO:0005739; P:GO:0006090; P:GO:0007052; P:GO:0010171; P:GO:0040011; F:GO:0004315; C:GO:0005811	-	EC:2.3.1.41	IPR002155; IPR016038; IPR016039; IPR020610; IPR020613; IPR020616; IPR020617; PTHR18919:SF7 (PANTHER)
Caenorhabditis briggsae	acetoacetyl- thiolase	9	C:GO:0005875; P:GO:0006633; C:GO:0005739; P:GO:0006090; P:GO:0007052; P:GO:0010171; P:GO:0040011; F:GO:0004315; C:GO:0005811	-	EC:2.3.1.41	IPR002155; IPR016038; IPR016039; IPR020610; IPR020613; IPR020616; IPR020617; PTHR18919:SF7 (PANTHER)
	-	0				-

Caenorhabditis elegans	uncoordi-ted family member (unc-5)	0		P:GO:0007165; F:GO:0005515		PTHR12582 (PANTHER), PTHR12582:SF2 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-unc-82 protein	3	P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	PTHR22971 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	ras and ef-hand domain containing	5	F:GO:0005509; P:GO:0007264; C:GO:0048471; P:GO:0015031; F:GO:0005525	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	P:GO:0007186; C:GO:0016021	-		SignalP (SIGNALP)
Mus musculus	stress-associated endoplasmic reticulum protein 1	17	P:GO:0001501; P:GO:0006486; C:GO:0005840; P:GO:0007009; P:GO:0009791; P:GO:0015031; C:GO:0016021; C:GO:0005789; P:GO:0010259; P:GO:0045727; P:GO:0048644; P:GO:0046622; P:GO:0006006; P:GO:0055085; P:GO:0060124; P:GO:0030968; P:GO:0032024	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				IPR004988
Caenorhabditis elegans	hypothetical protein F15A8.7 [Caenorhabditis elegans]	0				IPR006954
Caenorhabditis briggsae	briggsae cbr-wah-1 protein	0		P:GO:0007067; F:GO:0050660; C:GO:0005737; P:GO:0055114; F:GO:0016491; F:GO:0003824; P:GO:0008152; P:GO:0045454; F:GO:0005488		-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-cpg-4 protein	0				-
Caenorhabditis briggsae	briggsae cbr-cpg-4 protein	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-cpg-4 protein	0				-
	-	0				-
Caenorhabditis elegans	tbc (tre-2 bub2 cdc16) domain family member (tbc-1)	0		P:GO:0032313; C:GO:0005622; F:GO:0005097		IPR000195; PTHR13297 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	cg10671 cg10671-pa	1	P:GO:0000003	-		IPR019388; PTHR23129 (PANTHER), SignalP (SIGNALP)

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		C:GO:0016021; P:GO:0016042; P:GO:0006644		IPR013090; IPR016090
Caenorhabditis elegans	briggsae cbr-dpf-5 protein	3	C:GO:0005773; F:GO:0016787; C:GO:0009507	-		IPR001375; G3DSA:3.40.50.1820 (GENE3D), PTHR11731 (PANTHER), PTHR11731:SF7 (PANTHER), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-pqn-24 protein	0				-
Caenorhabditis elegans	atp-binding cassette sub-family f member 1	8	P:GO:0040035; P:GO:0009792; C:GO:0005840; F:GO:0043024; F:GO:0016887; F:GO:0005524; P:GO:0006412; F:GO:0043023	-	EC:3.6.5.3	IPR003439; IPR003593; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR19211 (PANTHER), PTHR19211:SF14 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	wd repeat protein 7	2	P:GO:0008593; P:GO:0007035	-		-
	-	0				-
Homo sapiens	mhc class ib antigen	5	P:GO:0006955; F:GO:0032393; C:GO:0016021; P:GO:0002474; C:GO:0042612	-		-
	-	0				-
Caenorhabditis elegans	hypothetical protein F40F4.6 [Caenorhabditis elegans]	1	P:GO:0040010	-		SignalP (SIGNALP)
	-	0				-
Loa loa	novel protein vertebrate fibronectin type iii domain containing protein family	0		P:GO:0008152; F:GO:0016787; F:GO:0016798; F:GO:0016162		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-vha-5 protein	5	F:GO:0005516; F:GO:0008553; P:GO:0015986; C:GO:0045202; C:GO:0000220	-	EC:3.6.3.6	IPR002490; PTHR11629:SF23 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0055114; F:GO:0005488; F:GO:0016491; P:GO:0008152; F:GO:0003824		-
Brugia malayi	d- primase	0		F:GO:0003676; P:GO:0006260; F:GO:0008270; F:GO:0003896; C:GO:0005575; C:GO:0005622		-

Loa loa	u3 small nucleolar r- (u3 snor-) associated protein	0		P:GO:0042254; P:GO:0006898; C:GO:0030529; C:GO:0005634; P:GO:0000003; F:GO:0003674; P:GO:0002119; C:GO:0005575; P:GO:0040039; P:GO:0040010; P:GO:0040007; P:GO:0008150; P:GO:0040035		SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-d--2 protein	0		F:GO:0004386; F:GO:0003677; P:GO:0006260; F:GO:0004003; P:GO:0006200; F:GO:0000166; F:GO:0003674; F:GO:0017111; F:GO:0005524; C:GO:0005575; P:GO:0008150		IPR014808; PTHR10887 (PANTHER), PTHR10887:SF14 (PANTHER)
Caenorhabditis elegans	uncoordi-ted protein isoform partially confirmed by transcript evidence	8	F:GO:0004872; P:GO:0006629; F:GO:0005219; P:GO:0006816; P:GO:0006874; P:GO:0055085; F:GO:0005509; C:GO:0016021	-		-
	-	0				-
Caenorhabditis elegans	trehalose 6-phosphate synthase	3	F:GO:0003825; P:GO:0034608; P:GO:0005992	-	EC:2.4.1.15	IPR000418
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	P:GO:0040010	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	major facilitator superfamily protein	3	P:GO:0055085; C:GO:0016021; P:GO:0019915	-		PTHR11662 (PANTHER), PTHR11662:SF21 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Strongylocentrotus purpuratus	ensangp00000010363	0				-
Caenorhabditis briggsae	briggsae cbr-smp-2 protein	0				-
Caenorhabditis briggsae	Hypothetical protein CBG11982 [Caenorhabditis briggsae]	0				-
	-	0				-
Taeniopygia guttata	eukaryotic translation initiation factor 1	5	C:GO:0005737; F:GO:0005515; P:GO:0006950; P:GO:0045948; F:GO:0003743	-		IPR001950; G3DSA:3.30.780.10 (GENE3D), PTHR10388 (PANTHER)

Caenorhabditis briggsae	Hypothetical protein CBG08488 [Caenorhabditis briggsae]	1	P:GO:0000003	-		PTHR11254 (PANTHER), PTHR11254:SF8 (PANTHER)
Loa loa	a-phase-promoting complex subunit 2	1	F:GO:0005515	-		IPR001373; PTHR11932 (PANTHER), PTHR11932:SF5 (PANTHER)
Caenorhabditis briggsae	alcohol dehydroge-se class-3	17	P:GO:0003016; F:GO:0008270; P:GO:0006069; F:GO:0018467; P:GO:0001523; C:GO:0005739; F:GO:0051903; P:GO:0055114; P:GO:0051409; P:GO:0051775; P:GO:0046294; P:GO:0045777; F:GO:0004024; F:GO:0042803; P:GO:0032496; P:GO:0018119; F:GO:0005504	-	EC:1.2.1.46; EC:1.1.1.284	-
	-	0				-
Loa loa	mothers against decapentaplegic homolog 4	17	P:GO:0007179; P:GO:0031325; P:GO:0043009; P:GO:0090100; P:GO:0048513; P:GO:0051128; P:GO:0040007; P:GO:0048646; P:GO:0048729; P:GO:0009952; C:GO:0005667; P:GO:0030154; P:GO:0048523; P:GO:0051239; P:GO:0010604; F:GO:0046332; P:GO:0006355	-		-
Brugia malayi	cation channel family protein	7	P:GO:0043052; F:GO:0004672; P:GO:0055085; P:GO:0010960; P:GO:0006811; C:GO:0016021; F:GO:0005216	-		PTHR13800 (PANTHER)
Caenorhabditis elegans	sushi domain containing 2	2	C:GO:0016021; P:GO:0007160	-		IPR005533; PTHR13802 (PANTHER), PTHR13802:SF2 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	eb-1 binding protein 2-like	4	P:GO:0040007; P:GO:0040035; P:GO:0006898; P:GO:0002119	-		IPR008610
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-pqn-45 protein	1	P:GO:0009792	-		-

Caenorhabditis elegans	briggsae cbr-pqn-45 protein	1	P:GO:0009792	-		-
Caenorhabditis elegans	acetoacetyl- synthetase	1	P:GO:0010033	-		PTHR11968 (PANTHER), PTHR11968:SF40 (PANTHER), PF11930 (PFAM)
Caenorhabditis elegans	caveolin 2	26	F:GO:0004871; P:GO:0009888; C:GO:0030133; P:GO:0042127; F:GO:0051219; C:GO:0005624; P:GO:0070836; F:GO:0031748; C:GO:0031234; P:GO:0006906; C:GO:0005794; P:GO:0048513; C:GO:0005829; C:GO:0009986; P:GO:0007088; P:GO:0006629; C:GO:0043234; P:GO:0007268; P:GO:0048278; C:GO:0048471; F:GO:0042803; C:GO:0005811; C:GO:0005901; P:GO:0060161; C:GO:0005887; F:GO:0019905	-		-
	-	0				-
	-	0				-
	-	0				-
Loa loa	prion-like-(q n-rich)-domain-bearing protein family member (pqn-44)	0				IPR012937; PTHR12974 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0040010; P:GO:0009792; P:GO:0000003	-		-
Caenorhabditis elegans	ddx55_caeel ame: full=probable atp-dependent r- helicase ddx55 homolog ame: full=dead box protein 55	0		F:GO:0004386; C:GO:0016020; P:GO:0017038; F:GO:0003677; F:GO:0016787; F:GO:0003676; F:GO:0000166; P:GO:0000003; F:GO:0003723; F:GO:0005524; F:GO:0008026; P:GO:0002119; P:GO:0040010; P:GO:0040007		-
Brugia malayi	angiomotin	1	F:GO:0005515	-		IPR009114; PTHR14826:SF2 (PANTHER)

Caenorhabditis briggsae	inorganic p hosphatase family member (pyp-1)	14	P:GO:0040010; C:GO:0016021; P:GO:0042766; P:GO:0006796; P:GO:0000003; P:GO:0035076; P:GO:0002119; F:GO:0000287; F:GO:0004427; P:GO:0040039; P:GO:0009792; C:GO:0005737; P:GO:0006350; C:GO:0016589	-	EC:3.6.1.1	IPR008162
	-	0				G3DSA:2.60.120.20 (GENE3D)
Caenorhabditis elegans	ras-related protein rab-6a	2	C:GO:0016023; F:GO:0000166	-		IPR001806; IPR005225; IPR013753; IPR015600; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	briggsae cbr-ced-5 protein	7	F:GO:0005083; P:GO:0043652; C:GO:0005886; F:GO:0032403; F:GO:0019899; P:GO:0040039; F:GO:0017124	-		PTHR23317 (PANTHER), PTHR23317:SF16 (PANTHER)
	-	0				-
Caenorhabditis remanei	tuftelin-interacting protein 11	10	P:GO:0006396; C:GO:0005681; F:GO:0003676; P:GO:0040007; C:GO:0016607; P:GO:0040035; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0009792	-		IPR022783; PTHR23329 (PANTHER), PTHR23329:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-tat-2 protein	7	C:GO:0016021; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0015914; F:GO:0000287; F:GO:0004012	-	EC:3.6.3.1	-
Loa loa	hypothetical protein LOAG_11376 [Loa loa]	0				IPR001781; PTHR18973 (PANTHER), PTHR18973:SF49 (PANTHER), SSF57716 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	protein-tyrosine phosphatase containing protein	3	F:GO:0004721; P:GO:0009792; P:GO:0000003	-	EC:3.1.3.16	IPR000242; IPR000387; IPR016130; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)

Caenorhabditis briggsae	glycogen synthase	7	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0005978; F:GO:0005515; F:GO:0004373; P:GO:0040011	-	EC:2.4.1.11	IPR008631
Caenorhabditis briggsae	Hypothetical protein CBG14225 [Caenorhabditis briggsae]	0				IPR010916; SignalP (SIGNALP)
	-	0				-
	-	0				-
Ciona intestinalis	transcription factor protein	4	F:GO:0003700; F:GO:0003677; C:GO:0016602; P:GO:0006355	-		IPR001289
Caenorhabditis briggsae	mosc domain-containing protein mitochondrial precursor	2	C:GO:0005743; F:GO:0005515	-		IPR005303; PTHR14237 (PANTHER), SignalP (SIGNALP), SSF141673 (SUPERFAMILY)
Caenorhabditis briggsae	mosc domain-containing protein mitochondrial precursor	2	C:GO:0005743; F:GO:0005515	-		IPR005303; PTHR14237 (PANTHER), SignalP (SIGNALP), SSF141673 (SUPERFAMILY)
Caenorhabditis elegans	ryanodine receptor homologue	9	P:GO:0055085; P:GO:0006629; C:GO:0005875; F:GO:0005509; C:GO:0016021; P:GO:0006874; P:GO:0006816; F:GO:0005219; P:GO:0006936	-		IPR000699; IPR015925; PTHR13715:SF11 (PANTHER)
	-	0				-
Brugia malayi	histone deacetylase family protein	4	F:GO:0004407; P:GO:0045449; C:GO:0005737; C:GO:0005634	-		SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	suppressor of t-cell receptor sig-ling 1	0		F:GO:0004619; F:GO:0004872; P:GO:0016070; F:GO:0003824; C:GO:0005622; F:GO:0016853		IPR013078; G3DSA:3.40.50.1240 (GENE3D), PTHR16469 (PANTHER), PTHR16469:SF5 (PANTHER), SSF53254 (SUPERFAMILY)
Caenorhabditis elegans	atp-dependent permease mdl2	5	F:GO:0042626; P:GO:0043581; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		IPR011527; IPR017940; G3DSA:1.20.1560.10 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF76 (PANTHER)
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
Caenorhabditis briggsae	bccip_caebr ame: full=protein bccip homolog	7	P:GO:0009792; P:GO:0002119; P:GO:0016246; P:GO:0040011; P:GO:0040007; P:GO:0006898; P:GO:0008406	-		-
Caenorhabditis elegans	glutaminyl-tr- synthase (glutamine-hydrolyzing)-like 1	2	F:GO:0016884; P:GO:0019915	-	EC:6.3.5.0	IPR000120; PTHR11895:SF7 (PANTHER)
Loa loa	ov39 antigen -like	0				SignalP (SIGNALP)

Caenorhabditis briggsae	briggsae cbr-gly-3 protein	4	F:GO:0004653; C:GO:0005795; P:GO:0009312; C:GO:0016020	-	EC:2.4.1.41	PTHR11675 (PANTHER), SSF53448 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-flp-13 protein	3	C:GO:0005576; P:GO:0007218; P:GO:0019915	-		IPR002544; PTHR20986 (PANTHER)
	-	0				-
	-	0				-
Loa loa	fanconi anemia complementation group d2 isoform	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	ain family member (clp-1)	7	C:GO:0005737; P:GO:0016540; F:GO:0004198; F:GO:0005509; P:GO:0008219; P:GO:0006508; C:GO:0016020	-		IPR001300; IPR022684; PTHR10183 (PANTHER), PTHR10183:SF45 (PANTHER), SSF54001 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-pmk-3 protein	4	P:GO:0006950; C:GO:0005634; F:GO:0004674; F:GO:0000166	-	EC:2.7.11.0	-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0007160; C:GO:0016021; C:GO:0005575		IPR005533; PTHR13802 (PANTHER), PTHR13802:SF1 (PANTHER)
Caenorhabditis elegans	briggsae cbr-scp-1 protein	1	P:GO:0009792	-		-
	-	0				-
Caenorhabditis elegans	af303255_1 guanylate-binding protein	4	C:GO:0016021; P:GO:0000003; F:GO:0003924; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR015894; G3DSA:3.40.50.300 (GENE3D), PTHR10751 (PANTHER), PTHR10751:SF3 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				IPR008139; IPR011001; SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein C07G1.2 [Caenorhabditis elegans]	0		P:GO:0006508; F:GO:0004252; F:GO:0005488; F:GO:0005044; F:GO:0003824; C:GO:0016020		IPR001190; IPR017448; G3DSA:3.10.250.10 (GENE3D)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		-
Brugia malayi	sh3 domain-binding protein 5-like	0		F:GO:0003674; P:GO:0008150; C:GO:0005575		IPR007940
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)

Homo sapiens	cathepsin z	6	C:GO:0005615; P:GO:0060441; C:GO:0005764; F:GO:0004197; P:GO:0006508; C:GO:0005783	-	EC:3.4.22.0	SignalP (SIGNALP)
Brugia malayi	neuroepithelial cell transforming gene 1	0		F:GO:0005089; P:GO:0035023; F:GO:0005085; P:GO:0001558; C:GO:0005634; P:GO:0006915; P:GO:0023034; C:GO:0005737; P:GO:0007165; C:GO:0005622; C:GO:0005829; P:GO:0008624; F:GO:0005509		IPR000219
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	histone-lysine n-methyltransferase	0		F:GO:0016740; C:GO:0048188; C:GO:0005694; F:GO:0008168; F:GO:0003677; C:GO:0005634; F:GO:0003676; F:GO:0000166; F:GO:0018024; P:GO:0016568; F:GO:0005515		IPR001214; G3DSA:2.170.270.10 (GENE3D), PTHR22884 (PANTHER), PTHR22884:SF17 (PANTHER), SSF82199 (SUPERFAMILY)
Haemonchus contortus	atp-binding sub-family b (mdr tap) member 1	5	P:GO:0055085; P:GO:0006629; F:GO:0042626; F:GO:0005524; C:GO:0005887	-		IPR001140; IPR011527; IPR017940; G3DSA:1.20.1560.10 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF96 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	phenylacetyl- ligase	3	P:GO:0019915; F:GO:0003824; P:GO:0006629	-		IPR000873; IPR020845; G3DSA:3.40.50.980 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF43 (PANTHER), SSF56801 (SUPERFAMILY)
Caenorhabditis briggsae	nol1 nop2 sun domain family	0		F:GO:0008168; F:GO:0016740; P:GO:0008150; C:GO:0005575		-
Loa loa	hypothetical protein LOAG_08240 [Loa loa]	0				-
	-	0				-
	-	0				-
Brugia malayi	wd40 associated region in tfiid subunit family protein	0		F:GO:0003743; P:GO:0045449; F:GO:0030528; C:GO:0005634		IPR007582; SignalP (SIGNALP)
Caenorhabditis elegans	carbonic anhydrase	4	P:GO:0044237; F:GO:0008270; F:GO:0004089; P:GO:0015976	-	EC:4.2.1.1	IPR001765; PTHR11002:SF1 (PANTHER)

Caenorhabditis elegans	eb module family protein	2	F:GO:0005488; F:GO:0003824	-		IPR006149; IPR006210; PD936484 (PRODOM)
	-	0				-
Mus musculus	5-oxoproli-se (atp-hydrolysing)	3	F:GO:0017168; P:GO:0006749; F:GO:0000166	-	EC:3.5.2.9	IPR002821; IPR003692; PTHR11365 (PANTHER)
Homo sapiens	mhc class i antigen	0				-
Caenorhabditis briggsae	regulator of presy-ptic morphology protein	4	P:GO:0030071; F:GO:0005515; F:GO:0008270; C:GO:0005680	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	isoleucyl-tr- synthetase	5	F:GO:0004822; F:GO:0008270; C:GO:0005739; P:GO:0006428; F:GO:0005524	-	EC:6.1.1.5	IPR002300; IPR002301; IPR014729; PTHR11946 (PANTHER), SSF52374 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	briggsae cbr-pqn-37 protein	0		C:GO:0016021; P:GO:0007186		SSF57501 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Loa loa	neurogenic locus notch homolog protein 2-like	0		P:GO:0007155; C:GO:0016020		IPR000436; IPR016060; PTHR19325 (PANTHER), PTHR19325:SF25 (PANTHER)
Caenorhabditis elegans	aldo keto reductase	2	F:GO:0016491; P:GO:0055114	-		IPR001395; IPR023210; PTHR11732:SF34 (PANTHER)
	-	0				-
Caenorhabditis elegans	- ca exchangers family member (ncx-2)	14	P:GO:0002026; P:GO:0055085; P:GO:0006814; C:GO:0030315; F:GO:0005432; P:GO:0040010; F:GO:0031072; P:GO:0045214; C:GO:0016021; P:GO:0000003; P:GO:0006874; C:GO:0005624; P:GO:0006816; P:GO:0007154	-		IPR004836; PTHR11878 (PANTHER)
Caenorhabditis briggsae	nematode cuticle collagen n-termi-l domain containing protein	2	P:GO:0040011; P:GO:0010171	-		PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER)
Pongo abelii	xap-5 protein	6	P:GO:0007283; F:GO:0004872; P:GO:0007275; P:GO:0007165; C:GO:0016021; C:GO:0005634	-		IPR007005

Caenorhabditis elegans	hypothetical protein W10D9.5 [Caenorhabditis elegans]	7	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040010; P:GO:0006886; C:GO:0005741; P:GO:0006898	-		-
Caenorhabditis elegans	temporarily assigned gene -me family member (tag-124)	0		F:GO:0003723; P:GO:0009451; F:GO:0009982		-
Caenorhabditis elegans	hypothetical protein Y37E11AL.6 [Caenorhabditis elegans]	0				IPR006210; IPR013032
Caenorhabditis elegans	hypothetical protein F35H10.10 [Caenorhabditis elegans]	4	P:GO:0007186; C:GO:0016021; P:GO:0007165; F:GO:0004930	-		IPR017871; PTHR11336 (PANTHER), PTHR11336:SF8 (PANTHER)
	-	0				-
Homo sapiens	cytochrome c oxidase subunit i	32	[illegible] F:GO:0004129; P:GO:0042127; P:GO:0051602; F:GO:0005515; P:GO:0010243; P:GO:0051412; C:GO:0005792; F:GO:0020037; P:GO:0007568; P:GO:0019371; F:GO:0009055; C:GO:0005743; C:GO:0016021; C:GO:0005789; P:GO:0045907; C:GO:0005794; P:GO:0032811; F:GO:0016702; F:GO:0004601; P:GO:0045987; C:GO:0070469; C:GO:0005635; P:GO:0046688; P:GO:0010700; P:GO:0021549; F:GO:0004666; F:GO:0008289;	-	EC:1.9.3.1; EC:1.13.11.0 ; EC:1.11.1.7; EC:1.14.99.1	-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	family with sequence similarity member a	6	P:GO:0009792; P:GO:0008340; P:GO:0040007; C:GO:0005634; P:GO:0002119; P:GO:0040011	-		IPR007005
	-	0				-
Caenorhabditis elegans	leukocyte receptor cluster member 4 protein	3	F:GO:0008415; C:GO:0016021; P:GO:0008654	-		IPR004299; PTHR13906 (PANTHER), PTHR13906:SF5 (PANTHER)
Caenorhabditis briggsae	cuticlin 1	0		P:GO:0010171		IPR001507; PTHR22907 (PANTHER)
Caenorhabditis elegans	hypothetical protein C15H9.9 [Caenorhabditis elegans]	1	F:GO:0005515	-		SignalP (SIGNALP)

	-	0					-
Caenorhabditis briggsae	heparan sulfate 3-o-sulfotransferase 4	6	F:GO:0008467; C:GO:0005794; P:GO:0030201; C:GO:0016021; C:GO:0005576; P:GO:0019915	-	EC:2.8.2.23	IPR000863; G3DSA:3.40.50.300 (GENE3D), PTHR10605 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	cu++ alpha polypeptide	58	F:GO:0016532; C:GO:0031526; P:GO:0010468; P:GO:0015677; P:GO:0031069; C:GO:0005923; P:GO:0048813; C:GO:0043005; C:GO:0005802; F:GO:0004008; C:GO:0030140; P:GO:0043588; P:GO:0010273; P:GO:0051542; C:GO:0005783; P:GO:0042417; P:GO:0051353; C:GO:0000299; C:GO:0030141; P:GO:0030199; C:GO:0016323; P:GO:0002082; F:GO:0032767; P:GO:0006754; P:GO:0042093; P:GO:0018205; P:GO:0006570; P:GO:0019430;	-	EC:3.6.3.4	IPR001757; IPR006121; IPR006403; IPR008250; IPR018303; G3DSA:2.70.150.10 (GENE3D), G3DSA:3.30.70.100 (GENE3D), PTHR11939:SF38 (PANTHER), SSF81653 (SUPERFAMILY), SSF81660 (SUPERFAMILY), SSF81665 (SUPERFAMILY)
Caenorhabditis elegans	serine threonine specific	0				-
Trichostrongylus vitrinus	protein rio1 ki-se	2	F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	SignalP (SIGNALP)
	-	0				IPR000571; PTHR15092 (PANTHER), PTHR15092:SF2 (PANTHER)
Bos taurus	eukaryotic translation initiation factor subunit m	4	C:GO:0005852; F:GO:0005515; P:GO:0045948; F:GO:0003743	-		PTHR15350 (PANTHER), PTHR15350:SF3 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-

Homo sapiens	milk fat globule-egf factor 8 protein variant	17	P:GO:0001525; P:GO:0006910; F:GO:0008429; C:GO:0009897; P:GO:0043627; P:GO:0050766; C:GO:0005615; P:GO:0006911; P:GO:0007155; F:GO:0005178; F:GO:0001786; C:GO:0031012; P:GO:0044419; P:GO:0008284; C:GO:0005737; C:GO:0019897; P:GO:0007338	-		-
Caenorhabditis briggsae	family protein	1	F:GO:0042802	-		IPR005627
Caenorhabditis elegans	briggsae cbr-daz-1 protein	1	F:GO:0003676	-		-
Caenorhabditis elegans	briggsae cbr-daz-1 protein	1	F:GO:0003676	-		-
Caenorhabditis elegans	briggsae cbr-daz-1 protein	1	F:GO:0003676	-		-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-ptr-14 protein	7	P:GO:0018996; C:GO:0016021; P:GO:0040018; P:GO:0006810; F:GO:0005215; F:GO:0008158; P:GO:0040011	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	r- interference and gene silencing protein	0		F:GO:0003676; F:GO:0003743; P:GO:0008150; C:GO:0005575		IPR003165; IPR012337; PTHR22891 (PANTHER)
Pongo abelii	cysteine- angiogenic 61	13	P:GO:0060710; P:GO:0051789; P:GO:0002041; P:GO:0001558; P:GO:0006935; P:GO:0060716; F:GO:0050840; P:GO:0010811; F:GO:0005520; F:GO:0008201; C:GO:0005576; P:GO:0008283; P:GO:0030198	-		-
	-	0				IPR000436; IPR016060; SignalP (SIGNALP)
	-	0				-
	-	0				-

Caenorhabditis elegans	suppressor with morphological effect on genitalia family member (smg-1)	2	F:GO:0005488; F:GO:0016772	-		IPR013889
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0055114; F:GO:0016491		IPR001534
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-sax-1 protein	12	P:GO:0007243; F:GO:0004674; P:GO:0048814; F:GO:0046872; P:GO:0035317; F:GO:0005524; P:GO:0022416; P:GO:0048800; C:GO:0005938; F:GO:0005515; C:GO:0005634; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR000961; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22985 (PANTHER), PTHR22985:SF33 (PANTHER)
Caenorhabditis elegans	transmembrane cell adhesion receptor mua-3	2	F:GO:0005509; F:GO:0005515	-		IPR000152; IPR006209; IPR006210; IPR013091; G3DSA:2.10.25.10 (GENE3D), PTHR22992 (PANTHER), PTHR22992:SF12 (PANTHER), SSF57196 (SUPERFAMILY)
	-	0				-
	-	0				-
Ancylostoma caninum	metalloprotease 1 precursor	1	F:GO:0008233	-		IPR000859; IPR001506; IPR013032; IPR019742; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF60 (PANTHER)
Caenorhabditis elegans	cmp-sialic acid transporter	5	P:GO:0015780; C:GO:0005794; F:GO:0005338; C:GO:0016021; P:GO:0044238	-		IPR004689; IPR007271; IPR021189; PTHR10231:SF10 (PANTHER), SSF103481 (SUPERFAMILY)
Caenorhabditis elegans	cmp-sialic acid transporter	5	P:GO:0015780; C:GO:0005794; F:GO:0005338; C:GO:0016021; P:GO:0044238	-		IPR004689; IPR007271; IPR021189; PTHR10231:SF10 (PANTHER), SSF103481 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG09106 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	upf0632 protein c2orf89-like	0		C:GO:0016021; C:GO:0016020		-
Caenorhabditis elegans	glutamyl-tr- amidotransferase a subunit	2	F:GO:0016884; P:GO:0019915	-	EC:6.3.5.0	-
Caenorhabditis briggsae	Hypothetical protein CBG18309 [Caenorhabditis briggsae]	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0055114; F:GO:0016491; F:GO:0020037		IPR008333; IPR017938; G3DSA:2.40.30.10 (GENE3D), PTHR19370 (PANTHER), PTHR19370:SF1 (PANTHER)
Caenorhabditis briggsae	upf0487 protein c17orf71-like protein	1	P:GO:0000184	-		IPR019354; PTHR13091 (PANTHER), SignalP (SIGNALP)
	-	0				-
Haemonchus contortus	hypothetical protein [Haemonchus contortus]	0				-

	-	0				-
Caenorhabditis elegans	iron-sulfur cluster assembly accessory protein	1	P:GO:0008152	-		IPR000361; IPR016092; PTHR10072:SF26 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein B0252.1 [Caenorhabditis elegans]	3	F:GO:0005488; F:GO:0004672; P:GO:0040010	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0009792		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-syd-2 protein	1	F:GO:0005515	-		PTHR12587 (PANTHER), PTHR12587:SF2 (PANTHER)
	-	0				-
Caenorhabditis elegans	cg5669	3	F:GO:0008270; F:GO:0003676; C:GO:0005622	-		-
Caenorhabditis briggsae	#NAME?	11	P:GO:0040010; P:GO:0008340; P:GO:0018991; F:GO:0030145; F:GO:0046537; P:GO:0010171; P:GO:0002119; P:GO:0006096; P:GO:0040011; P:GO:0009792; C:GO:0005737	-		IPR005995; IPR006124; IPR011258; IPR017849; IPR017850; SignalP (SIGNALP)
	-	0				-
Brugia malayi	nuclear pore glycoprotein p62	0		C:GO:0005643; F:GO:0017056; F:GO:0005515		IPR007758
Caenorhabditis briggsae	cral trio domain containing protein	1	P:GO:0040010	-		IPR011074; G3DSA:1.10.8.20 (GENE3D)
	-	0				-
Loa loa	cyclin-dependent ki-se 9	10	P:GO:0006367; C:GO:0005730; F:GO:0008353; C:GO:0008023; F:GO:0003677; F:GO:0005515; P:GO:0006368; F:GO:0000166; P:GO:0008283; P:GO:0006468	-	EC:2.7.11.23	G3DSA:1.10.510.10 (GENE3D)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	4	P:GO:0009792; P:GO:0010171; P:GO:0040017; P:GO:0006898	-		IPR002656; IPR006621; PTHR11161 (PANTHER)
Caenorhabditis briggsae	sideroflexin 2	4	C:GO:0016020; F:GO:0008324; P:GO:0006812; P:GO:0055085	-		IPR004686; PTHR11153:SF7 (PANTHER)
Caenorhabditis elegans	general substrate transporter:major facilitator superfamily mfs_1 transporter	6	C:GO:0016021; P:GO:0009792; P:GO:0040010; P:GO:0055085; F:GO:0005215; P:GO:0002119	-		IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11600 (PANTHER), PTHR11600:SF28 (PANTHER), SignalP (SIGNALP)

Brugia malayi	component of oligomeric golgi complex 6	1	C:GO:0017119	-		IPR010490
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	temporarily assigned gene -me family member (tag-163)	3	C:GO:0030054; F:GO:0005515; P:GO:0009987	-		IPR000980; IPR006020; IPR011993; IPR013625; PTHR12583 (PANTHER), PTHR12583:SF7 (PANTHER), SSF50729 (SUPERFAMILY), SSF55550 (SUPERFAMILY)
	-	0				-
	-	0				-
Tribolium castaneum	histone deacetylase 11	0		P:GO:0005975; F:GO:0016787; F:GO:0004650		-
Loa loa	rho gdp-dissociation inhibitor 2	2	C:GO:0005737; F:GO:0005094	-		-
Caenorhabditis elegans	briggsae cbr-gei-6 protein	0		F:GO:0016740; C:GO:0009986; F:GO:0004674; C:GO:0016020; F:GO:0004672; F:GO:0005083; F:GO:0003677; C:GO:0015629; F:GO:0000166; P:GO:0006468; F:GO:0005524; F:GO:0016301; P:GO:0006461; F:GO:0005515; P:GO:0008154; C:GO:0005618		-
Homo sapiens	fibronectin isoform cra_n	13	P:GO:0018149; P:GO:0016477; P:GO:0001525; P:GO:0008360; C:GO:0005793; C:GO:0031093; P:GO:0034446; F:GO:0005518; C:GO:0005577; F:GO:0008201; C:GO:0005578; F:GO:0005201; P:GO:0006953	-		PTHR19143 (PANTHER), PTHR19143:SF6 (PANTHER)
Caenorhabditis briggsae	mesoderm development candiate isoform cra_b	1	C:GO:0044464	-		IPR019330; PTHR17600 (PANTHER)
Teladorsagia circumcincta	class 3 lipase protein	2	F:GO:0004806; P:GO:0006629	-	EC:3.1.1.3	IPR002921; G3DSA:3.40.50.1820 (GENE3D), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0046872; P:GO:0008152; F:GO:0043874; P:GO:0019509		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0006508; F:GO:0008270		IPR016181
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	cmgc cdk protein ki-se	0		F:GO:0004672; F:GO:0005524; F:GO:0000166; P:GO:0006468; F:GO:0004674		PTHR11295 (PANTHER), PTHR11295:SF95 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	daf-16-dependent longevity (wt but not daf-16 lifespan increased) family member (ddl-3)	2	P:GO:0008340; P:GO:0040010	-		SignalP (SIGNALP)
Loa loa	hypothetical protein LOAG_07593 [Loa loa]	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	proteasome (macropain) 26s non- 12	6	P:GO:0051436; P:GO:0051437; C:GO:0005838; P:GO:0000003; P:GO:0031145; F:GO:0005515	-		-
Tetraodon nigroviridis	dead (asp-glu-ala-asp) box polypeptide 1	9	F:GO:0003723; F:GO:0008026; P:GO:0000245; F:GO:0005524; C:GO:0010494; F:GO:0005515; P:GO:0006446; P:GO:0007275; F:GO:0003724	-		IPR003877; PTHR12381 (PANTHER), PTHR12381:SF10 (PANTHER)
	-	0				-
Caenorhabditis elegans	post-gpi attachment to proteins factor 2	5	F:GO:0008565; P:GO:0006506; C:GO:0016021; C:GO:0000139; C:GO:0005789	-		IPR019402; PTHR12892 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				PTHR12187 (PANTHER), PTHR12187:SF2 (PANTHER)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG12630 [Caenorhabditis briggsae]	0		C:GO:0016020		-
Caenorhabditis elegans	abnormal embroygenesis family member (emb-27)	0		P:GO:0000003; P:GO:0040035; P:GO:0009792; P:GO:0007126; P:GO:0007067		IPR011990; IPR013026
Caenorhabditis briggsae	uncoordi-ted family member (unc-89)	0				IPR013098; IPR013783
Caenorhabditis elegans	briggsae cbr-hmg-5 protein	0		C:GO:0005694; F:GO:0003677; C:GO:0005634		IPR000910; IPR009071; PTHR13711 (PANTHER)
	-	0				-

Caenorhabditis elegans	utrophin	9	F:GO:0005277; P:GO:0015870; P:GO:0001954; P:GO:0007271; P:GO:0046716; F:GO:0005515; P:GO:0040017; C:GO:0016010; C:GO:0005737	-		IPR002017; IPR005829; G3DSA:1.20.58.60 (GENE3D), SSF46966 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-nsh-1 protein	0				-
	-	0				-
Tomato ringspot virus	polyprotein	1	F:GO:0016787	-		IPR001205; G3DSA:3.30.70.270 (GENE3D), SSF56672 (SUPERFAMILY)
	-	0				-
Brugia malayi	lethal family member (let-805)	8	P:GO:0018996; P:GO:0009792; P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		IPR013783
Caenorhabditis remanei	protein ki-se family member (kin-20)	14	P:GO:0040010; P:GO:0016055; F:GO:0004674; P:GO:0000003; F:GO:0005524; P:GO:0010171; P:GO:0002119; P:GO:0040011; P:GO:0032436; P:GO:0009792; C:GO:0005737; P:GO:0040018; C:GO:0005634; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017441; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF18 (PANTHER)
Mus musculus	transmembrane protein isoform cra_a	1	C:GO:0016021	-		-
	-	0				-
Brugia malayi	tsc-22 dip bun family protein	2	P:GO:0006970; F:GO:0005515	-		IPR000580
Caenorhabditis elegans	protein ki-se c	4	P:GO:0006468; F:GO:0046872; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR000008; G3DSA:2.60.40.150 (GENE3D)
Pongo abelii	complement component 4a (rodgers blood group)	5	C:GO:0005615; P:GO:0006957; F:GO:0005515; P:GO:0006958; F:GO:0004866	-		-

Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0030247; C:GO:0016021; F:GO:0016787; F:GO:0003676; P:GO:0016042; C:GO:0005576; F:GO:0003824; F:GO:0005044; P:GO:0006935; F:GO:0047391; P:GO:0008152; F:GO:0046872; P:GO:0006955		IPR002591; IPR017849; IPR017850; PTHR10151 (PANTHER), PTHR10151:SF28 (PANTHER)
	-	0				-
Caenorhabditis briggsae	uncoordi-ted family member (unc-43)	21	P:GO:0006468; F:GO:0004683; P:GO:0040018; P:GO:0040017; C:GO:0048786; P:GO:0008049; P:GO:0007616; C:GO:0005737; C:GO:0045211; F:GO:0046872; C:GO:0030425; P:GO:0007528; P:GO:0007067; C:GO:0030424; P:GO:0051932; C:GO:0005886; P:GO:0006952; F:GO:0005516; F:GO:0005524; P:GO:0051489; C:GO:0005954	-	EC:2.7.11.17	IPR000719; IPR011009; IPR015742; IPR017442; IPR020636; G3DSA:1.10.510.10 (GENE3D)
	-	0				-
Loa loa	briggsae cbr-hyl-2 protein	0		C:GO:0016021; C:GO:0016020		-
	-	0				SignalP (SIGNALP)
	-	0				IPR018801; SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	vent 1 transcription factor	2	F:GO:0003677; P:GO:0045449	-		-
	-	0				SignalP (SIGNALP)

Nematostella vectensis	forkhead box n4	26	F:GO:0016566; C:GO:0000785; P:GO:0008016; P:GO:0048813; P:GO:0043193; C:GO:0005701; P:GO:0007389; P:GO:0007517; P:GO:0007400; F:GO:0003704; C:GO:0005730; F:GO:0016563; C:GO:0005667; P:GO:0007391; P:GO:0048663; P:GO:0008105; F:GO:0003705; P:GO:0010551; P:GO:0048749; P:GO:0051090; F:GO:0003690; F:GO:0008301; F:GO:0010843; F:GO:0008134; P:GO:0007476; P:GO:0006325	-		IPR001766; IPR011991; IPR018122; SSF46785 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	myosin heavy chain	6	F:GO:0003779; C:GO:0016459; F:GO:0005524; F:GO:0003774; C:GO:0031672; P:GO:0007626	-		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	4	P:GO:0040026; P:GO:0007052; F:GO:0005515; P:GO:0051301	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-cdh-1 protein	5	P:GO:0002119; P:GO:0007155; P:GO:0040010; P:GO:0040011; C:GO:0016020	-		-
Caenorhabditis elegans	testis expressed 10	3	P:GO:0040010; P:GO:0006898; P:GO:0002119	-		IPR011989; IPR016024; PTHR16056 (PANTHER), PTHR16056:SF2 (PANTHER), PF12333 (PFAM)
	-	0				-
Xenopus laevis	sideroflexin 1	7	C:GO:0005743; F:GO:0005515; F:GO:0008324; P:GO:0030218; P:GO:0055085; C:GO:0016021; P:GO:0006826	-		IPR004686; PTHR11153:SF9 (PANTHER)
	-	0				SignalP (SIGNALP)

	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	inositol -trisphosphate receptor	3	P:GO:0006810; C:GO:0044464; F:GO:0005216	-		IPR015925; PTHR13715:SF2 (PANTHER)
	-	0				-
Haemonchus contortus	thioredoxin reductase 2	8	P:GO:0009987; C:GO:0005739; F:GO:0005515; F:GO:0000166; P:GO:0008152; F:GO:0050662; P:GO:0000305; F:GO:0004791	-	EC:1.8.1.9	IPR006338; IPR013027; PR00411 (PRINTS), G3DSA:3.50.50.60 (GENE3D), PTHR22912 (PANTHER), SSF51905 (SUPERFAMILY)
Loa loa	zag-1	6	F:GO:0030528; F:GO:0003700; F:GO:0043565; C:GO:0005634; F:GO:0008270; P:GO:0006355	-		-
Caenorhabditis elegans	s-adenosylmethionine mitochondrial carrier protein	4	C:GO:0016021; C:GO:0005739; F:GO:0005488; P:GO:0055085	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF45 (PANTHER)
	-	0				-
Caenorhabditis elegans	protein-tyrosine phosphatase containing protein	2	F:GO:0016791; P:GO:0009792	-	EC:3.1.3.0	IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-lam-3 protein	5	C:GO:0005606; P:GO:0030334; P:GO:0045995; P:GO:0030155; F:GO:0005102	-		-
	-	0				-
Caenorhabditis elegans	-d-dependent malic mitochondrial precursor	9	P:GO:0009060; F:GO:0046872; P:GO:0006090; F:GO:0051287; P:GO:0006108; P:GO:0055114; F:GO:0004473; C:GO:0005739; P:GO:0006800	-	EC:1.1.1.40	IPR016040; PTHR23406 (PANTHER), PTHR23406:SF2 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Brugia malayi	uncharacterized protein c4orf34 homolog	1	F:GO:0005515	-		IPR020309
	-	0				-
Homo sapiens	keratinocyte associated protein 2	4	C:GO:0008250; C:GO:0016021; F:GO:0004579; P:GO:0018279	-	EC:2.4.1.119	-

Caenorhabditis briggsae	briggsae cbr-cyp-33a1 protein	2	F:GO:0046872; P:GO:0040010	-		IPR001128; IPR002401; PTHR19383:SF67 (PANTHER)
Caenorhabditis elegans	daf-16 foxo germline tumor affecting family member (dct-6)	0				-
Caenorhabditis briggsae	trehalose 6-phosphate synthase	3	F:GO:0003825; P:GO:0034608; P:GO:0005992	-	EC:2.4.1.15	IPR001830; G3DSA:3.40.50.2000 (GENE3D), PTHR10788 (PANTHER), SignalP (SIGNALP), SSF53756 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-rap-1 protein	5	F:GO:0005525; C:GO:0005886; C:GO:0005829; P:GO:0007264; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001806; IPR003577; IPR005225; IPR013753; IPR020849; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF126 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Brugia malayi	co-repressor protein groucho	4	P:GO:0045449; P:GO:0009887; F:GO:0005515; P:GO:0007165	-		IPR001680; IPR009146; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR10814 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	peptidase (mitochondrial processing) alpha	5	F:GO:0046872; C:GO:0005743; F:GO:0004222; C:GO:0005759; P:GO:0006508	-	EC:3.4.24.0	IPR011237; IPR011249; IPR011765; PTHR11851 (PANTHER), PTHR11851:SF49 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	8	P:GO:0009792; P:GO:0002119; P:GO:0006468; F:GO:0005524; P:GO:0000003; P:GO:0040011; P:GO:0040007; F:GO:0004674	-	EC:2.7.11.0	IPR011009; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
	-	0				-

Caenorhabditis elegans	structural mainte-nce of chromosomes 1a	18	P:GO:0000075; P:GO:0007052; P:GO:0042770; C:GO:0000777; P:GO:0051301; C:GO:0005737; F:GO:0046982; F:GO:0003777; P:GO:0008380; P:GO:0007126; C:GO:0008280; C:GO:0000794; P:GO:0007064; P:GO:0009314; F:GO:0003682; P:GO:0032876; F:GO:0005524; P:GO:0006281	-		IPR003395; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR18937 (PANTHER), PTHR18937:SF12 (PANTHER), SSF52540 (SUPERFAMILY)
Macaca mulatta	eukaryotic translation initiation factor isoform 1	11	F:GO:0003743; C:GO:0016281; C:GO:0005829; F:GO:0003729; P:GO:0045948; P:GO:0031100; F:GO:0008026; P:GO:0006200; F:GO:0000339; F:GO:0005524; F:GO:0005515	-		IPR000629; IPR011545; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF2 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	eukaryotic translation initiation factor 3 subunit b	14	F:GO:0003743; P:GO:0040010; F:GO:0003723; P:GO:0008340; P:GO:0000003; C:GO:0005852; P:GO:0010171; P:GO:0019915; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0006446; P:GO:0006898; P:GO:0009792	-		SignalP (SIGNALP)
Caenorhabditis elegans	mitochondrial sorting of proteins (yeast msp) in nematode family member (mspn-1)	10	P:GO:0010171; P:GO:0002119; F:GO:0016887; F:GO:0005515; F:GO:0005524; C:GO:0016021; P:GO:0040007; P:GO:0006310; F:GO:0009378; P:GO:0006281	-		-
Caenorhabditis briggsae	pseudouridylate synthase 10	3	F:GO:0003723; P:GO:0001522; F:GO:0009982	-	EC:5.4.99.12	-

Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	P:GO:0009056; P:GO:0044238; F:GO:0003824	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Zea mays	reverse identical	0		F:GO:0003676; F:GO:0003723; F:GO:0000166; P:GO:0006278; F:GO:0004519; F:GO:0003677; F:GO:0003964		-
Caenorhabditis elegans	uncoordi-ted family member (unc-103)	4	F:GO:0005249; P:GO:0055085; P:GO:0006813; C:GO:0016021	-		IPR003938; IPR003967; IPR018490; G3DSA:1.10.287.630 (GENE3D), PTHR10217 (PANTHER), PTHR10217:SF15 (PANTHER)
Brugia malayi	phosphatidylinositol 3- and 4-ki-se family protein	5	P:GO:0002119; F:GO:0016301; F:GO:0005515; P:GO:0009987; P:GO:0019915	-		IPR000341; IPR015433; G3DSA:3.10.20.90 (GENE3D), PTHR10048:SF9 (PANTHER), SSF54236 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	ornithine decarboxylase	1	F:GO:0005515	-		IPR000183; IPR002433; IPR009006; IPR022643; IPR022644; IPR022657; G3DSA:3.20.20.10 (GENE3D), PTHR11482 (PANTHER), PTHR11482:SF4 (PANTHER), SSF51419 (SUPERFAMILY)
Caenorhabditis elegans	pyridoxal-5 -phosphate-dependent protein beta subunit	2	P:GO:0008152; F:GO:0030170	-		IPR001926; G3DSA:3.40.50.1100 (GENE3D), PTHR10314 (PANTHER), PTHR10314:SF8 (PANTHER)
	-	0				-
	-	0				-
Pan troglodytes	thioredoxin	14	C:GO:0005829; P:GO:0022900; P:GO:0007267; C:GO:0005739; F:GO:0015037; P:GO:0045454; P:GO:0000122; F:GO:0005515; P:GO:0006928; P:GO:0007165; C:GO:0005576; P:GO:0046826; P:GO:0008283; C:GO:0005634	-		IPR005746; IPR012335; IPR012336; IPR013766; IPR017936; IPR017937; PTHR10438:SF18 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	abnormal cell migration family member (mig-1)	2	P:GO:0023052; F:GO:0004888	-		-

Caenorhabditis elegans	titin	7	P:GO:0009792; P:GO:0002119; P:GO:0040018; F:GO:0003677; P:GO:0045449; P:GO:0000003; C:GO:0005634	-		IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF11 (PANTHER), SSF48726 (SUPERFAMILY)
Homo sapiens	proteasome (macropain) beta 1	9	P:GO:0051436; P:GO:0051437; F:GO:0004298; P:GO:0031145; F:GO:0005515; P:GO:0044419; C:GO:0005737; C:GO:0005839; C:GO:0005634	-	EC:3.4.25.0	G3DSA:3.60.20.10 (GENE3D), PTHR11599 (PANTHER), PTHR11599:SF8 (PANTHER), PS51476 (PROFILE), SignalP (SIGNALP), SSF56235 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	short chain dehydroge-se reductase family protein	1	P:GO:0008152	-		-
Caenorhabditis elegans	variable abnormal morphology family member (vab-19)	0				-
Brugia malayi	orb2 cg5735-pb	4	P:GO:0007616; F:GO:0000166; P:GO:0008049; F:GO:0003729	-		IPR000504; PTHR12566 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	zinc finger protein 291	0		F:GO:0046872; C:GO:0005783; F:GO:0008270; C:GO:0005634; C:GO:0005622		-
Caenorhabditis briggsae	zinc finger protein 291	0		F:GO:0046872; C:GO:0005783; F:GO:0008270; C:GO:0005634; C:GO:0005622		-
	-	0				-
	-	0				-
Brugia malayi	lmbr1-like conserved region family protein	1	C:GO:0016021	-		IPR006876; PTHR21355 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	atp-dependent r- helicase ddx54	6	F:GO:0008026; F:GO:0003723; P:GO:0040010; F:GO:0005524; C:GO:0016021; C:GO:0005634	-		IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF17 (PANTHER), SSF52540 (SUPERFAMILY)

Caenorhabditis elegans	-d-dependent malic mitochondrial precursor	15	P:GO:0060070; P:GO:0000122; F:GO:0003714; C:GO:0005759; P:GO:0006108; C:GO:0005667; F:GO:0016619; F:GO:0046872; P:GO:0030282; F:GO:0051287; P:GO:0045944; F:GO:0003690; P:GO:0055114; P:GO:0048625; P:GO:0045599	-	EC:1.1.1.38	IPR012302; IPR016040; PTHR23406 (PANTHER), PTHR23406:SF2 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				-
Brugia malayi	protein-tyrosine phosphatase containing protein	2	P:GO:0016311; F:GO:0004721	-	EC:3.1.3.16	SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0006508; F:GO:0004181; F:GO:0008270	-	EC:3.4.17.0	PTHR11705 (PANTHER), PTHR11705:SF12 (PANTHER)
	-	0				-
	-	0				-
	-	0				IPR015880
Homo sapiens	heterogeneous nuclear ribonucleoprotein a b	11	F:GO:0003729; P:GO:0001837; F:GO:0003688; F:GO:0005515; P:GO:0043193; F:GO:0003700; F:GO:0000166; C:GO:0030529; P:GO:0045892; C:GO:0005737; C:GO:0005634	-		SignalP (SIGNALP)
Ancylostoma ceylanicum	venom-allergen-like protein family member (vap-1)	0		P:GO:0040011; P:GO:0006898; C:GO:0005576		-
	-	0				-
Caenorhabditis elegans	large subunit ribosomal protein 14	8	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; P:GO:0018996; P:GO:0040010; P:GO:0000003; P:GO:0006412	-	EC:3.6.5.3	-
Caenorhabditis briggsae	large subunit ribosomal protein 14	8	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; P:GO:0018996; P:GO:0040010; P:GO:0000003; P:GO:0006412	-	EC:3.6.5.3	-
	-	0				-
	-	0				-

Onchocerca volvulus	cyclophilin-type peptidyl-prolyl cis-trans isomerase- bmcyp-1 fragment	5	P:GO:0006457; C:GO:0071011; P:GO:0000398; F:GO:0003755; C:GO:0071013	-	EC:5.2.1.8	-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	3	F:GO:0005515; P:GO:0007600; P:GO:0007165	-		IPR014756; PTHR11188 (PANTHER), PTHR11188:SF10 (PANTHER)
Caenorhabditis elegans	imprinted and ancient	0		F:GO:0003674; P:GO:0008150; P:GO:0006417; C:GO:0005575		IPR001498; IPR006575; IPR016135; IPR020568; G3DSA:3.30.230.30 (GENE3D)
	-	0				-
	-	0				-
Caenorhabditis briggsae	uncoordi-ted family member (unc-13)	10	F:GO:0004872; F:GO:0046872; P:GO:0006917; C:GO:0005794; P:GO:0023034; C:GO:0030054; P:GO:0006887; P:GO:0007165; C:GO:0045202; P:GO:0007588	-		-
Caenorhabditis briggsae	uncoordi-ted family member (unc-13)	10	F:GO:0004872; F:GO:0046872; P:GO:0006917; C:GO:0005794; P:GO:0023034; C:GO:0030054; P:GO:0006887; P:GO:0007165; C:GO:0045202; P:GO:0007588	-		IPR000008; IPR008973; IPR018029; G3DSA:2.60.40.150 (GENE3D), PTHR10480 (PANTHER)
Caenorhabditis briggsae	carnitine acetyltransferase	7	F:GO:0008415; C:GO:0005777; P:GO:0040011; P:GO:0033540; C:GO:0005783; C:GO:0005739; P:GO:0006091	-		IPR000542; PTHR22589:SF12 (PANTHER), SSF52777 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	calcium atpase	6	C:GO:0016021; F:GO:0015662; F:GO:0015085; P:GO:0006754; F:GO:0005524; P:GO:0006812	-		IPR001757; IPR004014; PTHR11939:SF76 (PANTHER)
Caenorhabditis elegans	m protein	0		F:GO:0003674; C:GO:0005737; P:GO:0006810; P:GO:0015031		-

Caenorhabditis briggsae	actin-related protein 2 3 complex subunit 5	10	P:GO:0043652; C:GO:0005856; P:GO:0016331; P:GO:0010631; P:GO:0040007; P:GO:0000003; P:GO:0034314; P:GO:0002119; P:GO:0009792; C:GO:0005737	-		-
	-	0				-
Caenorhabditis elegans	tm2 domain containing protein	1	P:GO:0044237	-		-
Caenorhabditis briggsae	abnormal go-d development family member (gon-2)	0		P:GO:0008406; C:GO:0016021; C:GO:0016020; P:GO:0055085; P:GO:0007067; P:GO:0006811; F:GO:0005216; P:GO:0006810		PTHR13800 (PANTHER)
Caenorhabditis elegans	1-acyl-sn-glycerol-3-phosphate acyltransferase	3	F:GO:0008415; C:GO:0016020; P:GO:0008152	-		-
Pan troglodytes	ephrin a1	0				-
Caenorhabditis elegans	tao ki-se 1	8	C:GO:0043231; F:GO:0004674; F:GO:0005524; P:GO:0042327; F:GO:0030295; F:GO:0019901; P:GO:0050790; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF27 (PANTHER)
Caenorhabditis elegans	amin (actin binding protein) alpha family member (fl--1)	0		P:GO:0006857; C:GO:0016021; C:GO:0016020; F:GO:0005215; P:GO:0006810		IPR013783; IPR014756; IPR017868; PTHR11915 (PANTHER), PTHR11915:SF55 (PANTHER)
	-	0				-
Caenorhabditis briggsae	low-density lipoprotein receptor-related protein 2	0		F:GO:0005509; F:GO:0004872; C:GO:0016021; C:GO:0016020; P:GO:0006898		G3DSA:2.10.25.10 (GENE3D), PTHR10529 (PANTHER)
Caenorhabditis elegans	isoform e	2	F:GO:0008324; P:GO:0006812	-		-
	-	0				-
Caenorhabditis briggsae	malonyl -acyl carrier protein transacylase	5	P:GO:0005975; F:GO:0016773; F:GO:0016301; P:GO:0008610; C:GO:0005739	-	EC:2.7.1.0	IPR001227; IPR014043; IPR016035; PTHR10982 (PANTHER), PTHR10982:SF4 (PANTHER)
Caenorhabditis briggsae	malonyl -acyl carrier protein transacylase	5	P:GO:0005975; F:GO:0016773; F:GO:0016301; P:GO:0008610; C:GO:0005739	-	EC:2.7.1.0	IPR001227; IPR014043; IPR016035; PTHR10982 (PANTHER), PTHR10982:SF4 (PANTHER)

Acyrthosiphon pisum	cg8213 cg8213-pa	0				IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR19355 (PANTHER), PTHR19355:SF171 (PANTHER)
	-	0				-
Aphid lethal paralysis virus	nonstructural polyprotein	1	F:GO:0016787	-		IPR000199; IPR009003; G3DSA:2.40.10.10 (GENE3D)
Caenorhabditis elegans	glycogen synthase	7	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0005978; F:GO:0005515; F:GO:0004373; P:GO:0040011	-	EC:2.4.1.11	IPR008631
Oncorhynchus keta	chromosome assembly factor caf-1	0		F:GO:0043565; F:GO:0003700; F:GO:0003677; C:GO:0005634; F:GO:0004879; F:GO:0008270; P:GO:0006355; F:GO:0004872; F:GO:0046872; P:GO:0006350; F:GO:0003707; P:GO:0045449		-
Caenorhabditis elegans	large subunit ribosomal protein 26	7	P:GO:0009792; P:GO:0002119; F:GO:0003735; P:GO:0040010; P:GO:0000003; C:GO:0015934; P:GO:0006412	-	EC:3.6.5.3	IPR005756; IPR005824; IPR005825; IPR008991; IPR014723; PTHR11143:SF2 (PANTHER)
Caenorhabditis elegans	large subunit ribosomal protein 26	8	P:GO:0009792; P:GO:0002119; F:GO:0003735; P:GO:0040010; P:GO:0000003; C:GO:0015934; C:GO:0005829; P:GO:0006414	-		IPR005756; IPR005824; IPR005825; IPR008991; IPR014723; PTHR11143:SF2 (PANTHER)
Caenorhabditis briggsae	large subunit ribosomal protein 26	7	P:GO:0009792; P:GO:0002119; F:GO:0003735; P:GO:0040010; P:GO:0000003; C:GO:0015934; P:GO:0006412	-	EC:3.6.5.3	-
Caenorhabditis briggsae	large subunit ribosomal protein 26	7	P:GO:0009792; P:GO:0002119; F:GO:0003735; P:GO:0040010; P:GO:0000003; C:GO:0015934; P:GO:0006412	-	EC:3.6.5.3	-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)

	-	0				IPR007807; PTHR10925 (PANTHER), PTHR10925:SF5 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	P:GO:0000003	-		-
Loa loa	tnni3 interacting ki-se	4	F:GO:0005515; F:GO:0004672; F:GO:0000166; C:GO:0044424	-		-
	-	0				-
	-	0				-
Brugia malayi	niemann-pick c1	11	P:GO:0033344; F:GO:0005515; C:GO:0016021; P:GO:0016242; P:GO:0008206; P:GO:0007041; P:GO:0006897; P:GO:0046686; C:GO:0005768; C:GO:0044446; P:GO:0042632	-		IPR003392; PTHR10796 (PANTHER), PTHR10796:SF35 (PANTHER), SSF82866 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Rattus norvegicus	beta 2	3	F:GO:0046872; F:GO:0016787; C:GO:0005739	-		G3DSA:3.60.15.10 (GENE3D), PTHR23131 (PANTHER)
Brugia malayi	utp--ammonia ligase	4	P:GO:0002119; P:GO:0040010; F:GO:0003883; P:GO:0006221	-	EC:6.3.4.2	-
Caenorhabditis elegans	rho guanine nucleotide exchange factor 17	2	P:GO:0009987; P:GO:0050789	-		PTHR12877 (PANTHER), PTHR12877:SF7 (PANTHER)
Caenorhabditis briggsae	cysteinyl-tr- cytoplasmic	3	F:GO:0004812; P:GO:0006418; F:GO:0000166	-		-
Caenorhabditis elegans	hypothetical protein H28G03.2 [Caenorhabditis elegans]	0		F:GO:0005515		-
	-	0				-

Homo sapiens	alpha isoform cra_a	36	P:GO:0043154; P:GO:0006457; P:GO:0042542; P:GO:0060561; C:GO:0032432; C:GO:0005626; P:GO:0010629; C:GO:0015630; P:GO:0007568; P:GO:0007517; P:GO:0002088; P:GO:0006936; C:GO:0005794; C:GO:0005829; P:GO:0006916; C:GO:0009986; P:GO:0031109; F:GO:0008017; P:GO:0001666; P:GO:0030308; P:GO:0006006; F:GO:0051082; P:GO:0009408; P:GO:0032387; C:GO:0030018; F:GO:0042803; P:GO:0051260; C:GO:0005886;	-		-
Caenorhabditis elegans	malate dehydroge-se	2	P:GO:0008152; F:GO:0016491	-		IPR003767; G3DSA:1.10.1530.10 (GENE3D)
	-	0				-
	-	0				-
Caenorhabditis briggsae	ykd6_caeel ame: full=uncharacterized protein	0				-
Caenorhabditis briggsae	threonyl-tr- synthetase	3	F:GO:0016874; P:GO:0044260; P:GO:0044238	-		IPR002314; G3DSA:3.30.930.10 (GENE3D), PTHR11451 (PANTHER), PTHR11451:SF5 (PANTHER), SSF55681 (SUPERFAMILY)
Caenorhabditis briggsae	phosphatidylinositide phosphatase sac1	9	P:GO:0040010; P:GO:0008340; C:GO:0016021; F:GO:0016791; P:GO:0002119; P:GO:0009792; C:GO:0005789; P:GO:0040018; C:GO:0005794	-	EC:3.1.3.0	IPR002013; PTHR11200 (PANTHER), PTHR11200:SF11 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0016888		-
Homo sapiens	poly binding protein 2	11	P:GO:0043161; F:GO:0003723; P:GO:0050687; F:GO:0031625; P:GO:0016071; P:GO:0008380; P:GO:0045087; F:GO:0003677; C:GO:0030529; C:GO:0005737; C:GO:0005634	-		IPR004088; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR10288 (PANTHER), PTHR10288:SF48 (PANTHER), SSF54791 (SUPERFAMILY)
	-	0				-

	-	0				-
Caenorhabditis briggsae	dm (doublesex mab-3) domain family member (dmd-7)	5	F:GO:0003700; F:GO:0005515; P:GO:0007548; C:GO:0005634; P:GO:0006355	-		IPR001275; PTHR12322 (PANTHER), PTHR12322:SF9 (PANTHER)
Caenorhabditis briggsae	zinc c2h2 type family protein	6	P:GO:0006952; P:GO:0000003; C:GO:0005622; F:GO:0008270; F:GO:0005515; P:GO:0006898	-		IPR007087; IPR015880
	-	0				SignalP (SIGNALP)
Loa loa	briggsae cbr-hyl-2 protein	0		P:GO:0006355; F:GO:0043565; C:GO:0016021; P:GO:0045449; C:GO:0016020; F:GO:0003677; F:GO:0003700; C:GO:0005634		PTHR12560 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	trehalose 6-phosphate synthase	2	F:GO:0016757; P:GO:0034608	-		IPR013200; G3DSA:3.40.50.1000 (GENE3D)
	-	0				SignalP (SIGNALP)
Caenorhabditis brenneri	sjogren syndrome antigen b	13	P:GO:0040010; F:GO:0003723; P:GO:0018991; C:GO:0005730; P:GO:0008033; P:GO:0040027; F:GO:0005515; F:GO:0000166; P:GO:0006898; C:GO:0030529; P:GO:0009792; P:GO:0008406; C:GO:0005737	-		IPR000504; IPR002344; IPR006630; IPR011991; IPR012677; IPR014886; PTHR22792 (PANTHER), PTHR22792:SF2 (PANTHER), SSF46785 (SUPERFAMILY), SSF54928 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	fatty acid elongation protein 3	5	P:GO:0018996; C:GO:0016021; P:GO:0008340; P:GO:0040010; P:GO:0007283	-		IPR002076
Brugia malayi	xpa-binding protein 2	11	P:GO:0040010; F:GO:0005488; P:GO:0000910; C:GO:0071011; P:GO:0000381; P:GO:0000003; P:GO:0006911; P:GO:0002119; C:GO:0071013; P:GO:0009792; P:GO:0001703	-		PTHR11246 (PANTHER), PTHR11246:SF5 (PANTHER)
	-	0				-

Homo sapiens	apolipoprotein a-i binding protein	3	C:GO:0005576; C:GO:0005739; F:GO:0005515	-		-
Caenorhabditis elegans	zinc finger ccch-type containing 14	2	P:GO:0006911; F:GO:0005488	-		IPR002483; G3DSA:1.20.1390.10 (GENE3D)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	amp-dependent synthetase and ligase	4	P:GO:0009792; P:GO:0000003; P:GO:0008152; F:GO:0003824	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		-
Caenorhabditis elegans	nucleolar complex protein 3 homolog	1	C:GO:0005730	-		PTHR14428 (PANTHER)
Loa loa	briggsae cbr-xpg-1 protein	0		P:GO:0009411; P:GO:0006295; F:GO:0003677; C:GO:0005634; F:GO:0004520; F:GO:0000405; F:GO:0042803; P:GO:0008340; P:GO:0009792; P:GO:0010225; C:GO:0016591; C:GO:0005675; F:GO:0047485; P:GO:0009650; F:GO:0003824; F:GO:0004519; F:GO:0004518; P:GO:0006289; P:GO:0035264; P:GO:0006283; F:GO:0003697; P:GO:0006281; P:GO:0043066; F:GO:0003690		IPR001044; IPR006084
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0006508; F:GO:0004185		IPR001563; IPR018202; G3DSA:3.40.50.1820 (GENE3D), PTHR11802:SF9 (PANTHER), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	statb_caeel ame: full=sig-l transducer and activator of transcription b ame: full=zinc finger protein stat-b	7	F:GO:0003700; F:GO:0004871; F:GO:0005515; F:GO:0005509; P:GO:0007165; C:GO:0005634; P:GO:0006355	-		-
	-	0				-
Caenorhabditis elegans	beta chain spectrin	1	F:GO:0003779	-		-
Danio rerio	mitochondrial protein 18 kda	6	P:GO:0006915; C:GO:0005743; F:GO:0004089; P:GO:0015976; C:GO:0016021; F:GO:0008270	-	EC:4.2.1.1	-
	-	0				-

	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	si:ch211- protein	3	F:GO:0005524; F:GO:0004835; P:GO:0006464	-	EC:6.3.2.25	IPR004344; IPR013816; PTHR12241:SF9 (PANTHER), SSF56059 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG19972 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	mgc53303 protein	0				-
Caenorhabditis elegans	briggsae cbr-dpf-5 protein	2	C:GO:0044444; C:GO:0043231	-		-
Caenorhabditis elegans	px domain containing protein	3	F:GO:0035091; F:GO:0005515; P:GO:0007154	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Loa loa	kelch motif family protein	2	P:GO:0046529; C:GO:0031463	-		-
Caenorhabditis elegans	apg4a protein	2	F:GO:0005515; F:GO:0008233	-		IPR000318; SignalP (SIGNALP)
Rhodobacter sphaeroides ATCC 17029	hypothetical protein Rsph17029_3116 [Rhodobacter sphaeroides ATCC 17029]	0				-
	-	0				-
Callithrix jacchus	ribosomal protein s7	8	C:GO:0005730; F:GO:0003735; F:GO:0003723; F:GO:0005515; P:GO:0006364; C:GO:0022627; P:GO:0042274; P:GO:0006414	-		IPR000554
	-	0				-
Caenorhabditis elegans	acid phosphatase lysosomal	1	C:GO:0005764	-		IPR000560; G3DSA:3.40.50.1240 (GENE3D), PTHR11567 (PANTHER), PTHR11567:SF20 (PANTHER), SSF53254 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG16766 [Caenorhabditis briggsae]	0				PTHR21579 (PANTHER), PTHR21579:SF2 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	sodium potassium adenosine triphosphatase	6	C:GO:0016021; P:GO:0015672; F:GO:0015077; F:GO:0015662; P:GO:0006754; F:GO:0005524	-		IPR001757; IPR008250; G3DSA:1.20.1110.10 (GENE3D), PTHR11939:SF100 (PANTHER), SignalP (SIGNALP), SSF81665 (SUPERFAMILY)
	-	0				-
	-	0				-

Caenorhabditis briggsae	serine threonine protein ki-se	12	P:GO:0043268; C:GO:0005856; C:GO:0005624; F:GO:0005524; F:GO:0005515; C:GO:0016324; C:GO:0016323; C:GO:0005737; P:GO:0006950; C:GO:0005634; F:GO:0004702; P:GO:0006468	-		IPR000719; IPR002290; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.10.20.90 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF71 (PANTHER), PF12202 (PFAM)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				IPR000742; IPR006210; IPR007110; IPR013032; IPR013783; G3DSA:2.10.25.10 (GENE3D), SSF57196 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG17944 [Caenorhabditis briggsae]	0				-
	-	0				-
	-	0				-
Ancylostoma caninum	secreted protein 5 precursor	0		C:GO:0005576		IPR014044; SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	hypothetical protein R144.11 [Caenorhabditis elegans]	6	P:GO:0040035; P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040018; P:GO:0002009	-		-
	-	0				-
Caenorhabditis elegans	metabotropic gaba-b receptor subtype 2	4	P:GO:0042048; P:GO:0031631; F:GO:0004888; C:GO:0016020	-		IPR001828; IPR002455; G3DSA:3.40.50.2300 (GENE3D), PTHR10519 (PANTHER), PTHR10519:SF4 (PANTHER), SSF53822 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG22133 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)
Caenorhabditis elegans	ga19517- partial	4	P:GO:0019915; C:GO:0016021; P:GO:0055085; F:GO:0005215	-		IPR005828; IPR016196; G3DSA:1.20.1250.20 (GENE3D), PTHR11600 (PANTHER), PTHR11600:SF44 (PANTHER), SignalP (SIGNALP)
	-	0				G3DSA:2.40.50.40 (GENE3D)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	F:GO:0005488	-		IPR020683; PTHR18958 (PANTHER), PTHR18958:SF37 (PANTHER)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG13938 [Caenorhabditis briggsae]	0		P:GO:0019752; F:GO:0003824; F:GO:0016831; F:GO:0030170		SignalP (SIGNALP)
Brugia malayi	exportin partial	0		F:GO:0005488; F:GO:0008536; P:GO:0006886; F:GO:0008565		IPR013598; PTHR11223 (PANTHER), PTHR11223:SF3 (PANTHER)
	-	0				-
	-	0				-

Caenorhabditis elegans	hypothetical protein Y54E5A.8 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0016787		-
	-	0				-
	-	0				-
Caenorhabditis elegans	pantothe-te ki-se 4	2	F:GO:0016301; F:GO:0000166	-		IPR002791; PTHR12280 (PANTHER), PTHR12280:SF3 (PANTHER)
Loa loa	actin family protein	0		C:GO:0005884; P:GO:0007010; F:GO:0005515		IPR004000; G3DSA:3.30.420.40 (GENE3D), PTHR11937:SF21 (PANTHER), SSF53067 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	: shorter than wild-type family member (dpy-10)	3	C:GO:0005576; F:GO:0042302; P:GO:0040002	-		IPR002486; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	map ki-se-interacting serine threonine-protein ki-se 1	9	P:GO:0040008; P:GO:0044267; F:GO:0004674; C:GO:0005874; C:GO:0005813; P:GO:0007017; F:GO:0000166; P:GO:0050794; C:GO:0005635	-	EC:2.7.11.0	-
	-	0				IPR007087; IPR015880
	-	0				-
	-	0				SignalP (SIGNALP)
Homo sapiens	ok sw-	12	F:GO:0003756; F:GO:0004656; C:GO:0005793; P:GO:0045454; C:GO:0009986; C:GO:0042470; C:GO:0005792; C:GO:0005788; F:GO:0005515; P:GO:0018401; C:GO:0005576; C:GO:0005886	-	EC:5.3.4.1; EC:1.14.11.2	-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	8	C:GO:0005737; F:GO:0005525; F:GO:0005515; P:GO:0006913; F:GO:0005509; P:GO:0006886; C:GO:0005634; P:GO:0007264	-		-
Ancylostoma ceylanicum	metalloprotease 1 precursor	4	F:GO:0004222; P:GO:0000003; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	-
	-	0				-
	-	0				-

Homo sapiens	polyubiquitin with 3 ub domains	6	P:GO:0006464; F:GO:0003735; F:GO:0005515; C:GO:0022627; C:GO:0005634; P:GO:0006414	-		IPR000626; IPR019955; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), PTHR10666:SF12 (PANTHER), SSF54236 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F47G3.1 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	tpr domain containing protein	3	P:GO:0040010; P:GO:0040017; F:GO:0005488	-		PTHR16091 (PANTHER)
	-	0				-
Caenorhabditis briggsae	2-hydroxyphytanoyl-coa lyase	3	F:GO:0030976; F:GO:0000287; F:GO:0003824	-		G3DSA:3.40.50.970 (GENE3D), PTHR18968 (PANTHER), PTHR18968:SF6 (PANTHER), SSF52518 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				IPR015157
	-	0				-
Brugia malayi	d--directed r- polymerase iii subunit rpc1	2	F:GO:0046872; F:GO:0016779	-	EC:2.7.7.0	IPR007081; IPR015700; PTHR19376 (PANTHER), SSF64484 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	mitogen-activated protein ki-se 14	25	P:GO:0001525; C:GO:0005654; P:GO:0009749; P:GO:0007265; F:GO:0004708; P:GO:0002062; F:GO:0008022; F:GO:0008339; P:GO:0046777; P:GO:0006928; P:GO:0000902; P:GO:0031663; C:GO:0044445; P:GO:0000077; P:GO:0007519; P:GO:0019395; P:GO:0006006; P:GO:0006935; P:GO:0045648; P:GO:0032495; P:GO:0045944; C:GO:0005625; F:GO:0005524; C:GO:0000922; P:GO:0051403	-		IPR000719; IPR002290; IPR003527; IPR008352; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF61 (PANTHER)
Caenorhabditis elegans	hypothetical protein B0252.1 [Caenorhabditis elegans]	1	P:GO:0040010	-		-
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis elegans	solute carrier family 23 (nucleobase transporters) member 2	7	P:GO:0055085; P:GO:0015882; F:GO:0015229; C:GO:0016021; F:GO:0015370; P:GO:0048513; C:GO:0016323	-		IPR006043; PTHR11119:SF8 (PANTHER)
Caenorhabditis elegans	asparagine-linked glycosylation 12 homolog (alpha- -mannosyltransferase) isoform cra_a	4	P:GO:0006488; F:GO:0000009; C:GO:0016020; C:GO:0005783	-		-
	-	0				-
Caenorhabditis elegans	protein	1	P:GO:0009886	-		-
Caenorhabditis elegans	Hypothetical protein F44A2.3 [Caenorhabditis elegans]	0		F:GO:0008289		PTHR10504 (PANTHER), PTHR10504:SF10 (PANTHER)
Caenorhabditis elegans	phosphorylase ki-se	9	C:GO:0005964; C:GO:0005886; F:GO:0004339; P:GO:0006508; F:GO:0008270; F:GO:0008237; P:GO:0005977; F:GO:0005516; F:GO:0004689	-	EC:3.2.1.3; EC:2.7.11.19	IPR008734; IPR008928; IPR011613; PTHR10749:SF2 (PANTHER)
Caenorhabditis briggsae	g-patch domain containing protein	3	P:GO:0019915; P:GO:0010171; P:GO:0002119	-		PTHR13384 (PANTHER), PTHR13384:SF8 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; C:GO:0016020; F:GO:0008375		IPR003406; PTHR19297:SF3 (PANTHER)
	-	0				-
Tribolium castaneum	oligopeptide transporter	0		P:GO:0006857; C:GO:0016021; C:GO:0016020; F:GO:0005215; P:GO:0006810		PTHR11654 (PANTHER), PTHR11654:SF13 (PANTHER), SignalP (SIGNALP)
Pongo abelii	capping protein (actin filament) gelsolin-like	11	C:GO:0031965; C:GO:0005730; P:GO:0051016; P:GO:0007076; P:GO:0051301; C:GO:0042470; C:GO:0000796; F:GO:0003779; C:GO:0008290; C:GO:0005576; P:GO:0030031	-		IPR007122; IPR007123; G3DSA:3.40.20.10 (GENE3D), PTHR11977:SF13 (PANTHER), SSF55753 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	dystrophin-like phenotype and capon related family member (dyc-1)	6	P:GO:0046662; F:GO:0030235; F:GO:0005515; P:GO:0040017; C:GO:0016010; P:GO:0046716	-		-

Caenorhabditis elegans	clc-type chloride channel family member (clh-3)	12	F:GO:0004872; F:GO:0005247; C:GO:0005902; C:GO:0005886; F:GO:0005515; P:GO:0055085; C:GO:0016021; C:GO:0005626; P:GO:0008152; F:GO:0003824; C:GO:0015629; P:GO:0006821	-		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis elegans	protein ki-se domain containing protein	3	P:GO:0006468; F:GO:0004687; F:GO:0005524	-	EC:2.7.11.18	IPR000719; IPR008271; IPR011009; IPR015730; IPR017442; IPR020636; G3DSA:3.30.200.20 (GENE3D)
Caenorhabditis elegans	tir (toll and interleukin 1 receptor) domain protein family member (tir-1)	5	P:GO:0007165; P:GO:0045087; C:GO:0031224; F:GO:0042802; F:GO:0004888	-		IPR000157; IPR001660; IPR010993; IPR011510; G3DSA:3.40.50.10140 (GENE3D), PTHR22998 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	hypothetical kda protein in chromosome	1	P:GO:0040010	-		SignalP (SIGNALP)
Caenorhabditis briggsae	d- polymerase gamma	11	P:GO:0008340; F:GO:0016772; P:GO:0007424; P:GO:0008406; F:GO:0003676; P:GO:0002009; P:GO:0006264; C:GO:0005912; P:GO:0030421; F:GO:0016788; C:GO:0005739	-		-
Ciona intestinalis	thrombospondin type 1 domain containing protein	0		P:GO:0006508; F:GO:0008237; F:GO:0004222; F:GO:0008233; C:GO:0005576		-
Caenorhabditis elegans	elongation factor-2 ki-se	5	F:GO:0008135; C:GO:0005829; F:GO:0004674; F:GO:0000166; P:GO:0006414	-	EC:2.7.11.0	IPR004166; IPR011009; PTHR14187 (PANTHER), PTHR14187:SF2 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	conserved oligomeric golgi component family member (cogc-3)	2	P:GO:0046907; C:GO:0044431	-		IPR007265; SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	yt6j_caeel ame: full=upf0027 protein	1	P:GO:0009886	-		IPR001233

Caenorhabditis elegans	organic cation transporter	4	C:GO:0016020; P:GO:0009987; P:GO:0006810; F:GO:0005215	-		IPR005828; IPR016196; PTHR11600 (PANTHER), PTHR11600:SF42 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	cy561_caeel ame: full= cytochrome b561 short=cytochrome b-561	0				-
Caenorhabditis elegans	n-6 adenine-specific d- methyltransferase 2	0		F:GO:0003676; P:GO:0006508; F:GO:0008168; F:GO:0003674; F:GO:0016740; P:GO:0008150; P:GO:0032259; C:GO:0005575		IPR002052; IPR019369; PTHR13200 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	i uaiaretic acid resistant family member (ndg-4)	3	P:GO:0009792; P:GO:0010171; P:GO:0040010	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	guanine-nucleotide exchange factor c3g	3	F:GO:0005085; C:GO:0005622; P:GO:0051056	-		IPR001895; IPR008937; PTHR23113:SF40 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein C17H12.2 [Caenorhabditis elegans]	0				IPR018795
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-ptr-14 protein	7	P:GO:0018996; C:GO:0016021; P:GO:0040018; P:GO:0006810; F:GO:0005215; F:GO:0008158; P:GO:0040011	-		IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER)
Pongo abelii	mannose-binding 2	6	C:GO:0000139; C:GO:0005789; F:GO:0005529; C:GO:0016021; C:GO:0033116; P:GO:0015031	-		-

Caenorhabditis elegans	briggsae cbr-acy-1 protein	11	P:GO:0006952; P:GO:0008219; C:GO:0016021; F:GO:0004016; P:GO:0007188; P:GO:0009190; P:GO:0042221; P:GO:0002119; P:GO:0040017; C:GO:0005886; P:GO:0030431	-	EC:4.6.1.1	IPR001054; PTHR11920 (PANTHER), PTHR11920:SF10 (PANTHER)
Caenorhabditis elegans	malate dehydroge-se	6	F:GO:0046872; F:GO:0051287; C:GO:0005759; F:GO:0016619; P:GO:0006108; P:GO:0055114	-	EC:1.1.1.38	IPR012302; IPR016040; PTHR23406 (PANTHER), PTHR23406:SF2 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-vab-2 protein	1	C:GO:0016020	-		IPR001799; IPR008972; PTHR11304:SF23 (PANTHER)
Caenorhabditis elegans	briggsae cbr-smgl-1 protein	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG01673 [Caenorhabditis briggsae]	1	F:GO:0005488	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-lmn-1 protein	2	C:GO:0005635; F:GO:0005515	-		IPR001322; IPR001664; IPR016044; G3DSA:1.20.5.170 (GENE3D), G3DSA:2.60.40.1260 (GENE3D), PTHR23239:SF11 (PANTHER), SSF74853 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0019915; P:GO:0040018; P:GO:0040011	-		-
Caenorhabditis elegans	tyrosyl-tr- synthetase	3	F:GO:0004812; P:GO:0006418; F:GO:0000166	-		IPR002307; G3DSA:1.10.240.10 (GENE3D), SSF52374 (SUPERFAMILY)
	-	0				-
	-	0				-
Ciona intestinalis	epidermal retinol dehydroge-se 2	6	P:GO:0042572; P:GO:0042574; C:GO:0000299; F:GO:0004745; P:GO:0043616; C:GO:0005789	-	EC:1.1.1.105	IPR002198; IPR002347; IPR016040; PTHR19410:SF36 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis briggsae	briggsae cbr-snr-5 protein	10	P:GO:0040027; F:GO:0003676; P:GO:0018996; F:GO:0005515; P:GO:0032940; P:GO:0000003; P:GO:0040007; P:GO:0006898; C:GO:0030529; P:GO:0040039	-		IPR001163; IPR006649; IPR010920; G3DSA:2.30.30.100 (GENE3D), PTHR11021 (PANTHER)
	-	0				-
Caenorhabditis elegans	cysteine synthase a	5	F:GO:0030170; F:GO:0004124; F:GO:0005515; P:GO:0006535; F:GO:0016740	-	EC:2.5.1.47	-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	5	C:GO:0005622; F:GO:0005515; P:GO:0007155; P:GO:0006895; P:GO:0015031	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-coq-8 protein	0		F:GO:0016301; F:GO:0005524; C:GO:0005739; F:GO:0016740; F:GO:0000166; P:GO:0008219		-
Brugia malayi	r- binding motif protein 15b	7	F:GO:0003676; C:GO:0005730; P:GO:0000381; P:GO:0006913; F:GO:0005515; P:GO:0016481; C:GO:0005654	-		IPR000504; IPR010912; IPR012677; IPR012921; IPR016194; G3DSA:2.40.290.10 (GENE3D), PTHR23189 (PANTHER), PTHR23189:SF9 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	nuclear hormone receptor family member (nhr-66)	3	P:GO:0050789; F:GO:0005515; P:GO:0007275	-		IPR000536; IPR008946; PTHR11865 (PANTHER), PTHR11865:SF235 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	phosphatidylinositol-glycan biosynthesis class w protein	4	F:GO:0008415; P:GO:0006506; C:GO:0005783; C:GO:0044425	-		IPR009447
	-	0				-
	-	0				-
	-	0				G3DSA:2.60.120.20 (GENE3D)
Caenorhabditis briggsae	n-acetyl galactosaminyl transferase 6	5	C:GO:0000139; F:GO:0004653; F:GO:0005529; F:GO:0046872; C:GO:0016021	-	EC:2.4.1.41	PTHR11675 (PANTHER), SSF53448 (SUPERFAMILY)

Caenorhabditis briggsae	n-acetyl galactosaminyl transferase 6	5	C:GO:0000139; F:GO:0004653; F:GO:0005529; F:GO:0046872; C:GO:0016021	-	EC:2.4.1.41	PTHR11675 (PANTHER), SSF53448 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-nsy-4 protein	1	C:GO:0016021	-		IPR010761; SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Ostertagia ostertagi	sxc1 protein	0		P:GO:0006508; F:GO:0008237; F:GO:0004222; F:GO:0008233		IPR003582; SignalP (SIGNALP)
Caenorhabditis elegans	hda6_caeel ame: full=histone deacetylase 6	0		F:GO:0016787; F:GO:0033558; F:GO:0008270		IPR000286; PTHR10625:SF19 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	protein-tyrosine phosphatase containing protein	2	F:GO:0004725; P:GO:0006470	-	EC:3.1.3.48	-
Brugia malayi	rab5 gdp gtp exchange factor	2	F:GO:0046872; F:GO:0005515	-		IPR003123; IPR013995; PTHR23101 (PANTHER), PTHR23101:SF2 (PANTHER), SSF109993 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	haloacid dehaloge-se-like hydrolase family protein	0		F:GO:0016787; P:GO:0008152; F:GO:0003824; F:GO:0016614; F:GO:0050660		-
	-	0				IPR008160; PTHR10499 (PANTHER), PTHR10499:SF115 (PANTHER)
	-	0				-
Caenorhabditis briggsae	3 saliva family protein	2	P:GO:0019915; C:GO:0016020	-		IPR004316; IPR018179; SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	ecotropic viral integration site	1	F:GO:0005515	-		PTHR22957 (PANTHER), PTHR22957:SF44 (PANTHER)
Caenorhabditis elegans	kinesin-like protein family member (klp-4)	7	C:GO:0000235; F:GO:0008017; P:GO:0007018; F:GO:0005524; P:GO:0051294; C:GO:0005871; F:GO:0003777	-		IPR001752; PTHR16012 (PANTHER), PTHR16012:SF65 (PANTHER), SSF52540 (SUPERFAMILY)

Caenorhabditis briggsae	cullin 5	10	C:GO:0005829; P:GO:0006511; F:GO:0031625; C:GO:0005624; C:GO:0031466; F:GO:0004842; P:GO:0006970; F:GO:0016931; P:GO:0051480; C:GO:0005634	-	EC:6.3.2.19	-
Caenorhabditis briggsae	tetratricopeptide repeat protein 39b	0		F:GO:0003674; F:GO:0005488; P:GO:0008150		IPR019412; SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	galnt11 protein	3	F:GO:0016757; C:GO:0005794; C:GO:0016020	-		IPR001173; G3DSA:3.90.550.10 (GENE3D), PTHR11675 (PANTHER), SSF53448 (SUPERFAMILY)
Nematostella vectensis	activin a receptor type ii-like 1	2	F:GO:0004871; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR23255 (PANTHER), PTHR23255:SF14 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	kiaa0528 protein	0		F:GO:0003674; C:GO:0008021; C:GO:0016020; P:GO:0008150; F:GO:0005515; F:GO:0005215; P:GO:0006810		-
	-	0				-
	-	0				-
Loa loa	hypothetical protein LOAG_14520 [Loa loa]	0				-
	-	0				-
Caenorhabditis briggsae	n-deacetylase n-sulfotransferase	5	C:GO:0000139; F:GO:0015016; F:GO:0016787; P:GO:0009987; C:GO:0016021	-	EC:2.8.2.8	PTHR10605 (PANTHER), PTHR10605:SF2 (PANTHER)
Caenorhabditis elegans	methylmalonic aciduria (cobalamin deficiency) cbld with homocystinuria	1	F:GO:0005515	-		IPR019362; PTHR13192 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	udp- ransferase family member (ugt-49)	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	C:GO:0016021	-		-
	-	0				-
Schistosoma mansoni	nuclear transcription factor y subunit beta	4	F:GO:0043565; F:GO:0005515; C:GO:0005634; P:GO:0006355	-		IPR003957; IPR009072; PTHR11064 (PANTHER)

Caenorhabditis briggsae	briggsae cbr-uaf-2 protein	11	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0003723; P:GO:0018996; F:GO:0005515; P:GO:0040011; P:GO:0040007; C:GO:0005634; F:GO:0008270; F:GO:0000166	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0017057; P:GO:0005975; F:GO:0016787; P:GO:0006098		IPR005900; G3DSA:3.40.50.1360 (GENE3D), SSF100950 (SUPERFAMILY)
Caenorhabditis briggsae	neurexin iv	0		P:GO:0009059; C:GO:0005919; C:GO:0005918; P:GO:0019991; P:GO:0008065; C:GO:0016021; P:GO:0007155; C:GO:0016020; P:GO:0016081; P:GO:0016080; P:GO:0021682; F:GO:0008897; P:GO:0045216; P:GO:0007163; F:GO:0004888; P:GO:0008104; F:GO:0000287; P:GO:0060857; C:GO:0005887; P:GO:0007391; P:GO:0008366; C:GO:0005886; P:GO:0035151		IPR013320; PTHR10127 (PANTHER), PTHR10127:SF11 (PANTHER)
Loa loa	hypothetical protein LOAG_01835 [Loa loa]	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Monosiga brevicollis MX1	snf2 family d--dependent atpase	5	P:GO:0009987; C:GO:0043229; P:GO:0044238; F:GO:0003676; F:GO:0004386	-		IPR000330; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10799 (PANTHER), PTHR10799:SF74 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	ifa-1	3	C:GO:0005882; F:GO:0005198; F:GO:0005515	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	g patch domain containing 3	3	F:GO:0003676; C:GO:0005622; F:GO:0000166	-		PTHR14390 (PANTHER)

Caenorhabditis briggsae	thyroid adenoma-associated protein homolog	0		F:GO:0003674; F:GO:0005488; P:GO:0008150; C:GO:0005575		IPR019442; PTHR14387 (PANTHER)
Caenorhabditis elegans	tyrosine ki-se receptor	4	P:GO:0006468; F:GO:0004713; P:GO:0040010; F:GO:0005524	-	EC:2.7.10.0	IPR000719; IPR001245; IPR011009; IPR020685; G3DSA:3.30.200.20 (GENE3D), PTHR23256:SF243 (PANTHER)
	-	0				-
Caenorhabditis elegans	in family member (ttn-1)	1	P:GO:0009792	-		IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF17 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Pongo abelii	family with sequence similarity member b	5	C:GO:0005737; C:GO:0005634; F:GO:0005515; N:GO:0071817; P:GO:0007059	-		IPR002744; PTHR12377 (PANTHER), SSF117916 (SUPERFAMILY)
Homo sapiens	loc23117 protein	1	C:GO:0016021	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	vacuolar protein sorting-associated protein	0		P:GO:0008104		PTHR16166 (PANTHER), PTHR16166:SF25 (PANTHER)
	-	0				-
Caenorhabditis briggsae	myo-inositol oxyge-se	5	C:GO:0005737; F:GO:0005506; P:GO:0055114; P:GO:0019310; F:GO:0050113	-	EC:1.13.99.1	IPR007828; SSF109604 (SUPERFAMILY)
Brugia malayi	importin beta-2	9	P:GO:0009792; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0016246; P:GO:0040010; P:GO:0000003; P:GO:0040011; P:GO:0006898	-		IPR011989
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG02784 [Caenorhabditis briggsae]	0				PTHR13298 (PANTHER), PTHR13298:SF2 (PANTHER)
Caenorhabditis elegans	furry homolog	1	F:GO:0005515	-		PTHR12295 (PANTHER), PTHR12295:SF6 (PANTHER)
	-	0				-
Caenorhabditis elegans	cation efflux family protein	4	C:GO:0016021; F:GO:0008324; P:GO:0006812; P:GO:0055085	-		IPR002524; G3DSA:3.30.70.1350 (GENE3D)
	-	0				-
	-	0				SignalP (SIGNALP)
Brugia malayi	hypothetical protein Bm1_04780 [Brugia malayi]	0				-
	-	0				-

Loa loa	transmembrane protein 186	0		C:GO:0005739; F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150		-
	-	0				-
Loa loa	hypothetical protein LOAG_00907 [Loa loa]	0		P:GO:0008104		PTHR16166 (PANTHER), PTHR16166:SF24 (PANTHER)
Caenorhabditis briggsae	gex interacting protein family member (gei-18)	0		P:GO:0009792; F:GO:0005515		PTHR22834 (PANTHER), PTHR22834:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	p21-activated ki-se family member (pak-2)	6	P:GO:0006468; F:GO:0005515; F:GO:0005524; P:GO:0006916; F:GO:0004674; C:GO:0005739	-	EC:2.7.11.0	-
Caenorhabditis elegans	osta1_caeel ame: full=organic solute transporter alpha-like protein	4	C:GO:0016021; P:GO:0009792; P:GO:0006810; F:GO:0005215	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-zip-2 protein	0		P:GO:0006355; F:GO:0043565; F:GO:0046983; F:GO:0003700; C:GO:0005634; F:GO:0003677		IPR004827; IPR011700; G3DSA:1.20.5.170 (GENE3D), PTHR23334 (PANTHER)
	-	0				-
Caenorhabditis briggsae	myosin heavy chain	6	C:GO:0032982; F:GO:0003779; F:GO:0005524; F:GO:0003774; C:GO:0031672; P:GO:0007626	-		-
Caenorhabditis elegans	nitrilase 1	11	P:GO:0009684; F:GO:0080061; P:GO:0000003; P:GO:0009617; P:GO:0019762; P:GO:0009970; C:GO:0009507; P:GO:0046686; F:GO:0080109; C:GO:0005886; C:GO:0048046	-		IPR000132; IPR003010
Homo sapiens	low quality protein: guanine nucleotide-binding protein subunit beta-2-like 1-like	5	F:GO:0019903; C:GO:0005737; C:GO:0043025; F:GO:0005102; C:GO:0005886	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-tnt-3 protein	2	P:GO:0043050; P:GO:0006952	-		-
	-	0				SignalP (SIGNALP)

	-	0				-
Caenorhabditis briggsae	adenylosucci-te synthetase	11	P:GO:0040010; F:GO:0004019; P:GO:0006164; P:GO:0040027; P:GO:0040035; F:GO:0000287; P:GO:0040011; P:GO:0006898; P:GO:0009792; C:GO:0005737; F:GO:0005525	-	EC:6.3.4.4	IPR001114; IPR018220; G3DSA:1.10.300.10 (GENE3D), G3DSA:3.40.440.10 (GENE3D), G3DSA:3.90.170.10 (GENE3D), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG16529 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	pecanex-like protein 1	1	P:GO:0040011	-		PTHR12372 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	major facilitator superfamily protein	1	P:GO:0007275	-		IPR005828; IPR016196; G3DSA:1.20.1250.20 (GENE3D), PTHR11600 (PANTHER), PTHR11600:SF42 (PANTHER), SignalP (SIGNALP)
Loa loa	egg laying defective family member (egl-44)	1	P:GO:0048675	-		IPR000818
Caenorhabditis briggsae	mitochondrial ribosomal protein l49	2	C:GO:0030529; C:GO:0005739	-		IPR007740
Caenorhabditis briggsae	cdk5 regulatory subunit associated protein 1-like 1	5	P:GO:0009451; F:GO:0046872; C:GO:0016021; F:GO:0003824; F:GO:0051539	-		IPR005839; G3DSA:3.80.30.20 (GENE3D), SSF102114 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein F10E7.6 [Caenorhabditis elegans]	2	P:GO:0040010; P:GO:0006898	-		-
	-	0				SignalP (SIGNALP)
Loa loa	tetratricopeptide repeat domain 21b	0		F:GO:0005488		IPR011990; PTHR14699 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	arp2 actin-related protein 2 homolog	14	C:GO:0005885; P:GO:0043652; P:GO:0040010; P:GO:0007126; P:GO:0016331; P:GO:0010631; P:GO:0034314; F:GO:0005524; C:GO:0042995; P:GO:0002119; F:GO:0003779; P:GO:0006898; P:GO:0009792; C:GO:0005737	-		-

Caenorhabditis elegans	arp2 actin-related protein 2 homolog	14	C:GO:0005885; P:GO:0043652; P:GO:0040010; P:GO:0007126; P:GO:0016331; P:GO:0010631; P:GO:0034314; F:GO:0005524; C:GO:0042995; P:GO:0002119; F:GO:0003779; P:GO:0006898; P:GO:0009792; C:GO:0005737	-		-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0016765		-
Caenorhabditis briggsae	protein-tyrosine phosphatase containing protein	5	F:GO:0004725; P:GO:0006470; P:GO:0009792; P:GO:0000003; F:GO:0008138	-	EC:3.1.3.48	IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
	-	0				-
Pongo abelii	small nuclear ribonucleoprotein polypeptide g	8	C:GO:0005683; C:GO:0005654; P:GO:0000387; C:GO:0005681; F:GO:0003723; F:GO:0005515; C:GO:0005829; P:GO:0000245	-		IPR001163; IPR006649; IPR010920; G3DSA:2.30.30.100 (GENE3D), PTHR10553 (PANTHER), PTHR10553:SF2 (PANTHER)
	-	0				-
	-	0				-
Loa loa	aldehyde dehydroge-se	2	P:GO:0008152; F:GO:0016491	-		IPR012394; IPR015590; IPR016161; IPR016163; SignalP (SIGNALP)
Macaca mulatta	prolyl 4- beta polypeptide	12	F:GO:0003756; F:GO:0004656; C:GO:0005793; P:GO:0045454; C:GO:0009986; C:GO:0042470; C:GO:0005792; C:GO:0005788; F:GO:0005515; P:GO:0018401; C:GO:0005576; C:GO:0005886	-	EC:5.3.4.1; EC:1.14.11.2	IPR012335; IPR012336; IPR013766; PTHR18929 (PANTHER)
Caenorhabditis briggsae	in family member (ttn-1)	3	P:GO:0009792; F:GO:0004672; F:GO:0000166	-		IPR013783
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0000003; F:GO:0008270; P:GO:0040010		PTHR22880 (PANTHER), PTHR22880:SF1 (PANTHER)
Caenorhabditis elegans	ribose-phosphate pyrophosphoki-se	4	F:GO:0016301; P:GO:0009165; F:GO:0004749; F:GO:0000287	-	EC:2.7.6.1	IPR005946; G3DSA:3.40.50.2020 (GENE3D), PTHR10210 (PANTHER), SSF53271 (SUPERFAMILY)

Caenorhabditis elegans	ribose-phosphate pyrophosphoki-se	4	F:GO:0016301; P:GO:0009165; F:GO:0004749; F:GO:0000287	-	EC:2.7.6.1	IPR005946; G3DSA:3.40.50.2020 (GENE3D), PTHR10210 (PANTHER), SignalP (SIGNALP), SSF53271 (SUPERFAMILY)
Caenorhabditis elegans	ribose-phosphate pyrophosphoki-se	5	F:GO:0016301; P:GO:0009165; C:GO:0043234; F:GO:0004749; F:GO:0000287	-	EC:2.7.6.1	IPR005946; G3DSA:3.40.50.2020 (GENE3D), PTHR10210 (PANTHER), SSF53271 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	immunoglobulin i-set domain containing protein	0		F:GO:0005509; F:GO:0003824		-
Pediculus humanus corporis	gtp-binding protein di-	5	C:GO:0016020; C:GO:0005622; F:GO:0003924; F:GO:0005525; P:GO:0007264	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR013753; IPR020849; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF117 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	olfactory ing defective family member (olrn-1)	0				-
	-	0				-
Caenorhabditis elegans	rap ran-gap family protein	0		F:GO:0005096; P:GO:0051056; C:GO:0005622		-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
Gallus gallus	multiple ankyrin repeats single kh domain protein	0		F:GO:0003723		IPR002110; IPR018201; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER), PTHR18958:SF281 (PANTHER)
Gallus gallus	multiple ankyrin repeats single kh domain protein	0		F:GO:0003723		IPR002110; IPR018201; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER), PTHR18958:SF281 (PANTHER)
	-	0				-
Populus trichocarpa	predicted protein [Populus trichocarpa]	4	F:GO:0020037; P:GO:0055114; F:GO:0004497; F:GO:0009055	-		-
Caenorhabditis briggsae	briggsae cbr-unc-68 protein	8	F:GO:0004872; P:GO:0006629; F:GO:0005219; P:GO:0006816; P:GO:0006874; P:GO:0055085; F:GO:0005509; C:GO:0016021	-		-
	-	0				-
Caenorhabditis elegans	ke (drosophila actin-binding) homolog family member (ketn-1)	1	P:GO:0000003	-		IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)

Homo sapiens	heavy polypeptide non- isoform cra_b	43	P:GO:0001525; C:GO:0030863; P:GO:0008360; C:GO:0031594; P:GO:0030048; F:GO:0030898; P:GO:0051295; C:GO:0005913; P:GO:0016337; F:GO:0043531; P:GO:0032796; P:GO:0015031; C:GO:0001772; P:GO:0050900; P:GO:0007229; C:GO:0005829; P:GO:0007520; F:GO:0000146; P:GO:0006509; P:GO:0043534; C:GO:0008305; C:GO:0005819; C:GO:0001726; P:GO:0007132; C:GO:0032154; P:GO:0000904; P:GO:0001768; F:GO:0043495;	-		IPR000897
Caenorhabditis briggsae	briggsae cbr-ego-1 protein	1	F:GO:0005515	-		-
Caenorhabditis elegans	zinc finger transcription factor family member (ztf-27)	1	F:GO:0005515	-		-
	-	0				SignalP (SIGNALP)
Ailuropoda melanoleuca	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	9	C:GO:0008250; C:GO:0019718; P:GO:0018279; C:GO:0016021; C:GO:0042470; P:GO:0015833; C:GO:0030867; F:GO:0005515; F:GO:0004579	-	EC:2.4.1.119	-
Caenorhabditis briggsae	sap30-binding protein	1	P:GO:0009987	-		IPR012479
Caenorhabditis briggsae	sap30-binding protein	0		P:GO:0006915; P:GO:0006350; F:GO:0005515; P:GO:0006917; C:GO:0005634		IPR012479
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	expulsion defective family member (aex-1)	2	P:GO:0003008; P:GO:0046903	-		-
Caenorhabditis elegans	threonine dehydratase deami-se	6	P:GO:0040035; F:GO:0005488; P:GO:0040010; P:GO:0040011; F:GO:0003824; P:GO:0002009	-		IPR001926; G3DSA:3.40.50.1100 (GENE3D), PTHR10314 (PANTHER), PTHR10314:SF17 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG03729 [Caenorhabditis briggsae]	0				-

Haemonchus contortus	briggsae cbr-trxr-2 protein	10	P:GO:0001666; C:GO:0005875; P:GO:0008340; C:GO:0005739; P:GO:0045454; F:GO:0004362; P:GO:0008152; F:GO:0042803; F:GO:0004791; P:GO:0006974	-	EC:1.8.1.7; EC:1.8.1.9	IPR001327; IPR006338; IPR013027; PR00411 (PRINTS), G3DSA:3.50.50.60 (GENE3D), PTHR22912 (PANTHER), SSF51905 (SUPERFAMILY)
	-	0				-
Cyathostominae sp. JM-2007a	briggsae cbr-tag-273 protein	2	F:GO:0008270; P:GO:0000003	-		SignalP (SIGNALP)
	-	0				-
Nippostrongylus brasiliensis	globin	6	F:GO:0020037; C:GO:0005576; C:GO:0005737; F:GO:0005344; P:GO:0015671; F:GO:0019825	-		IPR000971; IPR009050; IPR012085; IPR012292; SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0008152; F:GO:0003824		IPR004245; PTHR10974:SF5 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	estradiol 17-beta-dehydroge-se 12-b	9	P:GO:0009790; F:GO:0018454; F:GO:0005515; P:GO:0055114; F:GO:0045703; P:GO:0042761; C:GO:0016021; P:GO:0006508; C:GO:0005783	-	EC:1.1.1.36	IPR002198; IPR016040; PTHR19410:SF38 (PANTHER), SignalP (SIGNALP), SSF51735 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	jhd1_caebr ame: full= domain-containing histone demethylation protein 1 ame: full= -lysine-36 demethylase 1	9	P:GO:0016568; F:GO:0051864; F:GO:0046872; P:GO:0055114; P:GO:0045449; P:GO:0000003; F:GO:0016702; C:GO:0005634; P:GO:0006974	-	EC:1.14.11.27; EC:1.13.11.0	-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0017176; P:GO:0006506; C:GO:0016021		IPR009450; SignalP (SIGNALP)
	-	0				-
Caenorhabditis sp. PS1010	briggsae cbr-cdh-4 protein	7	P:GO:0007156; P:GO:0007163; C:GO:0005886; P:GO:0007411; F:GO:0005509; C:GO:0016021; P:GO:0007413	-		IPR002126; IPR015919; PTHR10596 (PANTHER), PTHR10596:SF74 (PANTHER)

Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	11	P:GO:0009103; C:GO:0005829; P:GO:0007265; F:GO:0004674; F:GO:0004871; C:GO:0016021; P:GO:0000165; F:GO:0005524; F:GO:0005515; P:GO:0009792; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR002290; IPR008271; IPR011009; IPR017441; IPR017442; IPR020636; IPR020646; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	11	P:GO:0009103; C:GO:0005829; P:GO:0007265; F:GO:0004674; F:GO:0004871; C:GO:0016021; P:GO:0000165; F:GO:0005524; F:GO:0005515; P:GO:0009792; P:GO:0006468	-	EC:2.7.11.0	-
	-	0				-
	-	0				-
Caenorhabditis elegans	yaf2_caeel ame: full=uncharacterized protein flags: precursor	0				-
Schistosoma mansoni	nonsense-mediated mr- decay protein 1	0		F:GO:0004386; F:GO:0003677; F:GO:0016787; F:GO:0000166; C:GO:0005737; F:GO:0008270; F:GO:0005524; P:GO:0000184; F:GO:0046872		-
Caenorhabditis briggsae	phosphatidylinositol-3-phosphate phosphatidylinositol 5-type iii	15	P:GO:0042147; C:GO:0005829; C:GO:0031901; P:GO:0046488; P:GO:0044267; F:GO:0008270; P:GO:0023034; P:GO:0034504; C:GO:0032593; F:GO:0016308; F:GO:0005524; F:GO:0005515; C:GO:0045121; C:GO:0012506; P:GO:0006898	-	EC:2.7.1.68	IPR002498; G3DSA:3.30.800.10 (GENE3D), SSF56104 (SUPERFAMILY)
Caenorhabditis elegans	fanci (fanconi anemia complex component i) homolog family member (fnci-1)	0				-
	-	0				-
Caenorhabditis elegans	sulfate transporter	3	C:GO:0016021; P:GO:0055085; F:GO:0005215	-		-

Macaca mulatta	-+ k+ alpha 1 polypeptide	20	F:GO:0005515; P:GO:0045989; P:GO:0045822; F:GO:0003869; C:GO:0005792; C:GO:0016323; C:GO:0042470; F:GO:0046872; P:GO:0006754; C:GO:0042383; F:GO:0005391; P:GO:0045823; P:GO:0042493; P:GO:0031947; C:GO:0005890; P:GO:0006813; P:GO:0002026; F:GO:0005524; P:GO:0008217; P:GO:0006814	-	EC:3.1.3.41; EC:3.6.3.9	IPR001757; G3DSA:3.40.1110.10 (GENE3D), PTHR11939:SF100 (PANTHER), SSF81660 (SUPERFAMILY)
Caenorhabditis elegans	melt_caeel ame: full=protein melted homolog	0		F:GO:0005488; C:GO:0016020; C:GO:0005886		-
Caenorhabditis elegans	sex peptide receptor	0		F:GO:0016740; C:GO:0016021; P:GO:0006729; P:GO:0055114; P:GO:0045434; F:GO:0008188; F:GO:0016491; P:GO:0048042; F:GO:0003824; F:GO:0050254; F:GO:0004872; P:GO:0008152; P:GO:0007186; C:GO:0005886; F:GO:0005488; F:GO:0004757		IPR017452; G3DSA:1.20.1070.10 (GENE3D), PTHR22751 (PANTHER), PTHR22751:SF12 (PANTHER), SignalP (SIGNALP), SSF81321 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	zinc c2h2 type family protein	0		F:GO:0008270; C:GO:0005622		IPR015880
	-	0				-
Caenorhabditis briggsae	kank1 protein	1	P:GO:0030837	-		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF169 (PANTHER)
Mus musculus	atp-binding sub-family a member 2	7	F:GO:0017111; C:GO:0016020; P:GO:0044238; C:GO:0043229; P:GO:0009987; P:GO:0065007; C:GO:0044444	-	EC:3.6.1.15	PTHR19229 (PANTHER), PTHR19229:SF31 (PANTHER)

Caenorhabditis elegans	yf26_caeel ame: full=protein	0		P:GO:0000003; P:GO:0040035; P:GO:0006898; P:GO:0002119; P:GO:0040007		PF10175 (PFAM)
Gallus gallus	extensin-like protein	0		F:GO:0016740; F:GO:0003677; P:GO:0006260; F:GO:0003887; F:GO:0005524; F:GO:0008270; P:GO:0055114; P:GO:0030261; F:GO:0016491; F:GO:0016779; C:GO:0016459; F:GO:0003824; F:GO:0003774; P:GO:0008152; F:GO:0005488		-
Brugia malayi	protein-tyrosine phosphatase containing protein	2	P:GO:0016311; F:GO:0004721	-	EC:3.1.3.16	IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF20 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis elegans	egl nine homolog 1	16	P:GO:0007411; P:GO:0060412; P:GO:0060347; F:GO:0005515; F:GO:0008270; P:GO:0043433; P:GO:0060711; C:GO:0005829; F:GO:0031543; P:GO:0055008; P:GO:0001666; F:GO:0005506; P:GO:0032364; P:GO:0030163; P:GO:0055114; F:GO:0031418	-		IPR002893; IPR005123; IPR006620; PTHR12907 (PANTHER), PS51471 (PROFILE), SSF144232 (SUPERFAMILY)
Caenorhabditis elegans	leucine-rich repeat serine threonine-protein ki-se 1	1	F:GO:0004672	-		IPR001611; IPR003591; PR00019 (PRINTS), G3DSA:3.80.10.10 (GENE3D), PTHR23154 (PANTHER), PTHR23154:SF107 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-sos-1 protein	0		P:GO:0051056; P:GO:0007264; F:GO:0005089; P:GO:0035023; F:GO:0003677; F:GO:0005085; C:GO:0005622		-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	r- polymerase rpb3 rpb11 dimerisation domain containing protein	1	F:GO:0016740	-		IPR009025; G3DSA:3.30.1360.10 (GENE3D), PTHR11800 (PANTHER), PTHR11800:SF13 (PANTHER)

Caenorhabditis elegans	egf-like domain containing protein	0				IPR000742; IPR013032; G3DSA:2.10.25.10 (GENE3D)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-cat-4 protein	11	P:GO:0046654; F:GO:0003934; F:GO:0046872; P:GO:0042438; P:GO:0006729; P:GO:0006730; F:GO:0005515; P:GO:0034607; C:GO:0005737; F:GO:0005525; P:GO:0042416	-	EC:3.5.4.16	IPR018247
Caenorhabditis elegans	hypothetical wd-repeat protein in chromosome	0				IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR12816 (PANTHER), PTHR12816:SF6 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Homo sapiens	optineurin	9	P:GO:0043001; C:GO:0016023; P:GO:0007165; P:GO:0008219; P:GO:0000042; F:GO:0008022; C:GO:0005802; C:GO:0048471; P:GO:0090161	-		-
Pediculus humanus corporis	histone h1	0		C:GO:0005694; F:GO:0005524; C:GO:0000786; P:GO:0006334; C:GO:0016459; F:GO:0003774; F:GO:0003677; C:GO:0005634		-
Caenorhabditis briggsae	thrombospondin type 1 domain containing protein	3	F:GO:0005044; F:GO:0030247; P:GO:0006955	-		-
Brugia malayi	rad9 family protein	0		P:GO:0006260; P:GO:0006281; F:GO:0005515		IPR007268; G3DSA:3.70.10.10 (GENE3D), SSF55979 (SUPERFAMILY)
Caenorhabditis briggsae	p-type atpase	5	C:GO:0016021; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0006812	-		-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG20437 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	briggsae cbr-pqn- protein	1	F:GO:0005488	-		IPR009060; PTHR16308 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-pqn- protein	1	F:GO:0005488	-		IPR009060; PTHR16308 (PANTHER)
	-	0				-
	-	0				-
	-	0				-

Haemonchus contortus	multidrug resistance protein 1	17	P:GO:0055085; P:GO:0015893; P:GO:0007595; P:GO:0048545; P:GO:0014045; F:GO:0015238; P:GO:0010212; C:GO:0005739; C:GO:0016021; F:GO:0042626; C:GO:0046581; C:GO:0009986; F:GO:0005524; P:GO:0046685; F:GO:0005515; P:GO:0014070; C:GO:0016324	-		IPR001140; IPR011527; IPR017940; G3DSA:1.20.1560.10 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF96 (PANTHER)
	-	0				-
Caenorhabditis elegans	uncoordi-ted protein isoform partially confirmed by transcript evidence	8	F:GO:0004872; P:GO:0006629; F:GO:0005219; P:GO:0006816; P:GO:0006874; P:GO:0055085; F:GO:0005509; C:GO:0016021	-		IPR020830
Caenorhabditis briggsae	-dh oxidase	3	P:GO:0008152; P:GO:0051301; F:GO:0003824	-		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	thymus-specific serine protease	0		P:GO:0006508; F:GO:0008236; C:GO:0016021; F:GO:0008233; P:GO:0008150; F:GO:0005515; C:GO:0005575		IPR008758; G3DSA:3.40.50.1820 (GENE3D), PTHR11010:SF4 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Loa loa	cttnbp2 n-termi-l like	0		C:GO:0015629; F:GO:0005515		-
Caenorhabditis elegans	hed family member (ptc-3)	10	P:GO:0007283; P:GO:0006461; P:GO:0009792; P:GO:0002119; C:GO:0005887; F:GO:0008158; P:GO:0040018; P:GO:0008544; P:GO:0018996; P:GO:0040011	-		IPR000731; PTHR10796 (PANTHER), PTHR10796:SF34 (PANTHER), PF12349 (PFAM)

Caenorhabditis briggsae	protein ki-se domain containing protein	8	C:GO:0005929; C:GO:0030425; F:GO:0005515; P:GO:0034606; F:GO:0004672; C:GO:0030424; P:GO:0034608; C:GO:0043025	-		IPR000719; IPR001245; IPR008266; IPR011009; IPR020685; IPR020764; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
Caenorhabditis elegans	rab3il1 protein	7	C:GO:0005829; P:GO:0006810; P:GO:0033365; C:GO:0005813; F:GO:0005515; P:GO:0042384; C:GO:0005634	-		IPR009449; PTHR14430 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0005515		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-hcp-4 protein	0		F:GO:0030247; C:GO:0016021; C:GO:0016020; F:GO:0008195; F:GO:0016787; P:GO:0007165; C:GO:0005576; F:GO:0005044; C:GO:0005622; F:GO:0005515; P:GO:0007050; P:GO:0008283; P:GO:0006955		-
Caenorhabditis briggsae	glutaredoxin-related protein	4	C:GO:0030018; P:GO:0002026; F:GO:0005515; P:GO:0010614	-		IPR002109; IPR004480; IPR012335; IPR012336; IPR013766
	-	0				-
	-	0				-
Caenorhabditis elegans	e430025e21rik protein	0		F:GO:0008289; P:GO:0000003; P:GO:0008150; C:GO:0005575; P:GO:0006810		IPR019393
Brugia malayi	hypothetical kda protein in chromosome	0		C:GO:0016021; C:GO:0016020		PTHR22746 (PANTHER), PTHR22746:SF6 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	excretory ca-l abnormal family member (exc-5)	4	F:GO:0005089; C:GO:0005622; P:GO:0035023; F:GO:0008270	-		IPR000219; PTHR12673 (PANTHER), PTHR12673:SF8 (PANTHER)
Caenorhabditis elegans	yka7_caeel ame: full=uncharacterized protein	0				-
	-	0				-
Loa loa	hypothetical protein LOAG_07907 [Loa loa]	1	F:GO:0005515	-		IPR001715
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-

Callithrix jacchus	proteasome (macropain) beta 10	9	P:GO:0051436; P:GO:0051437; F:GO:0004298; P:GO:0031145; P:GO:0006959; P:GO:0044419; C:GO:0005737; C:GO:0005839; C:GO:0005634	-	EC:3.4.25.0	-
Caenorhabditis elegans	o-phosphoseryl-tr- selenium transferase	6	C:GO:0005737; F:GO:0042802; F:GO:0030170; F:GO:0016740; F:GO:0016829; P:GO:0006412	-	EC:3.6.5.3	IPR008829; IPR019872
Caenorhabditis briggsae	uncoordi-ted family member (unc-22)	5	C:GO:0030018; F:GO:0008307; P:GO:0007498; F:GO:0004674; F:GO:0000166	-	EC:2.7.11.0	IPR003599; IPR007110; IPR013098; IPR013783; PTHR19900 (PANTHER), PTHR19900:SF7 (PANTHER), SSF48726 (SUPERFAMILY)
Brugia malayi	cell cycle protein	0		F:GO:0016740; F:GO:0004674; F:GO:0004672; P:GO:0006468; F:GO:0000166; P:GO:0051301; F:GO:0005524; F:GO:0016301; C:GO:0005575		IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF7 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-qui-1 protein	0		F:GO:0005524; F:GO:0000166		SignalP (SIGNALP)
Ancylostoma caninum	venom allergen-like protein	0		F:GO:0009055; P:GO:0019646; P:GO:0040011; C:GO:0005576		IPR001283; IPR014044; IPR018244; PTHR10334:SF11 (PANTHER)
Homo sapiens	biglycan	10	C:GO:0009986; F:GO:0050840; P:GO:0001974; P:GO:0019800; C:GO:0042383; F:GO:0005201; F:GO:0005515; F:GO:0005539; C:GO:0005578; C:GO:0030133	-		IPR001611; G3DSA:3.80.10.10 (GENE3D), PTHR23154 (PANTHER), PTHR23154:SF71 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)
Caenorhabditis elegans	phosphatidylinositol transfer membrane-associated 2	5	C:GO:0016021; P:GO:0008152; F:GO:0005509; C:GO:0005625; C:GO:0043231	-		IPR001666; G3DSA:3.30.530.20 (GENE3D), PTHR10658:SF6 (PANTHER), SSF55961 (SUPERFAMILY)
	-	0				-

Caenorhabditis elegans	ribosomal r- processing homolog	9	P:GO:0040010; P:GO:0008340; C:GO:0005730; P:GO:0000183; F:GO:0035064; N:GO:0071840; C:GO:0005677; C:GO:0033553; F:GO:0008168	-	EC:2.1.1.0	IPR007823; G3DSA:3.40.50.150 (GENE3D), SSF53335 (SUPERFAMILY)
Caenorhabditis elegans	rophin family member (stn-1)	8	P:GO:0007528; F:GO:0005515; P:GO:0040017; C:GO:0016010; F:GO:0005277; F:GO:0005246; P:GO:0015870; P:GO:0046716	-		IPR015482; PTHR10554:SF5 (PANTHER)
Loa loa	briggsae cbr-cki- protein	0		F:GO:0016301; P:GO:0045132; F:GO:0004861; P:GO:0007050; P:GO:0009792; P:GO:0007067; C:GO:0005634		IPR003175; G3DSA:4.10.365.10 (GENE3D), PTHR10265:SF6 (PANTHER)
	-	0				-
Ailuropoda melanoleuca	sec61-like protein	6	C:GO:0030176; F:GO:0015450; P:GO:0045047; F:GO:0005515; P:GO:0055085; F:GO:0043022	-		-
Caenorhabditis briggsae	protein ki-se domain containing protein	2	F:GO:0005488; F:GO:0004672	-		IPR000980; SSF55550 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-hmt-1 protein	0		F:GO:0005524; F:GO:0016887; F:GO:0000166; C:GO:0016021; F:GO:0042626; F:GO:0017111; P:GO:0055085; P:GO:0006810		PTHR19242 (PANTHER), PTHR19242:SF69 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	n -(beta-n-acetylglucosaminyl)-l-asparagi-se precursor (n4-(n-acetyl-beta-glucosaminyl)-l-asparagine amidase)	5	F:GO:0043621; C:GO:0005764; F:GO:0003948; P:GO:0006517; C:GO:0005783	-	EC:3.5.1.26	IPR000246; PTHR10188:SF6 (PANTHER), SSF56235 (SUPERFAMILY)
	-	0				-
	-	0				IPR007465
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR000782; PTHR10900 (PANTHER), PTHR10900:SF10 (PANTHER)
	-	0				-
Caenorhabditis elegans	beta like 1	1	F:GO:0042802	-		PTHR14978 (PANTHER)

Caenorhabditis elegans	cathepsin b-like cysteine protei-se	9	P:GO:0009792; P:GO:0002119; F:GO:0005515; P:GO:0040011; F:GO:0004197; P:GO:0040007; P:GO:0006898; P:GO:0006508; P:GO:0050790	-	EC:3.4.22.0	-
Caenorhabditis elegans	spectrin beta chain	0		F:GO:0005200; F:GO:0003779; F:GO:0016787; F:GO:0004725; C:GO:0008091		PTHR11915 (PANTHER), PTHR11915:SF48 (PANTHER)
Caenorhabditis briggsae	acid ceramidase-like	2	C:GO:0005764; P:GO:0006629	-		-
Caenorhabditis briggsae	uncoordi-ted family member (unc-53)	0		F:GO:0005524; F:GO:0003674; P:GO:0007049; F:GO:0000166; F:GO:0017111; C:GO:0005575		PTHR12784 (PANTHER), PTHR12784:SF5 (PANTHER)
Caenorhabditis briggsae	uncoordi-ted family member (unc-53)	0		F:GO:0005524; F:GO:0003674; P:GO:0007049; F:GO:0000166; F:GO:0017111; C:GO:0005575		PTHR12784 (PANTHER), PTHR12784:SF5 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Brugia malayi	uridine-cytidine ki-se 2	2	F:GO:0016301; P:GO:0006911	-		IPR000764; IPR006083; G3DSA:3.40.50.300 (GENE3D), PTHR10285 (PANTHER), SSF52540 (SUPERFAMILY)
Brugia malayi	hypothetical protein Bm1_25600 [Brugia malayi]	0		F:GO:0051082; P:GO:0006457; C:GO:0016272		-
Caenorhabditis briggsae	translocon-associated protein subunit alpha	1	P:GO:0009792	-		IPR005595; PTHR12924 (PANTHER)
	-	0				-
Caenorhabditis elegans	hypothetical protein H01M10.1 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Brugia malayi	c-termi-l binding protein 1	7	P:GO:0009987; C:GO:0043234; P:GO:0055114; F:GO:0004617; F:GO:0051287; F:GO:0005515; C:GO:0044451	-	EC:1.1.1.95	PTHR10996 (PANTHER), PTHR10996:SF11 (PANTHER)

Caenorhabditis elegans	tho complex 2	8	P:GO:0045132; P:GO:0040007; P:GO:0000003; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0051028	-		IPR021726; PTHR21597 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-unc-95 protein	1	F:GO:0046872	-		-
Caenorhabditis elegans	glycerol ki-se 5	2	P:GO:0005975; F:GO:0016773	-	EC:2.7.1.0	-
Caenorhabditis elegans	glycerol ki-se 5	2	P:GO:0005975; F:GO:0016772	-		IPR000577; IPR005999; IPR018484; IPR018485; G3DSA:3.30.420.40 (GENE3D), SSF53067 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	haloacid dehaloge-se-like hydrolase family protein	1	F:GO:0016787	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
	-	0				IPR001304; IPR016186; IPR016187; PTHR22801 (PANTHER), PTHR22801:SF9 (PANTHER), SignalP (SIGNALP)
	-	0				-
Ancylostoma ceylanicum	secreted protein 5 precursor	0		C:GO:0005576		IPR014044
	-	0				-
	-	0				-
Caenorhabditis elegans	alpha-l- tissue	7	C:GO:0005625; F:GO:0005529; P:GO:0016142; F:GO:0043169; P:GO:0006004; C:GO:0005764; F:GO:0004560	-	EC:3.2.1.51	IPR000933; IPR013781; IPR017853
	-	0				-
Pristionchus pacificus	briggsae cbr-egl-20 protein	12	F:GO:0005109; C:GO:0005615; P:GO:0007409; F:GO:0004871; C:GO:0005886; P:GO:0042074; P:GO:0007507; P:GO:0009952; C:GO:0005578; P:GO:0009798; P:GO:0060070; P:GO:0007223	-		IPR005817; PTHR12027:SF9 (PANTHER)
Caenorhabditis elegans	oate ligase family member (lpl-1)	0		P:GO:0000003; P:GO:0040010; P:GO:0006898; P:GO:0002119; P:GO:0040007; P:GO:0040018		IPR019346; SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein R07D5.2 [Caenorhabditis elegans]	0				SignalP (SIGNALP)

Caenorhabditis briggsae	atp-binding sub-family a member 7	2	F:GO:0016887; F:GO:0005524	-		-
Caenorhabditis elegans	tubulin beta-2c chain	8	P:GO:0009792; P:GO:0007018; F:GO:0005525; P:GO:0007067; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000217; IPR002453; IPR003008; IPR008280; IPR018316
	-	0				IPR001128; PTHR19383:SF66 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	secreted frizzled-related protein 2	12	P:GO:0001501; P:GO:0009888; F:GO:0004930; C:GO:0016021; P:GO:0030178; P:GO:0009790; P:GO:0006915; P:GO:0007165; F:GO:0004926; P:GO:0009887; P:GO:0030154; P:GO:0007186	-		IPR015526; IPR020067; PTHR11309:SF18 (PANTHER)
Caenorhabditis briggsae	talin 2	6	F:GO:0005200; C:GO:0005856; P:GO:0007016; C:GO:0005925; C:GO:0001726; F:GO:0005158	-		IPR000299; IPR002404; IPR002558; IPR011993; IPR015224; IPR015710; G3DSA:1.20.1490.10 (GENE3D), SSF109885 (SUPERFAMILY), SSF50729 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG05684 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)
Caenorhabditis briggsae	protein ki-se domain containing protein	0		F:GO:0016301; F:GO:0004672; F:GO:0005524; F:GO:0000166; P:GO:0006468; F:GO:0004674		G3DSA:1.10.510.10 (GENE3D), PTHR22984 (PANTHER)
Caenorhabditis elegans	daf-16 foxo germline tumor affecting family member (dct-6)	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	islet cell autoantigen 1	10	C:GO:0030425; C:GO:0000139; C:GO:0045202; P:GO:0043496; C:GO:0005795; P:GO:0042221; C:GO:0030667; F:GO:0019904; C:GO:0048471; P:GO:0046928	-		IPR010504; PTHR10164 (PANTHER), SSF103657 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	leucine-rich repeat-containing protein 47	1	F:GO:0005488	-		IPR001611; IPR007666; PR00019 (PRINTS), G3DSA:3.80.10.10 (GENE3D), PTHR23155 (PANTHER), PTHR23155:SF37 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	protein phosphatase 2a (two a) regulatory subunit family member (pptr-2)	8	F:GO:0008601; P:GO:0009792; P:GO:0002119; C:GO:0000159; F:GO:0005515; P:GO:0007165; P:GO:0040007; C:GO:0005634	-		IPR002554; IPR016024
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis briggsae	udp-glucose dehydroge-se	16	P:GO:0007427; F:GO:0003979; P:GO:0007224; P:GO:0016055; P:GO:0016319; P:GO:0055114; P:GO:0007507; F:GO:0042802; P:GO:0042048; P:GO:0015014; P:GO:0008543; F:GO:0051287; P:GO:0002121; P:GO:0007509; P:GO:0007428; P:GO:0030206	-	EC:1.1.1.22	IPR001732; IPR014028; IPR016040; PTHR11374:SF1 (PANTHER), SSF51735 (SUPERFAMILY)

Pediculus humanus corporis	luteinizing hormone receptor	0		F:GO:0004872; F:GO:0004871; C:GO:0005887; C:GO:0005886; P:GO:0010524; C:GO:0016021; F:GO:0051117; C:GO:0016020; P:GO:0050482; C:GO:0005783; F:GO:0004963; F:GO:0016500; F:GO:0004930; P:GO:0007200; P:GO:0007165; P:GO:0046886; F:GO:0042803; F:GO:0042802; P:GO:0007190; C:GO:0043235; P:GO:0042700; F:GO:0008528; C:GO:0005615; P:GO:0007188; P:GO:0050850; P:GO:0007186; F:GO:0005515;		PTHR23154 (PANTHER), PTHR23154:SF30 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	2-amino-3-carboxymuco-te-6-semialdehyde decarboxylase	5	P:GO:0006568; P:GO:0006769; F:GO:0001760; C:GO:0005829; P:GO:0046874	-	EC:4.1.1.45	IPR006992; G3DSA:3.20.20.140 (GENE3D), PTHR21240 (PANTHER), SSF51556 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	malic enzyme	6	F:GO:0046872; F:GO:0051287; C:GO:0005759; F:GO:0016619; P:GO:0006108; P:GO:0055114	-	EC:1.1.1.38	-
Caenorhabditis briggsae	briggsae cbr-ser-1 protein	0		F:GO:0004872; F:GO:0004871; F:GO:0004930; C:GO:0016021; P:GO:0007165; P:GO:0007186		-
Caenorhabditis elegans	wd-repeat protein	7	P:GO:0030334; C:GO:0005794; C:GO:0005829; C:GO:0010008; F:GO:0017137; C:GO:0048471; C:GO:0005874	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR14221 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	cadherin domain containing protein	1	C:GO:0016020	-		-
	-	0				-

	-	0				-
Caenorhabditis elegans	leucyl tr- synthetase family member (lrs-2)	4	C:GO:0005737; F:GO:0004823; P:GO:0006429; F:GO:0005524	-	EC:6.1.1.4	G3DSA:1.10.730.10 (GENE3D)
Caenorhabditis elegans	ribosomal protein l20	4	P:GO:0009792; F:GO:0003723; P:GO:0009987; C:GO:0030529	-		IPR005813; G3DSA:1.10.1900.20 (GENE3D), SSF74731 (SUPERFAMILY)
	-	0				-
Brugia malayi	smr domain containing protein	0				-
Caenorhabditis briggsae	mpp10 protein	4	P:GO:0040035; P:GO:0002119; P:GO:0040010; P:GO:0006898	-		IPR007151
Homo sapiens	cytochrome b- alpha polypeptide	33	P:GO:0001938; P:GO:0006810; P:GO:0071333; P:GO:0045730; P:GO:0071356; F:GO:0020037; P:GO:0042554; F:GO:0009055; C:GO:0005794; P:GO:0022900; P:GO:0003106; F:GO:0046982; P:GO:0071260; C:GO:0030425; P:GO:0048661; C:GO:0043025; P:GO:0050665; P:GO:0071480; P:GO:0006954; P:GO:0070555; P:GO:0071407; C:GO:0043020; C:GO:0030141; P:GO:0017004; P:GO:0014895; F:GO:0017124; P:GO:0045087;	-		IPR007732; SignalP (SIGNALP)
Caenorhabditis sp. PS1010	d- polymerase eta	4	P:GO:0044260; P:GO:0044238; F:GO:0016772; F:GO:0000166	-		IPR001126; IPR017963; G3DSA:3.30.70.270 (GENE3D), PTHR11076:SF11 (PANTHER), SSF56672 (SUPERFAMILY)
	-	0				-
	-	0				-
Brugia malayi	yemanuclein alpha	3	C:GO:0005634; F:GO:0003677; P:GO:0048477	-		-
Caenorhabditis briggsae	briggsae cbr-apt-10 protein	1	P:GO:0016192	-		-
Brugia malayi	viral a-type inclusion protein repeat containing protein	0				-
Ostertagia ostertagi	metalloprotease 1 precursor	3	F:GO:0004222; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	-

Caenorhabditis briggsae	phospholipase d3	0		C:GO:0016021; C:GO:0016020; F:GO:0070290; F:GO:0016787; P:GO:0016042; C:GO:0005789; F:GO:0003824; F:GO:0004630; C:GO:0005783; P:GO:0008152		IPR013582; G3DSA:3.30.870.10 (GENE3D), PTHR10185 (PANTHER)
Brugia malayi	roquin isoform 2	4	P:GO:0008340; P:GO:0009408; F:GO:0004842; F:GO:0005515	-	EC:6.3.2.19	IPR001841; IPR013083; IPR017907; PTHR13139 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	9	C:GO:0005887; P:GO:0015724; F:GO:0015108; F:GO:0015499; C:GO:0005624; P:GO:0009987; F:GO:0015380; P:GO:0015701; P:GO:0006821	-		IPR011547; PTHR11814 (PANTHER), PTHR11814:SF26 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	cerevisiae sec31-like 2	0				-
Caenorhabditis briggsae	translocon-associated protein subunit beta precursor	2	C:GO:0044464; P:GO:0009792	-		IPR008856
	-	0				-
Caenorhabditis briggsae	glutaredoxin-like protein	7	P:GO:0009792; F:GO:0009055; P:GO:0040015; P:GO:0045454; P:GO:0040010; P:GO:0000003; F:GO:0015035	-		IPR002109; IPR004480; IPR012335; IPR012336; IPR014434
Trichostrongylus vitrinus	serine threonine phosphatase	2	P:GO:0000003; F:GO:0004721	-	EC:3.1.3.16	IPR004843; IPR006186; G3DSA:3.60.21.10 (GENE3D), SSF56300 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	erv1 alr family protein	8	P:GO:0045454; P:GO:0040017; C:GO:0043231; P:GO:0040010; P:GO:0055114; F:GO:0016972; C:GO:0044444; C:GO:0016020	-	EC:1.8.3.2	IPR012335; IPR012336; IPR013766; IPR017937; PTHR18929 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	dedicator of cytokinesis protein 1	10	F:GO:0005085; F:GO:0005083; P:GO:0043652; F:GO:0005525; P:GO:0007520; C:GO:0005886; F:GO:0032403; F:GO:0051020; P:GO:0040039; F:GO:0017124	-		PTHR23317 (PANTHER), PTHR23317:SF16 (PANTHER)

Brugia malayi	high mobility group protein	10	P:GO:0040010; F:GO:0031492; P:GO:0040035; F:GO:0043621; P:GO:0002119; P:GO:0051101; C:GO:0035101; P:GO:0040011; P:GO:0009792; P:GO:0001672	-		-
	-	0				IPR018062; SignalP (SIGNALP)
Phaeodactylum tricornutum CCAP 1055/1	chromodomain-helicase-d--binding protein 1-like	0		F:GO:0004386; C:GO:0016585; F:GO:0016787; C:GO:0005634; F:GO:0003677; F:GO:0003676; F:GO:0016818; F:GO:0005524; P:GO:0006974; P:GO:0043044; F:GO:0031491; P:GO:0006338; F:GO:0000166; F:GO:0016887; F:GO:0004003; P:GO:0006281; F:GO:0005515; F:GO:0008026		IPR000330; PTHR10799 (PANTHER), PTHR10799:SF74 (PANTHER)
Loa loa	d--dependent r- polymerase family protein	0		F:GO:0016779; F:GO:0003899; F:GO:0016740; P:GO:0006350; F:GO:0003677		-
Caenorhabditis elegans	r- polymerase 1-2	12	F:GO:0003899; P:GO:0009303; P:GO:0017126; P:GO:0007566; C:GO:0005736; P:GO:0040007; P:GO:0040035; F:GO:0003677; P:GO:0002119; F:GO:0005515; F:GO:0032549; P:GO:0009792	-	EC:2.7.7.6	IPR007644; IPR015712; PTHR20856:SF1 (PANTHER), SSF64484 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)

Loa loa	adenylate cyclase 6	14	C:GO:0045121; F:GO:0005102; P:GO:0007193; F:GO:0008294; C:GO:0005624; P:GO:0009755; C:GO:0031528; C:GO:0016021; P:GO:0034199; F:GO:0046872; C:GO:0042383; C:GO:0005768; P:GO:0007189; F:GO:0005524	-		IPR001054; IPR018297; PTHR11920 (PANTHER), PTHR11920:SF14 (PANTHER)
	-	0				-
Brugia malayi	cpyc type	1	F:GO:0016740	-		IPR002109; IPR011767; IPR012335; IPR012336; IPR014025; PTHR10168 (PANTHER), PTHR10168:SF16 (PANTHER)
Caenorhabditis elegans	tubulointerstitial nephritis antigen-like	2	P:GO:0006508; F:GO:0004197	-	EC:3.4.22.0	-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG02477 [Caenorhabditis briggsae]	0		P:GO:0008104		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Macaca mulatta	elongin b	10	C:GO:0005829; F:GO:0003746; P:GO:0045944; C:GO:0005667; F:GO:0016251; P:GO:0006461; F:GO:0004842; F:GO:0005515; P:GO:0006368; C:GO:0030891	-	EC:6.3.2.19	SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	abnormal go-d development family member (gon-2)	7	P:GO:0071482; P:GO:0006810; F:GO:0005262; P:GO:0007601; P:GO:0007067; P:GO:0008406; C:GO:0005887	-		PTHR13800 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	numb related family member (num-1)	1	F:GO:0005515	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Schistosoma mansoni	hypothetical protein [Schistosoma mansoni]	0				-

Caenorhabditis elegans	variant sh3 domain containing protein	18	P:GO:0090130; P:GO:0007166; F:GO:0004871; F:GO:0005515; F:GO:0004435; P:GO:0048729; P:GO:0016319; P:GO:0007424; F:GO:0016491; P:GO:0042048; P:GO:0009395; P:GO:0006024; P:GO:0007367; P:GO:0015012; P:GO:0007165; P:GO:0002121; P:GO:0042331; P:GO:0007298	-	EC:3.1.4.11	IPR000980; IPR020685; IPR020700; SSF55550 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-twk-33 protein	3	C:GO:0016020; F:GO:0005216; P:GO:0006811	-		IPR013099; G3DSA:1.10.287.70 (GENE3D), PTHR11003 (PANTHER), PTHR11003:SF7 (PANTHER), SignalP (SIGNALP), SSF81324 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	F:GO:0005515; P:GO:0006974; P:GO:0008340	-		IPR007087
Homo sapiens	un-med protein product [Homo sapiens]	9	F:GO:0005525; C:GO:0005794; C:GO:0005886; F:GO:0005515; P:GO:0016192; P:GO:0007264; C:GO:0048471; F:GO:0003924; P:GO:0015031	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Loa loa	poly polymerase gamma	11	F:GO:0016779; P:GO:0040010; C:GO:0043231; P:GO:0031123; P:GO:0040035; P:GO:0010171; P:GO:0002119; F:GO:0000166; P:GO:0040011; P:GO:0002009; P:GO:0009792	-	EC:2.7.7.0	IPR002934; IPR007010; IPR007012; IPR011068; IPR014492; G3DSA:1.10.1410.10 (GENE3D), PTHR10682 (PANTHER), PTHR10682:SF8 (PANTHER), SSF81301 (SUPERFAMILY), SSF81631 (SUPERFAMILY)
	-	0				-
	-	0				-
Danio rerio	novel protein containing sea domains	0		P:GO:0006950		-
Caenorhabditis elegans	hypothetical protein F54H5.3 [Caenorhabditis elegans]	0		P:GO:0000003; P:GO:0019915		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)

Caenorhabditis briggsae	wingless-related mmtv integration site isoform cra_a	11	F:GO:0005102; P:GO:0060026; P:GO:0090090; P:GO:0007389; P:GO:0048513; C:GO:0009986; P:GO:0042060; P:GO:0016477; P:GO:0048598; P:GO:0045600; C:GO:0031012	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021		SignalP (SIGNALP)
Clostridium bartlettii DSM 16795	hep_hag family protein	0		F:GO:0005515		-
Caenorhabditis elegans	tr- (guanine-n -)-methyltransferase	5	P:GO:0030488; P:GO:0009792; F:GO:0008176; C:GO:0005634; F:GO:0000049	-	EC:2.1.1.33	IPR003358; G3DSA:3.40.50.150 (GENE3D), PTHR23417 (PANTHER), SSF53335 (SUPERFAMILY)
Brugia malayi	hypothetical protein [Brugia malayi]	0				IPR002550; PTHR12064 (PANTHER)
Brugia malayi	molybdenum cofactor synthesis protein 2 small subunit	2	C:GO:0005737; P:GO:0044237	-		IPR003749; IPR012675; IPR016155
Caenorhabditis elegans	hypothetical protein ZK1307.7 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	annexin a6	4	F:GO:0005515; C:GO:0044444; P:GO:0051239; F:GO:0005544	-		IPR001464; IPR018252; IPR018502; PTHR10502:SF30 (PANTHER)
	-	0				-
	-	0				-
Homo sapiens	transgelin 2	4	C:GO:0031965; F:GO:0005515; C:GO:0005886; P:GO:0007517	-		-
	-	0				-
	-	0				-
Angiostrongylus cantonensis	tnf receptor-associated protein 1	6	P:GO:0006457; P:GO:0006950; P:GO:0040010; F:GO:0005524; F:GO:0051082; C:GO:0005739	-		IPR001404; IPR020568; IPR020576; PTHR11528:SF24 (PANTHER), SSF110942 (SUPERFAMILY)
Caenorhabditis briggsae	abnormal cell migration family member (mig-15)	8	F:GO:0005083; P:GO:0006468; F:GO:0000155; F:GO:0005515; F:GO:0005524; P:GO:0007165; C:GO:0016020; F:GO:0004674	-	EC:2.7.11.0	IPR001180; PTHR22986 (PANTHER), PTHR22986:SF5 (PANTHER)
	-	0				-
Caenorhabditis elegans	protein phosphatase four regulatory subunit family member (ppfr-1)	0		P:GO:0000003; F:GO:0003674; F:GO:0005488; C:GO:0016021; C:GO:0005575		IPR011989; IPR016024; IPR021133; PTHR10648 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	cg32809 cg32809-pd	2	F:GO:0005515; P:GO:0008340	-		IPR022782; PTHR22741 (PANTHER), PTHR22741:SF2 (PANTHER)
Caenorhabditis elegans	briggsae cbr-npp-12 protein	0				PTHR23019 (PANTHER)

Canis familiaris	poly	19	F:GO:0047485; F:GO:0008270; P:GO:0042769; P:GO:0032869; C:GO:0005730; P:GO:0006284; P:GO:0000723; C:GO:0005667; P:GO:0045449; F:GO:0042802; P:GO:0016540; F:GO:0003677; F:GO:0051287; P:GO:0006471; P:GO:0040009; F:GO:0008134; C:GO:0005635; P:GO:0006366; F:GO:0003950	-	EC:2.4.2.30	IPR004102; PTHR15447 (PANTHER)
	-	0				IPR012394; IPR015590
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0003674; C:GO:0016020; P:GO:0008150; C:GO:0005575		SignalP (SIGNALP)
Caenorhabditis briggsae	bactericidal permeability increasing protein	0		F:GO:0008289		IPR001124; IPR017943; G3DSA:3.15.20.10 (GENE3D), PTHR10504 (PANTHER), PTHR10504:SF14 (PANTHER)
Caenorhabditis elegans	kynu_caeel ame: full=kynureni-se ame: full=l-kynurenine hydrolase	0				-
Caenorhabditis elegans	d--directed r- beta subunit family protein	6	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0005488; F:GO:0016779; P:GO:0040007	-	EC:2.7.7.0	IPR007644
Caenorhabditis briggsae	hspc154 protein	0				IPR013261; PTHR13032 (PANTHER), PTHR13032:SF4 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-max-1 protein	0		F:GO:0005488; C:GO:0005856; P:GO:0040010; P:GO:0008340		PTHR22903 (PANTHER), PTHR22903:SF2 (PANTHER)
	-	0				IPR015940; G3DSA:1.10.8.10 (GENE3D)
	-	0				-
	-	0				-
Loa loa	sister chromatid cohesion protein dcc1	5	C:GO:0000785; C:GO:0005654; F:GO:0005515; P:GO:0034088; C:GO:0000775	-		-
Caenorhabditis elegans	briggsae cbr-mup-4 protein	2	F:GO:0005509; F:GO:0005515	-		IPR000742; IPR006210; IPR013032; SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis briggsae	briggsae cbr-mup-4 protein	1	F:GO:0005515	-		PTHR22992 (PANTHER), PTHR22992:SF12 (PANTHER)
Caenorhabditis elegans	hypothetical protein T12D8.9 [Caenorhabditis elegans]	0				-
						IPR003961; IPR008957; IPR011009; IPR013098; IPR013783; PR00014 (PRINTS), G3DSA:3.30.200.20 (GENE3D), PTHR19900 (PANTHER), PTHR19900:SF7 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Brugia malayi	rab3 gtpase-activating protein catalytic subunit	4	F:GO:0005097; F:GO:0017137; C:GO:0005625; P:GO:0043087	-		PTHR21422 (PANTHER), PTHR21422:SF5 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-sgcb-1 protein	0		C:GO:0016012; C:GO:0016021; P:GO:0007010		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; C:GO:0016020; F:GO:0008375		-
Caenorhabditis elegans	phosphodiesterase i	1	F:GO:0016787	-		IPR002591; IPR017849; IPR017850; PTHR10151 (PANTHER)
Talaromyces stipitatus ATCC 10500	rr- promoter binding protein	0				-
Talaromyces stipitatus ATCC 10500	rr- promoter binding protein	0				-
Talaromyces stipitatus ATCC 10500	phosphatidylinositol glycan anchor class partial	0				-
Talaromyces stipitatus ATCC 10500	rr- promoter binding protein	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein Y119C1B.9 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG08295 [Caenorhabditis briggsae]	0		C:GO:0016021; P:GO:0007186		-
Pan troglodytes	-dh dehydroge-se	4	P:GO:0006120; F:GO:0008137; P:GO:0006810; C:GO:0005747	-	EC:1.6.5.3	-
Brugia malayi	malate dehydroge-se	2	P:GO:0008152; F:GO:0016491	-		IPR003767
Haemonchus contortus	multidrug resistance protein 3-like	5	F:GO:0042626; C:GO:0005886; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		-
	-	0				-
Caenorhabditis elegans	briggsae cbr-adm-4 protein	3	P:GO:0040010; F:GO:0016787; P:GO:0000003	-		IPR001590; IPR001762; G3DSA:3.40.390.10 (GENE3D), PTHR11905 (PANTHER), PTHR11905:SF3 (PANTHER), SSF55486 (SUPERFAMILY)
	-	0				-
Gallus gallus	c4b-binding protein alpha chain precursor	0				IPR000436; IPR016060; PTHR19325 (PANTHER), PTHR19325:SF51 (PANTHER), SignalP (SIGNALP)

	-	0				-
Caenorhabditis elegans	briggsae cbr-lin-25 protein	5	P:GO:0018991; C:GO:0005737; C:GO:0005634; P:GO:0007618; P:GO:0001708	-		-
Angiostrongylus cantonensis	bcl2-associated athanogene 2	3	F:GO:0005515; P:GO:0040002; P:GO:0040011	-		PTHR12334 (PANTHER)
Caenorhabditis briggsae	atpase type 13a1	5	C:GO:0016021; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0006812	-		IPR001757; PTHR11939:SF48 (PANTHER), SignalP (SIGNALP), SSF81665 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	biogenesis of lysosome-related organelles complex-1 subunit 2	0		F:GO:0003674; C:GO:0005737; C:GO:0005856; C:GO:0005815		-
	-	0				-
	-	0				-
Caenorhabditis elegans	flightless-	3	P:GO:0030239; F:GO:0003779; P:GO:0010004	-		IPR007122; IPR007123; G3DSA:3.40.20.10 (GENE3D), PTHR11977:SF6 (PANTHER), SSF55753 (SUPERFAMILY)
	-	0				-
Brugia malayi	exonuclease family protein	0		F:GO:0003676; F:GO:0004527; C:GO:0005622		G3DSA:3.30.420.10 (GENE3D), PTHR23044 (PANTHER), PTHR23044:SF8 (PANTHER)
Caenorhabditis elegans	briggsae cbr-s--2 protein	3	P:GO:0000003; P:GO:0007275; P:GO:0040007	-		-
Caenorhabditis briggsae	protein ki-se domain containing protein	4	P:GO:0006468; F:GO:0005524; P:GO:0040011; F:GO:0004674	-	EC:2.7.11.0	G3DSA:3.30.200.20 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
	-	0				-
Caenorhabditis elegans	lobulin-like cell adhesion molecule family member (igcm-3)	1	P:GO:0019915	-		-
	-	0				-
	-	0				-
Homo sapiens	isoform cra_a	8	C:GO:0005615; P:GO:0050679; F:GO:0008083; F:GO:0005125; P:GO:0007165; C:GO:0005739; P:GO:0007566; P:GO:0001835	-		-
	-	0				-
Caenorhabditis elegans	transmembrane emp24 domain-containing protein 7	3	C:GO:0016021; C:GO:0005783; P:GO:0006810	-		IPR000348; IPR009038; IPR015718; PTHR22811 (PANTHER), SignalP (SIGNALP), SSF101576 (SUPERFAMILY)

Caenorhabditis briggsae	isoform a	0		C:GO:0005739; F:GO:0004540; P:GO:0008033; C:GO:0005758; P:GO:0055085; P:GO:0008150; P:GO:0015031; C:GO:0005575		PTHR21622 (PANTHER)
Loa loa	exonuclease family protein	1	F:GO:0004527	-		IPR012337; G3DSA:3.30.420.10 (GENE3D), PTHR12801 (PANTHER), PTHR12801:SF19 (PANTHER)
Ailuropoda melanoleuca	triosephosphate isomerase	11	C:GO:0005829; P:GO:0006633; C:GO:0005625; P:GO:0006098; P:GO:0019682; F:GO:0004807; F:GO:0005515; P:GO:0006096; P:GO:0006094; C:GO:0005634; P:GO:0009790	-	EC:5.3.1.1	IPR000652; IPR013785; IPR020861
	-	0				-
	-	0				IPR013753; IPR015600; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), SSF52540 (SUPERFAMILY)
Loa loa	was protein member 3	1	F:GO:0005515	-		-
	-	0				SignalP (SIGNALP)
Loa loa	ww domain containing adaptor with coiled- isoform cra_a	2	C:GO:0005681; F:GO:0005515	-		IPR001202; G3DSA:2.20.70.10 (GENE3D), PTHR15911 (PANTHER), PTHR15911:SF4 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	msp domain protein	0		C:GO:0005856; C:GO:0016021; F:GO:0005198; P:GO:0040011		-
	-	0				-
Loa loa	notch gene homolog 4	6	F:GO:0005488; P:GO:0050789; P:GO:0060429; P:GO:0030154; P:GO:0007275; C:GO:0044464	-		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF37 (PANTHER)
	-	0				-
Caenorhabditis briggsae	isoleucyl-tr- synthetase	5	C:GO:0005737; P:GO:0006428; F:GO:0005524; F:GO:0004822; F:GO:0008270	-	EC:6.1.1.5	-
Ailuropoda melanoleuca	eukaryotic translation initiation factor subunit 6 interacting protein	6	F:GO:0003743; P:GO:0045948; C:GO:0005852; F:GO:0005515; C:GO:0005654; C:GO:0001650	-		IPR019382; PTHR13242 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-

Caenorhabditis briggsae	Hypothetical protein CBG10829 [Caenorhabditis briggsae]	0		P:GO:0006629; F:GO:0016787; F:GO:0004806		SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	zinc c2h2 type family protein	4	P:GO:0009792; P:GO:0000003; P:GO:0040007; P:GO:0002119	-		IPR015880
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	iesterase family member (pde-4)	3	F:GO:0046872; P:GO:0007165; F:GO:0004114	-	EC:3.1.4.17	IPR002073; PTHR11347 (PANTHER), PTHR11347:SF37 (PANTHER), SSF109604 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	scy1-like 2	5	P:GO:0006468; F:GO:0004672; C:GO:0043231; C:GO:0044444; F:GO:0005524	-		IPR000719; IPR001245; IPR011009; G3DSA:1.10.510.10 (GENE3D), PTHR12984 (PANTHER), PTHR12984:SF3 (PANTHER)
	-	0				SignalP (SIGNALP)
Ancylostoma caninum	metalloprotease 1 precursor	1	F:GO:0016787	-		IPR001506; IPR006026; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
	-	0				SSF52058 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	endoplasmic reticulum mannosyl-oligosaccharide -alpha-mannosidase	7	F:GO:0004559; C:GO:0005794; F:GO:0004571; P:GO:0048364; F:GO:0005509; P:GO:0006491; C:GO:0016020	-	EC:3.2.1.24; EC:3.2.1.113	SignalP (SIGNALP)
	-	0				-

Chlamydomonas reinhardtii	flagellar associated protein	0		F:GO:0005262; F:GO:0004386; F:GO:0016787; F:GO:0003676; F:GO:0005216; F:GO:0005524; C:GO:0016021; C:GO:0016020; C:GO:0019861; P:GO:0055085; F:GO:0000166; F:GO:0005488; P:GO:0017038; F:GO:0004623; P:GO:0006816; P:GO:0055114; P:GO:0006811; P:GO:0006810; C:GO:0000502; F:GO:0032440; F:GO:0005515; F:GO:0016740; F:GO:0016491		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF306 (PANTHER)
Caenorhabditis elegans	briggsae cbr-dys-1 protein	7	P:GO:0007271; F:GO:0005515; P:GO:0040017; C:GO:0016010; F:GO:0005277; P:GO:0015870; P:GO:0046716	-		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-sqv-8 protein	1	F:GO:0016757	-		IPR005027; G3DSA:3.90.550.10 (GENE3D), PTHR10896:SF5 (PANTHER), SSF53448 (SUPERFAMILY)
	-	0				-
	-	0				PR01503 (PRINTS)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	C:GO:0005576; F:GO:0008061; F:GO:0005515; P:GO:0006030	-		IPR006150; IPR007026; PTHR11201 (PANTHER), PTHR11201:SF241 (PANTHER)
Caenorhabditis elegans	gamma-tubulin interacting protein family member (gip-1)	0		C:GO:0000922; P:GO:0000226; C:GO:0016021; C:GO:0005815; P:GO:0009792; P:GO:0007020; F:GO:0005515		IPR007259

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	8	C:GO:0005737; C:GO:0005625; F:GO:0005515; P:GO:0030163; F:GO:0004046; P:GO:0006520; P:GO:0006508; F:GO:0008237	-	EC:3.5.1.14	IPR002933; G3DSA:3.40.630.10 (GENE3D), PTHR11014 (PANTHER), PTHR11014:SF8 (PANTHER), SSF53187 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	blooms syndrome d- helicase	7	F:GO:0043140; P:GO:0006260; F:GO:0003676; C:GO:0005622; F:GO:0005524; P:GO:0006310; P:GO:0006281	-		IPR004589; PTHR13710:SF14 (PANTHER)
	-	0				-
Ornithorhynchus anatinus	phospholipase a2 receptor 1	0				IPR001304; IPR016186; IPR016187; PTHR22802 (PANTHER), PTHR22802:SF10 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	3	C:GO:0034703; F:GO:0005261; P:GO:0055080	-		-
Angiostrongylus cantonensis	gtp-binding protein era homolog	3	F:GO:0005525; C:GO:0005622; F:GO:0003723	-		IPR009019; IPR011619; IPR015946; G3DSA:3.40.50.300 (GENE3D), PTHR11649 (PANTHER), PTHR11649:SF3 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	phosphopantothe-te-cysteine ligase	1	F:GO:0016874	-		IPR007085; PTHR12290 (PANTHER), PTHR12290:SF2 (PANTHER)
Drosophila simulans	exonuclease nef-sp	0		F:GO:0003676; F:GO:0004527; C:GO:0005622		IPR012337; IPR013520; G3DSA:3.30.420.10 (GENE3D), PTHR12801 (PANTHER), PTHR12801:SF11 (PANTHER)
Caenorhabditis elegans	polymerase (d- directed) epsilon	16	F:GO:0008270; F:GO:0003887; P:GO:0006260; P:GO:0040035; P:GO:0006297; F:GO:0003677; P:GO:0000731; F:GO:0005515; F:GO:0000166; P:GO:0040011; P:GO:0006997; P:GO:0000082; C:GO:0005654; P:GO:0002009; P:GO:0009792; F:GO:0003682	-	EC:2.7.7.7	-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	hypothetical protein Bm1_19685 [Brugia malayi]	0		P:GO:0008202		IPR000648; PTHR10972:SF11 (PANTHER)

	-	0				-
Loa loa	u4 tri-snrnp-associated protein 3	1	P:GO:0018991	-		-
Loa loa	briggsae cbr-vps- protein	2	P:GO:0016192; F:GO:0005515	-		IPR000169; IPR001619; G3DSA:3.40.50.1910 (GENE3D), PTHR11679:SF1 (PANTHER)
Caenorhabditis elegans	abnormal embryonic partitioning of cytoplasm family member (par-3)	8	C:GO:0005737; P:GO:0007163; P:GO:0040001; F:GO:0005515; P:GO:0007155; P:GO:0007369; C:GO:0016021; P:GO:0008406	-		-
	-	0				-
Caenorhabditis briggsae	carbamoyl-phosphate synthetase aspartate and dihydroorotase	8	F:GO:0004086; P:GO:0034404; P:GO:0046483; F:GO:0016743; F:GO:0016812; P:GO:0006520; F:GO:0000166; P:GO:0060041	-	EC:2.1.3.0; EC:3.5.2.0	IPR002474; G3DSA:3.50.30.20 (GENE3D), PTHR11405 (PANTHER), PTHR11405:SF3 (PANTHER)
	-	0				-
Caenorhabditis elegans	yqp1_caeel ame: full=uncharacterized protein	0				-
	-	0				-
Pongo abelii	d--binding protein b	14	F:GO:0003723; F:GO:0003690; C:GO:0070937; P:GO:0070934; P:GO:0006355; P:GO:0008380; F:GO:0016564; C:GO:0071204; C:GO:0010494; F:GO:0005515; F:GO:0003700; F:GO:0003697; P:GO:0006397; P:GO:0006366	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-vit-5 protein	3	P:GO:0009792; P:GO:0008340; P:GO:0040010	-		-
Caenorhabditis briggsae	briggsae cbr-vit-5 protein	3	P:GO:0009792; P:GO:0008340; P:GO:0040010	-		-
Caenorhabditis elegans	briggsae cbr-vit-5 protein	4	P:GO:0009792; P:GO:0008340; P:GO:0040010; F:GO:0005515	-		SignalP (SIGNALP)
	-	0				
Caenorhabditis elegans	briggsae cbr-vit-5 protein	4	P:GO:0009792; P:GO:0008340; P:GO:0040010; F:GO:0005515	-		SignalP (SIGNALP)

Caenorhabditis elegans	briggsae cbr-vit-5 protein	4	P:GO:0009792; F:GO:0005515; P:GO:0040010; P:GO:0008340	-		-
Caenorhabditis elegans	briggsae cbr-vit-5 protein	4	P:GO:0009792; F:GO:0005515; P:GO:0040010; P:GO:0008340	-		PTHR23345 (PANTHER)
Caenorhabditis elegans	vitellogenin structural genes (yolk protein genes) family member (vit-2)	0		P:GO:0006869; F:GO:0005515		-
Caenorhabditis elegans	vit-2	1	F:GO:0005515	-		-
Caenorhabditis elegans	briggsae cbr-vit-5 protein	4	P:GO:0009792; P:GO:0008340; P:GO:0040010; F:GO:0005515	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	amine oxidase (flavin containing) domain 1	7	P:GO:0016568; F:GO:0005488; P:GO:0019219; F:GO:0032453; P:GO:0055114; F:GO:0016491; P:GO:0006306	-		IPR002937; G3DSA:3.50.50.60 (GENE3D), PTHR10742 (PANTHER), PTHR10742:SF31 (PANTHER), SSF54373 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0006508; F:GO:0004181; F:GO:0008270	-	EC:3.4.17.0	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), PTHR11705:SF12 (PANTHER), SSF53187 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	hypothetical protein R02D3.7 [Caenorhabditis elegans]	0		F:GO:0008270; C:GO:0005622		IPR007087; IPR015880
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	glycine dehydroge-se	4	F:GO:0016491; F:GO:0046983; P:GO:0006544; C:GO:0005739	-		IPR015424; IPR020580; IPR020581
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	p-type atpase	5	C:GO:0016021; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0006812	-		IPR000695; IPR001757; IPR005834; G3DSA:1.20.1110.10 (GENE3D), PTHR11939:SF63 (PANTHER), SSF56784 (SUPERFAMILY), SSF81665 (SUPERFAMILY)
Caenorhabditis briggsae	moco sulphurase c-termi-l domain containing 2	2	C:GO:0005743; F:GO:0005515	-		IPR005302; IPR005303; IPR011037; PTHR14237 (PANTHER), SSF141673 (SUPERFAMILY)
Caenorhabditis briggsae	moco sulphurase c-termi-l domain containing 2	2	C:GO:0005743; F:GO:0005515	-		IPR005302; IPR005303; IPR011037; PTHR14237 (PANTHER), SignalP (SIGNALP), SSF141673 (SUPERFAMILY)
Caenorhabditis briggsae	tyrosine sulfotransferase	1	F:GO:0008146	-	EC:2.8.2.0	PTHR12788 (PANTHER)
Loa loa	hypothetical protein LOAG_09341 [Loa loa]	0				IPR000210; IPR011333; IPR013069
	-	0				-

	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				IPR007356; PTHR13563:SF4 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	l-3-hydroxyacyl-coenzyme a short chain	5	P:GO:0055114; P:GO:0006098; F:GO:0004616; P:GO:0006631; F:GO:0050662	-	EC:1.1.1.44	IPR006108; IPR006176; IPR006180; IPR008927; IPR013328; IPR016040; PTHR23309 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-lin-24 protein	1	F:GO:0005515	-		IPR004991; G3DSA:2.170.15.10 (GENE3D), SSF56973 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	sodium-independent organic anion transporter family protein	3	C:GO:0016020; P:GO:0009792; P:GO:0006810	-		IPR004156; PTHR11388:SF7 (PANTHER)
	-	0				IPR018271
	-	0				-
Caenorhabditis elegans	yng2_caeel ame: full=uncharacterized protein	0				SignalP (SIGNALP)
Caenorhabditis elegans	ytv2_caeel ame: full=uncharacterized zinc metalloprotease	0		P:GO:0006508; F:GO:0008233		-
Caenorhabditis elegans	atp-dependent r-	5	F:GO:0008026; F:GO:0003676; F:GO:0005515; P:GO:0006397; F:GO:0005524	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	swi snf matrix actin dependent regulator of subfamily member 1	12	F:GO:0030528; P:GO:0043044; P:GO:0007420; C:GO:0016585; F:GO:0003677; F:GO:0005524; F:GO:0031491; F:GO:0005515; P:GO:0043193; F:GO:0004386; F:GO:0008094; P:GO:0030182	-		IPR006118; IPR010916
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis sp. PS1010	briggsae cbr-cdh-4 protein	3	P:GO:0007163; P:GO:0007411; P:GO:0007413	-		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	meiosis-specific homolog	4	P:GO:0000239; P:GO:0000712; F:GO:0005515; C:GO:0005634	-		IPR000432; G3DSA:3.40.50.300 (GENE3D), PTHR11361:SF18 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-

Caenorhabditis elegans	in family member (ttn-1)	0		F:GO:0005524; F:GO:0004672; P:GO:0006468; P:GO:0009792		IPR013783
Loa loa	mitogen-activated protein ki-se ki-se ki-se 3	6	F:GO:0004674; P:GO:0000165; P:GO:0043123; F:GO:0005515; F:GO:0000166; P:GO:0046777	-	EC:2.7.11.0	IPR000719; IPR011009; IPR015748; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22986 (PANTHER)
Caenorhabditis elegans	cyclin y	9	P:GO:0045737; P:GO:0000086; F:GO:0016538; C:GO:0000308; P:GO:0051301; P:GO:0060828; F:GO:0005515; C:GO:0005634; C:GO:0005886	-		IPR006670; IPR011028; IPR013922
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Loa loa	cleavage and polyadenylation specificity factor subunit 2	7	P:GO:0040035; P:GO:0009792; F:GO:0005488; P:GO:0000910; P:GO:0016246; F:GO:0016787; P:GO:0006397	-		G3DSA:3.60.15.10 (GENE3D), PTHR11203 (PANTHER), PTHR11203:SF5 (PANTHER), SSF56281 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	6	P:GO:0002119; P:GO:0009792; P:GO:0000003; P:GO:0040007; F:GO:0008289; P:GO:0040011	-		IPR001124; IPR017943; G3DSA:3.15.20.10 (GENE3D), PTHR10504 (PANTHER), PTHR10504:SF14 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	exocyst complex component 2	5	P:GO:0045921; F:GO:0017160; F:GO:0047485; P:GO:0000003; C:GO:0000145	-		PTHR13043 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	receptor protein tyrosine	2	F:GO:0004725; P:GO:0006470	-	EC:3.1.3.48	-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	P:GO:0006915	-		IPR002213; G3DSA:3.40.50.2000 (GENE3D), PTHR11926:SF3 (PANTHER), SSF53756 (SUPERFAMILY)

Caenorhabditis briggsae	rac gtpase	16	P:GO:0007265; P:GO:0030032; P:GO:0007390; C:GO:0016020; P:GO:0006974; P:GO:0051017; P:GO:0007394; F:GO:0005525; P:GO:0051301; F:GO:0004767; P:GO:0035099; P:GO:0007254; P:GO:0008258; C:GO:0005622; F:GO:0003924; P:GO:0007435	-	EC:3.1.4.12; EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
	-	0				SignalP (SIGNALP)
Vitis vinifera	hypothetical protein [Vitis vinifera]	1	C:GO:0009507	-		-
Caenorhabditis briggsae	phosphatidylcholine:ceramide cholinephosphotransferase 1-like	6	F:GO:0033188; F:GO:0047493; P:GO:0016049; C:GO:0000138; C:GO:0030173; P:GO:0006686	-	EC:2.7.8.27; EC:2.7.8.3	IPR000326; PTHR21290 (PANTHER), PTHR21290:SF4 (PANTHER)
Caenorhabditis elegans	phosphoribosylglyci-mide formyltransferase	3	F:GO:0016879; F:GO:0004644; P:GO:0006189	-	EC:2.1.2.2	IPR001555; IPR002376; PTHR10520 (PANTHER), PTHR10520:SF9 (PANTHER)
	-	0				-
Callithrix jacchus	heterogeneous nuclear ribonucleoprotein l	9	C:GO:0005737; P:GO:0008380; C:GO:0030530; C:GO:0005654; C:GO:0045120; F:GO:0003723; F:GO:0005515; P:GO:0006397; F:GO:0000166	-		IPR012677; PTHR11546 (PANTHER), PTHR11546:SF5 (PANTHER)
Loa loa	hypothetical protein LOAG_01771 [Loa loa]	0		P:GO:0008150; C:GO:0005575		IPR006578
Caenorhabditis elegans	degeneration of certain neurons protein 1	1	P:GO:0006810	-		-
Loa loa	elegans protein partially confirmed by transcript evidence	0				IPR002861
Caenorhabditis briggsae	phosphatidylinositol polyphosphate 5-phosphatase	3	F:GO:0016788; P:GO:0000003; P:GO:0040013	-		IPR005135; IPR008962; G3DSA:3.60.10.10 (GENE3D), PTHR11200 (PANTHER), PTHR11200:SF26 (PANTHER)
Caenorhabditis briggsae	huntingtin-associated protein 1-like	9	F:GO:0050811; P:GO:0006493; P:GO:0006357; P:GO:0006836; F:GO:0019899; P:GO:0006605; C:GO:0005769; C:GO:0005634; C:GO:0005886	-		-

Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	6	F:GO:0003700; F:GO:0043565; F:GO:0003707; C:GO:0005634; F:GO:0008270; P:GO:0006355	-		-
Caenorhabditis elegans	ferm domain (-ezrin-radixin-moesin) family member (frm-1)	1	F:GO:0005515	-		-
Ascaris suum	thioredoxin	3	P:GO:0045454; F:GO:0016491; F:GO:0016209	-		-
	-	0				-
Brugia malayi	hypothetical protein Bm1_03880 [Brugia malayi]	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	C:GO:0005794; F:GO:0005515; F:GO:0000062	-		IPR009038; IPR018234; PTHR22973 (PANTHER), PTHR22973:SF4 (PANTHER), SSF101576 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Loa loa	tsc1 cg6147-pa	6	P:GO:0040008; P:GO:0048523; P:GO:0023033; P:GO:0042221; P:GO:0008361; P:GO:0007275	-		IPR007483
	-	0				-
	-	0				-
Rattus norvegicus	ribosomal protein l8	4	F:GO:0003735; C:GO:0022625; F:GO:0019843; P:GO:0006414	-		IPR002171; IPR012340; IPR016027; IPR022666; PTHR13691:SF3 (PANTHER)
Caenorhabditis elegans	briggsae cbr-rhgf-1 protein	1	F:GO:0005488	-		SignalP (SIGNALP)
Tribolium castaneum	dynein light chain cytoplasmic	11	P:GO:0046907; C:GO:0030286; P:GO:0008039; F:GO:0008092; C:GO:0005886; C:GO:0043186; C:GO:0016459; P:GO:0007017; C:GO:0005634; C:GO:0005829; F:GO:0003777	-		IPR001372
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	C:GO:0016021	-		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)

Caenorhabditis briggsae	clathrin heavy chain 1	17	C:GO:0030315; F:GO:0042277; F:GO:0031072; C:GO:0030132; C:GO:0005739; C:GO:0030130; P:GO:0006892; P:GO:0031623; F:GO:0030506; C:GO:0005624; C:GO:0042470; P:GO:0033572; P:GO:0007067; P:GO:0007030; C:GO:0005819; P:GO:0006886; F:GO:0005198	-		IPR000547; IPR001473; IPR011990; IPR015348; IPR016024; IPR016025; IPR016341; IPR022365; PTHR10292 (PANTHER), PTHR10292:SF1 (PANTHER), PF00637 (PFAM)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Loa loa	abnormal cell migration family member (mig-5)	4	C:GO:0005622; P:GO:0007275; F:GO:0004871; F:GO:0042802	-		IPR001158; IPR015506
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	vacuolar proton atpase	4	F:GO:0015078; C:GO:0033177; C:GO:0016021; P:GO:0015986	-		IPR002490; PTHR11629:SF23 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	cg10914 cg10914-pa	0		F:GO:0005525		G3DSA:3.40.50.300 (GENE3D), PTHR11089 (PANTHER), PTHR11089:SF1 (PANTHER)
	-	0				-
	-	0				IPR008840
Caenorhabditis elegans	heterogeneous nuclear ribonucleoprotein k	3	F:GO:0003676; F:GO:0005515; C:GO:0044424	-		IPR004087; IPR004088; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR10288 (PANTHER), PTHR10288:SF38 (PANTHER), SSF54791 (SUPERFAMILY)
Caenorhabditis briggsae	heterogeneous nuclear ribonucleoprotein k	3	F:GO:0003676; F:GO:0005515; C:GO:0044424	-		IPR004087; IPR004088; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR10288 (PANTHER), PTHR10288:SF38 (PANTHER), SSF54791 (SUPERFAMILY)
Caenorhabditis elegans	kh domain containing protein	2	F:GO:0005515; F:GO:0003723	-		-
Caenorhabditis briggsae	heterogeneous nuclear ribonucleoprotein	6	F:GO:0003723; F:GO:0005515; F:GO:0003697; C:GO:0030529; C:GO:0005634; P:GO:0006396	-		SignalP (SIGNALP)

Caenorhabditis elegans	heterogeneous nuclear ribonucleoprotein k	3	F:GO:0003676; F:GO:0005515; C:GO:0044424	-		IPR004087; IPR004088; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR10288 (PANTHER), PTHR10288:SF38 (PANTHER), SSF54791 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis sp. PS1010	elegans protein confirmed by transcript evidence	0				-
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	2	F:GO:0008270; F:GO:0005515	-		-
Nematostella vectensis	glutathione s-transferase kappa 1	1	F:GO:0016740	-		IPR001853; IPR012336; PTHR13887 (PANTHER)
Caenorhabditis elegans	hypothetical protein T14B4.1 [Caenorhabditis elegans]	0		F:GO:0003723; P:GO:0006396; F:GO:0008173		-
	-	0				-
Caenorhabditis briggsae	sy-ptotagmin xi	1	F:GO:0005515	-		-
Caenorhabditis elegans	fertilization defective (abnormal sperm) family member (fer-1)	0		C:GO:0016021		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	spectrin alpha chain	2	F:GO:0004725; F:GO:0005509	-	EC:3.1.3.48	IPR002017; IPR018159; G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF6 (PANTHER), SSF46966 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-rsr-1 protein	4	C:GO:0035145; C:GO:0071011; P:GO:0000398; C:GO:0071013	-		IPR002483; G3DSA:1.20.1390.10 (GENE3D), PTHR23148 (PANTHER), SSF101233 (SUPERFAMILY)
Caenorhabditis elegans	probable 60s ribosomal protein mitochondrial	7	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; P:GO:0040010; P:GO:0006898; P:GO:0006412	-	EC:3.6.5.3	IPR000911; IPR020783; PTHR11661:SF1 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-btf-1 protein	1	F:GO:0005488	-		IPR022707; SignalP (SIGNALP)
Loa loa	amp-activated protein ki-se gamma2 subunit-like	2	P:GO:0040035; P:GO:0040011	-		PTHR13780 (PANTHER)
Methanocella paludicola SANAE	d- repair and recombi-tion protein	3	P:GO:0006259; F:GO:0005488; F:GO:0017111	-	EC:3.6.1.15	IPR014774; IPR020588; G3DSA:3.40.50.300 (GENE3D), PTHR22942 (PANTHER), PTHR22942:SF15 (PANTHER), SSF52540 (SUPERFAMILY)
Brugia malayi	dedicator of cytokinesis family protein	0		F:GO:0005525; F:GO:0051020; F:GO:0005085		PTHR23317 (PANTHER), PTHR23317:SF26 (PANTHER)
Caenorhabditis elegans	lysocardiolipin acyltransferase 1	5	P:GO:0001885; P:GO:0035162; F:GO:0016740; F:GO:0005515; C:GO:0016020	-		IPR002052; PTHR10983 (PANTHER), PTHR10983:SF1 (PANTHER), SignalP (SIGNALP)

Loa loa	cleavage stimulation 3 pre- subunit 77kda	8	P:GO:0006378; P:GO:0009792; P:GO:0008380; F:GO:0003723; F:GO:0005515; P:GO:0000003; C:GO:0005634; P:GO:0006379	-		PTHR19980 (PANTHER)
	-	0				-
Caenorhabditis briggsae	msp domain protein	0		P:GO:0040017; C:GO:0005856; F:GO:0005198		IPR000535; IPR008962; PTHR22947 (PANTHER)
Caenorhabditis elegans	cdc45 cell division cycle 45-like (cerevisiae)	6	P:GO:0007049; C:GO:0005813; F:GO:0005515; P:GO:0006270; C:GO:0005654; F:GO:0003682	-		IPR003874
	-	0				-
Homo sapiens	basigin	16	P:GO:0046689; C:GO:0005739; P:GO:0007566; C:GO:0016021; C:GO:0000139; P:GO:0042475; F:GO:0005537; P:GO:0043434; F:GO:0015129; C:GO:0042470; P:GO:0046697; F:GO:0005515; C:GO:0045121; C:GO:0042383; P:GO:0007166; P:GO:0051591	-		IPR009151; PTHR10075 (PANTHER), PTHR10075:SF6 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	patched family protein	4	P:GO:0040018; P:GO:0018996; P:GO:0007275; P:GO:0040011	-		IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER), SSF82866 (SUPERFAMILY)
Brugia malayi	eukaryotic elongation selenocysteine-tr--specific	1	F:GO:0000166	-		-
Loa loa	uncoordi-ted family member (unc-89)	0				-
Caenorhabditis sp. PS1010	protocadherin alpha 8	5	P:GO:0007163; P:GO:0007411; P:GO:0007155; C:GO:0016020; P:GO:0007413	-		IPR002126; IPR015919; IPR020894; PTHR10596 (PANTHER), PTHR10596:SF76 (PANTHER)
	-	0				-
Caenorhabditis briggsae	clc-type chloride channel family member (clh-2)	6	P:GO:0009792; F:GO:0005247; P:GO:0055085; P:GO:0000003; C:GO:0016021; P:GO:0006821	-		IPR001807; PTHR11689:SF5 (PANTHER), SignalP (SIGNALP), SSF54631 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)

	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	lor sdh bifunctio-l protein conserved domain protein	1	F:GO:0003824	-		-
	-	0				-
Loa loa	nidogen 1	3	F:GO:0005488; P:GO:0044237; C:GO:0016020	-		-
Homo sapiens	elastin (supravalvular aortic williams-beuren syndrome) isoform cra_b	6	P:GO:0008015; F:GO:0030023; P:GO:0009887; C:GO:0005578; P:GO:0007585; P:GO:0008283	-		-
	-	0				-
Caenorhabditis briggsae	integrin alpha-ps	22	P:GO:0048468; P:GO:0002119; P:GO:0048699; F:GO:0030528; P:GO:0007424; P:GO:0032989; P:GO:0050789; F:GO:0004872; P:GO:0018991; P:GO:0040039; P:GO:0048513; P:GO:0006898; P:GO:0040007; P:GO:0032940; P:GO:0009792; P:GO:0065008; P:GO:0007155; P:GO:0007229; P:GO:0061061; C:GO:0005622; F:GO:0005488; C:GO:0008305	-		IPR000413; IPR013517; IPR013649; G3DSA:2.60.40.1460 (GENE3D), PTHR23220 (PANTHER), PTHR23220:SF11 (PANTHER), PS51470 (PROFILE), SSF69179 (SUPERFAMILY), SSF69318 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-vap-1 protein	3	C:GO:0005576; P:GO:0040011; P:GO:0006898	-		-
	-	0				-
Caenorhabditis elegans	phosphoserine phosphatase	4	C:GO:0005737; F:GO:0000287; F:GO:0004647; P:GO:0006564	-	EC:3.1.3.3	G3DSA:3.40.50.1000 (GENE3D), PTHR10000 (PANTHER), SignalP (SIGNALP), SSF56784 (SUPERFAMILY)
Caenorhabditis briggsae	glycolate oxidase	10	P:GO:0006979; C:GO:0005777; P:GO:0032787; F:GO:0008891; C:GO:0009570; C:GO:0005773; C:GO:0022626; C:GO:0016020; C:GO:0005634; C:GO:0048046	-		IPR000262; IPR008259; IPR012133; IPR013785; PTHR10578 (PANTHER), PTHR10578:SF9 (PANTHER), SSF51395 (SUPERFAMILY)

Caenorhabditis briggsae	hydroxyacid oxidase 1	12	P:GO:0006979; P:GO:0046487; C:GO:0005777; F:GO:0008891; P:GO:0001561; P:GO:0046296; C:GO:0009570; C:GO:0022626; F:GO:0010181; C:GO:0016020; C:GO:0005634; C:GO:0048046	-		IPR000262; IPR008259; IPR012133; IPR013785; PTHR10578 (PANTHER), PTHR10578:SF9 (PANTHER), SSF51395 (SUPERFAMILY)
Caenorhabditis briggsae	glycolate oxidase	10	P:GO:0006979; C:GO:0005777; P:GO:0032787; F:GO:0008891; C:GO:0009570; C:GO:0005773; C:GO:0022626; C:GO:0016020; C:GO:0005634; C:GO:0048046	-		IPR000262; IPR008259; IPR012133; IPR013785; PTHR10578 (PANTHER), PTHR10578:SF9 (PANTHER), SSF51395 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein Y51F10.10 [Caenorhabditis elegans]	0				-
	-	0				-
Brugia malayi	origin recognition complex subunit 5	0		P:GO:0006260; C:GO:0000808; C:GO:0005634		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				IPR013032
Loa loa	protein phosphatase regulatory subunit b epsilon isoform	7	C:GO:0005737; C:GO:0000159; P:GO:0007165; P:GO:0050790; F:GO:0005515; C:GO:0043231; F:GO:0008601	-		IPR002554; IPR016024
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR001534; SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	protein disulfide isomerase family member 6	12	P:GO:0002119; P:GO:0006457; C:GO:0005788; C:GO:0005793; C:GO:0005886; P:GO:0045454; F:GO:0005515; C:GO:0042470; F:GO:0005509; P:GO:0040011; F:GO:0003756; P:GO:0040007	-	EC:5.3.4.1	-
Caenorhabditis elegans	tripeptidyl peptidase ii	2	P:GO:0019915; F:GO:0070011	-		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis briggsae	ynv9_caeel ame: full=uncharacterized protein flags: precursor	1	F:GO:0005488	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-tsp-13 protein	2	P:GO:0030001; F:GO:0046872	-		IPR017969; PTHR19282 (PANTHER), PTHR19282:SF12 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	choline transporter-like family member (chtl-1)	6	P:GO:0002009; C:GO:0016021; P:GO:0040007; P:GO:0040035; P:GO:0040002; P:GO:0002119	-		-
	-	0				IPR003511
	-	0				-
Caenorhabditis elegans	dymeclin	4	P:GO:0009792; P:GO:0000003; F:GO:0005515; P:GO:0002119	-		IPR019142; PTHR12895 (PANTHER), PTHR12895:SF2 (PANTHER)
	-	0				-
Caenorhabditis elegans	run domain containing protein	0				-
Caenorhabditis elegans	protein ki-se domain containing protein	3	P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	PTHR22984 (PANTHER)
Loa loa	tafii55 protein conserved region containing protein	0		C:GO:0005669; P:GO:0006367; F:GO:0016251		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	tyrosi-se	0		F:GO:0046872; F:GO:0004503; P:GO:0055114; P:GO:0042438; F:GO:0016491; P:GO:0008152; F:GO:0004497; F:GO:0005515		SignalP (SIGNALP)
	-	0				-
	-	0				PTHR12846 (PANTHER), PTHR12846:SF2 (PANTHER)
Saccoglossus kowalevskii	protein c20orf11 homolog	1	F:GO:0005515	-		IPR006594; IPR006595; IPR013144; IPR013720; IPR019589; PTHR12864 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG08123 [Caenorhabditis briggsae]	2	P:GO:0007186; C:GO:0016021	-		PTHR22718 (PANTHER), PTHR22718:SF8 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-

Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0030247; C:GO:0016021; F:GO:0016787; F:GO:0003676; F:GO:0003824; C:GO:0005575; F:GO:0005044; P:GO:0008152; F:GO:0046872; P:GO:0006955		PTHR10151 (PANTHER), PTHR10151:SF28 (PANTHER)
Caenorhabditis briggsae	d- repair and recombi-tion protein rad54-like	8	P:GO:0006915; P:GO:0000003; F:GO:0003677; F:GO:0005524; F:GO:0005515; F:GO:0004386; F:GO:0008094; P:GO:0006974	-		PTHR10799 (PANTHER), PTHR10799:SF66 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis elegans	asparaginyl-tr- cytoplasmic	8	F:GO:0003676; P:GO:0006422; F:GO:0005515; F:GO:0004816; F:GO:0005524; P:GO:0006421; F:GO:0004815; C:GO:0005739	-	EC:6.1.1.22; EC:6.1.1.12	IPR002312; IPR004364; IPR006195; IPR018150; G3DSA:3.30.930.10 (GENE3D), PTHR22594:SF6 (PANTHER), SSF55681 (SUPERFAMILY)
Caenorhabditis elegans	trrap-like (transcription transformation domain-associated protein) family member (trr-1)	4	P:GO:0044238; C:GO:0043234; P:GO:0044260; C:GO:0044451	-		-
Loa loa	trrap-like (transcription transformation domain-associated protein) family member (trr-1)	4	P:GO:0044238; C:GO:0043234; P:GO:0044260; C:GO:0044451	-		-
	-	0				-
	-	0				-
	-	0				-
Loa loa	bm8 interacting protein 2d-2	0		P:GO:0008150; F:GO:0005515; C:GO:0005575; F:GO:0003677		IPR006578
Caenorhabditis briggsae	adamts family member (adt-2)	11	F:GO:0008270; P:GO:0040007; P:GO:0000003; P:GO:0018996; F:GO:0004222; P:GO:0006508; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0040011; C:GO:0016020	-	EC:3.4.24.0	-
	-	0				-

	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	ribosomal protein l16 containing protein	8	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; F:GO:0005515; P:GO:0040010; P:GO:0006412; F:GO:0019843	-	EC:3.6.5.3	IPR000114; PTHR12220:SF12 (PANTHER)
Danio rerio	wolfram syndrome 1	5	C:GO:0016020; P:GO:0048878; P:GO:0050789; P:GO:0009987; P:GO:0003008	-		-
Danio rerio	wolfram syndrome 1	5	C:GO:0016020; P:GO:0048878; P:GO:0050789; P:GO:0009987; P:GO:0003008	-		-
	-	0				-
Brugia malayi	atp-dependent helicase ddx1	7	F:GO:0003676; F:GO:0008026; P:GO:0000245; F:GO:0005524; P:GO:0001700; P:GO:0042254; P:GO:0006446	-		-
	-	0				-
Loa loa	r- recognition motif domain containing protein	2	F:GO:0003676; F:GO:0000166	-		-
Ascaris lumbricoides	gmp reductase	4	P:GO:0009117; F:GO:0046872; P:GO:0055114; F:GO:0003920	-	EC:1.7.1.7	-
Caenorhabditis elegans	ubiquitin specific peptidase 24	0		F:GO:0005488; F:GO:0016787; F:GO:0008234; F:GO:0008233; F:GO:0004221; P:GO:0006511		IPR000169; IPR001394; IPR018200; PTHR10420 (PANTHER), PTHR10420:SF47 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis elegans	amin (actin binding protein) alpha family member (fl--1)	0		F:GO:0003779		-
	-	0				-
Loa loa	expressed sequence	0				IPR010733
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR011009; IPR012877; G3DSA:3.90.1200.10 (GENE3D)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				IPR011009; IPR012877; G3DSA:3.90.1200.10 (GENE3D)
Caenorhabditis briggsae	briggsae cbr-dhs-27 protein	0		P:GO:0055114; F:GO:0005488; F:GO:0016491; P:GO:0008152; F:GO:0003824		IPR011009; IPR012877; G3DSA:3.90.1200.10 (GENE3D)

Caenorhabditis briggsae	briggsae cbr-dhs-27 protein	0		F:GO:0004672; F:GO:0005524; P:GO:0055114; F:GO:0005488; F:GO:0016491; P:GO:0008152; P:GO:0006468; F:GO:0003824		IPR011009; IPR012877; G3DSA:3.90.1200.10 (GENE3D)
	-	0				-
Mus musculus	mCG14133 [Mus musculus]	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-elpc-2 protein	7	P:GO:0006357; C:GO:0005730; C:GO:0016591; C:GO:0008023; F:GO:0003677; F:GO:0016944; C:GO:0005737	-		PTHR13729 (PANTHER)
	-	0				-
Loa loa	importin 8	0		F:GO:0005488; F:GO:0005509; C:GO:0005737; F:GO:0008262; P:GO:0008283; P:GO:0006886; C:GO:0005634; F:GO:0008565		-
	-	0				-
	-	0				-
Caenorhabditis elegans	anion bicarbo-te porter family member (abts-3)	5	F:GO:0005452; P:GO:0006820; P:GO:0009401; F:GO:0005351; C:GO:0016021	-		IPR003020; PTHR11453:SF16 (PANTHER)
Caenorhabditis elegans	vacuolar protein sorting-associated protein 4a	23	P:GO:0033993; C:GO:0005829; C:GO:0005764; P:GO:0000910; P:GO:0007049; C:GO:0030496; F:GO:0042623; P:GO:0006813; P:GO:0032367; F:GO:0008022; C:GO:0031902; C:GO:0005774; C:GO:0005769; F:GO:0005524; C:GO:0000815; F:GO:0019904; C:GO:0048471; P:GO:0008152; P:GO:0007032; F:GO:0017048; P:GO:0015031; C:GO:0005634; P:GO:0032510	-		IPR003593; IPR003959; IPR003960; IPR007330; IPR015415; G3DSA:1.10.8.60 (GENE3D), G3DSA:1.20.58.280 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23074 (PANTHER), PTHR23074:SF3 (PANTHER), SSF116846 (SUPERFAMILY), SSF52540 (SUPERFAMILY)

Caenorhabditis elegans	transmembrane cell surface protein homolog family member (ttyh-1)	0				IPR006990; PTHR12424:SF2 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Homo sapiens	ga-b protein	7	F:GO:0033919; P:GO:0005975; C:GO:0042470; C:GO:0005783; F:GO:0030246; C:GO:0005794; F:GO:0005515	-	EC:3.2.1.84	-
	-	0				-
	-	0				IPR013632; PTHR22942 (PANTHER), PTHR22942:SF10 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG14951 [Caenorhabditis briggsae]	3	P:GO:0040018; P:GO:0040035; P:GO:0002119	-		-
Caenorhabditis elegans	glycerol-3-phosphate acyltransferase 3	5	C:GO:0016021; P:GO:0019432; F:GO:0004366; C:GO:0005789; P:GO:0032006	-	EC:2.3.1.15	PTHR23063 (PANTHER), PTHR23063:SF2 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG13872 [Caenorhabditis briggsae]	0		C:GO:0016021; P:GO:0006814; F:GO:0008508; C:GO:0016020		-
Caenorhabditis briggsae	ryanodine receptor	7	P:GO:0006629; F:GO:0005219; P:GO:0006816; P:GO:0006874; P:GO:0055085; F:GO:0005509; C:GO:0016021	-		IPR015925; PTHR13715:SF3 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				IPR003582; PTHR21724 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	C:GO:0034703; F:GO:0005261; P:GO:0055080	-		SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	short coiled-coil protein	1	F:GO:0005515	-		-
	-	0				-
	-	0				IPR000436; IPR016060
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				IPR001412

Caenorhabditis elegans	r- binding motif protein 19	7	C:GO:0005737; C:GO:0005730; C:GO:0005654; P:GO:0048546; F:GO:0003723; P:GO:0040019; F:GO:0000166	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF63 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-pqn-70 protein	1	P:GO:0000003	-		PTHR21806 (PANTHER)
Caenorhabditis elegans	briggsae cbr-pqn-70 protein	1	P:GO:0000003	-		-
Brugia malayi	muts homolog 5 (coli)	8	C:GO:0000795; P:GO:0007292; F:GO:0003677; P:GO:0007129; F:GO:0005515; P:GO:0007131; P:GO:0007136; P:GO:0006950	-		IPR000432; IPR007696; G3DSA:3.40.50.300 (GENE3D), PTHR11361:SF20 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Brugia malayi	hepatocellular carcinoma-associated antigen 66	0				IPR013949; PTHR23271 (PANTHER), PTHR23271:SF1 (PANTHER)
Caenorhabditis elegans	multidrug resistance	7	P:GO:0000917; F:GO:0042626; F:GO:0005525; C:GO:0005622; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF62 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	low quality protein: collagen alpha-3 chain-like	1	P:GO:0040010	-		IPR002035; G3DSA:3.40.50.410 (GENE3D), SSF53300 (SUPERFAMILY)
Caenorhabditis elegans	low quality protein: collagen alpha-3 chain-like	1	P:GO:0040010	-		IPR002035; G3DSA:3.40.50.410 (GENE3D), SSF53300 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	yoq5_caeel ame: full=uncharacterized protein	0		F:GO:0005515		-
	-	0				-
	-	0				-
	-	0				-
	-	0				IPR011989
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0003674; P:GO:0045449; P:GO:0008150; C:GO:0005575; F:GO:0003700		PTHR13029 (PANTHER), PTHR13029:SF7 (PANTHER)

Caenorhabditis briggsae	briggsae cbr--s-39 protein	12	F:GO:0008270; F:GO:0005509; P:GO:0001885; P:GO:0035162; P:GO:0035124; F:GO:0004222; P:GO:0006508; F:GO:0005515; P:GO:0048264; P:GO:0030513; P:GO:0001568; P:GO:0001707	-	EC:3.4.24.0	IPR000859; PTHR10127 (PANTHER), PTHR10127:SF70 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-far-8 protein	0		F:GO:0008289		IPR008632
Haemonchus contortus	gata transcription factor	4	F:GO:0003700; F:GO:0043565; F:GO:0008270; P:GO:0006355	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0055114; F:GO:0009055; F:GO:0020037; F:GO:0005506; F:GO:0004497		IPR013078; G3DSA:3.40.50.1240 (GENE3D), PTHR16469 (PANTHER), PTHR16469:SF4 (PANTHER), SSF53254 (SUPERFAMILY)
Caenorhabditis briggsae	small calcium-binding mitochondrial carrier 2	4	C:GO:0005743; P:GO:0055085; F:GO:0005509; C:GO:0016021	-		IPR001993; IPR002067; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF34 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	sda1 domain containing 1	6	C:GO:0005730; P:GO:0002119; F:GO:0005488; P:GO:0006898; P:GO:0040007; P:GO:0051729	-		IPR012977; PTHR12730 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	P:GO:0023034; C:GO:0016021	-		-
Homo sapiens	basigin (ok blood group) isoform cra_d	16	P:GO:0046689; C:GO:0005739; P:GO:0007566; C:GO:0016021; C:GO:0000139; P:GO:0042475; F:GO:0005537; P:GO:0043434; F:GO:0015129; C:GO:0042470; P:GO:0046697; F:GO:0005515; C:GO:0045121; C:GO:0042383; P:GO:0007166; P:GO:0051591	-		-
	-	0				-

Loa loa	isoform a	19	C:GO:0000139; F:GO:0005458; F:GO:0005461; P:GO:0015784; F:GO:0005464; P:GO:0015787; F:GO:0005456; P:GO:0015790; P:GO:0055085; F:GO:0005460; F:GO:0005457; P:GO:0015788; F:GO:0005351; P:GO:0015783; C:GO:0016021; C:GO:0005783; F:GO:0005462; P:GO:0015782; P:GO:0015786	-		IPR013657; PTHR10778 (PANTHER), PTHR10778:SF4 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0008152; F:GO:0003824		IPR010770
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	4	P:GO:0009792; P:GO:0000003; P:GO:0040010; P:GO:0002119	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	carboxylase:pyruvate acetyl-coa propionyl-coa	8	P:GO:0044249; C:GO:0005875; F:GO:0005488; P:GO:0006090; F:GO:0016874; P:GO:0016051; C:GO:0005759; C:GO:0005811	-		IPR000089; IPR001882; IPR011053; G3DSA:2.40.50.100 (GENE3D), PTHR18866 (PANTHER), PTHR18866:SF10 (PANTHER)
Strongylocentrotus purpuratus	mgc82686 protein	5	F:GO:0003919; P:GO:0040010; P:GO:0006777; F:GO:0005524; P:GO:0006747	-	EC:2.7.7.2	IPR001453; PTHR23293 (PANTHER)
Caenorhabditis elegans	protein son-like	4	C:GO:0005622; F:GO:0003723; F:GO:0005515; P:GO:0006916	-		-
	-	0				-
Caenorhabditis briggsae	cdk5 regulatory subunit associated protein 1-like 1	5	P:GO:0009451; F:GO:0046872; C:GO:0016021; F:GO:0003824; F:GO:0051539	-		IPR005839
Caenorhabditis elegans	metabotropic gaba-b receptor subtype 2	3	C:GO:0016020; P:GO:0023052; F:GO:0004888	-		PTHR10519 (PANTHER), PTHR10519:SF4 (PANTHER), SignalP (SIGNALP)

Loa loa	novel protein (zgc:158710)	6	F:GO:0005097; F:GO:0004672; C:GO:0005622; F:GO:0005524; P:GO:0032313; P:GO:0006468	-		IPR000195; G3DSA:1.10.8.270 (GENE3D), PTHR22957 (PANTHER), PTHR22957:SF22 (PANTHER)
Caenorhabditis elegans	rsk-pninety (rsk-p90 ki-se) homolog family member (rskn-1)	8	C:GO:0005829; P:GO:0007243; F:GO:0004674; F:GO:0005524; F:GO:0005515; F:GO:0000287; C:GO:0005654; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR000961; IPR002290; IPR008271; IPR011009; IPR017441; IPR017442; IPR017892; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22985 (PANTHER), PTHR22985:SF67 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	cation transport regulator-like protein 1	0		F:GO:0003723; P:GO:0070059; F:GO:0016740; C:GO:0005829; F:GO:0005515; F:GO:0008146		IPR006840
Caenorhabditis brenneri	elegans protein partially confirmed by transcript evidence	5	P:GO:0009792; F:GO:0004672; P:GO:0040010; P:GO:0000003; F:GO:0000166	-		IPR000719; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	uncoordi-ted protein isoform partially confirmed by transcript evidence	11	P:GO:0055085; P:GO:0006629; C:GO:0005875; F:GO:0005509; C:GO:0016021; F:GO:0004872; P:GO:0006874; P:GO:0006816; C:GO:0005789; F:GO:0005219; P:GO:0006936	-		IPR000699; IPR015925; PTHR13715:SF11 (PANTHER)
Caenorhabditis elegans	rgm domain family member b-like	0		F:GO:0042802; C:GO:0045121; P:GO:0045941; C:GO:0005793; C:GO:0031225; P:GO:0007165; C:GO:0046658; C:GO:0005886; P:GO:0030509; P:GO:0007155		IPR009496
	-	0				IPR009072
	-	0				-

Caenorhabditis elegans	cytochrome c oxidase polypeptide vb	9	P:GO:0009792; P:GO:0002119; P:GO:0006629; C:GO:0005740; P:GO:0040010; P:GO:0000003; P:GO:0008340; P:GO:0019915; F:GO:0004129	-	EC:1.9.3.1	IPR002124; SignalP (SIGNALP), SSF57802 (SUPERFAMILY)
Loa loa	hypothetical protein LOAG_10859 [Loa loa]	0				PTHR10117 (PANTHER), PTHR10117:SF10 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	nuclear vcp-like	2	F:GO:0005524; F:GO:0017111	-	EC:3.6.1.15	-
	-	0				-
Caenorhabditis elegans	monocarboxylate transporter	5	C:GO:0016021; P:GO:0000003; P:GO:0040007; P:GO:0055085; P:GO:0002119	-		-
Caenorhabditis briggsae	nuclear receptor	7	F:GO:0003700; F:GO:0043565; P:GO:0008340; F:GO:0003707; C:GO:0005634; F:GO:0008270; P:GO:0006355	-		IPR001628; IPR008946; PTHR11865 (PANTHER), PTHR11865:SF197 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	3	C:GO:0034703; F:GO:0005261; P:GO:0055080	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	caveolin 1	66	P:GO:0006641; P:GO:0010524; F:GO:0016504; C:GO:0005925; P:GO:0033344; F:GO:0050998; C:GO:0005901; P:GO:0007584; P:GO:0033484; C:GO:0009925; P:GO:0010332; C:GO:0005625; P:GO:0009612; P:GO:0031116; P:GO:0051899; P:GO:0045807; P:GO:0051384; C:GO:0043234; C:GO:0000299; P:GO:0060056; P:GO:0007126; C:GO:0030141; C:GO:0005829; P:GO:0009967; P:GO:0006940; P:GO:0043409;	-		IPR001612; PTHR10844:SF2 (PANTHER)
Xenopus (Silurana) tropicalis	collagen alpha-6 chain- partial	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-cpg-3 protein	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-cpg-3 protein	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG02118 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	7	C:GO:0005737; P:GO:0040010; P:GO:0055114; P:GO:0006561; P:GO:0006898; F:GO:0004349; F:GO:0004350	-	EC:2.7.2.11; EC:1.2.1.41	IPR001048; IPR001057; IPR019797; PTHR11063 (PANTHER), PTHR11063:SF2 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	exoribonuclease 1	6	F:GO:0003676; C:GO:0005730; F:GO:0008408; F:GO:0005515; P:GO:0071044; C:GO:0005737	-		IPR012337; IPR013520; G3DSA:3.30.420.10 (GENE3D), PTHR23044 (PANTHER), PTHR23044:SF7 (PANTHER)

Loa loa	nucleolar protein 10	5	P:GO:0009792; P:GO:0002119; P:GO:0018991; P:GO:0040010; C:GO:0005634	-		IPR001680; IPR015943; PTHR14927 (PANTHER)
Caenorhabditis elegans	zinc-binding dehydroge-se family protein	4	F:GO:0008270; P:GO:0055114; F:GO:0005515; F:GO:0016491	-		IPR002085; IPR011032; IPR013149; IPR013154; IPR016040; G3DSA:3.90.180.10 (GENE3D), PTHR11695:SF38 (PANTHER), SSF51735 (SUPERFAMILY)
Teladorsagia circumcincta	parasitic stage specific protein 1	0				-
Caenorhabditis briggsae	glycoside hydrolase family 25 protein	1	F:GO:0005515	-		IPR013781; IPR017853; PTHR23208 (PANTHER), PTHR23208:SF13 (PANTHER), SignalP (SIGNALP)
Teladorsagia circumcincta	parasitic stage specific protein 1	0				-
Caenorhabditis elegans	coatomer protein subunit alpha	17	P:GO:0030157; C:GO:0030126; C:GO:0005829; P:GO:0040010; C:GO:0005625; P:GO:0006890; P:GO:0000003; C:GO:0005615; P:GO:0032940; C:GO:0005792; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0048205; P:GO:0006886; F:GO:0005198; P:GO:0009792	-		IPR001680; IPR006692; IPR010714; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR19876 (PANTHER), PTHR19876:SF1 (PANTHER), SSF82171 (SUPERFAMILY)
Caenorhabditis elegans	coatomer protein subunit alpha	17	P:GO:0030157; C:GO:0030126; C:GO:0005829; P:GO:0040010; C:GO:0005625; P:GO:0006890; P:GO:0000003; C:GO:0005615; P:GO:0032940; C:GO:0005792; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0048205; P:GO:0006886; F:GO:0005198; P:GO:0009792	-		IPR001680; IPR006692; IPR010714; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR19876 (PANTHER), PTHR19876:SF1 (PANTHER), SSF82171 (SUPERFAMILY)

Caenorhabditis elegans	coatomer protein subunit alpha	17	P:GO:0030157; C:GO:0030126; C:GO:0005829; P:GO:0040010; C:GO:0005625; P:GO:0006890; P:GO:0000003; C:GO:0005615; P:GO:0032940; C:GO:0005792; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0048205; P:GO:0006886; F:GO:0005198; P:GO:0009792	-		IPR001680; IPR006692; IPR010714; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR19876 (PANTHER), PTHR19876:SF1 (PANTHER), SSF82171 (SUPERFAMILY)
Caenorhabditis elegans	coatomer protein subunit alpha	17	P:GO:0030157; C:GO:0030126; C:GO:0005829; P:GO:0040010; C:GO:0005625; P:GO:0006890; P:GO:0000003; C:GO:0005615; P:GO:0032940; C:GO:0005792; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0048205; P:GO:0006886; F:GO:0005198; P:GO:0009792	-		IPR001680; IPR006692; IPR010714; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR19876 (PANTHER), PTHR19876:SF1 (PANTHER), SSF82171 (SUPERFAMILY)
Caenorhabditis elegans	coatomer protein subunit alpha	17	P:GO:0030157; C:GO:0030126; C:GO:0005829; P:GO:0040010; C:GO:0005625; P:GO:0006890; P:GO:0000003; C:GO:0005615; P:GO:0032940; C:GO:0005792; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0048205; P:GO:0006886; F:GO:0005198; P:GO:0009792	-		IPR001680; IPR006692; IPR010714; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR19876 (PANTHER), PTHR19876:SF1 (PANTHER), SSF82171 (SUPERFAMILY)

Caenorhabditis elegans	coatomer protein subunit alpha	17	P:GO:0030157; C:GO:0030126; C:GO:0005829; P:GO:0040010; C:GO:0005625; P:GO:0006890; P:GO:0000003; C:GO:0005615; P:GO:0032940; C:GO:0005792; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0048205; P:GO:0006886; F:GO:0005198; P:GO:0009792	-		IPR001680; IPR006692; IPR010714; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR19876 (PANTHER), PTHR19876:SF1 (PANTHER), SSF82171 (SUPERFAMILY)
Caenorhabditis elegans	coatomer protein subunit alpha	17	P:GO:0030157; C:GO:0030126; C:GO:0005829; P:GO:0040010; C:GO:0005625; P:GO:0006890; P:GO:0000003; C:GO:0005615; P:GO:0032940; C:GO:0005792; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0048205; P:GO:0006886; F:GO:0005198; P:GO:0009792	-		IPR001680; IPR006692; IPR010714; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR19876 (PANTHER), PTHR19876:SF1 (PANTHER), SSF82171 (SUPERFAMILY)
Caenorhabditis elegans	coatomer protein subunit alpha	17	P:GO:0030157; C:GO:0030126; C:GO:0005829; P:GO:0040010; C:GO:0005625; P:GO:0006890; P:GO:0000003; C:GO:0005615; P:GO:0032940; C:GO:0005792; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0048205; P:GO:0006886; F:GO:0005198; P:GO:0009792	-		IPR001680; IPR006692; IPR010714; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR19876 (PANTHER), PTHR19876:SF1 (PANTHER), SSF82171 (SUPERFAMILY)

Caenorhabditis elegans	coatomer protein subunit alpha	17	P:GO:0030157; C:GO:0030126; C:GO:0005829; P:GO:0040010; C:GO:0005625; P:GO:0006890; P:GO:0000003; C:GO:0005615; P:GO:0032940; C:GO:0005792; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0048205; P:GO:0006886; F:GO:0005198; P:GO:0009792	-		IPR001680; IPR006692; IPR010714; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR19876 (PANTHER), PTHR19876:SF1 (PANTHER), SSF82171 (SUPERFAMILY)
Caenorhabditis elegans	phospholipase b-like 2-like	1	C:GO:0005764	-		IPR007000
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	erin family member (cdh-10)	1	C:GO:0016020	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	4	P:GO:0000003; P:GO:0040010; P:GO:0006898; P:GO:0002119	-		-
	-	0				-
	-	0				-
	-	0				-
Loa loa	n-myristoyltransferase 1	10	C:GO:0005829; P:GO:0040010; F:GO:0004379; P:GO:0000003; P:GO:0018008; P:GO:0009249; P:GO:0002119; P:GO:0040011; P:GO:0006898; P:GO:0001701	-	EC:2.3.1.97	IPR000903; IPR016181; IPR022676; IPR022677; IPR022678
Loa loa	n-myristoyltransferase 1	10	C:GO:0005829; P:GO:0040010; F:GO:0004379; P:GO:0000003; P:GO:0018008; P:GO:0009249; P:GO:0002119; P:GO:0040011; P:GO:0006898; P:GO:0001701	-	EC:2.3.1.97	IPR000903; IPR016181; IPR022676; IPR022677; IPR022678
	-	0				SignalP (SIGNALP)
Loa loa	hypothetical protein LOAG_12000 [Loa loa]	0				-
Caenorhabditis elegans	methylmalonyl coenzyme a mutase	6	F:GO:0046872; F:GO:0004494; F:GO:0031419; C:GO:0005759; P:GO:0009791; P:GO:0008152	-	EC:5.4.99.2	IPR006158; PTHR23408 (PANTHER), PTHR23408:SF1 (PANTHER)

	-	0				SignalP (SIGNALP)
Streptomyces sp. ACT-1	lpxtg-motif cell wall anchor domain protein	0		C:GO:0009986		-
Hydra magnipapillata	scy1-like 3 (cerevisiae)	0		C:GO:0042995; F:GO:0004672; P:GO:0006468; F:GO:0003674; C:GO:0005794; F:GO:0005524; F:GO:0016301; C:GO:0005575; P:GO:0008150; F:GO:0005488		IPR000719; G3DSA:1.10.510.10 (GENE3D), PTHR12984 (PANTHER), PTHR12984:SF4 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	3	P:GO:0002119; P:GO:0040011; P:GO:0040007	-		-
Caenorhabditis briggsae	Hypothetical protein CBG00040 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	scp(small c-termi-l domain phosphatase)-like phosphatase family member (scpl-1)	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-pqn-87 protein	0				-
	-	0				-
Caenorhabditis elegans	laminin alpha chain	5	C:GO:0005606; P:GO:0030334; P:GO:0045995; P:GO:0030155; F:GO:0005102	-		IPR009254
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	hypothetical protein F32B5.7 [Caenorhabditis elegans]	0				-
	-	0				SignalP (SIGNALP)
Homo sapiens	mhc class ii antigen	10	C:GO:0005789; C:GO:0005887; C:GO:0042613; C:GO:0005794; P:GO:0002504; C:GO:0031902; P:GO:0007165; C:GO:0005765; F:GO:0032395; P:GO:0006955	-		-
Loa loa	gem-associated protein 6	3	P:GO:0008380; C:GO:0044428; P:GO:0006397	-		IPR009422
Caenorhabditis elegans	endonuclease exonuclease phosphatase family protein	1	F:GO:0004437	-		-
Caenorhabditis briggsae	mboat family protein	2	C:GO:0016020; F:GO:0016747	-	EC:2.3.1.0	IPR004299; PTHR13906 (PANTHER), PTHR13906:SF5 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	zinc-binding dehydroge-se family protein	1	P:GO:0008340	-		IPR002085; IPR011032; IPR013154; G3DSA:3.90.180.10 (GENE3D), PTHR11695:SF15 (PANTHER)

Caenorhabditis elegans	atpase	7	F:GO:0004222; P:GO:0030163; F:GO:0005524; C:GO:0016021; F:GO:0017111; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0; EC:3.6.1.15	G3DSA:3.40.50.300 (GENE3D), PTHR23076 (PANTHER), PTHR23076:SF11 (PANTHER)
Caenorhabditis elegans	hypothetical protein Y51F10.10 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	serine threonine-protein ki-se prp4 homolog	14	P:GO:0040010; F:GO:0004674; P:GO:0008360; C:GO:0071011; P:GO:0040035; F:GO:0005524; P:GO:0007155; P:GO:0002119; P:GO:0040011; P:GO:0000398; C:GO:0071013; P:GO:0002009; P:GO:0009792; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF17 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; C:GO:0016020		IPR021999; PTHR13167 (PANTHER), PTHR13167:SF6 (PANTHER)
Brugia malayi	nuclear receptor subfamily group member 2	1	F:GO:0070016	-		PTHR11865 (PANTHER), PTHR11865:SF205 (PANTHER)
	-	0				-
Caenorhabditis briggsae	acetoacetyl- synthetase	1	F:GO:0003824	-		PTHR11968 (PANTHER), PTHR11968:SF40 (PANTHER)
	-	0				-
Caenorhabditis elegans	6-phosphofructo-2-ki-se fructose- -biphosphatase 2 (6pf-2-k fru- -p2ase heart-type isozyme) (pfk-2 fbpase-2)	3	F:GO:0003873; P:GO:0006003; F:GO:0005524	-	EC:2.7.1.105	IPR001345; IPR003094; IPR013078; G3DSA:3.40.50.1240 (GENE3D), PTHR10606:SF11 (PANTHER), SSF53254 (SUPERFAMILY)
	-	0				-
Brugia malayi	hypothetical protein Bm1_07015 [Brugia malayi]	0				-
	-	0				-
Caenorhabditis elegans	brca1 interacting protein c-termi-l helicase 1	11	P:GO:0006412; C:GO:0005762; P:GO:0006357; F:GO:0004003; P:GO:0006302; F:GO:0003735; F:GO:0003677; F:GO:0005524; F:GO:0005515; P:GO:0000077; C:GO:0005634	-	EC:3.6.5.3	PTHR11472 (PANTHER), PTHR11472:SF6 (PANTHER)
Caenorhabditis elegans	briggsae cbr-rpy-1 protein	7	C:GO:0005856; C:GO:0045211; P:GO:0007268; C:GO:0030054; F:GO:0033130; P:GO:0019915; F:GO:0008270	-		PTHR10098 (PANTHER), PTHR10098:SF7 (PANTHER)

Caenorhabditis briggsae	pol ii c-termi-l interaction domain suppressor family member (cids-2)	1	F:GO:0005515	-		IPR006569
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	6	F:GO:0042802; F:GO:0016286; C:GO:0005886; N:GO:0071805; C:GO:0016021; F:GO:0005516	-		-
	-	0				-
Caenorhabditis elegans	xanthine dehydroge-se	9	F:GO:0004855; F:GO:0009055; F:GO:0005506; F:GO:0030151; F:GO:0004854; P:GO:0055114; P:GO:0008340; F:GO:0051537; F:GO:0050660	-	EC:1.17.3.2; EC:1.17.1.4	IPR008274; PTHR11908 (PANTHER), PTHR11908:SF9 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Loa loa	patched family protein	2	F:GO:0008158; C:GO:0016021	-		-
Brugia malayi	lim domain containing protein	3	F:GO:0046872; F:GO:0016491; P:GO:0008152	-		G3DSA:3.50.50.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF1 (PANTHER)
Bursaphelenchus xylophilus	60s ribosomal protein l5	9	P:GO:0040035; P:GO:0009792; P:GO:0010171; P:GO:0002119; C:GO:0005840; F:GO:0008097; F:GO:0003735; P:GO:0040010; P:GO:0006412	-	EC:3.6.5.3	IPR005484; IPR005485; G3DSA:3.30.420.100 (GENE3D), PTHR23410:SF1 (PANTHER), SSF53137 (SUPERFAMILY)
Caenorhabditis briggsae	uncoordi-ted family member (unc-61)	9	C:GO:0005875; F:GO:0005525; C:GO:0045172; F:GO:0005515; P:GO:0000910; P:GO:0007049; P:GO:0007349; C:GO:0005940; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000038; IPR016491; G3DSA:3.40.50.300 (GENE3D), PTHR18884:SF28 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	uncoordi-ted family member (unc-61)	9	C:GO:0005875; F:GO:0005525; C:GO:0045172; F:GO:0005515; P:GO:0000910; P:GO:0007049; P:GO:0007349; C:GO:0005940; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000038; IPR016491; G3DSA:3.40.50.300 (GENE3D), PTHR18884:SF28 (PANTHER), SSF52540 (SUPERFAMILY)

Caenorhabditis briggsae	uncoordi-ted family member (unc-61)	9	C:GO:0005875; F:GO:0005525; C:GO:0045172; F:GO:0005515; P:GO:0000910; P:GO:0007049; P:GO:0007349; C:GO:0005940; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000038; IPR016491; G3DSA:3.40.50.300 (GENE3D), PTHR18884:SF28 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	uncoordi-ted family member (unc-61)	9	C:GO:0005875; F:GO:0005525; C:GO:0045172; F:GO:0005515; P:GO:0000910; P:GO:0007049; P:GO:0007349; C:GO:0005940; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000038; IPR016491; G3DSA:3.40.50.300 (GENE3D), PTHR18884:SF28 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	ketosteroid isomerase	0		F:GO:0016853		G3DSA:3.10.450.50 (GENE3D), SSF54427 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	dedicator of cytokinesis 7	0		F:GO:0005525; F:GO:0008168; F:GO:0051020; F:GO:0005488; P:GO:0032259; F:GO:0005085		PTHR23317 (PANTHER), PTHR23317:SF27 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	P:GO:0040010; F:GO:0000166; P:GO:0006898	-		-
Macaca mulatta	galactoside- 3 binding protein	9	F:GO:0005044; C:GO:0005615; F:GO:0005515; P:GO:0007155; P:GO:0007165; C:GO:0016020; C:GO:0005634; C:GO:0005578; P:GO:0006968	-		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0005089; P:GO:0035023; C:GO:0005622; F:GO:0005085		-
Caenorhabditis briggsae	prefoldin subunit 2	9	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0006457; P:GO:0035046; P:GO:0040011; F:GO:0051082; P:GO:0040007; C:GO:0016272	-		SignalP (SIGNALP)

Loa loa	protein tyrosine receptor u	11	P:GO:0060070; C:GO:0005911; P:GO:0030336; F:GO:0004725; P:GO:0034109; P:GO:0034394; P:GO:0001757; P:GO:0008285; P:GO:0006470; P:GO:0016481; F:GO:0008013	-	EC:3.1.3.48	IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), SSF52799 (SUPERFAMILY)
Brugia malayi	replication factor c subunit 3	6	P:GO:0006260; C:GO:0005875; F:GO:0003689; C:GO:0005663; F:GO:0005515; F:GO:0005524	-		IPR003593; IPR003959; G3DSA:1.10.8.60 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR11669 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein T12B3.3 [Caenorhabditis elegans]	3	P:GO:0006071; F:GO:0008889; P:GO:0006629	-	EC:3.1.4.46	-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-ttr-37 protein	0				IPR001534; SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-bch-1 protein	5	F:GO:0003676; F:GO:0004003; F:GO:0005524; P:GO:0010569; C:GO:0005634	-		IPR006555; PTHR11472 (PANTHER), PTHR11472:SF4 (PANTHER)
Caenorhabditis elegans	protein unc-80 homolog isoform 2	3	C:GO:0034703; F:GO:0005261; P:GO:0055080	-		SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	3	P:GO:0009792; C:GO:0005886; F:GO:0005216	-		PTHR14499 (PANTHER), PTHR14499:SF6 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-tag-198 protein	2	P:GO:0006259; F:GO:0004531	-	EC:3.1.22.1	-
	-	0				-
Caenorhabditis briggsae	ribosomal protein	7	P:GO:0009792; P:GO:0002119; F:GO:0003735; P:GO:0040010; P:GO:0040019; C:GO:0015934; P:GO:0006412	-	EC:3.6.5.3	IPR005749; PTHR12934:SF1 (PANTHER)
Xenopus laevis	u3 small nucleolar homolog a	0		P:GO:0042254; C:GO:0030529; C:GO:0005634; P:GO:0006364; C:GO:0032040; F:GO:0003676; F:GO:0003674; C:GO:0005575; C:GO:0005730; P:GO:0008150		IPR006709; PTHR14150:SF12 (PANTHER)

Caenorhabditis briggsae	- ca exchangers family member (ncx-1)	13	P:GO:0055085; F:GO:0005432; P:GO:0008016; P:GO:0045214; C:GO:0016021; P:GO:0001947; P:GO:0000003; P:GO:0006816; P:GO:0007368; P:GO:0007154; P:GO:0009792; P:GO:0051480; P:GO:0042044	-		IPR003644; PTHR11878 (PANTHER), PTHR11878:SF4 (PANTHER), SSF141072 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein Y22D7AL.6 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
Caenorhabditis briggsae	4-nitrophenylphosphatase	1	F:GO:0016787	-		G3DSA:3.40.50.1000 (GENE3D), PTHR19288 (PANTHER), PTHR19288:SF11 (PANTHER), SSF56784 (SUPERFAMILY)
Pediculus humanus corporis	palmitoyltransferase zdhhc17	8	F:GO:0019706; F:GO:0004871; P:GO:0042953; F:GO:0015095; C:GO:0030660; P:GO:0043123; P:GO:0018345; F:GO:0005515	-		IPR001594; PTHR22883 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0005524; C:GO:0005856; F:GO:0000166; C:GO:0016459; F:GO:0003774		IPR000857; PTHR22692 (PANTHER), PTHR22692:SF2 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	polybromodomain protein	11	P:GO:0040010; P:GO:0006996; F:GO:0005488; P:GO:0040035; P:GO:0010171; P:GO:0002119; C:GO:0044446; P:GO:0040011; C:GO:0005694; P:GO:0002009; P:GO:0009792	-		IPR000910; IPR001025; IPR001487; IPR007087; IPR009071; IPR015880; IPR018359; PTHR16062 (PANTHER), PTHR16062:SF2 (PANTHER), SSF57667 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	chloride channel protein 2	1	C:GO:0005886	-		IPR000644; IPR001807; PTHR11689:SF5 (PANTHER), SSF54631 (SUPERFAMILY)
	-	0				IPR018111
Caenorhabditis briggsae	r--binding protein pno1	4	C:GO:0005730; P:GO:0040035; P:GO:0009792; F:GO:0003723	-		PTHR12826 (PANTHER), PTHR12826:SF4 (PANTHER)
Brugia malayi	bromodomain containing protein	1	F:GO:0005488	-		-
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	briggsae cbr-smgl-1 protein	0				-
	-	0				IPR007087; IPR015880
Caenorhabditis elegans	briggsae cbr-snt-5 protein	0		C:GO:0008021; C:GO:0016021; C:GO:0016020; P:GO:0006810		SignalP (SIGNALP)
Oscheius sp. (strain CEW1)	vitellogenin structural genes (yolk protein genes) family member (vit-6)	7	P:GO:0009792; F:GO:0005515; F:GO:0022892; P:GO:0006810; P:GO:0040010; P:GO:0033036; P:GO:0008340	-		-
Oscheius sp. (strain CEW1)	vitellogenin structural genes (yolk protein genes) family member (vit-6)	6	P:GO:0009792; F:GO:0005319; F:GO:0005515; P:GO:0040010; P:GO:0006869; P:GO:0008340	-		-
Caenorhabditis elegans	vitellogenin structural genes (yolk protein genes) family member (vit-6)	6	P:GO:0009792; F:GO:0005319; F:GO:0005515; P:GO:0040010; P:GO:0006869; P:GO:0008340	-		-
Oscheius sp. (strain CEW1)	vitellogenin structural genes (yolk protein genes) family member (vit-6)	6	P:GO:0009792; F:GO:0005319; F:GO:0005515; P:GO:0040010; P:GO:0006869; P:GO:0008340	-		-
Oscheius sp. (strain CEW1)	vitellogenin structural genes (yolk protein genes) family member (vit-6)	6	P:GO:0009792; F:GO:0005319; F:GO:0005515; P:GO:0040010; P:GO:0006869; P:GO:0008340	-		-
Caenorhabditis elegans	zinc finger	6	F:GO:0008270; F:GO:0003676; C:GO:0005622; P:GO:0046672; P:GO:0006099; P:GO:0030536	-		IPR007087; IPR013087; IPR015880; PTHR10042 (PANTHER), PTHR10042:SF3 (PANTHER), SSF57667 (SUPERFAMILY)
Homo sapiens	AF258561_1PP3686 [Homo sapiens]	4	C:GO:0016021; F:GO:0004872; P:GO:0030154; P:GO:0007399	-		-
Caenorhabditis briggsae	kinesin family member 3a	5	P:GO:0007018; F:GO:0005524; C:GO:0030529; F:GO:0003777; C:GO:0005874	-		IPR001752; PTHR16012 (PANTHER), PTHR16012:SF160 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Angiostrongylus cantonensis	elegans protein confirmed by transcript evidence	0		C:GO:0005737; P:GO:0007275		IPR007917; IPR022776
	-	0				-
	-	0				-

	-	0				-
Caenorhabditis briggsae	peroxisome biogenesis factor 13	7	P:GO:0016477; C:GO:0016021; C:GO:0005778; P:GO:0007399; P:GO:0007610; P:GO:0051641; P:GO:0015031	-		IPR001452; G3DSA:2.30.30.40 (GENE3D), PTHR19332 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Solanum demissum	endonuclease-reverse transcriptase	2	F:GO:0003677; F:GO:0008168	-	EC:2.1.1.0	-
Medicago truncatula	endonuclease-reverse transcriptase	3	F:GO:0003677; F:GO:0008168; F:GO:0000166	-	EC:2.1.1.0	-
Caenorhabditis elegans	trehalase family member (tre-4)	0		P:GO:0005991; C:GO:0016021		IPR001661; PTHR23403:SF1 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	cytochrome b5 reductase 4	10	F:GO:0016174; F:GO:0004128; P:GO:0006739; P:GO:0006801; P:GO:0055114; P:GO:0006091; F:GO:0020037; C:GO:0048471; F:GO:0050660; C:GO:0005783	-	EC:1.6.3.1; EC:1.6.2.2	SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Macaca mulatta	-+ k+ alpha 1 polypeptide	20	F:GO:0005515; P:GO:0045989; P:GO:0045822; F:GO:0003869; C:GO:0005792; C:GO:0016323; C:GO:0042470; F:GO:0046872; P:GO:0006754; C:GO:0042383; F:GO:0005391; P:GO:0045823; P:GO:0042493; P:GO:0031947; C:GO:0005890; P:GO:0006813; P:GO:0002026; F:GO:0005524; P:GO:0008217; P:GO:0006814	-	EC:3.1.3.41; EC:3.6.3.9	IPR001757; IPR006068; IPR006069; G3DSA:1.20.1110.10 (GENE3D), PTHR11939:SF23 (PANTHER), SSF81665 (SUPERFAMILY)
	-	0				-
	-	0				IPR003582; SignalP (SIGNALP)

Loa loa	ets domain-containing protein elk-3-like	5	F:GO:0003700; F:GO:0043565; F:GO:0005515; C:GO:0005634; P:GO:0006355	-		IPR000418; IPR011991; PTHR11849 (PANTHER), PTHR11849:SF12 (PANTHER), SSF46785 (SUPERFAMILY)
Loa loa	ets-domain containing protein	5	F:GO:0003700; F:GO:0043565; F:GO:0005515; C:GO:0005634; P:GO:0006355	-		IPR000418; IPR011991; PTHR11849 (PANTHER), PTHR11849:SF12 (PANTHER), SSF46785 (SUPERFAMILY)
Danio rerio	atp-binding sub-family member 1	40	P:GO:0046685; P:GO:0032496; F:GO:0005324; F:GO:0000166; P:GO:0010243; P:GO:0070327; C:GO:0005624; F:GO:0015432; F:GO:0046624; C:GO:0016323; F:GO:0015562; P:GO:0015911; P:GO:0043526; P:GO:0006855; C:GO:0005737; P:GO:0034775; F:GO:0019904; P:GO:0015711; P:GO:0060326; F:GO:0034634; P:GO:0030644; F:GO:0008559; F:GO:0015431; P:GO:0015722; P:GO:0009408; P:GO:0031427; P:GO:0033700;	-	EC:3.6.3.44	-
	-	0				-
	-	0				-

Brugia malayi	timeless homolog	0		P:GO:0042127; P:GO:0051301; C:GO:0000790; P:GO:0007067; P:GO:0007623; P:GO:0001658; C:GO:0005634; F:GO:0046982; P:GO:0010553; P:GO:0002009; P:GO:0030324; F:GO:0042803; P:GO:0048754; P:GO:0009628; P:GO:0006974; P:GO:0007049; P:GO:0001822; P:GO:0042753; P:GO:0009790; P:GO:0007275; P:GO:0033261; P:GO:0016481; F:GO:0005515; P:GO:0009582		IPR006906; PTHR22940 (PANTHER), PTHR22940:SF7 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	tetratricopeptide repeat domain 4	8	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0005488; P:GO:0040018; P:GO:0040010; P:GO:0040011; P:GO:0006898	-		IPR011990; IPR019734; PTHR22904 (PANTHER), PTHR22904:SF16 (PANTHER), SSF48452 (SUPERFAMILY)
	-	0				PTHR14043 (PANTHER), PTHR14043:SF3 (PANTHER)
	-	0				-
Caenorhabditis elegans	dicarbonyl l-xylulose reductase	7	P:GO:0006739; C:GO:0005903; C:GO:0005902; F:GO:0005515; P:GO:0005997; F:GO:0016616; C:GO:0016020	-	EC:1.1.1.0	IPR002198; IPR002347; IPR016040; PTHR19410:SF59 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	protein ki-se domain containing protein	1	P:GO:0007283	-		PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR013640
	-	0				PTHR11375 (PANTHER)
	-	0				-

Macaca mulatta	glucose phosphate isomerase	21	P:GO:0001525; P:GO:0006094; P:GO:0043154; P:GO:0007599; F:GO:0004347; F:GO:0008083; F:GO:0005125; P:GO:0006959; C:GO:0019717; P:GO:0051156; C:GO:0005615; C:GO:0016021; F:GO:0017176; P:GO:0046185; C:GO:0005829; P:GO:0043524; P:GO:0006506; P:GO:0006096; P:GO:0019242; F:GO:0048029; F:GO:0016866	-	EC:5.3.1.9; EC:2.4.1.198	IPR001672; G3DSA:3.40.50.10490 (GENE3D), PS51463 (PROFILE), SSF53697 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	major facilitator superfamily protein	2	P:GO:0055085; C:GO:0016021	-		PTHR11662 (PANTHER), PTHR11662:SF24 (PANTHER), SignalP (SIGNALP)
	-	0				-
Loa loa	hypothetical protein LOAG_01867 [Loa loa]	0				-
Caenorhabditis sp. PS1010	briggsae cbr-hum-7 protein	5	F:GO:0046872; C:GO:0016459; F:GO:0005524; P:GO:0007165; F:GO:0003774	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	P:GO:0002119	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Homo sapiens	microsomal glutathione s-transferase 3	8	C:GO:0005789; C:GO:0005792; P:GO:0006629; F:GO:0004364; P:GO:0010243; P:GO:0007165; C:GO:0016021; F:GO:0004602	-	EC:2.5.1.18; EC:1.11.1.9	IPR001129; IPR010916; G3DSA:1.20.120.550 (GENE3D), PTHR10250 (PANTHER), PTHR10250:SF1 (PANTHER)
Drosophila simulans	vacuolar protein sorting 45	8	F:GO:0000149; C:GO:0008021; P:GO:0006605; P:GO:0016082; P:GO:0006897; P:GO:0034058; P:GO:0006904; P:GO:0007040	-		IPR001619; G3DSA:3.40.50.2060 (GENE3D), PTHR11679:SF3 (PANTHER)
	-	0				-

	-	0				-
Caenorhabditis elegans	discs large	3	P:GO:0009987; F:GO:0005515; C:GO:0044464	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR23116 (PANTHER), PTHR23116:SF1 (PANTHER)
	-	0				-
Caenorhabditis elegans	hypothetical protein W03B1.9 [Caenorhabditis elegans]	0				-
Caenorhabditis brenneri	shc (src homology domain c-termi-l) adaptor homolog family member (shc-2)	1	F:GO:0005515	-		IPR000980; PTHR12583 (PANTHER), PTHR12583:SF5 (PANTHER), SSF55550 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	cytochrome p450 family protein partially confirmed by transcript evidence	6	F:GO:0020037; C:GO:0016021; P:GO:0055114; F:GO:0004497; F:GO:0009055; P:GO:0040010	-		-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				SignalP (SIGNALP)
Loa loa	briggsae cbr-snf-1 protein	3	C:GO:0016021; P:GO:0006810; F:GO:0015293	-		IPR000175; PTHR11616:SF12 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein Y119C1B.5 [Caenorhabditis elegans]	3	F:GO:0008270; F:GO:0005515; C:GO:0016021	-		SignalP (SIGNALP)
Caenorhabditis elegans	achain cekdm7a from complex with h3k4me3 peptide and nog	0		F:GO:0046872; F:GO:0008270; F:GO:0005515; C:GO:0005634		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	te-scin isoform h	3	P:GO:0000003; P:GO:0040039; P:GO:0007275	-		IPR013032; IPR013111; PTHR11201 (PANTHER), PTHR11201:SF148 (PANTHER)
	-	0				-
Homo sapiens	protein tyrosine receptor c-associated protein	3	P:GO:0006952; C:GO:0005886; C:GO:0016021	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	serologically defined colon cancer antigen 1	0		P:GO:0008150; C:GO:0005575		IPR008532; PTHR15239 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	regulator of g protein sig-ling family member (rgs-5)	0		F:GO:0016301; F:GO:0004871		IPR000342; IPR016137; PTHR13155 (PANTHER)
Branchiostoma floridae	elegans protein confirmed by transcript evidence	0				PTHR12496 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Homo sapiens	low density lipoprotein receptor-related protein 3	4	C:GO:0016021; F:GO:0004872; P:GO:0006898; C:GO:0005905	-		-
Brugia malayi	zinc c2h2 type family protein	2	C:GO:0005622; F:GO:0008270	-		IPR015880

Brugia malayi	zinc c2h2 type family protein	2	C:GO:0005622; F:GO:0008270	-		IPR015880
Caenorhabditis briggsae	dhx33 protein	2	F:GO:0004386; F:GO:0000166	-		IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR18934 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	briggsae cbr-bub-1 protein	3	P:GO:0009987; F:GO:0005488; P:GO:0007275	-		-
Arabidopsis lyrata subsp. lyrata	eukaryotic translation initiation factor	0		F:GO:0003676; F:GO:0003743		PTHR22891 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis briggsae	dedicator of cytokinesis protein 9	0		F:GO:0005525; F:GO:0051020; F:GO:0005085		IPR021816
Brugia malayi	ets-domain containing protein	4	F:GO:0003700; F:GO:0043565; C:GO:0005634; P:GO:0006355	-		-
Caenorhabditis briggsae	Hypothetical protein CBG17893 [Caenorhabditis briggsae]	0		F:GO:0046872; F:GO:0003676; F:GO:0000166; F:GO:0008270; P:GO:0006396; F:GO:0008173		IPR000504; IPR012677; SSF54928 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	ynpi_caeel ame: full=uncharacterized protein	0				IPR006627
	-	0				SignalP (SIGNALP)
Ixodes scapularis	sentrin-specific protease 8 isoform a	1	F:GO:0008233	-		IPR003653; PTHR22875 (PANTHER), PTHR22875:SF2 (PANTHER), SSF54001 (SUPERFAMILY)
Loa loa	domon domain containing protein	3	P:GO:0009056; P:GO:0044238; F:GO:0003824	-		IPR005018
	-	0				-
	-	0				-
Caenorhabditis elegans	pih1 domain-containing protein 1	5	F:GO:0016491; P:GO:0000492; F:GO:0050660; C:GO:0016020; C:GO:0070761	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	ccaat-binding protein nf-y:subunit=	6	P:GO:0045944; F:GO:0003677; F:GO:0016563; C:GO:0016602; F:GO:0005515; F:GO:0003700	-		IPR001289; PTHR12632:SF6 (PANTHER)
						IPR011042
Drosophila pseudoobscura pseudoobscura	tubulin-specific chaperone d	7	P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0046785; P:GO:0040011; P:GO:0040007; P:GO:0002009	-		PTHR12658 (PANTHER)

	-	0				-
	-	0				IPR003006; SignalP (SIGNALP)
Brugia malayi	tk fer protein ki-se	6	P:GO:0023052; F:GO:0004713; F:GO:0005515; C:GO:0005737; P:GO:0040018; P:GO:0006468	-	EC:2.7.10.0	IPR000719; IPR001245; IPR008266; IPR011009; IPR020685; IPR020764; G3DSA:1.10.510.10 (GENE3D)
Caenorhabditis elegans	met-10+ like-protein	1	F:GO:0016740	-		IPR003402; G3DSA:3.40.50.150 (GENE3D), PTHR23245 (PANTHER), PTHR23245:SF25 (PANTHER), SSF53335 (SUPERFAMILY)
Brugia malayi	kiaa1688 protein	1	C:GO:0005622	-		IPR000857; PTHR22692 (PANTHER), PTHR22692:SF2 (PANTHER)
						IPR008160; PTHR10499 (PANTHER), PTHR10499:SF114 (PANTHER)
Caenorhabditis elegans	-galactosyltransferase 7	7	C:GO:0005794; P:GO:0006029; P:GO:0048147; F:GO:0046525; P:GO:0043206; C:GO:0016021; P:GO:0006024	-	EC:2.4.1.133	IPR003859; G3DSA:3.90.550.10 (GENE3D), PTHR19300:SF1 (PANTHER), SSF53448 (SUPERFAMILY)
	-	0				-
	-	0				-
Loa loa	cadherin domain containing protein	5	C:GO:0016021; P:GO:0007156; F:GO:0005509; C:GO:0005886; F:GO:0004930	-		IPR002126; IPR015919; IPR020894; PTHR10596 (PANTHER), PTHR10596:SF73 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	membrane-associated tyrosine- and threonine-specific cdc2-inhibitory ki-se	12	C:GO:0019898; F:GO:0004674; P:GO:0051447; P:GO:0002119; F:GO:0005515; C:GO:0044444; P:GO:0007067; P:GO:0016310; C:GO:0005654; P:GO:0048477; P:GO:0051327; P:GO:0009790	-	EC:2.7.11.0	-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	threonine ammonia-lyase	0		P:GO:0006520; P:GO:0008152; F:GO:0003824; F:GO:0016829; F:GO:0030170; F:GO:0004794		G3DSA:3.40.50.1100 (GENE3D)

Brugia malayi	receptor protein tyrosine	1	F:GO:0016787	-		IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF80 (PANTHER), SSF52799 (SUPERFAMILY)
Homo sapiens	cd9 antigen	14	P:GO:0030168; P:GO:0009414; P:GO:0030913; P:GO:0007420; C:GO:0009986; P:GO:0008285; P:GO:0007155; F:GO:0005515; P:GO:0007342; P:GO:0006928; C:GO:0016324; P:GO:0014003; C:GO:0031092; C:GO:0005887	-		IPR008952; G3DSA:1.10.1450.10 (GENE3D), PTHR19282 (PANTHER), PTHR19282:SF18 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	3	P:GO:0040010; P:GO:0006898; P:GO:0002119	-		-
	-	0				IPR011990; IPR013026; SSF48452 (SUPERFAMILY)
Caenorhabditis elegans	phosphoribosylaminoimidazole phosphoribosylaminoimidazole succinocarboxamide synthetase	6	F:GO:0042802; F:GO:0016874; P:GO:0002119; P:GO:0009168; P:GO:0040007; F:GO:0016829	-		IPR000031; IPR001636; IPR013816; IPR018236; G3DSA:3.30.200.20 (GENE3D), PTHR11609:SF2 (PANTHER), SSF56104 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0040007; P:GO:0006898; P:GO:0002119	-		-
Caenorhabditis elegans	briggsae cbr-cyc- protein	11	P:GO:0009792; P:GO:0002119; P:GO:0040018; C:GO:0070469; F:GO:0009055; C:GO:0005759; F:GO:0020037; P:GO:0006810; P:GO:0040010; P:GO:0008340; P:GO:0022900	-		-
	-	0				-
Caenorhabditis briggsae	pftaire protein ki-se 1	11	C:GO:0005829; P:GO:0000086; C:GO:0000308; P:GO:0051301; F:GO:0005524; P:GO:0060828; F:GO:0004693; F:GO:0030332; C:GO:0005634; C:GO:0005886; P:GO:0006468	-	EC:2.7.11.22	IPR000719; IPR011009; IPR017441; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF95 (PANTHER)
	-	0				-

Caenorhabditis elegans	tr--dihydrouridine synthase 3-like	5	F:GO:0046872; F:GO:0003676; P:GO:0055114; F:GO:0050660; F:GO:0017150	-		IPR000571; IPR001269; PTHR11082:SF1 (PANTHER)
Caenorhabditis elegans	ubiquitin protein ligase e3 component n-recognin 3	4	P:GO:0009790; F:GO:0016874; F:GO:0005488; P:GO:0044267	-		PTHR21497 (PANTHER), PTHR21497:SF3 (PANTHER)
	-	0				-
Angiostrongylus cantonensis	c2 domain containing protein	1	P:GO:0009792	-		IPR000008; IPR008973; G3DSA:2.60.40.150 (GENE3D), PTHR10024 (PANTHER)
Caenorhabditis briggsae	intraflagellar transport 57 homolog	8	C:GO:0035085; P:GO:0007635; F:GO:0005515; P:GO:0042384; F:GO:0005198; C:GO:0005932; P:GO:0008104; P:GO:0006919	-		IPR019530
Caenorhabditis briggsae	polyadenylate-binding protein	3	P:GO:0009792; F:GO:0000166; F:GO:0003723	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF69 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
Ancylostoma Ceylanicum	macrophage migration inhibitory factor	25	P:GO:0006954; P:GO:0031325; P:GO:0009628; P:GO:0006955; P:GO:0048519; P:GO:0016043; P:GO:0002684; P:GO:0008544; P:GO:0044281; P:GO:0042127; P:GO:0007568; P:GO:0080090; P:GO:0007399; P:GO:0030330; F:GO:0005515; C:GO:0044424; P:GO:0048545; F:GO:0016860; P:GO:0032103; P:GO:0080135; P:GO:0033273; P:GO:0051239; P:GO:0051050; P:GO:0010604; C:GO:0005576	-		IPR001398; IPR014347; PTHR11954:SF5 (PANTHER), SSF55331 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	cdc23 (cell division cycle homolog)	20	C:GO:0005654; P:GO:0070979; P:GO:0000080; F:GO:0005515; P:GO:0051437; P:GO:0007080; P:GO:0006898; C:GO:0005680; P:GO:0051436; C:GO:0005829; P:GO:0007096; P:GO:0009792; P:GO:0002009; F:GO:0004842; P:GO:0007126; P:GO:0002119; P:GO:0010171; P:GO:0031145; P:GO:0030071; P:GO:0040035	-	EC:6.3.2.19	IPR011990; IPR013026; IPR019734; PTHR12558 (PANTHER), PTHR12558:SF10 (PANTHER), SSF48452 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	r- polymerase i large subunit	7	F:GO:0003899; C:GO:0005654; F:GO:0003677; C:GO:0005736; F:GO:0005515; P:GO:0006350; F:GO:0008270	-	EC:2.7.7.6	-
	-	0				-
	-	0				-
Brugia malayi	protein ki-se domain containing protein	10	P:GO:0006468; C:GO:0005929; C:GO:0030425; F:GO:0005515; P:GO:0034606; F:GO:0004713; C:GO:0030424; P:GO:0034608; F:GO:0005524; C:GO:0043025	-	EC:2.7.10.0	IPR000719; IPR001245; IPR011009; IPR020685; IPR020764; G3DSA:3.30.200.20 (GENE3D)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG02738 [Caenorhabditis briggsae]	0		P:GO:0006355; F:GO:0043565; P:GO:0045449; F:GO:0003700; C:GO:0005634; F:GO:0003677		-
Caenorhabditis elegans	tetratricopeptide repeat domain 17	3	P:GO:0040010; P:GO:0040017; F:GO:0005488	-		-
Caenorhabditis elegans	o-glycosyl hydrolase family 30 protein	3	F:GO:0016787; P:GO:0009987; P:GO:0044238	-		IPR001139; IPR013781; IPR017853
	-	0				-
	-	0				-

	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG18472 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein T26A8.1 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein T26A8.1 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
Pan troglodytes	phd finger protein 15	0		C:GO:0005829; P:GO:0043029; F:GO:0003700; P:GO:0006355; C:GO:0016605; C:GO:0005886; F:GO:0032403; P:GO:0008152; C:GO:0016021; C:GO:0016020; P:GO:0048538; P:GO:0048536; P:GO:0008633; P:GO:0001701; P:GO:0006281; F:GO:0003824; P:GO:0002262; P:GO:0048563; C:GO:0000300; C:GO:0005624; C:GO:0005622; P:GO:0006606; P:GO:0035148; F:GO:0004222; F:GO:0008270; F:GO:0016491; P:GO:0006310; P:GO:0007160;		PTHR12138 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Ancylostoma caninum	secreted protein 5 precursor	0		P:GO:0040011; C:GO:0005576		IPR001283; IPR002413; IPR014044; PTHR10334:SF11 (PANTHER)
Loa loa	cyclin g associated ki-se	5	C:GO:0005737; F:GO:0004672; P:GO:0009987; F:GO:0030332; F:GO:0000166	-		IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR23172 (PANTHER), PTHR23172:SF21 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				G3DSA:1.10.720.30 (GENE3D)
Caenorhabditis briggsae	calcitonin receptor	8	F:GO:0004948; P:GO:0007202; P:GO:0045762; C:GO:0016021; F:GO:0032841; P:GO:0007165; P:GO:0007186; C:GO:0005886	-		IPR000832; IPR017981; PTHR12011 (PANTHER), PTHR12011:SF15 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	s enesis abnormal family member (syg-1)	1	C:GO:0016020	-		IPR003598; IPR007110; IPR013098; IPR013783; PTHR11640 (PANTHER), PTHR11640:SF3 (PANTHER), SSF48726 (SUPERFAMILY)

Loa loa	briggsae cbr-ncr-1 protein	6	C:GO:0016020; P:GO:0044237; P:GO:0050896; P:GO:0030301; C:GO:0005768; P:GO:0050794	-		IPR000731; IPR003392; PTHR10796 (PANTHER), PTHR10796:SF35 (PANTHER), SignalP (SIGNALP), SSF82866 (SUPERFAMILY)
Haemonchus contortus	zinc metalloprotei-se toh-2 precursor	4	F:GO:0004222; P:GO:0009792; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	IPR000859
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		IPR011021; IPR014756; PTHR11188 (PANTHER), PTHR11188:SF13 (PANTHER)
	-	0				-
Caenorhabditis elegans	diacylglycerol acyltransferase	11	C:GO:0005829; F:GO:0004144; P:GO:0034379; C:GO:0016021; F:GO:0003846; C:GO:0005792; P:GO:0030073; P:GO:0019432; F:GO:0019992; C:GO:0005789; F:GO:0005504	-	EC:2.3.1.20; EC:2.3.1.22	PTHR10408 (PANTHER), SignalP (SIGNALP)
Pongo abelii	transporter atp-binding sub-family b (mdr tap)	19	F:GO:0046979; C:GO:0042825; P:GO:0019060; F:GO:0015197; C:GO:0005792; P:GO:0042270; F:GO:0043531; C:GO:0005829; F:GO:0046982; F:GO:0046978; P:GO:0046967; P:GO:0015833; F:GO:0042626; P:GO:0019885; P:GO:0055085; F:GO:0042605; F:GO:0042803; F:GO:0005524; C:GO:0005739	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	briggsae cbr-hum-5 protein	8	F:GO:0000146; F:GO:0030898; F:GO:0003779; C:GO:0016459; F:GO:0005524; C:GO:0030673; F:GO:0005516; C:GO:0005790	-		IPR001609; PTHR13140 (PANTHER), PTHR13140:SF31 (PANTHER), SSF52540 (SUPERFAMILY)

Caenorhabditis elegans	transcription factor mitochondrial	10	P:GO:0006519; P:GO:0044106; F:GO:0003712; C:GO:0042645; F:GO:0004497; P:GO:0006390; P:GO:0009056; P:GO:0006417; P:GO:0000154; F:GO:0000179	-		IPR001737; G3DSA:3.40.50.150 (GENE3D), SSF53335 (SUPERFAMILY)
Loa loa	hypothetical protein LOAG_04713 [Loa loa]	0		F:GO:0004500; P:GO:0006548		-
	-	0				PTHR10504 (PANTHER), PTHR10504:SF11 (PANTHER)
	-	0				-
	-	0				-
Macaca mulatta	cathepsin b	29	P:GO:0009749; C:GO:0005764; F:GO:0030984; P:GO:0051789; C:GO:0009897; C:GO:0005625; C:GO:0005739; P:GO:0045471; P:GO:0042981; C:GO:0005901; P:GO:0009611; F:GO:0032403; C:GO:0005615; P:GO:0006508; P:GO:0043434; F:GO:0004197; C:GO:0042470; P:GO:0007519; P:GO:0014070; P:GO:0070670; C:GO:0048471; C:GO:0016324; C:GO:0042383; P:GO:0050790; P:GO:0014075; P:GO:0060548; P:GO:0006914;	-	EC:3.4.22.0	-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	midasin homolog	6	P:GO:0043254; P:GO:0006355; F:GO:0005524; F:GO:0016887; F:GO:0008134; C:GO:0005634	-		G3DSA:3.40.50.300 (GENE3D), PTHR22908 (PANTHER), PTHR22908:SF13 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	camp-dependent protein ki-se catalytic	5	P:GO:0006468; F:GO:0004871; F:GO:0005524; P:GO:0007165; F:GO:0004703	-	EC:2.7.11.16	SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	cation transporting atpase family member (catp-1)	5	P:GO:0006811; F:GO:0016820; F:GO:0000166; P:GO:0008152; C:GO:0016020	-	EC:3.6.3.0	SignalP (SIGNALP)
Caenorhabditis elegans	xanthine dehydroge-se	14	C:GO:0005829; P:GO:0007595; F:GO:0051537; P:GO:0055114; F:GO:0009055; P:GO:0010044; F:GO:0004855; F:GO:0004854; F:GO:0043546; P:GO:0030856; F:GO:0050660; P:GO:0009115; F:GO:0005506; P:GO:0045453	-	EC:1.17.3.2; EC:1.17.1.4	-
Caenorhabditis briggsae	intracelllar ipase a family member (ipla-1)	2	F:GO:0046872; P:GO:0008356	-		-
Caenorhabditis briggsae	intracelllar ipase a family member (ipla-1)	1	P:GO:0008356	-		-
Caenorhabditis briggsae	ddhd domain containing 1	1	P:GO:0008356	-		IPR004177; PTHR15457 (PANTHER), PTHR15457:SF4 (PANTHER)
Caenorhabditis briggsae	ddhd domain containing 1	1	P:GO:0008356	-		-
	-	0				-
Caenorhabditis elegans	hypothetical protein C09G4.2 [Caenorhabditis elegans]	1	P:GO:0000003	-		-
Loa loa	adducin 1	0		F:GO:0046872; P:GO:0008150; C:GO:0005575		IPR001303; PTHR10672 (PANTHER), PTHR10672:SF3 (PANTHER)
Caenorhabditis elegans	hypothetical protein Y94H6A.5 [Caenorhabditis elegans]	3	F:GO:0016818; F:GO:0005488; P:GO:0040010	-	EC:3.6.1.0	-
	-	0				-
Caenorhabditis elegans	gl actin (drosophila neuroligin-like) homolog family member (nrx-1)	0				-
Brugia malayi	trrap-like (transcription transformation domain-associated protein) family member (trr-1)	0		F:GO:0005488; F:GO:0016773		-
Brugia malayi	mkiaa0368 protein	0		F:GO:0005488		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		-
	-	0				-

Pan troglodytes	peroxiredoxin 1	19	P:GO:0001501; P:GO:0032872; P:GO:0042744; P:GO:0034101; C:GO:0005759; P:GO:0042267; C:GO:0005719; F:GO:0020037; P:GO:0008283; C:GO:0042470; P:GO:0019430; F:GO:0008379; C:GO:0005730; C:GO:0005829; P:GO:0045454; P:GO:0042345; P:GO:0055114; F:GO:0042803; C:GO:0005782	-		IPR000866; IPR012335; IPR012336; IPR019479; G3DSA:3.30.1020.10 (GENE3D), PTHR10681 (PANTHER), PTHR10681:SF8 (PANTHER)
	-	0				-
Caenorhabditis briggsae	mucoidy inhibitor a	1	F:GO:0005515	-		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	dhhc zinc finger domain containing protein	1	F:GO:0046872	-		IPR001594; PTHR22883 (PANTHER)
	-	0				-
Loa loa	briggsae cbr-dpy-22 protein	8	P:GO:0040010; P:GO:0018991; P:GO:0040035; P:GO:0010171; P:GO:0040026; P:GO:0040011; P:GO:0009792; P:GO:0040018	-		IPR021990; PTHR12796 (PANTHER)
Caenorhabditis elegans	hypothetical protein Y54E10A.16 [Caenorhabditis elegans]	2	P:GO:0040039; P:GO:0000003	-		-
	-	0				-
Caenorhabditis briggsae	cold-shock d--binding domain containing protein	5	F:GO:0003723; F:GO:0043565; F:GO:0005515; C:GO:0030529; P:GO:0045893	-		IPR002059; IPR011129; IPR012340; IPR016027; IPR019844; PTHR11544 (PANTHER), PTHR11544:SF4 (PANTHER)
Caenorhabditis briggsae	cold-shock d--binding domain containing protein	5	F:GO:0003723; F:GO:0043565; F:GO:0005515; C:GO:0030529; P:GO:0045893	-		IPR002059; IPR011129; IPR012340; IPR016027; IPR019844; PTHR11544 (PANTHER), PTHR11544:SF4 (PANTHER)
Caenorhabditis briggsae	cold-shock d--binding domain containing protein	9	F:GO:0005515; P:GO:0006357; F:GO:0003697; C:GO:0005737; C:GO:0071204; P:GO:0048522; F:GO:0003723; P:GO:0048523; P:GO:0001701	-		-

Caenorhabditis briggsae	cold-shock d--binding domain containing protein	9	F:GO:0005515; P:GO:0006357; F:GO:0003697; C:GO:0005737; C:GO:0071204; P:GO:0048522; F:GO:0003723; P:GO:0048523; P:GO:0001701	-		-
Caenorhabditis briggsae	cold-shock d--binding domain containing protein	9	F:GO:0005515; P:GO:0006357; F:GO:0003697; C:GO:0005737; C:GO:0071204; P:GO:0048522; F:GO:0003723; P:GO:0048523; P:GO:0001701	-		SignalP (SIGNALP)
Caenorhabditis briggsae	cold-shock d--binding domain containing protein	9	F:GO:0005515; P:GO:0006357; F:GO:0003697; C:GO:0005737; C:GO:0071204; P:GO:0048522; F:GO:0003723; P:GO:0048523; P:GO:0001701	-		SignalP (SIGNALP)
Caenorhabditis briggsae	r- helicase	1	F:GO:0005488	-		-
	-	0				-
Caenorhabditis elegans	glioma tumor suppressor candidate region gene 2	4	P:GO:0000003; P:GO:0040007; P:GO:0006898; P:GO:0002119	-		IPR011687; PTHR14211:SF6 (PANTHER)
	-	0				-
Ancylostoma ceylanicum	metalloprotease 1 precursor	2	F:GO:0046872; F:GO:0008237	-		IPR000859; IPR013032; PTHR10127 (PANTHER), PTHR10127:SF60 (PANTHER)
Pongo abelii	parkinson disease (autosomal early onset) 7	16	P:GO:0060765; C:GO:0005829; P:GO:0008344; C:GO:0030424; C:GO:0005739; P:GO:0008219; P:GO:0051899; P:GO:0060081; P:GO:0032091; P:GO:0051583; F:GO:0005515; P:GO:0042743; P:GO:0042493; F:GO:0051920; P:GO:0042542; C:GO:0005634	-	EC:1.11.1.15	IPR002818; G3DSA:3.40.50.880 (GENE3D), PTHR11019 (PANTHER), PTHR11019:SF5 (PANTHER), SSF52317 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis elegans	iesterase family member (pde-4)	3	F:GO:0046872; P:GO:0007165; F:GO:0004114	-	EC:3.1.4.17	-
Brugia malayi	ubiquitin carboxyl-termi-l hydrolase family protein	1	F:GO:0016787	-		-
Cooperia oncophora	latrophilin-like protein 2	6	P:GO:0007218; C:GO:0016021; P:GO:0007165; C:GO:0005886; F:GO:0005529; F:GO:0004930	-		IPR000922; IPR001304; IPR013032; IPR016186; IPR016187; PTHR10690 (PANTHER), PTHR10690:SF4 (PANTHER)
Caenorhabditis briggsae	arginyl-tr- synthetase mitochondrial	4	C:GO:0005737; F:GO:0004814; P:GO:0006420; F:GO:0005524	-	EC:6.1.1.19	IPR001278; IPR001412; IPR014729; IPR015945; SSF52374 (SUPERFAMILY)
Caenorhabditis briggsae	sideroflexin 3	4	F:GO:0005371; P:GO:0055085; P:GO:0006812; C:GO:0031966	-		IPR004686; PTHR11153:SF9 (PANTHER)
Caenorhabditis elegans	camk protein ki-se	1	F:GO:0005515	-		IPR020636; IPR020659; G3DSA:1.10.510.10 (GENE3D)
	-	0				-
	-	0				-
Brugia malayi	patched family protein	11	P:GO:0009792; P:GO:0002119; F:GO:0008158; P:GO:0040018; P:GO:0001703; P:GO:0018996; P:GO:0000910; P:GO:0040010; P:GO:0000003; P:GO:0040011; C:GO:0016021	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Loa loa	polymerase iii (d- directed) polypeptide b	9	F:GO:0003899; P:GO:0009615; P:GO:0032728; P:GO:0045089; F:GO:0046872; F:GO:0003677; F:GO:0032549; P:GO:0006350; C:GO:0005634	-	EC:2.7.7.6	IPR015712; G3DSA:3.90.1100.10 (GENE3D), PTHR20856:SF8 (PANTHER), SSF64484 (SUPERFAMILY)
	-	0				-
	-	0				-
Ancylostoma caninum	transforming growth factor beta	2	P:GO:0040007; F:GO:0008083	-		IPR001111; IPR015615; PTHR11848:SF36 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0005524		IPR007588

Caenorhabditis elegans	d- polymerase theta	8	C:GO:0043231; P:GO:0006310; P:GO:0010468; P:GO:0006260; P:GO:0009640; F:GO:0003677; F:GO:0016740; F:GO:0016787	-		IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR11752 (PANTHER), PTHR11752:SF3 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				IPR000242; G3DSA:3.90.190.10 (GENE3D), SignalP (SIGNALP)
Ailuropoda melanoleuca	tropomyosin 4	11	C:GO:0002102; F:GO:0008307; C:GO:0030863; P:GO:0006928; P:GO:0006979; P:GO:0006936; F:GO:0003779; C:GO:0005862; C:GO:0031941; F:GO:0005509; C:GO:0001725	-		IPR000533; PTHR19269 (PANTHER), PTHR19269:SF13 (PANTHER)
Homo sapiens	AF370418_1PP14214 [Homo sapiens]	12	C:GO:0016942; P:GO:0048662; P:GO:0001558; P:GO:0009968; F:GO:0046872; P:GO:0014912; F:GO:0031994; P:GO:0001933; P:GO:0045663; C:GO:0005634; F:GO:0008160; P:GO:0043065	-		-
Caenorhabditis briggsae	enoyl coenzyme a hydratase domain containing 3	3	P:GO:0008152; C:GO:0005739; F:GO:0003824	-		IPR001753; G3DSA:3.90.226.10 (GENE3D), PTHR11941 (PANTHER), SSF52096 (SUPERFAMILY)
Caenorhabditis briggsae	enoyl coenzyme a hydratase domain containing 3	3	P:GO:0008152; C:GO:0005739; F:GO:0003824	-		IPR001753; G3DSA:3.90.226.10 (GENE3D), PTHR11941 (PANTHER), SSF52096 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	P:GO:0009792; C:GO:0016021	-		IPR010761; SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	glycogen synthase ki-se 3	0		F:GO:0016740; F:GO:0004674; F:GO:0004672; P:GO:0006468; F:GO:0000166; F:GO:0005524; P:GO:0002119; F:GO:0016301; P:GO:0040010		IPR011009; G3DSA:1.10.510.10 (GENE3D)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)

	-	0				-
	-	0				-
Nematostella vectensis	predicted protein [Nematostella vectensis]	0		F:GO:0005488; P:GO:0007155		IPR000436; IPR016060; SignalP (SIGNALP)
Callithrix jacchus	heterogeneous nuclear ribonucleoprotein a2 b1	11	C:GO:0005737; C:GO:0005730; P:GO:0050658; C:GO:0030530; C:GO:0005654; C:GO:0005681; F:GO:0003723; F:GO:0005515; F:GO:0043047; P:GO:0000398; F:GO:0000166	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF13 (PANTHER), SSF54928 (SUPERFAMILY)
Mus musculus	multiple coagulation factor deficiency protein 2 homolog	0		F:GO:0003674; P:GO:0016192; F:GO:0005509; C:GO:0005783; P:GO:0019752; C:GO:0005794; C:GO:0005576; P:GO:0006810		IPR011992; IPR018247; IPR018249; PTHR23104 (PANTHER)
Mus musculus	multiple coagulation factor deficiency protein 2 homolog	0		F:GO:0003674; P:GO:0016192; F:GO:0005509; C:GO:0005783; P:GO:0019752; C:GO:0005794; C:GO:0005576; P:GO:0006810		-
	-	0				-
Caenorhabditis briggsae	mitochondrial glutamate	3	C:GO:0016020; P:GO:0008340; P:GO:0006810	-		IPR001993; PTHR11896:SF23 (PANTHER)
Heligmosomoides polygyrus	transforming growth protein 2-like protein	2	P:GO:0040007; F:GO:0008083	-		-
Caenorhabditis briggsae	Hypothetical protein CBG08397 [Caenorhabditis briggsae]	0				-
Ailuropoda melanoleuca	general transcription factor	6	P:GO:0045449; F:GO:0003702; F:GO:0005515; C:GO:0016021; C:GO:0005634; P:GO:0006366	-		IPR002715; PTHR10351 (PANTHER)
Ixodes scapularis	elegans protein partially confirmed by transcript evidence	0		F:GO:0003676; F:GO:0004528; F:GO:0046872; C:GO:0016021; P:GO:0008152; F:GO:0016787; F:GO:0003824		PTHR10151 (PANTHER), PTHR10151:SF28 (PANTHER)
	-	0				-
Pongo abelii	d--damage-inducible transcript 4	4	P:GO:0009968; P:GO:0006915; C:GO:0005737; P:GO:0001666	-		-

Caenorhabditis elegans	ribosomal protein l11	15	P:GO:0040010; P:GO:0006917; C:GO:0005730; P:GO:0006364; P:GO:0042273; F:GO:0019843; F:GO:0003735; P:GO:0040035; P:GO:0006414; P:GO:0006605; P:GO:0002119; F:GO:0005515; P:GO:0040039; P:GO:0009792; C:GO:0022625	-		-
Brugia malayi	elongator subunit iki3	0		F:GO:0005488		IPR006849
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR001534
Caenorhabditis briggsae	uroca-se domain containing 1	2	P:GO:0006548; F:GO:0016153	-	EC:4.2.1.49	IPR000193
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG11167 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	protein ki-se chk2	11	P:GO:0006468; P:GO:0006919; P:GO:0045132; P:GO:0008630; P:GO:0009792; F:GO:0004674; P:GO:0000077; P:GO:0007281; C:GO:0044446; F:GO:0005488; C:GO:0005634	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017442; IPR020636; IPR020648; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
Caenorhabditis elegans	exportin crm1 homolog	19	P:GO:0042176; P:GO:0009615; C:GO:0005654; F:GO:0005515; P:GO:0046825; P:GO:0040010; F:GO:0008565; P:GO:0040011; P:GO:0051301; C:GO:0005829; C:GO:0000776; C:GO:0005635; P:GO:0009792; P:GO:0002119; C:GO:0005642; P:GO:0010171; P:GO:0010824; P:GO:0034504; C:GO:0030529	-		IPR011989; IPR014877; IPR016024; PTHR11223 (PANTHER), PTHR11223:SF2 (PANTHER)
	-	0				SignalP (SIGNALP)

Brugia malayi	lethal family member (let-23)	0		F:GO:0016740; C:GO:0016020; F:GO:0004672; P:GO:0006468; F:GO:0000166; P:GO:0007169; F:GO:0005524; F:GO:0004714; F:GO:0016301; C:GO:0005578; F:GO:0004713; F:GO:0004872; F:GO:0005515		G3DSA:2.10.220.10 (GENE3D)
Caenorhabditis elegans	protein yipf3	3	C:GO:0016021; C:GO:0005794; C:GO:0030133	-		IPR006977; PTHR15627 (PANTHER), PTHR15627:SF9 (PANTHER)
	-	0				-
Caenorhabditis elegans	mtk1 mekk4 homolog family member (mtk-1)	2	P:GO:0009792; P:GO:0016246	-		-
Caenorhabditis briggsae	rho gtpase activating protein 5	11	F:GO:0005100; F:GO:0042169; C:GO:0005622; P:GO:0030879; P:GO:0002053; P:GO:0008361; P:GO:0019915; P:GO:0007155; P:GO:0030335; F:GO:0003924; P:GO:0007266	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Brugia malayi	n-alpha-acetyltransferase auxiliary subunit	0		P:GO:0048659; C:GO:0005737; F:GO:0005515		PTHR21373 (PANTHER)
Caenorhabditis briggsae	r- binding identical	5	F:GO:0003723; P:GO:0009792; C:GO:0005622; P:GO:0006378; F:GO:0000166	-		IPR000504; IPR012677; IPR015465; PTHR10432 (PANTHER), SSF54928 (SUPERFAMILY)
Loa loa	d- helicase	9	F:GO:0043140; P:GO:0006260; F:GO:0003676; F:GO:0005515; F:GO:0005524; C:GO:0005634; P:GO:0006310; F:GO:0009378; P:GO:0006281	-		IPR004589; G3DSA:3.40.50.300 (GENE3D), PTHR13710:SF12 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-

Caenorhabditis briggsae	Hypothetical protein CBG07097 [Caenorhabditis briggsae]	0		F:GO:0005096; P:GO:0051056; P:GO:0007165; C:GO:0005622		-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	7	F:GO:0003700; F:GO:0043565; F:GO:0005515; F:GO:0003707; C:GO:0005634; F:GO:0008270; P:GO:0006355	-		IPR001628; IPR013088; PR00350 (PRINTS), PTHR11865 (PANTHER), PTHR11865:SF158 (PANTHER), SSF57716 (SUPERFAMILY)
Loa loa	wd repeat-containing protein 36	3	F:GO:0003824; C:GO:0032991; C:GO:0044424	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR13889 (PANTHER), PTHR13889:SF2 (PANTHER)
Ancylostoma ceylanicum	glutamate-cysteine ligase modifier subunit	5	P:GO:0009987; P:GO:0055114; F:GO:0016874; F:GO:0016491; F:GO:0005515	-		IPR023210; PTHR13295 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR001534
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR001534; SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-ugt-21 protein	0		F:GO:0016740; F:GO:0030246; C:GO:0016021; F:GO:0003700; C:GO:0005634; F:GO:0016758; F:GO:0016757; P:GO:0005975; P:GO:0030259; P:GO:0006355; F:GO:0005515; P:GO:0008152; P:GO:0045449		IPR002213; PTHR11926:SF3 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	peptide chain release factor 1	0		F:GO:0003747; P:GO:0006412; C:GO:0005737; F:GO:0016787; F:GO:0016149; P:GO:0006415		IPR005139; PTHR11075 (PANTHER), PTHR11075:SF11 (PANTHER), SSF75620 (SUPERFAMILY)
Loa loa	e2f transcription factor 4	11	P:GO:0051726; P:GO:0006355; P:GO:0009887; F:GO:0003677; F:GO:0003700; F:GO:0019904; F:GO:0008134; P:GO:0000082; C:GO:0005635; C:GO:0005654; C:GO:0005737	-		IPR003316; IPR011991; IPR015633; PTHR12081:SF24 (PANTHER), SSF144074 (SUPERFAMILY), SSF46785 (SUPERFAMILY)

Loa loa	e2f transcription factor 4	13	P:GO:0000083; P:GO:0009887; F:GO:0003677; P:GO:0008361; F:GO:0003700; P:GO:0042127; F:GO:0019904; F:GO:0008134; P:GO:0042384; C:GO:0005654; P:GO:0008015; P:GO:0002064; P:GO:0006884	-		IPR003316; IPR011991; IPR015633; PTHR12081:SF24 (PANTHER), SSF144074 (SUPERFAMILY), SSF46785 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	3	P:GO:0019915; P:GO:0040018; P:GO:0040011	-		IPR000615; IPR021134
Brugia malayi	in family member (ttn-1)	1	P:GO:0009792	-		IPR007110; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF17 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	cell death abnormality family member (ced-7)	4	P:GO:0043652; C:GO:0005886; P:GO:0012501; F:GO:0017111	-	EC:3.6.1.15	-
	-	0				-
Caenorhabditis briggsae	family protein	3	P:GO:0000003; F:GO:0008121; P:GO:0040010	-	EC:1.10.2.2	SignalP (SIGNALP)
Caenorhabditis briggsae	alpha-adaptin	13	F:GO:0008565; P:GO:0040010; F:GO:0008022; P:GO:0000003; C:GO:0030139; C:GO:0030131; C:GO:0005905; P:GO:0040011; P:GO:0006898; P:GO:0006886; P:GO:0009792; P:GO:0048488; C:GO:0005886	-		IPR002553; IPR011989; IPR016024; PTHR22780 (PANTHER), PTHR22780:SF4 (PANTHER)
Caenorhabditis briggsae	dimethyladenosine transferase	5	C:GO:0005737; P:GO:0032259; P:GO:0000154; C:GO:0005634; F:GO:0000179	-		-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0046872; F:GO:0008270; P:GO:0019915		PTHR10634 (PANTHER), PTHR10634:SF1 (PANTHER)
Branchiostoma floridae	deubiquiti-ting enzyme 3-like	0		F:GO:0046872; F:GO:0016787; F:GO:0008234; F:GO:0008270; F:GO:0008233; F:GO:0004221; P:GO:0006511		IPR001394; PTHR10420 (PANTHER), PTHR10420:SF51 (PANTHER), SignalP (SIGNALP), SSF54001 (SUPERFAMILY)
	-	0				-
	-	0				-

	-	0				-
	-	0				-
	-	0				-
Brugia malayi	spry domain-containing socs box protein ssb-4	0				IPR001496; IPR001870; IPR003877; IPR008985; IPR019775; PTHR12245 (PANTHER)
Caenorhabditis elegans	hed family member (ptc-3)	30	P:GO:0060644; P:GO:0000003; P:GO:0008544; F:GO:0005113; P:GO:0010157; P:GO:0040015; P:GO:0009612; P:GO:0040018; P:GO:0032526; P:GO:0043616; P:GO:0040011; P:GO:0030326; P:GO:0014070; P:GO:0018996; P:GO:0060603; F:GO:0008201; P:GO:0016485; F:GO:0008158; P:GO:0001843; P:GO:0007165; P:GO:0002119; P:GO:0050680; P:GO:0042493; P:GO:0008589; P:GO:0035137; C:GO:0005887; P:GO:0021904;	-		IPR003392; PTHR10796 (PANTHER), PTHR10796:SF34 (PANTHER), SignalP (SIGNALP), SSF82866 (SUPERFAMILY)
Caenorhabditis briggsae	protein ki-se domain containing protein	4	P:GO:0009792; F:GO:0004672; P:GO:0040010; F:GO:0000166	-		IPR011009; PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
Caenorhabditis elegans	hypothetical protein F43D9.1 [Caenorhabditis elegans]	0		C:GO:0016020; F:GO:0008158		PTHR10796 (PANTHER), PTHR10796:SF13 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein F26F12.3 [Caenorhabditis elegans]	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-asp-6 protein	5	P:GO:0008219; P:GO:0006508; F:GO:0004190; F:GO:0005515; P:GO:0040011	-	EC:3.4.23.0	IPR001461; IPR001969; IPR009007; IPR021109; PTHR13683:SF53 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	yl59_caeel ame: full=uncharacterized protein	0				SignalP (SIGNALP)
Caenorhabditis elegans	periodic tryptophan protein 2 homolog	1	C:GO:0044464	-		IPR000408; IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; PTHR19858 (PANTHER)
Caenorhabditis elegans	hypothetical protein R04B3.3 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				SignalP (SIGNALP)

Homo sapiens	type alpha 1 (ehlers-danlos syndrome type autosomal domi-nt) isoform cra_b	22	P:GO:0009314; P:GO:0018149; P:GO:0030168; P:GO:0048565; P:GO:0043206; C:GO:0005586; P:GO:0007229; P:GO:0050777; P:GO:0007507; P:GO:0007160; C:GO:0005615; F:GO:0046332; P:GO:0001501; F:GO:0048407; P:GO:0043588; P:GO:0030199; F:GO:0005178; P:GO:0007179; P:GO:0034097; P:GO:0032964; F:GO:0005201; P:GO:0001568	-		IPR000885; PTHR10499 (PANTHER), PTHR10499:SF71 (PANTHER), PS51461 (PROFILE)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0003676; F:GO:0004523		G3DSA:3.30.420.10 (GENE3D), PTHR10642 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Necator americanus	venom-allergen-like protein family member (vap-1)	0		P:GO:0040011; C:GO:0005576		IPR001283; IPR002413; IPR013032; IPR014044; PTHR10334:SF11 (PANTHER), SignalP (SIGNALP)
Ancylostoma duodenale	ancylostoma-secreted protein 1 precursor	0		C:GO:0005576		IPR014044; SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0004500; P:GO:0009792; C:GO:0005576; P:GO:0006548		IPR005018
	-	0				-
	-	0				-
Caenorhabditis elegans	serine protease	0		F:GO:0004252; C:GO:0016020; F:GO:0008061; C:GO:0005576; F:GO:0003824; F:GO:0005044; F:GO:0008233; P:GO:0006508; P:GO:0006030; F:GO:0005488		IPR001190; IPR002172; PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER)
Caenorhabditis briggsae	bro1 domain-containing protein brox	0		C:GO:0016020		PTHR23032 (PANTHER)
Caenorhabditis elegans	mitochondrial solute carrier	6	C:GO:0005743; F:GO:0022857; C:GO:0005811; P:GO:0006839; F:GO:0005509; C:GO:0016021	-		IPR001993; IPR002048; IPR002067; IPR002113; IPR011992; IPR018108; IPR018247; IPR018249; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF74 (PANTHER), SSF47473 (SUPERFAMILY)

	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG11187 [Caenorhabditis briggsae]	2	F:GO:0004672; P:GO:0040010	-		SignalP (SIGNALP)
Caenorhabditis elegans	protein ki-se domain containing protein	7	P:GO:0006935; F:GO:0005524; F:GO:0004713; P:GO:0007155; F:GO:0005515; P:GO:0007165; P:GO:0046777	-	EC:2.7.10.0	IPR000719; IPR001245; IPR008266; IPR011009; IPR020685; IPR020764; G3DSA:1.10.510.10 (GENE3D)
Caenorhabditis elegans	uncoordi-ted family member (unc-44)	2	C:GO:0016020; F:GO:0005515	-		-
Loa loa	uncoordi-ted family member (unc-44)	2	F:GO:0005515; P:GO:0007165	-		IPR002110; IPR018120; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER), PTHR18958:SF296 (PANTHER)
Haemonchus contortus	heat shock protein family member (hsp-)	0		P:GO:0006950; P:GO:0009408		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Homo sapiens	sbf1 protein	4	P:GO:0007283; P:GO:0016311; F:GO:0016791; C:GO:0044464	-	EC:3.1.3.0	IPR017906; PTHR10807 (PANTHER), PTHR10807:SF4 (PANTHER), SSF52799 (SUPERFAMILY)
Homo sapiens	mhc class ii antigen	9	C:GO:0005789; C:GO:0005887; C:GO:0042613; C:GO:0005794; P:GO:0002504; C:GO:0031902; C:GO:0005765; F:GO:0032395; P:GO:0006955	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	uncoordi-ted family member (unc-103)	0		F:GO:0005249; C:GO:0016021; C:GO:0016020; P:GO:0006813; P:GO:0055085; P:GO:0006811; F:GO:0005216; P:GO:0006810		-
Brugia malayi	clathrin-associated protein	7	P:GO:0016183; C:GO:0008021; P:GO:0007269; C:GO:0030122; F:GO:0005515; P:GO:0006886; P:GO:0033227	-		IPR011012; IPR015629; IPR022775; G3DSA:3.30.450.60 (GENE3D), PTHR11998 (PANTHER)

synthetic construct	proteasome (macropain) beta 3	9	P:GO:0051436; P:GO:0051437; F:GO:0004298; P:GO:0031145; F:GO:0005515; P:GO:0044419; C:GO:0005737; C:GO:0005839; C:GO:0005634	-	EC:3.4.25.0	IPR001353; G3DSA:3.60.20.10 (GENE3D), PTHR11599 (PANTHER), PTHR11599:SF7 (PANTHER), PS51476 (PROFILE), SSF56235 (SUPERFAMILY)
Loa loa	splicing factor u2af 26 kda subunit	14	F:GO:0003723; C:GO:0015030; C:GO:0005681; F:GO:0008270; P:GO:0040007; F:GO:0050733; C:GO:0016607; P:GO:0040035; P:GO:0018996; P:GO:0002119; F:GO:0000166; P:GO:0040011; P:GO:0000398; P:GO:0009792	-		IPR022272
Loa loa	splicing factor u2af 26 kda subunit	14	F:GO:0003723; C:GO:0015030; C:GO:0005681; F:GO:0008270; P:GO:0040007; F:GO:0050733; C:GO:0016607; P:GO:0040035; P:GO:0018996; P:GO:0002119; F:GO:0000166; P:GO:0040011; P:GO:0000398; P:GO:0009792	-		IPR000504; IPR000571; IPR009145; IPR012677; SSF54928 (SUPERFAMILY), SSF90229 (SUPERFAMILY)
Loa loa	splicing factor u2af 26 kda subunit	14	F:GO:0003723; C:GO:0015030; C:GO:0005681; F:GO:0008270; P:GO:0040007; F:GO:0050733; C:GO:0016607; P:GO:0040035; P:GO:0018996; P:GO:0002119; F:GO:0000166; P:GO:0040011; P:GO:0000398; P:GO:0009792	-		IPR022272
Homo sapiens	gamma-inducible protein 30	7	F:GO:0016491; P:GO:0019886; C:GO:0005764; P:GO:0048147; P:GO:0055114; P:GO:0050821; C:GO:0005576	-		IPR004911; PTHR13234:SF7 (PANTHER)

Trichoplax adhaerens	d- polymerase partial	0		F:GO:0004385; P:GO:0007005; P:GO:0000003; P:GO:0006264; C:GO:0005913; F:GO:0003677; C:GO:0005912; F:GO:0003676; P:GO:0006261; P:GO:0006260; P:GO:0016337; P:GO:0008340; F:GO:0008296; P:GO:0008406; P:GO:0035147; C:GO:0005739; F:GO:0003887; P:GO:0046328; P:GO:0007163; C:GO:0005760; P:GO:0035156; P:GO:0030421; P:GO:0007391; F:GO:0005515; P:GO:0007254; P:GO:0007562		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Xenopus laevis	d-se domain containing 3 variant 5	1	C:GO:0005739	-		IPR001130; IPR015992; G3DSA:3.20.20.140 (GENE3D), SSF51556 (SUPERFAMILY)
Macaca mulatta	cd82 molecule	0		C:GO:0005887; F:GO:0005515; C:GO:0005886		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-mup-4 protein	1	F:GO:0005515	-		-

Brugia malayi	structural mainte-nce of chromosomes 1a	17	P:GO:0000075; P:GO:0007052; P:GO:0042770; C:GO:0005737; F:GO:0046982; F:GO:0003777; C:GO:0000776; P:GO:0008380; P:GO:0007126; C:GO:0008280; C:GO:0000794; P:GO:0007064; P:GO:0009314; F:GO:0003682; P:GO:0032876; F:GO:0005524; P:GO:0006281	-		IPR010935; PTHR18937 (PANTHER), PTHR18937:SF12 (PANTHER)
Tetrahymena thermophila	lim domain containing protein	0		F:GO:0046872; F:GO:0008270; C:GO:0005575		IPR001781; PTHR18973 (PANTHER), PTHR18973:SF49 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; C:GO:0016020; F:GO:0016772		PTHR13205 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Cooperia oncophora	latrophilin-like protein 2	6	P:GO:0007218; C:GO:0016021; P:GO:0007165; C:GO:0005886; F:GO:0005529; F:GO:0004930	-		-
	-	0				-
Caenorhabditis briggsae	uncoordi-ted family member (unc-52)	2	P:GO:0030239; C:GO:0005578	-		IPR003599; IPR007110; IPR013783; SSF48726 (SUPERFAMILY)
Brugia malayi	tumor protein p53 binding protein 1	7	F:GO:0005488; C:GO:0044427; P:GO:0040007; P:GO:0040035; P:GO:0019915; P:GO:0002119; P:GO:0002009	-		IPR001357; G3DSA:3.40.50.10190 (GENE3D), PTHR15321 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG16818 [Caenorhabditis briggsae]	0				PTHR15180 (PANTHER)
	-	0				-
Loa loa	hypothetical protein LOAG_05263 [Loa loa]	0				-
	-	0				-
	-	0				-
Brugia malayi	proteasome (macropain) activator subunit 4	0		P:GO:0030154; F:GO:0005488; C:GO:0000502; C:GO:0016607; P:GO:0007275; P:GO:0007283; C:GO:0005634		-

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0006629; P:GO:0008152; F:GO:0016787; P:GO:0016042; F:GO:0005215; P:GO:0006810; C:GO:0030288		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	P:GO:0000003	-		SignalP (SIGNALP)
	-	0				-
	-	0				IPR005018
	-	0				-
Caenorhabditis briggsae	probable complex i intermediate-associated protein	0		F:GO:0003676; C:GO:0005739; F:GO:0000166		PTHR13194 (PANTHER), PTHR13194:SF8 (PANTHER)
	-	0				-
Caenorhabditis elegans	hypothetical protein B0207.7 [Caenorhabditis elegans]	0		F:GO:0004672; F:GO:0005524; F:GO:0000166; P:GO:0006468; F:GO:0004674		G3DSA:3.30.200.20 (GENE3D)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	e3 ubiquitin protein ligase	0		F:GO:0016874; F:GO:0008270		-
Brugia malayi	plasmid mainte-nce protein containing protein	1	C:GO:0016020	-		IPR005599
	-	0				-
	-	0				-
Caenorhabditis elegans	phe-zine biosynthesis-like protein domain containing	1	F:GO:0003824	-		IPR003719; G3DSA:3.10.310.10 (GENE3D), SSF54506 (SUPERFAMILY)
Caenorhabditis briggsae	domain iii family protein	5	P:GO:0000712; P:GO:0000239; F:GO:0003677; F:GO:0005515; C:GO:0005634	-		IPR000432; IPR007696; G3DSA:3.40.50.300 (GENE3D), PTHR11361:SF18 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein F12F6.1 [Caenorhabditis elegans]	0				-
	-	0				-
Homo sapiens	d-loop d- fusion protein	0				-

Homo sapiens	fibronectin 1	18	P:GO:0042060; P:GO:0018149; P:GO:0016477; P:GO:0001525; P:GO:0008360; C:GO:0005793; C:GO:0005604; P:GO:0007044; P:GO:0007160; C:GO:0031093; P:GO:0034446; F:GO:0005518; C:GO:0005577; C:GO:0016324; F:GO:0008201; F:GO:0005201; F:GO:0016504; P:GO:0006953	-		IPR000083; IPR016060; PTHR19143 (PANTHER), PTHR19143:SF6 (PANTHER), SSF57603 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	hypothetical protein Y34D9A.8 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	briggsae cbr-hmr-1 protein	15	C:GO:0005911; P:GO:0016339; F:GO:0005515; P:GO:0007412; F:GO:0005509; C:GO:0016021; P:GO:0050774; P:GO:0007156; P:GO:0048676; P:GO:0007413; P:GO:0031290; P:GO:0045467; P:GO:0016318; P:GO:0045463; P:GO:0048841	-		IPR002126; IPR020894; PTHR10596 (PANTHER), PTHR10596:SF114 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				SSF141739 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-nhr-76 protein	1	F:GO:0005515	-		IPR008946
	-	0				-
	-	0				SignalP (SIGNALP)
Angiostrongylus cantonensis	fatty acid-binding protein homolog	1	F:GO:0005515	-		IPR000463; IPR011038; IPR012674; PTHR22725 (PANTHER), SignalP (SIGNALP)
Angiostrongylus cantonensis	fatty acid-binding protein homolog	4	P:GO:0006810; F:GO:0005515; F:GO:0008289; F:GO:0005215	-		-
Caenorhabditis elegans	sig-l recognition particle 72 kda protein	2	F:GO:0005488; C:GO:0048500	-		IPR008940; PTHR14094 (PANTHER), PTHR14094:SF9 (PANTHER), SSF48452 (SUPERFAMILY)
	-	0				-
	-	0				IPR015848
	-	0				-

Caenorhabditis elegans	protein ki-se domain containing protein	5	P:GO:0044260; F:GO:0005488; F:GO:0004672; P:GO:0019915; P:GO:0044238	-		IPR011009; G3DSA:3.30.200.20 (GENE3D)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-hex-2 protein	0		F:GO:0004553; F:GO:0016787; P:GO:0005975; F:GO:0003824; F:GO:0043169		-
	-	0				-
	-	0				IPR000463; IPR011038; IPR012674
	-	0				-
Caenorhabditis briggsae	3-hydroxyacyl-coa dehyroge-se	14	C:GO:0005875; P:GO:0055114; P:GO:0040007; C:GO:0016507; P:GO:0019915; F:GO:0003857; P:GO:0002119; P:GO:0006635; F:GO:0050662; P:GO:0006898; F:GO:0016509; P:GO:0009792; C:GO:0005811; F:GO:0004300	-	EC:1.1.1.35; EC:1.1.1.211; EC:4.2.1.17	IPR001753; G3DSA:3.90.226.10 (GENE3D), PTHR11941 (PANTHER), SignalP (SIGNALP), SSF52096 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				IPR016186; IPR016187; PTHR22802 (PANTHER), PTHR22802:SF15 (PANTHER)
Caenorhabditis elegans	kelch-repeat containing protein family member (kel-3)	1	F:GO:0005515	-		IPR006652; IPR013089; IPR015915; PR00501 (PRINTS), PTHR23230:SF164 (PANTHER), SSF117281 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	gex interacting protein family member (gei-4)	1	F:GO:0005515	-		SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-sax-2 protein	1	F:GO:0005515	-		PTHR12295 (PANTHER), PTHR12295:SF6 (PANTHER)
Caenorhabditis elegans	dead deah box helicase family protein	2	F:GO:0004386; F:GO:0003676	-		IPR001650; IPR011545; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR11752 (PANTHER), PTHR11752:SF2 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-

Loa loa	cell division protein ki-se 7	20	P:GO:0009299; P:GO:0006367; P:GO:0000718; P:GO:0006468; F:GO:0008094; F:GO:0008022; F:GO:0004693; C:GO:0005624; C:GO:0005829; C:GO:0005675; P:GO:0009792; P:GO:0006368; C:GO:0005856; P:GO:0045448; P:GO:0045944; F:GO:0008353; F:GO:0032403; C:GO:0000307; F:GO:0005524; C:GO:0005739	-	EC:2.7.11.22; EC:2.7.11.23	-
Caenorhabditis elegans	polyketide synthase	3	P:GO:0008152; F:GO:0003824; F:GO:0048037	-		G3DSA:3.40.50.1820 (GENE3D)
Brugia malayi	protein-tyrosine phosphatase containing protein	1	F:GO:0004721	-	EC:3.1.3.16	IPR000242; IPR000387; IPR003595; IPR016130; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	uncoordi-ted protein isoform partially confirmed by transcript evidence	8	F:GO:0004872; P:GO:0006629; F:GO:0005219; P:GO:0006816; P:GO:0006874; P:GO:0055085; F:GO:0005509; C:GO:0016021	-		-
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	d- excision repair protein ercc-6	0		F:GO:0003676; F:GO:0004386; F:GO:0005524; F:GO:0003677		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Loa loa	hypothetical protein LOAG_09252 [Loa loa]	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-elt-3 protein	4	F:GO:0003700; F:GO:0043565; F:GO:0008270; P:GO:0006355	-		IPR000679; IPR013088; PTHR10071 (PANTHER), PTHR10071:SF15 (PANTHER), SSF57716 (SUPERFAMILY)

Bombyx mori	elegans protein partially confirmed by transcript evidence	0		F:GO:0005201; F:GO:0048407; F:GO:0005488; C:GO:0016021; C:GO:0005581; F:GO:0042302; F:GO:0005515; C:GO:0005587		-
Caenorhabditis briggsae	multiple coagulation factor deficiency isoform cra_b	1	P:GO:0009792	-		-
Loa loa	bromodomain containing protein	3	F:GO:0008270; F:GO:0003676; F:GO:0005515	-		IPR001878; PTHR13900 (PANTHER)
Caenorhabditis elegans	not-like (yeast ccr4 not complex component) family member (ntl-2)	13	F:GO:0030528; P:GO:0040010; P:GO:0008340; P:GO:0045449; F:GO:0042802; P:GO:0040035; P:GO:0019915; P:GO:0002119; P:GO:0040011; P:GO:0006898; P:GO:0002009; P:GO:0009792; P:GO:0040018	-		IPR007282; PTHR23326 (PANTHER)
Trichoplax adhaerens	long-chain-fatty-acid-- ligase	2	F:GO:0016877; P:GO:0008152	-		IPR000873; G3DSA:2.30.38.10 (GENE3D), G3DSA:3.30.300.30 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF44 (PANTHER), SSF56801 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-srb-17 protein	0		F:GO:0004888; C:GO:0016021; P:GO:0007606		IPR019408; SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG12496 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	prolyl oligopeptidase family protein	0		P:GO:0006508; F:GO:0004252; C:GO:0005737; F:GO:0008236; F:GO:0016787		G3DSA:3.40.50.1820 (GENE3D), PTHR11731 (PANTHER), PTHR11731:SF7 (PANTHER), SSF53474 (SUPERFAMILY)
Brugia malayi	nedd4 binding protein 2-like 1	0		F:GO:0005524; F:GO:0003674; P:GO:0001906; P:GO:0008150; C:GO:0005575		G3DSA:3.40.50.300 (GENE3D), PTHR13308 (PANTHER)
Macaca mulatta	pyrophosphatase 1	4	F:GO:0004427; P:GO:0071344; C:GO:0005737; F:GO:0000287	-	EC:3.6.1.1	IPR008162
	-	0				-
Caenorhabditis briggsae	peptidylprolyl isomerase	2	P:GO:0019915; P:GO:0009792	-		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
	-	0				-
	-	0				-

	-	0				-
Caenorhabditis briggsae	udp- ransferase family member (ugt-26)	0		P:GO:0030259; F:GO:0030246; P:GO:0005975; C:GO:0016021; F:GO:0016758		IPR002213; PTHR11926:SF3 (PANTHER)
	-	0				-
Brugia malayi	galactoki-se 2	2	P:GO:0008152; F:GO:0016772	-		IPR006203; IPR006204; IPR014721; IPR020568; PTHR10457 (PANTHER), PTHR10457:SF7 (PANTHER)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	5	P:GO:0006633; F:GO:0016717; F:GO:0005515; F:GO:0020037; P:GO:0055114	-	EC:1.14.19.0	IPR005804; PTHR19353 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	zinc finger protein 296-like	1	F:GO:0005515	-		IPR000504; IPR007087; IPR012677; IPR015880; PTHR10432 (PANTHER), PTHR10432:SF56 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	fyve finger-containing phosphoinositide ki-se	12	P:GO:0042147; C:GO:0031901; P:GO:0046488; P:GO:0044267; F:GO:0008270; P:GO:0034504; C:GO:0031982; F:GO:0016308; F:GO:0005524; F:GO:0005515; C:GO:0045121; P:GO:0006898	-	EC:2.7.1.68	IPR002498; G3DSA:3.30.810.10 (GENE3D), SSF56104 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-tag-168 protein	3	P:GO:0001539; F:GO:0003774; C:GO:0009288	-		IPR001452; IPR011511; G3DSA:2.30.30.40 (GENE3D), PTHR14234 (PANTHER), PTHR14234:SF1 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG01705 [Caenorhabditis briggsae]	0		F:GO:0008324; P:GO:0006812		-
Caenorhabditis elegans	transmembrane protein 39b	5	P:GO:0019915; P:GO:0040018; P:GO:0040017; P:GO:0010171; P:GO:0040010	-		IPR019397; PTHR12995 (PANTHER)
Caenorhabditis elegans	transmembrane protein 39b	5	P:GO:0019915; P:GO:0040018; P:GO:0040017; P:GO:0010171; P:GO:0040010	-		IPR019397; PTHR12995 (PANTHER)

Loa loa	nedd4 binding protein 2	0		P:GO:0009214; C:GO:0016020; F:GO:0004113; F:GO:0046404; P:GO:0016070; F:GO:0005524; F:GO:0003824; C:GO:0005575; C:GO:0005622; F:GO:0005515; F:GO:0004519; P:GO:0040010; P:GO:0001906		IPR010488; G3DSA:3.40.50.300 (GENE3D), PTHR13308 (PANTHER), PTHR13308:SF4 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	alcohol dehydroge-se	3	F:GO:0008270; P:GO:0055114; F:GO:0003939	-	EC:1.1.1.14	IPR002085; IPR013149; IPR016040; PTHR11695:SF38 (PANTHER), SignalP (SIGNALP), SSF51735 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	5	P:GO:0006548; P:GO:0016052; F:GO:0030246; F:GO:0004500; C:GO:0016021	-	EC:1.14.17.1	IPR000082
	-	0				-
	-	0				-
	-	0				-
Ailuropoda melanoleuca	lipolysis stimulated lipoprotein receptor	14	P:GO:0019216; C:GO:0034362; C:GO:0042627; F:GO:0030228; P:GO:0042953; C:GO:0005730; C:GO:0016021; P:GO:0001889; F:GO:0030169; P:GO:0007165; C:GO:0034361; C:GO:0005794; C:GO:0005886; P:GO:0009790	-		-
Caenorhabditis elegans	rnp-1 like r--binding protein	4	C:GO:0005622; P:GO:0009792; F:GO:0000166; F:GO:0003723	-		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0004563; P:GO:0005975		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0004563; P:GO:0005975		-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	protein disulfide	1	C:GO:0005622	-		IPR012335; IPR012336; IPR013766; PTHR18929 (PANTHER)
Tribolium castaneum	ubx6 -related	0		F:GO:0008270; C:GO:0005622		IPR000449; IPR009060; IPR015940; G3DSA:1.10.8.10 (GENE3D), PTHR13020 (PANTHER), PTHR13020:SF4 (PANTHER)
Caenorhabditis briggsae	amop domain containing protein	2	C:GO:0016021; P:GO:0007160	-		IPR005533; PTHR13802 (PANTHER), PTHR13802:SF2 (PANTHER)

	-	0				-
Caenorhabditis briggsae	lactation elevated 1	1	F:GO:0000166	-		IPR005654; G3DSA:3.40.50.300 (GENE3D)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG20463 [Caenorhabditis briggsae]	0				-
Homo sapiens	activating transcription factor 4 (tax-responsive enhancer element b67)	14	P:GO:0034976; P:GO:0045944; P:GO:0007214; C:GO:0005667; F:GO:0008022; C:GO:0032590; P:GO:0006520; F:GO:0043565; F:GO:0016563; F:GO:0046983; F:GO:0003700; P:GO:0006094; F:GO:0003704; C:GO:0005737	-		PTHR13044 (PANTHER), PTHR13044:SF2 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-rde-1 protein	0		P:GO:0055046; P:GO:0009561; P:GO:0033169; C:GO:0005739; F:GO:0003676; P:GO:0007143; C:GO:0005737; P:GO:0007140; C:GO:0005731; C:GO:0005730; F:GO:0035197		G3DSA:2.170.260.10 (GENE3D), PTHR22891 (PANTHER), SSF101690 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein H41C03.1 [Caenorhabditis elegans]	1	P:GO:0040010	-		PTHR23324 (PANTHER), PTHR23324:SF3 (PANTHER)
	-	0				-
Caenorhabditis elegans	protein ki-se domain containing protein	6	P:GO:0006468; F:GO:0005515; F:GO:0004713; F:GO:0005524; P:GO:0000003; F:GO:0004674	-	EC:2.7.10.0; EC:2.7.11.0	IPR000719; IPR001245; IPR008266; IPR011009; IPR018271; IPR020685; IPR020764; G3DSA:1.10.510.10 (GENE3D)
	-	0				-
	-	0				-
	-	0				-
Equus caballus	alpha-2-glycoprotein zinc-binding	0				-
Caenorhabditis elegans	zinc finger protein	2	F:GO:0008270; F:GO:0005515	-		IPR004457; PTHR10876 (PANTHER)
Homo sapiens	transcription factor-like 1	7	P:GO:0016568; C:GO:0043234; F:GO:0003677; P:GO:0000122; F:GO:0003700; C:GO:0005634; F:GO:0003702	-		-
	-	0				-

Caenorhabditis briggsae	zinc finger rad18 domain-containing protein c1orf124 homolog	6	P:GO:0002119; F:GO:0003677; C:GO:0016607; P:GO:0000003; P:GO:0040007; P:GO:0006281	-		IPR006640; PTHR21220 (PANTHER)
Caenorhabditis elegans	interferon gamma-inducible thiol reductase	0		C:GO:0005576		IPR004911; PTHR13234:SF2 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	2-amino-3-ketobutyrate coenzyme a mitochondrial	7	F:GO:0016874; F:GO:0030170; P:GO:0009058; F:GO:0016769; P:GO:0006520; F:GO:0008890; C:GO:0005739	-	EC:2.3.1.29	IPR004839; IPR011282; IPR015421; IPR015424; PTHR13693 (PANTHER)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG22805 [Caenorhabditis briggsae]	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	zinc finger protein 136	12	P:GO:0040032; C:GO:0031430; F:GO:0008270; P:GO:0007517; P:GO:0045449; P:GO:0030239; P:GO:0007626; F:GO:0003677; P:GO:0040011; F:GO:0017022; C:GO:0032982; C:GO:0005634	-		IPR007087; IPR013087; IPR015880; PTHR23224 (PANTHER), PTHR23224:SF184 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis briggsae	amop domain containing protein	1	P:GO:0007160	-		PTHR13802 (PANTHER), PTHR13802:SF2 (PANTHER)
Caenorhabditis elegans	ctd (carboxy-termi-l r- polymerase polypeptide a) small phosphatase like 2	2	P:GO:0016311; F:GO:0004721	-	EC:3.1.3.16	-
Caenorhabditis elegans	peroxisomal acyl-coenzyme a oxidase 3	8	F:GO:0003995; C:GO:0005739; P:GO:0033540; P:GO:0055114; F:GO:0050660; C:GO:0005782; F:GO:0016402; F:GO:0005504	-	EC:1.3.99.3	IPR006091; IPR009100; IPR012258; PTHR10909 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	5	F:GO:0030170; F:GO:0004124; F:GO:0005515; P:GO:0006535; F:GO:0016740	-	EC:2.5.1.47	IPR001926; G3DSA:3.40.50.1100 (GENE3D), PTHR10314 (PANTHER), PTHR10314:SF8 (PANTHER)

Plesiocystis pacifica SIR-1	b-box zinc finger	0		P:GO:0051301; C:GO:0005634; P:GO:0006464; P:GO:0009590; P:GO:0046907; P:GO:0007049; F:GO:0016905; P:GO:0042254; C:GO:0005737; F:GO:0005488; P:GO:0006364; C:GO:0020011; P:GO:0007059; P:GO:0045449; F:GO:0043565; F:GO:0016881; F:GO:0008270; C:GO:0005622; F:GO:0016740; C:GO:0005576		PTHR11071 (PANTHER), PTHR11071:SF54 (PANTHER)
Taeniopygia guttata	retrotransposon-like 1	0		C:GO:0016020; P:GO:0046907; P:GO:0006412; F:GO:0005524; P:GO:0007275; C:GO:0005575; F:GO:0004812; P:GO:0008150; C:GO:0020011		PTHR11071 (PANTHER), PTHR11071:SF54 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Brugia malayi	d-3-phosphoglycerate dehydroge-se	4	P:GO:0044238; F:GO:0016616; F:GO:0051287; F:GO:0016787	-	EC:1.1.1.0	-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				SSF57501 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-gon-1 protein	3	F:GO:0046872; F:GO:0008237; C:GO:0031012	-		IPR000884; G3DSA:2.20.100.10 (GENE3D), PTHR13723 (PANTHER), PTHR13723:SF30 (PANTHER)
Caenorhabditis elegans	clc-type chloride channel family member (clh-2)	6	P:GO:0009792; F:GO:0005247; P:GO:0055085; P:GO:0000003; C:GO:0016021; P:GO:0006821	-		IPR001807; PTHR11689:SF5 (PANTHER)
Caenorhabditis elegans	zo-1 (zonula occludens tight junctio-l protein) ortholog family member (zoo-1)	0				-
Loa loa	pou domain protein isoform b	5	F:GO:0030528; F:GO:0003700; F:GO:0043565; C:GO:0005634; P:GO:0006355	-		-
Caenorhabditis elegans	hypothetical protein W05F2.4 [Caenorhabditis elegans]	3	P:GO:0040018; P:GO:0040035; P:GO:0002119	-		-

Caenorhabditis elegans	transmembrane protein 48	6	P:GO:0006810; C:GO:0016021; P:GO:0000003; P:GO:0006997; C:GO:0005635; P:GO:0009792	-		IPR019049; PTHR13269 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Loa loa	breast cancer anti-estrogen resistance 3	4	P:GO:0006468; F:GO:0005515; F:GO:0004713; F:GO:0005524	-	EC:2.7.10.0	IPR000980; PTHR14247 (PANTHER), PTHR14247:SF3 (PANTHER), SSF55550 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-kin-32 protein	9	F:GO:0004674; C:GO:0005856; F:GO:0004871; F:GO:0005524; F:GO:0004713; C:GO:0005925; F:GO:0005515; P:GO:0007172; P:GO:0006468	-	EC:2.7.11.0; EC:2.7.10.0	-
	-	0				-
	-	0				-
Caenorhabditis briggsae	threonine dehydratase deami-se	4	F:GO:0004794; P:GO:0008152; F:GO:0030170; F:GO:0016597	-	EC:4.3.1.19	-
	-	0				-
Caenorhabditis elegans	hypothetical protein Y110A7A.21 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-nol-1 protein	8	P:GO:0040010; P:GO:0008340; P:GO:0000003; P:GO:0002119; P:GO:0040039; P:GO:0009792; P:GO:0040015; P:GO:0040019	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-ech-9 protein	3	P:GO:0006631; F:GO:0016491; F:GO:0050662	-		-
	-	0				PD035033 (PRODOM)
Caenorhabditis elegans	hypothetical protein Y20F4.2 [Caenorhabditis elegans]	0				PTHR13589 (PANTHER), PTHR13589:SF2 (PANTHER)
Homo sapiens	ubx domain-containing protein 1	0		P:GO:0031397; P:GO:0032435; F:GO:0051117; C:GO:0005737; P:GO:0043161; C:GO:0000502; C:GO:0005575; F:GO:0005515; F:GO:0031593; P:GO:0008150		SignalP (SIGNALP)
	-	0				-
	-	0				-

Caenorhabditis briggsae	nuclear hormone receptor family protein isoform confirmed by transcript evidence	4	F:GO:0046872; F:GO:0004879; F:GO:0003677; P:GO:0045449	-		IPR000536; IPR008946
	-	0				SignalP (SIGNALP)
Pongo abelii	cytoskeleton associated protein 1	6	P:GO:0030154; F:GO:0005515; P:GO:0007399; P:GO:0007023; C:GO:0005829; C:GO:0005874	-		IPR000938; PTHR18916 (PANTHER), PTHR18916:SF6 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	2	C:GO:0016021; P:GO:0006810	-		-
	-	0				-
	-	0				-
	-	0				-
Loa loa	calcium alpha subunit family member (cca-1)	7	P:GO:0051899; P:GO:0045760; P:GO:0043051; P:GO:0006816; P:GO:0055085; C:GO:0005891; F:GO:0008332	-		IPR005445; IPR005821; PTHR10037 (PANTHER), SignalP (SIGNALP), SSF81324 (SUPERFAMILY)
Ciona intestinalis	tpa: extracellular serine-rich (afu_orthologue afua_3g07870)	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	ync9_caeel ame: full=uncharacterized protein flags: precursor	0				-
Bos taurus	ribosomal protein l9	6	C:GO:0005730; C:GO:0005840; F:GO:0003735; C:GO:0005829; F:GO:0019843; P:GO:0006414	-		IPR000702; IPR002359; IPR020040; PTHR11655:SF2 (PANTHER)

Nematostella vectensis	leishmanolysin-like peptidase	0		P:GO:0051301; P:GO:0051225; P:GO:0007420; P:GO:0007067; F:GO:0016787; P:GO:0045842; F:GO:0046872; F:GO:0008237; P:GO:0007155; C:GO:0016020; P:GO:0007049; P:GO:0051298; F:GO:0008233; P:GO:0008406; P:GO:0007076; F:GO:0004222; P:GO:0006338; P:GO:0008354; P:GO:0006508; C:GO:0005737; P:GO:0007444; P:GO:0007100; F:GO:0008270; P:GO:0007052; C:GO:0031252		IPR001577; SSF55486 (SUPERFAMILY)
Caenorhabditis briggsae	oxidized-ldl responsive gene 2	2	P:GO:0006508; F:GO:0004197	-	EC:3.4.22.0	IPR000169; IPR000668; IPR013128; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF15 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis elegans	4-aminobutyrate aminotransferase	3	C:GO:0005759; P:GO:0006520; F:GO:0008483	-	EC:2.6.1.0	IPR004631; IPR005814; IPR015422; IPR015424
Caenorhabditis elegans	4-aminobutyrate aminotransferase	5	F:GO:0030170; C:GO:0005759; P:GO:0006520; F:GO:0003867; P:GO:0009448	-	EC:2.6.1.19	IPR004631; IPR005814; IPR015421; IPR015422; IPR015424
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Solanum demissum	endonuclease-reverse transcriptase	0		F:GO:0003723; F:GO:0008168; F:GO:0016740; P:GO:0006278; F:GO:0004519; F:GO:0003677; F:GO:0003964		-
Solanum demissum	endonuclease-reverse transcriptase	0		F:GO:0003723; F:GO:0008168; F:GO:0016740; P:GO:0006278; F:GO:0004519; F:GO:0003677; F:GO:0003964		-
	-	0				-

Caenorhabditis elegans	variable abnormal morphology family member (vab-10)	0		F:GO:0005509; P:GO:0007050; F:GO:0003779		-
	-	0				-
						IPR003598; IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	udp- ransferase family member (ugt-26)	2	P:GO:0008152; F:GO:0016740	-		IPR002213; PTHR11926:SF3 (PANTHER)
Loa loa	dead (asp-glu-ala-asp) box polypeptide 58	3	P:GO:0050896; F:GO:0005488; P:GO:0050789	-		IPR001650; IPR011545; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR14074 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
	-	0				IPR001757; G3DSA:3.40.50.1000 (GENE3D), PTHR11939:SF14 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	9	P:GO:0040010; F:GO:0046872; P:GO:0045449; F:GO:0003677; F:GO:0004879; P:GO:0002119; F:GO:0005515; P:GO:0009792; P:GO:0040018	-		IPR000536; IPR001628; IPR001723; IPR008946; IPR013088; PR00350 (PRINTS), PTHR11865 (PANTHER), PTHR11865:SF238 (PANTHER), SSF57716 (SUPERFAMILY)
	-	0				IPR000283
	-	0				-
Caenorhabditis elegans	scy1 protein ki-se	3	P:GO:0006468; F:GO:0005524; F:GO:0004672	-		-
Loa loa	tr- selenocysteine 1-associated protein 1	3	P:GO:0001514; F:GO:0005515; C:GO:0005634	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF68 (PANTHER), SSF54928 (SUPERFAMILY)

Ailuropoda melanoleuca	-+ k+ alpha 1 polypeptide	20	F:GO:0005515; P:GO:0045989; P:GO:0045822; F:GO:0003869; C:GO:0005792; C:GO:0016323; C:GO:0042470; F:GO:0046872; P:GO:0006754; C:GO:0042383; F:GO:0005391; P:GO:0045823; P:GO:0042493; P:GO:0031947; C:GO:0005890; P:GO:0006813; P:GO:0002026; F:GO:0005524; P:GO:0008217; P:GO:0006814	-	EC:3.1.3.41; EC:3.6.3.9	IPR001757; PTHR11939:SF100 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis brenneri	guanosine monophosphate reductase 2	7	P:GO:0009117; F:GO:0046872; P:GO:0009792; P:GO:0055114; F:GO:0003920; P:GO:0040007; P:GO:0002119	-	EC:1.7.1.7	IPR001093; IPR013785; PTHR11911 (PANTHER), PTHR11911:SF7 (PANTHER), SSF51412 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	briggsae cbr-tag-68 protein	5	F:GO:0003700; F:GO:0005515; C:GO:0005667; P:GO:0006355; P:GO:0007179	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	dicer ribonuclease type iii	9	P:GO:0009653; C:GO:0043005; P:GO:0016246; F:GO:0005515; P:GO:0007275; C:GO:0005737; F:GO:0004519; F:GO:0003723; P:GO:0035196	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	immunoglobulin i-set domain containing protein	6	C:GO:0005887; F:GO:0005114; F:GO:0034713; P:GO:0030511; P:GO:0040018; P:GO:0000003	-		-
	-	0				-
Caenorhabditis elegans	briggsae cbr-ttr-54 protein	0				IPR001534

Loa loa	heat shock transcription factor 1	5	F:GO:0003700; F:GO:0043565; C:GO:0005634; P:GO:0009408; P:GO:0006355	-		IPR000232; IPR011991; PTHR10015 (PANTHER), PTHR10015:SF17 (PANTHER), SSF46785 (SUPERFAMILY)
Pan troglodytes	isolog of yeast sui1 and rice gos2	0				-
Loa loa	tk fer protein ki-se	12	P:GO:0030098; P:GO:0048523; F:GO:0004674; F:GO:0005021; P:GO:0002320; P:GO:0023052; F:GO:0005524; F:GO:0005515; P:GO:0008284; P:GO:0040018; C:GO:0005887; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR001245; IPR011009; IPR020685; IPR020764; G3DSA:1.10.510.10 (GENE3D)
synthetic construct	transcription elongation factor b polypeptide 2	10	C:GO:0005829; F:GO:0003746; P:GO:0045944; C:GO:0005667; F:GO:0016251; P:GO:0006461; F:GO:0004842; F:GO:0005515; P:GO:0006368; C:GO:0030891	-	EC:6.3.2.19	IPR000626; IPR019955; G3DSA:3.10.20.90 (GENE3D), PTHR13248 (PANTHER), SSF54236 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	ched related family member (ptr-2)-like	13	P:GO:0009792; P:GO:0002119; F:GO:0008158; P:GO:0040018; P:GO:0001703; P:GO:0018996; P:GO:0000910; P:GO:0006810; P:GO:0040010; P:GO:0000003; P:GO:0040011; C:GO:0016021; F:GO:0005215	-		-
Brugia malayi	protein ki-se domain containing protein	4	F:GO:0005488; F:GO:0004672; P:GO:0040010; P:GO:0000003	-		IPR000719; IPR001245; IPR008266; IPR011009; IPR020685; IPR020764; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
Caenorhabditis briggsae	briggsae cbr-zyg-9 protein	1	F:GO:0005515	-		IPR000357; IPR011989; IPR016024; IPR021133; PTHR12609 (PANTHER)
	-	0				-
Brugia malayi	zinc finger protein 709-like	8	P:GO:0018991; F:GO:0008270; F:GO:0003676; P:GO:0006796; F:GO:0005515; F:GO:0000287; F:GO:0004427; C:GO:0005737	-	EC:3.6.1.1	IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)

Caenorhabditis elegans	briggsae cbr-dhs-7 protein	3	F:GO:0016491; P:GO:0008152; F:GO:0005488	-		-
Callithrix jacchus	enolase 1	15	P:GO:0009615; C:GO:0000015; P:GO:0000122; F:GO:0003714; F:GO:0004252; C:GO:0031430; C:GO:0009986; F:GO:0004634; P:GO:0006096; F:GO:0003677; P:GO:0030308; F:GO:0000287; F:GO:0003700; C:GO:0005886; C:GO:0005634	-	EC:3.4.21.0; EC:4.2.1.11	IPR020811; G3DSA:3.30.390.10 (GENE3D), PTHR11902 (PANTHER), SSF54826 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	cyclopropane-fatty-acyl-phospholipid synthase	1	F:GO:0008168	-	EC:2.1.1.0	-
	-	0				-
	-	0				-
Caenorhabditis briggsae	bwf1-like protein	0		F:GO:0004672; F:GO:0005524; F:GO:0003755; P:GO:0006457; P:GO:0006468; F:GO:0016853		IPR000409; PTHR13743 (PANTHER)
Caenorhabditis briggsae	retinol reti-ldehyde reductase	10	P:GO:0016477; F:GO:0005488; P:GO:0006710; C:GO:0043231; P:GO:0055114; F:GO:0009055; F:GO:0016491; C:GO:0044425; C:GO:0044444; P:GO:0008406	-		-
Pediculus humanus corporis	conserved hypothetical protein [Pediculus humanus corporis]	0				-
Pediculus humanus corporis	conserved hypothetical protein [Pediculus humanus corporis]	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0003840	-	EC:2.3.2.2	IPR000101; SSF56235 (SUPERFAMILY)
Caenorhabditis briggsae	low density lipid receptor-related	4	C:GO:0016021; F:GO:0004872; F:GO:0003824; F:GO:0005509	-		IPR000033; IPR001917; IPR006209; IPR006210; IPR011042; G3DSA:2.10.25.10 (GENE3D), PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER), SSF57196 (SUPERFAMILY), SSF63825 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-asm-1 protein	4	P:GO:0046513; F:GO:0004767; C:GO:0005576; P:GO:0006685	-	EC:3.1.4.12	G3DSA:3.60.21.10 (GENE3D), PTHR10340 (PANTHER), PTHR10340:SF13 (PANTHER)
	-	0				-

	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Asticcacaulis excentricus CB 48	gamma-glutamyltranspeptidase	0		F:GO:0003840; F:GO:0008415; F:GO:0016740		IPR000101; SSF56235 (SUPERFAMILY)
Saccoglossus kowalevskii	sestrin 2	0		C:GO:0005737; P:GO:0007050; C:GO:0005634		IPR006730; SSF69118 (SUPERFAMILY)
Brugia malayi	hypothetical protein Bm1_49115 [Brugia malayi]	0				-
	-	0				IPR004245; PTHR10974:SF17 (PANTHER)
Macaca mulatta	type alpha 2	8	F:GO:0005201; F:GO:0030674; C:GO:0005615; P:GO:0016337; C:GO:0005578; P:GO:0009749; P:GO:0030198; C:GO:0042383	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	#NAME?	20	P:GO:0008340; P:GO:0015672; P:GO:0035158; P:GO:0008360; P:GO:0051124; P:GO:0035159; P:GO:0019991; P:GO:0009612; P:GO:0006754; F:GO:0005391; P:GO:0001700; C:GO:0005918; P:GO:0007268; C:GO:0005890; P:GO:0009266; C:GO:0005634; F:GO:0005524; P:GO:0050905; P:GO:0001894; P:GO:0008344	-	EC:3.6.3.9	-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	rt05_caebr ame: full= 28s ribosomal protein mitochondrial	9	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; F:GO:0003723; P:GO:0040010; P:GO:0006898; P:GO:0006412; C:GO:0005739	-	EC:3.6.5.3	-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	4	P:GO:0040015; P:GO:0000003; P:GO:0040010; P:GO:0040011	-		PTHR22991 (PANTHER)
	-	0				SignalP (SIGNALP)

synthetic construct	eukaryotic translation elongation factor 1 alpha 1	10	C:GO:0005829; F:GO:0003746; C:GO:0005853; P:GO:0006414; P:GO:0006184; F:GO:0005515; C:GO:0043025; F:GO:0003924; F:GO:0005525; C:GO:0005634	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
	-	0				-
Brugia malayi	baculoviral iap repeat-containing 6	4	P:GO:0006916; P:GO:0019538; F:GO:0005515; F:GO:0019787	-		-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR009432
	-	0				-
	-	0				-
	-	0				-
Pongo abelii	eukaryotic translation initiation factor subunit 5 47kda	5	C:GO:0005852; F:GO:0005515; P:GO:0045948; F:GO:0003743; C:GO:0005829	-		PTHR10540 (PANTHER), PTHR10540:SF6 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; P:GO:0019915		PTHR23294 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	gem-interacting protein	3	F:GO:0005488; P:GO:0023052; P:GO:0050794	-		IPR000198; IPR008936; PTHR15228 (PANTHER), PTHR15228:SF1 (PANTHER)
Caenorhabditis elegans	ribosomal protein s27a	18	P:GO:0006412; C:GO:0005875; P:GO:0006511; F:GO:0008270; P:GO:0006355; F:GO:0003735; P:GO:0000003; P:GO:0018996; C:GO:0022627; P:GO:0010171; P:GO:0002119; P:GO:0042254; F:GO:0005515; P:GO:0006325; P:GO:0009792; P:GO:0040015; P:GO:0006950; C:GO:0005634	-	EC:3.6.5.3	IPR002906; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), PTHR10666:SF2 (PANTHER)
	-	0				IPR000626; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), PTHR10666:SF7 (PANTHER)
	-	0				-

Caenorhabditis briggsae	briggsae cbr-pgp-9 protein	0		F:GO:0005524; F:GO:0016887; C:GO:0016021; F:GO:0000166; F:GO:0042626; F:GO:0017111; P:GO:0055085; P:GO:0006810		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	dhx33 protein	2	F:GO:0004386; F:GO:0000166	-		-
	-	0				-
Caenorhabditis elegans	vacuolar protein sorting 13d	3	P:GO:0040010; P:GO:0002119; P:GO:0040011	-		-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-dhs-15 protein	5	P:GO:0009792; F:GO:0016491; F:GO:0005515; P:GO:0040010; P:GO:0055114	-		IPR002198; IPR016040; PTHR19410:SF76 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	midasin homolog	7	P:GO:0043254; P:GO:0006355; F:GO:0005524; F:GO:0016887; F:GO:0008134; F:GO:0051082; C:GO:0005634	-		G3DSA:3.40.50.300 (GENE3D), PTHR22908 (PANTHER), PTHR22908:SF13 (PANTHER)
Caenorhabditis briggsae	malate l-lactate dehydroge-se family protein	4	P:GO:0018991; P:GO:0055114; F:GO:0016491; P:GO:0040011	-		IPR003767; G3DSA:1.10.1530.10 (GENE3D), G3DSA:3.30.1370.60 (GENE3D)
Caenorhabditis briggsae	trp channel protein -nchung	9	P:GO:0055085; P:GO:0050974; C:GO:0016021; P:GO:0006811; P:GO:0045450; P:GO:0045451; F:GO:0005216; P:GO:0007605; P:GO:0009270	-		IPR020683; PTHR10582 (PANTHER), PTHR10582:SF2 (PANTHER)
Caenorhabditis elegans	abnormal dye filling family member (dyf-14)	0				-
	-	0				-
	-	0				-
Brugia malayi	mgc88946 protein	0				-
	-	0				-

Caenorhabditis elegans	hypothetical protein R05D3.12 [Caenorhabditis elegans]	0		F:GO:0003918; F:GO:0003916; P:GO:0006265; C:GO:0005694; F:GO:0003700; P:GO:0006259; F:GO:0003677; F:GO:0000166; F:GO:0005524; P:GO:0006355; F:GO:0016853		-
	-	0				-
	-	0				-
	-	0				-
Haemonchus contortus	thioredoxin reductase 3 isoform 1	11	C:GO:0005829; C:GO:0043231; P:GO:0055114; P:GO:0006749; P:GO:0032501; C:GO:0005792; F:GO:0000166; F:GO:0050662; F:GO:0015036; P:GO:0032502; F:GO:0004791	-	EC:1.8.1.9	IPR006338; IPR012335; IPR012999; IPR013027; PR00411 (PRINTS), G3DSA:3.50.50.60 (GENE3D), PTHR22912 (PANTHER), SSF51905 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Pongo abelii	marcks-like 1	4	P:GO:0008284; F:GO:0005516; P:GO:0016192; C:GO:0005886	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	low-density lipoprotein receptor related family member (lrp-1)	3	F:GO:0004872; C:GO:0016021; F:GO:0005509	-		IPR000152; IPR011042
Caenorhabditis briggsae	xanthine dehydroge-se	8	F:GO:0004855; F:GO:0009055; F:GO:0005506; F:GO:0004854; P:GO:0055114; P:GO:0008340; F:GO:0051537; F:GO:0050660	-	EC:1.17.3.2; EC:1.17.1.4	IPR002346; IPR016166; IPR016169; PTHR11908 (PANTHER), PTHR11908:SF9 (PANTHER)
Caenorhabditis elegans	trehalose 6-phosphate synthase	3	F:GO:0003825; P:GO:0034608; P:GO:0005992	-	EC:2.4.1.15	IPR001830; G3DSA:3.40.50.2000 (GENE3D), PTHR10788 (PANTHER), SSF53756 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	williams-beuren syndrome chromosome region 16 protein	0				IPR000408; IPR009091; PTHR22870 (PANTHER), PTHR22870:SF11 (PANTHER)
	-	0				-

Caenorhabditis elegans	troponin c	6	P:GO:0000003; P:GO:0040007; F:GO:0005509; F:GO:0005515; C:GO:0009536; P:GO:0002119	-		IPR002048; IPR011992; IPR018247; IPR018248; IPR018249; PTHR23050 (PANTHER), PTHR23050:SF16 (PANTHER), SSF47473 (SUPERFAMILY)
Caenorhabditis elegans	failed axon connections protein	1	P:GO:0007409	-		PTHR12289 (PANTHER), PTHR12289:SF17 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	C:GO:0016021	-		IPR010761; SignalP (SIGNALP)
Caenorhabditis briggsae	msp-domain protein 1 variant	5	C:GO:0044297; P:GO:0019915; P:GO:0040018; P:GO:0000003; C:GO:0031143	-		-
Tribolium castaneum	required for meiotic nuclear division 5 homolog a	0		P:GO:0008150; C:GO:0005575		IPR013083; PTHR12170 (PANTHER), PTHR12170:SF3 (PANTHER)
Loa loa	#NAME?	1	F:GO:0016813	-	EC:3.5.3.0	G3DSA:3.75.10.10 (GENE3D), PTHR12737 (PANTHER), PTHR12737:SF5 (PANTHER)
Caenorhabditis briggsae	pdz domain	0		F:GO:0005515		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR10910 (PANTHER), PTHR10910:SF10 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-pph-5 protein	0		F:GO:0046872; F:GO:0005488; C:GO:0005737; P:GO:0006470; F:GO:0016787; F:GO:0004722; F:GO:0004721; C:GO:0005634		IPR013235
Caenorhabditis elegans	vacuolar protein sorting 13d	1	P:GO:0008104	-		PTHR16166 (PANTHER), PTHR16166:SF24 (PANTHER)
	-	0				-
Bos taurus	endothelial differentiation-related factor 1	13	P:GO:0019216; P:GO:0043388; F:GO:0005516; P:GO:0006355; F:GO:0043565; F:GO:0003700; P:GO:0045446; P:GO:0007275; F:GO:0004402; F:GO:0003713; C:GO:0005669; C:GO:0005737; F:GO:0008168	-	EC:2.3.1.48; EC:2.1.1.0	IPR013729; PTHR10245 (PANTHER), PTHR10245:SF1 (PANTHER)
Caenorhabditis elegans	hypothetical protein C05E11.6 [Caenorhabditis elegans]	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	betaine aldehyde dehydroge-se	2	F:GO:0016491; P:GO:0006350	-		IPR015590; IPR016161; IPR016162; G3DSA:2.30.30.330 (GENE3D), PTHR11699:SF47 (PANTHER), PF05708 (PFAM)

Caenorhabditis elegans	briggsae cbr-nhr-45 protein	0		F:GO:0043565; F:GO:0003700; F:GO:0003677; C:GO:0005634; F:GO:0008270; P:GO:0006355; F:GO:0004872; F:GO:0005515; F:GO:0046872; P:GO:0006350; F:GO:0003707; P:GO:0045449		-
	-	0				-
	-	0				-
	-	0				-
	-	0				IPR000990; SignalP (SIGNALP)
Danio rerio	serine threonine-protein ki-se pak 4	0		F:GO:0016301; F:GO:0005524; F:GO:0016740; F:GO:0000166; P:GO:0006468; F:GO:0004674; C:GO:0005575		PTHR22986 (PANTHER), PTHR22986:SF88 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein H20J04.9 [Caenorhabditis elegans]	0		F:GO:0008168; P:GO:0008152		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	7	P:GO:0040035; C:GO:0005921; P:GO:0040010; P:GO:0040011; C:GO:0016021; P:GO:0019915; P:GO:0002009	-		-
	-	0				-
Caenorhabditis elegans	yeast mon (monensin-resistant) homolog family member (mon-2)	1	P:GO:0006810	-		-
Caenorhabditis elegans	protein mon2-like protein	1	P:GO:0006810	-		IPR016024; PTHR10663 (PANTHER), PTHR10663:SF5 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
	-	0				-

Ailuropoda melanoleuca	sig-l transducer and activator of transcription 1	30	F:GO:0005515; P:GO:0007260; P:GO:0042542; P:GO:0032869; P:GO:0006366; P:GO:0006919; P:GO:0009612; P:GO:0006355; P:GO:0008015; P:GO:0031663; F:GO:0005509; P:GO:0014070; C:GO:0005737; C:GO:0005730; P:GO:0019221; C:GO:0030425; P:GO:0034097; P:GO:0048661; P:GO:0007249; F:GO:0043565; P:GO:0006917; C:GO:0030424; F:GO:0005062; P:GO:0042493; P:GO:0051591; F:GO:0003700; P:GO:0007584;	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	exosome component 8	1	F:GO:0005515	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	pumilio homolog 2	2	F:GO:0003723; F:GO:0005515	-		IPR001313; IPR011989; IPR016024; PTHR12537 (PANTHER), PTHR12537:SF12 (PANTHER)
Loa loa	pumilio homolog 2	2	F:GO:0003723; F:GO:0005515	-		IPR001313; IPR011989; IPR016024; PTHR12537 (PANTHER), PTHR12537:SF12 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	erin family member (cdh-12)	0				-

Caenorhabditis briggsae	briggsae cbr-hmr-1 protein	15	C:GO:0005911; P:GO:0016339; F:GO:0005515; P:GO:0007412; F:GO:0005509; C:GO:0016021; P:GO:0050774; P:GO:0007156; P:GO:0048676; P:GO:0007413; P:GO:0031290; P:GO:0045467; P:GO:0016318; P:GO:0045463; P:GO:0048841	-		IPR002126; IPR015919; IPR020894; PTHR10596 (PANTHER), PTHR10596:SF113 (PANTHER)
	-	0				-
Loa loa	cpb-2	1	F:GO:0003676	-		PTHR12566 (PANTHER)
Loa loa	hypothetical protein LOAG_07811 [Loa loa]	0		P:GO:0009792		-
Caenorhabditis briggsae	prion-like-(q n-rich)-domain-bearing protein family member (pqn-83)	0		P:GO:0000003; P:GO:0040011; P:GO:0002119		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				PTHR13190 (PANTHER), PTHR13190:SF2 (PANTHER)
Caenorhabditis briggsae	exs family protein	3	P:GO:0018991; P:GO:0010171; P:GO:0040010	-		-
Culex quinquefasciatus	phosphatidylethanolamine-binding protein	0				IPR001858; IPR008914; PTHR11362 (PANTHER)
	-	0				-
Bunostomum phlebotomum	-dh dehydroge-se subunit 1	4	C:GO:0016021; P:GO:0055114; C:GO:0005739; F:GO:0008137	-	EC:1.6.5.3	IPR001694; IPR018086
	-	0				-
Brugia malayi	cytochrome p450	1	F:GO:0046872	-		-
Brugia malayi	lung seven transmembrane receptor family protein	0		F:GO:0004872; C:GO:0016021		-
Caenorhabditis elegans	gata zinc finger family protein	1	F:GO:0005488	-		-
	-	0				-
Caenorhabditis briggsae	proline oxidase	6	P:GO:0055114; F:GO:0004657; P:GO:0006537; P:GO:0042331; C:GO:0005759; P:GO:0006562	-	EC:1.5.99.8	IPR002872; IPR015659; G3DSA:3.20.20.220 (GENE3D), SSF51730 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-unc-8 protein	3	C:GO:0016021; F:GO:0005272; P:GO:0006814	-		IPR001873; IPR020903; G3DSA:1.10.287.820 (GENE3D), PTHR11690:SF17 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; C:GO:0016020		IPR013057; PTHR22950 (PANTHER), SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	mrp-4	23	F:GO:0034040; F:GO:0005324; F:GO:0046624; C:GO:0016323; F:GO:0015562; P:GO:0015911; P:GO:0043526; P:GO:0006855; C:GO:0005737; P:GO:0034775; P:GO:0060326; F:GO:0034634; F:GO:0008559; F:GO:0015431; P:GO:0033700; P:GO:0046618; P:GO:0006200; C:GO:0005887; P:GO:0030335; F:GO:0005524; P:GO:0043215; P:GO:0006979; P:GO:0042908	-	EC:3.6.3.44	IPR001140; IPR011527; IPR017940; G3DSA:1.20.1560.10 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF15 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	cell adhesion	8	P:GO:0018996; P:GO:0009792; P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		IPR003961; IPR008957; IPR013783; PR00014 (PRINTS)
Homo sapiens	giy-yig domain containing 2	7	C:GO:0033557; F:GO:0008821; F:GO:0046872; P:GO:0000724; F:GO:0017108; F:GO:0005515; P:GO:0010792	-	EC:3.1.22.4	PTHR20208 (PANTHER), PTHR20208:SF7 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	membrane calcium atpase family member (mca-1)	0				-
Ancylostoma ceylanicum	kunitz type serine protease inhibitor	1	F:GO:0030414	-		IPR002223; IPR020901; PTHR10083 (PANTHER), PTHR10083:SF39 (PANTHER), SignalP (SIGNALP)
Loa loa	d- topoisomerase ii	3	P:GO:0006259; F:GO:0003916; F:GO:0000166	-		IPR002205; IPR013757; IPR013760; PTHR10169 (PANTHER), PTHR10169:SF2 (PANTHER)
Caenorhabditis elegans	dephospho- ki-se	3	F:GO:0016301; C:GO:0044464; F:GO:0000166	-		IPR001977; G3DSA:3.40.50.300 (GENE3D), PTHR10695 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	alkylation repair homolog 6	1	F:GO:0003824	-		IPR005123; G3DSA:2.60.120.590 (GENE3D), PS51471 (PROFILE), SSF51197 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)

Loa loa	thiamin pyrophosphoki-se 1	0		C:GO:0009536; F:GO:0016301; F:GO:0005524; P:GO:0006772; F:GO:0016740; F:GO:0004788; P:GO:0009229		IPR007373; G3DSA:2.60.120.320 (GENE3D), PTHR13622 (PANTHER), PTHR13622:SF1 (PANTHER), PF04265 (PFAM)
Caenorhabditis elegans	yxd2_caeel ame: full=uncharacterized serine carboxypeptidase	0		P:GO:0006508; F:GO:0004185		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis elegans	atp-binding cassette sub-family a member	3	C:GO:0016021; F:GO:0016887; F:GO:0000166	-		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	endoplasmic reticulum metallopeptidase 1	4	P:GO:0001541; F:GO:0008233; C:GO:0016020; C:GO:0005783	-		IPR007484; G3DSA:3.40.630.10 (GENE3D), PTHR12147 (PANTHER), SSF53187 (SUPERFAMILY)
Caenorhabditis elegans	enolase-phosphatase e1	3	P:GO:0019509; F:GO:0043874; C:GO:0044424	-	EC:3.1.3.77	IPR010041; G3DSA:3.40.50.1000 (GENE3D), SSF56784 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein C15F1.5 [Caenorhabditis elegans]	0		F:GO:0008270		IPR013083; IPR017907
Caenorhabditis elegans	briggsae cbr-ltd-1 protein	1	F:GO:0008270	-		IPR001781; SSF57716 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	sfrs protein ki-se 3	11	P:GO:0007276; P:GO:0000910; F:GO:0004674; P:GO:0040035; P:GO:0007519; P:GO:0002119; F:GO:0005515; F:GO:0000166; P:GO:0009792; P:GO:0051729; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF118 (PANTHER)
Caenorhabditis elegans	serine threonine-protein ki-se srpk3	11	P:GO:0007276; P:GO:0000910; F:GO:0004674; P:GO:0040035; P:GO:0007519; P:GO:0002119; F:GO:0005515; F:GO:0000166; P:GO:0009792; P:GO:0051729; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF118 (PANTHER)

Caenorhabditis elegans	serine arginine-rich protein specific ki-se 1	16	P:GO:0007276; P:GO:0000910; P:GO:0007243; F:GO:0004674; P:GO:0050684; P:GO:0000245; P:GO:0040035; F:GO:0005524; P:GO:0002119; F:GO:0005515; F:GO:0000287; P:GO:0009792; P:GO:0051729; C:GO:0016020; C:GO:0005634; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF118 (PANTHER)
Caenorhabditis elegans	sfrs protein ki-se 3	11	P:GO:0007276; P:GO:0000910; F:GO:0004674; P:GO:0040035; P:GO:0007519; P:GO:0002119; F:GO:0005515; F:GO:0000166; P:GO:0009792; P:GO:0051729; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF118 (PANTHER)
	-	0				-
Ornithorhynchus anatinus	upf0420 protein c16orf58	1	C:GO:0016021	-		IPR006968; PTHR12770:SF10 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0000166; C:GO:0005634		PTHR12202 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	mkiaa1517 protein	10	P:GO:0040010; P:GO:0008340; P:GO:0000003; P:GO:0002119; F:GO:0005515; F:GO:0000166; F:GO:0004386; P:GO:0006898; P:GO:0009792; P:GO:0016246	-		IPR011709; PTHR18934 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Loa loa	hypothetical protein LOAG_09182 [Loa loa]	0				-
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis elegans	d- excision repair protein rad2	1	F:GO:0004518	-		IPR001044; IPR006084; IPR006085; G3DSA:3.40.50.1010 (GENE3D), PTHR11081:SF4 (PANTHER), SSF88723 (SUPERFAMILY)
Caenorhabditis elegans	sirtuin 1	31	P:GO:0006471; P:GO:0006343; C:GO:0033553; P:GO:0006281; F:GO:0008022; P:GO:0006344; C:GO:0005677; C:GO:0016605; P:GO:0031937; P:GO:0033158; F:GO:0003950; P:GO:0043433; F:GO:0002039; P:GO:0007569; P:GO:0051097; P:GO:0043518; P:GO:0045444; P:GO:0042127; C:GO:0005737; P:GO:0016575; F:GO:0016564; F:GO:0042802; F:GO:0042393; C:GO:0005635; P:GO:0006260; P:GO:0045768; P:GO:0034983;	-	EC:2.4.2.30	IPR003000; G3DSA:3.30.1600.10 (GENE3D), G3DSA:3.40.50.1220 (GENE3D), SSF52467 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	rio ki-se 2	2	F:GO:0016301; F:GO:0000166	-		IPR011009; IPR018934; IPR018935; G3DSA:3.90.1200.10 (GENE3D), PTHR10593 (PANTHER), PTHR10593:SF1 (PANTHER)
Caenorhabditis briggsae	atg2 autophagy related 2 homolog b (cerevisiae)	0				PTHR13190 (PANTHER), PTHR13190:SF8 (PANTHER)
	-	0				SignalP (SIGNALP)
Loa loa	myosin light chain ki-se	4	C:GO:0005737; F:GO:0005515; F:GO:0004674; F:GO:0000166	-	EC:2.7.11.0	IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG22082 [Caenorhabditis briggsae]	2	P:GO:0007186; C:GO:0016021	-		-
	-	0				IPR017985; PD968187 (PRODOM)
Caenorhabditis elegans	guanine nucleotide exchange factor	3	F:GO:0005085; C:GO:0005622; P:GO:0051056	-		IPR001895; IPR008937; PTHR23113:SF20 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	stress-activated protein ki-se jnk	4	F:GO:0004707; P:GO:0006468; F:GO:0005515; F:GO:0005524	-	EC:2.7.11.24	IPR011009; IPR020636; IPR020648; G3DSA:1.10.510.10 (GENE3D)
	-	0				-
	-	0				-

Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	3	P:GO:0040010; P:GO:0008152; F:GO:0003824	-		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	3	P:GO:0040010; P:GO:0008152; F:GO:0003824	-		IPR002114; IPR002198; IPR002347; IPR016040; PTHR19410:SF76 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	3	P:GO:0040010; P:GO:0008152; F:GO:0003824	-		IPR002114; IPR002198; IPR002347; IPR016040; PTHR19410:SF76 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Brugia malayi	short-chain dehydroge-se reductase sdr	2	F:GO:0003824; P:GO:0008152	-		IPR002198; IPR016040; PTHR19410:SF98 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Ostertagia ostertagi	aspartyl protease inhibitor 1	3	C:GO:0005576; F:GO:0008233; F:GO:0019828	-		IPR010480; SignalP (SIGNALP), SSF55149 (SUPERFAMILY)
Ostertagia ostertagi	aspartyl protease inhibitor 1	3	C:GO:0005576; F:GO:0008233; F:GO:0019828	-		IPR010480; SignalP (SIGNALP), SSF55149 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG05491 [Caenorhabditis briggsae]	2	F:GO:0016627; P:GO:0008152	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	protein-tyrosine phosphatase containing protein	3	F:GO:0004721; P:GO:0009792; P:GO:0000003	-	EC:3.1.3.16	IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				IPR003961; SignalP (SIGNALP)
Callithrix jacchus	atp h+ mitochondrial f1 gamma polypeptide 1	5	F:GO:0046933; C:GO:0000275; P:GO:0042776; F:GO:0046961; C:GO:0005759	-	EC:3.6.3.14	IPR000131; G3DSA:3.40.1380.10 (GENE3D), PTHR11693:SF5 (PANTHER)
	-	0				-
Caenorhabditis briggsae	attractin	4	P:GO:0018991; C:GO:0016021; P:GO:0040010; P:GO:0040011	-		IPR002049; G3DSA:2.10.25.10 (GENE3D), PTHR10574 (PANTHER), PTHR10574:SF3 (PANTHER), SSF57196 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-nhr-69 protein	7	F:GO:0008270; F:GO:0003707; P:GO:0006355; F:GO:0042802; F:GO:0043565; F:GO:0003700; C:GO:0005634	-		IPR000536; IPR001628; IPR001723; IPR008946; IPR013088; PR00545 (PRINTS), PTHR11865 (PANTHER), PTHR11865:SF196 (PANTHER), SSF57716 (SUPERFAMILY)

Caenorhabditis briggsae	briggsae cbr-nhr-69 protein	7	F:GO:0008270; F:GO:0003707; P:GO:0006355; F:GO:0042802; F:GO:0043565; F:GO:0003700; C:GO:0005634	-		IPR000536; IPR001628; IPR001723; IPR008946; IPR013088; PR00545 (PRINTS), PTHR11865 (PANTHER), PTHR11865:SF196 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis briggsae	dnpep_caeel ame: full= aspartyl aminopeptidase	0		F:GO:0046872; P:GO:0006508; F:GO:0008237; C:GO:0005773; F:GO:0004177; F:GO:0016787; F:GO:0008233; F:GO:0008270		-
Loa loa	dy-ctin subunit 1	0		C:GO:0030286; C:GO:0005737; C:GO:0005856; F:GO:0003774; C:GO:0005874		IPR000938; IPR023092; PTHR18916 (PANTHER), PTHR18916:SF2 (PANTHER)
Caenorhabditis remanei	membrane calcium atpase family member (mca-1)	5	F:GO:0005388; C:GO:0016021; P:GO:0006754; F:GO:0005524; P:GO:0006816	-	EC:3.6.3.8	IPR001757; PTHR11939:SF75 (PANTHER)
Angiostrongylus cantonensis	briggsae cbr-lec-8 protein	0		F:GO:0005529		-
	-	0				-
	-	0				IPR000276
Camponotus floridanus	probable phospholipid-transporting atpase id	0				IPR001757; PTHR11939:SF19 (PANTHER)
Caenorhabditis sp. PS1010	elegans protein partially confirmed by transcript evidence	0		P:GO:0006508; F:GO:0004181; F:GO:0008270		-
Camponotus floridanus	peroxisome biogenesis factor 1	13	P:GO:0040010; P:GO:0007031; C:GO:0005777; C:GO:0016021; F:GO:0004872; P:GO:0000003; F:GO:0004176; P:GO:0006508; F:GO:0004713; F:GO:0005524; F:GO:0005515; F:GO:0004252; P:GO:0006468	-	EC:2.7.10.0; EC:3.4.21.0	IPR003959; G3DSA:3.40.50.300 (GENE3D), PTHR23077 (PANTHER), PTHR23077:SF12 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	sidekick homolog 2	1	C:GO:0016020	-		IPR003961; IPR008957; IPR013783; PR00014 (PRINTS), PTHR10489 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Teladorsagia circumcincta	long family member (lon-1)	2	F:GO:0005515; C:GO:0005576	-		-
	-	0				-

Caenorhabditis elegans	hypothetical protein T25B9.10 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	kynureni-se (l-kynurenine hydrolase)	13	C:GO:0005829; P:GO:0019805; C:GO:0005625; C:GO:0005739; P:GO:0019441; P:GO:0009435; P:GO:0034516; P:GO:0043420; F:GO:0030429; P:GO:0034341; F:GO:0042803; F:GO:0030170; P:GO:0019442	-	EC:3.7.1.3	IPR010111; IPR015422; IPR015424
Caenorhabditis elegans	briggsae cbr-phy-3 protein	0		F:GO:0005506; F:GO:0031418; F:GO:0016705; F:GO:0016702; P:GO:0055114; F:GO:0016491; F:GO:0004656; C:GO:0005783; F:GO:0005488		-
Caenorhabditis elegans	profilin	9	C:GO:0005737; P:GO:0009792; F:GO:0003779; P:GO:0000910; P:GO:0000003; P:GO:0008340; P:GO:0040011; C:GO:0015629; P:GO:0030036	-		-
Caenorhabditis elegans	nedd8-activating enzyme e1 regulatory subunit	3	F:GO:0003824; P:GO:0008152; F:GO:0005488	-		IPR009036; IPR016040; PTHR10953 (PANTHER), PTHR10953:SF29 (PANTHER)
	-	0				-
	-	0				PTHR22986 (PANTHER), PTHR22986:SF67 (PANTHER)
	-	0				-
Caenorhabditis elegans	c2 domain containing protein	0				-
Caenorhabditis elegans	hypothetical protein D1007.15 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein D1007.15 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Brugia malayi	hypothetical wd-repeat protein in chromosome	0				PTHR12816 (PANTHER), PTHR12816:SF6 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	tropomodulin	3	C:GO:0005856; P:GO:0000003; F:GO:0005523	-		IPR004934; PTHR10901:SF7 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	xanthine molybdopterin binding subunit	4	F:GO:0046872; F:GO:0016725; F:GO:0051536; P:GO:0008340	-		IPR000674; IPR008274; PTHR11908 (PANTHER), PTHR11908:SF9 (PANTHER)

Caenorhabditis briggsae	polybromodomain protein	7	P:GO:0040035; P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040010; P:GO:0040011; P:GO:0002009	-		IPR001487; PTHR16062 (PANTHER), PTHR16062:SF2 (PANTHER)
Caenorhabditis elegans	ribonuclease l inhibitor homolog	17	P:GO:0006413; P:GO:0040010; P:GO:0016049; F:GO:0051536; C:GO:0005739; F:GO:0043024; P:GO:0016071; P:GO:0040035; F:GO:0009055; C:GO:0005852; F:GO:0005524; P:GO:0010171; P:GO:0002119; F:GO:0016887; P:GO:0040011; P:GO:0009792; P:GO:0043524	-		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0005488; P:GO:0007067		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	zinc carboxypeptidase family protein	3	P:GO:0006508; F:GO:0004181; F:GO:0008270	-	EC:3.4.17.0	G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), PTHR11705:SF12 (PANTHER), SSF53187 (SUPERFAMILY)
Caenorhabditis remanei	aha-1	18	F:GO:0030528; P:GO:0009056; P:GO:0040010; P:GO:0030522; F:GO:0016788; F:GO:0008270; P:GO:0006355; F:GO:0004872; F:GO:0043565; P:GO:0010171; P:GO:0009410; P:GO:0002119; F:GO:0005515; P:GO:0040017; F:GO:0003700; P:GO:0007165; C:GO:0005634; P:GO:0045941	-		IPR001067; IPR011598; PTHR23042 (PANTHER), PTHR23042:SF7 (PANTHER)

Brugia malayi	short chain dehydroge-se reductase family protein	3	P:GO:0055114; F:GO:0016491; F:GO:0005488	-		IPR002198; IPR016040; PTHR19410:SF85 (PANTHER), SignalP (SIGNALP), SSF51735 (SUPERFAMILY)
	-	0				-
Loa loa	intermediate filament protein	6	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0018991; P:GO:0040011; P:GO:0040007	-		IPR001322; IPR001664; G3DSA:2.60.40.1260 (GENE3D), PTHR23239:SF12 (PANTHER), SSF74853 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	ferm domain containing 6	3	C:GO:0005856; C:GO:0005737; F:GO:0005488	-		IPR000299; IPR014352; IPR018979; IPR019748; IPR019749; G3DSA:3.10.20.90 (GENE3D), SSF54236 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	dead box atp-dependent r-	3	F:GO:0003676; F:GO:0005524; F:GO:0008026	-		IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF45 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	low-density lipoprotein	0		P:GO:0015031; C:GO:0016021; C:GO:0016020; P:GO:0006898; C:GO:0005624; F:GO:0004872; F:GO:0005515; F:GO:0005041; F:GO:0050750; F:GO:0005509		IPR002172; PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	fancm (fanconi anemia complex component m) homolog family member (fncm-1)	0		P:GO:0000003		-
Culex quinquefasciatus	plasma glutamate carboxypeptidase	0		P:GO:0006508; F:GO:0004180; F:GO:0008233		G3DSA:3.40.630.10 (GENE3D), PTHR12053 (PANTHER), PTHR12053:SF2 (PANTHER)
	-	0				-
Loa loa	arsenite-resistance protein	3	P:GO:0008340; P:GO:0031053; C:GO:0005654	-		IPR007042; IPR021933; PTHR13165 (PANTHER)
Loa loa	arsenite-resistance protein	3	P:GO:0008340; P:GO:0031053; C:GO:0005654	-		IPR007042; IPR021933; PTHR13165 (PANTHER)
	-	0				-
Callithrix jacchus	PREDICTED: stathmin-like [Callithrix jacchus]	0				-
Caenorhabditis briggsae	briggsae cbr-gly-8 protein	0		F:GO:0016740; F:GO:0016757		-
Homo sapiens	isoform cra_b	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis elegans	phosphoethanolamine ransferase family member (pmt-1)	9	P:GO:0009792; P:GO:0002119; F:GO:0008757; P:GO:0032940; P:GO:0009877; P:GO:0009312; P:GO:0040017; P:GO:0040010; P:GO:0000003	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	smu-1 suppressor of mec-8 and unc-52 homolog (elegans)	1	C:GO:0044424	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR22848 (PANTHER)
Loa loa	pdz domain containing protein	4	P:GO:0009792; P:GO:0040007; P:GO:0040035; P:GO:0002119	-		-
	-	0				-
Caenorhabditis elegans	hypothetical protein H41C03.1 [Caenorhabditis elegans]	1	P:GO:0040010	-		-
Caenorhabditis elegans	briggsae cbr-acy-3 protein	0		P:GO:0009190; F:GO:0016849		-
Caenorhabditis elegans	diphthamide biosynthesis protein 2	1	P:GO:0040002	-		IPR002728; IPR010014
Caenorhabditis briggsae	protein	5	F:GO:0005432; P:GO:0006816; P:GO:0055085; C:GO:0016021; P:GO:0007154	-		-
Caenorhabditis briggsae	briggsae cbr-tag-280 protein	0				IPR019319; PTHR13411 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Loa loa	dis3-like exonuclease 2	1	F:GO:0004518	-		-
Loa loa	dis3-like exonuclease 2	1	F:GO:0004518	-		-
	-	0				-
Caenorhabditis elegans	transformation transcription domain-associated protein	1	F:GO:0016772	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-dpf-5 protein	0				-
Brugia malayi	mucosa associated lymphoid tissue lymphoma translocation protein isoform b	0		P:GO:0000003; P:GO:0006508; F:GO:0004197; F:GO:0005515		PTHR22576 (PANTHER), PTHR22576:SF1 (PANTHER)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG07070 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	udp-n-acetylglucosamine pyrophosphorylase	4	F:GO:0016779; P:GO:0009792; P:GO:0000003; P:GO:0040010	-	EC:2.7.7.0	IPR002618; G3DSA:3.90.550.10 (GENE3D), PTHR11952:SF2 (PANTHER), SSF53448 (SUPERFAMILY)
Caenorhabditis elegans	utp--glucose-1-phosphate uridylyltransferase family protein	4	P:GO:0009792; P:GO:0000003; P:GO:0040010; F:GO:0016740	-		IPR002618; G3DSA:3.90.550.10 (GENE3D), PTHR11952:SF2 (PANTHER), SSF53448 (SUPERFAMILY)

Caenorhabditis elegans	udp-n-acetylglucosamine pyrophosphorylase	6	F:GO:0016779; P:GO:0009792; P:GO:0008152; P:GO:0000003; P:GO:0040010; P:GO:0009847	-	EC:2.7.7.0	IPR002618; G3DSA:3.90.550.10 (GENE3D), PTHR11952:SF2 (PANTHER), SSF53448 (SUPERFAMILY)
Caenorhabditis elegans	utp--glucose-1-phosphate uridylyltransferase family protein	4	P:GO:0009792; P:GO:0000003; P:GO:0040010; F:GO:0016740	-		IPR002618; G3DSA:3.90.550.10 (GENE3D), PTHR11952:SF2 (PANTHER), SSF53448 (SUPERFAMILY)
Caenorhabditis elegans	udp-n-acetylglucosamine pyrophosphorylase	6	F:GO:0016779; P:GO:0009792; P:GO:0008152; P:GO:0000003; P:GO:0040010; P:GO:0009847	-	EC:2.7.7.0	IPR002618; G3DSA:3.90.550.10 (GENE3D), PTHR11952:SF2 (PANTHER), SSF53448 (SUPERFAMILY)
Caenorhabditis elegans	udp-n-acetylglucosamine pyrophosphorylase	6	F:GO:0016779; P:GO:0009792; P:GO:0008152; P:GO:0000003; P:GO:0040010; P:GO:0009847	-	EC:2.7.7.0	IPR002618; G3DSA:3.90.550.10 (GENE3D), PTHR11952:SF2 (PANTHER), SSF53448 (SUPERFAMILY)
	-	0				-
	-	0				-
Brugia malayi	death-associated protein ki-se 1	7	F:GO:0005516; P:GO:0007243; F:GO:0005524; C:GO:0015629; F:GO:0016301; P:GO:0008624; P:GO:0006468	-		IPR002110; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER)
	-	0				-
Caenorhabditis briggsae	dead (asp-glu-ala-asp) box polypeptide partial	4	F:GO:0003676; F:GO:0005524; F:GO:0008270; F:GO:0008026	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis brenneri	isoleucyl-tr- synthetase	5	F:GO:0004822; F:GO:0008270; P:GO:0006428; F:GO:0005524; C:GO:0005759	-	EC:6.1.1.5	IPR002300; IPR002301; IPR014729; PTHR11946 (PANTHER)
Caenorhabditis elegans	nuclear receptor subfamily group member 6	13	F:GO:0008270; P:GO:0009628; F:GO:0004887; P:GO:0000122; F:GO:0043565; P:GO:0019915; P:GO:0032501; F:GO:0005515; F:GO:0003700; P:GO:0007165; F:GO:0003707; C:GO:0005634; P:GO:0009605	-		IPR001628; IPR013088; PR00350 (PRINTS), PTHR11865 (PANTHER), PTHR11865:SF218 (PANTHER), SSF57716 (SUPERFAMILY)
	-	0				-

Caenorhabditis sp. PS1010	hypothetical protein Csp3_JD06.005 [Caenorhabditis sp. PS1010]	0		C:GO:0016020; F:GO:0005337; P:GO:0006810		IPR002259; PTHR10332:SF6 (PANTHER)
Xenopus laevis	alpha cardiac myosin heavy chain	0		P:GO:0055010; P:GO:0006936; C:GO:0005859; C:GO:0048471; P:GO:0008152; F:GO:0000146; F:GO:0016887; P:GO:0055009; P:GO:0001701; P:GO:0007522; P:GO:0008217; P:GO:0043462; F:GO:0046982; F:GO:0008270; F:GO:0042803; F:GO:0005524; C:GO:0030017; P:GO:0030049; C:GO:0030016; P:GO:0030048; F:GO:0008307; F:GO:0000166; P:GO:0030239; P:GO:0008016; C:GO:0043292; P:GO:0007512; C:GO:0016459;		-
Haemonchus contortus	legumain	8	C:GO:0005737; P:GO:0009792; F:GO:0008233; P:GO:0040015; C:GO:0045177; C:GO:0043231; P:GO:0000003; P:GO:0006508	-		IPR001096; PTHR12000:SF4 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	legumain	8	C:GO:0005737; P:GO:0009792; F:GO:0008233; P:GO:0040015; C:GO:0045177; C:GO:0043231; P:GO:0000003; P:GO:0006508	-		IPR001096; PTHR12000:SF4 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	spastic paraplegia 7	6	P:GO:0030163; F:GO:0005524; C:GO:0016021; F:GO:0017111; P:GO:0006508; F:GO:0008270	-	EC:3.6.1.15	G3DSA:3.40.50.300 (GENE3D), PTHR23076 (PANTHER), PTHR23076:SF2 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	spastic paraplegia 7	6	P:GO:0030163; F:GO:0005524; C:GO:0016021; F:GO:0017111; P:GO:0006508; F:GO:0008270	-	EC:3.6.1.15	G3DSA:3.40.50.300 (GENE3D), PTHR23076 (PANTHER), PTHR23076:SF2 (PANTHER), SSF52540 (SUPERFAMILY)

Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
	-	0				-
Loa loa	ras-related gtp binding a	10	P:GO:0006915; F:GO:0005525; C:GO:0005794; P:GO:0045919; F:GO:0051219; P:GO:0019048; C:GO:0005634; F:GO:0046982; P:GO:0007264; F:GO:0042803	-		IPR006762; G3DSA:3.40.50.300 (GENE3D), PTHR11259:SF1 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	af221132_1diacylglycerol acyltransferase	1	C:GO:0016020	-		-
Caenorhabditis briggsae	briggsae cbr-pmt-2 protein	0		F:GO:0008168; P:GO:0008152		-
	-	0				SignalP (SIGNALP)
Camponotus floridanus	serine threonine protein ki-se	0		F:GO:0004674; F:GO:0042302; F:GO:0004672; F:GO:0016787; P:GO:0006468; F:GO:0000166; F:GO:0003674; F:GO:0005524; F:GO:0016301; C:GO:0005575; P:GO:0008152; P:GO:0008150		IPR008160; PTHR10499 (PANTHER), PTHR10499:SF114 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Ailuropoda melanoleuca	transmembrane protein	8	C:GO:0030663; C:GO:0005792; C:GO:0005793; F:GO:0005515; P:GO:0016192; C:GO:0016021; C:GO:0042589; P:GO:0015031	-		SignalP (SIGNALP)
Brugia malayi	k acetyltransferase 2b	13	F:GO:0004402; C:GO:0000123; F:GO:0019901; C:GO:0031672; P:GO:0045736; C:GO:0031674; C:GO:0000776; P:GO:0042326; F:GO:0003713; F:GO:0004861; P:GO:0045944; C:GO:0042641; P:GO:0016573	-	EC:2.3.1.48	IPR016181; PTHR22880 (PANTHER), PTHR22880:SF2 (PANTHER)
	-	0				-
Caenorhabditis elegans	glycoprotein hormone alpha 2	4	P:GO:0006952; C:GO:0016021; C:GO:0005615; F:GO:0005179	-		IPR004133; IPR018245

	-	0				-
	-	0				-
Haemonchus contortus	ligand-gated ion channel family member (lgc-41)	6	C:GO:0045211; C:GO:0030054; F:GO:0005515; F:GO:0005230; P:GO:0006811; C:GO:0016021	-		IPR006201; IPR006202; IPR018000; PTHR18945:SF16 (PANTHER)
	-	0				-
	-	0				-
Homo sapiens	argininosucci-te synthetase 1	22	C:GO:0005764; P:GO:0006526; C:GO:0070852; P:GO:0001889; P:GO:0007584; C:GO:0005741; P:GO:0000050; P:GO:0043434; F:GO:0005524; P:GO:0051384; F:GO:0005515; P:GO:0042493; P:GO:0001822; P:GO:0010043; P:GO:0032496; P:GO:0006953; F:GO:0004055; C:GO:0005783; P:GO:0000053; F:GO:0015643; C:GO:0005634; C:GO:0043204	-	EC:6.3.4.5	IPR001518; G3DSA:1.20.5.470 (GENE3D), SSF69864 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	phospholipid-transporting atpase	6	F:GO:0043492; F:GO:0022892; F:GO:0016820; F:GO:0000166; P:GO:0008152; C:GO:0016020	-	EC:3.6.3.0	-
Ancylostoma caninum	metalloprotease 1 precursor	2	F:GO:0046872; F:GO:0008237	-		IPR013032; PTHR10127 (PANTHER), PTHR10127:SF60 (PANTHER)
	-	0				-
Caenorhabditis elegans	nucleolar complex-associated protein	1	C:GO:0005730	-		IPR011501
Brugia malayi	calcium atpase	6	F:GO:0005388; C:GO:0016021; P:GO:0006754; F:GO:0005524; P:GO:0006816; C:GO:0005576	-	EC:3.6.3.8	-
Caenorhabditis elegans	uncoordi-ted family member (unc-44)	5	C:GO:0016021; P:GO:0007156; F:GO:0005509; F:GO:0005515; C:GO:0005886	-		-

Caenorhabditis briggsae	pat2_caebr ame: full=integrin alpha pat-2 ame: full=paralyzed arrest at two-fold protein 2 flags: precursor	11	P:GO:0009792; F:GO:0004872; P:GO:0002119; P:GO:0007229; P:GO:0018991; P:GO:0032940; P:GO:0007155; P:GO:0040007; P:GO:0006898; P:GO:0040039; C:GO:0008305	-		-
	-	0				-
Caenorhabditis elegans	ubiquinone biosynthesis protein	15	P:GO:0040010; P:GO:0008340; P:GO:0051094; C:GO:0005739; F:GO:0046914; P:GO:0055114; P:GO:0006744; P:GO:0045333; P:GO:0000003; F:GO:0016491; P:GO:0019538; P:GO:0042493; P:GO:0006119; P:GO:0030534; P:GO:0048520	-		IPR009078; IPR011566; IPR012347
Caenorhabditis briggsae	transmembrane protein 68	6	F:GO:0008415; P:GO:0045454; C:GO:0016020; P:GO:0008152; F:GO:0016491; F:GO:0016209	-		IPR002123; PTHR22753 (PANTHER), PTHR22753:SF2 (PANTHER), SignalP (SIGNALP)
	-	0				-
Macaca mulatta	small subunit 1	8	C:GO:0005737; P:GO:0008284; C:GO:0005886; F:GO:0004198; F:GO:0005509; P:GO:0006508; C:GO:0005634; F:GO:0046982	-		-
	-	0				-
Loa loa	fh1 fh2 domain-containing protein 3	4	P:GO:0030036; C:GO:0005856; C:GO:0005737; F:GO:0003779	-		SignalP (SIGNALP)
Macaca mulatta	b chain activator-bound structure of human pyruvate ki-se m2	9	F:GO:0004743; F:GO:0005515; F:GO:0030955; F:GO:0005524; F:GO:0000287; P:GO:0006096; P:GO:0012501; C:GO:0005634; C:GO:0005829	-	EC:2.7.1.40	IPR001697; IPR011037; IPR015793; IPR015806

Loa loa	polymerase iii (d- directed) polypeptide 155kda	9	F:GO:0003899; P:GO:0009615; F:GO:0008270; P:GO:0032728; P:GO:0045087; F:GO:0003677; F:GO:0032549; P:GO:0006351; C:GO:0005666	-	EC:2.7.7.6	IPR015700; PTHR19376 (PANTHER), SSF64484 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis elegans	lethal essential for life l2efl	2	P:GO:0009408; F:GO:0042802	-		-
	-	0				-
Loa loa	nuclear hormone receptor family member (nhr-23)	6	F:GO:0003700; F:GO:0043565; F:GO:0003707; C:GO:0005634; F:GO:0008270; P:GO:0006355	-		IPR001628; IPR008946; IPR013088; PR00350 (PRINTS), PTHR11865 (PANTHER), PTHR11865:SF178 (PANTHER), SSF57716 (SUPERFAMILY)
Loa loa	hypothetical protein LOAG_12429 [Loa loa]	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical tyrosi-se-like protein in chromosome	4	F:GO:0005515; F:GO:0046872; P:GO:0008152; F:GO:0016491	-		IPR002227; IPR008922; PTHR11474 (PANTHER), PTHR11474:SF1 (PANTHER)
	-	0				IPR000436; IPR016060; SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein T09B4.7 [Caenorhabditis elegans]	0		F:GO:0005524; F:GO:0004672; F:GO:0000166; P:GO:0006468		-
Loa loa	tpr domain containing protein	0		F:GO:0005488		IPR011990; SSF48452 (SUPERFAMILY)
Angiostrongylus cantonensis	homeobox family member	5	F:GO:0003700; F:GO:0030528; F:GO:0043565; C:GO:0005634; P:GO:0006355	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				PTHR12751 (PANTHER), PTHR12751:SF3 (PANTHER)
	-	0				-
Sordaria macrospora	un-med protein product [Sordaria macrospora]	0				-
Loa loa	hypothetical protein LOAG_01266 [Loa loa]	0				IPR015943; IPR017986; IPR019781; PTHR22847 (PANTHER), PTHR22847:SF48 (PANTHER)
Brugia malayi	zinc c2h2 type family protein	1	F:GO:0005488	-		IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)
Loa loa	zinc finger protein	0		F:GO:0003676; C:GO:0005783; C:GO:0005794; P:GO:0006886; F:GO:0008270; C:GO:0005622		-
	-	0				IPR012335; PTHR18929 (PANTHER)

Caenorhabditis briggsae	cg7840-pa	6	F:GO:0016491; P:GO:0016095; C:GO:0044425; P:GO:0006488; C:GO:0005783; P:GO:0019348	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				IPR018114
Caenorhabditis briggsae	briggsae cbr-unc-104 protein	10	F:GO:0003777; P:GO:0007411; P:GO:0048490; P:GO:0007528; C:GO:0005874; P:GO:0008345; P:GO:0047496; F:GO:0005524; P:GO:0016188; C:GO:0005871	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	-dh oxidase	2	P:GO:0008152; F:GO:0003824	-		IPR001155; IPR013785; PTHR22893 (PANTHER), PTHR22893:SF6 (PANTHER), SSF51395 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein Y41D4A.7 [Caenorhabditis elegans]	0				-
Schizosaccharomyces pombe	histone acetyltransferase mst2	14	P:GO:0009880; P:GO:0045941; F:GO:0004402; P:GO:0006323; P:GO:0009952; P:GO:0001502; C:GO:0070776; P:GO:0048703; F:GO:0003713; P:GO:0030099; P:GO:0043966; P:GO:0016481; C:GO:0000790; P:GO:0010172	-	EC:2.3.1.48	IPR002717; IPR016181; PTHR10615 (PANTHER), PTHR10615:SF29 (PANTHER)
	-	0				-
Caenorhabditis elegans	pdxp protein	1	F:GO:0003824	-		G3DSA:3.40.50.1000 (GENE3D), PTHR19288 (PANTHER), PTHR19288:SF11 (PANTHER), SSF56784 (SUPERFAMILY)
Caenorhabditis elegans	gex interacting protein family member (gei-11)	1	P:GO:0007275	-		IPR015495; PTHR10641:SF13 (PANTHER)
Caenorhabditis elegans	gex interacting protein family member (gei-11)	1	P:GO:0007275	-		-
Caenorhabditis briggsae	phosphoglycolate phosphatase	1	F:GO:0003824	-		IPR005834; G3DSA:3.40.50.1000 (GENE3D), PTHR12725 (PANTHER), PTHR12725:SF4 (PANTHER), SignalP (SIGNALP), SSF56784 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-

	-	0				-
Caenorhabditis elegans	carbonic anhydrase	0		F:GO:0046872; P:GO:0006730; F:GO:0008270; F:GO:0016829; F:GO:0004089; C:GO:0005575		IPR001148; PTHR18952:SF34 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-coq-8 protein	0				-
Caenorhabditis briggsae	ubiquinol-cytochrome c reductase hinge protein variant 1	2	P:GO:0055114; F:GO:0016491	-		IPR003422; IPR023184
Caenorhabditis elegans	ankyrin repeat and fyve domain containing 1	4	P:GO:0009792; F:GO:0005488; P:GO:0040010; C:GO:0010008	-		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF248 (PANTHER)
Caenorhabditis briggsae	oligopeptide transporter	3	C:GO:0016021; P:GO:0006857; F:GO:0042936	-		-
Caenorhabditis elegans	lfi-1	4	F:GO:0005515; C:GO:0044430; C:GO:0005694; P:GO:0009987	-		IPR006829; IPR009053; PD936484 (PRODOM), PTHR23159 (PANTHER), PTHR23159:SF6 (PANTHER)
Caenorhabditis elegans	lfi-1	4	F:GO:0005515; C:GO:0044430; C:GO:0005694; P:GO:0009987	-		IPR006829; IPR009053; PD936484 (PRODOM), PTHR23159 (PANTHER), PTHR23159:SF6 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG11012 [Caenorhabditis briggsae]	0		F:GO:0004623; C:GO:0016021; P:GO:0016042; P:GO:0006644; F:GO:0005515		-
Caenorhabditis elegans	vermilion	35	P:GO:0043892; P:GO:0001752; P:GO:0035071; P:GO:0048069; P:GO:0035224; P:GO:0050770; P:GO:0019441; P:GO:0008348; P:GO:0006911; P:GO:0007418; F:GO:0020037; P:GO:0007377; P:GO:0046843; P:GO:0040010; P:GO:0007254; C:GO:0005737; F:GO:0004833; P:GO:0007386; P:GO:0009997; F:GO:0016564; P:GO:0035277; F:GO:0042802; P:GO:0007376; P:GO:0001736; P:GO:0046844; F:GO:0043565; P:GO:0007484; P:GO:0007365;	-	EC:1.13.11.11	IPR004981
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	hypothetical protein T27E4.7 [Caenorhabditis elegans]	0				-
	-	0				PTHR19229 (PANTHER), PTHR19229:SF18 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	tailless	7	F:GO:0003700; F:GO:0043565; F:GO:0005515; F:GO:0003707; C:GO:0005634; F:GO:0008270; P:GO:0006355	-		-
Caenorhabditis elegans	dihydrouridine synthase domain containing protein	6	F:GO:0003677; P:GO:0055114; F:GO:0050660; F:GO:0008270; F:GO:0017150; P:GO:0008033	-		-
	-	0				-
Drosophila pseudoobscura pseudoobscura	chromosome 9 open reading frame 4	0		F:GO:0004500; C:GO:0016021; P:GO:0006548		IPR005018; PTHR23130 (PANTHER), PTHR23130:SF3 (PANTHER)
Caenorhabditis briggsae	actin binding	2	P:GO:0009792; P:GO:0040010	-		IPR013784; IPR019008; PTHR13605 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	ufm1-conjugating enzyme 1	3	F:GO:0071568; F:GO:0005515; P:GO:0071569	-		-
Caenorhabditis elegans	carrier protein	4	F:GO:0005488; C:GO:0005743; P:GO:0055085; C:GO:0016021	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF38 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Loa loa	hypothetical protein LOAG_12576 [Loa loa]	0				-
Loa loa	hypothetical protein LOAG_12576 [Loa loa]	0				-
Loa loa	nucleoredoxin	2	F:GO:0004791; C:GO:0005634	-	EC:1.8.1.9	IPR000866; IPR012335; IPR012336; PTHR13871 (PANTHER), PTHR13871:SF6 (PANTHER)
Caenorhabditis briggsae	beta chain spectrin	3	C:GO:0044459; P:GO:0016044; F:GO:0003779	-		IPR001605; IPR001849; IPR002017; IPR011993; IPR018159; G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF48 (PANTHER), SSF46966 (SUPERFAMILY), SSF50729 (SUPERFAMILY)
Caenorhabditis briggsae	beta chain spectrin	3	C:GO:0044459; P:GO:0016044; F:GO:0003779	-		IPR001605; IPR001849; IPR002017; IPR011993; IPR018159; G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF48 (PANTHER), SSF46966 (SUPERFAMILY), SSF50729 (SUPERFAMILY)

Caenorhabditis briggsae	beta chain spectrin	3	C:GO:0044459; P:GO:0016044; F:GO:0003779	-		IPR001605; IPR001849; IPR002017; IPR011993; IPR018159; G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF48 (PANTHER), SSF46966 (SUPERFAMILY), SSF50729 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Ailuropoda melanoleuca	protein phosphatase catalytic alpha-like isoform 2	15	P:GO:0006470; P:GO:0030324; C:GO:0005829; P:GO:0007049; C:GO:0005730; F:GO:0046872; F:GO:0042802; P:GO:0051301; C:GO:0005741; F:GO:0004722; P:GO:0046822; C:GO:0070688; P:GO:0005977; P:GO:0048754; F:GO:0008599	-		-
	-	0				-
	-	0				-
Brugia malayi	transcription factor cp2-like 1	0		P:GO:0000902; F:GO:0003677; C:GO:0005634; P:GO:0006357; P:GO:0019079; F:GO:0016566; P:GO:0000122; P:GO:0006694; C:GO:0016020; P:GO:0008340; F:GO:0016565; P:GO:0007431; F:GO:0003700; P:GO:0016481; P:GO:0001525; C:GO:0005737; P:GO:0007028; F:GO:0003714; P:GO:0045449; P:GO:0002070; P:GO:0045927; P:GO:0007565		PTHR11037 (PANTHER)
	-	0				-
Caenorhabditis elegans	moz sas family protein	1	F:GO:0005488	-		PTHR10615 (PANTHER), PTHR10615:SF25 (PANTHER)
Caenorhabditis briggsae	u632_caeel ame: full=upf0632 protein flags: precursor	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-rsr-2 protein	4	P:GO:0040035; P:GO:0040027; P:GO:0008340; P:GO:0040007	-		-
	-	0				-

Loa loa	innexin protein 13	5	P:GO:0040035; C:GO:0005921; P:GO:0040010; P:GO:0040011; P:GO:0002009	-		IPR000990; SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-taf-5 protein	0		P:GO:0045449; F:GO:0030528; C:GO:0005634		-
Ciona intestinalis	riboflavin ki-se	4	F:GO:0008531; F:GO:0005488; P:GO:0009231; C:GO:0005829	-	EC:2.7.1.26	IPR015865
Caenorhabditis briggsae	briggsae cbr-ptr-14 protein	4	P:GO:0018996; C:GO:0016020; P:GO:0040018; P:GO:0040011	-		IPR003392
Caenorhabditis elegans	gamma-glutamyltranspeptidase family protein	1	F:GO:0003840	-	EC:2.3.2.2	IPR000101; SSF56235 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	sterol regulatory element-binding protein cleavage-activating protein	12	P:GO:0045540; P:GO:0006994; C:GO:0016021; C:GO:0005794; P:GO:0009792; C:GO:0031090; P:GO:0007165; C:GO:0044446; F:GO:0005070; C:GO:0012505; C:GO:0005783; C:GO:0005625	-		IPR000731; PF12349 (PFAM), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	lethal giant discs 1	1	F:GO:0005515	-		IPR006608
	-	0				-
Caenorhabditis elegans	molybdenum cofactor synthesis domain protein	2	P:GO:0006777; F:GO:0003824	-		IPR001453; IPR008284; IPR020817; PTHR10192 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	tr- modification gtpase family protein	2	F:GO:0005488; P:GO:0009987	-		IPR021629; PTHR12691 (PANTHER), PTHR12691:SF3 (PANTHER), SignalP (SIGNALP)
	-	0				-
	malic enzyme	6	F:GO:0046872; F:GO:0051287; C:GO:0005759; F:GO:0016619; P:GO:0006108; P:GO:0055114	-	EC:1.1.1.38	IPR001891; IPR012301; G3DSA:3.40.50.10380 (GENE3D), PTHR23406 (PANTHER), PTHR23406:SF2 (PANTHER), SSF53223 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-ego-1 protein	1	F:GO:0005515	-		SignalP (SIGNALP)

Caenorhabditis briggsae	ns1 binding protein	0		C:GO:0005634; F:GO:0003674; P:GO:0055114; F:GO:0016491; C:GO:0005575; F:GO:0005515; P:GO:0008150; C:GO:0005856; F:GO:0045480		-
Parvibaculum lavamentivorans DS-1	fad linked oxidase domain protein	1	F:GO:0016491	-		PTHR11748 (PANTHER), PTHR11748:SF6 (PANTHER)
Caenorhabditis elegans	dachsous 1	7	P:GO:0002119; P:GO:0007156; C:GO:0005886; P:GO:0040010; F:GO:0005509; P:GO:0040011; C:GO:0016021	-		IPR002126; IPR015919; PTHR10596 (PANTHER), PTHR10596:SF80 (PANTHER)
	-	0				-
Loa loa	hypothetical protein LOAG_03210 [Loa loa]	0				IPR011333; IPR013069
	-	0				-
Caenorhabditis elegans	vacuolar protein sorting-associated protein 45	7	C:GO:0043231; P:GO:0000003; P:GO:0018996; P:GO:0002119; C:GO:0044444; P:GO:0006898; P:GO:0051649	-		IPR001619; G3DSA:3.40.50.1910 (GENE3D), PTHR11679:SF3 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Saccoglossus kowalevskii	PREDICTED: hypothetical protein [Saccoglossus kowalevskii]	0		F:GO:0046872; C:GO:0016020; F:GO:0008270; F:GO:0005515; F:GO:0005215; P:GO:0006810		-
Loa loa	dep domain-containing	0		P:GO:0040010		PTHR13179 (PANTHER)
Loa loa	dep domain-containing	0		P:GO:0040010		PTHR13179 (PANTHER)
Caenorhabditis elegans	hypothetical protein F54C1.1 [Caenorhabditis elegans]	5	P:GO:0005975; P:GO:0030259; C:GO:0016021; F:GO:0030246; F:GO:0016758	-	EC:2.4.1.0	-
	-	0				-
	-	0				IPR013032
	-	0				-
Caenorhabditis elegans	hypothetical protein Y73C8B.1 [Caenorhabditis elegans]	0				IPR010463
	-	0				IPR001283; IPR014044; PTHR10334:SF11 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	helicase srcap-like	1	P:GO:0000003	-		SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein T07F8.4 [Caenorhabditis elegans]	1	P:GO:0000003	-		SignalP (SIGNALP)

Homo sapiens	translocase of outer mitochondrial membrane 7 homolog	5	F:GO:0015450; C:GO:0016021; C:GO:0005742; F:GO:0004872; P:GO:0006626	-		IPR012621; PTHR16463 (PANTHER)
Monosiga brevicollis MX1	hypothetical protein [Monosiga brevicollis MX1]	0				-
Monosiga brevicollis MX1	fibrillin 2- partial	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	P:GO:0009792; P:GO:0005975; F:GO:0004133; P:GO:0043170	-		-
	-	0				SignalP (SIGNALP)
Pongo abelii	solute carrier family 25 (mitochondrial carrier adenine nucleotide translocator) member 6	8	P:GO:0006915; F:GO:0005515; P:GO:0055085; F:GO:0005471; C:GO:0005744; C:GO:0016021; C:GO:0042645; P:GO:0044419	-		IPR001993; IPR002113; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF35 (PANTHER)
Caenorhabditis elegans	hypothetical protein C18C4.7 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	briggsae cbr-pif-1 protein	0		F:GO:0016887		-
Caenorhabditis briggsae	briggsae cbr-pgp-3 protein	8	C:GO:0009986; C:GO:0005624; P:GO:0042493; F:GO:0005515; F:GO:0008559; P:GO:0055085; F:GO:0005524; C:GO:0016021	-	EC:3.6.3.44	-
Caenorhabditis briggsae	- h exchanger family member (nhx-9)	3	P:GO:0009792; F:GO:0015299; P:GO:0006812	-		IPR006153; SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	8	P:GO:0006810; C:GO:0016021; P:GO:0040007; P:GO:0045449; F:GO:0005524; P:GO:0010171; P:GO:0002119; F:GO:0016887	-		IPR003495; G3DSA:3.40.50.300 (GENE3D), PTHR19241 (PANTHER), PTHR19241:SF30 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-hrd-1 protein	8	F:GO:0008270; P:GO:0030433; C:GO:0005730; C:GO:0016021; F:GO:0016881; P:GO:0006916; F:GO:0005515; C:GO:0005789	-	EC:6.3.2.0	IPR001841; IPR013083; IPR018957; PTHR12477 (PANTHER), PTHR12477:SF11 (PANTHER), SignalP (SIGNALP), SSF57850 (SUPERFAMILY)

Caenorhabditis elegans	briggsae cbr-hrd-1 protein	8	F:GO:0008270; P:GO:0030433; C:GO:0005730; C:GO:0016021; F:GO:0016881; P:GO:0006916; F:GO:0005515; C:GO:0005789	-	EC:6.3.2.0	IPR001841; IPR013083; IPR018957; PTHR12477 (PANTHER), PTHR12477:SF11 (PANTHER), SignalP (SIGNALP), SSF57850 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein C50B8.5 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				-
Brugia malayi	receptor family ligand binding region containing protein	4	F:GO:0004872; P:GO:0009190; F:GO:0016849; F:GO:0000166	-		IPR001828; G3DSA:3.40.50.2300 (GENE3D), SSF53822 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Macaca mulatta	ribosomal protein l5	8	C:GO:0005730; P:GO:0006364; P:GO:0042273; F:GO:0003735; P:GO:0006414; F:GO:0005515; C:GO:0022625; F:GO:0008097	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				PTHR13190 (PANTHER), PTHR13190:SF2 (PANTHER)
Leishmania infantum JPCM5	heavy chain non-muscle	15	P:GO:0051234; P:GO:0007010; F:GO:0005515; P:GO:0007275; F:GO:0000166; C:GO:0044430; C:GO:0015629; P:GO:0006928; F:GO:0003774; C:GO:0043234; P:GO:0030154; P:GO:0002376; P:GO:0048646; C:GO:0044459; C:GO:0005938	-		PD936484 (PRODOM)
Caenorhabditis elegans	vacuolar protein sorting vps16	11	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0008340; C:GO:0031902; P:GO:0006886; P:GO:0040011; P:GO:0008219; C:GO:0005765; P:GO:0040007; P:GO:0048565	-		IPR006925; PTHR12811 (PANTHER)
	-	0				SignalP (SIGNALP)

Caenorhabditis briggsae	myosin heavy nonmuscle or smooth muscle	4	C:GO:0016459; F:GO:0005524; F:GO:0051015; F:GO:0003774	-		IPR001609; PTHR13140 (PANTHER), PTHR13140:SF23 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	6	F:GO:0046872; F:GO:0051287; C:GO:0005759; F:GO:0016619; P:GO:0006108; P:GO:0055114	-	EC:1.1.1.38	-
	-	0				-
Caenorhabditis elegans	d- polymerase i	4	P:GO:0006259; F:GO:0004527; F:GO:0003676; F:GO:0016779	-	EC:2.7.7.0	IPR001098; G3DSA:1.10.150.20 (GENE3D), G3DSA:3.30.70.370 (GENE3D), PTHR10133 (PANTHER), SSF56672 (SUPERFAMILY)
Loa loa	isy1-like splicing family protein	3	P:GO:0018996; P:GO:0040035; P:GO:0002119	-		IPR009360; PTHR13021:SF7 (PANTHER)
Caenorhabditis briggsae	myosin heavy chain	6	C:GO:0032982; F:GO:0003779; F:GO:0005524; F:GO:0003774; C:GO:0031672; P:GO:0007626	-		IPR015650; PTHR13140 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
Angiostrongylus cantonensis	ttk protein ki-se	8	P:GO:0000278; P:GO:0006468; P:GO:0007051; P:GO:0023052; F:GO:0004674; F:GO:0042802; P:GO:0048522; F:GO:0005524	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22974 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	f-box spry domain-containing protein 1-like	6	C:GO:0030054; P:GO:0007274; C:GO:0042734; C:GO:0031594; C:GO:0045211; P:GO:0045886	-		IPR001870; IPR003877; IPR008985; PTHR12245 (PANTHER)
Caenorhabditis briggsae	g in family member (glb-29)	3	F:GO:0020037; P:GO:0015671; F:GO:0019825	-		IPR009050; IPR012292
Caenorhabditis elegans	transmembrane protein 144	1	P:GO:0002119	-		IPR012435; SignalP (SIGNALP)
Strongylocentrotus purpuratus	pdcd6ip protein	0				G3DSA:1.20.120.560 (GENE3D), PTHR23030 (PANTHER), PTHR23030:SF11 (PANTHER)
Caenorhabditis elegans	briggsae cbr-tnt-3 protein	2	P:GO:0043050; P:GO:0006952	-		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-coq-8 protein	2	F:GO:0004672; C:GO:0005739	-		IPR004147; PTHR10566 (PANTHER), PTHR10566:SF7 (PANTHER)

Caenorhabditis briggsae	dedicator of cytokinesis	7	F:GO:0005083; P:GO:0043652; C:GO:0005886; F:GO:0032403; F:GO:0019899; P:GO:0040039; F:GO:0017124	-		-
	-	0				-
	-	0				-
Homo sapiens	dipeptidyl-peptidase 7	9	F:GO:0008239; C:GO:0016023; C:GO:0005764; F:GO:0005515; F:GO:0004177; C:GO:0005576; F:GO:0008236; P:GO:0006508; C:GO:0005829	-	EC:3.4.11.0	IPR008758; PTHR11010:SF10 (PANTHER)
Macrovipera lebetina	c-type lectin	0		F:GO:0005488; F:GO:0005529; C:GO:0005576		IPR001304; IPR016186; IPR016187; PTHR22801 (PANTHER), PTHR22801:SF9 (PANTHER), SignalP (SIGNALP)
	-	0				-
Brugia malayi	hexoki-se family protein	5	P:GO:0060361; F:GO:0005515; F:GO:0005524; P:GO:0006096; F:GO:0004396	-	EC:2.7.1.1	IPR001312; IPR022673; G3DSA:3.40.367.20 (GENE3D), SSF53067 (SUPERFAMILY)
Heliconius melpomene	endonuclease-reverse transcriptase -e01	0		F:GO:0003723; P:GO:0006278; F:GO:0004519; F:GO:0003677; F:GO:0003964		-
	-	0				-
Caenorhabditis elegans	briggsae cbr-ymel-1 protein	6	F:GO:0016887; P:GO:0030163; F:GO:0005524; C:GO:0016021; P:GO:0006508; F:GO:0008237	-		IPR003593; IPR003959; IPR003960; G3DSA:3.40.50.300 (GENE3D), PTHR23076 (PANTHER), PTHR23076:SF10 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-ymel-1 protein	7	C:GO:0005743; F:GO:0016887; F:GO:0004222; P:GO:0030163; F:GO:0005524; C:GO:0016021; P:GO:0006508	-	EC:3.4.24.0	IPR000642; IPR003593; IPR003959; IPR003960; IPR005936; G3DSA:1.10.8.60 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23076 (PANTHER), PTHR23076:SF10 (PANTHER), SSF140990 (SUPERFAMILY), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-ymel-1 protein	7	C:GO:0005743; F:GO:0016887; F:GO:0004222; P:GO:0030163; F:GO:0005524; C:GO:0016021; P:GO:0006508	-	EC:3.4.24.0	IPR000642; IPR003593; IPR003959; IPR003960; IPR005936; G3DSA:1.10.8.60 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23076 (PANTHER), PTHR23076:SF10 (PANTHER), SSF140990 (SUPERFAMILY), SSF52540 (SUPERFAMILY)

Caenorhabditis elegans	briggsae cbr-glr-1 protein	19	F:GO:0005234; C:GO:0030054; C:GO:0030288; P:GO:0007215; C:GO:0030425; P:GO:0040007; C:GO:0043195; P:GO:0060992; F:GO:0004971; P:GO:0006811; C:GO:0030666; P:GO:0051968; P:GO:0002119; C:GO:0045211; C:GO:0043025; P:GO:0050803; P:GO:0009792; C:GO:0008328; C:GO:0014069	-		IPR001320; IPR001508; IPR001638; IPR015683; G3DSA:3.40.190.10 (GENE3D), PTHR18966:SF29 (PANTHER), SSF53850 (SUPERFAMILY)
	-	0				-
Loa loa	hypothetical protein LOAG_04165 [Loa loa]	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	clathrin coat assembly protein	19	F:GO:0004984; F:GO:0008565; P:GO:0048072; P:GO:0016183; C:GO:0016021; C:GO:0008021; P:GO:0040007; P:GO:0000003; P:GO:0007608; P:GO:0006727; P:GO:0010171; P:GO:0002119; P:GO:0007269; C:GO:0030117; F:GO:0005515; P:GO:0006886; P:GO:0009792; P:GO:0007040; F:GO:0005549	-		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	multiple coagulation factor deficiency 2	3	P:GO:0009792; P:GO:0006810; C:GO:0044444	-		IPR011992; IPR018247; IPR018249; PTHR23104 (PANTHER), SignalP (SIGNALP), SSF47473 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
synthetic construct	and pleckstrin domain protein 1 (chondrocyte-derived)	6	C:GO:0005737; C:GO:0005856; F:GO:0005089; C:GO:0019898; F:GO:0008092; P:GO:0035023	-		-
	-	0				-
	-	0				-

	-	0				-
	-	0				-
Caenorhabditis elegans	polymerase iii (d- directed) polypeptide 155kda	9	F:GO:0003899; P:GO:0009615; F:GO:0008270; P:GO:0032728; P:GO:0045087; F:GO:0003677; F:GO:0032549; P:GO:0006351; C:GO:0005666	-	EC:2.7.7.6	IPR000722; IPR006592; IPR015700; PTHR19376 (PANTHER), SignalP (SIGNALP), SSF64484 (SUPERFAMILY)
Caenorhabditis elegans	deoxyribose-phosphate aldolase	3	C:GO:0005737; F:GO:0004139; P:GO:0009264	-	EC:4.1.2.4	IPR002915; IPR011343; IPR013785; SSF51569 (SUPERFAMILY)
Caenorhabditis elegans	small nuclear r- activating polypeptide 50kda	6	P:GO:0040007; P:GO:0040035; P:GO:0002119; P:GO:0006898; P:GO:0002009; P:GO:0009792	-		IPR022042; PTHR13421 (PANTHER), PTHR13421:SF5 (PANTHER)
Brugia malayi	variant sh3 domain containing protein	4	P:GO:0050807; F:GO:0005089; C:GO:0005622; P:GO:0035023	-		IPR001452; G3DSA:2.30.30.40 (GENE3D), PTHR22826 (PANTHER), PTHR22826:SF16 (PANTHER)
	-	0				-
Caenorhabditis briggsae	zip zinc transporter family protein	4	P:GO:0030001; C:GO:0016021; F:GO:0046873; P:GO:0055085	-		PTHR11040 (PANTHER), PTHR11040:SF6 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	4	P:GO:0030001; C:GO:0016021; F:GO:0046873; P:GO:0055085	-		IPR003689; PTHR11040 (PANTHER), PTHR11040:SF6 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	quinine non-avoider family member (qui-1)	0				-
	-	0				-
	-	0				-
Brugia malayi	zinc c2h2 type family protein	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		PTHR12358 (PANTHER), PTHR12358:SF12 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein T07D1.3 [Caenorhabditis elegans]	0		P:GO:0055114; F:GO:0016491; C:GO:0016021		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	boid related family member (rom-4)	0		C:GO:0016021		-
Caenorhabditis briggsae	tbc1 domain member 10a	5	F:GO:0005097; C:GO:0005622; F:GO:0030165; P:GO:0032313; C:GO:0005902	-		IPR000195; G3DSA:1.10.8.270 (GENE3D), PTHR22957 (PANTHER), PTHR22957:SF49 (PANTHER)
Caenorhabditis elegans	carnitine o-acyltransferase	4	F:GO:0008415; P:GO:0042594; P:GO:0010038; P:GO:0006979	-		IPR000542; PTHR22589:SF8 (PANTHER), SignalP (SIGNALP), SSF52777 (SUPERFAMILY)

Caenorhabditis elegans	progestin and adipoq receptor family member v	1	C:GO:0016021	-		IPR004254; PTHR20855:SF4 (PANTHER), SignalP (SIGNALP)
Homo sapiens	mhc class ib antigen	5	P:GO:0006955; F:GO:0032393; C:GO:0016021; P:GO:0002474; C:GO:0042612	-		IPR001039; IPR011161; IPR011162; PTHR16675 (PANTHER), PTHR16675:SF53 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	periodic tryptophan protein 2 homolog	3	F:GO:0004871; P:GO:0007165; C:GO:0016020	-		PTHR19858 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	organic cation transporter	5	P:GO:0055085; C:GO:0016021; P:GO:0006811; P:GO:0019915; F:GO:0005215	-		PTHR11600 (PANTHER), PTHR11600:SF44 (PANTHER)
Caenorhabditis elegans	hypothetical protein F36H9.7 [Caenorhabditis elegans]	0				IPR000472; G3DSA:2.10.60.10 (GENE3D), SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0000003; P:GO:0005975; P:GO:0009792; P:GO:0019915		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0000003; P:GO:0005975; P:GO:0009792; P:GO:0019915		-
	-	0				IPR002057
Xenopus (Silurana) tropicalis	chromosome transmission fidelity protein 8 homolog	0		P:GO:0006260; F:GO:0003674; P:GO:0007049; P:GO:0008150; C:GO:0005575; C:GO:0005634; F:GO:0003677		IPR018607
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	P:GO:0006952; F:GO:0005488	-		IPR002198; IPR016040; PTHR19410:SF18 (PANTHER), SignalP (SIGNALP), SSF51735 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-acy-3 protein	0		P:GO:0009190; F:GO:0016849		PTHR11920 (PANTHER), PTHR11920:SF6 (PANTHER)
Caenorhabditis briggsae	nuclear receptor nhr-1	8	F:GO:0042802; F:GO:0003700; F:GO:0043565; F:GO:0003707; P:GO:0019915; C:GO:0005634; F:GO:0008270; P:GO:0006355	-		IPR000536; IPR008946; PTHR11865 (PANTHER), PTHR11865:SF218 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis briggsae	leucine-rich repeat protein shoc-2	7	C:GO:0000164; P:GO:0008543; P:GO:0040025; P:GO:0046579; F:GO:0019888; F:GO:0019903; C:GO:0005634	-		IPR001611; IPR003591; PR00019 (PRINTS), G3DSA:3.80.10.10 (GENE3D), PTHR23155 (PANTHER), PTHR23155:SF38 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG22233 [Caenorhabditis briggsae]	3	P:GO:0007411; P:GO:0019915; P:GO:0007413	-		PTHR23051 (PANTHER)
Caenorhabditis briggsae	histidine acid phosphatase family protein	0		F:GO:0016787; C:GO:0016021; C:GO:0016020; F:GO:0003993; P:GO:0008150; C:GO:0005575		IPR000560; G3DSA:3.40.50.1240 (GENE3D), PTHR11567 (PANTHER), PTHR11567:SF13 (PANTHER), SSF53254 (SUPERFAMILY)
	-	0				-
Pongo abelii	complement 1 subcomponent q polypeptide gamma	7	C:GO:0005730; P:GO:0006958; P:GO:0030853; P:GO:0045650; P:GO:0045087; C:GO:0005576; C:GO:0005737	-		IPR001073; IPR008983; PTHR10499 (PANTHER), PTHR10499:SF33 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	receptor protein tyrosine	2	F:GO:0004721; P:GO:0006470	-	EC:3.1.3.16	IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF35 (PANTHER)
	-	0				-
Macaca mulatta	eukaryotic translation initiation factor 3 subunit 2 beta	5	C:GO:0005852; F:GO:0005515; P:GO:0045948; F:GO:0003743; C:GO:0005829	-		-
Ailuropoda melanoleuca	spectrin alpha brain-like isoform 2	20	C:GO:0005829; F:GO:0047485; C:GO:0030018; F:GO:0005516; C:GO:0016328; C:GO:0043234; C:GO:0015630; F:GO:0005509; P:GO:0031532; F:GO:0032403; C:GO:0005624; C:GO:0008091; F:GO:0003779; C:GO:0032437; F:GO:0005200; F:GO:0046982; F:GO:0019905; C:GO:0005916; P:GO:0051693; F:GO:0030507	-		-
	-	0				-

Homo sapiens	solute carrier family 25 (mitochondrial carrier citrate transporter) member 1	6	C:GO:0005743; F:GO:0005515; P:GO:0006843; P:GO:0055085; C:GO:0016021; F:GO:0015137	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF62 (PANTHER)
Brugia malayi	uncoordi-ted protein 40	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	f-box leucine rich repeat protein	0				G3DSA:3.80.10.10 (GENE3D), PTHR23125 (PANTHER), PTHR23125:SF31 (PANTHER), SSF52047 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein T04C4.1 [Caenorhabditis elegans]	0				-
	-	0				IPR002085; PTHR11695:SF3 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	fatty acid amide hydrolase 2	2	F:GO:0016884; C:GO:0016021	-	EC:6.3.5.0	IPR000120; PTHR11895:SF5 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Brugia malayi	collagen col-34	1	F:GO:0042302	-		-
Caenorhabditis briggsae	leucine rich repeat family protein	0		F:GO:0005515		G3DSA:3.80.10.10 (GENE3D), PTHR13824 (PANTHER), PTHR13824:SF6 (PANTHER), SSF52047 (SUPERFAMILY)
Caenorhabditis briggsae	endonuclease iv	4	P:GO:0009792; F:GO:0046872; F:GO:0004519; P:GO:0006974	-		IPR001719; IPR012307; IPR013022; IPR018246
Caenorhabditis briggsae	briggsae cbr-spon-1 protein	1	F:GO:0004867	-		IPR000884; IPR002223; G3DSA:2.20.100.10 (GENE3D), PTHR11311 (PANTHER), PTHR11311:SF2 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	protein ki-se domain containing protein	2	P:GO:0007283; F:GO:0016301	-		G3DSA:3.30.200.20 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
	-	0				-
Caenorhabditis briggsae	myo-2	4	C:GO:0032982; F:GO:0003779; F:GO:0005524; F:GO:0003774	-		-
	-	0				-
Caenorhabditis briggsae	prolyl 4-hydroxylase	6	F:GO:0031418; F:GO:0005506; F:GO:0004656; P:GO:0055114; F:GO:0016702; C:GO:0005783	-	EC:1.14.11.2; EC:1.13.11.0	IPR005123; PTHR10869 (PANTHER), PTHR10869:SF13 (PANTHER)

Caenorhabditis elegans	sucrase- intesti-l	6	C:GO:0016324; F:GO:0030246; F:GO:0004339; F:GO:0004558; P:GO:0005983; C:GO:0016021	-	EC:3.2.1.3; EC:3.2.1.20	IPR000322; PTHR22762:SF10 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-grk-1 protein	1	F:GO:0004672	-		-
	-	0				-
Loa loa	briggsae cbr-snf-1 protein	0		F:GO:0005328; C:GO:0016020; P:GO:0006836; C:GO:0005887		SignalP (SIGNALP)
Caenorhabditis elegans	peroxisome biogenesis factor 10	5	P:GO:0006412; P:GO:0007031; F:GO:0016874; C:GO:0005778; F:GO:0005515	-	EC:3.6.5.3	IPR006845; PTHR23350 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	phosphorylase alpha 1 -like isoform 1	6	C:GO:0005737; F:GO:0016301; F:GO:0004339; C:GO:0043231; P:GO:0005977; F:GO:0005516	-	EC:3.2.1.3	IPR008734; IPR011613; PTHR10749:SF2 (PANTHER)
Caenorhabditis elegans	phosphorylase alpha 1 -like isoform 1	6	C:GO:0005737; F:GO:0016301; F:GO:0004339; C:GO:0043231; P:GO:0005977; F:GO:0005516	-	EC:3.2.1.3	IPR008734; IPR011613; PTHR10749:SF2 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	cyclin m2	3	P:GO:0006811; C:GO:0005886; C:GO:0016021	-		IPR000644; PTHR12064 (PANTHER), PTHR12064:SF6 (PANTHER)
Caenorhabditis elegans	mgc53303 protein	0				-
Brugia malayi	protein-tyrosine phosphatase containing protein	1	F:GO:0004721	-	EC:3.1.3.16	IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
	-	0				-
Ailuropoda melanoleuca	eukaryotic translation initiation factor subunit 8	6	C:GO:0005852; F:GO:0005515; P:GO:0045948; F:GO:0003743; C:GO:0005829; F:GO:0043022	-		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)

Brugia malayi	serine threonine-protein phosphatase 2a 65 kda regulatory subunit a alpha isoform	27	P:GO:0006275; C:GO:0016020; P:GO:0006672; C:GO:0000159; P:GO:0006461; F:GO:0003823; P:GO:0010033; C:GO:0015630; P:GO:0042518; P:GO:0030155; C:GO:0005829; F:GO:0046982; P:GO:0030111; C:GO:0000775; P:GO:0008380; P:GO:0006917; P:GO:0030308; P:GO:0007059; P:GO:0000188; P:GO:0045595; F:GO:0008601; P:GO:0006470; P:GO:0045449; P:GO:0019932; C:GO:0005625; C:GO:0005634; C:GO:0005739	-		IPR000357; IPR011989; IPR016024; IPR021133; PTHR10648 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Homo sapiens	heat shock 70kda protein 1a	18	F:GO:0047485; P:GO:0042026; P:GO:0090084; C:GO:0005739; P:GO:0030308; F:GO:0031625; C:GO:0016607; F:GO:0044183; P:GO:0006916; P:GO:0008285; C:GO:0016234; F:GO:0005524; P:GO:0006402; C:GO:0048471; C:GO:0030529; F:GO:0051082; P:GO:0006986; C:GO:0005783	-		IPR001023; IPR013126; G3DSA:1.20.1270.10 (GENE3D), G3DSA:2.60.34.10 (GENE3D), PTHR19375:SF1 (PANTHER), SSF100920 (SUPERFAMILY), SSF100934 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	P:GO:0019915	-		IPR010291; PTHR23294 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	pyridoxal-phosphate dependent enzyme family protein	2	P:GO:0008152; F:GO:0030170	-		-
	-	0				-

Caenorhabditis elegans	protein ki-se domain containing protein	8	C:GO:0005929; C:GO:0030425; F:GO:0005515; P:GO:0034606; F:GO:0004672; C:GO:0030424; P:GO:0034608; C:GO:0043025	-		IPR000719; IPR001245; IPR011009; IPR017441; IPR020685; IPR020764; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
Loa loa	hypothetical protein LOAG_04203 [Loa loa]	0				-
Angiostrongylus cantonensis	vacuolar membrane pq loop repeat protein	0				IPR006603; PF04193 (PFAM), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-nhr-43 protein	0		F:GO:0043565; F:GO:0003700; F:GO:0003677; C:GO:0005634; F:GO:0008270; P:GO:0006355; F:GO:0004872; F:GO:0046872; P:GO:0006350; F:GO:0003707; P:GO:0045449		IPR000536; IPR008946; PTHR11865 (PANTHER), PTHR11865:SF235 (PANTHER)
Caenorhabditis elegans	phosphate permease	9	P:GO:0016192; C:GO:0016021; F:GO:0005315; P:GO:0040027; P:GO:0040035; C:GO:0030117; P:GO:0006886; P:GO:0009792; P:GO:0006817	-		IPR001204; PTHR11101:SF12 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-inf-1 protein	18	P:GO:0008340; P:GO:0000003; F:GO:0005515; F:GO:0008026; P:GO:0040010; P:GO:0040011; F:GO:0003743; C:GO:0016281; P:GO:0045948; C:GO:0005829; P:GO:0019915; P:GO:0009792; P:GO:0002119; P:GO:0051789; F:GO:0003723; P:GO:0006200; F:GO:0005524; P:GO:0044419	-		IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF2 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	hypothetical protein T05B11.7 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein C27H5.2 [Caenorhabditis elegans]	1	F:GO:0005515	-		-

Caenorhabditis elegans	atpase inhibitor-like protein	4	F:GO:0004857; P:GO:0045980; P:GO:0050830; C:GO:0005739	-		IPR007648; G3DSA:1.20.5.500 (GENE3D), PTHR23407 (PANTHER), PTHR23407:SF2 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Homo sapiens	r- binding motif protein isoform cra_a	13	C:GO:0035145; F:GO:0003729; C:GO:0005681; P:GO:0006417; C:GO:0005730; C:GO:0016607; P:GO:0008380; F:GO:0005515; F:GO:0000166; P:GO:0006397; C:GO:0005737; P:GO:0000184; P:GO:0051028	-		-
	-	0				-
	-	0				PF12349 (PFAM), SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	transducin -like 1 x-linked receptor 1 isoform 1	14	P:GO:0060070; F:GO:0042393; F:GO:0003714; P:GO:0043161; C:GO:0017053; F:GO:0047485; C:GO:0005730; F:GO:0016563; P:GO:0010553; C:GO:0000118; P:GO:0045944; C:GO:0005876; F:GO:0008013; F:GO:0010843	-		IPR001680; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR22846 (PANTHER), PTHR22846:SF2 (PANTHER), SSF117289 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-hum-7 protein	0		F:GO:0046872; F:GO:0005524; F:GO:0000166; P:GO:0007165; F:GO:0003774; C:GO:0016459; C:GO:0005622		-
	-	0				IPR018247; SignalP (SIGNALP)
Caenorhabditis elegans	uncoordi-ted family member (unc-26)	12	P:GO:0048790; F:GO:0003723; F:GO:0004519; F:GO:0004439; P:GO:0016311; C:GO:0043195; C:GO:0012506; F:GO:0000166; F:GO:0004445; F:GO:0004527; P:GO:0050803; P:GO:0048488	-	EC:3.1.3.36; EC:3.1.3.56	IPR002013; PTHR11200 (PANTHER), PTHR11200:SF10 (PANTHER)
	-	0				-

	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	gcn5-related n-acetyltransferase	1	F:GO:0008415	-		IPR000182; IPR016181; PTHR10545 (PANTHER), PTHR10545:SF3 (PANTHER)
Caenorhabditis elegans	inositol triphosphate receptor family member (itr-1)	5	P:GO:0006816; F:GO:0005220; P:GO:0055085; C:GO:0016021; C:GO:0005783	-		IPR015925; PTHR13715:SF2 (PANTHER)
Caenorhabditis elegans	r- polymerase domain 2 family protein	4	F:GO:0003899; F:GO:0003677; P:GO:0006350; C:GO:0005634	-	EC:2.7.7.6	IPR007081; IPR015699; PTHR19376 (PANTHER), SSF64484 (SUPERFAMILY)
Caenorhabditis elegans	calsequestrin family protein	1	F:GO:0005509	-		IPR001393; SignalP (SIGNALP)
Caenorhabditis elegans	transmembrane protein with metallophosphoesterase domain	0		F:GO:0004565; F:GO:0046872; F:GO:0016787; C:GO:0016021; C:GO:0016020; P:GO:0008150		G3DSA:3.60.21.10 (GENE3D), SignalP (SIGNALP), SSF56300 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein T23E7.6 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	briggsae cbr-lam-1 protein	3	C:GO:0005578; F:GO:0003824; F:GO:0005515	-		IPR002049; IPR008211; IPR013015; IPR013032; PR00011 (PRINTS), G3DSA:2.10.25.10 (GENE3D), PTHR10574 (PANTHER), PTHR10574:SF35 (PANTHER), SignalP (SIGNALP), SSF57196 (SUPERFAMILY)
	-	0				IPR003582; SignalP (SIGNALP)
	-	0				-
Bacillus thuringiensis IBL 200	protein	0		F:GO:0003676; C:GO:0016021; C:GO:0016020; P:GO:0008150; C:GO:0005575		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein T19E7.6 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	fatty acid desaturase	0		P:GO:0006629; P:GO:0055114; F:GO:0016491		IPR021863
	-	0				-
	-	0				IPR002350
	-	0				-
Periplaneta americana	delta protein	4	F:GO:0005515; C:GO:0044464; P:GO:0007389; P:GO:0045665	-		IPR000742; IPR001774; IPR006209; IPR006210; IPR013032; IPR013111; PD936484 (PRODOM), G3DSA:2.10.25.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF220 (PANTHER), SSF57196 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-pde-6 protein	5	P:GO:0007411; F:GO:0004871; F:GO:0046872; F:GO:0004114; P:GO:0007165	-	EC:3.1.4.17	IPR002073; IPR023088; PTHR11347 (PANTHER), PTHR11347:SF38 (PANTHER), SSF109604 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	6	P:GO:0009056; P:GO:0018991; F:GO:0004553; P:GO:0006665; P:GO:0040011; C:GO:0016020	-	EC:3.2.1.0	IPR006775; PTHR12654 (PANTHER), PF12215 (PFAM)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-gon-1 protein	1	F:GO:0008233	-		-
	-	0				SignalP (SIGNALP)
Angiostrongylus cantonensis	heat shock protein family member (hsp-)	1	P:GO:0006950	-		IPR001436; IPR002068; IPR008978; G3DSA:2.60.40.790 (GENE3D), PTHR11527 (PANTHER), PTHR11527:SF28 (PANTHER)
Caenorhabditis briggsae	myg1 protein	3	C:GO:0005634; C:GO:0005739; P:GO:0043473	-		IPR003226
Caenorhabditis briggsae	Hypothetical protein CBG04590 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR001810; G3DSA:1.20.1280.50 (GENE3D)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	activator of 90 kda heat shock protein atpase homolog	0		F:GO:0001671; C:GO:0005737; P:GO:0006950; F:GO:0051087		-
	-	0				-
Brugia malayi	hypothetical protein Bm1_00020 [Brugia malayi]	0		P:GO:0007229; C:GO:0016021; C:GO:0016020; P:GO:0007275; F:GO:0004872; P:GO:0007160; C:GO:0008305; F:GO:0005488; P:GO:0007155		-
Harpegnathos saltator	histone-lysine n-methyltransferase setmar	0		F:GO:0016740; F:GO:0004803; P:GO:0006313; F:GO:0008168; C:GO:0005634; F:GO:0003677; F:GO:0016787; F:GO:0008270; F:GO:0018024; P:GO:0016568; P:GO:0015074; P:GO:0006281; C:GO:0005575; F:GO:0046872; F:GO:0004519		IPR011991; IPR013196; PTHR23016 (PANTHER)
	-	0				IPR008973; G3DSA:2.60.40.150 (GENE3D)
	-	0				-
	-	0				PTHR18937 (PANTHER), PTHR18937:SF13 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	acyl ydroge-se family member (acdh-11)	1	F:GO:0016491	-		-
	-	0				-
Caenorhabditis elegans	yrdc domain containing protein	0		P:GO:0051051; C:GO:0005624		IPR006070; IPR017945; PTHR17490 (PANTHER)
Brugia malayi	transcription elongation factor 1 homolog	5	F:GO:0046872; F:GO:0003746; P:GO:0045449; C:GO:0005634; P:GO:0006414	-		-
Caenorhabditis elegans	pwp2_caeel ame: full=periodic tryptophan protein 2 homolog	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	heavy unconventio-l myosin protein 7	5	F:GO:0046872; C:GO:0016459; F:GO:0005524; P:GO:0007165; F:GO:0003774	-		SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR009959; G3DSA:3.10.450.50 (GENE3D), SSF54427 (SUPERFAMILY)
Caenorhabditis briggsae	ke (drosophila actin-binding) homolog family member (ketn-1)	1	P:GO:0000003	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	protein sec13 homolog	15	P:GO:0051216; P:GO:0040007; P:GO:0000003; P:GO:0010171; P:GO:0070278; C:GO:0000776; P:GO:0002119; F:GO:0005515; P:GO:0006888; P:GO:0040011; P:GO:0006997; P:GO:0006898; P:GO:0006886; P:GO:0009792; C:GO:0031080	-		IPR011046; IPR015943; IPR019781; PTHR11024 (PANTHER), PTHR11024:SF2 (PANTHER)
	-	0				IPR016186; SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	wd repeat-containing protein 75	0				IPR015943; PTHR10219 (PANTHER), PTHR10219:SF1 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		IPR002223; PTHR10083 (PANTHER), PTHR10083:SF35 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	fps oncogene isoform c	8	P:GO:0007411; F:GO:0005488; P:GO:0008594; C:GO:0005912; P:GO:0051017; P:GO:0046664; F:GO:0004713; P:GO:0007394	-	EC:2.7.10.0	IPR000719; IPR001245; IPR008266; IPR011009; IPR020685; IPR020764; G3DSA:1.10.510.10 (GENE3D)

Caenorhabditis brenneri	solute carrier family 35 member b1	5	P:GO:0009792; P:GO:0055085; P:GO:0040010; P:GO:0000003; C:GO:0016021	-		IPR013657; PTHR10778 (PANTHER), PTHR10778:SF10 (PANTHER), SignalP (SIGNALP), SSF103481 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-gcy-28 protein	4	F:GO:0005488; P:GO:0044238; F:GO:0016829; P:GO:0044237	-		G3DSA:3.40.50.2300 (GENE3D), PTHR11920 (PANTHER), PTHR11920:SF2 (PANTHER)
	-	0				IPR000719; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22971 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Brugia malayi	dead h (asp-glu-ala-asp his) box polypeptide 26b	0		F:GO:0003674; P:GO:0008150; C:GO:0005634		PTHR12957 (PANTHER), PTHR12957:SF4 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	glucose-6-phosphate 1-dehydroge-se	4	P:GO:0006006; F:GO:0004345; P:GO:0055114; F:GO:0005488	-	EC:1.1.1.49	IPR001282; IPR016040; IPR022674; SSF51735 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-dlk-1 protein	0		F:GO:0016740; F:GO:0004674; C:GO:0045202; F:GO:0004672; C:GO:0030054; P:GO:0006468; F:GO:0000166; F:GO:0005524; F:GO:0016301; F:GO:0004709; F:GO:0046872		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				G3DSA:3.40.50.980 (GENE3D), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	6	P:GO:0040035; P:GO:0005975; F:GO:0008974; F:GO:0004849; F:GO:0005524; P:GO:0008340	-	EC:2.7.1.19; EC:2.7.1.48	IPR000764; IPR006083; G3DSA:3.40.50.2020 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR10285 (PANTHER), SSF52540 (SUPERFAMILY), SSF53271 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	6	P:GO:0040035; P:GO:0005975; F:GO:0008974; F:GO:0004849; F:GO:0005524; P:GO:0008340	-	EC:2.7.1.19; EC:2.7.1.48	IPR000764; IPR006083; G3DSA:3.40.50.2020 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR10285 (PANTHER), SSF52540 (SUPERFAMILY), SSF53271 (SUPERFAMILY)
	-	0				-
	-	0				-

Callithrix jacchus	lactate dehydroge-se b	9	F:GO:0042802; C:GO:0005625; F:GO:0051287; P:GO:0006089; F:GO:0004459; P:GO:0055114; P:GO:0019674; P:GO:0006096; C:GO:0005739	-	EC:1.1.1.27	-
	-	0				-
Caenorhabditis elegans	hexosaminidase d	4	F:GO:0004553; F:GO:0005488; P:GO:0044238; C:GO:0044424	-	EC:3.2.1.0	IPR013781; IPR017853
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-sand-1 protein	0				-
Loa loa	hr1 repeat family protein	3	P:GO:0009987; F:GO:0004674; F:GO:0000166	-	EC:2.7.11.0	IPR000861; IPR011072
	-	0				-
	-	0				-
	-	0				-
Strongylocentrotus purpuratus	cytochrome p450	1	F:GO:0005515	-		IPR001128; IPR002401
	-	0				SignalP (SIGNALP)
Brugia malayi	zinc c2h2 type family protein	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		-
Caenorhabditis briggsae	ribosome biogenesis protein	4	F:GO:0003924; C:GO:0005634; P:GO:0042254; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR012948; PTHR12858 (PANTHER), PTHR12858:SF2 (PANTHER)
	-	0				-
Caenorhabditis elegans	-dh:flavin oxidoreductase -dh oxidase	6	F:GO:0050660; F:GO:0047540; P:GO:0055114; F:GO:0018673; F:GO:0016758; F:GO:0010181	-	EC:1.3.1.31; EC:1.14.13.40; EC:2.4.1.0	IPR001155; IPR013785; PTHR22893 (PANTHER), PTHR22893:SF6 (PANTHER), SSF51395 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	2	P:GO:0006810; C:GO:0044425	-		IPR011547; IPR018045; PTHR11814 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-rbc-2 protein	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-lam-3 protein	1	C:GO:0031012	-		-
	-	0				-
	-	0				-
Loa loa	d- polymerase epsilon	7	F:GO:0005488; P:GO:0040035; F:GO:0016740; P:GO:0040011; P:GO:0006997; P:GO:0002009; P:GO:0009792	-		IPR006133; PTHR10670 (PANTHER)
	-	0				-

	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	abnormal cell lineage family member (lin-3)	0		F:GO:0008083; P:GO:0040025; C:GO:0016021		-
Caenorhabditis elegans	abnormal cell lineage family member (lin-3)	0		F:GO:0008083; P:GO:0040025; C:GO:0016021		SignalP (SIGNALP)
Caenorhabditis elegans	abnormal cell lineage family member (lin-3)	0		F:GO:0008083; P:GO:0040025; C:GO:0016021		SignalP (SIGNALP)
Caenorhabditis elegans	abnormal cell lineage family member (lin-3)	0		F:GO:0008083; P:GO:0040025; C:GO:0016021		SignalP (SIGNALP)
Ailuropoda melanoleuca	alpha-actinin-1-like isoform 4	13	C:GO:0005829; C:GO:0030018; F:GO:0017166; F:GO:0005509; P:GO:0051271; C:GO:0005730; P:GO:0042981; P:GO:0048041; C:GO:0031143; C:GO:0005925; F:GO:0003779; C:GO:0015629; F:GO:0005178	-		-
	-	0				-
Caenorhabditis elegans	beta- -glucuronosyltransferase	2	C:GO:0016021; F:GO:0015018	-	EC:2.4.1.135	IPR005027; G3DSA:3.90.550.10 (GENE3D), PTHR10896:SF2 (PANTHER), SSF53448 (SUPERFAMILY)
	-	0				-
Loa loa	transcription accessory protein	1	P:GO:0009987	-		IPR018974; G3DSA:1.10.3500.10 (GENE3D), PTHR10724 (PANTHER)
	-	0				IPR003511; PTHR21518 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	pyruvate dehydroge-se	8	F:GO:0004739; P:GO:0040010; C:GO:0005739; P:GO:0055114; P:GO:0006096; P:GO:0006898; P:GO:0048477; P:GO:0009792	-	EC:1.2.4.1	IPR001017; G3DSA:3.40.50.970 (GENE3D), PTHR11516 (PANTHER), PTHR11516:SF3 (PANTHER), SSF52518 (SUPERFAMILY)
Caenorhabditis briggsae	kinesin-like protein family member (klp-4)	5	P:GO:0007018; F:GO:0005515; F:GO:0005524; F:GO:0003777; C:GO:0005874	-		-
Homo sapiens	type alpha 1	4	F:GO:0048407; P:GO:0007155; C:GO:0005589; C:GO:0042383	-		-

	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	xanthine dehydroge-se	10	P:GO:0008340; F:GO:0051537; P:GO:0055114; F:GO:0009055; F:GO:0004855; F:GO:0004854; F:GO:0043546; F:GO:0050660; P:GO:0009115; F:GO:0005506	-	EC:1.17.3.2; EC:1.17.1.4	-
	-	0				-
Caenorhabditis elegans	prolyl-tr- synthetase	1	C:GO:0005739	-		IPR002314; IPR002316; IPR006195; G3DSA:3.30.930.10 (GENE3D), PTHR11451 (PANTHER), PTHR11451:SF3 (PANTHER), SSF55681 (SUPERFAMILY)
	-	0				-
Callithrix jacchus	aldolase fructose-bisphosphate	21	P:GO:0006941; F:GO:0070061; P:GO:0007015; P:GO:0008360; C:GO:0005739; P:GO:0043627; C:GO:0070062; F:GO:0042802; P:GO:0009408; P:GO:0006754; C:GO:0031674; P:GO:0035094; F:GO:0003779; P:GO:0046716; C:GO:0015629; P:GO:0006096; C:GO:0019861; F:GO:0015631; F:GO:0004332; P:GO:0032496; P:GO:0030388	-	EC:4.1.2.13	IPR000741; IPR013785; SSF51569 (SUPERFAMILY)
	-	0				-
	-	0				IPR000980; PTHR14247 (PANTHER), PTHR14247:SF6 (PANTHER), SSF55550 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	probable valyl-tr- synthetase	3	F:GO:0004812; P:GO:0006418; F:GO:0000166	-		IPR002300; IPR002303; IPR014729; PTHR11946 (PANTHER), SignalP (SIGNALP), SSF52374 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	hypothetical protein Y70D2A.1 [Caenorhabditis elegans]	0		C:GO:0016021; P:GO:0007186		PTHR22751 (PANTHER), PTHR22751:SF8 (PANTHER)
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis elegans	yeast bub homolog family member (bub-1)	0		P:GO:0000910; F:GO:0004674; C:GO:0000776; P:GO:0006468; P:GO:0000003; P:GO:0051301; F:GO:0005524; P:GO:0002119; P:GO:0009792; P:GO:0002009; F:GO:0005515; P:GO:0040011; P:GO:0040035		-
	-	0				-
Loa loa	mediator of r- polymerase ii transcription subunit 19	8	P:GO:0006357; P:GO:0040035; F:GO:0016455; P:GO:0002119; F:GO:0005515; C:GO:0016592; P:GO:0048477; P:GO:0040018	-		IPR019403; PTHR22536 (PANTHER)
Caenorhabditis briggsae	programmed cell death 11	8	P:GO:0040010; P:GO:0006396; F:GO:0005488; P:GO:0018991; P:GO:0002119; P:GO:0009792; P:GO:0008406; C:GO:0044424	-		IPR003029; IPR012340; IPR016027; IPR022967; PTHR23270 (PANTHER)
	-	0				-
Caenorhabditis elegans	Hypothetical protein C01B10.11 [Caenorhabditis elegans]	0		P:GO:0040011		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Loa loa	hypothetical protein LOAG_01892 [Loa loa]	0				PTHR21191 (PANTHER), PTHR21191:SF3 (PANTHER), SignalP (SIGNALP)
Pan troglodytes	ubiquitin a-52 residue ribosomal protein fusion product 1	8	F:GO:0030528; F:GO:0003735; P:GO:0006414; C:GO:0022627; P:GO:0016567; F:GO:0005515; C:GO:0005634; P:GO:0045941	-		IPR000626; IPR001975; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), PTHR10666:SF9 (PANTHER), SSF54236 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein C23H3.5 [Caenorhabditis elegans]	0		P:GO:0040017; P:GO:0000003; P:GO:0040035; P:GO:0006898; P:GO:0009792		-
	-	0				-

Brugia malayi	hypothetical protein [Brugia malayi]	0		F:GO:0005488		-
Brugia malayi	poly(adp-ribose) glycohydrolase 63 kda-like	0		P:GO:0005975; F:GO:0004649		IPR007724
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	mitofusin 1	5	P:GO:0008053; C:GO:0016021; C:GO:0005741; F:GO:0003924; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	
	-	0				-
Caenorhabditis briggsae	dipeptidyl peptidase	0		P:GO:0006508; F:GO:0008236; F:GO:0016787; C:GO:0016021; C:GO:0016020		PTHR11731 (PANTHER), PTHR11731:SF23 (PANTHER)
	-	0				-
	-	0				IPR018056; SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-sptf-3 protein	0				-
Homo sapiens	glutathione peroxidase 4	18	C:GO:0005829; P:GO:0006644; P:GO:0042744; C:GO:0005625; C:GO:0005743; F:GO:0004602; P:GO:0055114; P:GO:0007283; P:GO:0006749; P:GO:0007568; F:GO:0043295; P:GO:0032355; P:GO:0006325; P:GO:0007275; C:GO:0005635; F:GO:0008430; P:GO:0050727; F:GO:0047066	-	EC:1.11.1.9; EC:1.11.1.12	-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	prolyl tr- synthetase family member (prs-2)	0		F:GO:0004827; F:GO:0005524; P:GO:0006412; F:GO:0004812; C:GO:0005737; F:GO:0000166; P:GO:0006433; P:GO:0006418		IPR004154
Brugia malayi	hypothetical protein Bm1_45825 [Brugia malayi]	0				-
	-	0				-
Caenorhabditis elegans	cg8392	11	C:GO:0005737; P:GO:0009792; P:GO:0002119; C:GO:0005839; P:GO:0000003; P:GO:0040011; P:GO:0040007; P:GO:0006974; C:GO:0005634; F:GO:0004298; P:GO:0051603	-	EC:3.4.25.0	IPR000243; IPR001353; IPR016050; G3DSA:3.60.20.10 (GENE3D), PTHR11599 (PANTHER), PTHR11599:SF4 (PANTHER), PS51476 (PROFILE), SSF56235 (SUPERFAMILY)

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0019915; C:GO:0005576		IPR001283; IPR014044; PTHR10334:SF11 (PANTHER)
	-	0				-
Caenorhabditis elegans	serine threonine-protein ki-se pak	18	P:GO:0007010; P:GO:0000122; P:GO:0007347; F:GO:0004702; F:GO:0005515; P:GO:0016319; P:GO:0045315; P:GO:0048813; C:GO:0005913; P:GO:0007517; P:GO:0007405; F:GO:0043565; F:GO:0003700; C:GO:0005634; F:GO:0005524; C:GO:0031523; P:GO:0035190; P:GO:0000187	-		IPR000719; IPR011009; IPR015750; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22986 (PANTHER)
	-	0				-
Pan troglodytes	chemokine (c-c motif) ligand 19	9	P:GO:0006935; C:GO:0005615; P:GO:0006954; F:GO:0008009; P:GO:0006874; P:GO:0007165; P:GO:0006955; P:GO:0009615; P:GO:0007154	-		IPR000827; IPR001811; G3DSA:2.40.50.40 (GENE3D), PTHR12015 (PANTHER), PTHR12015:SF7 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0006355; P:GO:0006281; F:GO:0003702; C:GO:0005634		IPR004598
Caenorhabditis elegans	b-box zinc finger family protein	0		F:GO:0046872; P:GO:0030071; C:GO:0005680; F:GO:0008270; F:GO:0005515; C:GO:0005622		PTHR12846 (PANTHER), PTHR12846:SF2 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	P:GO:0040011	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	vps53- n-termi-l family protein	0				-
	-	0				-
Acyrthosiphon pisum	PREDICTED: similar to conserved hypothetical protein [Acyrthosiphon pisum]	0				IPR004245; PTHR10974:SF17 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	8	F:GO:0004383; F:GO:0004674; C:GO:0016021; P:GO:0019932; F:GO:0008528; F:GO:0005524; P:GO:0006468; P:GO:0006182	-	EC:4.6.1.2; EC:2.7.11.0	-
	-	0				-
Caenorhabditis elegans	poly(adp-ribose) metabolism enzyme family member (pme-3)	2	P:GO:0005975; P:GO:0045132	-		IPR007724; SignalP (SIGNALP)
Caenorhabditis elegans	frizzled smoothened family membrane region containing protein	0		F:GO:0004888; C:GO:0016021; C:GO:0016020; F:GO:0004930; F:GO:0004926; P:GO:0007275; P:GO:0007166; P:GO:0007165; F:GO:0004872; F:GO:0004871; P:GO:0007186; P:GO:0016055		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-kel-10 protein	0		F:GO:0005515		IPR006652; IPR013089; IPR015916; PR00501 (PRINTS), PTHR23230:SF184 (PANTHER), SSF117281 (SUPERFAMILY)
Ailuropoda melanoleuca	heat shock 70kda protein 1a	18	F:GO:0047485; P:GO:0042026; P:GO:0090084; C:GO:0005739; P:GO:0030308; F:GO:0031625; C:GO:0016607; F:GO:0044183; P:GO:0006916; P:GO:0008285; C:GO:0016234; F:GO:0005524; P:GO:0006402; C:GO:0048471; C:GO:0030529; F:GO:0051082; P:GO:0006986; C:GO:0005783	-		IPR019651
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-tsp-8 protein	1	C:GO:0016020	-		IPR018499; PTHR19282 (PANTHER), PTHR19282:SF65 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG02143 [Caenorhabditis briggsae]	0		P:GO:0007165; F:GO:0005515		-

Loa loa	dynein heavy chain	5	P:GO:0007018; C:GO:0030286; F:GO:0016887; F:GO:0005524; F:GO:0003777	-		PTHR10676 (PANTHER), PTHR10676:SF4 (PANTHER)
Caenorhabditis elegans	briggsae cbr-spp-15 protein	1	P:GO:0006629	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-atm-1 protein	0		F:GO:0016301; F:GO:0005524; F:GO:0016740; F:GO:0000166; F:GO:0016773; C:GO:0000785		-
Homo sapiens	immunoglobulin heavy chain variable region	0				IPR013106; IPR013783; PTHR23266 (PANTHER), PTHR23266:SF10 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis briggsae	beta esterase (agap005371-pa)	1	F:GO:0005515	-		IPR002018; IPR019826; G3DSA:3.40.50.1820 (GENE3D), PTHR11559:SF6 (PANTHER), SSF53474 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Loa loa	ser thr protein phosphatase family protein	1	F:GO:0004721	-	EC:3.1.3.16	-
Caenorhabditis elegans	nuclear vcp-like	2	F:GO:0017111; F:GO:0005524	-	EC:3.6.1.15	-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	ribulose-phosphate 3-epimerase	6	C:GO:0005625; P:GO:0009052; C:GO:0005792; F:GO:0004750; F:GO:0048029; F:GO:0005515	-	EC:5.1.3.1	IPR000056; IPR011060; IPR013785
Caenorhabditis elegans	ribulose-phosphate 3-epimerase	6	C:GO:0005625; P:GO:0009052; C:GO:0005792; F:GO:0004750; F:GO:0048029; F:GO:0005515	-	EC:5.1.3.1	IPR000056; IPR011060; IPR013785
Brugia malayi	ubiquitin-conjugating enzyme family protein	1	P:GO:0019538	-		-
	-	0				-
Caenorhabditis briggsae	tubulin-specific chaperone e	3	P:GO:0009987; P:GO:0008340; P:GO:0016043	-		IPR001611; IPR018087; G3DSA:3.80.10.10 (GENE3D), PTHR23154 (PANTHER), SSF52058 (SUPERFAMILY)

Bos taurus	filamin alpha	28	F:GO:0004871; C:GO:0005802; P:GO:0043433; P:GO:0034394; C:GO:0015629; P:GO:0051220; P:GO:0050821; C:GO:0005576; C:GO:0005829; F:GO:0001948; P:GO:0051764; P:GO:0043123; F:GO:0051015; F:GO:0048365; P:GO:0045022; P:GO:0007195; F:GO:0042803; F:GO:0034989; P:GO:0031532; F:GO:0034988; C:GO:0005886; F:GO:0008134; P:GO:0042177; C:GO:0005634; P:GO:0042993; C:GO:0005938; P:GO:0043113	-		-
	-	0				-
Caenorhabditis elegans	trpa cation channel homolog family member (trpa-1)	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Xenopus laevis	dolichyl pyrophosphate man9 c2 alpha- -glucosyltransferase	4	P:GO:0006487; F:GO:0046527; P:GO:0000003; C:GO:0016020	-		IPR004856
	-	0				-
	-	0				-
Loa loa	yoq5_caeel ame: full=uncharacterized protein	1	F:GO:0005515	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-tag-241 protein	0				-
	-	0				-
Caenorhabditis briggsae	ras family protein	6	F:GO:0005525; C:GO:0005622; C:GO:0016020; P:GO:0007264; F:GO:0003924; P:GO:0015031	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR013753; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF28 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	innexin family protein	3	C:GO:0016021; C:GO:0005921; F:GO:0008234	-		SignalP (SIGNALP)
Caenorhabditis elegans	high incidence of males (increased x chromosome loss) family member (him-6)	0				-

Caenorhabditis elegans	glycerol-3-phosphate dehydroge-se	9	C:GO:0009331; P:GO:0007629; P:GO:0006641; F:GO:0004367; P:GO:0006127; F:GO:0051287; P:GO:0046168; F:GO:0042803; C:GO:0005811	-	EC:1.1.1.8	IPR006109; IPR006168; IPR008927; IPR011128; IPR013328; IPR016040; IPR017751; SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-itx-1 protein	0				-
Caenorhabditis elegans	methyltransferase like 5	4	F:GO:0008649; F:GO:0003676; F:GO:0005515; P:GO:0032259	-		PTHR23290 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	alkmo_caeel ame: full=alkylglycerol monooxyge-se homolog ame: full=transmembrane protein 195 homolog	0		P:GO:0055114; F:GO:0016491; F:GO:0005506; C:GO:0005783; P:GO:0006633		-
Caenorhabditis elegans	dipeptidyl peptidase four family member (dpf-6)	0		F:GO:0008236; F:GO:0016787		-
Loa loa	gpi transamidase subunit pig-u family protein	0		C:GO:0005789; P:GO:0006506; C:GO:0016021		IPR009600; SignalP (SIGNALP)
	-	0				-
Caenorhabditis sp. PS1010	hypothetical protein Csp3_JD03.001 [Caenorhabditis sp. PS1010]	0		F:GO:0005089; P:GO:0035023; C:GO:0005622		-
Saccoglossus kowalevskii	receptor for egg jelly 6-like	0				IPR000436; IPR016060; PTHR19325 (PANTHER), PTHR19325:SF25 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0005488; P:GO:0007155		IPR000436; IPR016060; PTHR19325 (PANTHER), PTHR19325:SF25 (PANTHER)
Caenorhabditis elegans	low-density lipoprotein receptor-related protein 2-like	8	C:GO:0043231; F:GO:0005509; C:GO:0016021; F:GO:0004872; F:GO:0005515; C:GO:0044444; P:GO:0008152; P:GO:0006898	-		IPR002172; IPR006210; G3DSA:2.10.25.10 (GENE3D), PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER), SSF57196 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Brugia malayi	t family of potassium channels family member (twk-2)	0				-
	-	0				SignalP (SIGNALP)
	-	0				IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG16316 [Caenorhabditis briggsae]	0		C:GO:0016021; C:GO:0016020		-
Caenorhabditis elegans	cullin 2	1	F:GO:0005515	-		IPR001373; IPR016159; G3DSA:1.20.1310.10 (GENE3D)

Caenorhabditis elegans	excitatory gaba receptor exp-1a	7	P:GO:0010171; F:GO:0004872; C:GO:0045211; C:GO:0030054; F:GO:0005230; P:GO:0006811; C:GO:0016021	-		IPR006201; IPR006202; IPR018000; PTHR18945:SF8 (PANTHER)
	-	0				-
Caenorhabditis elegans	variable abnormal morphology family member (vab-10)	1	F:GO:0005488	-		IPR002017; IPR018159; G3DSA:1.20.58.60 (GENE3D), SSF46966 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	rap ran-gap family protein	1	F:GO:0005515	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	sushi domain containing	2	C:GO:0016021; P:GO:0007160	-		PTHR13802 (PANTHER), PTHR13802:SF1 (PANTHER)
	-	0				PTHR12846 (PANTHER), PTHR12846:SF2 (PANTHER)
Caenorhabditis elegans	serine threonine-protein phosphatase dullard	10	P:GO:0006470; F:GO:0043169; F:GO:0004563; P:GO:0006998; C:GO:0009536; P:GO:0005975; F:GO:0004722; P:GO:0007275; C:GO:0005635; C:GO:0005789	-	EC:3.2.1.52	IPR004274; G3DSA:3.40.50.1000 (GENE3D), SignalP (SIGNALP), SSF56784 (SUPERFAMILY)
Caenorhabditis elegans	protein unc-79 homolog	0		C:GO:0016021; C:GO:0016020		PTHR21696 (PANTHER)
Haemonchus contortus	glutathione peroxidase	4	F:GO:0004602; P:GO:0055114; C:GO:0005739; P:GO:0006979	-	EC:1.11.1.9	IPR000889; IPR012335; IPR012336
Haemonchus contortus	glutathione peroxidase	4	F:GO:0004602; P:GO:0055114; C:GO:0005739; P:GO:0006979	-	EC:1.11.1.9	IPR000889; IPR012335; IPR012336
Loa loa	uncoordi-ted family member (unc-103)	4	F:GO:0005249; P:GO:0055085; P:GO:0006813; C:GO:0016021	-		-
	-	0				-
	-	0				-
Oryctolagus cuniculus	small nuclear ribonucleoprotein polypeptides b and b1	8	F:GO:0042802; F:GO:0071208; C:GO:0005683; C:GO:0005654; P:GO:0000387; C:GO:0005681; C:GO:0005829; C:GO:0071204	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0005509	-		-

Loa loa	haloacid dehaloge-se-like hydrolase family protein	2	P:GO:0008152; F:GO:0003824	-		-
Caenorhabditis elegans	leucine rich repeat family protein	7	P:GO:0040010; P:GO:0045449; P:GO:0016334; P:GO:0000003; P:GO:0016336; F:GO:0005515; P:GO:0009792	-		IPR001611; G3DSA:3.80.10.10 (GENE3D), PTHR10588 (PANTHER), PTHR10588:SF23 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)
Vitis vinifera	protein	0				-
	-	0				-
Homo sapiens	neural precursor cell developmentally down-regulated 8	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	contactin associated 2	0		P:GO:0021987; P:GO:0007420; P:GO:0008038; P:GO:0034613; C:GO:0016021; P:GO:0007155; C:GO:0016020; P:GO:0021794; F:GO:0005102; P:GO:0021761; C:GO:0070852; C:GO:0008076; C:GO:0030673; P:GO:0007165; P:GO:0019226; C:GO:0030425; P:GO:0007610; P:GO:0045163; C:GO:0005886; C:GO:0044224; P:GO:0071109; P:GO:0021756		PTHR10127 (PANTHER), PTHR10127:SF2 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Loa loa	briggsae cbr-pan-1 protein	0		F:GO:0005515		SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-che-11 protein	0		F:GO:0005488; F:GO:0003824		IPR022100; PTHR15722 (PANTHER), PTHR15722:SF7 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	diacylglycerol o-acyltransferase 1	1	C:GO:0016021	-		SignalP (SIGNALP)
	-	0				-
Loa loa	r--binding protein 1	6	P:GO:0008380; F:GO:0003723; F:GO:0005515; C:GO:0005634; P:GO:0008406; F:GO:0000166	-		IPR000504; IPR012677; PTHR10548 (PANTHER), SSF54928 (SUPERFAMILY)
Loa loa	r--binding protein 1	6	P:GO:0008380; F:GO:0003723; F:GO:0005515; C:GO:0005634; P:GO:0008406; F:GO:0000166	-		IPR000504; IPR012677; PTHR10548 (PANTHER), SSF54928 (SUPERFAMILY)

Caenorhabditis briggsae	protein yipf4	3	F:GO:0005488; C:GO:0005622; C:GO:0016021	-		-
	-	0				-
	-	0				-
Brugia malayi	zinc c2h2 type family protein	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		-
Loa loa	sodium bicarbo-te cotransporter	3	C:GO:0016020; F:GO:0015380; P:GO:0006810	-		IPR003020; SignalP (SIGNALP)
Caenorhabditis elegans	uncoordi-ted family member (unc-89)	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				IPR008160; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER)
	-	0				-
Trichostrongylus colubriformis	globin	6	F:GO:0020037; C:GO:0005615; C:GO:0005737; F:GO:0005344; P:GO:0015671; F:GO:0019825	-		-
Caenorhabditis elegans	hypothetical protein K11H12.9 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
Caenorhabditis elegans	cadherin domain containing protein	6	P:GO:0007218; C:GO:0016021; P:GO:0007156; F:GO:0005509; C:GO:0005886; F:GO:0004930	-		-
Loa loa	hypothetical protein LOAG_04806 [Loa loa]	0				-
Homo sapiens	complement c1s subcomponent precursor	8	F:GO:0005509; P:GO:0006958; P:GO:0045087; P:GO:0010001; P:GO:0006508; F:GO:0004252; C:GO:0005578; P:GO:0051591	-	EC:3.4.21.0	IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR19355 (PANTHER), PTHR19355:SF44 (PANTHER)
	-	0				-
Caenorhabditis elegans	erv1 alr family protein	2	P:GO:0048518; P:GO:0040011	-		IPR005746; IPR012335; IPR012336; IPR013766; IPR017936; IPR017937; PTHR18929 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	dve (defective proventriculus in drosophila) homolog family member (dve-1)	5	F:GO:0003700; F:GO:0043565; F:GO:0005515; C:GO:0005634; P:GO:0006355	-		IPR001356; IPR009057; IPR012287; PTHR15116 (PANTHER), PTHR15116:SF7 (PANTHER)
Caenorhabditis elegans	astacin family metalloendopeptidase farm-1	2	F:GO:0046872; F:GO:0016787	-		IPR003582
	-	0				-

Brugia malayi	mixed-lineage leukemia mll	1	F:GO:0005488	-		IPR001214; IPR001965; IPR003616; IPR003888; IPR003889; IPR015722; IPR018516; IPR018518; G3DSA:2.170.270.10 (GENE3D), PTHR22884 (PANTHER), SSF82199 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	ef hand family protein	1	P:GO:0009792	-		IPR018247; PTHR23104 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Pongo abelii	pctaire protein ki-se 1	4	P:GO:0006468; F:GO:0005515; F:GO:0005524; F:GO:0004693	-	EC:2.7.11.22	-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Macaca mulatta	eukaryotic translation initiation factor isoform 1	10	F:GO:0003729; C:GO:0016281; F:GO:0008026; F:GO:0005515; P:GO:0031100; F:GO:0005524; F:GO:0000339; F:GO:0003743; C:GO:0005829; P:GO:0006412	-	EC:3.6.5.3	IPR011545; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF2 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0004888; C:GO:0016021; C:GO:0016020; F:GO:0004930; P:GO:0007166; P:GO:0007165; F:GO:0004872; F:GO:0004871; P:GO:0007186; C:GO:0005886		-
Gallus gallus	tubulin alpha-1c chain-like	6	P:GO:0007018; F:GO:0005525; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Caenorhabditis briggsae	yq58_caeel ame: full=uncharacterized protein	0				PTHR13100 (PANTHER)
Caenorhabditis elegans	adenylyl cyclase-associated protein	2	P:GO:0008078; F:GO:0003779	-		IPR001837; IPR013992
Caenorhabditis elegans	Hypothetical protein C30F12.5a [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)

	-	0				-
	-	0				PTHR13373 (PANTHER), PTHR13373:SF2 (PANTHER)
Branchiostoma floridae	zinc finger protein 490	0		F:GO:0046872; P:GO:0006355; F:GO:0003676; F:GO:0008270; F:GO:0003677; C:GO:0005634; C:GO:0005622		IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Brugia malayi	timeless protein	0				-
Caenorhabditis briggsae	complexin precursor	4	C:GO:0005829; F:GO:0019905; P:GO:0006836; P:GO:0006887	-		-
	-	0				SignalP (SIGNALP)
Pediculus humanus corporis	g-protein sig-lling modulator	1	F:GO:0005515	-		IPR011990; IPR013026; IPR019734; PTHR10098 (PANTHER), PTHR10098:SF11 (PANTHER), SSF48452 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-lpr-2 protein	2	C:GO:0016021; F:GO:0005488	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	serine threonine protein ki-se	7	P:GO:0043254; P:GO:0006355; F:GO:0016874; F:GO:0005524; F:GO:0016887; F:GO:0008134; C:GO:0005634	-		IPR011704; G3DSA:3.40.50.300 (GENE3D), PTHR22908 (PANTHER), PTHR22908:SF13 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Loa loa	serine threonine protein phosphatase	1	F:GO:0004721	-	EC:3.1.3.16	IPR004843; IPR006186; G3DSA:3.60.21.10 (GENE3D), SSF56300 (SUPERFAMILY)
	-	0				IPR008160; PTHR10499 (PANTHER), PTHR10499:SF125 (PANTHER)
Caenorhabditis briggsae	mitogen-activated protein ki-se	3	F:GO:0004707; P:GO:0006468; F:GO:0005524	-	EC:2.7.11.24	-
	-	0				-
Loa loa	trehalose 6-phosphate synthase	3	F:GO:0016757; P:GO:0034608; P:GO:0005992	-		-
Caenorhabditis briggsae	dual-specificity protein	3	F:GO:0004725; P:GO:0006470; F:GO:0008138	-	EC:3.1.3.48	-
Brugia malayi	mgc84124 protein	0		F:GO:0003676		-
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	mannosyl-oligosaccharide alpha- -mannosidase	7	C:GO:0000139; F:GO:0004571; P:GO:0006487; F:GO:0005509; P:GO:0008340; P:GO:0042221; C:GO:0016021	-	EC:3.2.1.113	IPR001382; PTHR11742:SF6 (PANTHER)
	-	0				PTHR21512 (PANTHER), PTHR21512:SF6 (PANTHER)
Caenorhabditis elegans	ataxia telangiectasia mutated	4	F:GO:0016301; F:GO:0005524; F:GO:0016773; C:GO:0000785	-	EC:2.7.1.0	IPR000403; IPR011009; IPR015519; PTHR11139 (PANTHER)
Caenorhabditis briggsae	receptor tyrosine ki-se-like orphan receptor	0		F:GO:0016787; P:GO:0006468; F:GO:0005044; F:GO:0005524; F:GO:0016301; C:GO:0016021; F:GO:0008236; C:GO:0016020; F:GO:0008233; F:GO:0004672; F:GO:0004872; F:GO:0004252; F:GO:0000166; F:GO:0003824; P:GO:0006508; F:GO:0005488; F:GO:0016740; F:GO:0005515; F:GO:0004713; P:GO:0007596; C:GO:0005576		IPR000001; IPR013806
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	transmembrane protein adipocyte-associated 1 isoform 1	1	C:GO:0016021	-		IPR018781; SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	lethal family member (let-716)	8	P:GO:0009792; P:GO:0002119; F:GO:0005488; C:GO:0005622; P:GO:0018991; P:GO:0040010; P:GO:0008406; P:GO:0006396	-		IPR003029; IPR016027; IPR022967; SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0003674; C:GO:0005575		IPR019410; G3DSA:3.40.50.150 (GENE3D), PTHR14614 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis elegans	serine threonine protein	7	C:GO:0005737; P:GO:0006468; F:GO:0046872; P:GO:0007275; F:GO:0005524; C:GO:0005634; F:GO:0004674	-	EC:2.7.11.0	IPR011009; IPR017442; IPR020636; IPR020666; G3DSA:1.10.510.10 (GENE3D)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				PTHR11232 (PANTHER), PTHR11232:SF2 (PANTHER)
	-	0				-
	-	0				-
Brugia malayi	tyrosine-protein ki-se fps85d	2	F:GO:0005488; F:GO:0004672	-		IPR000980; IPR020685; IPR020764; SSF55550 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-grl-4 protein	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
Loa loa	beta like 1	1	F:GO:0042802	-		PTHR14978 (PANTHER)
	-	0				-
	-	0				IPR018469
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; F:GO:0005529; C:GO:0005578; F:GO:0005201; P:GO:0040010; P:GO:0007160; F:GO:0005509; P:GO:0007155; F:GO:0005488		-
Caenorhabditis elegans	temporarily assigned gene -me family member (tag-344)	0		F:GO:0004672; P:GO:0030154; F:GO:0005524; F:GO:0000287; F:GO:0000166; P:GO:0006468; F:GO:0004674		-
Caenorhabditis briggsae	kiaa0999 protein	7	C:GO:0005737; P:GO:0006468; F:GO:0046872; P:GO:0007275; F:GO:0005524; C:GO:0005634; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017442; IPR020636; IPR020666; G3DSA:1.10.510.10 (GENE3D)
Caenorhabditis elegans	briggsae cbr-dep-1 protein	12	P:GO:0006470; P:GO:0007417; C:GO:0030424; C:GO:0016021; P:GO:0040027; P:GO:0040026; F:GO:0005001; P:GO:0008045; P:GO:0007424; C:GO:0045177; C:GO:0005886; F:GO:0004728	-		IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF75 (PANTHER), SSF52799 (SUPERFAMILY)

	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	atp-binding sub-family member 8	4	F:GO:0016887; P:GO:0006810; C:GO:0016020; F:GO:0000166	-		IPR001140; IPR011527; IPR017940; G3DSA:1.20.1560.10 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF77 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-elks-1 protein	5	P:GO:0044260; F:GO:0005515; P:GO:0044238; P:GO:0050794; C:GO:0044444	-		IPR019323; PD968187 (PRODOM), PTHR18861 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-elks-1 protein	1	F:GO:0005515	-		-
Caenorhabditis elegans	briggsae cbr-elks-1 protein	5	P:GO:0044260; F:GO:0005515; P:GO:0044238; P:GO:0050794; C:GO:0044444	-		IPR019323; PD968187 (PRODOM), PTHR18861 (PANTHER)
Caenorhabditis elegans	briggsae cbr-elks-1 protein	5	P:GO:0044260; F:GO:0005515; P:GO:0044238; P:GO:0050794; C:GO:0044444	-		IPR019323; PD968187 (PRODOM), PTHR18861 (PANTHER)
	-	0				IPR013032
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
	-	0				-
Caenorhabditis briggsae	ring finger protein 26	1	F:GO:0005488	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	dystrophin-like phenotype and capon related family member (dyc-1)	5	P:GO:0046662; F:GO:0005515; P:GO:0040017; C:GO:0016010; P:GO:0046716	-		-
	-	0				-
Xenopus laevis	sumo ligase	0		F:GO:0016874; F:GO:0008270		-
Caenorhabditis elegans	cg12367 cg12367-pa	0		F:GO:0003674; P:GO:0006457; P:GO:0008150; F:GO:0003725; C:GO:0005622		G3DSA:3.40.50.150 (GENE3D)
Strongylocentrotus purpuratus	contactin associated protein	0				IPR001304; IPR016186; IPR016187
	-	0				-
Caenorhabditis elegans	kinesin-like protein family member (klp-12)	4	P:GO:0009792; F:GO:0005515; P:GO:0007067; F:GO:0003824	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR16012 (PANTHER), PTHR16012:SF173 (PANTHER)

Chlorella variabilis	succinyl- alpha subunit	0		F:GO:0016874; F:GO:0004776; F:GO:0004775; F:GO:0000166; F:GO:0005524; P:GO:0006099; F:GO:0003824; F:GO:0003878; P:GO:0008152; F:GO:0005488		IPR016102; PTHR11117 (PANTHER)
	-	0				-
Angiostrongylus cantonensis	-nos3 protein	1	F:GO:0005488	-		-
	-	0				-
Pan troglodytes	copine v	2	C:GO:0043025; C:GO:0043005	-		IPR000008; IPR008973; IPR018029; G3DSA:2.60.40.150 (GENE3D), PTHR10857 (PANTHER)
Trichoplax adhaerens	ring finger protein 138	0		F:GO:0016874; F:GO:0019901; F:GO:0008270; C:GO:0005575; C:GO:0005622; F:GO:0005515; F:GO:0046872; P:GO:0016055; P:GO:0008150		IPR001841; IPR013083; IPR017907; PTHR10825 (PANTHER), SSF57850 (SUPERFAMILY)
	-	0				-
Loa loa	leucyl-tr- synthetase	4	C:GO:0005737; F:GO:0004823; P:GO:0006429; F:GO:0005524	-	EC:6.1.1.4	IPR002300; IPR002302; IPR014729; PTHR11946 (PANTHER), SSF52374 (SUPERFAMILY)
Caenorhabditis elegans	ulk protein ki-se	4	P:GO:0006468; F:GO:0005524; P:GO:0000003; F:GO:0004674	-	EC:2.7.11.0	-
	-	0				-
Ancylostoma caninum	lyr motif-containing protein 4	0		F:GO:0003674; P:GO:0008150; C:GO:0005575; C:GO:0005634		IPR008139; IPR011001; PTHR21579 (PANTHER), PTHR21579:SF6 (PANTHER), SignalP (SIGNALP)
Ancylostoma caninum	lyr motif-containing protein 4	0		C:GO:0005739; F:GO:0003674; P:GO:0008150; C:GO:0005575; C:GO:0005634		-
Caenorhabditis briggsae	acyl- thioesterase ii	1	P:GO:0019915	-		IPR003703; G3DSA:3.10.129.10 (GENE3D), PTHR11066:SF7 (PANTHER), SSF54637 (SUPERFAMILY)

Macaca mulatta	amyloid beta a4 protein	53	C:GO:0043198; F:GO:0016504; F:GO:0008233; C:GO:0019717; P:GO:0050885; F:GO:0008201; P:GO:0035235; F:GO:0004867; P:GO:0007176; P:GO:0050803; P:GO:0016358; C:GO:0031594; P:GO:0000085; F:GO:0046872; C:GO:0035253; P:GO:0040014; P:GO:0030900; P:GO:0001967; P:GO:0051402; P:GO:0008542; C:GO:0030424; C:GO:0051233; P:GO:0016199; P:GO:0045944; P:GO:0007219; C:GO:0005887; C:GO:0048471;	-		-
Brugia malayi	leucine-rich repeat-containing protein 47	1	F:GO:0003824	-		-
Angiostrongylus cantonensis	cuticular collagen	6	P:GO:0019915; P:GO:0006952; C:GO:0016021; F:GO:0042302; P:GO:0010171; F:GO:0005515	-		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG04283 [Caenorhabditis briggsae]	0		F:GO:0008270; F:GO:0005515; F:GO:0004842		-
Caenorhabditis elegans	yrr5_caeel ame: full=uncharacterized protein	0				-
Danio rerio	-nos homolog 1	2	C:GO:0005737; F:GO:0046872	-		IPR008705
Caenorhabditis elegans	atp-binding sub-family d member 4	4	F:GO:0016887; P:GO:0006810; C:GO:0016020; F:GO:0000166	-		IPR010509; PTHR11384 (PANTHER), PTHR11384:SF3 (PANTHER)
	-	0				-

Pongo abelii	keratin 18	11	P:GO:0043000; P:GO:0007049; P:GO:0033209; C:GO:0034451; F:GO:0005515; C:GO:0045095; C:GO:0048471; P:GO:0044419; P:GO:0009653; F:GO:0005198; P:GO:0043066	-		-
Caenorhabditis elegans	abc transporter	11	P:GO:0070574; C:GO:0016021; C:GO:0005743; F:GO:0042626; P:GO:0015886; C:GO:0043190; F:GO:0015232; C:GO:0005774; F:GO:0005524; F:GO:0015086; P:GO:0046686	-		G3DSA:1.20.1560.10 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF69 (PANTHER), SignalP (SIGNALP)
	-	0				-
Loa loa	myosin xviiia	0		F:GO:0005524; F:GO:0003774; F:GO:0005515; C:GO:0016459		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	coenzyme q3 methyltransferase (cerevisiae)	6	P:GO:0006071; P:GO:0002119; P:GO:0006744; F:GO:0008171; P:GO:0008340; C:GO:0005739	-		IPR013216; G3DSA:3.40.50.150 (GENE3D), PTHR23134 (PANTHER), SSF53335 (SUPERFAMILY)
Caenorhabditis briggsae	coenzyme q3 methyltransferase (cerevisiae)	6	P:GO:0006071; P:GO:0002119; P:GO:0006744; F:GO:0008171; P:GO:0008340; C:GO:0005739	-		-
Caenorhabditis elegans	atg2b protein	0		F:GO:0003674; P:GO:0008150		IPR015412; PTHR13190 (PANTHER), PTHR13190:SF2 (PANTHER)
Brugia malayi	in family member (ttn-1)	4	P:GO:0009792; P:GO:0006468; F:GO:0004672; F:GO:0005524	-		IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF5 (PANTHER), SSF48726 (SUPERFAMILY)
Brugia malayi	cop9 sig-losome complex subunit 6	1	P:GO:0050821	-		IPR000555; PTHR10540 (PANTHER), PTHR10540:SF8 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	histidine ammonia-lyase	6	C:GO:0005625; P:GO:0006548; F:GO:0005515; P:GO:0009058; C:GO:0005829; F:GO:0004397	-	EC:4.3.1.3	IPR001106; IPR008948; G3DSA:1.20.200.10 (GENE3D)
	-	0				-

Caenorhabditis briggsae	zinc c2h2 type family protein	0		F:GO:0046872; P:GO:0006355; F:GO:0003676; F:GO:0008270; C:GO:0005622		IPR007087; IPR015880
	-	0				IPR016160
Caenorhabditis briggsae	briggsae cbr-dyb-1 protein	9	F:GO:0005277; P:GO:0015870; F:GO:0046872; P:GO:0007271; F:GO:0005515; P:GO:0007529; P:GO:0046716; P:GO:0040017; C:GO:0016010	-		PTHR11915 (PANTHER), PTHR11915:SF16 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0005515		PTHR10316 (PANTHER), PTHR10316:SF7 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0005515		PTHR10316 (PANTHER), PTHR10316:SF7 (PANTHER)
	-	0				SignalP (SIGNALP)
Loa loa	protein-tyrosine phosphatase containing protein	6	P:GO:0009987; F:GO:0004725; F:GO:0005515; C:GO:0005737; C:GO:0005634; C:GO:0005886	-	EC:3.1.3.48	IPR000242; IPR000387; IPR003595; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis elegans	statb_caeel ame: full=sig-l transducer and activator of transcription b ame: full=zinc finger protein stat-b	7	F:GO:0003700; F:GO:0004871; F:GO:0005515; F:GO:0005509; P:GO:0007165; C:GO:0005634; P:GO:0006355	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Pongo abelii	adp-ribosylation factor 5	9	F:GO:0005525; C:GO:0005794; C:GO:0005886; F:GO:0005515; P:GO:0016192; P:GO:0007264; C:GO:0048471; F:GO:0003924; P:GO:0015031	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR006689; G3DSA:3.40.50.300 (GENE3D), PTHR11711:SF30 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	arginine serine-rich splicing factor	4	P:GO:0009792; P:GO:0008380; F:GO:0003723; F:GO:0005515	-		-
Caenorhabditis elegans	arginine serine-rich splicing factor	4	F:GO:0003723; P:GO:0009792; P:GO:0008380; F:GO:0005515	-		IPR000504; IPR012677; PTHR10548 (PANTHER), SSF54928 (SUPERFAMILY)

Caenorhabditis elegans	arginine serine-rich splicing factor	4	P:GO:0009792; P:GO:0008380; F:GO:0003723; F:GO:0005515	-		-
	-	0				-
Caenorhabditis elegans	hypothetical protein F19C7.1 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	ankyrin repeat domain 50	3	F:GO:0005515; P:GO:0006974; P:GO:0008340	-		IPR002110; IPR020683; PTHR18958 (PANTHER)
Homo sapiens	af061732_1my029 protein	0				SignalP (SIGNALP)
Brugia malayi	hypothetical protein Bm1_21590 [Brugia malayi]	0				IPR021752
	-	0				-
Caenorhabditis elegans	atypical protein ki-se c	27	P:GO:0007314; P:GO:0007338; P:GO:0045176; P:GO:0006468; C:GO:0035003; P:GO:0007369; F:GO:0008270; P:GO:0046667; P:GO:0007613; P:GO:0045197; P:GO:0045186; P:GO:0007506; F:GO:0019904; C:GO:0045179; P:GO:0016332; P:GO:0030011; P:GO:0002052; P:GO:0045196; P:GO:0001738; C:GO:0030864; F:GO:0005524; P:GO:0007294; P:GO:0045167; P:GO:0007416; P:GO:0055059; F:GO:0004697; C:GO:0016324	-	EC:2.7.11.13	IPR000961; IPR015745; IPR017892; PTHR22985 (PANTHER)
Loa loa	hypothetical protein LOAG_07145 [Loa loa]	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-frl-1 protein	2	F:GO:0005515; P:GO:0016043	-		IPR003104; IPR015425; IPR018247; PTHR23213 (PANTHER), PTHR23213:SF24 (PANTHER)

Loa loa	d- repair and recombi-tion protein rad54-like	18	P:GO:0000003; F:GO:0008094; F:GO:0008270; F:GO:0070087; P:GO:0006355; P:GO:0000724; P:GO:0051276; P:GO:0030900; P:GO:0006306; C:GO:0005720; F:GO:0003677; P:GO:0006915; P:GO:0007126; P:GO:0042493; P:GO:0010212; F:GO:0003682; F:GO:0005524; F:GO:0003678	-		IPR000330; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10799 (PANTHER), PTHR10799:SF66 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Pediculus humanus corporis	mitochondrial 2-oxoglutarate malate carrier protein	6	F:GO:0005488; C:GO:0005743; P:GO:0055085; P:GO:0006839; C:GO:0016021; F:GO:0005215	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF78 (PANTHER)
Brugia malayi	rab6	6	P:GO:0009792; P:GO:0046907; P:GO:0007165; F:GO:0000166; P:GO:0015031; C:GO:0044424	-		IPR013753; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF27 (PANTHER)
Caenorhabditis elegans	hypothetical protein C06E7.2 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	zinc finger ccch-type containing 12d	10	C:GO:0005737; P:GO:0030154; F:GO:0004519; P:GO:0006915; F:GO:0003676; F:GO:0005515; P:GO:0007275; P:GO:0008152; C:GO:0005634; F:GO:0008270	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-nhr-78 protein	3	F:GO:0004872; F:GO:0005515; P:GO:0006350	-		IPR001628; IPR008946; IPR013088; PTHR11865 (PANTHER), PTHR11865:SF235 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis elegans	Hypothetical protein F10E7.9 [Caenorhabditis elegans]	0		C:GO:0016021; C:GO:0016020; P:GO:0055085		-
	-	0				IPR001664; PTHR23239:SF1 (PANTHER)

	-	0				PTHR22776 (PANTHER), PTHR22776:SF1 (PANTHER)
Caenorhabditis elegans	protein unc-45 homolog a	5	C:GO:0030018; F:GO:0005488; P:GO:0048738; P:GO:0030239; P:GO:0007519	-		IPR011990; IPR013026; PTHR22904 (PANTHER), PTHR22904:SF28 (PANTHER), SSF48452 (SUPERFAMILY)
Caenorhabditis briggsae	d--binding protein smubp-	2	F:GO:0005488; F:GO:0017111	-	EC:3.6.1.15	IPR000606; PTHR10887 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	mannose-1-phosphate guanyltransferase	2	P:GO:0009058; F:GO:0016779	-	EC:2.7.7.0	IPR001451; IPR005835; IPR011004; IPR018357; G3DSA:2.160.10.10 (GENE3D), G3DSA:3.90.550.10 (GENE3D), PTHR22572 (PANTHER), PTHR22572:SF15 (PANTHER), SSF53448 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	8	P:GO:0006810; F:GO:0005083; C:GO:0045202; F:GO:0042802; C:GO:0019717; P:GO:0007289; P:GO:0006914; C:GO:0005886	-		-
Homo sapiens	preli domain containing 1	4	P:GO:0006955; C:GO:0005730; P:GO:0007275; C:GO:0005739	-		IPR006797; PTHR11158 (PANTHER), PTHR11158:SF16 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		IPR007087; IPR012317; IPR015880
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	5	P:GO:0002119; P:GO:0040010; P:GO:0000003; P:GO:0040011; P:GO:0006898	-		-
Caenorhabditis briggsae	protein kri1 homolog	8	P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0040010; P:GO:0040011; P:GO:0019915; P:GO:0006898; P:GO:0002009	-		IPR007851; IPR018034
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	monocyte to macrophage differentiation protein	1	C:GO:0016021	-		-
Caenorhabditis briggsae	puromycin-sensitive aminopeptidase	2	F:GO:0005488; F:GO:0070011	-		IPR001930; IPR014782; IPR015568; SSF55486 (SUPERFAMILY), SSF63737 (SUPERFAMILY)
	-	0				-
Homo sapiens	immunoglobulin heavy chain variable region	0				-

Caenorhabditis elegans	chaperone protein	1	F:GO:0005488	-		IPR001623; IPR015609; PTHR11821:SF25 (PANTHER)
Loa loa	coenzyme q biosynthesis family member (coq-2)	5	F:GO:0004659; P:GO:0006744; P:GO:0008340; C:GO:0016021; C:GO:0005739	-		PTHR11048 (PANTHER), PTHR11048:SF2 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	Hypothetical protein Y32H12A.2b [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				-
	-	0				IPR017441; G3DSA:3.30.200.20 (GENE3D)
Caenorhabditis briggsae	liprin alpha (lar-interacting protein alpha) (sy-pse defective protein 2)	4	F:GO:0005515; C:GO:0009986; C:GO:0005737; P:GO:0007160	-		-
	-	0				-
Caenorhabditis elegans	briggsae cbr-mre-11 protein	0		P:GO:0006259; C:GO:0005634; F:GO:0016787; P:GO:0006974; P:GO:0006302; P:GO:0006281; F:GO:0004527; F:GO:0004519; F:GO:0030145; F:GO:0004518; P:GO:0007126		-
	-	0				-
Loa loa	camk camkl nuak protein ki-se	0				-
	-	0				-
	-	0				-
	-	0				-
Danio rerio	transmembrane protein 67	0		F:GO:0051082; P:GO:0030433; P:GO:0042384; P:GO:0048754; C:GO:0005789; C:GO:0016021; C:GO:0016020; C:GO:0005929; C:GO:0005783; C:GO:0005813; C:GO:0005737; P:GO:0010826; C:GO:0060170; C:GO:0030659; C:GO:0042995; C:GO:0005932; C:GO:0005856; F:GO:0005515; C:GO:0005886		-
	-	0				-
	-	0				-

Haemonchus contortus	myosin heavy chain	6	C:GO:0032982; F:GO:0003779; F:GO:0005524; F:GO:0003774; C:GO:0031672; P:GO:0007626	-		-
Homo sapiens	protein ki-se c substrate 80k-h	14	F:GO:0004558; F:GO:0005080; F:GO:0003723; P:GO:0051291; P:GO:0007243; F:GO:0005509; C:GO:0017177; C:GO:0005768; P:GO:0016310; F:GO:0016301; P:GO:0007154; F:GO:0035091; C:GO:0005794; P:GO:0050830	-	EC:3.2.1.20	SignalP (SIGNALP)
Caenorhabditis elegans	protein ki-se domain containing protein	7	P:GO:0006468; P:GO:0009103; F:GO:0005515; F:GO:0005524; P:GO:0007165; C:GO:0016020; F:GO:0004674	-	EC:2.7.11.0	IPR020675; IPR020680
	-	0				-
	-	0				-
Caenorhabditis briggsae	vacuolar proton atpases	3	F:GO:0015078; C:GO:0033177; P:GO:0015986	-		IPR002490
	-	0				-
	-	0				-
Caenorhabditis elegans	anion transporter	4	C:GO:0016020; P:GO:0006814; P:GO:0055085; F:GO:0005215	-		IPR001898; PTHR10283 (PANTHER), PTHR10283:SF15 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	rap ran-gap family protein	5	F:GO:0005096; P:GO:0051056; F:GO:0005515; P:GO:0050790; C:GO:0048471	-		-
Haemonchus contortus	thioredoxin reductase 2	10	P:GO:0030097; P:GO:0010269; F:GO:0004791; P:GO:0000305; P:GO:0042542; P:GO:0007507; F:GO:0050662; C:GO:0005739; F:GO:0042803; F:GO:0000166	-	EC:1.8.1.9	IPR004099; IPR006338; PR00411 (PRINTS), G3DSA:3.50.50.60 (GENE3D), PTHR22912 (PANTHER), SSF51905 (SUPERFAMILY)

Caenorhabditis briggsae	slc22a5-prov partial	6	C:GO:0016021; P:GO:0009792; P:GO:0040010; P:GO:0055085; F:GO:0005215; P:GO:0002119	-		-
Caenorhabditis elegans	prion protein interacting protein	1	F:GO:0005488	-		-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	5	C:GO:0005789; F:GO:0008484; C:GO:0016021; P:GO:0016254; F:GO:0051267	-	EC:3.1.6.0	IPR017849; IPR017850; PTHR23072 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	pleckstrin homology domain family h (with 4 domain) member 1	4	C:GO:0005856; P:GO:0008340; F:GO:0005488; P:GO:0040010	-		IPR000299; IPR000857; IPR014352; IPR019748; IPR019749; PTHR22903 (PANTHER), PTHR22903:SF2 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	saccharopine dehydroge-se	3	F:GO:0016491; P:GO:0055114; F:GO:0005488	-		IPR005097; IPR007698; IPR007886; IPR016040; G3DSA:1.10.1870.10 (GENE3D), G3DSA:3.30.360.10 (GENE3D), G3DSA:3.40.50.1770 (GENE3D), PTHR11133 (PANTHER), PTHR11133:SF1 (PANTHER), SSF51735 (SUPERFAMILY), SSF52283 (SUPERFAMILY), SSF55347 (SUPERFAMILY)
Brugia malayi	member ras oncogene family	24	C:GO:0000785; C:GO:0005654; P:GO:0007052; C:GO:0042470; F:GO:0005525; P:GO:0030521; P:GO:0006611; P:GO:0051301; P:GO:0006184; P:GO:0006259; F:GO:0004767; C:GO:0005829; C:GO:0005643; P:GO:0007067; F:GO:0003713; P:GO:0007286; P:GO:0007165; P:GO:0045893; F:GO:0003682; F:GO:0003924; P:GO:0006606; F:GO:0050681; P:GO:0006405; P:GO:0044419	-	EC:3.1.4.12; EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR002041; IPR005225; IPR013753; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF269 (PANTHER), SSF52540 (SUPERFAMILY)

Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	11	P:GO:0040010; F:GO:0008270; P:GO:0006355; F:GO:0043565; P:GO:0002119; F:GO:0005515; F:GO:0003700; F:GO:0003707; P:GO:0009792; P:GO:0040018; C:GO:0005634	-		IPR001628; IPR013088; PR00350 (PRINTS), PTHR11865 (PANTHER), PTHR11865:SF238 (PANTHER), SSF57716 (SUPERFAMILY)
	-	0				IPR015880
	-	0				SignalP (SIGNALP)
	-	0				-
Macaca mulatta	cellular nucleic acid binding isoform 2	11	C:GO:0005829; F:GO:0008270; F:GO:0003727; P:GO:0045944; F:GO:0005515; F:GO:0003700; F:GO:0003697; P:GO:0008284; P:GO:0006695; C:GO:0005783; C:GO:0005634	-		IPR001878; IPR013084; PTHR23002 (PANTHER), PTHR23002:SF11 (PANTHER), SSF57756 (SUPERFAMILY)
Loa loa	hypothetical protein LOAG_06433 [Loa loa]	0				-
Brugia malayi	hypothetical protein [Brugia malayi]	3	F:GO:0008173; P:GO:0006396; F:GO:0000166	-		-
	-	0				-
Pongo abelii	s100 calcium binding protein a4	10	F:GO:0050786; P:GO:0001837; C:GO:0043005; F:GO:0005509; C:GO:0005730; P:GO:0043123; F:GO:0048306; C:GO:0048471; F:GO:0046982; F:GO:0042803	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	myb-like d--binding domain containing protein	0		F:GO:0003677		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Oesophagostomum dentatum	fmrf-like peptide family member (flp-1)	1	P:GO:0007218	-		IPR002544; PTHR20986 (PANTHER)

Caenorhabditis briggsae	briggsae cbr-unc-68 protein	11	P:GO:0055085; P:GO:0006629; C:GO:0005875; F:GO:0005509; C:GO:0016021; F:GO:0004872; P:GO:0006874; P:GO:0006816; C:GO:0005789; F:GO:0005219; P:GO:0006936	-		IPR015925; PTHR13715:SF11 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	guanine nucleotide exchange factor for ras-like gtpases n-termi-l motif family protein	5	F:GO:0005085; F:GO:0008603; P:GO:0051056; P:GO:0001932; C:GO:0005952	-		-
Caenorhabditis elegans	augmenter of liver regeneration	6	F:GO:0016972; P:GO:0055114; C:GO:0005739; P:GO:0007283; F:GO:0005515; P:GO:0008283	-	EC:1.8.3.2	IPR006863; IPR017905; PTHR12645 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	uncoordi-ted family member (unc-89)	0				IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF17 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	hypothetical protein Y69A2AR.31 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	heat repeat-containing protein 7a-like	1	F:GO:0005488	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR001534; SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR001534
Loa loa	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR001534; SignalP (SIGNALP)
Pongo abelii	apoptosis regulatory protein siva-like	14	P:GO:0006917; F:GO:0001618; F:GO:0008270; C:GO:0005739; F:GO:0008656; P:GO:0032088; P:GO:0008635; F:GO:0005164; P:GO:0019987; P:GO:0007165; F:GO:0005175; P:GO:0044419; C:GO:0005654; P:GO:0006924	-		IPR006058; IPR022773
	-	0				-

Caenorhabditis elegans	clathrin-associated protein	7	P:GO:0016183; C:GO:0008021; P:GO:0007269; C:GO:0030122; F:GO:0005515; P:GO:0006886; P:GO:0033227	-		IPR015629; PTHR11998 (PANTHER)
Caenorhabditis elegans	solute carrier family 27 (fatty acid transporter) member 1	0		F:GO:0016874; C:GO:0016021; P:GO:0008152; F:GO:0003824		-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	briggsae cbr-vps-35 protein	2	P:GO:0006897; C:GO:0005768	-		IPR005378
	-	0				-
Haemonchus contortus	briggsae cbr-asp-2 protein	3	P:GO:0008219; F:GO:0005515; F:GO:0008233	-		IPR001461; IPR009007; IPR021109; PTHR13683:SF53 (PANTHER)
Caenorhabditis elegans	cytoplasmic fmr1 interacting protein 1	12	P:GO:0016477; F:GO:0048365; P:GO:0048675; C:GO:0001726; P:GO:0030032; C:GO:0005845; F:GO:0051015; C:GO:0019717; C:GO:0048471; P:GO:0010172; C:GO:0030027; P:GO:0031529	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	ethanolamine ki-se	2	F:GO:0016301; P:GO:0008654	-		IPR011009; IPR020003
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		PTHR12905 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-ric-4 protein	1	C:GO:0044464	-		IPR000727; G3DSA:1.20.5.110 (GENE3D), PTHR19305 (PANTHER)
	-	0				-
	-	0				-
	-	0				IPR000276

Loa loa	d- replication licensing factor mcm7	22	C:GO:0000785; F:GO:0008094; F:GO:0005515; P:GO:0006974; P:GO:0006268; P:GO:0006355; P:GO:0008283; F:GO:0003697; C:GO:0005829; P:GO:0040039; P:GO:0030174; P:GO:0009792; P:GO:0042325; P:GO:0042493; C:GO:0042555; P:GO:0010171; F:GO:0003682; P:GO:0071364; F:GO:0005524; F:GO:0003678; P:GO:0040035; P:GO:0000910	-		IPR001208; IPR003593; IPR008050; IPR012340; IPR016027; IPR018525; G3DSA:3.30.1640.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR11630 (PANTHER), SSF52540 (SUPERFAMILY)
Loa loa	d- replication licensing factor mcm7	22	C:GO:0000785; F:GO:0008094; F:GO:0005515; P:GO:0006974; P:GO:0006268; P:GO:0006355; P:GO:0008283; F:GO:0003697; C:GO:0005829; P:GO:0040039; P:GO:0030174; P:GO:0009792; P:GO:0042325; P:GO:0042493; C:GO:0042555; P:GO:0010171; F:GO:0003682; P:GO:0071364; F:GO:0005524; F:GO:0003678; P:GO:0040035; P:GO:0000910	-		IPR001208; IPR003593; IPR008050; IPR012340; IPR016027; IPR018525; G3DSA:3.30.1640.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR11630 (PANTHER), SSF52540 (SUPERFAMILY)

Loa loa	d- replication licensing factor mcm7	22	C:GO:0000785; F:GO:0008094; F:GO:0005515; P:GO:0006974; P:GO:0006268; P:GO:0006355; P:GO:0008283; F:GO:0003697; C:GO:0005829; P:GO:0040039; P:GO:0030174; P:GO:0009792; P:GO:0042325; P:GO:0042493; C:GO:0042555; P:GO:0010171; F:GO:0003682; P:GO:0071364; F:GO:0005524; F:GO:0003678; P:GO:0040035; P:GO:0000910	-		IPR001208; IPR003593; IPR008050; IPR012340; IPR016027; IPR018525; G3DSA:3.30.1640.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR11630 (PANTHER), SSF52540 (SUPERFAMILY)
Loa loa	d- replication licensing factor mcm7	22	C:GO:0000785; F:GO:0008094; F:GO:0005515; P:GO:0006974; P:GO:0006268; P:GO:0006355; P:GO:0008283; F:GO:0003697; C:GO:0005829; P:GO:0040039; P:GO:0030174; P:GO:0009792; P:GO:0042325; P:GO:0042493; C:GO:0042555; P:GO:0010171; F:GO:0003682; P:GO:0071364; F:GO:0005524; F:GO:0003678; P:GO:0040035; P:GO:0000910	-		IPR001208; IPR003593; IPR008050; IPR012340; IPR016027; IPR018525; G3DSA:3.30.1640.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR11630 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	udp- ransferase family member (ugt-60)	4	P:GO:0005975; P:GO:0030259; F:GO:0030246; F:GO:0016758	-	EC:2.4.1.0	-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Homo sapiens	golgi membrane protein 1	2	C:GO:0005887; C:GO:0005794	-		PTHR15896 (PANTHER), PTHR15896:SF5 (PANTHER)
	-	0				-
Brugia malayi	paz piwi domain-containing family member (ppw-1)	0		P:GO:0016246		-

Caenorhabditis briggsae	atp synthase beta subunit	17	P:GO:0001525; F:GO:0046961; C:GO:0005929; F:GO:0005515; F:GO:0008553; P:GO:0006933; P:GO:0006898; P:GO:0006172; F:GO:0046933; F:GO:0030228; F:GO:0005509; P:GO:0042777; P:GO:0006629; P:GO:0007165; C:GO:0000275; P:GO:0006200; F:GO:0005524	-	EC:3.6.3.14; EC:3.6.3.6	IPR000194; IPR000793; IPR003593; IPR004100; IPR005722; IPR018118; IPR020003; G3DSA:1.10.1140.10 (GENE3D), G3DSA:2.40.10.170 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR15184 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis brenneri	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	poly(adp-ribose) metabolism enzyme family member (pme-3)	2	P:GO:0005975; P:GO:0045132	-		IPR007724; SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	tk fer protein ki-se	9	C:GO:0005929; C:GO:0030425; F:GO:0005515; P:GO:0034606; F:GO:0004672; C:GO:0030424; P:GO:0034608; C:GO:0043025; F:GO:0000166	-		IPR000980; IPR020685; IPR020764; SSF55550 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein Y32H12A.6 [Caenorhabditis elegans]	0		F:GO:0016491; C:GO:0016021; F:GO:0010181		-
	-	0				-
	-	0				-
	ubiquitin-like protein 5	1	C:GO:0005737	-		-
	-	0				-
Pongo abelii	kelch domain containing 7b	0		P:GO:0008150; C:GO:0005575		-
Ixodes scapularis	elmo domain-containing protein 1	0		F:GO:0003674; C:GO:0005856; P:GO:0006909; P:GO:0008150; C:GO:0005575		IPR006816; PTHR12771 (PANTHER), PTHR12771:SF1 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-ddl-3 protein	3	P:GO:0008340; F:GO:0005488; P:GO:0040010	-		IPR011990; PTHR13143 (PANTHER), SSF48452 (SUPERFAMILY)

Brugia malayi	integrator complex subunit 4	11	P:GO:0006810; P:GO:0040010; F:GO:0005488; P:GO:0040035; P:GO:0010171; P:GO:0019915; P:GO:0002119; P:GO:0040011; P:GO:0009792; P:GO:0001703; P:GO:0016246	-		IPR011989; PTHR20938 (PANTHER)
	-	0				-
Caenorhabditis elegans	oligopeptide transporter	6	F:GO:0016248; C:GO:0005624; F:GO:0015198; P:GO:0051956; F:GO:0015291; C:GO:0016020	-		PTHR11654 (PANTHER), PTHR11654:SF11 (PANTHER)
	-	0				-
Caenorhabditis elegans	d- polymerase zeta catalytic subunit	4	P:GO:0006261; F:GO:0003887; F:GO:0003677; F:GO:0000166	-	EC:2.7.7.7	IPR006134; PTHR10322 (PANTHER), PTHR10322:SF5 (PANTHER), SSF56672 (SUPERFAMILY)
Caenorhabditis remanei	degeneration of certain neurons protein 1	3	C:GO:0016020; F:GO:0005216; P:GO:0006811	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	P:GO:0055085; C:GO:0016021	-		IPR011701; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11662 (PANTHER), PTHR11662:SF11 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans ada-2 isoform b	0		P:GO:0010171; P:GO:0040027; P:GO:0006898; P:GO:0000003; F:GO:0008270; P:GO:0009792; P:GO:0008340; C:GO:0005622; P:GO:0040011; P:GO:0040010		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	af067448_1hemoglobi-se-type cysteine protei-se	7	P:GO:0009792; C:GO:0043231; C:GO:0044444; P:GO:0000003; F:GO:0004197; P:GO:0006508; F:GO:0004674	-	EC:3.4.22.0; EC:2.7.11.0	IPR001096; PTHR12000:SF4 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-

Ailuropoda melanoleuca	casein ki-se epsilon	14	C:GO:0005829; P:GO:0006281; F:GO:0004674; P:GO:0042752; P:GO:0030178; P:GO:0032922; F:GO:0005524; P:GO:0090263; F:GO:0005515; P:GO:0034613; P:GO:0007165; P:GO:0032436; C:GO:0005634; P:GO:0006468	-	EC:2.7.11.0	G3DSA:3.30.200.20 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF18 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	uncoordi-ted family member (unc-22)	5	C:GO:0030018; F:GO:0008307; P:GO:0007498; F:GO:0004674; F:GO:0000166	-	EC:2.7.11.0	IPR003598; IPR007110; IPR013098; IPR013783; G3DSA:1.10.510.10 (GENE3D), PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein T06D8.1 [Caenorhabditis elegans]	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein Y73B6BL.35 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	hypothetical protein T04F3.1 [Caenorhabditis elegans]	1	F:GO:0003824	-		-
	-	0				-
Caenorhabditis briggsae	tbc (tre-2 bub2 cdc16) domain family member (tbc-19)	0		P:GO:0032313; C:GO:0005622; F:GO:0005097		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	exosome complex exonuclease rrp4	5	F:GO:0000175; F:GO:0005515; C:GO:0000178; C:GO:0005634; F:GO:0008312	-		PTHR21321 (PANTHER), PTHR21321:SF2 (PANTHER)
Caenorhabditis briggsae	membrane associated ring finger	0		F:GO:0008270		IPR011016; IPR013083; IPR018957; PTHR12267 (PANTHER), SignalP (SIGNALP), SSF57850 (SUPERFAMILY)
Caenorhabditis briggsae	dimethylglycine dehydroge-se	6	C:GO:0005737; P:GO:0006546; F:GO:0016491; F:GO:0004047; P:GO:0055085; C:GO:0016020	-	EC:2.1.2.10	IPR006076; G3DSA:3.50.50.60 (GENE3D), PTHR13847 (PANTHER), PTHR13847:SF15 (PANTHER), SignalP (SIGNALP), SSF51905 (SUPERFAMILY)
	-	0				-
	-	0				-
Brugia malayi	hypothetical protein [Brugia malayi]	0				IPR022091
Caenorhabditis briggsae	db module family protein	0				IPR002602; PTHR12974 (PANTHER), PTHR12974:SF2 (PANTHER)
	-	0				-
Caenorhabditis briggsae	fh1 fh2 domain-containing protein 3	2	F:GO:0003779; P:GO:0030036	-		PTHR23213 (PANTHER), PTHR23213:SF3 (PANTHER)

Caenorhabditis elegans	prolyl 4-hydroxylase	6	F:GO:0031418; F:GO:0005506; F:GO:0004656; P:GO:0055114; F:GO:0016702; C:GO:0005783	-	EC:1.14.11.2 ; EC:1.13.11.0	PTHR10869 (PANTHER), PTHR10869:SF13 (PANTHER)
Caenorhabditis elegans	suppressor of cytokine sig-ling 7	7	F:GO:0005488; P:GO:0044238; P:GO:0050789; P:GO:0044260; P:GO:0023033; C:GO:0044464; P:GO:0043412	-		IPR000980; PTHR10385 (PANTHER), PTHR10385:SF17 (PANTHER), SSF55550 (SUPERFAMILY)
Gallus gallus	phd finger protein	2	P:GO:0009987; C:GO:0005622	-		IPR001841; IPR001965; IPR011011; PTHR12420 (PANTHER), PTHR12420:SF3 (PANTHER), SSF57889 (SUPERFAMILY)
Caenorhabditis briggsae	fk506 binding protein 2 isoform cra_b	5	P:GO:0006457; P:GO:0040010; C:GO:0044464; P:GO:0008340; F:GO:0003755	-	EC:5.2.1.8	IPR001179; G3DSA:3.10.50.40 (GENE3D), PTHR10516:SF9 (PANTHER), SSF54534 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	P:GO:0044238; P:GO:0019915; F:GO:0016757	-		IPR002213; G3DSA:3.40.50.2000 (GENE3D), PTHR11926:SF3 (PANTHER), SSF53756 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG00897 [Caenorhabditis briggsae]	0				PTHR23125 (PANTHER), PTHR23125:SF32 (PANTHER)
	-	0				IPR015880
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	briggsae cbr-cln- protein	26	P:GO:0008340; C:GO:0043005; C:GO:0005802; C:GO:0000139; C:GO:0030176; P:GO:0016236; P:GO:0006898; C:GO:0005624; C:GO:0005764; P:GO:0046662; P:GO:0007042; P:GO:0009792; P:GO:0006681; C:GO:0005795; C:GO:0005769; P:GO:0050877; C:GO:0008021; P:GO:0019222; P:GO:0042987; P:GO:0001575; C:GO:0005901; P:GO:0006684; P:GO:0015809; C:GO:0005634; P:GO:0043066; P:GO:0006678	-		IPR003492; SignalP (SIGNALP)
Ancylostoma duodenale	elegans protein partially confirmed by transcript evidence	0		P:GO:0040011; C:GO:0005576		IPR001283; IPR014044; SignalP (SIGNALP)

Caenorhabditis briggsae	glycine c-acetyltransferase (2-amino-3-ketobutyrate-coenzyme a ligase)	6	F:GO:0016874; F:GO:0030170; C:GO:0005743; P:GO:0009058; F:GO:0016769; F:GO:0008890	-	EC:2.3.1.29	IPR011282; IPR015421; IPR015424; PTHR13693 (PANTHER)
	-	0				-
Caenorhabditis elegans	short chain dehydroge-se reductase family protein	3	P:GO:0008152; F:GO:0003824; F:GO:0005488	-		IPR002198; IPR002347; IPR016040; PTHR19410:SF98 (PANTHER), SignalP (SIGNALP), SSF51735 (SUPERFAMILY)
Lodderomyces elongisporus NRRL YB-4239	n-glycosylase d- lyase	0		F:GO:0003684; C:GO:0016021; F:GO:0005375; P:GO:0006289; F:GO:0003677; F:GO:0008534; F:GO:0003906; P:GO:0006284; F:GO:0016829; P:GO:0006281; F:GO:0003824; P:GO:0006825		IPR011257; G3DSA:1.10.340.30 (GENE3D), PTHR10242 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	bestrophin 2	3	C:GO:0016021; F:GO:0005524; F:GO:0008026	-		IPR000615; IPR021134; SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein F59C12.3 [Caenorhabditis elegans]	1	F:GO:0005515	-		-
	-	0				-
Oryza sativa Japonica Group	surface-anchored protein	1	C:GO:0044464	-		PTHR16469 (PANTHER)
Oryza sativa Japonica Group	surface-anchored protein	0		C:GO:0009986; P:GO:0006397; F:GO:0008061; C:GO:0005634; P:GO:0008380; C:GO:0005739; C:GO:0019867; C:GO:0005576; F:GO:0003743; C:GO:0005618; P:GO:0006030		-
	-	0				-
Macacine herpesvirus 4	prb3 protein	1	F:GO:0005488	-		-
Paramecium tetraurelia strain d4-2	surface-anchored protein	0		C:GO:0009986; C:GO:0005739; F:GO:0008061; C:GO:0019867; C:GO:0005576; F:GO:0004872; F:GO:0003743; C:GO:0005618; P:GO:0006030		PTHR16469 (PANTHER)
Oryza sativa Japonica Group	surface-anchored protein	1	C:GO:0044464	-		PTHR16469 (PANTHER)
	-	0				SignalP (SIGNALP)

	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-rbc-1 protein	0				PTHR13950 (PANTHER), PTHR13950:SF1 (PANTHER)
Caenorhabditis briggsae	tk fer protein ki-se	7	F:GO:0004674; F:GO:0005524; F:GO:0004713; F:GO:0005515; C:GO:0044424; P:GO:0040018; P:GO:0006468	-	EC:2.7.11.0; EC:2.7.10.0	IPR000719; IPR001245; IPR008266; IPR011009; IPR020685; IPR020764; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
Apis mellifera	tubulin alpha-1 chain	6	P:GO:0007018; F:GO:0005525; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0017057; P:GO:0006098		G3DSA:3.40.50.1360 (GENE3D), SSF100950 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	immunoglobulin i-set domain containing protein	0		C:GO:0005604; P:GO:0006468; P:GO:0016338; P:GO:0070593; F:GO:0005524; C:GO:0016021; P:GO:0007156; F:GO:0008237; C:GO:0016020; F:GO:0008233; C:GO:0031012; F:GO:0005509; F:GO:0030414; F:GO:0004222; F:GO:0005021; C:GO:0030054; P:GO:0008218; P:GO:0007399; C:GO:0005938; P:GO:0007162; F:GO:0008270; C:GO:0005578; C:GO:0005887; F:GO:0005515; C:GO:0005886; C:GO:0005576; P:GO:0018298		-
	-	0				PTHR16193 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				PTHR10201 (PANTHER), PTHR10201:SF5 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	C:GO:0016021; P:GO:0006865; F:GO:0015171; P:GO:0055085	-		-

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	C:GO:0005737; P:GO:0006546; F:GO:0016491; F:GO:0004047	-	EC:2.1.2.10	-
Caenorhabditis elegans	expulsion defective family member (aex-3)	7	P:GO:0007618; P:GO:0030421; P:GO:0018991; F:GO:0017112; P:GO:0007268; P:GO:0050794; C:GO:0044464	-		PTHR13008 (PANTHER)
	-	0				-
Caenorhabditis briggsae	integrin alpha-ps2	8	P:GO:0009792; P:GO:0002119; P:GO:0018991; P:GO:0032940; P:GO:0040007; P:GO:0006898; P:GO:0040039; C:GO:0008305	-		G3DSA:2.130.10.130 (GENE3D), PTHR23220 (PANTHER), PTHR23220:SF11 (PANTHER)
	-	0				-
	-	0				-
Brugia malayi	swim zinc finger family protein	0		F:GO:0008270		PTHR22619 (PANTHER)
Caenorhabditis elegans	suppressor of activated let-60 ras family member (sur-2)	3	P:GO:0044260; P:GO:0090304; P:GO:0010467	-		IPR021629
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-sec-3 protein	5	P:GO:0007126; P:GO:0000003; P:GO:0040010; F:GO:0005515; P:GO:0040011	-		IPR019160
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	2	P:GO:0055085; C:GO:0016021	-		G3DSA:1.20.1250.20 (GENE3D), PTHR11662 (PANTHER), PTHR11662:SF17 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-unc-68 protein	8	F:GO:0004872; P:GO:0006629; F:GO:0005219; P:GO:0006816; P:GO:0006874; P:GO:0055085; F:GO:0005509; C:GO:0016021	-		IPR001870; IPR003877; IPR008985; IPR015925; PTHR13715:SF11 (PANTHER)
	-	0				-
	-	0				-
Loa loa	pinin sdk mema protein conserved region containing protein	0		F:GO:0046872; F:GO:0035091; F:GO:0016788; F:GO:0000166; P:GO:0007154; F:GO:0008270; F:GO:0005515; C:GO:0005634		IPR006786; PTHR12707 (PANTHER)

Caenorhabditis briggsae	briggsae cbr-gas-1 protein	14	F:GO:0048038; P:GO:0006979; P:GO:0008340; F:GO:0008137; C:GO:0005747; F:GO:0046872; P:GO:0040007; F:GO:0051539; F:GO:0051287; P:GO:0006120; P:GO:0002119; F:GO:0005515; P:GO:0006898; P:GO:0009792	-	EC:1.6.5.3	-
Brugia malayi	briggsae cbr-clk-2 protein	0		C:GO:0016020; C:GO:0005694; C:GO:0005634; F:GO:0000166; C:GO:0005737; F:GO:0017111; F:GO:0003674; F:GO:0005524; F:GO:0004872; F:GO:0005488		PTHR15830 (PANTHER)
Loa loa	calcium homeostasis endoplasmic reticulum protein	4	C:GO:0005737; P:GO:0065007; F:GO:0003676; P:GO:0009987	-		IPR000061; IPR006569; IPR006903; PTHR12323 (PANTHER), SSF109905 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	tetratricopeptide repeat protein 38	0		F:GO:0005488; F:GO:0005044; C:GO:0016020		-
	-	0				PTHR23317 (PANTHER), PTHR23317:SF16 (PANTHER)
Caenorhabditis briggsae	beta- -glucuronosyltransferase	2	C:GO:0016020; F:GO:0015018	-	EC:2.4.1.135	IPR005027; G3DSA:3.90.550.10 (GENE3D), SSF53448 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Loa loa	rab5-interacting protein	1	F:GO:0005515	-		IPR010742; PF07019 (PFAM)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis briggsae	probable e3 ubiquitin-protein ligase mycbp2	4	P:GO:0030071; F:GO:0005515; F:GO:0008270; C:GO:0005680	-		IPR012983; PTHR12846 (PANTHER), PTHR12846:SF2 (PANTHER)
Caenorhabditis elegans	gcn1 general control of amino-acid synthesis 1-like 1	4	C:GO:0005840; F:GO:0008135; F:GO:0005515; P:GO:0000003	-		IPR000357; IPR011989; IPR016024; IPR021133; PTHR23346 (PANTHER), PTHR23346:SF7 (PANTHER), PF12348 (PFAM)
Caenorhabditis briggsae	maltase-glucoamylase-like protein	0		F:GO:0004553; F:GO:0030246; P:GO:0008152; F:GO:0016787; P:GO:0005975; F:GO:0004558; F:GO:0016798; F:GO:0003824		IPR000322; PTHR22762:SF11 (PANTHER)
	-	0				-

	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021		-
Caenorhabditis elegans	btb and math domain containing family member (bath-44)	2	F:GO:0005515; P:GO:0000003	-		-
	-	0				-
Loa loa	zinc c2h2 type family protein	3	F:GO:0008270; F:GO:0003676; C:GO:0005622	-		-
Monodelphis domestica	briggsae cbr-rab-14 protein	23	C:GO:0005829; C:GO:0042599; P:GO:0045176; C:GO:0005764; C:GO:0042175; P:GO:0007264; F:GO:0001948; P:GO:0032880; C:GO:0005795; P:GO:0006913; F:GO:0004767; C:GO:0005624; P:GO:0007589; C:GO:0005770; C:GO:0005769; C:GO:0005791; C:GO:0030140; F:GO:0003924; C:GO:0048471; C:GO:0016324; P:GO:0006886; C:GO:0005634; F:GO:0005525	-	EC:3.1.4.12; EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
	-	0				-
Caenorhabditis elegans	trove domain member 2	3	F:GO:0005515; P:GO:0040010; C:GO:0030529	-		IPR008858; PTHR14202 (PANTHER), SSF140864 (SUPERFAMILY), SSF53300 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Loa loa	bestrophin family protein	0		P:GO:0040011; P:GO:0040018		IPR000615; IPR021134
Caenorhabditis briggsae	ferm domain (-ezrin-radixin-moesin) family member (frm-8)	0		F:GO:0005515		PTHR13436 (PANTHER), PTHR13436:SF1 (PANTHER)
Loa loa	hypothetical protein LOAG_11670 [Loa loa]	0				IPR001810; IPR022364; G3DSA:1.20.1280.50 (GENE3D), G3DSA:3.80.10.10 (GENE3D), SSF52058 (SUPERFAMILY)
Caenorhabditis elegans	lethal family member (let-805)	8	P:GO:0018996; P:GO:0009792; P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		PTHR19143 (PANTHER), PTHR19143:SF2 (PANTHER)

Caenorhabditis briggsae	patched family protein	10	P:GO:0040025; F:GO:0008158; P:GO:0040018; P:GO:0018996; P:GO:0040002; P:GO:0006810; P:GO:0040011; C:GO:0016021; P:GO:0019915; F:GO:0005215	-		-
Enterococcus casseliflavus EC20	ycf2	0		C:GO:0009986; F:GO:0008061; F:GO:0000166; F:GO:0017111; F:GO:0005524; C:GO:0005576; C:GO:0005618; C:GO:0009570; P:GO:0006030; C:GO:0009507; F:GO:0005488; C:GO:0009536		-
Enterococcus casseliflavus EC20	protein	0		C:GO:0009986; F:GO:0008061; F:GO:0000166; F:GO:0017111; F:GO:0005524; F:GO:0005179; C:GO:0005576; C:GO:0005618; C:GO:0009570; P:GO:0006030; C:GO:0009507; F:GO:0005488; C:GO:0009536		-
	-	0				IPR006162; SignalP (SIGNALP)
	-	0				-
Angiostrongylus cantonensis	zinc finger c-x8-c-x5-c-x3-h type	1	F:GO:0046872	-		PTHR14493 (PANTHER), PTHR14493:SF6 (PANTHER)
Angiostrongylus cantonensis	briggsae cbr-prx-11 protein	0				-
Caenorhabditis briggsae	chronic lymphocytic leukemia deletion region gene 6 protein	0				PTHR20951 (PANTHER)
	-	0				SignalP (SIGNALP)
Haemonchus contortus	legumain [Haemonchus contortus]	0		P:GO:0006508; F:GO:0004197		IPR001096; PTHR12000:SF3 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG15176 [Caenorhabditis briggsae]	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		-
Loa loa	twik (kcnk-like) family of potassium alpha subunit 7	4	C:GO:0016021; P:GO:0006813; F:GO:0005267; P:GO:0055085	-		PTHR11003 (PANTHER), PTHR11003:SF7 (PANTHER), SignalP (SIGNALP)

Caenorhabditis briggsae	briggsae cbr-cdh-1 protein	5	P:GO:0002119; P:GO:0007155; P:GO:0040010; P:GO:0040011; C:GO:0016020	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	pci domain-containing protein 2	5	P:GO:0000003; P:GO:0010171; P:GO:0040010; P:GO:0002119; P:GO:0040011	-		IPR000717; PTHR12732 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	protein ki-se domain containing protein	3	P:GO:0040022; F:GO:0016301; P:GO:0051729	-		PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0005515		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	4	P:GO:0040018; P:GO:0000003; P:GO:0010171; P:GO:0002119	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0005524; C:GO:0016021; F:GO:0008026		IPR000615; IPR021134
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Haemonchus contortus	ligand-gated ion channel family member (lgc-41)	5	C:GO:0016021; C:GO:0030054; C:GO:0045211; F:GO:0005230; P:GO:0006811	-		-
Oryctolagus cuniculus	alpha 1 type i collagen	15	P:GO:0001957; P:GO:0070208; P:GO:0010812; P:GO:0060325; P:GO:0043588; C:GO:0005584; F:GO:0005515; P:GO:0001649; P:GO:0001958; F:GO:0005201; P:GO:0001568; C:GO:0005737; P:GO:0015031; P:GO:0060351; P:GO:0060346	-		IPR008160; PTHR10499 (PANTHER), PTHR10499:SF122 (PANTHER)
	-	0				-
Nematostella vectensis	ornithine aminotransferase	2	F:GO:0030170; F:GO:0008483	-	EC:2.6.1.0	IPR005814; IPR010164; IPR015421; IPR015424

Caenorhabditis briggsae	immunoglobulin i-set domain containing protein	0		P:GO:0016311; F:GO:0016791; P:GO:0006470; F:GO:0016787; F:GO:0004725; P:GO:0009792; F:GO:0004721		IPR003961; IPR008957; IPR013783; PTHR10489 (PANTHER), PTHR10489:SF4 (PANTHER)
Caenorhabditis elegans	immunoglobulin i-set domain containing protein	0				IPR002602; IPR003961; IPR006150; IPR008957; IPR013783; PTHR10489 (PANTHER), PTHR10489:SF4 (PANTHER)
Macaca mulatta	PREDICTED: hypothetical protein LOC695354 [Macaca mulatta]	0				-
Brugia malayi	f-box only protein 11	9	C:GO:0005737; F:GO:0005515; P:GO:0016567; P:GO:0006511; F:GO:0004842; F:GO:0016274; C:GO:0005634; F:GO:0008270; C:GO:0000151	-	EC:6.3.2.19	IPR006626; IPR011050; IPR012334; PTHR22990 (PANTHER), PTHR22990:SF6 (PANTHER)
	-	0				-
Saccoglossus kowalevskii	-d-dependent epimerase dehydratase	4	F:GO:0016491; P:GO:0044237; F:GO:0050662; P:GO:0044238	-		IPR000534; IPR016040; SignalP (SIGNALP), SSF51735 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Brugia malayi	wapl (drosophila wings apart-like cohesin interactor) family member (wapl-1)	0		P:GO:0000003; P:GO:0040011; P:GO:0040010; P:GO:0018991		IPR012502; PTHR22100 (PANTHER), PTHR22100:SF7 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	inositol triphosphate receptor family member (itr-1)	11	P:GO:0055085; P:GO:0000280; P:GO:0006979; P:GO:0051209; P:GO:0007629; C:GO:0016021; P:GO:0016319; F:GO:0005220; P:GO:0007591; P:GO:0030322; C:GO:0005783	-		IPR000493; IPR003608; IPR015925; IPR016093; G3DSA:2.80.10.50 (GENE3D), PTHR13715:SF2 (PANTHER)
Danio rerio	disco-interacting protein 2 homolog b	4	P:GO:0008152; F:GO:0008134; C:GO:0005634; F:GO:0050564	-	EC:6.3.2.26	IPR010506; PTHR22754 (PANTHER), PTHR22754:SF9 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-sfxn-2 protein	4	F:GO:0008324; P:GO:0055085; P:GO:0006812; C:GO:0016020	-		IPR004686; PTHR11153:SF7 (PANTHER), SignalP (SIGNALP)
Loa loa	cyclic amp-regulated 21-like	0		F:GO:0003676; P:GO:0034605; F:GO:0003674; C:GO:0005737		IPR001374; G3DSA:3.30.1370.50 (GENE3D), PTHR15672 (PANTHER), PTHR15672:SF8 (PANTHER), SSF82708 (SUPERFAMILY)

Brugia malayi	cyclic amp-regulated 21-like	0		F:GO:0003676; P:GO:0034605; F:GO:0003674; C:GO:0005737		IPR001374; G3DSA:3.30.1370.50 (GENE3D), PTHR15672 (PANTHER), PTHR15672:SF8 (PANTHER), SSF82708 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	troponin i	0		F:GO:0005515		-
Brugia malayi	g protein-coupled receptor ki-se-interactor 1	8	F:GO:0008060; P:GO:0008277; F:GO:0046872; C:GO:0005925; P:GO:0050790; F:GO:0031267; C:GO:0005737; P:GO:0044237	-		IPR013724; PTHR23180 (PANTHER), PTHR23180:SF18 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG22835 [Caenorhabditis briggsae]	0		F:GO:0046872; P:GO:0055114; F:GO:0009055; F:GO:0016491; F:GO:0020037; F:GO:0005506; F:GO:0004497		-
	-	0				-
Haemochus contortus	alpha 1b	10	F:GO:0005200; P:GO:0007018; F:GO:0005525; F:GO:0019904; P:GO:0000226; P:GO:0051258; C:GO:0005829; F:GO:0046982; C:GO:0005881; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000217; IPR002452; IPR003008; IPR008280; IPR017975; IPR018316; IPR023123
Mus musculus	rab3 gtpase-activating protein catalytic subunit	0		F:GO:0005096; P:GO:0050790; C:GO:0005737; F:GO:0017137; P:GO:0043087; C:GO:0005625; F:GO:0005097		PTHR21422 (PANTHER), PTHR21422:SF5 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	alkyldihydroxyacetonephosphate synthase	6	F:GO:0050660; P:GO:0009792; F:GO:0016491; P:GO:0040007; F:GO:0016740; P:GO:0002119	-		-
	-	0				-

Caenorhabditis elegans	briggsae cbr-hhat-2 protein	0		C:GO:0016021; C:GO:0016020; P:GO:0055085; P:GO:0015031; F:GO:0015450; P:GO:0006810		SignalP (SIGNALP)
Brugia malayi	hypothetical protein Bm1_31875 [Brugia malayi]	0		F:GO:0005488		-
Loa loa	tir (toll and interleukin 1 receptor) domain protein family member (tir-1)	5	P:GO:0007165; P:GO:0045087; C:GO:0031224; F:GO:0042802; F:GO:0004888	-		-
Caenorhabditis elegans	membrane-bound transcription factor site 2	3	P:GO:0044238; C:GO:0044464; F:GO:0016787	-		IPR001193; IPR008915; PTHR13325 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	regulator of g protein sig-ling domain containing protein	0		F:GO:0004871		IPR000342; IPR016137; G3DSA:1.10.196.10 (GENE3D), PTHR10845 (PANTHER), PTHR10845:SF14 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG02636 [Caenorhabditis briggsae]	0		P:GO:0010171; P:GO:0044237; F:GO:0050662; P:GO:0000003; P:GO:0002119; P:GO:0009792; P:GO:0055114; F:GO:0016491; F:GO:0003854; F:GO:0003824; P:GO:0040011; P:GO:0008152; P:GO:0006694; F:GO:0005488		PTHR10366 (PANTHER), PTHR10366:SF19 (PANTHER)
Caenorhabditis elegans	fanci (fanconi anemia complex component i) homolog family member (fnci-1)	0				-
	-	0				-
Brugia malayi	dappu_310999-like protein	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	4	P:GO:0007186; C:GO:0016021; P:GO:0007165; F:GO:0004930	-		IPR000276; G3DSA:1.20.1070.10 (GENE3D), PTHR19264 (PANTHER), PTHR19264:SF33 (PANTHER), SignalP (SIGNALP)
	-	0				-
Bos taurus	PREDICTED: hypothetical protein [Bos taurus]	0				-
Bos taurus	PREDICTED: hypothetical protein [Bos taurus]	3	C:GO:0016020; F:GO:0005272; P:GO:0006814	-		-

Caenorhabditis briggsae	pdf receptor homolog family member (pdfr-1)	0		F:GO:0004888; C:GO:0016021; C:GO:0016020; F:GO:0004930; P:GO:0007166; P:GO:0007165; F:GO:0004872; F:GO:0004871; P:GO:0007186; C:GO:0005886		-
Caenorhabditis briggsae	pdf receptor homolog family member (pdfr-1)	1	F:GO:0004871	-		PTHR12011 (PANTHER), PTHR12011:SF14 (PANTHER)
Caenorhabditis elegans	pdf receptor homolog family member (pdfr-1)	0		F:GO:0004888; C:GO:0016021; C:GO:0016020; F:GO:0004930; P:GO:0007166; P:GO:0007165; F:GO:0004872; F:GO:0004871; P:GO:0007186; C:GO:0005886		PTHR12011 (PANTHER), PTHR12011:SF14 (PANTHER)
Caenorhabditis briggsae	pdf receptor homolog family member (pdfr-1)	1	F:GO:0004871	-		PTHR12011 (PANTHER), PTHR12011:SF14 (PANTHER)
	-	0				-
Caenorhabditis elegans	tata-binding protein-associated factor 172	3	F:GO:0005524; F:GO:0004386; F:GO:0003677	-		IPR000330; PTHR10799 (PANTHER), PTHR10799:SF72 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0000003; P:GO:0040011; P:GO:0040010; P:GO:0006898; F:GO:0008270; P:GO:0002119; P:GO:0040007; C:GO:0005622		IPR007087; IPR015880
	-	0				-
Caenorhabditis elegans	blooms syndrome d-	16	C:GO:0031981; P:GO:0032508; F:GO:0005515; F:GO:0000403; P:GO:0007131; F:GO:0043140; P:GO:0000731; C:GO:0044427; P:GO:0045003; F:GO:0000739; P:GO:0048523; P:GO:0000732; P:GO:0019219; F:GO:0005524; P:GO:0060255; P:GO:0006260	-		IPR004589; G3DSA:3.40.50.300 (GENE3D), PTHR13710:SF14 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	lethal family member (let-23)	1	F:GO:0016301	-		IPR006211; IPR006212; IPR009030; IPR020685; IPR020688; G3DSA:2.10.220.10 (GENE3D), G3DSA:3.80.20.20 (GENE3D)

Angiostrongylus cantonensis	elegans protein confirmed by transcript evidence	0				IPR021010; SSF141739 (SUPERFAMILY)
Pongo abelii	dus1l protein	4	F:GO:0050660; P:GO:0055114; F:GO:0017150; P:GO:0008033	-		-
	-	0				-
Caenorhabditis elegans	stem-loop binding protein	13	F:GO:0003730; P:GO:0040010; P:GO:0006915; P:GO:0044260; P:GO:0090304; P:GO:0007076; P:GO:0040035; P:GO:0010171; P:GO:0002009; C:GO:0005737; C:GO:0005634; P:GO:0009790; P:GO:0016246	-		PTHR17408 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG18685 [Caenorhabditis briggsae]	0		F:GO:0003676; F:GO:0000166		-
Loa loa	hypothetical protein LOAG_10662 [Loa loa]	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Saccoglossus kowalevskii	threonine dehydratase	6	P:GO:0040035; F:GO:0005488; P:GO:0040010; P:GO:0040011; F:GO:0003824; P:GO:0002009	-		IPR001926; G3DSA:3.40.50.1100 (GENE3D), PTHR10314 (PANTHER), PTHR10314:SF17 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Homo sapiens	non-structural mainte-nce of chromosomes element 1 homolog	6	P:GO:0023034; F:GO:0005515; C:GO:0005634; F:GO:0008270; P:GO:0006310; P:GO:0006281	-		-
Caenorhabditis briggsae	eukaryotic translation initiation factor subunit 10 150 170kda	6	F:GO:0003743; C:GO:0043229; C:GO:0005829; C:GO:0005852; F:GO:0005515; P:GO:0001732	-		IPR000717; PTHR14005 (PANTHER)
Caenorhabditis briggsae	eukaryotic translation initiation factor subunit 10 150 170kda	6	F:GO:0003743; C:GO:0043229; C:GO:0005829; C:GO:0005852; F:GO:0005515; P:GO:0001732	-		IPR000717; PTHR14005 (PANTHER)
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	5	P:GO:0007160; P:GO:0008218; F:GO:0005509; P:GO:0018298; C:GO:0016020	-		IPR011042; PTHR10529 (PANTHER), PTHR10529:SF4 (PANTHER), SSF63825 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	wgr domain containing protein	1	F:GO:0016740	-		IPR008893; PTHR15447 (PANTHER), SSF142921 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG08489 [Caenorhabditis briggsae]	0		C:GO:0016021; C:GO:0016020		SignalP (SIGNALP)
Caenorhabditis elegans	dead (asp-glu-ala-asp) box polypeptide 49	3	F:GO:0003676; F:GO:0005524; F:GO:0008026	-		IPR011545; IPR014001; IPR014014; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF12 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Brugia malayi	in family member (ttn-1)	0		F:GO:0005524; F:GO:0004672; P:GO:0006468; P:GO:0009792		IPR007110; IPR013783; PTHR19900 (PANTHER), PTHR19900:SF1 (PANTHER), SSF48726 (SUPERFAMILY)
Macaca fascicularis	ribosomal protein l8	4	F:GO:0003735; C:GO:0022625; F:GO:0019843; P:GO:0006414	-		IPR002171; IPR008991; IPR014722; IPR014726; IPR022669; IPR022671; PTHR13691:SF4 (PANTHER)
Caenorhabditis sp. PS1010	f-box domain containing protein	3	P:GO:0006508; F:GO:0004181; F:GO:0008270	-	EC:3.4.17.0	-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG01711 [Caenorhabditis briggsae]	0				-
Pongo abelii	trafficking protein particle complex subunit 5	7	P:GO:0006182; F:GO:0005515; F:GO:0020037; C:GO:0030008; P:GO:0016192; F:GO:0004383; C:GO:0005783	-	EC:4.6.1.2	IPR007194; IPR011644; G3DSA:3.30.1380.20 (GENE3D), PTHR20902 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	pqq enzyme repeat family protein	1	P:GO:0006898	-		PTHR21573 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-abf-2 protein	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	histone-lysine n- h3 lysine-9 specific 3	5	P:GO:0007127; P:GO:0006357; P:GO:0007281; P:GO:0034968; F:GO:0005488	-		IPR001214; IPR007728; G3DSA:2.170.270.10 (GENE3D), PTHR22884 (PANTHER), PTHR22884:SF22 (PANTHER), SSF82199 (SUPERFAMILY)
	-	0				-
	-	0				-
Brugia malayi	hypothetical protein Bm1_43305 [Brugia malayi]	0				-
Ancylostoma caninum	forkhead transcription factor daf-16	4	F:GO:0003700; F:GO:0043565; C:GO:0005634; P:GO:0006355	-		-

Caenorhabditis briggsae	- h exchanger family member (nhx-9)	5	F:GO:0015385; P:GO:0055085; P:GO:0006885; C:GO:0016021; P:GO:0006814	-		IPR006153; SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	motor axon guidance family member (max-1)	2	P:GO:0008340; P:GO:0040010	-		PTHR22903 (PANTHER), PTHR22903:SF2 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	tnni3 interacting ki-se	8	C:GO:0005737; P:GO:0006468; F:GO:0046872; F:GO:0005524; F:GO:0008022; C:GO:0005634; F:GO:0004674; F:GO:0031013	-	EC:2.7.11.0	-
	-	0				-
Caenorhabditis elegans	elongator complex protein 3	12	F:GO:0051536; P:GO:0006357; C:GO:0005730; C:GO:0016591; F:GO:0046872; F:GO:0008607; C:GO:0008023; F:GO:0003677; F:GO:0005515; F:GO:0004402; F:GO:0016944; C:GO:0005737	-	EC:2.3.1.48	PTHR11135 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-eel-1 protein	0		F:GO:0005488; F:GO:0016881; C:GO:0005622; P:GO:0006464		SignalP (SIGNALP)
	-	0				-
	-	0				-
						IPR008160; PTHR10499 (PANTHER), PTHR10499:SF114 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Brugia malayi	uncoordi-ted family member (unc-52)	2	P:GO:0030239; C:GO:0005578	-		IPR013783; PTHR10574 (PANTHER), PTHR10574:SF20 (PANTHER)
	-	0				-
	-	0				-
Ornithorhynchus anatinus	phosphoenolpyruvate cytosolic	12	P:GO:0006107; C:GO:0005625; F:GO:0030145; P:GO:0042593; P:GO:0014823; F:GO:0019003; P:GO:0046327; F:GO:0031406; P:GO:0006094; F:GO:0004613; C:GO:0005737; F:GO:0005525	-	EC:4.1.1.32	IPR008209; IPR008210; IPR013035; G3DSA:2.170.8.10 (GENE3D), SSF53795 (SUPERFAMILY)

Caenorhabditis elegans	lethal isoform b	0		F:GO:0015662; C:GO:0016020; P:GO:0006754; P:GO:0006812		PTHR13219 (PANTHER)
Caenorhabditis elegans	lethal isoform b	0		F:GO:0015662; C:GO:0016020; P:GO:0006754; P:GO:0006812		PTHR13219 (PANTHER)
	-	0				-
Caenorhabditis elegans	Hypothetical protein C25A1.7a [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				PTHR13436 (PANTHER), PTHR13436:SF1 (PANTHER)
Caenorhabditis briggsae	patched family protein	5	P:GO:0018996; C:GO:0016021; P:GO:0040018; F:GO:0008158; P:GO:0040011	-		IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER), SSF82866 (SUPERFAMILY)
Loa loa	iesterase family member (pde-6)	0		P:GO:0007411; F:GO:0003824; P:GO:0007165		-
Caenorhabditis briggsae	ubr1_caeel ame: full=e3 ubiquitin-protein ligase ubr-1 ame: full=n-recognin-1 ame: full=ubiquitin-protein ligase e3-alpha	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	ras family protein	9	C:GO:0005737; F:GO:0005525; C:GO:0005886; F:GO:0005515; P:GO:0006913; P:GO:0006886; C:GO:0005634; P:GO:0007264; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
	-	0				IPR008138; IPR008139; IPR011001
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Pongo abelii	plexin d1	8	P:GO:0001569; F:GO:0017154; C:GO:0005622; C:GO:0005886; F:GO:0005515; P:GO:0007165; P:GO:0060666; C:GO:0016021	-		-

Caenorhabditis elegans	abnormal cell migration family member (mig-15)	10	F:GO:0005083; P:GO:0007243; F:GO:0004674; P:GO:0045060; F:GO:0005524; F:GO:0005515; F:GO:0000155; C:GO:0016020; P:GO:0006950; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF82 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-inx- protein	7	P:GO:0040035; P:GO:0009792; P:GO:0007631; P:GO:0040010; P:GO:0030421; P:GO:0040011; P:GO:0002009	-		IPR000990; SignalP (SIGNALP)
Caenorhabditis elegans	zinc finger protein	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		IPR007087; IPR015880; SSF57667 (SUPERFAMILY)
Caenorhabditis elegans	zinc finger protein	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		IPR007087; IPR015880; SSF57667 (SUPERFAMILY)
Brugia malayi	hypothetical protein [Brugia malayi]	4	P:GO:0000003; P:GO:0040010; P:GO:0006898; P:GO:0002119	-		IPR007590
	-	0				IPR014044
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	valyl-tr- synthetase	3	F:GO:0004812; P:GO:0006418; F:GO:0000166	-		IPR002303; IPR009080; IPR013155; IPR014729; G3DSA:1.10.730.10 (GENE3D), PTHR11946 (PANTHER), SSF52374 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein C01B7.5 [Caenorhabditis elegans]	0		F:GO:0005515		IPR001478; G3DSA:2.30.42.10 (GENE3D)
Caenorhabditis elegans	sensory axon guidance family member (sax-2)	1	F:GO:0005515	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	homeodomain interacting protein ki-se family member (hpk-1)	1	P:GO:0008340	-		-
	-	0				-
Caenorhabditis elegans	autophagy-specific gene isoform b	12	F:GO:0004674; P:GO:0050804; F:GO:0019894; P:GO:0001558; P:GO:0000003; P:GO:0051124; P:GO:0008088; F:GO:0005524; P:GO:0035069; P:GO:0006914; P:GO:0006468; P:GO:0032007	-	EC:2.7.11.0	-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-lem-3 protein	1	P:GO:0007413	-		-

Caenorhabditis briggsae	phosphatidylethanolamine-binding protein	2	P:GO:0002119; P:GO:0009792	-		-
	-	0				-
Caenorhabditis elegans	nephrosis 2-like protein	2	F:GO:0032934; C:GO:0016020	-		IPR001107; IPR001972; SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0004888; C:GO:0016020; P:GO:0007606		SignalP (SIGNALP)
Caenorhabditis elegans	excretory ca-l abnormal family member (exc-5)	0				PTHR12673 (PANTHER), PTHR12673:SF8 (PANTHER)
Caenorhabditis elegans	n-alpha-acetyltransferase auxiliary subunit	0		P:GO:0048659; C:GO:0005737; F:GO:0005515		PTHR21373 (PANTHER)
Caenorhabditis elegans	ptb domain-containing engulfment adapter protein 1	2	P:GO:0012501; F:GO:0005515	-		IPR006020; IPR011993; PTHR11232 (PANTHER), PTHR11232:SF11 (PANTHER), SSF50729 (SUPERFAMILY)
Caenorhabditis briggsae	r--dependent r- polymerase	1	F:GO:0005515	-		-
Pongo abelii	small nuclear ribonucleoprotein f	7	C:GO:0005683; C:GO:0005654; P:GO:0000387; C:GO:0005681; F:GO:0003723; F:GO:0005515; C:GO:0005829	-		IPR001163; IPR006649; IPR010920; G3DSA:2.30.30.100 (GENE3D), PTHR11021 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical r--binding protein	0		F:GO:0003676; F:GO:0000166; P:GO:0009792		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF57 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	in family member (ttn-1)	1	P:GO:0009792	-		IPR013783
Caenorhabditis briggsae	briggsae cbr-ers-2 protein	0		F:GO:0016874; C:GO:0016021; P:GO:0006418; F:GO:0000166; C:GO:0005737; P:GO:0006412; F:GO:0005524; F:GO:0004818; P:GO:0016485; F:GO:0004812; F:GO:0016876; P:GO:0006424; P:GO:0043039		IPR000738; IPR009068

Harpegnathos saltator	26s protease regulatory subunit 8	15	P:GO:0051437; P:GO:0006366; F:GO:0003712; F:GO:0031531; P:GO:0043193; P:GO:0051436; P:GO:0043069; C:GO:0005737; C:GO:0005730; C:GO:0000502; P:GO:0016481; F:GO:0016887; F:GO:0008233; P:GO:0031145; F:GO:0005524	-		G3DSA:1.10.8.60 (GENE3D), PTHR23073 (PANTHER), PTHR23073:SF12 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis briggsae	briggsae cbr-hid-1 protein	0		F:GO:0003674; C:GO:0016020; P:GO:0008150; C:GO:0005575		IPR019142; PTHR21575 (PANTHER), PTHR21575:SF9 (PANTHER)
Homo sapiens	transgelin 2	4	C:GO:0031965; F:GO:0005515; C:GO:0005886; P:GO:0007517	-		-
Caenorhabditis elegans	gl actin (drosophila neuroligin-like) homolog family member (nrx-1)	0				-
Loa loa	hypothetical protein LOAG_01905 [Loa loa]	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	solute carrier family 9 (sodium hydrogen exchanger) member 7	5	F:GO:0015385; P:GO:0055085; P:GO:0006885; C:GO:0016021; P:GO:0006814	-		IPR002090; SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-pgp-1 protein	4	F:GO:0042626; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		-
Homo sapiens	hCG2041296 [Homo sapiens]	0				-
Caenorhabditis elegans	atp-binding sub-family d member 2	8	P:GO:0055085; C:GO:0005739; C:GO:0016021; F:GO:0042626; C:GO:0005778; F:GO:0005524; F:GO:0005515; P:GO:0008152	-		IPR010509; PTHR11384 (PANTHER), PTHR11384:SF12 (PANTHER)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG19257 [Caenorhabditis briggsae]	0		P:GO:0002119		-
	-	0				-
	-	0				-

Caenorhabditis elegans	cysteine synthase	0		F:GO:0016740; F:GO:0030170; P:GO:0019344; F:GO:0016829; F:GO:0003824; P:GO:0006535; F:GO:0004124; P:GO:0008152; P:GO:0008652		G3DSA:3.40.50.1100 (GENE3D), PTHR10314 (PANTHER), PTHR10314:SF8 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	protein ki-se domain-containing protein	2	F:GO:0005488; F:GO:0004672	-		-
Caenorhabditis briggsae	Hypothetical protein CBG18604 [Caenorhabditis briggsae]	0		F:GO:0046872; P:GO:0055114; F:GO:0009055; F:GO:0016491; F:GO:0020037; F:GO:0005506; F:GO:0004497		-
Loa loa	domon domain-containing protein	2	P:GO:0009056; P:GO:0044238	-		-
Pongo abelii	phosphatidic acid phosphatase type 2c	6	P:GO:0016311; F:GO:0004721; C:GO:0016021; F:GO:0008195; F:GO:0042392; C:GO:0005886	-	EC:3.1.3.16; EC:3.1.3.4	-
	-	0				SignalP (SIGNALP)
						IPR009443
Brugia malayi	in family member (ttn-1)	1	P:GO:0009792	-		-
	-	0				-
	-	0				-
Angiostrongylus cantonensis	zinc finger c-x8-c-x5-c-x3-h type	1	F:GO:0005515	-		PTHR14493 (PANTHER), PTHR14493:SF1 (PANTHER)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG08295 [Caenorhabditis briggsae]	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0019915; P:GO:0040018; P:GO:0040011	-		-
	-	0				-
Caenorhabditis elegans	briggsae cbr-swm-1 protein	1	F:GO:0005515	-		-
Caenorhabditis elegans	briggsae cbr-swm-1 protein	1	F:GO:0005515	-		IPR002919; IPR013032; G3DSA:2.10.25.10 (GENE3D), PTHR23259 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Loa loa	hypothetical protein LOAG_12108 [Loa loa]	0		C:GO:0016021		SignalP (SIGNALP)
Caenorhabditis elegans	transmembrane protein 38a	3	C:GO:0016021; F:GO:0005261; P:GO:0015672	-		IPR007866; PTHR12454:SF2 (PANTHER)

Homo sapiens	-dh dehydroge-se	5	P:GO:0006120; P:GO:0007605; F:GO:0008137; P:GO:0006810; C:GO:0005747	-	EC:1.6.5.3	SignalP (SIGNALP)
Loa loa	lycan alpha homolog family member (sgca-1)	0		C:GO:0016012; F:GO:0005509; C:GO:0016020; F:GO:0005515		IPR008908
Caenorhabditis elegans	tetratricopeptide repeat domain 39a	0		F:GO:0003674; F:GO:0005488; P:GO:0008150; C:GO:0005575		IPR019412; SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein C29F5.1 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	nmda receptor glutamate-binding chain	1	F:GO:0005515	-		IPR006214; PTHR23291:SF14 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	c2 domain containing protein	2	P:GO:0009792; C:GO:0016020	-		IPR000008; IPR008973; IPR018029; G3DSA:2.60.40.150 (GENE3D), PTHR10774 (PANTHER), PTHR10774:SF1 (PANTHER)
Caenorhabditis elegans	c2 domain containing protein	2	P:GO:0009792; C:GO:0016020	-		IPR000008; IPR008973; IPR018029; G3DSA:2.60.40.150 (GENE3D), PTHR10774 (PANTHER), PTHR10774:SF1 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	zinc finger bed domain-containing protein 1	0		F:GO:0004803; F:GO:0003677; C:GO:0005634; F:GO:0003676; C:GO:0005737; F:GO:0003674; F:GO:0046983; F:GO:0005515; F:GO:0046872; C:GO:0000228; P:GO:0008150		IPR012337; PTHR23272 (PANTHER)
Angiostrongylus cantonensis	homeobox protein 1aa	16	P:GO:0007411; F:GO:0030528; P:GO:0021561; P:GO:0016337; P:GO:0006355; P:GO:0021570; F:GO:0043565; P:GO:0010171; P:GO:0007413; P:GO:0002119; F:GO:0003700; P:GO:0040011; C:GO:0005737; P:GO:0040018; C:GO:0005634; P:GO:0009790	-		-
	-	0				-

	-	0				-
Caenorhabditis sp. PS1010	briggsae cbr-cdh-4 protein	5	P:GO:0007409; F:GO:0005515; P:GO:0007155; P:GO:0007420; C:GO:0016020	-		IPR002126; IPR015919; PTHR10596 (PANTHER), PTHR10596:SF74 (PANTHER)
	-	0				-
	-	0				-
	-	0				IPR000436; IPR016060
Nematostella vectensis	leishmanolysin-like (metallopeptidase m8 family) isoform cra_a	1	C:GO:0044464	-		IPR001577; G3DSA:3.90.132.10 (GENE3D), SSF55486 (SUPERFAMILY)
Loa loa	short chain dehydroge-se reductase family protein	2	P:GO:0009058; F:GO:0016616	-	EC:1.1.1.0	IPR002198; IPR016040; PTHR19410:SF36 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	#NAME?	5	P:GO:0055114; F:GO:0016491; P:GO:0040010; P:GO:0002119; P:GO:0040011	-		IPR001395; IPR018170; IPR023210; PTHR11732:SF34 (PANTHER)
Caenorhabditis briggsae	protein	23	F:GO:0004674; P:GO:0002119; P:GO:0006325; C:GO:0032991; P:GO:0001751; P:GO:0007169; P:GO:0044238; P:GO:0016246; F:GO:0008565; P:GO:0044260; P:GO:0040039; P:GO:0040010; P:GO:0006898; P:GO:0006606; P:GO:0009792; P:GO:0048523; C:GO:0044428; P:GO:0040035; P:GO:0003002; P:GO:0007476; C:GO:0044444; C:GO:0044427; F:GO:0005488	-	EC:2.7.11.0	IPR001494; IPR011989; IPR016024; PTHR10997 (PANTHER), PTHR10997:SF8 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
synthetic construct	ribosome binding protein 1 homolog 180kda	7	F:GO:0004872; C:GO:0030176; C:GO:0005840; P:GO:0055085; P:GO:0007165; P:GO:0006412; P:GO:0015031	-	EC:3.6.5.3	PTHR18939 (PANTHER)
Caenorhabditis elegans	creb homolog family member (crh-1)	0				-
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis briggsae	amop domain containing protein	2	C:GO:0016021; P:GO:0007160	-		IPR005533; PTHR13802 (PANTHER), PTHR13802:SF2 (PANTHER)
Loa loa	briggsae cbr-gcy-12 protein	1	F:GO:0003824	-		-
	-	0				-
Homo sapiens	isoform cra_a	0		F:GO:0003674; P:GO:0008150		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-dmd-6 protein	6	F:GO:0003700; F:GO:0003677; F:GO:0005515; P:GO:0007548; C:GO:0005634; P:GO:0006355	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG23067 [Caenorhabditis briggsae]	0		P:GO:0006508; F:GO:0016491; F:GO:0004190; C:GO:0016021		-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis briggsae	Hypothetical protein CBG01673 [Caenorhabditis briggsae]	1	F:GO:0005488	-		PTHR22908 (PANTHER), PTHR22908:SF13 (PANTHER)
	matrix metalloprotei-se 7	7	C:GO:0005615; P:GO:0042127; F:GO:0004222; P:GO:0030574; P:GO:0006508; F:GO:0008270; C:GO:0005578	-	EC:3.4.24.0	IPR001818; G3DSA:3.40.390.10 (GENE3D), PTHR10201 (PANTHER), PTHR10201:SF34 (PANTHER), SSF55486 (SUPERFAMILY)
Brugia malayi	strictosidine synthase	1	F:GO:0003824	-		IPR004141; IPR011042; PTHR10426:SF6 (PANTHER), SSF63829 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-pro-1 protein	4	P:GO:0030154; P:GO:0007506; P:GO:0006364; C:GO:0005634	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Arthroderma otae CBS 113480	adp-ribosylation factor	0		F:GO:0005525; P:GO:0007264; F:GO:0000166; C:GO:0005622		-
Homo sapiens	histone h1 transcription factor large subunit 2a	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-tag-275 protein	1	F:GO:0016787	-		PTHR11905 (PANTHER), PTHR11905:SF6 (PANTHER)
	-	0				-
	-	0				-

	-	0				-
Caenorhabditis briggsae	briggsae cbr-tag-308 protein	0				-
	-	0				-
Caenorhabditis sp. PS1010	zinc carboxypeptidase family protein	3	P:GO:0006508; F:GO:0004181; F:GO:0008270	-	EC:3.4.17.0	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), PTHR11705:SF12 (PANTHER), SSF53187 (SUPERFAMILY)
	-	0				IPR008160; PTHR10499 (PANTHER), PTHR10499:SF114 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
uncultured archaeon	conserved hypothetical protein, DUF255 family [uncultured archaeon]	0		F:GO:0003824		PTHR12145 (PANTHER)
Caenorhabditis briggsae	-dh-cytochrome b5 reductase 2	7	P:GO:0009792; P:GO:0002119; F:GO:0016491; P:GO:0032940; P:GO:0040010; P:GO:0055114; P:GO:0006898	-		IPR001433; G3DSA:3.40.50.80 (GENE3D), PTHR19370 (PANTHER), PTHR19370:SF3 (PANTHER), SSF52343 (SUPERFAMILY)
Saccoglossus kowalevskii	lethal giant	2	P:GO:0009987; C:GO:0044424	-		IPR000664; IPR011046; IPR013577; IPR015943; PTHR10241 (PANTHER), PTHR10241:SF10 (PANTHER)
	-	0				-
	-	0				IPR001159; IPR014720
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG02103 [Caenorhabditis briggsae]	0				-
	-	0				IPR000436
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	uncharacterized protein kiaa1409	0		F:GO:0005488		PTHR21696 (PANTHER)
Brugia malayi	set domain containing protein	0		F:GO:0046872; P:GO:0006355; F:GO:0003676; F:GO:0008270; C:GO:0005634; C:GO:0005622		-
Loa loa	hypothetical protein LOAG_14239 [Loa loa]	0				-
	-	0				-
Caenorhabditis briggsae	malate dehydroge-se mitochondrial variant 1	7	F:GO:0030060; F:GO:0005488; C:GO:0005739; P:GO:0055114; P:GO:0006108; P:GO:0006099; P:GO:0006096	-	EC:1.1.1.37	IPR001236; IPR001252; IPR001557; IPR010097; IPR015955; IPR016040; IPR022383; PTHR11540 (PANTHER), SignalP (SIGNALP), SSF51735 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	8	F:GO:0004383; F:GO:0004674; P:GO:0023034; C:GO:0016021; F:GO:0008528; F:GO:0005524; P:GO:0006468; P:GO:0006182	-	EC:4.6.1.2; EC:2.7.11.0	IPR001054; IPR018297; PTHR11920 (PANTHER), PTHR11920:SF40 (PANTHER)
	-	0				IPR006564; IPR007527

Caenorhabditis elegans	hypothetical protein W03F11.5 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Harpegnathos saltator	f-actin-capping protein subunit alpha	6	C:GO:0030863; P:GO:0030036; C:GO:0071203; F:GO:0003779; C:GO:0008290; C:GO:0016020	-		-
	-	0				-
Caenorhabditis briggsae	cyclin a	6	P:GO:0007283; P:GO:0007141; F:GO:0005515; P:GO:0007275; C:GO:0005829; C:GO:0015630	-		IPR004367; IPR006670; IPR006671; IPR011028; IPR013763; IPR014400; IPR015453; PTHR10177 (PANTHER)
	-	0				-
Caenorhabditis elegans	zinc finger in n-recognin family protein	0		P:GO:0030163; F:GO:0008270; F:GO:0004842; F:GO:0005515		PTHR21497 (PANTHER), PTHR21497:SF6 (PANTHER)
	-	0				-
	-	0				-
Ailuropoda melanoleuca	lim domain containing isoform cra_a	1	F:GO:0008270	-		IPR001781; PTHR18973 (PANTHER), PTHR18973:SF106 (PANTHER), SSF57716 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Ailuropoda melanoleuca	n-acetyltransferase 5	4	P:GO:0008152; C:GO:0005737; F:GO:0004596; C:GO:0005634	-	EC:2.3.1.88	IPR016181; PTHR23091 (PANTHER), PTHR23091:SF5 (PANTHER)
	-	0				-
Caenorhabditis elegans	chaperone protein	8	C:GO:0005737; P:GO:0006260; F:GO:0046872; P:GO:0006457; F:GO:0031072; F:GO:0005524; F:GO:0051082; P:GO:0009408	-		IPR001623; IPR015609; PTHR11821:SF88 (PANTHER)
Caenorhabditis elegans	histone deacetylase	10	F:GO:0032129; P:GO:0030466; P:GO:0000183; F:GO:0031078; C:GO:0030874; P:GO:0006348; P:GO:0016575; C:GO:0000118; P:GO:0030702; P:GO:0031060	-		-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				IPR002485; PTHR22989 (PANTHER)
	-	0				-

Caenorhabditis elegans	-nchung cg5842-pa	4	C:GO:0016021; F:GO:0005216; P:GO:0006811; P:GO:0055085	-		-
						IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF14 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	hypothetical protein Bm1_56075 [Brugia malayi]	0				G3DSA:3.80.10.10 (GENE3D), SSF52047 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F53A9.4 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	protein	3	F:GO:0004222; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	IPR001506; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF80 (PANTHER), SSF55486 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	uncoordi-ted protein isoform partially confirmed by transcript evidence	7	P:GO:0006629; F:GO:0005219; P:GO:0006816; P:GO:0006874; P:GO:0055085; F:GO:0005509; C:GO:0016021	-		-
Loa loa	uncoordi-ted family member (unc-89)	0				IPR008957; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF5 (PANTHER)
	-	0				-
Pongo abelii	mitochondrial import receptor subunit tom40 homolog	10	P:GO:0044070; P:GO:0034765; F:GO:0015288; C:GO:0005742; F:GO:0008320; C:GO:0000299; P:GO:0006626; C:GO:0031307; F:GO:0008308; C:GO:0046930	-		IPR001925; PTHR10802 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis briggsae	fk506 binding protein 12-rapamycin associated protein 1	27	P:GO:0046777; F:GO:0004674; P:GO:0030838; P:GO:0032868; P:GO:0032314; C:GO:0005829; P:GO:0016049; C:GO:0031931; C:GO:0012505; P:GO:0048565; P:GO:0043200; P:GO:0018107; P:GO:0031529; P:GO:0050731; P:GO:0045859; P:GO:0051496; P:GO:0007281; P:GO:0018105; C:GO:0031932; F:GO:0051219; P:GO:0010592; P:GO:0031929; P:GO:0045792; P:GO:0030163; C:GO:0005634; P:GO:0016242; C:GO:0016020	-	EC:2.7.11.0	IPR011989; PTHR11139 (PANTHER), PTHR11139:SF9 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-asp-6 protein	4	P:GO:0008219; F:GO:0005515; P:GO:0040011; F:GO:0008233	-		IPR001461; IPR009007; IPR021109; PTHR13683:SF53 (PANTHER)
Caenorhabditis elegans	briggsae cbr-cdh-1 protein	5	P:GO:0002119; P:GO:0007155; P:GO:0040010; P:GO:0040011; C:GO:0016020	-		IPR002126; IPR015919; PTHR10596 (PANTHER), PTHR10596:SF77 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-sur-2 protein	0		P:GO:0006350; P:GO:0045449; C:GO:0005634		IPR021629
	-	0				-
Brugia malayi	breast adenocarcinoma marker	5	P:GO:0009792; F:GO:0019904; C:GO:0031902; C:GO:0005829; P:GO:0015031	-		IPR005024; PTHR10476 (PANTHER), PTHR10476:SF4 (PANTHER)
Caenorhabditis elegans	lethal family member (let-805)	8	P:GO:0018996; P:GO:0009792; P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		-
Caenorhabditis briggsae	ankyrin repeat domain 13c	1	C:GO:0005783	-		IPR021832; PTHR12447 (PANTHER)
	-	0				-

	-	0				-
Necator americanus	briggsae cbr-clec-87 protein	0		F:GO:0003674; F:GO:0005488; C:GO:0016021; P:GO:0008150; F:GO:0005529; C:GO:0005575		-
Caenorhabditis elegans	gabab2 receptor subunit	0				-
	-	0				-
	-	0				-
	-	0				-
Ailuropoda melanoleuca	collagen alpha-2 chain-like	17	P:GO:0042476; F:GO:0030674; P:GO:0070208; P:GO:0043589; P:GO:0008217; F:GO:0042802; C:GO:0005615; F:GO:0046332; P:GO:0001501; F:GO:0048407; C:GO:0005584; P:GO:0030199; P:GO:0007179; F:GO:0005201; P:GO:0001568; P:GO:0007266; C:GO:0005886	-		IPR008160; PTHR10499 (PANTHER), PTHR10499:SF123 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-set-27 protein	0				-
	-	0				-
	-	0				-
	-	0				-
Ailuropoda melanoleuca	sub1 homolog (cerevisiae)	6	P:GO:0006357; C:GO:0005730; C:GO:0005667; F:GO:0003697; F:GO:0003713; P:GO:0045941	-		SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG15947 [Caenorhabditis briggsae]	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	d--directed r- polymerase iii subunit	7	P:GO:0009792; P:GO:0002119; P:GO:0016246; P:GO:0040010; P:GO:0000003; P:GO:0040011; P:GO:0006898	-		IPR006886
Loa loa	apoptosis inhibitor 5	0		P:GO:0006916; F:GO:0005488; P:GO:0008150; C:GO:0005575		IPR008383; IPR011989; IPR016024; PTHR12758 (PANTHER)
	-	0				-

	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	atp-binding sub-family a member 1	0		P:GO:0015914; C:GO:0005887; C:GO:0005886; P:GO:0010875; P:GO:0043691; P:GO:0008152; C:GO:0016021; C:GO:0016020; F:GO:0016887; P:GO:0071222; P:GO:0033700; F:GO:0008509; P:GO:0045332; P:GO:0055099; P:GO:0033344; F:GO:0070653; F:GO:0017127; F:GO:0005524; P:GO:0030301; F:GO:0000166; P:GO:0042158; P:GO:0042157; C:GO:0043231; P:GO:0006497; C:GO:0005901; P:GO:0055085; P:GO:0008203; P:GO:0002790;		PTHR19229 (PANTHER), PTHR19229:SF25 (PANTHER), SignalP (SIGNALP)
	-	0				IPR007087
Caenorhabditis elegans	lbp bpi cetp n-termi-l domain containing protein	6	P:GO:0002119; P:GO:0009792; P:GO:0000003; P:GO:0040007; F:GO:0008289; P:GO:0040011	-		IPR017943; PTHR10504 (PANTHER), PTHR10504:SF10 (PANTHER)
	-	0				-
	-	0				-
Ailuropoda melanoleuca	eukaryotic translation initiation factor 3 subunit 2 beta	5	C:GO:0005852; F:GO:0005515; P:GO:0045948; F:GO:0003743; C:GO:0005829	-		PTHR19877 (PANTHER), PTHR19877:SF1 (PANTHER)
Caenorhabditis elegans	egf lag seven-pass g-type receptor 3	8	F:GO:0004871; P:GO:0048598; P:GO:0023052; P:GO:0007399; P:GO:0007155; P:GO:0048513; P:GO:0008104; C:GO:0016020	-		SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0040013; C:GO:0044297; C:GO:0043005	-		-
	-	0				-
	-	0				-

Caenorhabditis briggsae	briggsae cbr-hum-7 protein	4	F:GO:0005515; C:GO:0016459; P:GO:0023052; F:GO:0000166	-		-
Caenorhabditis briggsae	briggsae cbr-hmr-1 protein	1	F:GO:0005515	-		IPR002126; IPR015919; PTHR10596 (PANTHER), PTHR10596:SF73 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-teg-1 protein	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-tat-2 protein	7	C:GO:0016021; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0015914; F:GO:0000287; F:GO:0004012	-	EC:3.6.3.1	IPR001757; PTHR11939:SF19 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	lethal family member (let-805)	8	P:GO:0018996; P:GO:0009792; P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		IPR008957; IPR013783
Heligmosomoides polygyrus	glutathione s-transferase	4	P:GO:0008340; P:GO:0040010; F:GO:0005515; F:GO:0016740	-		IPR004046; IPR010987; IPR017933; PTHR11571 (PANTHER), PTHR11571:SF6 (PANTHER)
Pongo abelii	peptidyl-tr- hydrolase 2	4	F:GO:0004045; P:GO:0006915; P:GO:0006412; C:GO:0005739	-	EC:3.1.1.29; EC:3.6.5.3	IPR002833; G3DSA:3.40.1490.10 (GENE3D), PTHR12649 (PANTHER), SSF102462 (SUPERFAMILY)
Oryctolagus cuniculus	tissue inhibitor of metalloprotei-se 3	16	P:GO:0051045; P:GO:0007417; P:GO:0006917; P:GO:0043627; F:GO:0046872; C:GO:0005604; P:GO:0007601; F:GO:0005515; P:GO:0051593; P:GO:0007568; P:GO:0014070; F:GO:0008191; C:GO:0005737; P:GO:0043200; P:GO:0042246; P:GO:0009612	-		IPR001820; IPR008993; IPR015612; G3DSA:3.90.370.10 (GENE3D)
Caenorhabditis briggsae	briggsae cbr-mup-4 protein	4	F:GO:0004872; F:GO:0005515; F:GO:0005509; C:GO:0016020	-		-

	-	0				-
Caenorhabditis elegans	fanci (fanconi anemia complex component i) homolog family member (fnci-1)	0				-
Caenorhabditis elegans	rio ki-se 3	4	P:GO:0006468; F:GO:0005515; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR011009; IPR018934; IPR018935; G3DSA:3.90.1200.10 (GENE3D), PTHR10593 (PANTHER), PTHR10593:SF6 (PANTHER)
Caenorhabditis briggsae	sig-l sequence beta	5	P:GO:0009792; F:GO:0005048; P:GO:0006613; C:GO:0016021; C:GO:0005783	-		IPR008856; SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG19248 [Caenorhabditis briggsae]	0		F:GO:0008289		PTHR10504 (PANTHER), PTHR10504:SF10 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	egg laying defective family member (egl-15)	3	F:GO:0004672; C:GO:0016020; F:GO:0000166	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	riken cd- isoform cra_a	0		F:GO:0003674; C:GO:0005575		-
Caenorhabditis briggsae	novel protein (zgc:100846)	0		F:GO:0003674; P:GO:0008150; C:GO:0005575		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-tag-164 protein	0		C:GO:0016021		-
	-	0				-
	-	0				-
Ostertagia ostertagi	ladder protein	1	F:GO:0019841	-		-
	-	0				-
Caenorhabditis briggsae	and ph domain-containing protein 3	4	F:GO:0005089; C:GO:0005622; P:GO:0035023; F:GO:0008270	-		IPR011993; PTHR12673 (PANTHER), PTHR12673:SF8 (PANTHER), SSF50729 (SUPERFAMILY)
	-	0				-
Homo sapiens	novel protein	1	C:GO:0005737	-		IPR010630; PTHR14199 (PANTHER)
Brugia malayi	ribosomal r- adenine dimethylase family protein	1	F:GO:0008649	-		-
Caenorhabditis briggsae	ring finger r- polymerase ii elongation	1	F:GO:0046872	-		IPR001841; IPR013083; IPR017907; IPR018957; PTHR13712 (PANTHER), PTHR13712:SF74 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis briggsae	ring finger r- polymerase ii elongation	1	F:GO:0046872	-		IPR001841; IPR013083; IPR017907; IPR018957; PTHR13712 (PANTHER), PTHR13712:SF74 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis briggsae	r- binding identical	3	F:GO:0003676; P:GO:0009792; F:GO:0000166	-		SignalP (SIGNALP)
	-	0				-

	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	rap ran-gap family protein	3	F:GO:0005096; C:GO:0005622; P:GO:0051056	-		-
Caenorhabditis briggsae	protein ki-se	4	P:GO:0006468; F:GO:0005524; P:GO:0000003; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
	-	0				-
	-	0				IPR008162; PTHR12623 (PANTHER), PTHR12623:SF8 (PANTHER)
	-	0				-
Homo sapiens	-dh dehydroge-se	4	P:GO:0006120; F:GO:0008137; P:GO:0006810; C:GO:0005747	-	EC:1.6.5.3	SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	w e related abc transporte family member (wht-7)	3	F:GO:0017111; C:GO:0016020; F:GO:0000166	-	EC:3.6.1.15	IPR003439; IPR003593; IPR013525; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR19241 (PANTHER), PTHR19241:SF30 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis briggsae	g in family member (glb-10)	0		F:GO:0005344; F:GO:0020037; F:GO:0019825; P:GO:0015671; F:GO:0005506; P:GO:0006810		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	zinc finger c-x8-c-x5-c-x3-h type	2	F:GO:0005515; F:GO:0046872	-		PTHR14493 (PANTHER), PTHR14493:SF1 (PANTHER)
	-	0				-
	-	0				-
Loa loa	hypothetical protein LOAG_07427 [Loa loa]	0				-
Caenorhabditis elegans	zinc finger protein 423	2	F:GO:0005488; P:GO:0032502	-		IPR007087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis elegans	zinc finger protein zfp-like	0		P:GO:0040027; C:GO:0005634; F:GO:0003676; F:GO:0008270; F:GO:0003674; P:GO:0006355; C:GO:0005575; C:GO:0005622; F:GO:0046872; P:GO:0008150		IPR007087; IPR015880; PTHR23224 (PANTHER), PTHR23224:SF461 (PANTHER), SSF57667 (SUPERFAMILY)
	-	0				-
	-	0				-

Danio rerio	galactoki-se 1	8	P:GO:0046835; F:GO:0005534; F:GO:0005515; P:GO:0019402; C:GO:0044464; F:GO:0005524; P:GO:0006012; F:GO:0004335	-	EC:2.7.1.6	IPR013750; G3DSA:3.30.70.890 (GENE3D), PTHR10457 (PANTHER), PTHR10457:SF6 (PANTHER), SSF55060 (SUPERFAMILY)
	-	0				-
	-	0				-
Meloidogyne incognita	briggsae cbr-flp-7 protein	1	P:GO:0007218	-		IPR002544; PTHR20986 (PANTHER), SignalP (SIGNALP)
	-	0				-
Brugia malayi	comm domain containing 4	0		F:GO:0003674; C:GO:0005737; P:GO:0008150; F:GO:0005515		IPR009886
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	ankyrin unc44	0		P:GO:0006355; F:GO:0005524; P:GO:0006915; F:GO:0005488; F:GO:0000166; F:GO:0043565; F:GO:0017111; F:GO:0003700		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF250 (PANTHER)
Caenorhabditis elegans	wd repeat and fyve domain-containing protein 3	3	C:GO:0005737; F:GO:0005488; F:GO:0003831	-	EC:2.4.1.38	-
Branchiostoma floridae	hypothetical protein BRAFLDRAFT_118457 [Branchiostoma floridae]	0		F:GO:0005488; F:GO:0005509; F:GO:0005529		IPR000436; IPR016060; SignalP (SIGNALP)
Caenorhabditis briggsae	eb module family protein	4	P:GO:0018991; P:GO:0040010; P:GO:0040035; P:GO:0040011	-		IPR006149
Caenorhabditis elegans	glycine dehydroge-se	6	P:GO:0006546; F:GO:0004375; F:GO:0030170; F:GO:0009055; P:GO:0055114; F:GO:0016829	-	EC:1.4.4.2	IPR015421; IPR015424; IPR020580; IPR020581
Lodderomyces elongisporus NRRL YB-4239	26s proteasome regulatory subunit rpn6	0		F:GO:0005488; C:GO:0000502		-
	-	0				-
Brugia malayi	protein-tyrosine phosphatase containing protein	0		P:GO:0016311; F:GO:0016791; P:GO:0006470; F:GO:0016787; F:GO:0004725; F:GO:0004721		-

Ailuropoda melanoleuca	actin related protein 2 3 complex subunit 2	9	C:GO:0005885; C:GO:0031252; C:GO:0042995; C:GO:0005925; F:GO:0003779; P:GO:0006928; F:GO:0005200; C:GO:0005794; P:GO:0030838	-		IPR007188; G3DSA:3.30.1460.20 (GENE3D), SSF69645 (SUPERFAMILY)
Caenorhabditis elegans	xrp2 protein	3	F:GO:0005488; P:GO:0044238; P:GO:0044237	-		IPR006599; IPR012945; IPR017901; PTHR15440 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-rpm-1 protein	1	F:GO:0005488	-		PTHR12846 (PANTHER), PTHR12846:SF2 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-cab-1 protein	7	C:GO:0005623; P:GO:0040007; P:GO:0050896; P:GO:0009792; P:GO:0002119; P:GO:0007268; P:GO:0050794	-		SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-cab-1 protein	5	P:GO:0007268; C:GO:0016021; P:GO:0009792; P:GO:0040007; P:GO:0002119	-		SignalP (SIGNALP)
	-	0				-
	-	0				IPR004827
Caenorhabditis elegans	wap four-disulfide core domain 8	1	C:GO:0005737	-		-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Brugia malayi	guanine nucleotide exchange factor	5	F:GO:0005086; P:GO:0032012; C:GO:0005622; F:GO:0008060; F:GO:0017022	-		IPR000904; G3DSA:1.10.1000.11 (GENE3D), PTHR10663 (PANTHER), PTHR10663:SF16 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0055114; F:GO:0005488; F:GO:0016491; P:GO:0008152; F:GO:0003824		IPR002198; PTHR19410:SF18 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG05033 [Caenorhabditis briggsae]	2	P:GO:0008152; F:GO:0016787	-		IPR002018; G3DSA:3.40.50.1820 (GENE3D), PTHR11559:SF30 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG12007 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	shc (src homology domain c-termi-l) adaptor homolog family member (shc-2)	0		F:GO:0005515		IPR006020; IPR011993; PTHR12583 (PANTHER), PTHR12583:SF5 (PANTHER), SSF50729 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis elegans	patched family protein	10	P:GO:0009792; P:GO:0002119; P:GO:0040018; P:GO:0001703; P:GO:0018996; P:GO:0000910; P:GO:0040010; P:GO:0000003; P:GO:0040011; C:GO:0016020	-		IPR003392; PTHR10796 (PANTHER), PTHR10796:SF32 (PANTHER)
Caenorhabditis briggsae	isoform cra_a	3	P:GO:0055114; F:GO:0016491; C:GO:0005739	-		IPR015904
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	cg3603-pa	2	P:GO:0008152; F:GO:0003824	-		IPR002198; IPR016040; PTHR19410:SF88 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Brugia malayi	reticulocyte binding-like protein 2b	0		F:GO:0005525; F:GO:0003676; F:GO:0003924; F:GO:0000166		-
Caenorhabditis elegans	protein ki-se domain containing protein	3	F:GO:0004672; P:GO:0040011; F:GO:0000166	-		PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
	-	0				-
Loa loa	kelch-like 18	1	F:GO:0005515	-		IPR006652; IPR013089; IPR015916; PTHR23230:SF164 (PANTHER), SSF117281 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0004672; F:GO:0005524; F:GO:0005488; P:GO:0006468; P:GO:0019915; F:GO:0004674		-
	-	0				-
Caenorhabditis elegans	briggsae cbr-sbp-1 protein	1	F:GO:0005515	-		PTHR12565 (PANTHER), PTHR12565:SF3 (PANTHER), SignalP (SIGNALP)
Pongo abelii	eukaryotic translation initiation factor 3 subunit k	8	C:GO:0005852; F:GO:0003723; F:GO:0005515; P:GO:0045948; F:GO:0003743; C:GO:0005634; C:GO:0005829; F:GO:0043022	-		IPR009374; IPR016020; IPR016024; SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Loa loa	cwf19-like protein 1	1	F:GO:0003824	-		PTHR12072 (PANTHER)
Caenorhabditis elegans	cral trio domain containing protein	1	P:GO:0040010	-		PTHR23324 (PANTHER), PTHR23324:SF3 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	briggsae cbr-casy-1 protein	6	P:GO:0009792; C:GO:0005615; F:GO:0005515; C:GO:0032809; P:GO:0008355; C:GO:0043231	-		-
Caenorhabditis elegans	cationic amino acid transporter 4	5	P:GO:0019915; C:GO:0016021; P:GO:0006865; F:GO:0015171; P:GO:0055085	-		IPR002293; IPR015606; SignalP (SIGNALP)
Caenorhabditis briggsae	#NAME?	4	F:GO:0046872; P:GO:0019509; P:GO:0055114; F:GO:0051213	-		IPR004313; IPR011051; IPR014710
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Loa loa	hypothetical protein LOAG_04198 [Loa loa]	0		F:GO:0003723; F:GO:0003725; C:GO:0005622		IPR001159; PTHR12813 (PANTHER), PTHR12813:SF5 (PANTHER), SSF54768 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	ytv2_caeel ame: full=uncharacterized zinc metalloprotease	0		P:GO:0006508; F:GO:0008233		-
Caenorhabditis briggsae	d--directed r- polymerase iii largest subunit	4	F:GO:0046872; F:GO:0003899; F:GO:0003677; P:GO:0006350	-	EC:2.7.7.6	IPR007080; IPR015700; PTHR19376 (PANTHER), SignalP (SIGNALP), SSF64484 (SUPERFAMILY)
	-	0				-
Loa loa	sarcoglycan complex subunit protein	0		C:GO:0016012; P:GO:0040013; C:GO:0016021; P:GO:0007010; F:GO:0005515		IPR006875; PTHR12939 (PANTHER), PTHR12939:SF1 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG24916 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	eps (human endocytosis) related family member (eps-8)	1	F:GO:0005515	-		SignalP (SIGNALP)
Caenorhabditis elegans	eps (human endocytosis) related family member (eps-8)	0		P:GO:0007173; F:GO:0004872; F:GO:0005515		IPR001452; IPR011511; G3DSA:2.30.30.40 (GENE3D), PTHR12287 (PANTHER), PTHR12287:SF1 (PANTHER)
Caenorhabditis elegans	eps (human endocytosis) related family member (eps-8)	1	F:GO:0005515	-		SignalP (SIGNALP)
Loa loa	atp-dependent clp protease atp-binding subunit	8	P:GO:0006457; F:GO:0008233; F:GO:0016887; C:GO:0005622; F:GO:0005524; F:GO:0051082; F:GO:0008134; P:GO:0006355	-		IPR004487; IPR013093; G3DSA:3.40.50.300 (GENE3D), PTHR11262 (PANTHER), SSF52540 (SUPERFAMILY)

Pongo abelii	eukaryotic translation initiation factor subunit 5 47kda	5	C:GO:0005829; C:GO:0005852; F:GO:0005515; P:GO:0006413; F:GO:0003743	-		PTHR10540 (PANTHER)
	-	0				-
Caenorhabditis briggsae	ankyrin repeats-like	8	F:GO:0008381; F:GO:0015276; P:GO:0055085; P:GO:0050974; P:GO:0006811; P:GO:0050968; C:GO:0016021; P:GO:0050960	-		SignalP (SIGNALP)
Caenorhabditis elegans	and ph domain containing 2	4	F:GO:0005089; C:GO:0005622; P:GO:0035023; F:GO:0008270	-		IPR000219; PTHR12673 (PANTHER), PTHR12673:SF8 (PANTHER)
Macaca mulatta	amyloid beta precursor protein (peptidase nexin- alzheimer disease) isoform cra_c	53	[illegible] C:GO:0043198; F:GO:0016504; F:GO:0008233; C:GO:0019717; P:GO:0050885; F:GO:0008201; P:GO:0035235; F:GO:0004867; P:GO:0007176; P:GO:0050803; P:GO:0016358; C:GO:0031594; P:GO:0000085; F:GO:0046872; C:GO:0035253; P:GO:0040014; P:GO:0030900; P:GO:0001967; P:GO:0051402; P:GO:0008542; C:GO:0030424; C:GO:0051233; P:GO:0016199; P:GO:0045944; P:GO:0007219; C:GO:0005887; C:GO:0048471;	-		PTHR23103 (PANTHER), PTHR23103:SF7 (PANTHER)
	-	0				-
Caenorhabditis briggsae	bystin-like	8	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0007155; P:GO:0040010; P:GO:0007565; P:GO:0006898; C:GO:0044424	-		IPR007955

Ailuropoda melanoleuca	filamin alpha	28	F:GO:0004871; C:GO:0005802; P:GO:0043433; P:GO:0034394; C:GO:0015629; P:GO:0050821; P:GO:0051220; C:GO:0005576; C:GO:0005829; F:GO:0001948; P:GO:0051764; P:GO:0043123; F:GO:0051015; F:GO:0048365; P:GO:0045022; P:GO:0007195; F:GO:0042803; F:GO:0034989; P:GO:0031532; F:GO:0034988; C:GO:0005886; F:GO:0008134; P:GO:0042177; C:GO:0005634; P:GO:0042993; C:GO:0005938; P:GO:0043113	-		IPR013783; IPR017868; PTHR11915 (PANTHER), PTHR11915:SF24 (PANTHER)
						SignalP (SIGNALP)
Brugia malayi	bromodomain containing protein	0		F:GO:0003674; P:GO:0008150; F:GO:0005515; C:GO:0005575		IPR001487; IPR018359; PTHR22880 (PANTHER), PTHR22880:SF20 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	5	F:GO:0004672; P:GO:0032582; F:GO:0003677; F:GO:0005515; P:GO:0007362	-		IPR001487; IPR018359; PTHR22880 (PANTHER), PTHR22880:SF20 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	5	C:GO:0016021; P:GO:0040010; F:GO:0004573; P:GO:0009311; P:GO:0040011	-	EC:3.2.1.106	IPR004888; PTHR10412 (PANTHER)
	-	0				SignalP (SIGNALP)
Loa loa	zinc c2h2 type family protein	1	F:GO:0005488	-		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-

Caenorhabditis remanei	tpa_inf: eukaryotic translation elongation factor 1a	8	C:GO:0005737; P:GO:0009792; P:GO:0002119; P:GO:0007276; F:GO:0003746; F:GO:0005525; P:GO:0006414; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Caenorhabditis elegans	tumor suppressor candidate 4	0		C:GO:0005789; P:GO:0006506; C:GO:0016021; P:GO:0008150; C:GO:0005575		IPR009348; PTHR12991 (PANTHER), PTHR12991:SF10 (PANTHER)
Brugia malayi	eph receptor b1	1	F:GO:0005515	-		IPR001660; IPR010993; IPR013761; IPR021129
Caenorhabditis briggsae	Hypothetical protein CBG13967 [Caenorhabditis briggsae]	0		F:GO:0005488		IPR018556
Caenorhabditis elegans	rad54-like (cerevisiae)	12	P:GO:0000003; P:GO:0006310; F:GO:0070087; P:GO:0006355; P:GO:0006306; C:GO:0005720; F:GO:0003677; P:GO:0006915; P:GO:0007126; F:GO:0005524; F:GO:0003678; P:GO:0006281	-		IPR000330; PTHR10799 (PANTHER), PTHR10799:SF66 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	uncoordi-ted family member (unc-44)	3	C:GO:0016020; P:GO:0007155; F:GO:0005515	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	5	C:GO:0016021; P:GO:0006865; C:GO:0009986; F:GO:0015171; P:GO:0055085	-		IPR002293; PTHR11785:SF76 (PANTHER)
Caenorhabditis elegans	acyl-coenzyme a oxidase pristanoyl	7	C:GO:0005777; P:GO:0055114; P:GO:0006635; F:GO:0003995; F:GO:0050660; P:GO:0006911; F:GO:0003997	-	EC:1.3.99.3; EC:1.3.3.6	IPR012258; PTHR10909 (PANTHER)
Danio rerio	drebrin- isoform cra_a	5	C:GO:0005829; F:GO:0003779; F:GO:0042802; C:GO:0042995; N:GO:0035556	-		-
Danio rerio	drebrin- isoform cra_a	5	C:GO:0005829; F:GO:0003779; F:GO:0042802; C:GO:0042995; N:GO:0035556	-		-

Danio rerio	drebrin- isoform cra_a	5	C:GO:0005829; F:GO:0003779; F:GO:0042802; C:GO:0042995; N:GO:0035556	-		-
Caenorhabditis briggsae	Hypothetical protein CBG21978 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	yrr5_caeel ame: full=uncharacterized protein	0				-
Caenorhabditis briggsae	cysteinyl tr- synthetase family member (crs-1)	2	P:GO:0006412; F:GO:0000166	-	EC:3.6.5.3	SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-tag-321 protein	0				IPR019537; PTHR21706 (PANTHER), PTHR21706:SF7 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Macaca mulatta	heat shock 70 kda protein 1a partial	18	F:GO:0047485; P:GO:0042026; P:GO:0090084; C:GO:0005739; P:GO:0030308; F:GO:0031625; C:GO:0016607; F:GO:0044183; P:GO:0006916; P:GO:0008285; C:GO:0016234; F:GO:0005524; P:GO:0006402; C:GO:0048471; C:GO:0030529; F:GO:0051082; P:GO:0006986; C:GO:0005783	-		-
Teladorsagia circumcincta	long family member (lon-1)	2	F:GO:0005515; C:GO:0005576	-		-
Caenorhabditis elegans	tata-binding protein-associated factor 172	1	F:GO:0005488	-		IPR000330; IPR019825; PTHR10799 (PANTHER), PTHR10799:SF72 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Brugia malayi	suppressor of ty 5 homolog (cerevisiae)	7	P:GO:0006354; P:GO:0006357; P:GO:0040007; P:GO:0040035; P:GO:0002119; F:GO:0003711; P:GO:0009792	-		IPR005824; PTHR11125 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		IPR011992; PTHR23055 (PANTHER), PTHR23055:SF8 (PANTHER)
Schizosaccharomyces japonicus yFS275	vacuolar atp synthase subunit b	7	P:GO:0016337; F:GO:0046933; P:GO:0008219; P:GO:0015986; P:GO:0015988; F:GO:0046961; C:GO:0033180	-	EC:3.6.3.14	-
Loa loa	ubiquitin-conjugating enzyme family protein	3	P:GO:0051246; F:GO:0019787; P:GO:0043687	-		IPR016135; PTHR11621 (PANTHER), PTHR11621:SF9 (PANTHER)

Caenorhabditis elegans	c inesis defect family member (cyk-3)	4	P:GO:0009792; P:GO:0006511; F:GO:0005509; F:GO:0004221	-	EC:3.1.2.15	-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F18C5.10 [Caenorhabditis elegans]	0		F:GO:0005515		-
Callithrix jacchus	cd63 antigen	11	C:GO:0005765; C:GO:0043234; P:GO:0045807; C:GO:0031088; F:GO:0032403; C:GO:0031902; C:GO:0030658; P:GO:0045785; P:GO:0030855; P:GO:0010633; C:GO:0005887	-		IPR000301; IPR018499; IPR018503; PTHR19282 (PANTHER), PTHR19282:SF51 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Homo sapiens	granulysin isoform 519	5	P:GO:0050832; P:GO:0006968; C:GO:0005615; P:GO:0042742; P:GO:0031640	-		IPR011001; PTHR15541 (PANTHER)
Caenorhabditis elegans	6-phosphofructo-2-ki-se fructose- -biphosphatase 4	3	P:GO:0006003; F:GO:0005524; F:GO:0003873	-	EC:2.7.1.105	IPR003094; IPR013079; G3DSA:3.40.50.300 (GENE3D), PTHR10606:SF11 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Loa loa	d- gyrase topoisomerase a subunit family protein	9	P:GO:0000910; P:GO:0006355; F:GO:0005524; F:GO:0003700; F:GO:0003918; C:GO:0005694; P:GO:0006265; C:GO:0005654; P:GO:0009792	-	EC:5.99.1.3	IPR001154; IPR002205; IPR013758; IPR013760; PTHR10169 (PANTHER), PTHR10169:SF2 (PANTHER)
Loa loa	retinoblastoma binding protein 5	7	C:GO:0071339; F:GO:0042800; F:GO:0010843; P:GO:0043627; P:GO:0051568; F:GO:0005515; P:GO:0006974	-		IPR001680; IPR011046; IPR015943; IPR019781; PTHR12816 (PANTHER), PTHR12816:SF6 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	ef hand family protein	0		F:GO:0005509; P:GO:0005975; F:GO:0003824		IPR011992; IPR018247; PTHR19237 (PANTHER), PTHR19237:SF1 (PANTHER), SignalP (SIGNALP), SSF47473 (SUPERFAMILY)

Caenorhabditis briggsae	ef hand family protein	0		F:GO:0005509; P:GO:0005975; F:GO:0003824		IPR011992; IPR018247; PTHR19237 (PANTHER), PTHR19237:SF1 (PANTHER), SignalP (SIGNALP), SSF47473 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0005488; F:GO:0005044; C:GO:0016020		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Pongo abelii	v-raf murine sarcoma 3611 viral oncogene homolog	9	P:GO:0006468; F:GO:0046872; F:GO:0005515; F:GO:0005524; F:GO:0004709; P:GO:0007243; C:GO:0005626; C:GO:0005829; C:GO:0005739	-	EC:2.7.11.25	IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR23257 (PANTHER), PTHR23257:SF43 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	frizzled smoothened family membrane region containing protein	8	P:GO:0007186; F:GO:0004926; C:GO:0016021; P:GO:0007165; P:GO:0007275; F:GO:0042813; P:GO:0016055; F:GO:0004930	-		IPR000539; IPR015526; IPR017981; PTHR11309:SF18 (PANTHER), SignalP (SIGNALP)
Loa loa	r- recognition motif domain containing protein	1	F:GO:0005488	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF30 (PANTHER), SSF54928 (SUPERFAMILY)
Loa loa	r- recognition motif domain containing protein	1	F:GO:0005488	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF30 (PANTHER), SSF54928 (SUPERFAMILY)
Loa loa	r- recognition motif domain containing protein	1	F:GO:0005488	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF30 (PANTHER), SSF54928 (SUPERFAMILY)
Loa loa	r- recognition motif domain containing protein	1	F:GO:0005488	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF30 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	oligo- -glucosidase	1	F:GO:0016787	-		IPR006047; IPR013781; IPR017853; PTHR10357 (PANTHER), PTHR10357:SF11 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	alpha amylase	2	C:GO:0005886; F:GO:0003824	-		-
Caenorhabditis elegans	alpha catalytic domain containing protein	2	C:GO:0005886; F:GO:0003824	-		-
Caenorhabditis elegans	alpha catalytic domain containing protein	2	C:GO:0005886; F:GO:0003824	-		-
Loa loa	sec14-like protein 5	3	C:GO:0005622; P:GO:0006810; F:GO:0005215	-		IPR006797; PTHR11158 (PANTHER)
	-	0				-

Caenorhabditis briggsae	protein	4	F:GO:0004725; P:GO:0006470; P:GO:0006412; F:GO:0004045	-	EC:3.1.3.48; EC:3.6.5.3; EC:3.1.1.29	-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	inositol monophosphatase domain containing 1	1	F:GO:0004437	-		-
Mus musculus	small nuclear ribonucleoprotein e	8	C:GO:0005683; C:GO:0005654; P:GO:0000387; C:GO:0005681; F:GO:0003723; F:GO:0005515; C:GO:0005829; P:GO:0000245	-		IPR010920; G3DSA:2.30.30.100 (GENE3D), PTHR11193 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	exostoses -like 3	6	P:GO:0007166; P:GO:0007275; F:GO:0008375; C:GO:0044464; P:GO:0009987; P:GO:0008152	-		IPR004263; PTHR11062 (PANTHER), PTHR11062:SF5 (PANTHER)
	-	0				-
Caenorhabditis briggsae	saccharopine dehydroge-se	0		F:GO:0005488; P:GO:0008152; C:GO:0016021; F:GO:0003824		IPR005097; IPR016040; PTHR12286 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	protein white	8	C:GO:0016021; P:GO:0006355; F:GO:0003677; F:GO:0005524; P:GO:0010171; F:GO:0016887; F:GO:0003700; C:GO:0005634	-		IPR013525; PTHR19241 (PANTHER), PTHR19241:SF31 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	ligand-gated ion channel family member (lgc-43)	5	C:GO:0016021; C:GO:0030054; C:GO:0045211; F:GO:0005230; P:GO:0006811	-		IPR006201; PTHR18945:SF9 (PANTHER)
Loa loa	uncharacterized protein family upf0005 containing protein	0		F:GO:0004872; C:GO:0016021; C:GO:0016020; F:GO:0005515		IPR006214; PTHR23291:SF14 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	ammd protein	1	P:GO:0008152	-		IPR013094; G3DSA:3.40.50.1820 (GENE3D), SSF53474 (SUPERFAMILY)
	-	0				-

Caenorhabditis elegans	serine or cysteine protease inhibitor	7	F:GO:0008233; P:GO:0008380; F:GO:0004867; F:GO:0003723; F:GO:0005515; C:GO:0005634; P:GO:0008406	-		-
	-	0				-
Caenorhabditis elegans	trehalose 6-phosphate synthase	2	F:GO:0016757; P:GO:0034608	-		-
Apis mellifera	set domain and mariner transposase fusion	0				PTHR23016 (PANTHER)
Caenorhabditis elegans	uba and wwe domain containing 1	7	C:GO:0005737; C:GO:0005730; P:GO:0016574; F:GO:0003677; F:GO:0005515; P:GO:0000209; F:GO:0004842	-	EC:6.3.2.19	IPR010314
Caenorhabditis briggsae	yq42_caeel ame: full=uncharacterized protein	0				G3DSA:3.40.50.10180 (GENE3D), PTHR12227 (PANTHER), SSF82544 (SUPERFAMILY)
Caenorhabditis elegans	mofrl family protein	0				G3DSA:3.40.50.10180 (GENE3D), PTHR12227 (PANTHER), SSF82544 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Loa loa	nuclear cap-binding protein subunit 1	13	P:GO:0000184; C:GO:0005654; F:GO:0005515; P:GO:0006406; P:GO:0031442; P:GO:0006379; C:GO:0005829; C:GO:0005845; P:GO:0006446; F:GO:0003723; C:GO:0030529; P:GO:0006370; P:GO:0000387	-		IPR015172; IPR015174; IPR016021; IPR016024; PTHR12412 (PANTHER), PTHR12412:SF2 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	in family member (ttn-1)	4	P:GO:0009792; P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF17 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	long-chain-fatty-acid-- ligase 1	6	C:GO:0005829; C:GO:0043231; P:GO:0046320; C:GO:0044446; C:GO:0031090; F:GO:0004467	-	EC:6.2.1.3	IPR000873; G3DSA:3.40.50.980 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF8 (PANTHER), SignalP (SIGNALP), SSF56801 (SUPERFAMILY)

Caenorhabditis briggsae	long-chain-fatty-acid-- ligase 1	6	C:GO:0005829; C:GO:0043231; P:GO:0046320; C:GO:0044446; C:GO:0031090; F:GO:0004467	-	EC:6.2.1.3	IPR000873; G3DSA:3.40.50.980 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF8 (PANTHER), SignalP (SIGNALP), SSF56801 (SUPERFAMILY)
Haemonchus contortus	hexoki-se family protein	17	P:GO:0018105; C:GO:0005829; P:GO:0018108; F:GO:0004672; C:GO:0005739; C:GO:0005901; P:GO:0010359; P:GO:0018107; F:GO:0005536; P:GO:0046835; F:GO:0005524; F:GO:0016887; P:GO:0006096; F:GO:0042803; P:GO:0046777; P:GO:0043066; F:GO:0004340	-	EC:2.7.1.2	IPR001312; IPR022672; G3DSA:3.30.420.40 (GENE3D), SSF53067 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0009792		IPR003677; PTHR21593 (PANTHER)
	-	0				-
Caenorhabditis briggsae	lipase family protein	2	P:GO:0006629; F:GO:0004806	-	EC:3.1.1.3	IPR002921; G3DSA:3.40.50.1820 (GENE3D), SSF53474 (SUPERFAMILY)
Ailuropoda melanoleuca	lactate dehydroge-se a	8	P:GO:0031668; C:GO:0019861; F:GO:0005515; F:GO:0004459; P:GO:0055114; P:GO:0006096; C:GO:0005829; C:GO:0005739	-	EC:1.1.1.27	IPR001236; IPR001557; IPR016040; PTHR11540 (PANTHER), PTHR11540:SF3 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	lethal k05819-like	0		F:GO:0015662; C:GO:0016020; P:GO:0006754; P:GO:0006812		IPR000864; G3DSA:3.40.1110.10 (GENE3D), PTHR13219 (PANTHER)

Caenorhabditis briggsae	uncoordi-ted family member (unc-26)	25	P:GO:0016082; C:GO:0012506; P:GO:0046856; P:GO:0050803; F:GO:0008022; P:GO:0016191; P:GO:0032526; P:GO:0007612; C:GO:0019717; P:GO:0046549; F:GO:0017120; F:GO:0003676; P:GO:0034097; F:GO:0004445; P:GO:0007420; P:GO:0048260; P:GO:0014015; P:GO:0050808; F:GO:0004439; F:GO:0032403; C:GO:0043195; C:GO:0030118; P:GO:0048790; F:GO:0017124; P:GO:0048015	-	EC:3.1.3.56; EC:3.1.3.36	IPR002013
	-	0				-
Caenorhabditis briggsae	briggsae cbr-nol-9 protein	0		P:GO:0000003; P:GO:0006974		SignalP (SIGNALP)
Caenorhabditis elegans	#NAME?	10	P:GO:0006814; C:GO:0005890; F:GO:0005391; P:GO:0030317; F:GO:0046872; P:GO:0006813; P:GO:0006754; F:GO:0005524; P:GO:0030641; P:GO:0015991	-	EC:3.6.3.9	-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-let-418 protein	14	C:GO:0005700; F:GO:0031491; F:GO:0008026; P:GO:0040027; P:GO:0048813; C:GO:0016581; P:GO:0007517; P:GO:0046580; F:GO:0046872; F:GO:0003677; P:GO:0001709; P:GO:0042766; F:GO:0003678; F:GO:0016564	-		-
	-	0				-

Haemonchus contortus	metalloprotease 1 precursor	2	F:GO:0046872; F:GO:0008237	-		IPR000859; IPR001506; IPR006026; IPR013032; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	r- recognition	9	P:GO:0002009; F:GO:0003676; P:GO:0009792; P:GO:0000003; P:GO:0040007; P:GO:0010171; F:GO:0000166; P:GO:0002119; P:GO:0040011	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF54 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	copine domain atypical protein isoform partially confirmed by transcript evidence	0		F:GO:0046872; F:GO:0008270; F:GO:0005515		SignalP (SIGNALP)
Brugia malayi	myosin xviiia	0		F:GO:0008094; P:GO:0006259; P:GO:0006916; F:GO:0042802; F:GO:0003677; C:GO:0005634; C:GO:0005737; F:GO:0000166; C:GO:0005794; F:GO:0005524; C:GO:0005793; C:GO:0016459; F:GO:0003774; C:GO:0005730; F:GO:0005515; C:GO:0005856		IPR001609; PTHR13140 (PANTHER), PTHR13140:SF10 (PANTHER), SSF52540 (SUPERFAMILY)
Homo sapiens	complement component 4a (rodgers blood group)	5	C:GO:0005615; P:GO:0006957; F:GO:0005515; P:GO:0006958; F:GO:0004866	-		-
Caenorhabditis briggsae	Hypothetical protein CBG08978 [Caenorhabditis briggsae]	0		F:GO:0046872; F:GO:0008270; F:GO:0005515		IPR006575; IPR016135
Caenorhabditis elegans	glycine c-acetyltransferase (2-amino-3-ketobutyrate-coenzyme a ligase)	6	F:GO:0016874; F:GO:0030170; C:GO:0005743; P:GO:0009058; F:GO:0016769; F:GO:0008890	-	EC:2.3.1.29	IPR004839; IPR011282; IPR015422; IPR015424; PTHR13693 (PANTHER)
Brugia malayi	kiaa1378 protein	1	F:GO:0005515	-		-
Brugia malayi	kiaa1378 protein	1	F:GO:0005515	-		-
	-	0				-
Caenorhabditis elegans	erin family member (cdh-12)	0				-
	-	0				-
	-	0				-
	-	0				-

Gallus gallus	mannose c type 2	0		C:GO:0009986; C:GO:0016021; C:GO:0016020; F:GO:0005529; P:GO:0006897; P:GO:0007165; F:GO:0005518; F:GO:0004872; C:GO:0005886; F:GO:0005488		IPR001304; IPR016186; IPR016187; PTHR22803 (PANTHER)
	-	0				-
Caenorhabditis elegans	ymx3_caeel ame: full=uncharacterized protein	0		F:GO:0008270		-
	-	0				-
	-	0				-
Dictyocaulus viviparus	ll20 15kda ladder antigen	1	F:GO:0008289	-		PTHR21693 (PANTHER)
	-	0				-
Caenorhabditis elegans	high incidence of males (increased x chromosome loss) family member (him-6)	0				SignalP (SIGNALP)
Homo sapiens	membrane-associated tyrosine- and threonine-specific cdc2-inhibitory ki-se	10	F:GO:0004674; C:GO:0000139; P:GO:0007088; C:GO:0005624; F:GO:0005524; F:GO:0005515; C:GO:0005654; P:GO:0000079; C:GO:0005789; P:GO:0006468	-	EC:2.7.11.0	-
Brugia malayi	protein ki-se domain containing protein	0		F:GO:0016740; P:GO:0006950; F:GO:0004674; F:GO:0004672; P:GO:0006468; F:GO:0000166; C:GO:0005737; F:GO:0005524; P:GO:0007275; F:GO:0016301; C:GO:0005938; F:GO:0046872		-
Homo sapiens	lysosomal-associated membrane protein 1	9	C:GO:0005887; C:GO:0005624; C:GO:0005771; C:GO:0042383; C:GO:0042470; C:GO:0009897; C:GO:0005765; C:GO:0010008; P:GO:0006914	-		-
Caenorhabditis elegans	major sperm protein	7	F:GO:0005515; P:GO:0040017; P:GO:0040010; C:GO:0044464; P:GO:0000003; P:GO:0008340; P:GO:0019915	-		IPR000535; IPR008962; PTHR22920 (PANTHER)

Caenorhabditis briggsae	briggsae cbr-gtl-2 protein	4	P:GO:0043052; P:GO:0006810; P:GO:0010960; C:GO:0016020	-		PTHR13800 (PANTHER)
Caenorhabditis elegans	laminin alpha- 2 chain	10	P:GO:0030155; P:GO:0045995; C:GO:0005606; P:GO:0030334; F:GO:0005102; P:GO:0060429; P:GO:0030154; P:GO:0048513; P:GO:0009653; P:GO:0016043	-		IPR000034; IPR018031; PTHR10574 (PANTHER), PTHR10574:SF25 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG08814 [Caenorhabditis briggsae]	0				-
	-	0				-
	-	0				-
Tribolium castaneum	coiled-coil domain-containing protein 93	0				IPR019159; PTHR16441 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	rap gtpase-activating protein	3	C:GO:0005622; P:GO:0051056; F:GO:0005515	-		PTHR15711 (PANTHER)
	-	0				-
	-	0				-
Oryctolagus cuniculus	actin-related protein 2 3 complex subunit 3	7	C:GO:0005737; F:GO:0005200; C:GO:0005885; P:GO:0030833; P:GO:0006928; C:GO:0030027; F:GO:0003779	-		IPR007204
Caenorhabditis briggsae	serine threonine protein ki-se	6	P:GO:0006468; F:GO:0030295; F:GO:0019901; F:GO:0004674; F:GO:0000166; C:GO:0044424	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF27 (PANTHER)
Brugia malayi	short chain dehydroge-se reductase family protein	3	P:GO:0055114; F:GO:0016491; F:GO:0005488	-		IPR002198; IPR016040; PTHR19410:SF36 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0005488		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0005488		IPR011989
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-

Callithrix jacchus	x-ray repair complementing defective repair in chinese hamster cells 6 (ku 70kda)	22	P:GO:0050769; F:GO:0008022; C:GO:0005624; P:GO:0010552; P:GO:0006303; C:GO:0005958; P:GO:0033151; C:GO:0005737; F:GO:0016563; C:GO:0005667; C:GO:0043564; P:GO:0006266; C:GO:0000783; P:GO:0000723; P:GO:0019047; P:GO:0010212; F:GO:0003691; F:GO:0051575; F:GO:0004003; F:GO:0010843; P:GO:0019059; F:GO:0005524	-		IPR003034; G3DSA:1.10.720.30 (GENE3D), SSF68906 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	huth_caeel ame: full=probable histidine ammonia-lyase short=histidase	0		P:GO:0009058; F:GO:0016841; P:GO:0006548; P:GO:0006547; C:GO:0005737; F:GO:0016829; F:GO:0003824; F:GO:0004397; F:GO:0005515		-
Homo sapiens	basigin	16	P:GO:0046689; C:GO:0005739; P:GO:0007566; C:GO:0016021; C:GO:0000139; P:GO:0042475; F:GO:0005537; P:GO:0043434; F:GO:0015129; C:GO:0042470; P:GO:0046697; F:GO:0005515; C:GO:0045121; C:GO:0042383; P:GO:0007166; P:GO:0051591	-		-
	-	0				IPR001304; IPR016186; IPR016187
Caenorhabditis elegans	-+ k+ alpha 3a polypeptide	7	P:GO:0006814; F:GO:0005391; C:GO:0016021; F:GO:0046872; P:GO:0006813; P:GO:0006754; F:GO:0005524	-	EC:3.6.3.9	-

Streptococcus pneumoniae CCRI 1974M2	immunoglobulin a1 protease	0		C:GO:0009986; F:GO:0004222; C:GO:0016021; C:GO:0016020; F:GO:0016787; F:GO:0008270; F:GO:0008237; F:GO:0016829; F:GO:0004634; C:GO:0005576; F:GO:0008233; P:GO:0009405; F:GO:0046872; C:GO:0005618		-
Loa loa	related to oncogene abl family member (abl-1)	7	F:GO:0004715; F:GO:0030145; F:GO:0005515; P:GO:0018108; F:GO:0005524; F:GO:0000287; P:GO:0007165	-	EC:2.7.10.2	-
Caenorhabditis elegans	iesterase family member (pde-4)	1	F:GO:0016787	-		IPR002073; PTHR11347 (PANTHER), PTHR11347:SF37 (PANTHER), SSF109604 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0005096; P:GO:0007165; F:GO:0005515; C:GO:0005622		-
Ailuropoda melanoleuca	elongation factor 2	8	F:GO:0003746; P:GO:0006414; P:GO:0006184; F:GO:0005515; F:GO:0003924; C:GO:0030529; C:GO:0005737; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Nematostella vectensis	mannose receptor c type 1-like isoform 1	0		F:GO:0005488; F:GO:0005509; F:GO:0005044; P:GO:0007155; C:GO:0016020; F:GO:0005529		IPR001304; IPR016186; IPR016187; IPR018378; PTHR22802 (PANTHER), PTHR22802:SF16 (PANTHER)
Caenorhabditis elegans	protein yippee-like 1	0				IPR004910; PTHR13847 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	meckelin (meckel syndrome type 3 protein homolog) (transmembrane protein 67)	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-pro-2 protein	11	P:GO:0007506; F:GO:0005488; P:GO:0040007; P:GO:0019915; P:GO:0002119; P:GO:0030154; P:GO:0006898; P:GO:0009792; P:GO:0051729; C:GO:0005634; P:GO:0016246	-		-

Caenorhabditis elegans	Hypothetical protein F26G1.2a [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	beta chain spectrin	1	F:GO:0003779	-		IPR002017; IPR018159; G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF48 (PANTHER), SSF46966 (SUPERFAMILY)
Haemonchus contortus	cysteine protei-se	9	P:GO:0009792; P:GO:0002119; F:GO:0005515; P:GO:0040011; F:GO:0004197; P:GO:0040007; P:GO:0006898; P:GO:0006508; P:GO:0050790	-	EC:3.4.22.0	IPR000169; IPR000668; IPR013128; IPR015643; G3DSA:3.90.70.10 (GENE3D), SSF54001 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	stim (mammalian stromal interaction molecule) homolog family member (stim-1)	0		F:GO:0005509		IPR001660; IPR010993; IPR011510; IPR013761; PTHR15136 (PANTHER), PTHR15136:SF1 (PANTHER)
	-	0				-
Loa loa	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis briggsae	briggsae cbr-pme-5 protein	0				-
Caenorhabditis briggsae	related to yeast vacuolar protein sorting factor family member (vps-39)	7	P:GO:0009792; P:GO:0010171; F:GO:0005515; P:GO:0000003; C:GO:0030897; P:GO:0008219; P:GO:0002009	-		IPR019452; PTHR12894 (PANTHER), PTHR12894:SF10 (PANTHER)
Brugia malayi	importin-beta n-termi-l domain containing protein	0		F:GO:0005488; P:GO:0006886; F:GO:0008565		-
Loa loa	glucosyl glucuronosyl transferases	5	P:GO:0005975; P:GO:0030259; C:GO:0016021; F:GO:0030246; F:GO:0016758	-	EC:2.4.1.0	IPR002213; G3DSA:3.40.50.2000 (GENE3D), SSF53756 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	cation efflux family protein	5	C:GO:0016021; P:GO:0000003; F:GO:0008324; P:GO:0006812; P:GO:0055085	-		IPR002524; G3DSA:1.20.1510.10 (GENE3D), SignalP (SIGNALP)
Caenorhabditis briggsae	miz-type zinc finger transcription factor family member (miz-1)	0				-
Caenorhabditis elegans	calcium calmodulin-dependent protein ki-se ki-se alpha	10	C:GO:0005829; F:GO:0005516; P:GO:0032147; C:GO:0005625; P:GO:0032793; F:GO:0005524; P:GO:0019722; F:GO:0004683; C:GO:0005634; P:GO:0006468	-	EC:2.7.11.17	-

Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	F:GO:0005515; P:GO:0007600; P:GO:0007165	-		-
Acyrthosiphon pisum	briggsae cbr-lig-4 protein	0		P:GO:0006260; F:GO:0005524; F:GO:0016874; P:GO:0006281; F:GO:0003910; P:GO:0006310; F:GO:0003677; C:GO:0005622		IPR001357; G3DSA:3.40.50.10190 (GENE3D), PTHR10459 (PANTHER), PTHR10459:SF7 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	nuclear hormone receptor family member (nhr-105)	5	F:GO:0046872; F:GO:0004879; F:GO:0003677; P:GO:0045449; F:GO:0005515	-		IPR000536; IPR008946; PTHR11865 (PANTHER), PTHR11865:SF197 (PANTHER)
Canis familiaris	a-phase-promoting complex subunit 11	12	C:GO:0005829; F:GO:0008270; P:GO:0051436; P:GO:0051437; P:GO:0070979; P:GO:0051301; P:GO:0031145; F:GO:0004842; F:GO:0005515; P:GO:0007067; C:GO:0005654; C:GO:0005680	-	EC:6.3.2.19	SignalP (SIGNALP)
Caenorhabditis elegans	glycogen synthase ki-se 3 beta	33	F:GO:0004674; P:GO:0007052; P:GO:0002119; P:GO:0032091; C:GO:0005829; P:GO:0016481; P:GO:0001947; P:GO:0005977; F:GO:0008013; F:GO:0002039; C:GO:0034747; F:GO:0050321; P:GO:0040010; F:GO:0034236; P:GO:0046827; P:GO:0006983; P:GO:0031333; P:GO:0030178; P:GO:0043066; P:GO:0009792; P:GO:0060070; F:GO:0005524; P:GO:0031334; P:GO:0018105; P:GO:0071109; F:GO:0051059; C:GO:0030877;	-	EC:2.7.11.0; EC:2.7.11.26	IPR000719; IPR002290; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF114 (PANTHER)

Caenorhabditis briggsae	hypothetical tyrosi-se-like protein in chromosome	4	F:GO:0005515; F:GO:0046872; P:GO:0008152; F:GO:0016491	-		IPR002227; IPR008922; PTHR11474 (PANTHER), PTHR11474:SF1 (PANTHER)
	-	0				-
	-	0				-
Ailuropoda melanoleuca	eukaryotic translation initiation factor subunit 6 interacting protein	6	F:GO:0003743; P:GO:0045948; C:GO:0005852; F:GO:0005515; C:GO:0005654; C:GO:0001650	-		-
	-	0				-
Saccoglossus kowalevskii	scavenger receptor class a- serine protease (agap001979-pa)	0		F:GO:0004252; C:GO:0016021; C:GO:0016020; P:GO:0009792; C:GO:0031012; F:GO:0003824; F:GO:0005044; F:GO:0008233; F:GO:0004872; P:GO:0006508; F:GO:0005509; P:GO:0007155		IPR002172; PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER)
Caenorhabditis briggsae	tubulin-specific chaperone	7	P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0046785; P:GO:0040011; P:GO:0040007; P:GO:0002009	-		PTHR12658 (PANTHER)
Caenorhabditis briggsae	chromosome 1 open reading frame 50	1	F:GO:0005515	-		IPR019534; PTHR14553 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	mariner transposase	2	P:GO:0006313; F:GO:0004803	-		-
Caenorhabditis elegans	mariner transposase	2	P:GO:0006313; F:GO:0004803	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	uncoordi-ted protein isoform partially confirmed by transcript evidence	8	F:GO:0004872; P:GO:0006629; F:GO:0005219; P:GO:0006816; P:GO:0006874; P:GO:0055085; F:GO:0005509; C:GO:0016021	-		IPR015925; PTHR13715:SF17 (PANTHER)
	-	0				SignalP (SIGNALP)

Loa loa	polymerase iii (d- directed) polypeptide 155kda	9	F:GO:0003899; P:GO:0009615; F:GO:0008270; P:GO:0032728; P:GO:0045087; F:GO:0003677; F:GO:0032549; P:GO:0006351; C:GO:0005666	-	EC:2.7.7.6	IPR007081; IPR007083; IPR015700; PTHR19376 (PANTHER), SSF64484 (SUPERFAMILY)
Ailuropoda melanoleuca	eukaryotic translation initiation factor 5a	24	C:GO:0005840; P:GO:0006406; F:GO:0003746; P:GO:0007568; F:GO:0047485; P:GO:0006611; C:GO:0005789; F:GO:0003743; P:GO:0006452; F:GO:0043022; C:GO:0005829; C:GO:0005643; C:GO:0030425; P:GO:0008284; P:GO:0008612; C:GO:0043025; P:GO:0006917; F:GO:0017070; C:GO:0005642; P:GO:0055085; P:GO:0045905; P:GO:0051149; P:GO:0045901; P:GO:0043066	-		IPR001884; IPR012340; IPR014722; IPR016027; IPR020189; PTHR11673:SF2 (PANTHER)
Caenorhabditis elegans	sig-l transducer and activator of transcription 5b	17	F:GO:0003700; F:GO:0004871; P:GO:0006519; N:GO:2000026; P:GO:0030098; P:GO:0019752; P:GO:0023033; P:GO:0007165; P:GO:0022414; P:GO:0051251; P:GO:0045595; F:GO:0005515; F:GO:0005509; C:GO:0005634; P:GO:0009725; P:GO:0009308; P:GO:0006355	-		IPR001217; IPR011992; PTHR11801:SF3 (PANTHER), SSF55550 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0005515		-
Callithrix jacchus	ribosomal protein s13	7	F:GO:0003729; C:GO:0005730; F:GO:0003735; P:GO:0006414; C:GO:0022627; P:GO:0033119; F:GO:0005515	-		IPR000589; IPR009068; PTHR11885 (PANTHER), PTHR11885:SF1 (PANTHER)

	-	0				SignalP (SIGNALP)
Brugia malayi	denn madd domain containing 4c	0		F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150		IPR001194; IPR002885; IPR005112; PTHR12296 (PANTHER)
Loa loa	pan domain containing protein	0				-
Caenorhabditis briggsae	briggsae cbr-ndg-4 protein	3	P:GO:0009792; P:GO:0010171; P:GO:0040010	-		PTHR11161 (PANTHER)
Caenorhabditis briggsae	solute carrier family 39 (metal ion transporter) member 13	4	C:GO:0016020; P:GO:0006829; F:GO:0005385; P:GO:0055085	-		IPR003689; PTHR16950 (PANTHER), PTHR16950:SF6 (PANTHER)
Caenorhabditis elegans	cationic amino acid transporter	4	C:GO:0016021; P:GO:0006865; F:GO:0015171; P:GO:0055085	-		-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0006629; C:GO:0016021; F:GO:0016787; F:GO:0004806		G3DSA:3.40.50.1820 (GENE3D), SSF53474 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	uncoordi-ted family member (unc-103)	9	P:GO:0055085; P:GO:0000160; P:GO:0051291; P:GO:0006355; P:GO:0006813; F:GO:0005242; P:GO:0007165; F:GO:0000155; C:GO:0005887	-		IPR003938; PTHR10217 (PANTHER), PTHR10217:SF15 (PANTHER), SignalP (SIGNALP), SSF81324 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	hypothetical protein ZK470.1 [Caenorhabditis elegans]	0		C:GO:0016021		-
Caenorhabditis elegans	transcription factor dp-1-like	11	P:GO:0006357; P:GO:0006915; P:GO:0007049; C:GO:0005667; P:GO:0008544; F:GO:0003677; F:GO:0003700; F:GO:0019904; F:GO:0003713; P:GO:0045893; P:GO:0008283	-		IPR003316; IPR011991; IPR015648; PTHR12548:SF2 (PANTHER)
Brugia malayi	transcription factor dp-1	6	P:GO:0006357; P:GO:0007049; F:GO:0019904; F:GO:0003713; C:GO:0005654; P:GO:0008283	-		IPR003316; IPR011991; IPR014889; IPR015648; SSF144074 (SUPERFAMILY), SSF46785 (SUPERFAMILY)

Brugia malayi	snf2 family n-termi-l domain containing protein	9	P:GO:0007411; P:GO:0006917; F:GO:0003676; P:GO:0046328; P:GO:0051276; P:GO:0008347; C:GO:0000775; C:GO:0005700; F:GO:0004386	-		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Monodelphis domestica	haloacid dehaloge-se-like hydrolase domain containing 1a	2	F:GO:0005488; F:GO:0003824	-		-
Caenorhabditis briggsae	tryptophanyl-tr- synthetase	7	P:GO:0007031; F:GO:0008270; F:GO:0004830; C:GO:0005778; P:GO:0006436; F:GO:0005524; F:GO:0005515	-	EC:6.1.1.2	IPR001412; IPR002305; IPR002306; IPR014729; SSF52374 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-sma-4 protein	0		P:GO:0007179; C:GO:0005667; F:GO:0003700; C:GO:0005634; P:GO:0006355; C:GO:0005622; F:GO:0005515; P:GO:0006350; P:GO:0045449		-
	-	0				-

Caenorhabditis briggsae	histone deacetylase 6	45	F:GO:0031593; P:GO:0090035; P:GO:0010870; P:GO:0060765; C:GO:0005901; F:GO:0016566; C:GO:0031252; P:GO:0043065; P:GO:0060632; C:GO:0000118; C:GO:0005829; P:GO:0045861; P:GO:0090042; P:GO:0009967; P:GO:0070845; F:GO:0008013; P:GO:0010469; P:GO:0016236; P:GO:0070301; F:GO:0051879; C:GO:0030286; F:GO:0070840; P:GO:0016575; P:GO:0070848; C:GO:0048471; F:GO:0008270; P:GO:0006515;	-		IPR000286; PTHR10625:SF19 (PANTHER), SignalP (SIGNALP), SSF52768 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	ccaat enhancer-binding protein zeta	8	F:GO:0005488; P:GO:0040007; P:GO:0000003; P:GO:0002119; P:GO:0006898; P:GO:0009792; P:GO:0006350; C:GO:0005634	-		PTHR12048 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	mitochondrial ribosomal protein s5	10	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; F:GO:0003723; F:GO:0005515; P:GO:0040010; P:GO:0006898; P:GO:0006412; C:GO:0005739	-	EC:3.6.5.3	IPR000851; IPR005324; IPR014721; IPR020568; PTHR13718:SF3 (PANTHER)
	-	0				-
Loa loa	elegans protein confirmed by transcript evidence	1	F:GO:0005488	-		-

Caenorhabditis elegans	eb module family protein	0		F:GO:0016810; F:GO:0008061; P:GO:0005975; F:GO:0016491; C:GO:0005576; F:GO:0003824; F:GO:0005515; F:GO:0004867; P:GO:0006030		-
Loa loa	exportin 5	0		P:GO:0015031; C:GO:0005634; P:GO:0031047; P:GO:0006810; C:GO:0005737; F:GO:0003723; C:GO:0005575; C:GO:0005730; F:GO:0005515; F:GO:0000049; P:GO:0006611; F:GO:0005488		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	tln1 protein	0		F:GO:0005515		-
	-	0				-
Caenorhabditis briggsae	replication protein a 32 kda subunit	9	P:GO:0044260; F:GO:0005515; P:GO:0007275; P:GO:0006974; P:GO:0090304; P:GO:0048856; C:GO:0044428; P:GO:0007126; P:GO:0022414	-		IPR011991; IPR012340; IPR014892; IPR016027; PTHR13989 (PANTHER), SSF46785 (SUPERFAMILY)
Caenorhabditis briggsae	transmembrane protein 195	4	F:GO:0016491; P:GO:0044255; P:GO:0044281; C:GO:0044464	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	phospholipase d3	3	P:GO:0008152; C:GO:0016021; F:GO:0003824	-		IPR001736; G3DSA:3.30.870.10 (GENE3D), PTHR10185 (PANTHER)
Brugia malayi	pdz domain containing protein	0		F:GO:0005515		-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	polymerase (d- directed) epsilon	12	P:GO:0006281; F:GO:0008270; F:GO:0003887; P:GO:0006260; P:GO:0040035; F:GO:0003677; F:GO:0000166; P:GO:0040011; P:GO:0006997; P:GO:0002009; P:GO:0001701; C:GO:0005634	-	EC:2.7.7.7	IPR013697; PTHR10670 (PANTHER)

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	15	P:GO:0006468; P:GO:0045199; F:GO:0005515; P:GO:0046843; F:GO:0004713; P:GO:0007394; C:GO:0016021; P:GO:0042110; P:GO:0007254; F:GO:0004674; P:GO:0048522; P:GO:0043277; P:GO:0042981; F:GO:0005524; C:GO:0005938	-	EC:2.7.10.0; EC:2.7.11.0	-
	-	0				-
Caenorhabditis elegans	briggsae cbr-inx-12 protein	5	P:GO:0040035; C:GO:0005921; P:GO:0040010; P:GO:0040011; P:GO:0002009	-		IPR000990
	-	0				-
Homo sapiens	hematological and neurological expressed 1	1	C:GO:0005634	-		-
	-	0				-
Caenorhabditis elegans	hypothetical protein K04G7.1 [Caenorhabditis elegans]	3	P:GO:0009792; P:GO:0000003; P:GO:0006898	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	clc-type chloride channel family member (clh-2)	10	P:GO:0009792; F:GO:0005247; C:GO:0005902; F:GO:0005515; P:GO:0055085; P:GO:0000003; C:GO:0016021; C:GO:0005626; C:GO:0015629; P:GO:0006821	-		-
Caenorhabditis briggsae	exportin 7	4	C:GO:0005737; C:GO:0005643; F:GO:0005049; P:GO:0006611	-		PTHR12596 (PANTHER), PTHR12596:SF2 (PANTHER)
Caenorhabditis elegans	phosphatidylinositol-3-phosphate phosphatidylinositol 5-type iii	6	P:GO:0046488; F:GO:0005515; F:GO:0005524; P:GO:0044267; F:GO:0008270; F:GO:0016307	-		IPR002498; G3DSA:3.30.800.10 (GENE3D)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-

Saccoglossus kowalevskii	serine threonine-protein phosphatase 4 catalytic subunit	10	C:GO:0030289; F:GO:0004704; P:GO:0016311; F:GO:0046872; C:GO:0005813; P:GO:0000226; F:GO:0004722; F:GO:0005515; C:GO:0005634; P:GO:0006468	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				PTHR12565 (PANTHER), PTHR12565:SF3 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	sentrin sumo-specific protease senp7	5	P:GO:0040035; P:GO:0009792; P:GO:0010171; P:GO:0018991; P:GO:0040010	-		IPR003653; PTHR12438 (PANTHER), PTHR12438:SF1 (PANTHER), SSF54001 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	g in family member (glb-23)	2	F:GO:0005488; P:GO:0040011	-		IPR000971; IPR009050; IPR012292
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-bub-1 protein	0		F:GO:0004672; F:GO:0005524; F:GO:0000166; P:GO:0006468; F:GO:0004674		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	briggsae cbr-sax-2 protein	1	F:GO:0005515	-		-
Caenorhabditis briggsae	golgi apparatus protein 1	4	C:GO:0000139; F:GO:0005515; P:GO:0040010; C:GO:0016021	-		SignalP (SIGNALP)
Caenorhabditis briggsae	golgi apparatus protein 1	4	C:GO:0000139; F:GO:0005515; P:GO:0040010; C:GO:0016021	-		SignalP (SIGNALP)
Caenorhabditis briggsae	golgi apparatus protein 1	4	C:GO:0000139; F:GO:0005515; P:GO:0040010; C:GO:0016021	-		SignalP (SIGNALP)
Caenorhabditis briggsae	cathepsin a	3	P:GO:0019915; F:GO:0004185; P:GO:0006508	-	EC:3.4.16.0	IPR001563; IPR018202; G3DSA:3.40.50.1820 (GENE3D), PTHR11802:SF9 (PANTHER), SSF53474 (SUPERFAMILY)
Caenorhabditis briggsae	cysteinyl tr- synthetase family member (crs-1)	2	P:GO:0006412; F:GO:0000166	-	EC:3.6.5.3	IPR015803

Ailuropoda melanoleuca	proteasome (macropain) beta 2	10	P:GO:0010243; P:GO:0051436; P:GO:0051437; F:GO:0004298; P:GO:0031145; P:GO:0014070; P:GO:0044419; C:GO:0005737; C:GO:0005839; C:GO:0005634	-	EC:3.4.25.0	IPR001353; G3DSA:3.60.20.10 (GENE3D), PTHR11599 (PANTHER), PTHR11599:SF6 (PANTHER), PS51476 (PROFILE), SSF56235 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Angiostrongylus cantonensis	26s proteasome regulatory chain 4	6	C:GO:0005737; F:GO:0008233; P:GO:0030163; F:GO:0005524; C:GO:0000502; F:GO:0017111	-	EC:3.6.1.15	IPR003959; G3DSA:3.40.50.300 (GENE3D), PTHR23073 (PANTHER), PTHR23073:SF9 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	domain containing protein	1	F:GO:0031072	-		IPR001623; PTHR15606 (PANTHER), PTHR15606:SF1 (PANTHER)
	-	0				-
Brugia malayi	sterol carrier protein 2	12	P:GO:0006470; P:GO:0006996; F:GO:0016747; C:GO:0005777; C:GO:0005625; C:GO:0000795; F:GO:0008289; F:GO:0008420; P:GO:0019915; P:GO:0007127; F:GO:0005515; P:GO:0006694	-	EC:2.3.1.0	IPR002198; IPR003033; IPR016038; IPR016039; IPR020613; IPR020617; G3DSA:3.30.1050.10 (GENE3D), PTHR19410:SF115 (PANTHER)
Brugia malayi	non-specific lipid-transfer protein	13	P:GO:0006470; P:GO:0007031; C:GO:0005777; C:GO:0005625; C:GO:0005739; P:GO:0006637; C:GO:0000795; F:GO:0004770; F:GO:0008420; F:GO:0016740; P:GO:0007127; F:GO:0005515; P:GO:0006694	-		IPR002198; IPR003033; IPR016038; IPR016039; IPR020613; IPR020617; G3DSA:3.30.1050.10 (GENE3D), PTHR19410:SF115 (PANTHER)

Brugia malayi	sterol carrier protein 2	12	P:GO:0006470; P:GO:0006996; F:GO:0016747; C:GO:0005777; C:GO:0005625; C:GO:0000795; F:GO:0008289; F:GO:0008420; P:GO:0019915; P:GO:0007127; F:GO:0005515; P:GO:0006694	-	EC:2.3.1.0	IPR002198; IPR003033; IPR016038; IPR016039; IPR020613; IPR020617; G3DSA:3.30.1050.10 (GENE3D), PTHR19410:SF115 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	briggsae cbr-gosr- protein	4	P:GO:0015031; C:GO:0000139; C:GO:0016021; F:GO:0005515	-		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; F:GO:0004867		SignalP (SIGNALP)
Caenorhabditis elegans	c2 domain containing protein	2	P:GO:0009792; C:GO:0016021	-		IPR000008; IPR008973; IPR018029; IPR020477; G3DSA:2.60.40.150 (GENE3D), PTHR10774 (PANTHER), PTHR10774:SF1 (PANTHER)
Caenorhabditis elegans	myosin-rhogap myr	5	F:GO:0046872; C:GO:0016459; F:GO:0005524; P:GO:0007165; F:GO:0003774	-		IPR000198; IPR008936; PTHR13140 (PANTHER), PTHR13140:SF30 (PANTHER)
	-	0				-
Brugia malayi	ubiquitin-conjugating enzyme e2 a	15	P:GO:0009411; P:GO:0006301; P:GO:0006511; P:GO:0033522; P:GO:0070936; C:GO:0001741; P:GO:0070979; F:GO:0031625; P:GO:0051246; F:GO:0004842; F:GO:0005524; P:GO:0060135; P:GO:0051865; P:GO:0008284; P:GO:0001701	-	EC:6.3.2.19	-

Caenorhabditis elegans	ubiquitin-conjugating enzyme e2 a	15	P:GO:0009411; P:GO:0006301; P:GO:0006511; P:GO:0033522; P:GO:0070936; C:GO:0001741; P:GO:0070979; F:GO:0031625; P:GO:0051246; F:GO:0004842; F:GO:0005524; P:GO:0060135; P:GO:0051865; P:GO:0008284; P:GO:0001701	-	EC:6.3.2.19	IPR000608; IPR016135; PTHR11621 (PANTHER), PTHR11621:SF33 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0003676; P:GO:0000003; F:GO:0008270; P:GO:0009792; C:GO:0005622		IPR007087; IPR013087; IPR015880; PTHR23229 (PANTHER)
	-	0				-
Entamoeba histolytica HM-1:IMSS	myosin heavy chain	0		F:GO:0016787; F:GO:0005524; F:GO:0000156; F:GO:0046872; P:GO:0006974; C:GO:0016459; F:GO:0004871; F:GO:0000166; C:GO:0005737; F:GO:0003779; P:GO:0007165; F:GO:0004518; F:GO:0017111; P:GO:0000160; F:GO:0008757; F:GO:0003774; F:GO:0008168; F:GO:0008270; P:GO:0006281; F:GO:0005515; F:GO:0016740; P:GO:0006935; F:GO:0008984; C:GO:0032982		-
	-	0				SignalP (SIGNALP)

Pongo abelii	filamin a	28	F:GO:0004871; C:GO:0005802; P:GO:0043433; P:GO:0034394; C:GO:0015629; P:GO:0050821; P:GO:0051220; C:GO:0005576; C:GO:0005829; F:GO:0001948; P:GO:0051764; P:GO:0043123; F:GO:0051015; F:GO:0048365; P:GO:0045022; P:GO:0007195; F:GO:0042803; F:GO:0034989; P:GO:0031532; F:GO:0034988; C:GO:0005886; F:GO:0008134; P:GO:0042177; C:GO:0005634; P:GO:0042993; C:GO:0005938; P:GO:0043113	-		-
Caenorhabditis briggsae	fibulin 1	6	F:GO:0005201; C:GO:0005615; F:GO:0005509; C:GO:0031012; F:GO:0005515; C:GO:0005625	-		IPR000152; IPR000742; IPR001881; IPR013032; IPR013091; IPR018097; G3DSA:2.10.25.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF89 (PANTHER), SSF57196 (SUPERFAMILY)
Bos taurus	sig-l recognition particle receptor subunit alpha	10	C:GO:0005785; C:GO:0016021; F:GO:0004872; P:GO:0006184; F:GO:0005515; P:GO:0007165; F:GO:0003924; P:GO:0006614; F:GO:0005525; F:GO:0005047	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	SignalP (SIGNALP)
	-	0				-
Teladorsagia circumcincta	nicotinic acetylcholine receptor non-alpha subunit	6	F:GO:0004872; C:GO:0045211; C:GO:0030054; P:GO:0006811; C:GO:0016021; F:GO:0004889	-		-
Caenorhabditis briggsae	kelch-like 18	1	F:GO:0005515	-		-
Caenorhabditis elegans	thioredoxin domain-containing protein 14-like protein	3	P:GO:0045454; C:GO:0016021; P:GO:0040010	-		-
Caenorhabditis elegans	prolyl carboxy peptidase like family member (pcp-2)	2	C:GO:0016021; F:GO:0008236	-		IPR008758; PTHR11010:SF4 (PANTHER)
	-	0				-
	-	0				-

	-	0				-
Caenorhabditis elegans	polymerase iii (d- directed) polypeptide 155kda	8	F:GO:0003899; F:GO:0008270; P:GO:0032728; P:GO:0045087; F:GO:0003677; F:GO:0032549; P:GO:0006351; C:GO:0005666	-	EC:2.7.7.6	IPR007066; IPR015700; PTHR19376 (PANTHER), SSF64484 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	peroxidasin homolog	4	F:GO:0020037; P:GO:0055114; F:GO:0004601; P:GO:0006979	-	EC:1.11.1.7	IPR002007; IPR010255; PTHR11475 (PANTHER), PTHR11475:SF9 (PANTHER)
Caenorhabditis elegans	hypothetical protein T22B11.2 [Caenorhabditis elegans]	3	C:GO:0016021; P:GO:0008340; F:GO:0008378	-		PTHR23033 (PANTHER), PTHR23033:SF1 (PANTHER)
Caenorhabditis elegans	leucine-rich repeat serine threonine-protein ki-se 1	2	F:GO:0016301; F:GO:0000166	-		-
	-	0				SignalP (SIGNALP)
Brugia malayi	hypothetical protein Bm1_40230 [Brugia malayi]	0				-
	-	0				-
	-	0				-
	-	0				PS51257 (PROFILE), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Homo sapiens	aurora ki-se a-interacting protein	7	P:GO:0045862; C:GO:0005739; P:GO:0045839; F:GO:0005515; P:GO:0016310; F:GO:0016301; C:GO:0005634	-		IPR013177

Ailuropoda melanoleuca	member ras oncogene family	23	C:GO:0000785; C:GO:0005654; P:GO:0007052; C:GO:0042470; F:GO:0005525; P:GO:0030521; P:GO:0006611; P:GO:0051301; P:GO:0006184; P:GO:0006259; C:GO:0005829; C:GO:0005643; P:GO:0007067; F:GO:0003713; P:GO:0007286; P:GO:0007165; P:GO:0045893; F:GO:0003682; F:GO:0003924; P:GO:0006606; F:GO:0050681; P:GO:0006405; P:GO:0044419	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	acetoacetyl- synthetase	3	P:GO:0006629; F:GO:0030729; F:GO:0003987	-	EC:6.2.1.16; EC:6.2.1.1	PTHR11968 (PANTHER), PTHR11968:SF40 (PANTHER)
	-	0				-
Caenorhabditis elegans	coiled-coil domain containing 109a	1	C:GO:0005739	-		IPR006769; PTHR13462:SF5 (PANTHER), SignalP (SIGNALP)
Brugia malayi	2-amino-3-ketobutyrate coenzyme a mitochondrial precursor	5	F:GO:0030170; F:GO:0016769; F:GO:0008890; P:GO:0009058; F:GO:0016874	-	EC:2.3.1.29	IPR004839; IPR011282; IPR015421; IPR015424; PTHR13693 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	#NAME?	0		F:GO:0016740; P:GO:0032259; P:GO:0006370; F:GO:0008168; F:GO:0003676; P:GO:0000003; F:GO:0004483; P:GO:0080009; C:GO:0005622		-
	-	0				SignalP (SIGNALP)

Loa loa	risc-loading complex subunit tarbp2	0		F:GO:0003725; P:GO:0046782; F:GO:0003723; P:GO:0050689; C:GO:0005634; C:GO:0016442; F:GO:0035197; F:GO:0042803; F:GO:0016301; P:GO:0031047; C:GO:0048471; P:GO:0006417; P:GO:0035280; C:GO:0005737; P:GO:0045070; P:GO:0031054; P:GO:0030423; C:GO:0005622; P:GO:0030422; F:GO:0005515		IPR001159; IPR014720; PTHR10910 (PANTHER), PTHR10910:SF7 (PANTHER), SSF54768 (SUPERFAMILY)
Loa loa	risc-loading complex subunit tarbp2	0		F:GO:0003725; P:GO:0046782; F:GO:0003723; P:GO:0050689; C:GO:0005634; C:GO:0016442; F:GO:0035197; F:GO:0042803; F:GO:0016301; P:GO:0031047; C:GO:0048471; P:GO:0006417; P:GO:0035280; C:GO:0005737; P:GO:0045070; P:GO:0031054; P:GO:0030423; C:GO:0005622; P:GO:0030422; F:GO:0005515		IPR001159; IPR014720; PTHR10910 (PANTHER), PTHR10910:SF7 (PANTHER), SSF54768 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Pongo abelii	ornithine decarboxylase antizyme 1	3	P:GO:0006596; F:GO:0008073; F:GO:0005515	-		IPR002993; IPR016181; PTHR10279:SF2 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0006898; C:GO:0005576		IPR001283; IPR014044
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)

Tetraodon nigroviridis	with fg repeats 1	13	F:GO:0005515; F:GO:0008270; P:GO:0007275; C:GO:0016023; P:GO:0006406; P:GO:0007283; C:GO:0005794; C:GO:0005643; P:GO:0032312; F:GO:0003677; P:GO:0030154; F:GO:0003723; F:GO:0008060	-		IPR001164; PTHR23180 (PANTHER), PTHR23180:SF12 (PANTHER)
	-	0				SignalP (SIGNALP)
Ostertagia ostertagi	heat shock protein family member (hsp-)	1	P:GO:0009408	-		IPR001436; IPR002068; IPR008978; G3DSA:2.60.40.790 (GENE3D), PTHR11527 (PANTHER), PTHR11527:SF28 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG21226 [Caenorhabditis briggsae]	0		F:GO:0016888		-
Homo sapiens	serine or cysteine protei-se inhibitor clade g member 1	8	F:GO:0004867; P:GO:0001869; P:GO:0006958; C:GO:0005615; C:GO:0031093; F:GO:0005515; P:GO:0008015; P:GO:0007596	-		IPR000215; IPR015553
Ailuropoda melanoleuca	secreted cysteine-rich	8	F:GO:0050840; P:GO:0042127; C:GO:0031093; F:GO:0005518; P:GO:0071363; P:GO:0001503; F:GO:0005509; C:GO:0005604	-		-
	-	0				-
Pongo abelii	-rdilysin (n-arginine dibasic convertase)	10	P:GO:0016477; C:GO:0005829; P:GO:0007528; F:GO:0008270; P:GO:0051044; C:GO:0009986; F:GO:0004222; P:GO:0052548; F:GO:0048408; P:GO:0008283	-	EC:3.4.24.0	PTHR11851 (PANTHER), PTHR11851:SF65 (PANTHER)
	-	0				-
Caenorhabditis elegans	rad54 homolog b	2	F:GO:0005488; P:GO:0050896	-		IPR018838
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-

Caenorhabditis elegans	tubulin-specific chaperone d	7	P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0046785; P:GO:0040011; P:GO:0040007; P:GO:0002009	-		PTHR12658 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-unc- protein	0		F:GO:0008270		PTHR21696 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	mgc69166 protein	0		F:GO:0016740; F:GO:0003677		IPR017956
Caenorhabditis elegans	briggsae cbr-vhp-1 protein	1	F:GO:0004721	-	EC:3.1.3.16	IPR001763; SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Pan troglodytes	fau	3	C:GO:0005840; F:GO:0003735; P:GO:0006412	-	EC:3.6.5.3	IPR006846
	-	0				-
Caenorhabditis elegans	briggsae cbr-unc-95 protein	1	F:GO:0008270	-		-
Ciona intestinalis	proclotting enzyme	0		P:GO:0006508; F:GO:0004252; F:GO:0008236; F:GO:0016787; F:GO:0003824; F:GO:0008233		IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D)
Caenorhabditis elegans	proteasome activator complex	0		F:GO:0005488; C:GO:0000502		-
Caenorhabditis briggsae	briggsae cbr-frm-2 protein	8	C:GO:0005737; C:GO:0005856; P:GO:0007391; P:GO:0008258; C:GO:0019898; P:GO:0046665; F:GO:0008092; P:GO:0007390	-		IPR000299; IPR000798; IPR011993; IPR014352; IPR014847; IPR018979; IPR018980; IPR019747; IPR019748; IPR019749; IPR019750; G3DSA:3.10.20.90 (GENE3D), PTHR23280 (PANTHER), SSF50729 (SUPERFAMILY), SSF54236 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	cleavage and polyadenylation specific factor 73kda	9	P:GO:0006378; P:GO:0008380; C:GO:0005847; F:GO:0004521; F:GO:0003729; F:GO:0005515; P:GO:0006398; P:GO:0006379; F:GO:0008409	-		IPR011108; IPR021718; G3DSA:3.60.15.10 (GENE3D), PTHR11203 (PANTHER), PTHR11203:SF11 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	methyltransferase 11 domain containing 1	3	P:GO:0009792; P:GO:0000003; F:GO:0016740	-		IPR015324
	-	0				-
	-	0				-

Caenorhabditis elegans	solute carrier family 13 (sodium-dependent dicarboxylate transporter) member 3	14	C:GO:0030054; F:GO:0015141; C:GO:0016021; P:GO:0071422; P:GO:0015810; F:GO:0015362; C:GO:0005813; P:GO:0003333; C:GO:0005624; F:GO:0015137; F:GO:0015183; P:GO:0071436; P:GO:0015746; P:GO:0015807	-		IPR001898; PTHR10283 (PANTHER), PTHR10283:SF15 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	large subunit ribosomal protein 16	9	P:GO:0006412; P:GO:0009107; P:GO:0040007; F:GO:0003735; F:GO:0051539; C:GO:0015934; P:GO:0002119; P:GO:0009792; F:GO:0016992	-	EC:3.6.5.3; EC:2.8.1.8	IPR005755; IPR005822
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Loa loa	atp-binding cassette sub-family d member 4	7	P:GO:0055085; C:GO:0016021; F:GO:0042626; C:GO:0005622; P:GO:0006355; F:GO:0005524; F:GO:0008134	-		IPR010509; PTHR11384 (PANTHER), PTHR11384:SF3 (PANTHER)
	-	0				-
Caenorhabditis briggsae	uncharacterized cog2106 family protein	4	P:GO:0009792; P:GO:0040010; P:GO:0006898; P:GO:0002119	-		IPR003750; G3DSA:3.40.1280.10 (GENE3D), SSF75217 (SUPERFAMILY)
Caenorhabditis briggsae	reti-l pigment epithelium 65	7	P:GO:0008286; P:GO:0007468; P:GO:0042574; P:GO:0007601; F:GO:0003834; F:GO:0005515; F:GO:0004744	-	EC:1.14.99.36; EC:5.2.1.3	IPR004294; PTHR10543:SF4 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	immunoglobulin i-set domain containing protein	0				IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF11 (PANTHER), SSF48726 (SUPERFAMILY)

Caenorhabditis elegans	beta-adrenergic receptor ki-se	0		P:GO:0006468; F:GO:0005524; F:GO:0016301; P:GO:0007186; F:GO:0004674; F:GO:0004672; P:GO:0007603; F:GO:0004872; F:GO:0004871; F:GO:0004703; F:GO:0001664; F:GO:0000166; P:GO:0016310; P:GO:0007165; P:GO:0008277; P:GO:0007474; P:GO:0016060; F:GO:0035091; F:GO:0016740; F:GO:0050254		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				G3DSA:3.80.10.10 (GENE3D)
	-	0				-
	-	0				-
Caenorhabditis elegans	laminin alpha chain	12	P:GO:0001764; P:GO:0048514; P:GO:0030155; P:GO:0045995; C:GO:0005606; P:GO:0030334; F:GO:0005102; P:GO:0008045; P:GO:0030903; P:GO:0031290; P:GO:0007634; P:GO:0070831	-		IPR002049; IPR013032; PR00011 (PRINTS), G3DSA:2.10.25.10 (GENE3D), PTHR10574 (PANTHER), PTHR10574:SF38 (PANTHER), SSF57196 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein B0041.5 [Caenorhabditis elegans]	0		P:GO:0007411; P:GO:0019915; P:GO:0007413		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	rn207_caeel ame: full=probable ring finger protein 207 homolog	3	F:GO:0008270; C:GO:0005622; F:GO:0005515	-		PTHR22635 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	tpr domain containing protein	0		F:GO:0003723; F:GO:0005488; P:GO:0008150		IPR001440; IPR011990; IPR013026; IPR019734; PTHR23184 (PANTHER), PTHR23184:SF1 (PANTHER), SSF48452 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein F41H10.4 [Caenorhabditis elegans]	1	F:GO:0005515	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein F54D11.2 [Caenorhabditis elegans]	0				-

Caenorhabditis elegans	major facilitator superfamily protein	2	C:GO:0016021; P:GO:0055085	-		IPR011701; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11662 (PANTHER), PTHR11662:SF19 (PANTHER), SignalP (SIGNALP)
Loa loa	tyrosyl-d- phosphodiesterase 1	0		P:GO:0000012; P:GO:0008219; C:GO:0005634; F:GO:0016787; P:GO:0006974; F:GO:0017005; C:GO:0005737; P:GO:0006302; P:GO:0006281; F:GO:0004527; F:GO:0003697; F:GO:0008081; F:GO:0005515; F:GO:0004518; F:GO:0003690		IPR010347; G3DSA:3.30.870.10 (GENE3D), SSF56024 (SUPERFAMILY)
Caenorhabditis elegans	major intrinsic protein	10	P:GO:0050829; P:GO:0008340; F:GO:0015204; F:GO:0015168; F:GO:0015250; P:GO:0000003; P:GO:0045087; P:GO:0006833; P:GO:0015793; C:GO:0016323	-		IPR000425; IPR022357; PTHR19139:SF11 (PANTHER)
Brugia malayi	abc transporter family protein	4	F:GO:0042626; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		-
Homo sapiens	nfs1 nitrogen fixation 1 homolog (cerevisiae)	9	C:GO:0005829; P:GO:0018283; F:GO:0046872; P:GO:0000096; P:GO:0006461; F:GO:0031071; C:GO:0005759; F:GO:0042803; C:GO:0005634	-	EC:2.8.1.7	PTHR14360 (PANTHER), PTHR14360:SF2 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	7	F:GO:0030528; P:GO:0006355; F:GO:0043565; C:GO:0000776; F:GO:0005515; F:GO:0003700; C:GO:0005634	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-

Loa loa	pim-3 oncogene	7	P:GO:0016572; F:GO:0005515; P:GO:0043066; P:GO:0046777; F:GO:0004674; P:GO:0007346; F:GO:0000166	-	EC:2.7.11.0	IPR018378
Caenorhabditis elegans	hypothetical protein H35B03.1 [Caenorhabditis elegans]	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG05433 [Caenorhabditis briggsae]	0		F:GO:0046872; F:GO:0016491; P:GO:0008152		-
	-	0				-
Ailuropoda melanoleuca	heat shock protein hsp 90-alpha	22	P:GO:0001764; P:GO:0034619; C:GO:0016323; C:GO:0042470; F:GO:0030911; C:GO:0005829; P:GO:0070096; C:GO:0009986; F:GO:0030235; P:GO:0045429; P:GO:0007165; F:GO:0051082; P:GO:0042026; P:GO:0010592; F:GO:0042803; C:GO:0005625; F:GO:0005524; P:GO:0045585; P:GO:0006986; P:GO:0006839; C:GO:0016324; C:GO:0031012	-		IPR001404; IPR020576; SSF110942 (SUPERFAMILY)
Caenorhabditis briggsae	sterol carrier protein x	9	F:GO:0032934; F:GO:0008415; F:GO:0016491; C:GO:0005777; F:GO:0005515; P:GO:0019915; P:GO:0008152; P:GO:0007031; C:GO:0005739	-		-
Brugia malayi	dap (death associated protein ki-se) like ki-se family member (dlk-1)	7	P:GO:0006468; F:GO:0046872; C:GO:0030054; F:GO:0005515; F:GO:0005524; F:GO:0004709; C:GO:0045202	-	EC:2.7.11.25	-

Brugia malayi	krr1 family protein	8	P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0040010; P:GO:0040011; P:GO:0019915; P:GO:0006898; P:GO:0002009	-		IPR007851; IPR018034
Caenorhabditis briggsae	glit-1	1	P:GO:0040010	-		IPR002018; G3DSA:3.40.50.1820 (GENE3D), PTHR11559:SF32 (PANTHER), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	myosin light chain ki-se	3	P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR000900; IPR011009; IPR017441; IPR017442; IPR020675; IPR020680; G3DSA:3.30.200.20 (GENE3D)
Ancylostoma ceylanicum	secreted protein 5 precursor	0		P:GO:0040011; C:GO:0005576		IPR014044
Caenorhabditis briggsae	3-demethylubiquinone-9 3-methyltransferase	2	F:GO:0008168; P:GO:0044238	-	EC:2.1.1.0	-
Caenorhabditis elegans	ke (drosophila actin-binding) homolog family member (ketn-1)	1	P:GO:0000003	-		-
Rhodopseudomonas palustris BisA53	amp-dependent synthetase and ligase	0		F:GO:0016874; P:GO:0008152; F:GO:0003824		SignalP (SIGNALP)
Loa loa	ubiquitously transcribed sex (x y) chromosome tetratricopeptide repeat protein	5	P:GO:0040035; P:GO:0009792; P:GO:0040018; P:GO:0040010; P:GO:0040011	-		PTHR14017 (PANTHER)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021		IPR016196; PTHR23294 (PANTHER)
	-	0				-
Caenorhabditis elegans	asparagine synthetase domain-containing protein 1	0		P:GO:0006529; P:GO:0006541; P:GO:0008652; F:GO:0004066		G3DSA:3.60.20.10 (GENE3D)
	-	0				-
	-	0				-
Caenorhabditis briggsae	nicoti-mide nucleotide transhydroge-se	11	F:GO:0031177; C:GO:0005746; F:GO:0008750; C:GO:0016021; P:GO:0055114; P:GO:0006099; F:GO:0051287; F:GO:0003957; P:GO:0010467; F:GO:0050661; P:GO:0015992	-	EC:1.6.1.2; EC:1.6.1.1	IPR004003; IPR006162; IPR007698; IPR008143; IPR016040; G3DSA:3.40.50.1220 (GENE3D), PTHR10160 (PANTHER), PTHR10160:SF2 (PANTHER), SSF51735 (SUPERFAMILY), SSF52467 (SUPERFAMILY)
	-	0				-
	-	0				-
Anaeromyxobacter dehalogenans 2CP-C	threonine ammonia- catabolic	4	F:GO:0030170; P:GO:0009097; F:GO:0016597; F:GO:0004794	-	EC:4.3.1.19	IPR001926; G3DSA:3.40.50.1100 (GENE3D), PTHR10314 (PANTHER), PTHR10314:SF17 (PANTHER)

Caenorhabditis elegans	briggsae cbr-asp-1 protein	0		P:GO:0006508; F:GO:0004190; F:GO:0016787; F:GO:0008233		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	F:GO:0005044; F:GO:0005488; C:GO:0016020	-		SignalP (SIGNALP)
Caenorhabditis elegans	nematode astacin protease family member (-s-29)	0		P:GO:0006508; F:GO:0008237; C:GO:0016021; F:GO:0008270		SignalP (SIGNALP)
	-	0				IPR006130
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				IPR000436
Caenorhabditis elegans	valosin containing protein	11	C:GO:0000785; C:GO:0035101; F:GO:0016887; F:GO:0008289; F:GO:0032403; P:GO:0006810; P:GO:0007049; F:GO:0005524; C:GO:0005829; P:GO:0034214; P:GO:0051301	-		IPR003338; IPR003593; IPR003959; IPR003960; IPR004201; IPR009010; G3DSA:3.10.330.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23077 (PANTHER), PTHR23077:SF18 (PANTHER), SSF52540 (SUPERFAMILY), SSF54585 (SUPERFAMILY)
Caenorhabditis briggsae	succi-te dehydroge-se	10	P:GO:0006810; P:GO:0040010; P:GO:0022900; F:GO:0048039; C:GO:0016021; C:GO:0005749; P:GO:0006099; P:GO:0002119; F:GO:0020037; P:GO:0009792	-		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-tkr-1 protein	8	P:GO:0048265; C:GO:0005886; F:GO:0004995; F:GO:0005515; P:GO:0007165; P:GO:0007186; C:GO:0016021; P:GO:0019915	-		-
Caenorhabditis briggsae	protein phosphatase 1 regulatory subunit 7	5	P:GO:0040035; P:GO:0009792; F:GO:0005515; P:GO:0040011; P:GO:0006898	-		IPR003603; G3DSA:3.80.10.10 (GENE3D), PTHR10588 (PANTHER), PTHR10588:SF28 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)

Caenorhabditis briggsae	Hypothetical protein CBG13279 [Caenorhabditis briggsae]	0		F:GO:0004540; F:GO:0004526; P:GO:0008033; P:GO:0016070; C:GO:0005634		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein Y61A9LA.11 [Caenorhabditis elegans]	0				IPR013869
	-	0				-
Loa loa	amop domain containing protein	0		P:GO:0007160; C:GO:0016021		-
Brugia malayi	ancient conserved domain protein	0		F:GO:0004872; F:GO:0004871; F:GO:0004930; C:GO:0016021; P:GO:0007165; P:GO:0007186		IPR002550; PTHR12064 (PANTHER), PTHR12064:SF6 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	5	P:GO:0046686; C:GO:0005764; P:GO:0040010; P:GO:0008340; C:GO:0016021	-		IPR012336; PTHR12289 (PANTHER), PTHR12289:SF2 (PANTHER)
Loa loa	lycerol ki-se family member (dgk-1)	9	F:GO:0004143; F:GO:0008270; F:GO:0003676; P:GO:0023034; F:GO:0005515; F:GO:0000166; F:GO:0019992; P:GO:0007165; P:GO:0007205	-	EC:2.7.1.107	IPR001206; PTHR11255 (PANTHER), PTHR11255:SF8 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-cdh-12 protein	0		F:GO:0005509; P:GO:0007156; P:GO:0007155; C:GO:0016021; C:GO:0016020; C:GO:0005886		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	d- gyrase topoisomerase a subunit family protein	0		F:GO:0003918; F:GO:0003916; P:GO:0006265; C:GO:0005694; F:GO:0003700; P:GO:0006259; C:GO:0005634; F:GO:0003677; F:GO:0000166; F:GO:0005524; C:GO:0005654; P:GO:0006355; F:GO:0016853		IPR002205; IPR013757; PTHR10169 (PANTHER), PTHR10169:SF2 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	atp-binding sub-family a member 3	6	F:GO:0016887; F:GO:0003872; C:GO:0005945; F:GO:0005524; P:GO:0006096; C:GO:0016021	-	EC:2.7.1.11	G3DSA:3.40.50.300 (GENE3D), PTHR19229 (PANTHER), PTHR19229:SF27 (PANTHER)
Caenorhabditis elegans	glucosylceramidase precursor (beta-glucocerebrosidase) (acid beta-glucosidase) (d-glucosyl-n-acylsphingosine glucohydrolase)	3	F:GO:0016798; P:GO:0009987; P:GO:0044238	-		-
Homo sapiens	-dh dehydroge-se	5	P:GO:0006120; F:GO:0008137; P:GO:0006810; C:GO:0005747; C:GO:0016021	-	EC:1.6.5.3	PTHR17098 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Dugesia japonica	zinc c2h2 type family protein	28	C:GO:0005929; P:GO:0007548; P:GO:0021938; F:GO:0008270; P:GO:0001649; F:GO:0008022; P:GO:0021696; P:GO:0007283; P:GO:0021521; P:GO:0009913; P:GO:0060032; F:GO:0016563; C:GO:0005829; P:GO:0050767; F:GO:0008017; P:GO:0021508; P:GO:0019101; F:GO:0003705; P:GO:0019099; P:GO:0045944; P:GO:0031290; P:GO:0009954; F:GO:0003682; P:GO:0045740; P:GO:0048855; C:GO:0005634; C:GO:0035301	-		-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				PTHR20846 (PANTHER)
Caenorhabditis elegans	fatty acid desaturase	3	P:GO:0055114; F:GO:0016491; P:GO:0006629	-		IPR005804; IPR013032
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	F:GO:0022891; C:GO:0016021; P:GO:0055085	-		-
	-	0				-

Caenorhabditis elegans	hypothetical protein K09H11.1 [Caenorhabditis elegans]	0		F:GO:0016627; F:GO:0050660; F:GO:0016787; F:GO:0003995; P:GO:0006468; F:GO:0005524; P:GO:0055114; F:GO:0004713; F:GO:0016491; F:GO:0003824; P:GO:0006508; P:GO:0008152		-
	-	0				PTHR22775 (PANTHER), PTHR22775:SF8 (PANTHER)
	-	0				-
Caenorhabditis elegans	statb_caeel ame: full=sig-l transducer and activator of transcription b ame: full=zinc finger protein stat-b	7	F:GO:0003700; F:GO:0004871; F:GO:0005515; F:GO:0005509; P:GO:0007165; C:GO:0005634; P:GO:0006355	-		-
Homo sapiens	thymidine phosphorylase	14	P:GO:0001525; F:GO:0005161; P:GO:0006220; P:GO:0006213; P:GO:0006260; P:GO:0006935; P:GO:0000002; P:GO:0009887; P:GO:0006206; P:GO:0030154; F:GO:0016154; F:GO:0004645; F:GO:0009032; F:GO:0008083	-	EC:2.4.2.2; EC:2.4.1.1; EC:2.4.2.4	-
Ancylostoma caninum	briggsae cbr-vap-1 protein	0		P:GO:0040011; P:GO:0006898; C:GO:0005576		-
Caenorhabditis elegans	hypothetical protein ZC581.9 [Caenorhabditis elegans]	1	F:GO:0005488	-		-
Caenorhabditis briggsae	transmembrane protein 57	1	C:GO:0044464	-		IPR019130
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	C:GO:0005737	-		IPR010504; PTHR12141 (PANTHER), PTHR12141:SF1 (PANTHER), SSF103657 (SUPERFAMILY)
	-	0				-
	-	0				-
Bombyx mori	endonuclease-reverse transcriptase	1	F:GO:0003824	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	P:GO:0008152; F:GO:0005515; F:GO:0016740	-		IPR002213; PTHR11926:SF3 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein Y59C2A.1 [Caenorhabditis elegans]	0				PTHR11705 (PANTHER)
Ancylostoma caninum	secreted protein asp-2	0		P:GO:0040011; C:GO:0005576		IPR001283; IPR002413; IPR014044; PTHR10334:SF11 (PANTHER)

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0008340; C:GO:0005576		SignalP (SIGNALP)
Ancylostoma caninum	elegans protein partially confirmed by transcript evidence	0		P:GO:0040011; C:GO:0005576		SignalP (SIGNALP)
Ancylostoma caninum	secreted protein asp-2	0		P:GO:0040011; C:GO:0005576		SignalP (SIGNALP)
Streptomyces viridochromogenes DSM 40736	hypothetical protein SvirD4_18528 [Streptomyces viridochromogenes DSM 40736]	0				-
Caenorhabditis elegans	briggsae cbr-dys-1 protein	7	P:GO:0007271; F:GO:0005515; P:GO:0040017; C:GO:0016010; F:GO:0005277; P:GO:0015870; P:GO:0046716	-		-
Caenorhabditis elegans	tbc (tre-2 bub2 cdc16) domain family member (tbc-11)	0		P:GO:0032313; C:GO:0005622		-
	-	0				-
Caenorhabditis elegans	juvenile hormone diol ki-se	1	F:GO:0003824	-		IPR011992; IPR018247; IPR018249; SSF47473 (SUPERFAMILY)
Caenorhabditis briggsae	galt_caeel ame: full=probable galactose-1-phosphate uridylyltransferase short=gal-1-p uridylyltransferase ame: full=udp-glucose--hexose-1-phosphate uridylyltransferase	2	C:GO:0005829; F:GO:0008108	-	EC:2.7.7.12	IPR001937; IPR005849; IPR011146; IPR011151
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	briggsae cbr-nsy-1 protein	3	F:GO:0005515; F:GO:0004672; F:GO:0000166	-		-
	-	0				-
Danio rerio	nucleolar and coiled-body phosphoprotein 1-like	0				SignalP (SIGNALP)
Rhodococcus jostii RHA1	nolc1l protein	0		P:GO:0030261; F:GO:0003677		SignalP (SIGNALP)
Rhodococcus jostii RHA1	nucleolar and coiled-body phosphoprotein 1-like	0		P:GO:0030261; F:GO:0003677		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-cln- protein	9	P:GO:0008340; C:GO:0016020; P:GO:0006665; C:GO:0005794; P:GO:0046662; P:GO:0009792; P:GO:0016043; C:GO:0044446; P:GO:0006873	-		IPR003492; SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				IPR016059
	-	0				-
	-	0				-
Caenorhabditis elegans	component of oligomeric golgi complex 1	1	F:GO:0005515	-		IPR014812
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0005488; C:GO:0016021		-
	-	0				-

	-	0				-
	-	0				-
Caenorhabditis elegans	cg9125-pa	0				PTHR12395 (PANTHER)
	-	0				IPR016135
Caenorhabditis briggsae	dihydroorotate dehydroge-se	8	P:GO:0043065; F:GO:0004158; C:GO:0016021; C:GO:0005743; P:GO:0055114; P:GO:0006222; P:GO:0090140; P:GO:0006207	-	EC:1.3.3.1	IPR012135; IPR013785; PTHR11938 (PANTHER), PTHR11938:SF7 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Loa loa	hypothetical protein LOAG_10773 [Loa loa]	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG18219 [Caenorhabditis briggsae]	0				-
Caenorhabditis brenneri	protein ki-se domain containing protein	2	F:GO:0016301; P:GO:0040010	-		PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
Caenorhabditis elegans	solute carrier family 2 (facilitated glucose fructose transporter) member 5	4	P:GO:0009792; C:GO:0005886; F:GO:0005353; P:GO:0008643	-		IPR005828; IPR005829; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11600 (PANTHER), PTHR11600:SF12 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Loa loa	neuralized family protein	4	F:GO:0008270; F:GO:0005515; P:GO:0009792; P:GO:0000003	-		IPR006573; PTHR12429 (PANTHER)
	-	0				-
Caenorhabditis elegans	vitellogenin receptor	3	F:GO:0004872; C:GO:0016021; F:GO:0005509	-		IPR011042; PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER)
	-	0				-
Caenorhabditis elegans	transmembrane 9 superfamily protein member 4	5	P:GO:0035010; P:GO:0050829; C:GO:0016021; P:GO:0006911; F:GO:0005215	-		IPR004240; PTHR10766:SF12 (PANTHER)
	-	0				-
Caenorhabditis elegans	immunoglobulin i-set domain containing protein	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Branchiostoma floridae	atp-binding cassette sub-family b member mitochondrial	7	P:GO:0071585; P:GO:0070574; F:GO:0008559; C:GO:0016021; C:GO:0005774; F:GO:0005524; F:GO:0015086	-	EC:3.6.3.44	G3DSA:1.20.1560.10 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF69 (PANTHER), SignalP (SIGNALP)
	-	0				IPR008937; PTHR23113:SF22 (PANTHER)

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				IPR019395; PTHR13624 (PANTHER), PTHR13624:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	ring finger protein 146	1	F:GO:0005488	-		IPR004170; PTHR13417 (PANTHER), SSF117839 (SUPERFAMILY)
Caenorhabditis elegans	chondroitin synthase	7	P:GO:0040035; P:GO:0009792; P:GO:0000910; P:GO:0048871; P:GO:0006898; C:GO:0016020; F:GO:0016758	-	EC:2.4.1.0	IPR003378; IPR008428; SignalP (SIGNALP)
Caenorhabditis elegans	chondroitin synthase	7	P:GO:0040035; P:GO:0009792; P:GO:0000910; P:GO:0048871; P:GO:0006898; C:GO:0016020; F:GO:0016758	-	EC:2.4.1.0	IPR003378; IPR008428; SignalP (SIGNALP)
	-	0				IPR002857
	-	0				SignalP (SIGNALP)
Homo sapiens	actin binding 1a	26	C:GO:0030670; P:GO:0043029; F:GO:0043548; P:GO:0030217; C:GO:0030027; P:GO:0008360; P:GO:0048873; F:GO:0008022; C:GO:0031941; C:GO:0001891; P:GO:0050918; P:GO:0006816; P:GO:0051126; P:GO:0032796; P:GO:0001845; P:GO:0042102; C:GO:0001772; P:GO:0034097; P:GO:0031589; F:GO:0051015; F:GO:0042803; C:GO:0030864; P:GO:0030335; P:GO:0045087; C:GO:0005634; P:GO:0030595	-		IPR015048; IPR015505
	-	0				-
	-	0				-
Caenorhabditis elegans	major facilitator superfamily protein	0		C:GO:0016021; C:GO:0016020; P:GO:0055085; F:GO:0005215; P:GO:0006810		PTHR11600 (PANTHER), PTHR11600:SF28 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-

Ailuropoda melanoleuca	squamous cell carcinoma antigen recognized by t cells	7	P:GO:0007050; C:GO:0005829; C:GO:0015030; P:GO:0045585; C:GO:0005681; P:GO:0000387; P:GO:0008629	-		IPR005011
Bos taurus	secreted cysteine-rich	0		P:GO:0071363; P:GO:0001503; C:GO:0005604; F:GO:0050840; C:GO:0005578; C:GO:0031012; F:GO:0005518; C:GO:0005576; C:GO:0031093; F:GO:0005515; P:GO:0042127; F:GO:0005509		-
Caenorhabditis elegans	transport integral membrane protein	8	C:GO:0009986; P:GO:0006833; F:GO:0015168; P:GO:0000003; F:GO:0015204; C:GO:0016021; F:GO:0015250; P:GO:0015793	-		IPR000425; PTHR19139:SF11 (PANTHER), SignalP (SIGNALP)
Brugia malayi	enhancer of ezh	0		F:GO:0003677		IPR001214; G3DSA:2.170.270.10 (GENE3D), PTHR22884 (PANTHER), PTHR22884:SF18 (PANTHER), SSF82199 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	proto-oncogene serine threonine-protein ki-se pim-1	11	F:GO:0004674; F:GO:0030145; P:GO:0043433; F:GO:0005524; F:GO:0008134; P:GO:0007275; P:GO:0046777; P:GO:0008283; P:GO:0043066; C:GO:0005737; P:GO:0031659	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22984 (PANTHER)
						IPR003961; IPR008957; IPR013783; PR00014 (PRINTS), PTHR19900 (PANTHER), PTHR19900:SF7 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-

Homo sapiens	cd44 antigen isoform 5 precursor	30	F:GO:0005057; P:GO:0007160; P:GO:0070374; P:GO:0033138; P:GO:0001558; P:GO:0033189; F:GO:0051219; P:GO:0016337; C:GO:0016323; F:GO:0005540; P:GO:0043518; P:GO:0031175; P:GO:0001955; P:GO:0014070; P:GO:0001658; P:GO:0033031; P:GO:0060442; C:GO:0043234; C:GO:0009897; P:GO:0050731; F:GO:0004872; F:GO:0005518; C:GO:0005887; C:GO:0005634; P:GO:0002246; P:GO:0016477;	-		IPR001231; PTHR10225 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG12788 [Caenorhabditis briggsae]	0		F:GO:0046872; F:GO:0008270		-
Haemonchus contortus	elegans protein confirmed by transcript evidence	3	F:GO:0005515; F:GO:0005529; P:GO:0000003	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG01673 [Caenorhabditis briggsae]	0		C:GO:0005634; F:GO:0000166; F:GO:0008134; F:GO:0017111; F:GO:0005524; F:GO:0016887; P:GO:0006355; C:GO:0005622; P:GO:0043254		PTHR22908 (PANTHER), PTHR22908:SF13 (PANTHER)
Loa loa	fyve finger-containing phosphoinositide	11	P:GO:0042147; C:GO:0031901; P:GO:0044238; P:GO:0034504; F:GO:0046872; F:GO:0016308; F:GO:0005515; C:GO:0045121; F:GO:0000166; P:GO:0006898; P:GO:0044237	-	EC:2.7.1.68	-
Homo sapiens	c2orf28 protein	2	C:GO:0005886; C:GO:0016021	-		SignalP (SIGNALP)
Brugia malayi	serine threonine-protein phosphatase pp1	1	F:GO:0004721	-	EC:3.1.3.16	IPR006186; G3DSA:3.60.21.10 (GENE3D), SSF56300 (SUPERFAMILY)

	-	0				-
Caenorhabditis elegans	cytochrome p450 family protein partially confirmed by transcript evidence	3	P:GO:0008340; F:GO:0016491; F:GO:0005506	-		IPR001128; IPR002401; IPR017972; PTHR19383:SF59 (PANTHER)
Caenorhabditis briggsae	dual oxidase maturation factor 1	2	P:GO:0008104; C:GO:0044425	-		IPR018469; SignalP (SIGNALP)
Nematostella vectensis	d- polymerase catalytic subunit a	11	P:GO:0040035; P:GO:0009792; F:GO:0003887; P:GO:0006260; F:GO:0003677; P:GO:0006997; P:GO:0040011; C:GO:0005634; F:GO:0008270; F:GO:0000166; P:GO:0002009	-	EC:2.7.7.7	-
	-	0				-
Ancylostoma caninum	kunitz-like protease inhibitor precursor	0		F:GO:0008233; F:GO:0004867		IPR002223; PTHR10083 (PANTHER), PTHR10083:SF17 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG03564 [Caenorhabditis briggsae]	0				-
Brugia malayi	suppressor with morphological effect on genitalia family member (smg-1)	0		F:GO:0016740; F:GO:0004674; F:GO:0000166; C:GO:0005737; F:GO:0005524; F:GO:0016301; P:GO:0000184; F:GO:0016773; F:GO:0046872; F:GO:0005488		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	histone	6	P:GO:0009792; P:GO:0002119; C:GO:0005694; P:GO:0000003; P:GO:0040007; P:GO:0045132	-		-
Caenorhabditis briggsae	linker histone h1 and h5 family protein	5	P:GO:0009792; P:GO:0002119; F:GO:0005515; C:GO:0043229; P:GO:0040007	-		PTHR13138 (PANTHER)
Caenorhabditis elegans	histone 1	5	P:GO:0009792; P:GO:0002119; P:GO:0000003; C:GO:0043229; P:GO:0040007	-		-

Pongo abelii	fibrillarin	9	C:GO:0001652; C:GO:0031428; C:GO:0015030; F:GO:0003723; F:GO:0005515; P:GO:0016074; P:GO:0006364; F:GO:0008168; P:GO:0008033	-	EC:2.1.1.0	IPR000692; G3DSA:3.30.200.20 (GENE3D)
	-	0				-
Caenorhabditis elegans	protein ki-se epsilon	14	F:GO:0008047; P:GO:0006917; P:GO:0023034; F:GO:0004871; F:GO:0046872; F:GO:0005524; P:GO:0050730; P:GO:0007165; F:GO:0019901; F:GO:0004699; C:GO:0005783; C:GO:0005634; C:GO:0005886; F:GO:0017124	-		IPR000719; IPR011009; IPR015745; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22985 (PANTHER), SignalP (SIGNALP)
Strongylocentrotus purpuratus	alpha-2-macroglobulin receptor	0		F:GO:0005509; F:GO:0004872; P:GO:0008283; C:GO:0043025; C:GO:0005887; C:GO:0005886; P:GO:0010875; F:GO:0032403; P:GO:0006898; C:GO:0016021; C:GO:0016020; P:GO:0043277; P:GO:0007205; C:GO:0005624; P:GO:0030178; P:GO:0032429; F:GO:0005230; P:GO:0042157; C:GO:0005905; C:GO:0030425; P:GO:0006629; C:GO:0030136; F:GO:0070325; F:GO:0034185; F:GO:0005515; P:GO:0045768; F:GO:0002020;		IPR000033; IPR011042; PTHR10529 (PANTHER), SSF63825 (SUPERFAMILY)
	-	0				-
Drosophila grimshawi	elegans protein partially confirmed by transcript evidence	1	F:GO:0016787	-		IPR002018; G3DSA:3.40.50.1820 (GENE3D), PTHR11559:SF6 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
	-	0				-

Caenorhabditis briggsae	protein-tyrosine phosphatase containing protein	4	P:GO:0016311; F:GO:0004721; P:GO:0009792; P:GO:0000003	-	EC:3.1.3.16	IPR000242; IPR000387; IPR003595; IPR016130; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	beta-actin	21	C:GO:0005829; P:GO:0045214; F:GO:0019894; C:GO:0030016; P:GO:0035148; P:GO:0040007; P:GO:0040035; F:GO:0042802; C:GO:0035267; F:GO:0005524; P:GO:0002119; C:GO:0045179; F:GO:0050998; P:GO:0006928; C:GO:0031941; F:GO:0005200; P:GO:0006898; C:GO:0030529; C:GO:0070688; P:GO:0009792; P:GO:0051592	-		IPR004000; IPR004001; IPR020902; G3DSA:2.30.36.70 (GENE3D), G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), SSF53067 (SUPERFAMILY)
Macaca mulatta	zinc finger protein 706	2	F:GO:0008270; C:GO:0005622	-		IPR007087; IPR007513; IPR015880; PTHR21213 (PANTHER), SSF118359 (SUPERFAMILY)
	-	0				-
Ancylostoma ceylanicum	fasciclin domain containing protein	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				IPR000436; SignalP (SIGNALP)
Caenorhabditis elegans	polyphosphoinositide phosphatase	11	P:GO:0043473; P:GO:0030384; P:GO:0007626; F:GO:0017120; C:GO:0055037; F:GO:0005515; P:GO:0010976; P:GO:0007033; C:GO:0010008; C:GO:0005794; C:GO:0005783	-		-
	-	0				-
Caenorhabditis elegans	-related c-terminus containing protein	0		F:GO:0003674; C:GO:0009507; P:GO:0008150; C:GO:0005575		IPR000631; IPR017953; G3DSA:3.40.1190.20 (GENE3D), PTHR12592 (PANTHER), SSF53613 (SUPERFAMILY)
Caenorhabditis elegans	nuclear inhibitor of protein phosphatase-1	5	F:GO:0005515; P:GO:0008152; P:GO:0008283; C:GO:0044424; F:GO:0008599	-		-

Loa loa	myst histone	0		F:GO:0016740; C:GO:0000785; F:GO:0003682; F:GO:0004402; C:GO:0005634; F:GO:0008270; P:GO:0006333; F:GO:0016747; C:GO:0005622; F:GO:0008415; P:GO:0045449		IPR016181; IPR016197; G3DSA:2.30.30.270 (GENE3D), PTHR10615 (PANTHER), PTHR10615:SF35 (PANTHER), PF11717 (PFAM)
Caenorhabditis briggsae	map-ki-se activating death domain	14	P:GO:0007618; P:GO:0030421; P:GO:0018991; P:GO:0051726; C:GO:0016021; F:GO:0005123; P:GO:0042981; F:GO:0017112; P:GO:0007268; F:GO:0030295; P:GO:0007166; P:GO:0000187; C:GO:0005737; C:GO:0005886	-		-
	-	0				-
Pediculus humanus corporis	very low-density lipoprotein receptor	24	P:GO:0010951; P:GO:0006898; P:GO:0007205; C:GO:0005624; P:GO:0007568; P:GO:0008283; P:GO:0010875; F:GO:0070325; P:GO:0045768; P:GO:0042157; F:GO:0046872; C:GO:0030425; P:GO:0030178; F:GO:0005319; C:GO:0043025; P:GO:0006629; C:GO:0005768; F:GO:0002020; P:GO:0032429; F:GO:0032403; P:GO:0043277; C:GO:0030136; C:GO:0005887; F:GO:0034185	-		IPR000033; IPR011042; PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER), SSF63825 (SUPERFAMILY)

Caenorhabditis elegans	variable abnormal morphology family member (vab-10)	12	P:GO:0007050; F:GO:0008017; P:GO:0016055; C:GO:0015630; F:GO:0005509; P:GO:0007163; C:GO:0005938; F:GO:0003779; C:GO:0015629; P:GO:0006928; P:GO:0006620; P:GO:0001707	-		IPR001589; IPR001715; PTHR11915 (PANTHER), PTHR11915:SF49 (PANTHER)
	-	0				-
	-	0				IPR005552; PTHR23248:SF5 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-dve-1 protein	5	F:GO:0003700; F:GO:0043565; F:GO:0005515; C:GO:0005634; P:GO:0006355	-		IPR001356; IPR009057; IPR012287; PTHR15116 (PANTHER), PTHR15116:SF7 (PANTHER)
	-	0				IPR000436; IPR016060; SignalP (SIGNALP)
	-	0				IPR000436; IPR016060; SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	d-aspartate oxidase	6	P:GO:0009792; P:GO:0055114; F:GO:0003884; F:GO:0005488; F:GO:0008445; F:GO:0047821	-	EC:1.4.3.3; EC:1.4.3.1; EC:1.4.3.7	G3DSA:3.30.9.10 (GENE3D), PTHR11530 (PANTHER), SSF54373 (SUPERFAMILY)
	-	0				-
Branchiostoma floridae	hyaluronidase family protein	2	F:GO:0008080; P:GO:0008152	-		IPR011496; IPR017853; PTHR13170 (PANTHER), PTHR13170:SF7 (PANTHER)
Loa loa	hypothetical protein LOAG_09315 [Loa loa]	4	P:GO:0002009; P:GO:0040010; P:GO:0040035; P:GO:0002119	-		-
Caenorhabditis elegans	dachsous 1	3	P:GO:0002119; P:GO:0040010; P:GO:0040011	-		IPR002126; IPR015919; PTHR10596 (PANTHER), PTHR10596:SF74 (PANTHER)

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0005215; C:GO:0016021; C:GO:0016020; P:GO:0006810; P:GO:0008272; F:GO:0008271; F:GO:0000030; P:GO:0006493; P:GO:0055085; C:GO:0005886		-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Pongo abelii	bifunctio-l aminoacyl-tr- synthetase	10	C:GO:0005829; F:GO:0003723; C:GO:0005625; P:GO:0006424; F:GO:0004827; P:GO:0006461; F:GO:0005524; F:GO:0005515; F:GO:0004818; P:GO:0006433	-	EC:6.1.1.15; EC:6.1.1.17	-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-adm-2 protein	1	F:GO:0005488	-		IPR000742; IPR013032; PTHR11905 (PANTHER), PTHR11905:SF15 (PANTHER)
	-	0				-
Homo sapiens	cytochrome c oxidase subunit viia polypeptide 2	3	F:GO:0009055; F:GO:0004129; C:GO:0005746	-	EC:1.9.3.1	IPR003177; PTHR10510:SF1 (PANTHER)
Caenorhabditis briggsae	tripartite motif protein	3	P:GO:0006915; F:GO:0008270; F:GO:0005515	-		IPR011042; PTHR13712 (PANTHER), PTHR13712:SF9 (PANTHER)
	-	0				SignalP (SIGNALP)
Brugia malayi	cohesin subunit sa-	1	F:GO:0005515	-		PTHR11199 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	h transporter (pgp related) family member (haf-9)	6	F:GO:0015197; F:GO:0042626; P:GO:0015833; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		IPR001140; IPR011527; IPR017940; G3DSA:1.20.1560.10 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF82 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0016787; F:GO:0004091		-
Caenorhabditis elegans	sys1 golgi-localized integral membrane protein homolog	1	C:GO:0016020	-		IPR019185; PTHR12952 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	high incidence of males (increased x chromosome loss) family member (him-4)	0		F:GO:0005509		IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF8 (PANTHER)

Loa loa	loc733359 protein	0		F:GO:0003676; F:GO:0004526; P:GO:0008033; F:GO:0016787; F:GO:0005515; C:GO:0005730; C:GO:0005634		G3DSA:3.30.110.20 (GENE3D), PTHR15314 (PANTHER), PF12328 (PFAM), SignalP (SIGNALP), SSF82704 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	leucine-rich repeats and immunoglobulin-like domains 2	6	C:GO:0005887; F:GO:0005114; F:GO:0034713; P:GO:0030511; P:GO:0040018; P:GO:0000003	-		IPR001611; G3DSA:3.80.10.10 (GENE3D), PTHR23154 (PANTHER), PTHR23154:SF103 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	6	P:GO:0009792; P:GO:0002119; P:GO:0040010; P:GO:0000003; P:GO:0040011; F:GO:0008168	-	EC:2.1.1.0	SignalP (SIGNALP)
Caenorhabditis briggsae	r- recognition	2	F:GO:0003676; F:GO:0000166	-		-
Caenorhabditis briggsae	briggsae cbr-vab-19 protein	3	C:GO:0005886; F:GO:0005515; C:GO:0045177	-		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF169 (PANTHER)
Brugia malayi	dy-ctin 4	4	C:GO:0005737; C:GO:0005856; P:GO:0035046; F:GO:0005515	-		IPR008603
Caenorhabditis briggsae	briggsae cbr-fbl-1 protein	3	C:GO:0005576; F:GO:0005509; F:GO:0005515	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Ailuropoda melanoleuca	sodium potassium-transporting atpase subunit alpha-1 precursor	20	F:GO:0005515; P:GO:0045989; P:GO:0045822; F:GO:0003869; C:GO:0005792; C:GO:0016323; C:GO:0042470; F:GO:0046872; P:GO:0006754; C:GO:0042383; F:GO:0005391; P:GO:0045823; P:GO:0042493; P:GO:0031947; C:GO:0005890; P:GO:0006813; P:GO:0002026; F:GO:0005524; P:GO:0008217; P:GO:0006814	-	EC:3.1.3.41; EC:3.6.3.9	-

Loa loa	n-acetylated-alpha-linked acidic dipeptidase-like protein	0		C:GO:0016021; C:GO:0016020; F:GO:0016787; F:GO:0016805; F:GO:0003674; F:GO:0008237; F:GO:0003824; C:GO:0005575; C:GO:0016324; F:GO:0008233; P:GO:0006508; F:GO:0046872; F:GO:0004181; F:GO:0004180; P:GO:0008150; C:GO:0005886		PTHR10404 (PANTHER), PTHR10404:SF15 (PANTHER)
	-	0				-
Mycoplasma arthritidis 158L3-1	virulence-associated lipoprotein mia	0				-
Ancylostoma caninum	secreted protein 4 precursor	0		C:GO:0005576		-
Caenorhabditis briggsae	briggsae cbr-dep-1 protein	2	P:GO:0040026; P:GO:0040027	-		-
	-	0				-
Caenorhabditis briggsae	probable e3 ubiquitin-protein ligase mycbp2	9	F:GO:0008270; F:GO:0004842; F:GO:0005515; P:GO:0016198; P:GO:0021986; P:GO:0030071; P:GO:0031290; C:GO:0005737; C:GO:0005680	-	EC:6.3.2.19	IPR000315; PTHR12846 (PANTHER), PTHR12846:SF2 (PANTHER)
Homo sapiens	immunoglobulin heavy chain variable region	0				IPR013106; IPR013783; PTHR23266 (PANTHER), PTHR23266:SF11 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	briggsae cbr-eat-3 protein	2	F:GO:0003924; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001401; G3DSA:3.40.50.300 (GENE3D), PTHR11566 (PANTHER), PTHR11566:SF8 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
Homo sapiens	mhc class ii antigen	8	C:GO:0005789; C:GO:0042613; C:GO:0005794; P:GO:0002504; C:GO:0031902; C:GO:0005765; C:GO:0016021; P:GO:0006955	-		IPR000353; IPR011162; IPR014745; PTHR19944 (PANTHER), PTHR19944:SF26 (PANTHER)
Caenorhabditis elegans	glycosyl hydrolases family 31 protein	0		F:GO:0004553; F:GO:0030246; F:GO:0016787; P:GO:0005975; F:GO:0003824		-
	-	0				IPR012877
	-	0				-

Caenorhabditis briggsae	malate cytoplasmic	8	F:GO:0005488; C:GO:0005811; F:GO:0030060; P:GO:0006108; P:GO:0055114; P:GO:0006099; P:GO:0006096; C:GO:0005829	-	EC:1.1.1.37	IPR001236; IPR001252; IPR001557; IPR010945; IPR011274; IPR015955; IPR016040; IPR022383; SSF51735 (SUPERFAMILY)
Caenorhabditis briggsae	malate cytoplasmic	8	F:GO:0005488; C:GO:0005811; F:GO:0030060; P:GO:0006108; P:GO:0055114; P:GO:0006099; P:GO:0006096; C:GO:0005829	-	EC:1.1.1.37	IPR001236; IPR001252; IPR001557; IPR010945; IPR011274; IPR015955; IPR016040; IPR022383; SSF51735 (SUPERFAMILY)
Loa loa	protein-tyrosine phosphatase containing protein	2	F:GO:0004721; P:GO:0044237	-	EC:3.1.3.16	IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-smg-1 protein	2	F:GO:0005488; F:GO:0016772	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Bos taurus	cold shock domain-containing protein e1	6	F:GO:0003723; C:GO:0005743; P:GO:0006355; P:GO:0008584; F:GO:0003677; F:GO:0005515	-		PTHR12913 (PANTHER)
	-	0				-
Caenorhabditis elegans	esterase fe4	2	F:GO:0016787; P:GO:0008152	-		IPR002018; IPR019819; G3DSA:3.40.50.1820 (GENE3D), PTHR11559:SF30 (PANTHER), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	cystinosin	6	P:GO:0015811; P:GO:0003333; C:GO:0045335; F:GO:0015171; C:GO:0005765; C:GO:0016021	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-unc-40 protein	2	P:GO:0016358; P:GO:0001841	-		IPR000408; IPR003961; IPR008957; IPR013783; PR00014 (PRINTS), PTHR10489 (PANTHER), PTHR10489:SF55 (PANTHER)
Caenorhabditis elegans	briggsae cbr-unc-40 protein	2	P:GO:0016358; P:GO:0001841	-		IPR000408; IPR003961; IPR008957; IPR013783; PR00014 (PRINTS), PTHR10489 (PANTHER), PTHR10489:SF55 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0006139; F:GO:0005524; F:GO:0019205		-
Brugia malayi	domon domain containing protein	0		F:GO:0004500; P:GO:0006548		-

Caenorhabditis briggsae	myosin heavy nonmuscle or smooth muscle	34	P:GO:0006941; P:GO:0046664; P:GO:0045200; C:GO:0016461; P:GO:0035159; P:GO:0031036; P:GO:0035072; P:GO:0007443; P:GO:0007395; P:GO:0045214; P:GO:0035017; P:GO:0007297; C:GO:0031672; P:GO:0046663; F:GO:0003779; F:GO:0000146; P:GO:0001736; F:GO:0008307; F:GO:0032027; P:GO:0008258; P:GO:0051259; P:GO:0016203; C:GO:0032154; C:GO:0045179; P:GO:0045184; C:GO:0005863; P:GO:0035317; P:GO:0007427;	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	discoidin domain receptor family member (ddr-2)	9	F:GO:0004872; P:GO:0006468; F:GO:0005515; P:GO:0007155; P:GO:0040010; F:GO:0004716; F:GO:0005524; C:GO:0016021; F:GO:0004674	-	EC:2.7.11.0	-
	-	0				-
	-	0				-

Caenorhabditis elegans	tyrosine-protein ki-se fyn	37	P:GO:0001764; P:GO:0060027; P:GO:0071363; P:GO:0050966; F:GO:0043548; P:GO:0007243; P:GO:0008360; F:GO:0004715; P:GO:0046777; P:GO:0045471; P:GO:0007612; C:GO:0005792; P:GO:0006816; P:GO:0001702; P:GO:0030900; P:GO:0050798; C:GO:0005829; F:GO:0042610; F:GO:0001948; P:GO:0051480; F:GO:0042802; P:GO:0050852; P:GO:0018108; P:GO:0042493; C:GO:0005768; C:GO:0005740; F:GO:0015631;	-	EC:2.7.10.2	-
Caenorhabditis briggsae	family with sequence similarity member b1	0		P:GO:0006508; F:GO:0008236; F:GO:0016787; C:GO:0005576		G3DSA:3.40.50.1820 (GENE3D), PTHR12277 (PANTHER), PTHR12277:SF8 (PANTHER), SSF53474 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-ltd-1 protein	1	F:GO:0008270	-		-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-rhgf-2 protein	0		P:GO:0035023; P:GO:0009792; C:GO:0005622		-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein Y48G1A.3 [Caenorhabditis elegans]	0		F:GO:0046872; F:GO:0008270		-
Angiostrongylus cantonensis	serine protease inhibitor precursor	0				IPR002919; IPR013032; G3DSA:2.10.25.10 (GENE3D), SignalP (SIGNALP)
Loa loa	ubiquitin family	0		C:GO:0005737		IPR000626; IPR015496; IPR019955; G3DSA:3.10.20.90 (GENE3D), SSF54236 (SUPERFAMILY)
Caenorhabditis elegans	mh2 domain containing protein	5	F:GO:0003700; F:GO:0005515; C:GO:0005667; P:GO:0006355; P:GO:0007179	-		IPR003619; IPR013019; IPR013790; PTHR13703:SF19 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-

Pongo abelii	-dh dehydroge-se	4	P:GO:0006810; C:GO:0005747; C:GO:0016021; P:GO:0022900	-		IPR019329; PTHR13327 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	regulator of g protein sig-ling family member (rgs-5)	0		F:GO:0016301; F:GO:0004871		IPR000342; IPR016137; G3DSA:1.10.196.10 (GENE3D)
	-	0				-
	-	0				-
	-	0				-
Loa loa	loc445829 protein	0		F:GO:0046872; F:GO:0008270; F:GO:0005515		IPR000108; IPR001452; G3DSA:2.30.30.40 (GENE3D), PTHR10661 (PANTHER), PTHR10661:SF1 (PANTHER)
Loa loa	loc445829 protein	0				IPR000108; IPR001452; G3DSA:2.30.30.40 (GENE3D), PTHR10661 (PANTHER), PTHR10661:SF1 (PANTHER)
Loa loa	loc445829 protein	0				IPR000108; IPR001452; G3DSA:2.30.30.40 (GENE3D), PTHR10661 (PANTHER), PTHR10661:SF1 (PANTHER)
Anguilla japonica	mannose c type 2	0		C:GO:0009986; C:GO:0016021; C:GO:0016020; F:GO:0005529; P:GO:0006897; P:GO:0007218; P:GO:0007165; F:GO:0005518; C:GO:0005575; F:GO:0004872; P:GO:0008150; F:GO:0005509; F:GO:0005488		IPR001304; IPR016186; IPR016187; PTHR22803 (PANTHER)
	-	0				-
Caenorhabditis briggsae	dedicator of cytokinesis 2	9	F:GO:0005085; F:GO:0005083; P:GO:0043652; F:GO:0005525; C:GO:0005886; F:GO:0032403; F:GO:0051020; P:GO:0040039; F:GO:0017124	-		PTHR23317 (PANTHER), PTHR23317:SF16 (PANTHER)
	-	0				-
Loa loa	ef hand family protein	0		F:GO:0005509		IPR011992; IPR018247; IPR018249; PTHR23055 (PANTHER), PTHR23055:SF7 (PANTHER), SSF47473 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	P:GO:0006810	-		-

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	12	P:GO:0009792; P:GO:0040018; P:GO:0019373; F:GO:0009055; F:GO:0004497; F:GO:0020037; P:GO:0040017; P:GO:0040010; P:GO:0055114; P:GO:0000003; P:GO:0008340; C:GO:0016021	-		IPR001128; PTHR19383:SF176 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	ras-related protein rab-	4	F:GO:0005525; P:GO:0007264; F:GO:0003924; P:GO:0015031	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001806; IPR013753; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF250 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	dynein light chain	5	C:GO:0043229; P:GO:0007049; F:GO:0042802; P:GO:0019060; C:GO:0005737	-		IPR005334; PTHR21255:SF4 (PANTHER)
Caenorhabditis elegans	beta-lactamase family protein	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG05472 [Caenorhabditis briggsae]	4	F:GO:0003723; P:GO:0001522; F:GO:0009982; P:GO:0008033	-	EC:5.4.99.12	-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	alp enigma encoding family member (alp-1)	1	F:GO:0042802	-		IPR006643; PTHR18973 (PANTHER), PTHR18973:SF57 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	bridging integrator 2	2	F:GO:0005515; C:GO:0005737	-		IPR001452; IPR003005; IPR004148; PD968187 (PRODOM), G3DSA:2.30.30.40 (GENE3D), PTHR10321 (PANTHER), PTHR10321:SF7 (PANTHER), SSF103657 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-amph-1 protein	2	F:GO:0005515; C:GO:0005737	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	dipeptidyl anminopeptidase	3	P:GO:0006508; F:GO:0004252; F:GO:0004177	-	EC:3.4.21.0; EC:3.4.11.0	-
Bos taurus	cold shock domain-containing protein e1	6	F:GO:0003723; C:GO:0005743; P:GO:0006355; P:GO:0008584; F:GO:0003677; F:GO:0005515	-		PTHR12913 (PANTHER)

Brugia malayi	egg laying defective family member (egl-15)	3	P:GO:0009987; F:GO:0005488; F:GO:0004672	-		-
	-	0				-
	-	0				-
Loa loa	phosphatidylcholine:ceramide cholinephosphotransferase	0		P:GO:0006686; F:GO:0016740; C:GO:0016021; F:GO:0047493		PTHR21290 (PANTHER), PTHR21290:SF3 (PANTHER), SignalP (SIGNALP)
Danio rerio	3-hydroxyisobutyryl- mitochondrial precursor	5	P:GO:0009792; P:GO:0040010; F:GO:0016787; P:GO:0009083; C:GO:0005739	-		SignalP (SIGNALP)
Caenorhabditis elegans	vacuolar atp synthase subunit b	17	F:GO:0046961; P:GO:0007605; P:GO:0007588; P:GO:0006885; C:GO:0033180; F:GO:0046933; C:GO:0005624; P:GO:0015988; P:GO:0016337; C:GO:0016323; P:GO:0001503; P:GO:0015986; C:GO:0016471; P:GO:0008219; C:GO:0012505; F:GO:0005524; C:GO:0016324	-	EC:3.6.3.14	IPR004100; G3DSA:3.40.50.300 (GENE3D), PTHR15184 (PANTHER), PTHR15184:SF11 (PANTHER), SSF52540 (SUPERFAMILY)
Loa loa	polyubiquitin precursor	5	C:GO:0005737; P:GO:0000003; P:GO:0040007; C:GO:0005634; P:GO:0002119	-		IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), PTHR10666:SF9 (PANTHER), SignalP (SIGNALP), SSF54236 (SUPERFAMILY)
Loa loa	polyubiquitin precursor	5	C:GO:0005737; P:GO:0000003; P:GO:0040007; C:GO:0005634; P:GO:0002119	-		IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), PTHR10666:SF9 (PANTHER), SSF54236 (SUPERFAMILY)
Mus musculus	ribosomal protein s18	7	F:GO:0003735; P:GO:0007275; P:GO:0051726; C:GO:0022627; P:GO:0006417; F:GO:0019843; P:GO:0006414	-		IPR001892; IPR010979; IPR018269; G3DSA:1.10.8.50 (GENE3D), G3DSA:4.10.910.10 (GENE3D), PTHR10871 (PANTHER), PTHR10871:SF2 (PANTHER)
	-	0				-
Brugia malayi	small family member (sma-1)	1	F:GO:0003779	-		-
	-	0				-
	-	0				-

Pediculus humanus corporis	ubiquitin carboxyl-termi-l hydrolase 3	10	F:GO:0042393; P:GO:0060564; P:GO:0031647; P:GO:0090231; F:GO:0004843; P:GO:0016578; F:GO:0004221; P:GO:0051322; C:GO:0000790; P:GO:0006281	-	EC:3.1.2.15	IPR001607; IPR013083; PTHR10420 (PANTHER), PTHR10420:SF58 (PANTHER)
	-	0				-
	-	0				-
Brugia malayi	msp-domain protein 2	2	C:GO:0005856; F:GO:0005198	-		IPR008962
	-	0				-
	-	0				-
Haemonchus contortus	cathepsin l-like cysteine protei-se	3	F:GO:0005515; F:GO:0004197; P:GO:0006508	-	EC:3.4.22.0	IPR000169; IPR000668; IPR013128; IPR013201; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF57 (PANTHER), SignalP (SIGNALP), SSF54001 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0046872; F:GO:0008270; F:GO:0005515; C:GO:0005622		IPR011042; IPR013017; PTHR13712 (PANTHER), PTHR13712:SF9 (PANTHER), SSF101898 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0005509		PTHR12294 (PANTHER), PTHR12294:SF2 (PANTHER)
	-	0				-
Caenorhabditis elegans	lin-12 and glp-1 x-hybridizing protein isoform partially confirmed by transcript evidence	0		P:GO:0005975; F:GO:0016810; F:GO:0003824		-
Caenorhabditis briggsae	r1ap1_caebr ame: full=rag1-activating protein 1 homolog	5	F:GO:0004181; P:GO:0007476; P:GO:0006911; P:GO:0019915; C:GO:0016020	-	EC:3.4.17.0	IPR004316; IPR018179; SignalP (SIGNALP)
Brugia malayi	chloride channel protein 7	4	F:GO:0005247; P:GO:0055085; C:GO:0016021; P:GO:0006821	-		IPR001807; PTHR11689:SF15 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein F52H2.7 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	snf related ki-se	2	F:GO:0004672; F:GO:0000166	-		IPR015940; IPR020636; IPR020661; G3DSA:1.10.510.10 (GENE3D), G3DSA:1.10.8.10 (GENE3D)
Caenorhabditis elegans	snf related ki-se	2	F:GO:0004672; F:GO:0000166	-		IPR015940; IPR020636; IPR020661; G3DSA:1.10.510.10 (GENE3D), G3DSA:1.10.8.10 (GENE3D)
Caenorhabditis briggsae	briggsae cbr-ndg-4 protein	3	P:GO:0009792; P:GO:0010171; P:GO:0040010	-		PTHR11161 (PANTHER)

Caenorhabditis elegans	uncoordi-ted family member (unc-89)	0		P:GO:0000902; P:GO:0009190; P:GO:0006468; F:GO:0003677; P:GO:0007264; F:GO:0016849; F:GO:0005524; P:GO:0035023; F:GO:0004672; F:GO:0005089; F:GO:0005085; C:GO:0000786; P:GO:0006334; F:GO:0005488; P:GO:0045214; F:GO:0008307; C:GO:0005622; F:GO:0005515; F:GO:0004713		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	ophagy (yeast atg homolog) family member (atg-11)	0				-
	-	0				PTHR10887 (PANTHER)
	-	0				-
	-	0				-
Canis familiaris	protein phosphatase 1g isoform 3	0				-
	-	0				-
Branchiostoma floridae	homolog 1	3	P:GO:0031167; F:GO:0003676; F:GO:0008168	-	EC:2.1.1.0	IPR002877; IPR015507; G3DSA:3.40.50.150 (GENE3D), SSF53335 (SUPERFAMILY)
Caenorhabditis elegans	nuclear receptor nhr-61	0		F:GO:0043565; F:GO:0003700; C:GO:0005634; F:GO:0004879; F:GO:0008270; P:GO:0009792; P:GO:0040018; P:GO:0002119; P:GO:0006355; F:GO:0005515; P:GO:0040010; P:GO:0040007; F:GO:0003707		PTHR11865 (PANTHER), PTHR11865:SF238 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	multiple pdz domain protein family member (mpz-1)	0		C:GO:0016021		PTHR19964 (PANTHER), PTHR19964:SF5 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-hum-7 protein	5	F:GO:0046872; C:GO:0016459; F:GO:0005524; P:GO:0007165; F:GO:0003774	-		-

Loa loa	protein serine ki-se h1	8	C:GO:0005815; F:GO:0004674; C:GO:0016607; F:GO:0005524; C:GO:0005789; C:GO:0005794; C:GO:0005886; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017442; IPR020636; G3DSA:1.10.510.10 (GENE3D), PTHR22982:SF12 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	sig-l transducer and activator of transcription	10	C:GO:0005737; F:GO:0042802; F:GO:0003700; F:GO:0004871; F:GO:0003677; P:GO:0007275; F:GO:0005509; P:GO:0007165; C:GO:0005634; P:GO:0006355	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Pongo abelii	ribosomal protein l27a	5	F:GO:0003735; F:GO:0003723; F:GO:0005515; C:GO:0022625; P:GO:0006414	-		SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				IPR021454
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Ailuropoda melanoleuca	golgi apparatus protein 1	5	C:GO:0000139; C:GO:0005797; P:GO:0006886; F:GO:0005102; C:GO:0016021	-		PTHR11884 (PANTHER)
Cyanothece sp. PCC 7822	alpha beta hydrolase fold protein	1	F:GO:0016787	-		IPR000073; IPR000639; G3DSA:3.40.50.1820 (GENE3D), PTHR10992 (PANTHER), PTHR10992:SF22 (PANTHER), SSF53474 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Nippostrongylus brasiliensis	glbc_nipbr ame: full= cuticular isoform flags: precursor	1	F:GO:0046872	-		SignalP (SIGNALP)
Caenorhabditis elegans	lethal family member (let-805)	8	P:GO:0018996; P:GO:0009792; P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		-
	-	0				-

Caenorhabditis elegans	splicing factor subunit 3	8	P:GO:0040035; P:GO:0010171; F:GO:0003676; P:GO:0018996; F:GO:0005515; C:GO:0005634; F:GO:0008270; P:GO:0040039	-		PTHR12786 (PANTHER), PTHR12786:SF2 (PANTHER)
Caenorhabditis elegans	inositol -trisphosphate receptor	1	P:GO:0006810	-		IPR015925; PTHR13715:SF2 (PANTHER)
						SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0005488		-
Caenorhabditis elegans	in family member (ttn-1)	4	P:GO:0009792; P:GO:0006468; F:GO:0004672; F:GO:0005524	-		-
Caenorhabditis elegans	temporarily assigned gene -me family member (tag-289)	0				PTHR13906 (PANTHER), PTHR13906:SF5 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	P:GO:0000003	-		PTHR23028 (PANTHER), PTHR23028:SF6 (PANTHER)
	-	0				-
Caenorhabditis briggsae	major facilitator superfamily protein	1	C:GO:0016021	-		-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-nhr-45 protein	2	F:GO:0005515; P:GO:0006350	-		IPR008946; PTHR11865 (PANTHER), PTHR11865:SF235 (PANTHER)
	-	0				-
						-
	-	0				-
Loa loa	protein tyrosine non-receptor type 23	0		P:GO:0016311; F:GO:0016791; C:GO:0016023; C:GO:0031410; P:GO:0006470; F:GO:0016787; F:GO:0004725; F:GO:0004721		IPR004328; IPR022407; G3DSA:1.20.120.560 (GENE3D), G3DSA:1.20.140.50 (GENE3D), G3DSA:1.25.40.280 (GENE3D), PTHR23030 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical ring finger protein in chromosome	8	P:GO:0009792; P:GO:0010171; F:GO:0046872; P:GO:0040018; P:GO:0018996; P:GO:0040010; P:GO:0000003; P:GO:0008219	-		-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG12817 [Caenorhabditis briggsae]	0				-
	-	0				-

Homo sapiens	immunoglobulin heavy chain variable region	0				IPR003596; IPR013106; IPR013783; PTHR23266 (PANTHER), PTHR23266:SF11 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis briggsae	variable abnormal morphology family member (vab-8)	0		P:GO:0007018; C:GO:0005874; F:GO:0000166; C:GO:0005737; F:GO:0005524; P:GO:0007275; F:GO:0003777; P:GO:0030154; F:GO:0003774; P:GO:0007399		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	r- binding motif protein 28	1	F:GO:0005488	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF50 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-mab- protein	5	F:GO:0003700; F:GO:0003677; P:GO:0007548; C:GO:0005634; P:GO:0006355	-		-
	-	0				-
Ancylostoma caninum	c-type lectin family member (clec-266)	0		F:GO:0003674; F:GO:0005488; C:GO:0016021; P:GO:0008150; F:GO:0005529; C:GO:0005575		IPR001304; IPR016186; IPR016187; PTHR22802 (PANTHER), PTHR22802:SF15 (PANTHER)
Loa loa	leishmanolysin-like (metallopeptidase m8 family)	3	P:GO:0000278; P:GO:0006996; P:GO:0000279	-		IPR001577; G3DSA:3.10.170.20 (GENE3D), SSF55486 (SUPERFAMILY)
Pongo abelii	heavy polypeptide 1	12	F:GO:0003777; C:GO:0005829; P:GO:0006810; C:GO:0005874; F:GO:0042623; P:GO:0006200; P:GO:0007052; C:GO:0005868; F:GO:0005524; P:GO:0007018; F:GO:0005515; C:GO:0005794	-		-
	-	0				-
Caenorhabditis elegans	pdz domain containing 8	4	P:GO:0023034; F:GO:0046872; C:GO:0016021; F:GO:0005515	-		SignalP (SIGNALP)
Caenorhabditis briggsae	pre-mr--splicing factor atp-dependent r- helicase prp16	4	F:GO:0003676; F:GO:0005524; F:GO:0005515; F:GO:0008026	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-

	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-qui-1 protein	0				PTHR19871 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Ciona intestinalis	protein tyrosine phosphatase	1	F:GO:0016791	-	EC:3.1.3.0	IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), SSF52799 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	fatty-acid amide hydrolase 2	1	C:GO:0005811	-		IPR000120; IPR020556; PTHR11895:SF5 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	fatty-acid amide hydrolase 2	1	C:GO:0005811	-		IPR000120; IPR020556; PTHR11895:SF5 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	fatty-acid amide hydrolase 2	1	C:GO:0005811	-		IPR000120; IPR020556; PTHR11895:SF5 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	ras family small gtpase	3	F:GO:0008270; F:GO:0005515; P:GO:0008340	-		-
Caenorhabditis briggsae	briggsae cbr-ins-1 protein	0		F:GO:0005179; C:GO:0005576		IPR016179

Loa loa	activin receptor-like ki-se 7	28	P:GO:0006468; P:GO:0009749; P:GO:0001541; P:GO:0030901; P:GO:0007181; P:GO:0032868; P:GO:0021766; P:GO:0001834; P:GO:0046676; P:GO:0014070; C:GO:0005737; F:GO:0016361; P:GO:0019915; C:GO:0009986; F:GO:0046872; P:GO:0021549; P:GO:0007165; P:GO:0002021; P:GO:0042493; P:GO:0030154; F:GO:0070700; C:GO:0048179; P:GO:0007368; P:GO:0033993; F:GO:0005524; P:GO:0043065;	-		IPR000719; IPR011009; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR23255 (PANTHER), PTHR23255:SF14 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	nudix hydrolase	3	F:GO:0030145; P:GO:0009132; F:GO:0016818	-	EC:3.6.1.0	IPR000086; IPR015797; IPR020084; PTHR12992 (PANTHER), PS51462 (PROFILE)
	-	0				-
Caenorhabditis elegans	uroca-te hydratase	2	P:GO:0006548; F:GO:0016153	-	EC:4.2.1.49	IPR000193
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-dpy-22 protein	10	P:GO:0040010; P:GO:0018991; P:GO:0040035; P:GO:0010171; P:GO:0040026; P:GO:0040011; P:GO:0009792; P:GO:0040018; P:GO:0006350; C:GO:0005634	-		-
Caenorhabditis briggsae	ypi7_caeel ame: full=uncharacterized f-box protein	0				IPR001810; G3DSA:1.20.1280.50 (GENE3D)
	-	0				IPR016186
Caenorhabditis elegans	ribosomal large p2	5	P:GO:0009792; C:GO:0005840; F:GO:0003735; P:GO:0040010; P:GO:0006414	-		IPR001813; PTHR21141 (PANTHER), PTHR21141:SF5 (PANTHER)
	-	0				-

Angiostrongylus cantonensis	elegans protein confirmed by transcript evidence	3	F:GO:0046872; P:GO:0019509; F:GO:0043874	-	EC:3.1.3.77	-
	-	0				-
Homo sapiens	mhc class ib antigen	5	P:GO:0006955; F:GO:0032393; C:GO:0016021; P:GO:0002474; C:GO:0042612	-		IPR001039; IPR011161; IPR011162; PTHR16675 (PANTHER), PTHR16675:SF53 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	multidrug resistance protein 2 (atp-binding cassette protein c)	1	F:GO:0017111	-	EC:3.6.1.15	-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	prolyl 4-hydroxylase	6	F:GO:0031418; F:GO:0005506; F:GO:0004656; P:GO:0055114; F:GO:0016702; C:GO:0005783	-	EC:1.14.11.2; EC:1.13.11.0	-
Caenorhabditis elegans	briggsae cbr-acs-11 protein	0		P:GO:0008152; F:GO:0003824		G3DSA:3.40.50.980 (GENE3D), SignalP (SIGNALP), SSF56801 (SUPERFAMILY)
Caenorhabditis elegans	yhb8_caeel ame: full=uncharacterized protein flags: precursor	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG12661 [Caenorhabditis briggsae]	0				PTHR21068 (PANTHER), PTHR21068:SF8 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-abt-4 protein	2	F:GO:0016887; F:GO:0005524	-		PTHR19229 (PANTHER), PTHR19229:SF27 (PANTHER), SignalP (SIGNALP)
	-	0				IPR001859; SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0016787		IPR002018; G3DSA:3.40.50.1820 (GENE3D), PTHR11559:SF6 (PANTHER), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-psr-1 protein	10	F:GO:0005515; P:GO:0006397; P:GO:0010468; F:GO:0032452; F:GO:0016491; C:GO:0044464; P:GO:0070077; P:GO:0048513; P:GO:0008380; P:GO:0019219	-		SSF51197 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG17703 [Caenorhabditis briggsae]	0		F:GO:0008270; C:GO:0005634		IPR012935
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	protein-s isoprenylcysteine o-methyltransferase	4	F:GO:0004671; C:GO:0016021; P:GO:0006481; C:GO:0005783	-	EC:2.1.1.100	IPR007269; PTHR12714 (PANTHER), SignalP (SIGNALP)

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0005488		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-cnt-2 protein	11	C:GO:0005829; P:GO:0006810; F:GO:0008060; P:GO:0032312; F:GO:0008270; P:GO:0000003; F:GO:0005515; F:GO:0003924; P:GO:0009792; C:GO:0005634; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001020; IPR001806; IPR013753; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR23180 (PANTHER), PTHR23180:SF6 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	protein ki-se c	13	F:GO:0008047; P:GO:0006917; P:GO:0023034; F:GO:0004871; F:GO:0046872; F:GO:0019899; F:GO:0005524; P:GO:0050730; P:GO:0007165; F:GO:0004699; C:GO:0005783; C:GO:0005634; C:GO:0005886	-		-
Caenorhabditis briggsae	briggsae cbr-apd-3 protein	12	P:GO:0016192; F:GO:0008565; P:GO:0061088; P:GO:0040007; P:GO:0010171; P:GO:0002119; C:GO:0030117; F:GO:0005515; P:GO:0006886; P:GO:0009792; P:GO:0006726; C:GO:0005794	-		IPR002553; IPR011989; PTHR22781 (PANTHER), PTHR22781:SF9 (PANTHER)
Brugia malayi	fes cip4 homology domain containing protein	0		P:GO:0007165; C:GO:0005622		-
	-	0				-
Caenorhabditis elegans	eb module family protein	2	F:GO:0016810; P:GO:0005975	-		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	e3 ubiquitin-protein ligase ubr7	1	F:GO:0003824	-		SignalP (SIGNALP)
Caenorhabditis briggsae	e3 ubiquitin-protein ligase ubr7	1	F:GO:0003824	-		SignalP (SIGNALP)
Caenorhabditis briggsae	e3 ubiquitin-protein ligase ubr7	1	F:GO:0003824	-		SignalP (SIGNALP)
	-	0				-

Loa loa	mitogen-activated protein ki-se erk-	3	P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	PTHR11295 (PANTHER), PTHR11295:SF111 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG21465 [Caenorhabditis briggsae]	0				G3DSA:3.30.70.340 (GENE3D), PTHR11705 (PANTHER), PTHR11705:SF10 (PANTHER)
	-	0				-
	-	0				-
Bitis gabonica	trypsin inhibitor-7 precursor	2	C:GO:0005576; F:GO:0008233	-		-
Homo sapiens	atp h+ mitochondrial f1 gamma polypeptide 1	10	F:GO:0046961; F:GO:0005515; F:GO:0008270; C:GO:0005759; P:GO:0006172; F:GO:0046933; P:GO:0042776; F:GO:0003677; C:GO:0000275; P:GO:0006200	-	EC:3.6.3.14	-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis elegans	homeobox domain containing protein	7	P:GO:0040010; F:GO:0003676; P:GO:0040035; P:GO:0002119; P:GO:0040011; P:GO:0006898; P:GO:0002009	-		-
	-	0				-
Caenorhabditis remanei	calcium atpase	5	F:GO:0005388; C:GO:0016021; P:GO:0006754; F:GO:0005524; P:GO:0006816	-	EC:3.6.3.8	IPR001757; IPR008250; G3DSA:1.20.1110.10 (GENE3D), PTHR11939:SF75 (PANTHER), SignalP (SIGNALP), SSF81665 (SUPERFAMILY)
Caenorhabditis briggsae	isocitrate dehydroge-se	7	F:GO:0051287; F:GO:0005515; P:GO:0055114; F:GO:0000287; P:GO:0006099; F:GO:0004449; C:GO:0005739	-	EC:1.1.1.41	IPR001804; PTHR11835:SF5 (PANTHER), SSF53659 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein B0399.1 [Caenorhabditis elegans]	0		F:GO:0015269; C:GO:0016021; P:GO:0006813; F:GO:0005516		-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	lamin b1	3	F:GO:0005515; C:GO:0005635; C:GO:0005882	-		IPR001664; IPR016044; PTHR23239:SF11 (PANTHER)
	-	0				-

	-	0				-
Caenorhabditis elegans	gamma-glutamyltranspeptidase family protein	0		F:GO:0005179; F:GO:0003840; C:GO:0005576		IPR000101
Pongo abelii	gram domain-containing protein 1a isoform 2	1	C:GO:0016021	-		-
Drosophila ananassae	vacuolar proton pump	3	F:GO:0015078; C:GO:0033177; P:GO:0015986	-		IPR002490; PTHR11629:SF23 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans fln-1 isoform partially confirmed by transcript evidence	1	F:GO:0003779	-		-
Caenorhabditis elegans	briggsae cbr--s-39 protein	8	F:GO:0008270; P:GO:0008586; F:GO:0005509; P:GO:0051605; P:GO:0007415; F:GO:0004222; P:GO:0006508; P:GO:0008045	-	EC:3.4.24.0	IPR000859; PTHR10127 (PANTHER), PTHR10127:SF70 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-unc-14 protein	0				-
	-	0				-
Caenorhabditis briggsae	cytoplasmic intermediate filament protein	11	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0018991; P:GO:0018996; F:GO:0005515; C:GO:0005882; P:GO:0040010; P:GO:0040011; P:GO:0006898; F:GO:0005198	-		G3DSA:1.20.5.170 (GENE3D)
	-	0				-
	-	0				-
Callithrix jacchus	src homology 2 domain containing transforming protein d	0		F:GO:0005085; P:GO:0007254; C:GO:0045202; P:GO:0023034; C:GO:0030054; C:GO:0005575; C:GO:0005622; F:GO:0030971; F:GO:0005515; F:GO:0005070; P:GO:0007264; F:GO:0019904; C:GO:0045211; P:GO:0008150; C:GO:0005886		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	uncoordi-ted family member (unc-62)	0		F:GO:0005515		-
	-	0				SignalP (SIGNALP)
	-	0				-

Haemonchus contortus	ligand-gated ion channel subunit	5	C:GO:0016021; C:GO:0030054; C:GO:0045211; F:GO:0005230; P:GO:0006811	-		-
Angiostrongylus cantonensis	ribosomal protein l13	9	P:GO:0009792; P:GO:0002119; F:GO:0003735; F:GO:0003723; F:GO:0005515; P:GO:0000003; C:GO:0022625; P:GO:0040007; P:GO:0006414	-		-
Loa loa	elegans protein partially confirmed by transcript evidence	0		F:GO:0008270; C:GO:0005622		IPR007087; IPR015880
	-	0				-
	-	0				-
Caenorhabditis briggsae	yqy2_caeel ame: full=uncharacterized protein	0		P:GO:0008152; F:GO:0008080		-
Caenorhabditis elegans	atp-binding-cassette protein	4	C:GO:0016021; F:GO:0016887; F:GO:0005524; P:GO:0010171	-		G3DSA:3.40.50.300 (GENE3D), PTHR19241 (PANTHER), PTHR19241:SF30 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	m-phase phosphoprotein 10 (u3 small nucleolar ribonucleoprotein)	8	P:GO:0040010; C:GO:0005730; P:GO:0040035; P:GO:0008380; P:GO:0002119; F:GO:0005515; C:GO:0030529; P:GO:0006898	-		IPR007151
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	pre-mr--processing factor 17	9	P:GO:0040007; P:GO:0000003; P:GO:0010171; F:GO:0016740; P:GO:0002119; P:GO:0040039; P:GO:0002009; P:GO:0001703; P:GO:0016246	-		PTHR19852 (PANTHER), PTHR19852:SF7 (PANTHER)
Caenorhabditis elegans	briggsae cbr-glo-4 protein	4	P:GO:0009987; F:GO:0003824; F:GO:0005488; P:GO:0008152	-		IPR000408; IPR009091; PTHR22870 (PANTHER), PTHR22870:SF14 (PANTHER)
Caenorhabditis elegans	briggsae cbr-glo-4 protein	4	P:GO:0009987; F:GO:0003824; F:GO:0005488; P:GO:0008152	-		IPR000408; IPR009091; PTHR22870 (PANTHER), PTHR22870:SF14 (PANTHER)

Caenorhabditis elegans	briggsae cbr-glo-4 protein	0		F:GO:0046872; F:GO:0016874; F:GO:0008270; F:GO:0016881; C:GO:0005622; P:GO:0006464		IPR000408; IPR009091; PTHR22870 (PANTHER), PTHR22870:SF14 (PANTHER)
Caenorhabditis elegans	briggsae cbr-glo-4 protein	0		F:GO:0046872; F:GO:0016874; F:GO:0008270; F:GO:0016881; C:GO:0005622; P:GO:0006464		IPR000408; IPR009091; PTHR22870 (PANTHER), PTHR22870:SF14 (PANTHER)
Caenorhabditis elegans	briggsae cbr-glo-4 protein	0		F:GO:0016874; F:GO:0003682; F:GO:0008536; F:GO:0008270; P:GO:0006464; C:GO:0005575; C:GO:0005622; F:GO:0016881; F:GO:0046872; P:GO:0008150		IPR000408; IPR009091; PTHR22870 (PANTHER), PTHR22870:SF14 (PANTHER)
Caenorhabditis elegans	briggsae cbr-glo-4 protein	0		F:GO:0016874; F:GO:0003682; F:GO:0008536; F:GO:0008270; P:GO:0006464; C:GO:0005575; C:GO:0005622; F:GO:0016881; F:GO:0046872; P:GO:0008150		IPR000408; IPR009091; PTHR22870 (PANTHER), PTHR22870:SF14 (PANTHER)
Caenorhabditis elegans	briggsae cbr-glo-4 protein	0		F:GO:0016874; F:GO:0003682; F:GO:0008536; F:GO:0008270; P:GO:0006464; C:GO:0005575; C:GO:0005622; F:GO:0016881; F:GO:0046872; P:GO:0008150		IPR000408; IPR009091; PTHR22870 (PANTHER), PTHR22870:SF14 (PANTHER)
Caenorhabditis elegans	briggsae cbr-glo-4 protein	0		F:GO:0016874; F:GO:0003682; F:GO:0008536; F:GO:0008270; P:GO:0006464; C:GO:0005575; C:GO:0005622; F:GO:0016881; F:GO:0046872; P:GO:0008150		IPR000408; IPR009091; PTHR22870 (PANTHER), PTHR22870:SF14 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	galaxin-like 2	0				-
	-	0				SignalP (SIGNALP)

Vitis vinifera	serine threonine protein	5	C:GO:0000164; F:GO:0046872; F:GO:0004722; P:GO:0006470; P:GO:0019915	-		IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF19 (PANTHER), SSF56300 (SUPERFAMILY)
Nematostella vectensis	elegans protein confirmed by transcript evidence	3	F:GO:0005488; F:GO:0016491; P:GO:0044237	-		-
Caenorhabditis elegans	drosophila sos homolog family member (sos-1)	0				-
Homo sapiens	un-med protein product [Homo sapiens]	7	P:GO:0006915; C:GO:0031965; F:GO:0004871; C:GO:0016021; P:GO:0043123; F:GO:0050699; C:GO:0005789	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	mediator complex subunit 26	11	P:GO:0008340; P:GO:0006357; P:GO:0040007; F:GO:0016455; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0006898; C:GO:0016592; P:GO:0009792	-		IPR017923; PTHR11477 (PANTHER), SignalP (SIGNALP)
Loa loa	briggsae cbr-nsy-1 protein	4	P:GO:0006468; F:GO:0005515; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	-
Caenorhabditis elegans	in family member (ttn-1)	0		F:GO:0005524; F:GO:0004672; F:GO:0000166; P:GO:0006468; P:GO:0009792; F:GO:0004674		IPR013783; PTHR19897 (PANTHER), PTHR19897:SF17 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
Brugia malayi	nuclear receptor nhr-67	0		F:GO:0043565; F:GO:0003700; F:GO:0003677; C:GO:0005634; F:GO:0004879; F:GO:0008270; P:GO:0006355; F:GO:0004872; F:GO:0046872; P:GO:0006350; F:GO:0003707; P:GO:0045449		IPR008946
	-	0				-

Homo sapiens	eukaryotic translation elongation factor 1 delta	7	F:GO:0003746; F:GO:0004871; C:GO:0005853; F:GO:0005515; P:GO:0043123; C:GO:0005829; P:GO:0006414	-		IPR001326; IPR018940; PTHR11595 (PANTHER), PTHR11595:SF3 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	ser thr protein phosphatase family protein	0		F:GO:0016787; F:GO:0004721		IPR006186
	-	0				-
	-	0				-
Caenorhabditis briggsae	heat shock protein 70-c	3	F:GO:0005524; P:GO:0006950; C:GO:0005788	-		IPR001023; IPR013126; IPR018181; G3DSA:3.30.30.30 (GENE3D), G3DSA:3.30.420.40 (GENE3D), PTHR19375:SF1 (PANTHER), SignalP (SIGNALP), SSF53067 (SUPERFAMILY)
Caenorhabditis briggsae	heat shock protein 70-c	3	F:GO:0005524; P:GO:0006950; C:GO:0005788	-		IPR001023; IPR013126; IPR018181; G3DSA:3.30.30.30 (GENE3D), G3DSA:3.30.420.40 (GENE3D), PTHR19375:SF1 (PANTHER), SignalP (SIGNALP), SSF53067 (SUPERFAMILY)
	-	0				-
Loa loa	general transcription factor iih subunit 1	7	P:GO:0006367; P:GO:0045944; F:GO:0008353; F:GO:0005515; P:GO:0006368; C:GO:0005675; F:GO:0008094	-	EC:2.7.11.23	IPR005607; PTHR12856 (PANTHER), SSF140383 (SUPERFAMILY)
Xenopus (Silurana) tropicalis	dhx33 protein	4	F:GO:0008026; F:GO:0003676; F:GO:0005524; C:GO:0009536	-		IPR002464; G3DSA:3.40.50.300 (GENE3D), PTHR18934 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	flavin monooxyge-se	7	F:GO:0004499; F:GO:0050661; P:GO:0055114; P:GO:0000003; C:GO:0031227; C:GO:0016021; F:GO:0050660	-	EC:1.14.13.8	IPR020946; G3DSA:3.50.50.60 (GENE3D), PTHR23023 (PANTHER), PTHR23023:SF4 (PANTHER), SSF51905 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	#NAME?	7	P:GO:0006814; F:GO:0005391; C:GO:0016021; F:GO:0046872; P:GO:0006813; P:GO:0006754; F:GO:0005524	-	EC:3.6.3.9	IPR001757; G3DSA:3.40.1110.10 (GENE3D), PTHR11939:SF100 (PANTHER), SSF81660 (SUPERFAMILY)
Caenorhabditis elegans	retinoblastoma-binding protein 5	0				IPR001680; IPR015943; PTHR12816 (PANTHER), PTHR12816:SF6 (PANTHER), SSF101908 (SUPERFAMILY)
Loa loa	u2-associated sr140 protein	1	F:GO:0003676	-		IPR000504; IPR012677; PTHR23140 (PANTHER), SSF54928 (SUPERFAMILY)

Caenorhabditis briggsae	ylw1_caeel ame: full=uncharacterized protein	0				-
	-	0				-
Caenorhabditis briggsae	yl4m_caeel ame: full=uncharacterized protein	0				IPR010463; IPR016059; G3DSA:3.40.50.1820 (GENE3D), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	unc-13 protein	4	P:GO:0016079; F:GO:0005488; C:GO:0043195; C:GO:0045211	-		IPR019558; PTHR10480 (PANTHER)
	-	0				-
Caenorhabditis elegans	phosphatidylserine receptor	0		F:GO:0070815; C:GO:0005634; F:GO:0016702; P:GO:0055114; P:GO:0016568; F:GO:0016491; P:GO:0018395; F:GO:0004872; F:GO:0005515; F:GO:0046872; P:GO:0006350; P:GO:0045449		-
Loa loa	cleavage and polyadenylation specific factor 3-like	4	C:GO:0005737; P:GO:0043484; F:GO:0016787; C:GO:0005634	-		IPR022712; PTHR11203 (PANTHER), PTHR11203:SF8 (PANTHER)
Homo sapiens	txndc5 protein	6	P:GO:0006892; C:GO:0005788; P:GO:0016044; P:GO:0045454; P:GO:0006916; F:GO:0016853	-		-
	-	0				-
Ascaris suum	dtdp-glucose -dehydratase	9	P:GO:0002119; P:GO:0006694; F:GO:0003854; P:GO:0018991; P:GO:0045226; P:GO:0040017; F:GO:0050662; P:GO:0040007; F:GO:0008831	-	EC:1.1.1.145; EC:1.1.1.133	IPR001509; IPR016040; PTHR10366 (PANTHER), PTHR10366:SF41 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis briggsae	myotonin-protein ki-se	2	F:GO:0004672; F:GO:0000166	-		IPR000095; IPR001180; IPR001849; IPR002219; IPR011993; IPR020454; G3DSA:3.30.60.20 (GENE3D), PTHR22988 (PANTHER), PTHR22988:SF2 (PANTHER), PS50219 (PROFILE), SSF50729 (SUPERFAMILY), SSF57889 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein F16H11.1 [Caenorhabditis elegans]	0		C:GO:0016021; P:GO:0055085		SignalP (SIGNALP)
Caenorhabditis elegans	temporarily assigned gene -me family member (tag-308)	0				PTHR10857 (PANTHER)

Homo sapiens	transporter atp-binding sub-family b (mdr tap)	19	F:GO:0046979; C:GO:0042825; P:GO:0019060; F:GO:0015197; C:GO:0005792; P:GO:0042270; F:GO:0043531; C:GO:0005829; F:GO:0046982; F:GO:0046978; P:GO:0046967; P:GO:0015833; F:GO:0042626; P:GO:0019885; P:GO:0055085; F:GO:0042605; F:GO:0042803; F:GO:0005524; C:GO:0005739	-		G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF79 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	glutamyl-tr- amidotransferase subunit	2	F:GO:0016884; P:GO:0019915	-	EC:6.3.5.0	IPR000120; PTHR11895:SF7 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Danio rerio	loc398277 protein	11	P:GO:0035121; P:GO:0016055; F:GO:0003676; F:GO:0046872; P:GO:0045449; F:GO:0016881; P:GO:0030902; P:GO:0030903; C:GO:0044424; P:GO:0001707; P:GO:0009952	-	EC:6.3.2.0	-
Drosophila virilis	isoform b	0		F:GO:0003674; P:GO:0006974; P:GO:0008150; C:GO:0005575		PTHR12175 (PANTHER)
Loa loa	elegans protein partially confirmed by transcript evidence	0		F:GO:0020037; F:GO:0005506; C:GO:0016021; P:GO:0019373; F:GO:0009055; P:GO:0000003; P:GO:0040018; P:GO:0055114; F:GO:0016491; C:GO:0005575; P:GO:0008340; P:GO:0040011; P:GO:0040010; F:GO:0046872; F:GO:0004497		IPR001128; PTHR19383:SF176 (PANTHER)

Caenorhabditis elegans	suppressor of lineage defect family member (sli-1)	7	P:GO:0007166; F:GO:0004871; C:GO:0005634; F:GO:0005509; F:GO:0008270; F:GO:0005515; F:GO:0016874	-		IPR003153; PTHR23007 (PANTHER), PTHR23007:SF4 (PANTHER)
Homo sapiens	pyridoxal ki-se	13	F:GO:0030170; P:GO:0008283; F:GO:0031403; F:GO:0030955; F:GO:0005524; F:GO:0000287; F:GO:0031402; F:GO:0008478; P:GO:0042823; F:GO:0008270; C:GO:0005829; F:GO:0042803; P:GO:0008615	-	EC:2.7.1.35	-
	-	0				-
Brugia malayi	protein ki-se domain containing protein	0		F:GO:0016301; F:GO:0004672; F:GO:0005524; F:GO:0000166; P:GO:0006468; F:GO:0004674		G3DSA:3.10.20.240 (GENE3D), SSF54277 (SUPERFAMILY)
Caenorhabditis briggsae	midasin nuclear aaa atpase	6	P:GO:0043254; P:GO:0006355; F:GO:0005524; F:GO:0016887; F:GO:0008134; C:GO:0005634	-		IPR011704; G3DSA:3.40.50.300 (GENE3D), PTHR22908 (PANTHER), PTHR22908:SF13 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	dead deah box helicase family protein	2	F:GO:0005488; F:GO:0016462	-		-
Drosophila melanogaster	isoform h	9	F:GO:0004872; F:GO:0005247; C:GO:0005902; F:GO:0005515; P:GO:0055085; C:GO:0016021; C:GO:0005626; C:GO:0015629; P:GO:0006821	-		IPR000644; IPR001807; PTHR11689:SF5 (PANTHER), SSF54631 (SUPERFAMILY)
Ailuropoda melanoleuca	transmembrane emp24 protein transport domain containing 9	4	C:GO:0016021; C:GO:0005789; C:GO:0005793; P:GO:0006810	-		IPR000348; IPR015719; PTHR22811 (PANTHER)
Loa loa	myosin xviiia	0		F:GO:0005524; F:GO:0003774; F:GO:0005515; C:GO:0016459		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-

	-	0				-
	-	0				-
Caenorhabditis elegans	expulsion defective family member (aex-3)	11	P:GO:0016192; P:GO:0007618; P:GO:0030421; P:GO:0018991; C:GO:0016021; P:GO:0051726; P:GO:0042981; C:GO:0008021; F:GO:0017112; P:GO:0007269; P:GO:0000187	-		PTHR13008 (PANTHER)
Ancylostoma caninum	venom-allergen-like protein family member (vap-1)	0		F:GO:0009055; P:GO:0019646; P:GO:0040011; C:GO:0005576		-
	-	0				-
Caenorhabditis elegans	cub domain containing protein	0		F:GO:0004872; F:GO:0016787		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	isoform b	1	P:GO:0045454	-		IPR012335; IPR012336; IPR013766; PTHR19991 (PANTHER)
	-	0				-
	-	0				-
Arabidopsis lyrata subsp. lyrata	sy-ptotagmin cytoplasmic r- interacting protein	0		P:GO:0016556; F:GO:0003727; F:GO:0003725; F:GO:0003723; C:GO:0005634; F:GO:0003676; F:GO:0004131; P:GO:0050821; C:GO:0030895; C:GO:0005783; C:GO:0005720; P:GO:0008150; F:GO:0000166; P:GO:0006397; C:GO:0005737; C:GO:0005622; F:GO:0005515; C:GO:0005575; F:GO:0003729		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF41 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		-
	-	0				-
Brugia malayi	expulsion defective family member (exp-2)	5	C:GO:0008076; F:GO:0005249; F:GO:0005515; P:GO:0055085; P:GO:0006813	-		G3DSA:1.10.287.70 (GENE3D), PTHR11537 (PANTHER), PTHR11537:SF50 (PANTHER), SignalP (SIGNALP)

Brugia malayi	gtp-binding protein	15	P:GO:0040010; P:GO:0007446; P:GO:0042594; P:GO:0007264; C:GO:0005622; P:GO:0000003; P:GO:0045727; P:GO:0030307; P:GO:0040011; F:GO:0003924; P:GO:0000082; P:GO:0090070; P:GO:0040015; C:GO:0016020; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				PS51257 (PROFILE), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				IPR012877
	-	0				-
Haemonchus contortus	latrophilin-like protein 2	7	F:GO:0004930; F:GO:0005529; C:GO:0005886; P:GO:0007165; P:GO:0007420; C:GO:0016021; P:GO:0007218	-		IPR000832; IPR017981; PTHR12011 (PANTHER), PTHR12011:SF56 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	23	F:GO:0003700; P:GO:0051049; F:GO:0008289; P:GO:0051649; P:GO:0032787; F:GO:0004872; P:GO:0044283; P:GO:0009653; P:GO:0045941; P:GO:0023033; P:GO:0007165; P:GO:0010565; P:GO:0051128; P:GO:0010033; P:GO:0010646; P:GO:0060341; F:GO:0005515; P:GO:0065008; F:GO:0043565; P:GO:0019216; P:GO:0050732; C:GO:0005634; P:GO:0006355	-		IPR000536; IPR008946; PTHR11865 (PANTHER), PTHR11865:SF218 (PANTHER)
	-	0				SignalP (SIGNALP)

Brugia malayi	p-loop atpase fused to an acetyltransferase	5	P:GO:0009792; P:GO:0040007; P:GO:0040035; P:GO:0002119; P:GO:0040011	-		PTHR10925 (PANTHER), PTHR10925:SF5 (PANTHER)
Caenorhabditis briggsae	n-acetylglucosaminyltransferase v	0				PTHR15075 (PANTHER)
Loa loa	protein phosphatase-5	5	C:GO:0005737; F:GO:0046872; F:GO:0004722; P:GO:0006470; C:GO:0005634	-		IPR004843; IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF12 (PANTHER), SSF56300 (SUPERFAMILY)
Homo sapiens	galactoside- 3 binding protein	9	F:GO:0005044; C:GO:0005615; F:GO:0005515; P:GO:0007155; P:GO:0007165; C:GO:0016020; C:GO:0005634; C:GO:0005578; P:GO:0006968	-		PTHR19331 (PANTHER), PTHR19331:SF8 (PANTHER)
	-	0				-
synthetic construct	jumping translocation breakpoint	2	C:GO:0005887; C:GO:0005624	-		-
Caenorhabditis briggsae	briggsae cbr-dhs-29 protein	5	P:GO:0006694; C:GO:0016021; P:GO:0055114; F:GO:0005488; F:GO:0003854	-	EC:1.1.1.145	SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR001534
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0016972; P:GO:0055114; P:GO:0045454		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	variant sh3 domain containing protein	12	F:GO:0004435; P:GO:0001525; P:GO:0008016; P:GO:0001570; P:GO:0048844; P:GO:0009395; F:GO:0004871; P:GO:0031101; P:GO:0035477; F:GO:0005515; P:GO:0007165; P:GO:0060218	-	EC:3.1.4.11	IPR001192; IPR001711; IPR017946; PTHR10336 (PANTHER), PTHR10336:SF22 (PANTHER)

Caenorhabditis elegans	uncoordi-ted family member (unc-89)	13	P:GO:0003007; F:GO:0005198; P:GO:0014866; F:GO:0004672; P:GO:0016310; P:GO:0006936; C:GO:0031672; F:GO:0008092; C:GO:0031674; P:GO:0048738; P:GO:0050790; C:GO:0044446; C:GO:0005634	-		-
Caenorhabditis briggsae	alanyl-tr- synthetase	4	F:GO:0003676; F:GO:0016876; P:GO:0006412; P:GO:0043039	-	EC:6.1.1.0; EC:3.6.5.3	IPR018163; IPR018164; PTHR11777 (PANTHER)
Brugia malayi	protein-tyrosine phosphatase containing protein	3	F:GO:0004725; P:GO:0006470; F:GO:0008138	-	EC:3.1.3.48	IPR000242; IPR000387; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
	-	0				-
Callithrix jacchus	hematological and neurological expressed 1	0		F:GO:0003674; P:GO:0008150; C:GO:0005575; C:GO:0005634		PTHR21558 (PANTHER), PTHR21558:SF1 (PANTHER)
	-	0				-
Adineta vaga	transposase	0				-
Caenorhabditis elegans	motile sperm domain containing 3	1	F:GO:0005515	-		IPR000535; IPR008962
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; P:GO:0008152; F:GO:0003824		IPR004245; PTHR10974:SF5 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG18218 [Caenorhabditis briggsae]	5	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0040010; P:GO:0006898	-		IPR007015; PTHR13213:SF5 (PANTHER)
	-	0				IPR001820; IPR008993; IPR015613; G3DSA:3.90.370.10 (GENE3D)
	-	0				-
Homo sapiens	guanylate ki-se 1	3	F:GO:0004385; F:GO:0005524; P:GO:0006163	-	EC:2.7.4.8	SignalP (SIGNALP)

Caenorhabditis elegans	myosin type ii heavy	0		P:GO:0007018; C:GO:0005694; C:GO:0005875; F:GO:0005083; C:GO:0005874; P:GO:0023034; F:GO:0000166; F:GO:0005524; P:GO:0009792; F:GO:0003777; P:GO:0051276; C:GO:0016459; F:GO:0003774; F:GO:0005515; F:GO:0046872		PD936484 (PRODOM)
Caenorhabditis elegans	loc398558 protein	5	P:GO:0040035; P:GO:0040027; P:GO:0040010; P:GO:0040019; P:GO:0006898	-		IPR002687; IPR012974; IPR012976; PTHR10894 (PANTHER), SignalP (SIGNALP), SSF89124 (SUPERFAMILY)
Caenorhabditis briggsae	sec14-like protein 2	0		F:GO:0008289; C:GO:0005737; P:GO:0045449; P:GO:0006810; F:GO:0005215; C:GO:0005622; C:GO:0005634		IPR001251; PTHR23324 (PANTHER), PTHR23324:SF6 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F37C4.4 [Caenorhabditis elegans]	3	P:GO:0009792; P:GO:0000003; P:GO:0008340	-		-
	-	0				-
Strongylocentrotus purpuratus	ensangp00000010363	0		F:GO:0003674; C:GO:0005575		PTHR22930 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis briggsae	protein ki-se mu	8	C:GO:0005737; P:GO:0006468; F:GO:0046872; P:GO:0045087; P:GO:0023034; F:GO:0004697; F:GO:0005524; C:GO:0016020	-	EC:2.7.11.13	IPR000719; IPR008271; IPR011009; IPR015727; IPR017442; G3DSA:1.10.510.10 (GENE3D)
	-	0				-
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis briggsae	u5 small nuclear ribonucleoprotein 200 kda helicase	9	P:GO:0018991; C:GO:0005681; F:GO:0008026; P:GO:0040007; P:GO:0008380; F:GO:0003677; F:GO:0005524; P:GO:0002119; P:GO:0009792	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	ankyrin repeat domain 50	3	F:GO:0005515; P:GO:0006974; P:GO:0008340	-		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF269 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	coelomocyte uptake defective family member (cup-5)	0				-
Caenorhabditis elegans	coelomocyte uptake defective family member (cup-5)	3	P:GO:0006874; C:GO:0005764; P:GO:0006914	-		-
Caenorhabditis elegans	coelomocyte uptake defective family member (cup-5)	3	P:GO:0006874; C:GO:0005764; P:GO:0006914	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
Desulfovibrio desulfuricans subsp. desulfuricans str. G20	atp-dependent clp atp-binding subunit	7	F:GO:0008233; P:GO:0044267; F:GO:0046872; F:GO:0016887; F:GO:0005515; F:GO:0000166; C:GO:0005759	-		IPR004487; IPR019489; G3DSA:1.10.8.60 (GENE3D), PTHR11262 (PANTHER)
Brugia malayi	ser thr protein phosphatase family protein	1	F:GO:0004721	-	EC:3.1.3.16	IPR004843; IPR006186; G3DSA:3.60.21.10 (GENE3D), SSF56300 (SUPERFAMILY)
	-	0				-
Pan troglodytes	PREDICTED: hypothetical protein [Pan troglodytes]	0				-
Caenorhabditis elegans	aldehyde dehydroge-se	4	P:GO:0055114; F:GO:0004028; P:GO:0006081; F:GO:0005488	-		IPR015590; IPR016161; IPR016163; PTHR11699:SF46 (PANTHER)
	-	0				-
Brugia malayi	timeless protein	0		F:GO:0046872; F:GO:0008270; F:GO:0005515; F:GO:0003677		IPR007725; PTHR22940 (PANTHER), PTHR22940:SF6 (PANTHER)
Caenorhabditis briggsae	sig-l peptide peptidase family protein	4	P:GO:0040008; P:GO:0000003; C:GO:0044425; P:GO:0007275	-		IPR007369; PTHR12174:SF4 (PANTHER)
Caenorhabditis briggsae	sig-l peptide peptidase family protein	4	P:GO:0040008; P:GO:0000003; C:GO:0044425; P:GO:0007275	-		IPR007369; PTHR12174:SF4 (PANTHER)
	-	0				SignalP (SIGNALP)

	-	0				-
Caenorhabditis elegans	eif4e binding protein	7	P:GO:0006629; P:GO:0040010; C:GO:0043005; P:GO:0010468; P:GO:0000003; P:GO:0006898; C:GO:0044424	-		IPR007146; PTHR13237 (PANTHER), PTHR13237:SF3 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-inft-1 protein	1	F:GO:0005488	-		IPR015425; PTHR23213 (PANTHER), PTHR23213:SF18 (PANTHER)
Mus musculus	eukaryotic translation initiation factor isoform cra_i	5	P:GO:0006412; C:GO:0005737; P:GO:0006915; P:GO:0048522; C:GO:0005634	-	EC:3.6.5.3	-
	-	0				-
	-	0				-
Homo sapiens	immunoglobulin j chain	3	C:GO:0005576; F:GO:0003823; P:GO:0006959	-		PD021296 (PRODOM)
Caenorhabditis briggsae	sarcolemmal membrane-associated protein	2	C:GO:0044444; C:GO:0043229	-		-
Caenorhabditis briggsae	sarcolemmal membrane-associated protein	2	C:GO:0044444; C:GO:0043229	-		-
Brugia malayi	myotubularin-related family protein	0		P:GO:0016311; F:GO:0016791		PTHR10807 (PANTHER), PTHR10807:SF4 (PANTHER)
	-	0				-
Branchiostoma floridae	domain-containing histone demethylation protein 1d	14	N:GO:0035575; F:GO:0051864; F:GO:0008270; F:GO:0032454; F:GO:0035064; F:GO:0071558; P:GO:0071557; P:GO:0030901; N:GO:0035574; P:GO:0033169; P:GO:0070544; P:GO:0045893; F:GO:0005506; C:GO:0005634	-	EC:1.14.11.27	IPR001965; IPR011011; IPR013083; IPR019787; PTHR23123 (PANTHER)
	-	0				-
Caenorhabditis briggsae	in family member (ttn-1)	0		F:GO:0005524; F:GO:0004672; P:GO:0006468; P:GO:0009792		IPR013783; PTHR19900 (PANTHER), PTHR19900:SF1 (PANTHER)
	-	0				-
Caenorhabditis elegans	hypothetical transporter	4	P:GO:0055085; P:GO:0040011; C:GO:0016021; P:GO:0007413	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Loa loa	af326938_1 xg314	0				-

	-	0				-
Camponotus floridanus	myosin light chain	0		F:GO:0017022; F:GO:0005509; F:GO:0032036; F:GO:0008092; C:GO:0016461; F:GO:0042623; C:GO:0016459		IPR011992; IPR018249; PTHR23048 (PANTHER), SSF47473 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				IPR001289; PTHR12632:SF6 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	wd repeat domain 24	0		F:GO:0003674; P:GO:0008150		-
	-	0				-
	-	0				-
Loa loa	briggsae cbr-wts-1 protein	2	F:GO:0016301; F:GO:0005515	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	transmembrane 9 superfamily protein member 3	1	C:GO:0016021	-		-
Brugia malayi	serine arginine repetitive matrix protein 1	8	F:GO:0003677; C:GO:0005681; F:GO:0003723; F:GO:0005515; P:GO:0000375; C:GO:0016607; P:GO:0006397; C:GO:0016363	-		IPR002483; G3DSA:1.20.1390.10 (GENE3D), PTHR23148 (PANTHER), SSF101233 (SUPERFAMILY)

Homo sapiens	achain structural basis of pp2a and sgo interaction	27	P:GO:0006275; C:GO:0016020; P:GO:0006672; C:GO:0000159; P:GO:0006461; F:GO:0003823; P:GO:0010033; C:GO:0015630; P:GO:0042518; P:GO:0030155; C:GO:0005829; F:GO:0046982; P:GO:0030111; C:GO:0000775; P:GO:0008380; P:GO:0006917; P:GO:0030308; P:GO:0007059; P:GO:0000188; P:GO:0045595; F:GO:0008601; P:GO:0006470; P:GO:0045449; P:GO:0019932; C:GO:0005625; C:GO:0005634; C:GO:0005739	-		-
Hydra magnipapillata	low quality protein: protein mon2 homolog	2	P:GO:0015031; F:GO:0005488	-		-
Caenorhabditis sp. PS1010	elegans protein confirmed by transcript evidence	3	P:GO:0009792; P:GO:0040010; P:GO:0040011	-		IPR000504; IPR002343; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF36 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis sp. PS1010	elegans protein partially confirmed by transcript evidence	3	P:GO:0009792; P:GO:0040010; P:GO:0040011	-		IPR000504; IPR002343; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF36 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis sp. PS1010	elegans protein partially confirmed by transcript evidence	3	P:GO:0009792; P:GO:0040010; P:GO:0040011	-		IPR000504; IPR002343; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF36 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Loa loa	tb2 hva22 family protein	0		F:GO:0004872		IPR004345; PTHR12300:SF13 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	P:GO:0006810	-		IPR013099; G3DSA:1.10.287.70 (GENE3D), PTHR11003 (PANTHER), PTHR11003:SF7 (PANTHER), SignalP (SIGNALP), SSF81324 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-apt-10 protein	0		C:GO:0030131; P:GO:0016192; P:GO:0006886; P:GO:0006897; F:GO:0005515		-
	-	0				-

Caenorhabditis briggsae	Hypothetical protein CBG02628 [Caenorhabditis briggsae]	0		F:GO:0016740; F:GO:0004674; F:GO:0004672; P:GO:0006468; F:GO:0000166; F:GO:0005524; F:GO:0016301; F:GO:0004713; F:GO:0005515		SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-ccb-1 protein	12	C:GO:0030315; C:GO:0016529; P:GO:0070588; P:GO:0070978; F:GO:0004872; F:GO:0015270; P:GO:0006612; F:GO:0005515; C:GO:0005891; P:GO:0006936; P:GO:0051925; F:GO:0008331	-		IPR000584; IPR008144; G3DSA:3.40.50.300 (GENE3D), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
Homo sapiens	granulin	8	C:GO:0005615; P:GO:0050679; F:GO:0008083; F:GO:0005125; P:GO:0007165; C:GO:0005739; P:GO:0007566; P:GO:0001835	-		PTHR12274 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Haemonchus contortus	superoxide dismutase	13	F:GO:0005507; P:GO:0008340; P:GO:0010038; F:GO:0008270; C:GO:0005739; P:GO:0060378; P:GO:0055114; F:GO:0004784; C:GO:0005615; P:GO:0009410; F:GO:0042803; P:GO:0019430; P:GO:0051597	-	EC:1.15.1.1	IPR001424; IPR018152; PTHR10003:SF12 (PANTHER), SignalP (SIGNALP)
	-	0				-
Gallus gallus	sy-ptotagmin-like 1	3	C:GO:0005886; F:GO:0005515; P:GO:0006887	-		IPR000008; IPR008973; IPR018029; G3DSA:2.60.40.150 (GENE3D), PTHR10024 (PANTHER)
	-	0				-
Homo sapiens	estradiol-specific single chain antibody fragment	0				IPR013106; IPR013783; PTHR23267 (PANTHER), PTHR23267:SF14 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-

	-	0				-
Caenorhabditis briggsae	d- polymerase i family protein	7	F:GO:0005488; P:GO:0030421; P:GO:0008340; P:GO:0006264; F:GO:0016791; F:GO:0016740; P:GO:0008406	-	EC:3.1.3.0	IPR001098; IPR002297; IPR019760; G3DSA:1.10.150.20 (GENE3D), SSF56672 (SUPERFAMILY)
	-	0				-
Brugia malayi	yhb8_caeel ame: full=uncharacterized protein flags: precursor	0				-
	-	0				-
Caenorhabditis elegans	protein-tyrosine phosphatase containing protein	1	F:GO:0004721	-	EC:3.1.3.16	IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	amiloride-sensitive sodium channel family protein	4	P:GO:0006811; C:GO:0016020; F:GO:0005216; P:GO:0007413	-		IPR001873; G3DSA:1.10.287.820 (GENE3D), PTHR11690:SF11 (PANTHER)
	-	0				-
Caenorhabditis elegans	serine threonine protein rio1 family	0		P:GO:0006468; C:GO:0005634; C:GO:0005694; F:GO:0005524; F:GO:0016301; C:GO:0016020; F:GO:0004674; P:GO:0006350; F:GO:0004672; F:GO:0008772; F:GO:0016791; F:GO:0003824; F:GO:0000166; C:GO:0005737; C:GO:0000781; P:GO:0045449; F:GO:0016773; F:GO:0004713; F:GO:0016740; P:GO:0006006; P:GO:0009103		IPR008266; G3DSA:1.10.510.10 (GENE3D), PTHR12209 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	P:GO:0006541; F:GO:0004359; F:GO:0005515; C:GO:0005759	-	EC:3.5.1.2	IPR002110; IPR015868; IPR020683; PTHR12544:SF3 (PANTHER)

Callithrix jacchus	vimentin	12	F:GO:0005200; P:GO:0006928; C:GO:0005886; C:GO:0031252; C:GO:0030424; C:GO:0016363; C:GO:0045098; P:GO:0045103; F:GO:0019901; F:GO:0008022; C:GO:0005829; P:GO:0044419	-		IPR001664; IPR006821; IPR016044; PTHR23239:SF27 (PANTHER)
Caenorhabditis elegans	briggsae cbr-gck-2 protein	4	P:GO:0006468; F:GO:0005083; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF75 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-cdh-12 protein	2	C:GO:0016020; P:GO:0007155	-		-
Ancylostoma ceylanicum	venom-allergen-like protein family member (vap-1)	1	P:GO:0040011	-		IPR001283; IPR014044; IPR018244; PTHR10334:SF11 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	mothers against decapentaplegic homolog 5	22	P:GO:0001525; P:GO:0009880; P:GO:0006468; P:GO:0007179; P:GO:0060048; P:GO:0001657; C:GO:0016021; C:GO:0005829; F:GO:0016563; C:GO:0005667; F:GO:0031625; P:GO:0007165; P:GO:0030218; P:GO:0007281; F:GO:0003700; P:GO:0002051; P:GO:0045944; F:GO:0030618; P:GO:0071407; P:GO:0045669; P:GO:0030509; P:GO:0001880	-		IPR001132; IPR008984; IPR013790; IPR017855; PTHR13703:SF19 (PANTHER)
	-	0				-
Homo sapiens	immunoglobulin heavy chain variable region	0				IPR013783; PTHR23266 (PANTHER), PTHR23266:SF7 (PANTHER), SignalP (SIGNALP), SSF48726 (SUPERFAMILY)
	-	0				-
Ixodes scapularis	rolling pebbles	0		F:GO:0046872; P:GO:0055114; F:GO:0005488; F:GO:0016491; F:GO:0008270; F:GO:0032440; F:GO:0005515		SignalP (SIGNALP)

Caenorhabditis elegans	integrin-linked ki-se	13	P:GO:0007016; F:GO:0004674; P:GO:0007229; P:GO:0007160; F:GO:0005524; C:GO:0005925; F:GO:0005515; P:GO:0009966; P:GO:0007475; P:GO:0016203; F:GO:0004623; F:GO:0004715; P:GO:0006468	-	EC:2.7.11.0; EC:3.1.1.4; EC:2.7.10.2	IPR000719; IPR001245; IPR011009; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR23257 (PANTHER), PTHR23257:SF30 (PANTHER)
Caenorhabditis elegans	60kd inner membrane protein	2	C:GO:0016020; C:GO:0005739	-		IPR001708; PTHR12428:SF3 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	protein ki-se domain containing protein	1	F:GO:0000166	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
Brugia malayi	lobulin-like cell adhesion molecule family member (igcm-3)	1	P:GO:0019915	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	uncoordi-ted family member (unc-62)	6	P:GO:0001654; P:GO:0045944; F:GO:0043565; F:GO:0005515; F:GO:0003700; C:GO:0005634	-		PTHR11850 (PANTHER), PTHR11850:SF8 (PANTHER)
Caenorhabditis elegans	tnni3 interacting ki-se	8	C:GO:0005737; P:GO:0006468; F:GO:0046872; F:GO:0005524; F:GO:0008022; C:GO:0005634; F:GO:0004674; F:GO:0031013	-	EC:2.7.11.0	IPR000719; IPR001245; IPR011009; G3DSA:1.10.510.10 (GENE3D), PTHR23257 (PANTHER), PTHR23257:SF63 (PANTHER)
Caenorhabditis briggsae	vacuolar membrane protein pep11	8	P:GO:0009792; P:GO:0010171; F:GO:0005488; P:GO:0040018; P:GO:0018996; P:GO:0040010; P:GO:0000003; P:GO:0008219	-		PTHR23323 (PANTHER), PTHR23323:SF24 (PANTHER), PF00637 (PFAM)
Caenorhabditis briggsae	tyrosine-protein phosphatase non-receptor type 4	8	C:GO:0005737; F:GO:0004725; C:GO:0005856; F:GO:0004872; C:GO:0019898; F:GO:0050254; F:GO:0008092; P:GO:0006470	-	EC:3.1.3.48; EC:2.7.11.14	-
Caenorhabditis elegans	flavin containing monooxyge-se 5	6	C:GO:0005789; F:GO:0004497; C:GO:0031224; F:GO:0050662; P:GO:0008152; F:GO:0000166	-		IPR002257; IPR020946; G3DSA:3.50.50.60 (GENE3D), PTHR23023 (PANTHER), PTHR23023:SF4 (PANTHER), SSF51905 (SUPERFAMILY)

Pan troglodytes	brain protein i3	9	P:GO:0012502; C:GO:0005765; C:GO:0016021; F:GO:0001540; C:GO:0005624; F:GO:0005524; C:GO:0048471; P:GO:0010977; C:GO:0005794	-		-
Caenorhabditis elegans	hypothetical protein Y23B4A.2 [Caenorhabditis elegans]	0		P:GO:0007218		SignalP (SIGNALP)
Caenorhabditis elegans	Hypothetical protein T07H6.4 [Caenorhabditis elegans]	0		F:GO:0030414; C:GO:0005576		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				IPR004988
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F09E10.7 [Caenorhabditis elegans]	0				-
	-	0				-
Caenorhabditis elegans	cation chloride cotransporter	2	P:GO:0055085; C:GO:0016021	-		IPR004841; PTHR11827 (PANTHER), PTHR11827:SF6 (PANTHER)
Caenorhabditis elegans	cation chloride cotransporter	2	P:GO:0055085; C:GO:0016021	-		IPR004841; PTHR11827 (PANTHER), PTHR11827:SF6 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	solute carrier organic anion transporter member 1c1-like	3	P:GO:0055085; C:GO:0016021; F:GO:0005215	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-btf-1 protein	3	F:GO:0005524; F:GO:0004386; F:GO:0003677	-		IPR000330; PTHR10799 (PANTHER), PTHR10799:SF72 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Callithrix jacchus	mitochondrial ribosomal protein s21	4	C:GO:0005763; C:GO:0005743; F:GO:0003735; P:GO:0006412	-	EC:3.6.5.3	-
Caenorhabditis elegans	carbonic anhydrase mitochondrial	1	F:GO:0016829	-		IPR001148; IPR018338; PTHR18952:SF34 (PANTHER)
Pongo abelii	n-methylpurine-d- glycosylase	6	F:GO:0003684; P:GO:0006307; P:GO:0045007; F:GO:0042802; F:GO:0003905; C:GO:0005654	-	EC:3.2.2.21	IPR003180; IPR011034
	-	0				-
Loa loa	organic cation transporter	4	P:GO:0006915; C:GO:0016021; F:GO:0015101; P:GO:0006810	-		PTHR11600 (PANTHER), PTHR11600:SF35 (PANTHER), SignalP (SIGNALP)
	-	0				IPR017452; G3DSA:1.20.1070.10 (GENE3D), PTHR22751 (PANTHER), PTHR22751:SF8 (PANTHER), SignalP (SIGNALP)

Caenorhabditis briggsae	ribosomal protein l4	4	C:GO:0005840; F:GO:0003735; P:GO:0006412; F:GO:0005515	-	EC:3.6.5.3	-
	-	0				-
	-	0				-
Caenorhabditis briggsae	zinc finger protein	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		-
	-	0				-
	-	0				-
Brugia malayi	squamous cell carcinoma antigen recognized by t-cells 3	9	P:GO:0040010; F:GO:0005488; P:GO:0008340; P:GO:0000910; P:GO:0018991; P:GO:0002119; P:GO:0040011; P:GO:0006898; P:GO:0009792	-		IPR000504; IPR003107; IPR012677; PTHR23269 (PANTHER), SSF54928 (SUPERFAMILY)
Brugia malayi	squamous cell carcinoma antigen recognized by t-cells 3	9	P:GO:0040010; F:GO:0005488; P:GO:0008340; P:GO:0000910; P:GO:0018991; P:GO:0002119; P:GO:0040011; P:GO:0006898; P:GO:0009792	-		IPR000504; IPR003107; IPR012677; PTHR23269 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	atp-dependent d- helicase recq	7	F:GO:0043140; P:GO:0006260; F:GO:0003676; C:GO:0005622; F:GO:0005524; P:GO:0006310; P:GO:0006281	-		IPR004589; G3DSA:3.40.50.300 (GENE3D), PTHR13710:SF14 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Homo sapiens	tyrosine ki-se binding protein	7	F:GO:0005057; C:GO:0005887; P:GO:0023034; F:GO:0016301; F:GO:0005515; P:GO:0007165; P:GO:0006968	-		-
Caenorhabditis elegans	spermidine synthase	1	F:GO:0016740	-		IPR001045; G3DSA:3.40.50.150 (GENE3D), PTHR11558:SF11 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				IPR017907
	-	0				-

Caenorhabditis elegans	filamin abp280 repeat family protein	7	P:GO:0009792; P:GO:0010171; C:GO:0005840; F:GO:0003735; P:GO:0007126; P:GO:0000003; P:GO:0006412	-	EC:3.6.5.3	IPR001298; IPR013783; IPR014756; IPR017868; PTHR11915 (PANTHER), PTHR11915:SF24 (PANTHER)
Caenorhabditis elegans	elegans fln-1 isoform partially confirmed by transcript evidence	4	P:GO:0051179; P:GO:0007293; P:GO:0048610; P:GO:0030725	-		IPR001298; IPR013783; IPR014756; IPR017868; PTHR11915 (PANTHER), PTHR11915:SF24 (PANTHER)
Caenorhabditis elegans	elegans fln-1 isoform partially confirmed by transcript evidence	10	C:GO:0005840; P:GO:0006412; P:GO:0048610; P:GO:0051179; P:GO:0009792; P:GO:0007126; F:GO:0003735; P:GO:0010171; P:GO:0007293; P:GO:0030725	-	EC:3.6.5.3	IPR001298; IPR013783; IPR014756; IPR017868; PTHR11915 (PANTHER), PTHR11915:SF24 (PANTHER)
Caenorhabditis elegans	mitochondrial chaperone bcs1	8	P:GO:0040010; P:GO:0000003; P:GO:0002119; F:GO:0000166; P:GO:0033108; P:GO:0006898; P:GO:0009792; C:GO:0044464	-		PTHR23070 (PANTHER), PTHR23070:SF2 (PANTHER)
	-	0				-
Caenorhabditis elegans	fanci (fanconi anemia complex component i) homolog family member (fnci-1)	0				-
Caenorhabditis briggsae	mitochondrial folate transporter carrier	7	F:GO:0005488; C:GO:0005743; P:GO:0055085; P:GO:0040010; P:GO:0008340; C:GO:0016021; F:GO:0005215	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF73 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	ef hand family protein	2	P:GO:0009792; F:GO:0005509	-		IPR018247; PTHR23104 (PANTHER)
Caenorhabditis briggsae	phospholipid-transporting atpase 1 (aminophospholipid flippase 1)	7	C:GO:0016021; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0015914; F:GO:0000287; F:GO:0004012	-	EC:3.6.3.1	IPR001757; IPR005834; IPR006539; IPR018303; G3DSA:3.40.1110.10 (GENE3D), G3DSA:3.40.50.1000 (GENE3D), PTHR11939:SF18 (PANTHER), SignalP (SIGNALP), SSF56784 (SUPERFAMILY), SSF81660 (SUPERFAMILY), SSF81665 (SUPERFAMILY)

Caenorhabditis briggsae	phospholipid-transporting atpase 1 (aminophospholipid flippase 1)	7	C:GO:0016021; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0015914; F:GO:0000287; F:GO:0004012	-	EC:3.6.3.1	IPR001757; IPR005834; IPR006539; IPR018303; G3DSA:3.40.1110.10 (GENE3D), G3DSA:3.40.50.1000 (GENE3D), PTHR11939:SF18 (PANTHER), SignalP (SIGNALP), SSF56784 (SUPERFAMILY), SSF81660 (SUPERFAMILY), SSF81665 (SUPERFAMILY)
Caenorhabditis elegans	uncoordi-ted family member (unc-53)	0		P:GO:0007049		PTHR12784 (PANTHER), PTHR12784:SF1 (PANTHER)
Caenorhabditis elegans	uncoordi-ted family member (unc-53)	0		F:GO:0004386; C:GO:0005634; F:GO:0016787; F:GO:0000166; F:GO:0017111; F:GO:0005524; C:GO:0005730; P:GO:0007399; P:GO:0007049		IPR003593; IPR003959; G3DSA:3.40.50.300 (GENE3D), PTHR12784 (PANTHER), PTHR12784:SF1 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	uncoordi-ted family member (unc-53)	0		F:GO:0004386; C:GO:0005634; F:GO:0016787; F:GO:0000166; F:GO:0017111; F:GO:0005524; C:GO:0005730; P:GO:0007399; P:GO:0007049		IPR003593; IPR003959; G3DSA:3.40.50.300 (GENE3D), PTHR12784 (PANTHER), PTHR12784:SF1 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	uncoordi-ted family member (unc-53)	0		P:GO:0007049		PTHR12784 (PANTHER), PTHR12784:SF1 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	voltage gated chloride channel family protein	6	P:GO:0009792; F:GO:0005247; P:GO:0055085; P:GO:0000003; C:GO:0016021; P:GO:0006821	-		IPR001807; PTHR11689:SF5 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	hypothetical tyrosi-se-like protein in chromosome	1	F:GO:0005488	-		-
Homo sapiens	legumain	7	C:GO:0005770; P:GO:0040015; C:GO:0005764; C:GO:0045177; F:GO:0004197; P:GO:0006508; F:GO:0004674	-	EC:3.4.22.0; EC:2.7.11.0	IPR001096; PTHR12000:SF3 (PANTHER)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG24703 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)
	-	0				IPR000953; IPR016197; G3DSA:2.40.50.40 (GENE3D)

Macaca mulatta	biogenesis of lysosomal organelles complex- subunit 1	7	P:GO:0006892; P:GO:0016044; F:GO:0005515; P:GO:0060155; P:GO:0032438; C:GO:0031083; C:GO:0005739	-		IPR009395; PTHR13073 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-rpm-1 protein	0		F:GO:0046872; P:GO:0030071; C:GO:0005680; F:GO:0008270; F:GO:0005515; C:GO:0005622		PTHR12846 (PANTHER), PTHR12846:SF2 (PANTHER)
Caenorhabditis elegans	utp21 specific wd40 associated domain containing protein	0		C:GO:0032040; P:GO:0006364		-
Caenorhabditis briggsae	briggsae cbr-bub-1 protein	11	P:GO:0000910; P:GO:0010564; P:GO:0040035; F:GO:0016740; C:GO:0000776; P:GO:0002119; F:GO:0005515; P:GO:0040011; C:GO:0000779; P:GO:0002009; P:GO:0009792	-		IPR000719; IPR011009; IPR015661; IPR017442; G3DSA:1.10.510.10 (GENE3D), SignalP (SIGNALP)
Caenorhabditis elegans	atp-dependent transporter	2	F:GO:0016887; F:GO:0000166	-		-
Homo sapiens	mhc class i antigen	7	P:GO:0006955; F:GO:0032393; C:GO:0005576; P:GO:0044419; C:GO:0005887; P:GO:0002474; C:GO:0042612	-		-
Caenorhabditis briggsae	rrp1_caeel ame: full=ribosomal r- processing protein 1 homolog ame: full=rrp1-like protein	5	P:GO:0009792; P:GO:0002119; P:GO:0040010; P:GO:0000003; P:GO:0006898	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-

Harpegnathos saltator	ras-like gtp-binding protein rho1	45	C:GO:0005856; F:GO:0005525; P:GO:0045665; P:GO:0050771; P:GO:0030838; P:GO:0043123; P:GO:0006357; P:GO:0030521; P:GO:0007160; F:GO:0017022; P:GO:0045727; P:GO:0050773; C:GO:0005625; P:GO:0009749; P:GO:0009612; P:GO:0042346; P:GO:0051384; P:GO:0050772; P:GO:0045785; P:GO:0043524; P:GO:0033144; P:GO:0045471; P:GO:0043525; C:GO:0030424; P:GO:0043124; P:GO:0001666; P:GO:0043280; P:GO:0043200;	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	r- polymerase i large subunit	2	F:GO:0005488; F:GO:0016779	-	EC:2.7.7.0	IPR007081; IPR015699; PTHR19376 (PANTHER), SSF64484 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Brugia malayi	ankyrin repeat and zinc finger domain-containing protein 1	0		F:GO:0046872; P:GO:0008150; F:GO:0008270; C:GO:0005622		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF206 (PANTHER)
Brugia malayi	f-box domain containing protein	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	cation transport regulator homolog 2 (coli)	0		P:GO:0006915; F:GO:0003674; C:GO:0005737; P:GO:0008150		-

Ectocarpus siliculosus	regulator of nonsense transcripts 1	16	P:GO:0000184; C:GO:0000785; F:GO:0005515; F:GO:0000166; P:GO:0006406; P:GO:0006449; C:GO:0005737; F:GO:0046872; P:GO:0009790; F:GO:0003723; F:GO:0003682; F:GO:0004004; P:GO:0071044; P:GO:0006260; P:GO:0007049; P:GO:0006281	-		PTHR10887 (PANTHER)
	-	0				-
Caenorhabditis briggsae	abelson interacting isoform a	5	P:GO:0030030; F:GO:0005515; P:GO:0048513; C:GO:0044464; N:GO:0071842	-		-
	-	0				-
Sus scrofa	protein disulfide isomerase family member 3	11	F:GO:0004629; F:GO:0003756; P:GO:0043065; P:GO:0006606; P:GO:0045454; F:GO:0004197; C:GO:0042470; C:GO:0005788; F:GO:0005515; P:GO:0007165; P:GO:0006621	-	EC:5.3.4.1; EC:3.4.22.0	IPR012336; PTHR18929 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	phenylalanine hydroxylase	14	P:GO:0006979; P:GO:0008340; P:GO:0040002; P:GO:0055114; P:GO:0042438; P:GO:0006559; P:GO:0000003; F:GO:0004510; F:GO:0005515; P:GO:0006569; F:GO:0016597; P:GO:0009792; F:GO:0004505; F:GO:0005506	-	EC:1.14.16.4 ; EC:1.14.16.1	IPR001273; IPR019774; PS51410 (PROFILE)
Loa loa	briggsae cbr-dys-1 protein	2	P:GO:0065007; P:GO:0009987	-		-
	-	0				-

Loa loa	bone morphogenetic protein receptor 1	18	P:GO:0007411; F:GO:0048185; P:GO:0006468; P:GO:0016319; P:GO:0007179; P:GO:0040018; F:GO:0004703; P:GO:0048813; P:GO:0007405; P:GO:0009411; F:GO:0016361; P:GO:0007165; P:GO:0007455; C:GO:0048179; P:GO:0007346; P:GO:0032924; F:GO:0005524; P:GO:0007476	-	EC:2.7.11.16	IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR23255 (PANTHER), PTHR23255:SF14 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	cytochrome b5 reductase 4	5	P:GO:0065008; F:GO:0016651; F:GO:0046872; C:GO:0044444; P:GO:0044237	-		IPR001199; PTHR19370 (PANTHER), PTHR19370:SF1 (PANTHER)
Xenopus (Silurana) tropicalis	-scent polypeptide-associated complex alpha subunit	12	P:GO:0006412; C:GO:0016459; F:GO:0003677; F:GO:0005524; F:GO:0003774; F:GO:0017025; C:GO:0005854; P:GO:0044419; F:GO:0003713; P:GO:0015031; C:GO:0005634; P:GO:0045941	-	EC:3.6.5.3	IPR000449
	-	0				-
Caenorhabditis briggsae	briggsae cbr-ocrl-1 protein	0		P:GO:0000003; P:GO:0040013; P:GO:0007165; F:GO:0004437; C:GO:0005622		G3DSA:3.60.10.10 (GENE3D), PTHR11200 (PANTHER), PTHR11200:SF26 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	p21-activated pak	2	F:GO:0004672; F:GO:0000166	-		-
Caenorhabditis elegans	yc27b_caeel ame: full=ig-like and fibronectin type-iii domain-containing protein flags: precursor	0				IPR007110; IPR013783
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	gtpase activating protein and vps9 domains 1	0		F:GO:0005096; P:GO:0051056; P:GO:0007165; C:GO:0005622		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-

	-	0				-
	-	0				SignalP (SIGNALP)
Pongo abelii	proteasome (macropain) alpha 6	9	F:GO:0003723; C:GO:0005739; P:GO:0051436; P:GO:0051437; F:GO:0004298; P:GO:0031145; F:GO:0005515; C:GO:0019773; C:GO:0005634	-	EC:3.4.25.0	IPR001353; G3DSA:3.60.20.10 (GENE3D), PTHR11599 (PANTHER), PTHR11599:SF11 (PANTHER), PS51475 (PROFILE), SSF56235 (SUPERFAMILY)
Harpegnathos saltator	methyltransferase-like protein 13	1	F:GO:0003824	-		G3DSA:3.40.50.150 (GENE3D), PTHR12176 (PANTHER), SSF53335 (SUPERFAMILY)
Ascaris suum	msp domain protein	1	P:GO:0040011	-		IPR000535; IPR008962; PTHR22947 (PANTHER)
Caenorhabditis elegans	hypothetical protein K11H12.9 [Caenorhabditis elegans]	0				IPR000719; IPR011009; G3DSA:1.10.510.10 (GENE3D)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; C:GO:0016020; P:GO:0055085; P:GO:0006810		-
Caenorhabditis elegans	eb module family protein	2	F:GO:0005488; F:GO:0003824	-		IPR000742; IPR006149; IPR006210; IPR013032; PTHR11201 (PANTHER), PTHR11201:SF128 (PANTHER)
Caenorhabditis elegans	immunoglobulin i-set domain containing protein	9	P:GO:0021940; P:GO:0060749; C:GO:0005615; P:GO:0000186; P:GO:0050730; P:GO:0048754; P:GO:0007173; C:GO:0005886; F:GO:0005154	-		SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	P:GO:0044237; F:GO:0016740; P:GO:0044238	-		IPR002213; PTHR11926:SF3 (PANTHER)
	-	0				-
Caenorhabditis briggsae	laminin gamma-1	0		F:GO:0016740; F:GO:0004714; P:GO:0007155; C:GO:0005578; C:GO:0031012		IPR002049; IPR013032; G3DSA:2.10.25.10 (GENE3D), PTHR10574 (PANTHER), PTHR10574:SF12 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	briggsae cbr-toh-1 protein	3	F:GO:0004222; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	-
	-	0				-
Caenorhabditis briggsae	glucose inhibited division protein a	1	P:GO:0008152	-		PTHR11806 (PANTHER)
	-	0				-
Loa loa	dolichyl pyrophosphate glc1man9 c2 alpha- -glucosyltransferase	2	C:GO:0044464; F:GO:0003824	-		IPR004856; SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-flp-13 protein	3	C:GO:0005576; P:GO:0007218; P:GO:0019915	-		IPR002544
Caenorhabditis elegans	preli domain containing 1	2	C:GO:0005730; C:GO:0005739	-		SignalP (SIGNALP)

Caenorhabditis elegans	d- polymerase epsilon catalytic subunit	17	F:GO:0008270; F:GO:0003887; P:GO:0006260; P:GO:0040035; P:GO:0006297; F:GO:0003677; P:GO:0000731; F:GO:0005515; F:GO:0000166; P:GO:0040011; P:GO:0006997; P:GO:0000082; F:GO:0004527; C:GO:0005654; P:GO:0002009; P:GO:0009792; F:GO:0003682	-	EC:2.7.7.7	PTHR10670 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0005525; P:GO:0007264; F:GO:0000166; C:GO:0005622; P:GO:0015031		IPR013684; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF228 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein T08B1.1 [Caenorhabditis elegans]	6	C:GO:0016021; P:GO:0009792; P:GO:0040010; P:GO:0055085; F:GO:0005215; P:GO:0002119	-		-
	-	0				-
Brugia malayi	hypothetical protein Bm1_20905 [Brugia malayi]	0		F:GO:0005488		-
Caenorhabditis elegans	metallophosphoesterase domain-containing	1	F:GO:0016787	-		PTHR12905 (PANTHER), SSF56300 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	fyve zinc finger family protein	9	P:GO:0046488; P:GO:0023034; F:GO:0005515; F:GO:0005524; P:GO:0044267; C:GO:0016020; F:GO:0008270; F:GO:0016307; C:GO:0048471	-		IPR000306; IPR011011; IPR013083; IPR017455; PTHR22835 (PANTHER), PTHR22835:SF42 (PANTHER)
Caenorhabditis elegans	yc91_caeel ame: full=uncharacterized mfs-type transporter	2	P:GO:0040011; P:GO:0007413	-		SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-rab-39 protein	3	P:GO:0015031; F:GO:0005525; P:GO:0007264	-		G3DSA:3.40.50.300 (GENE3D)
	-	0				-

Caenorhabditis briggsae	alpha 2 (congenital muscular dystrophy)	8	P:GO:0035141; P:GO:0008104; P:GO:0007517; P:GO:0016337; P:GO:0035138; P:GO:0050794; C:GO:0005604; F:GO:0005198	-		IPR002049; G3DSA:2.10.25.10 (GENE3D), PTHR10574 (PANTHER), PTHR10574:SF56 (PANTHER), SSF57196 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	fyve finger-containing phosphoinositide	4	F:GO:0005488; F:GO:0016740; C:GO:0016020; C:GO:0048471	-		-
Caenorhabditis briggsae	egg laying defective family member (egl-15)	0		F:GO:0016740; C:GO:0016021; C:GO:0016020; F:GO:0004672; P:GO:0006468; F:GO:0000166; F:GO:0005524; F:GO:0016301; F:GO:0004713; F:GO:0004872; F:GO:0005515		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR009673; SignalP (SIGNALP)
	-	0				-
	-	0				PTHR22986 (PANTHER), PTHR22986:SF27 (PANTHER)
Caenorhabditis elegans	hypothetical protein F46E10.11 [Caenorhabditis elegans]	0		P:GO:0040011; P:GO:0002119		-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0032313; C:GO:0005622; F:GO:0005097		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG12930 [Caenorhabditis briggsae]	0				-
	-	0				-
Loa loa	elegans protein partially confirmed by transcript evidence	7	F:GO:0043565; P:GO:0031643; F:GO:0003700; P:GO:0045893; P:GO:0022010; C:GO:0016020; C:GO:0005634	-		IPR007888; G3DSA:2.60.40.1390 (GENE3D), PTHR13029 (PANTHER), PTHR13029:SF7 (PANTHER)
Brugia malayi	hypothetical protein Bm1_05520 [Brugia malayi]	0				-

Camponotus floridanus	serine arginine repetitive matrix 2	0		F:GO:0004180; P:GO:0008284; P:GO:0007000; F:GO:0003674; F:GO:0005198; P:GO:0042306; F:GO:0003700; C:GO:0015030; P:GO:0008150; P:GO:0033979; P:GO:0006397; F:GO:0034513; F:GO:0005488; F:GO:0034512; P:GO:0045941; P:GO:0008380; F:GO:0008139; C:GO:0030532; C:GO:0005730; C:GO:0005654; F:GO:0005515; C:GO:0005681; C:GO:0005575		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG20503 [Caenorhabditis briggsae]	0				-
	-	0				-
	-	0				-
	-	0				-
Loa loa	cbp p300 homolog family member (cbp-1)	37	P:GO:0022603; P:GO:0051649; P:GO:0032989; C:GO:0043234; F:GO:0005102; P:GO:0007283; P:GO:0018076; P:GO:0040039; F:GO:0008013; P:GO:0040010; P:GO:0001666; P:GO:0032270; F:GO:0003713; P:GO:0045944; P:GO:0043967; C:GO:0005737; P:GO:0040026; P:GO:0007399; P:GO:0048646; P:GO:0009792; F:GO:0008270; P:GO:0060341; F:GO:0003677; P:GO:0010038; N:GO:0071844; P:GO:0048545; P:GO:0018996;	-	EC:2.3.1.48	PTHR13808 (PANTHER)

Caenorhabditis briggsae	isoform d	0		F:GO:0005488; P:GO:0040011; P:GO:0006898; P:GO:0002119; P:GO:0040007		-
Caenorhabditis briggsae	gtp-binding protein alpha g-o	15	P:GO:0007419; P:GO:0016055; F:GO:0004871; P:GO:0007186; P:GO:0007507; P:GO:0019991; C:GO:0005834; P:GO:0030866; F:GO:0005515; P:GO:0008356; P:GO:0007165; F:GO:0003924; P:GO:0060857; P:GO:0001737; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001019; IPR001408; IPR011025; G3DSA:3.40.50.300 (GENE3D), PTHR10218:SF76 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	cdk5 regulatory subunit-associated protein 1-like 1	5	F:GO:0046872; F:GO:0051539; C:GO:0016020; F:GO:0003824; P:GO:0009451	-		IPR005839
	-	0				-
Loa loa	sec14 and spectrin domains 1	13	F:GO:0010314; F:GO:0005545; C:GO:0034704; F:GO:0031210; F:GO:0005515; F:GO:0070273; F:GO:0001786; F:GO:0043325; F:GO:0080025; F:GO:0070300; P:GO:0051925; F:GO:0032266; F:GO:0005546	-		-
Caenorhabditis elegans	trehalase	0		P:GO:0005991; C:GO:0016021; F:GO:0003824; P:GO:0009792; P:GO:0002119; P:GO:0040007; F:GO:0004555		IPR001661; IPR018232; PTHR23403:SF1 (PANTHER)

Caenorhabditis elegans	frizzled homolog 4	14	P:GO:0016055; F:GO:0046983; P:GO:0050896; P:GO:0007154; P:GO:0023060; P:GO:0031589; P:GO:0030154; P:GO:0090047; P:GO:0001553; P:GO:0045449; P:GO:0048514; C:GO:0005886; F:GO:0004888; P:GO:0003008	-		IPR000539; IPR015526; PTHR11309:SF13 (PANTHER)
Caenorhabditis elegans	briggsae cbr-cdh-1 protein	4	P:GO:0002119; P:GO:0040010; P:GO:0040011; C:GO:0016020	-		PTHR10596 (PANTHER), PTHR10596:SF75 (PANTHER)
	-	0				SignalP (SIGNALP)
Ailuropoda melanoleuca	26s protease regulatory subunit 6a	13	F:GO:0008233; F:GO:0017111; C:GO:0000502; P:GO:0051436; P:GO:0051437; P:GO:0031145; F:GO:0005524; F:GO:0003714; P:GO:0001824; C:GO:0048471; P:GO:0044419; F:GO:0003713; C:GO:0005634	-	EC:3.6.1.15	G3DSA:1.10.8.60 (GENE3D), PTHR23073 (PANTHER), PTHR23073:SF7 (PANTHER), SSF52540 (SUPERFAMILY)
Loa loa	protein ki-se domain containing protein	4	P:GO:0006468; F:GO:0005515; F:GO:0004713; F:GO:0005524	-	EC:2.7.10.0	IPR020685; IPR020764
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein ZC487.1 [Caenorhabditis elegans]	2	F:GO:0005524; F:GO:0003824	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	intraflagellar transport 140 homolog	0		F:GO:0005488		PTHR15722 (PANTHER), PTHR15722:SF7 (PANTHER)

Anopheles gambiae str. PEST	bmp type ii receptor	29	P:GO:0030901; P:GO:0048813; C:GO:0005901; P:GO:0045906; P:GO:0010595; P:GO:0045669; P:GO:0048010; P:GO:0030513; P:GO:0010862; P:GO:0001707; P:GO:0048570; P:GO:0001947; P:GO:0007274; P:GO:0007165; F:GO:0000166; P:GO:0014916; C:GO:0005887; P:GO:0009952; F:GO:0005515; P:GO:0009267; P:GO:0007528; F:GO:0005026; P:GO:0006366; P:GO:0003085; P:GO:0010634; P:GO:0048286; P:GO:0030308; P:GO:0007368;	-		IPR000719; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR23255 (PANTHER), PTHR23255:SF13 (PANTHER)
	-	0				-
Loa loa	hypothetical protein LOAG_04618 [Loa loa]	0		F:GO:0003676		-
Caenorhabditis elegans	briggsae cbr-swm-1 protein	1	F:GO:0005515	-		-
Homo sapiens	antigen cd18	14	C:GO:0008305; P:GO:0006915; P:GO:0007267; P:GO:0006954; P:GO:0008360; P:GO:0007229; F:GO:0001948; F:GO:0004872; P:GO:0007160; P:GO:0050730; F:GO:0019901; P:GO:0007159; P:GO:0007275; P:GO:0030593	-		IPR001169; IPR015439; IPR015812; G3DSA:2.10.25.10 (GENE3D)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Loa loa	sh2 domain containing protein	0		F:GO:0016301; F:GO:0004672; F:GO:0005524; F:GO:0016740; F:GO:0000166; F:GO:0004713; P:GO:0006468; F:GO:0005515		IPR000980; IPR020685; IPR020764
	-	0				-
	-	0				-

Ciona intestinalis	glucosamine-6-phosphate deami-se 1	9	C:GO:0005737; P:GO:0007340; F:GO:0004342; P:GO:0006002; P:GO:0046370; P:GO:0006044; F:GO:0016787; P:GO:0006043; P:GO:0006091	-	EC:3.5.99.6	-
Caenorhabditis briggsae	briggsae cbr-nhr-97 protein	4	F:GO:0004872; F:GO:0005488; P:GO:0006350; P:GO:0000003	-		IPR000536; IPR008946; PTHR11865 (PANTHER), PTHR11865:SF138 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-spd-2 protein	0		C:GO:0005737; P:GO:0007049; C:GO:0005856; P:GO:0007275; F:GO:0005515; C:GO:0005814		IPR008962
Caenorhabditis briggsae	briggsae cbr-spd-2 protein	0		C:GO:0005737; P:GO:0007049; C:GO:0005856; P:GO:0007275; F:GO:0005515; C:GO:0005814		IPR008962
Caenorhabditis briggsae	briggsae cbr-spd-2 protein	0		C:GO:0005737; P:GO:0007049; C:GO:0005856; P:GO:0007275; F:GO:0005515; C:GO:0005814		IPR008962
Pongo abelii	solute carrier family member 3	8	F:GO:0015333; P:GO:0006857; F:GO:0005427; P:GO:0030163; P:GO:0055085; C:GO:0005765; C:GO:0016021; P:GO:0015031	-		-
Caenorhabditis elegans	protein ki-se domain containing protein	6	P:GO:0006468; P:GO:0040018; F:GO:0005515; F:GO:0004713; F:GO:0005524; F:GO:0004674	-	EC:2.7.10.0; EC:2.7.11.0	-
Caenorhabditis briggsae	alix (apoptosis-linked gene 2 interacting protein x) homolog family member (alx-1)	0				G3DSA:1.20.140.50 (GENE3D)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Ixodes scapularis	conserved hypothetical protein [Ixodes scapularis]	0				IPR018307

Loa loa	protein ki-se domain containing protein	4	P:GO:0006468; F:GO:0005515; F:GO:0004713; F:GO:0005524	-	EC:2.7.10.0	IPR001245; IPR011009; IPR020685; IPR020764; G3DSA:1.10.510.10 (GENE3D)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-pgp-1 protein	4	F:GO:0042626; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF96 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-ars-1 protein	0		P:GO:0006419; F:GO:0003676; F:GO:0000166; C:GO:0005737; P:GO:0006412; F:GO:0005524; F:GO:0004813; F:GO:0016876; P:GO:0043039		IPR018164; PTHR11777 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG08614 [Caenorhabditis briggsae]	0		F:GO:0016301; F:GO:0005524; F:GO:0004765; P:GO:0005975		-
	-	0				-
	-	0				-
	-	0				PTHR14027 (PANTHER), PTHR14027:SF2 (PANTHER)
	-	0				-
Caenorhabditis briggsae	d--directed r- polymerase i largest	5	F:GO:0003899; F:GO:0003677; P:GO:0006350; C:GO:0005634; F:GO:0008270	-	EC:2.7.7.6	IPR007081; IPR015699; PTHR19376 (PANTHER), SSF64484 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-toh-1 protein	3	F:GO:0004222; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Loa loa	zinc finger	0		F:GO:0005216; C:GO:0016021; C:GO:0016020; P:GO:0006813; P:GO:0006811; P:GO:0006810; F:GO:0003676; F:GO:0008270; C:GO:0005622; P:GO:0055085; F:GO:0005249		IPR015880; PTHR23224 (PANTHER), PTHR23224:SF401 (PANTHER), SSF57667 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-rrf-3 protein	1	P:GO:0009792	-		-
	-	0				-

Harpegnathos saltator	histone	4	C:GO:0000786; F:GO:0003677; P:GO:0006334; C:GO:0005634	-		IPR002119; IPR007125; IPR009072; SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	ankyrin repeat and fyve domain containing 1	7	P:GO:0009792; F:GO:0005545; F:GO:0046872; F:GO:0016773; F:GO:0016301; P:GO:0040010; F:GO:0016787	-	EC:2.7.1.0	IPR000306; IPR002110; IPR011011; IPR013083; IPR017455; IPR020683; PTHR13856 (PANTHER), PTHR13856:SF45 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Brugia malayi	trm44_caeel ame: full=probable tr- (uracil-o -)-methyltransferase	0		F:GO:0003676; F:GO:0008168; C:GO:0005737; P:GO:0008033; F:GO:0016740; F:GO:0008270		-
	-	0				-
Caenorhabditis elegans	dead deah box helicase family protein	2	P:GO:0000003; P:GO:0040010	-		SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-nhr-11 protein	3	F:GO:0004872; F:GO:0005515; P:GO:0006350	-		-
Nematostella vectensis	cytochrome family subfamily polypeptide 2	0		F:GO:0046872; P:GO:0055114; F:GO:0009055; F:GO:0016491; F:GO:0020037; F:GO:0005506; F:GO:0004497; C:GO:0005575		SignalP (SIGNALP)
Caenorhabditis briggsae	intermediate filament protein	4	C:GO:0005882; C:GO:0005737; F:GO:0005198; F:GO:0005515	-		IPR001322; IPR001664; G3DSA:2.60.40.1260 (GENE3D), PTHR23239:SF13 (PANTHER), SSF74853 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-pqn-73 protein	1	P:GO:0040035	-		-
Brugia malayi	bromodomain adjacent to zinc finger 2b	1	F:GO:0005488	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		C:GO:0016020		IPR011646; PTHR18958 (PANTHER), PTHR18958:SF283 (PANTHER)
	-	0				-
Caenorhabditis elegans	protein ki-se domain containing protein	3	P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
	-	0				-
	-	0				-

Caenorhabditis elegans	neurogenic locus notch	3	C:GO:0016020; P:GO:0009987; P:GO:0032502	-		IPR000152; IPR000742; IPR001881; IPR006209; IPR013032; IPR018097; PR00010 (PRINTS), G3DSA:2.10.25.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF220 (PANTHER), SSF57196 (SUPERFAMILY)
Brugia malayi	protein-tyrosine phosphatase containing protein	0		P:GO:0016311; F:GO:0016791; P:GO:0006470; F:GO:0016787; F:GO:0004725; F:GO:0004721		-
Caenorhabditis elegans	zinc zz type family protein	7	P:GO:0007271; F:GO:0005515; P:GO:0040017; C:GO:0016010; F:GO:0005277; P:GO:0015870; P:GO:0046716	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	gata zinc finger family protein	6	F:GO:0003700; F:GO:0043565; F:GO:0005515; C:GO:0005634; F:GO:0008270; P:GO:0006355	-		IPR000679; IPR013088; PTHR10071 (PANTHER), PTHR10071:SF14 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis elegans	beta-lactamase	0		F:GO:0016787; F:GO:0004091		PTHR10566 (PANTHER), PTHR10566:SF6 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F41G3.21 [Caenorhabditis elegans]	0		F:GO:0005515		-
	-	0				-

Caenorhabditis elegans	myosin heavy chain	25	P:GO:0001525; P:GO:0008360; P:GO:0030048; P:GO:0015031; C:GO:0005829; F:GO:0000146; P:GO:0006509; P:GO:0043534; C:GO:0008305; C:GO:0001726; C:GO:0032154; F:GO:0043495; F:GO:0051015; C:GO:0001725; F:GO:0016887; F:GO:0042803; P:GO:0031532; P:GO:0030224; P:GO:0030220; F:GO:0005516; C:GO:0005634; F:GO:0005524; C:GO:0016459; P:GO:0000910; C:GO:0005826	-		IPR001609; PTHR13140 (PANTHER), PTHR13140:SF23 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0					-
	-	0					-
Caenorhabditis briggsae	briggsae cbr-mup-4 protein	2	F:GO:0005509; F:GO:0005515	-			IPR000152; IPR000742; IPR006209; IPR006210; IPR013091; G3DSA:2.10.25.10 (GENE3D), PTHR22992 (PANTHER), PTHR22992:SF12 (PANTHER), SSF57196 (SUPERFAMILY)
	-	0					-
Macaca mulatta	poly binding protein 2	11	P:GO:0043161; F:GO:0003723; P:GO:0050687; F:GO:0031625; P:GO:0016071; P:GO:0008380; P:GO:0045087; F:GO:0003677; C:GO:0030529; C:GO:0005737; C:GO:0005634	-			PTHR10288 (PANTHER), PTHR10288:SF48 (PANTHER)
Caenorhabditis elegans	phosphatidylinositol 4-ki-se type 2-beta	4	F:GO:0016301; C:GO:0044464; F:GO:0016773; F:GO:0000166	-		EC:2.7.1.0	IPR000403; PTHR12865 (PANTHER)
Caenorhabditis elegans	phosphatidylinositol 4-ki-se type 2-beta	1	F:GO:0016773	-		EC:2.7.1.0	IPR000403; PTHR12865 (PANTHER)
Caenorhabditis briggsae	yqd7_caeel ame: full=uncharacterized protein	0					-
	-	0					-
	-	0					-
Nippostrongylus brasiliensis	fk506 binding protein 9	4	P:GO:0006457; P:GO:0008340; F:GO:0003755; P:GO:0040010	-		EC:5.2.1.8	SignalP (SIGNALP)
	-	0					-

	-	0				-
Caenorhabditis briggsae	neutral alpha-glucosidase ab-like	7	F:GO:0033919; P:GO:0005975; C:GO:0042470; C:GO:0005783; F:GO:0030246; C:GO:0005794; F:GO:0005515	-	EC:3.2.1.84	IPR000322; PTHR22762:SF7 (PANTHER)
	-	0				-
Caenorhabditis elegans	rab6 interacting protein 1	0		F:GO:0017137; C:GO:0005794; F:GO:0005515		IPR001194; PTHR12296 (PANTHER), PTHR12296:SF3 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				PTHR11865 (PANTHER), PTHR11865:SF138 (PANTHER), SignalP (SIGNALP)
Ailuropoda melanoleuca	dead (asp-glu-ala-asp) box polypeptide 17	7	F:GO:0003724; F:GO:0008026; F:GO:0003723; F:GO:0008186; F:GO:0005524; C:GO:0005634; P:GO:0006396	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-pqn-48 protein	0				IPR004911; PTHR13234:SF3 (PANTHER)
Loa loa	hypothetical protein LOAG_06866 [Loa loa]	2	P:GO:0040010; F:GO:0005509	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	glycosyl hydrolase family catalytic domain containing protein	3	F:GO:0004553; P:GO:0005975; F:GO:0043169	-	EC:3.2.1.0	IPR013781; IPR015883; IPR017853; PTHR21040 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	briggsae cbr-dpy-19 protein	2	C:GO:0016020; P:GO:0007275	-		-
	-	0				-
Caenorhabditis briggsae	aldehyde dehydroge-se	4	F:GO:0004029; P:GO:0055114; C:GO:0005739; F:GO:0042802	-	EC:1.2.1.3	IPR015590; IPR016160; IPR016161; IPR016162; PTHR11699:SF46 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	temporarily assigned gene -me family member (tag-308)	0				-
Brugia malayi	protein ki-se domain containing protein	0		F:GO:0016301; F:GO:0004672; F:GO:0005524; F:GO:0004713; P:GO:0006468; F:GO:0005515		-
	-	0				-

	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	briggsae cbr-nsy-4 protein	1	C:GO:0016021	-		IPR010761; SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	laminin a	1	C:GO:0031012	-		IPR001791; IPR008985; IPR012680; IPR013320; IPR015447; PTHR10127 (PANTHER)
Caenorhabditis elegans	axin-like family member (axl-1)	4	P:GO:0007411; P:GO:0000003; P:GO:0030178; F:GO:0019901	-		-
Caenorhabditis briggsae	solute carrier family 8 member 3	8	F:GO:0005432; P:GO:0009792; P:GO:0006816; F:GO:0031072; P:GO:0055085; P:GO:0000003; C:GO:0016021; P:GO:0007154	-		-
	-	0				-
Caenorhabditis elegans	briggsae cbr-mog-1 protein	1	F:GO:0005515	-		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	troponin t	3	P:GO:0043050; P:GO:0006952; P:GO:0040017	-		PTHR11521 (PANTHER), PTHR11521:SF1 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	4	F:GO:0005515; F:GO:0016740; P:GO:0019915; P:GO:0008152	-		IPR002213; G3DSA:3.40.50.2000 (GENE3D), PTHR11926:SF3 (PANTHER), SSF53756 (SUPERFAMILY)
	-	0				-
Oryctolagus cuniculus	alpha 1 type i collagen	0				-
	-	0				-
Caenorhabditis briggsae	u2 small nuclear	9	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0003676; P:GO:0040010; P:GO:0008340; P:GO:0040011; P:GO:0006898; C:GO:0030529	-		IPR011989; IPR016024; PTHR12097 (PANTHER)
Loa loa	ino80 complex subunit d	0		F:GO:0003674; P:GO:0008150		-
Caenorhabditis briggsae	venom dipeptidylpeptidase iv	0		F:GO:0005179; P:GO:0006508; F:GO:0004252; F:GO:0008236; C:GO:0016021; C:GO:0016020; C:GO:0005576		IPR002469; G3DSA:2.140.10.30 (GENE3D), PTHR11731 (PANTHER), PTHR11731:SF17 (PANTHER)

Ciona intestinalis	au r- binding protein enoyl-coenzyme a hydratase	3	C:GO:0005875; F:GO:0003824; F:GO:0017091	-		IPR001753; G3DSA:3.90.226.10 (GENE3D), PTHR11941 (PANTHER), SSF52096 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0005096; P:GO:0007165; F:GO:0005515; C:GO:0005622		-
	-	0				-
Loa loa	sec14-like protein 5	3	C:GO:0005622; P:GO:0006810; F:GO:0005215	-		IPR006797
Caenorhabditis briggsae	briggsae cbr-set-31 protein	0		F:GO:0016740; C:GO:0000785; F:GO:0003682; F:GO:0008168; C:GO:0005634; F:GO:0003677; P:GO:0006306; F:GO:0008270; P:GO:0006333; F:GO:0018024; P:GO:0016568; F:GO:0005515		IPR001214; G3DSA:2.170.270.10 (GENE3D), SSF82199 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150; C:GO:0005575		PTHR13167 (PANTHER), PTHR13167:SF2 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0003674; P:GO:0008150		PTHR13167 (PANTHER), PTHR13167:SF2 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0003674; P:GO:0008150		PTHR13167 (PANTHER), PTHR13167:SF2 (PANTHER), SignalP (SIGNALP)
Macaca mulatta	plexin b2	6	C:GO:0016021; C:GO:0005622; F:GO:0004872; F:GO:0005515; P:GO:0007165; P:GO:0050772	-		PTHR22625 (PANTHER), PTHR22625:SF1 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	3	P:GO:0019915; P:GO:0009792; P:GO:0040010	-		-
	-	0				SignalP (SIGNALP)
						IPR009443
						IPR003598; IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF8 (PANTHER), SSF48726 (SUPERFAMILY)

Caenorhabditis elegans	myosin ig	6	F:GO:0003779; C:GO:0016459; F:GO:0005524; F:GO:0003774; P:GO:0008152; F:GO:0005516	-		IPR001609; PTHR13140 (PANTHER), PTHR13140:SF31 (PANTHER), SSF52540 (SUPERFAMILY)
Loa loa	multiple pdz domain protein family member (mpz-1)	2	F:GO:0005515; C:GO:0016021	-		-
Caenorhabditis briggsae	topoisomerase iii alpha	8	P:GO:0007276; P:GO:0006268; P:GO:0007126; F:GO:0008270; F:GO:0003917; F:GO:0000166; C:GO:0005694; P:GO:0006265	-	EC:5.99.1.2	IPR000380; IPR003601; IPR013497; IPR013824
Caenorhabditis briggsae	sig-l peptide peptidase-like 2b	3	C:GO:0016020; F:GO:0004190; F:GO:0005515	-	EC:3.4.23.0	IPR006639; IPR007369; PTHR12174:SF21 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-rom-2 protein	4	C:GO:0016021; P:GO:0007165; F:GO:0005509; F:GO:0004252	-	EC:3.4.21.0	SignalP (SIGNALP)
	-	0				-
	-	0				-
Branchiostoma floridae	tyrosine-protein ki-se btk29a	0		C:GO:0016021; C:GO:0016020; F:GO:0005529; P:GO:0006811; P:GO:0006810; F:GO:0008270; P:GO:0007218; F:GO:0005230; F:GO:0005515; F:GO:0046872; F:GO:0005509; P:GO:0007155; F:GO:0005488		IPR001304; IPR016186; IPR016187; PTHR22800 (PANTHER), PTHR22800:SF11 (PANTHER)
	-	0				-
	-	0				-
Scapharca broughtonii	serine racemase	3	F:GO:0030170; P:GO:0006520; F:GO:0047689	-	EC:5.1.1.13	-
	-	0				-
Loa loa	four domain-type voltage-gated ion channel alpha-1 subunit	4	C:GO:0016021; F:GO:0005216; P:GO:0006811; P:GO:0055085	-		PTHR10037 (PANTHER), PTHR10037:SF60 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	plexin a	4	P:GO:0016199; F:GO:0005515; C:GO:0044464; F:GO:0004888	-		IPR001627; IPR015943; PTHR22625 (PANTHER), PTHR22625:SF11 (PANTHER)
Ancylostoma caninum	elegans protein partially confirmed by transcript evidence	3	C:GO:0016021; F:GO:0004222; P:GO:0006508	-	EC:3.4.24.0	IPR000718; IPR018497; G3DSA:3.40.390.10 (GENE3D), PTHR11733:SF15 (PANTHER), SSF55486 (SUPERFAMILY)
	-	0				-

Caenorhabditis elegans	briggsae cbr-elpc-4 protein	0		C:GO:0005634; C:GO:0005737; F:GO:0008607; C:GO:0033588; P:GO:0006357; C:GO:0008023; F:GO:0005515; P:GO:0006350; P:GO:0045449		-
	-	0				-
	-	0				-
Caenorhabditis elegans	autophagy protein 9	1	P:GO:0009792	-		IPR007241; PTHR13038:SF1 (PANTHER)
	-	0				SignalP (SIGNALP)
Loa loa	abnormal cell migration family member (mig-15)	14	F:GO:0005515; C:GO:0016020; P:GO:0016055; P:GO:0046777; F:GO:0005083; C:GO:0005737; C:GO:0005730; F:GO:0004674; C:GO:0005856; F:GO:0000155; P:GO:0007256; P:GO:0031532; P:GO:0048814; F:GO:0005524	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF83 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	mgc83607 protein	5	P:GO:0030514; P:GO:0008344; C:GO:0016021; C:GO:0043025; P:GO:0045886	-		IPR008521; SSF103481 (SUPERFAMILY)
Caenorhabditis elegans	mgc83607 protein	5	P:GO:0030514; P:GO:0008344; C:GO:0016021; C:GO:0043025; P:GO:0045886	-		IPR008521; SSF103481 (SUPERFAMILY)
Brugia malayi	protein-tyrosine phosphatase containing protein	3	P:GO:0016311; F:GO:0004721; F:GO:0005515	-	EC:3.1.3.16	IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	hexosaminidase a	16	P:GO:0042552; C:GO:0005764; F:GO:0004563; F:GO:0005488; P:GO:0048667; P:GO:0050885; P:GO:0001501; P:GO:0019953; P:GO:0019915; P:GO:0030203; P:GO:0006689; P:GO:0050884; P:GO:0007605; P:GO:0007628; P:GO:0007040; C:GO:0016020	-	EC:3.2.1.52	IPR001540; IPR013781; IPR015883; IPR017853
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	8	C:GO:0005606; P:GO:0030334; P:GO:0045995; P:GO:0030155; P:GO:0031581; P:GO:0008544; F:GO:0005102; F:GO:0005198	-		IPR002049; G3DSA:2.10.25.10 (GENE3D), PTHR10574 (PANTHER), PTHR10574:SF56 (PANTHER), SSF57196 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein C49H3.3 [Caenorhabditis elegans]	0				IPR018784
Brugia malayi	paired amphipathic helix repeat family protein	3	F:GO:0003714; P:GO:0045892; C:GO:0016580	-		IPR003822; IPR013194; PTHR12346 (PANTHER)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0006898; P:GO:0002119; P:GO:0040007		SignalP (SIGNALP)
Brugia malayi	vacuolar protein sorting protein	1	F:GO:0005488	-		PTHR23323 (PANTHER)
Harpegnathos saltator	serine threonine-protein phosphatase 4 catalytic subunit	10	C:GO:0030289; F:GO:0004704; P:GO:0016311; F:GO:0046872; C:GO:0005813; P:GO:0000226; F:GO:0004722; F:GO:0005515; C:GO:0005634; P:GO:0006468	-		IPR004843; IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF22 (PANTHER), SSF56300 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	abnormal cell lineage family member (lin-2)	13	P:GO:0016080; P:GO:0008360; P:GO:0007163; C:GO:0005954; F:GO:0004385; F:GO:0004713; F:GO:0005524; P:GO:0007155; F:GO:0005515; P:GO:0016081; P:GO:0007628; F:GO:0004683; P:GO:0006468	-	EC:2.7.4.8; EC:2.7.10.0; EC:2.7.11.17	IPR008144; G3DSA:3.40.50.300 (GENE3D), PTHR23122 (PANTHER), PTHR23122:SF7 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
Loa loa	tnni3 interacting ki-se	3	P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	-
	-	0				SignalP (SIGNALP)
Callithrix jacchus	rho-related gtp-binding	18	P:GO:0007160; P:GO:0006357; P:GO:0033144; P:GO:0000902; F:GO:0005525; P:GO:0030521; F:GO:0004767; F:GO:0017022; P:GO:0043524; P:GO:0043123; P:GO:0007264; P:GO:0007519; P:GO:0045666; P:GO:0051496; F:GO:0003924; C:GO:0005886; C:GO:0005634; C:GO:0005739	-	EC:3.1.4.12; EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
	-	0				PTHR11909 (PANTHER), PTHR11909:SF12 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Loa loa	elegans protein partially confirmed by transcript evidence	0		F:GO:0022891; C:GO:0016021; C:GO:0016020; F:GO:0005351; P:GO:0055085; P:GO:0009792; F:GO:0005215; P:GO:0006810		IPR005828; IPR016196; IPR020846; PTHR11600 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis elegans	ck1 worm6 protein ki-se	0		F:GO:0016301; F:GO:0005524; F:GO:0004672; F:GO:0000166; P:GO:0006468		IPR000719; IPR017441; G3DSA:3.30.200.20 (GENE3D)
Caenorhabditis elegans	protein kri1 homolog	8	P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0040010; P:GO:0040011; P:GO:0019915; P:GO:0006898; P:GO:0002009	-		-
Loa loa	expulsion defective family member (exp-2)	5	C:GO:0008076; F:GO:0005249; F:GO:0005515; P:GO:0055085; P:GO:0006813	-		-
	-	0				-
	-	0				-
Macaca mulatta	beta 1 (fibronectin beta antigen cd29 includes msk12)	30	C:GO:0005925; F:GO:0005178; P:GO:0045596; P:GO:0008354; C:GO:0031594; C:GO:0032587; P:GO:0007160; P:GO:0055007; C:GO:0019717; P:GO:0030183; C:GO:0042470; P:GO:0001708; P:GO:0045214; P:GO:0031175; P:GO:0007229; F:GO:0046982; C:GO:0009986; C:GO:0008305; P:GO:0008284; C:GO:0042383; P:GO:0007156; P:GO:0051726; F:GO:0042802; P:GO:0033631; P:GO:0000082; P:GO:0007159; F:GO:0004872; P:GO:0001701;	-		IPR001169; IPR013032; IPR013111; IPR015438; IPR015812; G3DSA:2.10.25.10 (GENE3D), SSF57196 (SUPERFAMILY)
Caenorhabditis elegans	uncoordi-ted family member (unc-22)	3	P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR013098; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-pod-1 protein	0				IPR001680; IPR011046; IPR015049; IPR015505; IPR015943; IPR019781
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis elegans	protein o-fucosyltransferase 1	0		F:GO:0008417; P:GO:0006493		-
Caenorhabditis briggsae	Hypothetical protein CBG14320 [Caenorhabditis briggsae]	0				-

	-	0				-
	-	0				-
Caenorhabditis briggsae	uncoordi-ted family member (unc-83)	0				-
						IPR010939; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF9 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0008104		-
Caenorhabditis elegans	-dc (-+-coupled dicarboxylate transporter) family member (-c-3)	4	C:GO:0016020; P:GO:0006814; P:GO:0055085; F:GO:0005215	-		IPR000215
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				IPR002542
	-	0				-
Caenorhabditis elegans	tyrosine-protein phosphatase non-receptor type 4	7	F:GO:0004726; C:GO:0005856; C:GO:0019898; F:GO:0050254; F:GO:0008092; C:GO:0005886; P:GO:0006470	-	EC:2.7.11.14	IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF58 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis briggsae	inositol -trisphosphate receptor	5	P:GO:0006816; F:GO:0005220; P:GO:0055085; C:GO:0016021; C:GO:0005783	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0000003		-
	-	0				-
Loa loa	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis briggsae	flavodoxin family protein	0		F:GO:0016491; C:GO:0016021; F:GO:0010181		-
Brugia malayi	trehalase family protein	2	C:GO:0016020; F:GO:0016798	-		IPR001661; PTHR23403:SF1 (PANTHER)
Caenorhabditis elegans	briggsae cbr-haf-6 protein	8	P:GO:0055085; C:GO:0016021; F:GO:0042626; C:GO:0043190; C:GO:0005624; F:GO:0005524; P:GO:0008152; C:GO:0005740	-		IPR003439; G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF77 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	54s ribosomal protein l19	7	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; P:GO:0040010; P:GO:0006898; P:GO:0006412	-	EC:3.6.5.3	IPR000911; IPR020783; PTHR11661:SF1 (PANTHER)
Caenorhabditis elegans	k+ channel tetramerization protein	6	P:GO:0009792; C:GO:0008076; F:GO:0005249; F:GO:0005515; P:GO:0040011; P:GO:0006813	-		IPR000210; IPR011333; PTHR21637 (PANTHER)

Pongo abelii	lymphocyte antigen 6 locus e	9	P:GO:0055010; P:GO:0048242; P:GO:0035265; P:GO:0042415; C:GO:0031225; P:GO:0007166; P:GO:0001701; P:GO:0030325; C:GO:0005887	-		IPR001526; IPR016054; G3DSA:2.10.60.10 (GENE3D), SignalP (SIGNALP), SSF57302 (SUPERFAMILY)
Homo sapiens	fk506 binding protein isoform cra_a	0		P:GO:0001708; P:GO:0030513; C:GO:0031966; F:GO:0003755; P:GO:0009953; P:GO:0030510; C:GO:0005740; P:GO:0006915; C:GO:0016021; C:GO:0016020; P:GO:0043010; P:GO:0021904; C:GO:0005739; F:GO:0005488; F:GO:0016853; P:GO:0021915; C:GO:0030176; P:GO:0006457; P:GO:0035264; P:GO:0010468; P:GO:0007224		-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-mec-5 protein	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	F:GO:0003824; F:GO:0005488; P:GO:0040010	-		SignalP (SIGNALP)
Caenorhabditis briggsae	epithelial fusion failure family member (eff-1)	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	myosin heavy chain	4	F:GO:0003779; C:GO:0016459; F:GO:0005524; F:GO:0003774	-		-
	-	0				-

Caenorhabditis elegans	exosome complex exonuclease rrp41	18	F:GO:0005515; C:GO:0016020; P:GO:0040010; P:GO:0040018; F:GO:0016740; P:GO:0008406; F:GO:0004527; P:GO:0006396; P:GO:0009792; C:GO:0043234; P:GO:0002119; C:GO:0005740; C:GO:0031974; F:GO:0003723; P:GO:0010171; P:GO:0071044; C:GO:0005634; P:GO:0006626	-		IPR001247; IPR015847; IPR020568; PTHR11953 (PANTHER)
Caenorhabditis elegans	exosome complex exonuclease rrp41	18	F:GO:0005515; C:GO:0016020; P:GO:0040010; P:GO:0040018; F:GO:0016740; P:GO:0008406; F:GO:0004527; P:GO:0006396; P:GO:0009792; C:GO:0043234; P:GO:0002119; C:GO:0005740; C:GO:0031974; F:GO:0003723; P:GO:0010171; P:GO:0071044; C:GO:0005634; P:GO:0006626	-		IPR001247; IPR015847; IPR020568; PTHR11953 (PANTHER)
	-	0				-
	ap-2 complex subunit mu-1	14	P:GO:0016192; C:GO:0005829; C:GO:0030125; C:GO:0030132; C:GO:0005739; C:GO:0030133; F:GO:0008289; C:GO:0030131; C:GO:0005778; C:GO:0030666; P:GO:0050690; F:GO:0005515; F:GO:0005215; P:GO:0006886	-		IPR008968; IPR015629; G3DSA:2.60.40.1170 (GENE3D), PTHR11998 (PANTHER)
	-	0				-
Caenorhabditis briggsae	angiogenic factor with g patch and fha domains 1	4	F:GO:0005488; P:GO:0032502; C:GO:0005622; P:GO:0009987	-		PTHR23106 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-

Loa loa	nucleolar protein 10	5	P:GO:0009792; P:GO:0002119; P:GO:0018991; P:GO:0040010; C:GO:0005634	-		PTHR14927 (PANTHER)
Brugia malayi	elegans protein confirmed by transcript evidence	0		C:GO:0005737; F:GO:0005515		-
Brugia malayi	retinoic acid receptor rxr-alpha-like	21	F:GO:0003700; F:GO:0070644; F:GO:0003708; F:GO:0046872; P:GO:0048738; P:GO:0008203; P:GO:0009653; P:GO:0022414; F:GO:0003713; P:GO:0045944; P:GO:0010033; P:GO:0048384; P:GO:0006766; P:GO:0030154; F:GO:0042809; F:GO:0046982; F:GO:0046966; C:GO:0005634; P:GO:0032526; F:GO:0003706; P:GO:0010553	-		IPR000536; IPR008946; PR00545 (PRINTS), PTHR11865 (PANTHER), PTHR11865:SF190 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Teladorsagia circumcincta	class 3 lipase protein	1	F:GO:0016787	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG08295 [Caenorhabditis briggsae]	0				-
Loa loa	r- pseudouridylate synthase domain containing 4	1	F:GO:0003824	-		-
	-	0				-
Angiostrongylus cantonensis	fyve zinc finger family protein	2	F:GO:0008270; F:GO:0005515	-		IPR000306; IPR011011; IPR013083; IPR015390; IPR017455; PD936484 (PRODOM)
	-	0				-
Loa loa	lethal family member (let-19)	0		F:GO:0016455; P:GO:0009792; C:GO:0016592		PTHR12950 (PANTHER), PTHR12950:SF3 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	protein ki-se domain containing protein	4	P:GO:0006468; F:GO:0005515; F:GO:0004713; F:GO:0005524	-	EC:2.7.10.0	IPR000719; IPR001245; IPR011009; IPR020685; IPR020764; G3DSA:1.10.510.10 (GENE3D)

Harpegnathos saltator	ran	21	C:GO:0000785; C:GO:0005654; P:GO:0007052; C:GO:0042470; F:GO:0005525; P:GO:0030521; P:GO:0051301; P:GO:0006611; F:GO:0004767; P:GO:0006259; C:GO:0005829; C:GO:0005643; P:GO:0007067; F:GO:0003713; P:GO:0007165; P:GO:0045893; F:GO:0003682; F:GO:0003924; F:GO:0050681; P:GO:0006405; P:GO:0044419	-	EC:3.1.4.12; EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Caenorhabditis elegans	briggsae cbr-mvb-12 protein	0				IPR018798; PS51497 (PROFILE)
	-	0				-
Caenorhabditis elegans	briggsae cbr-orai-1 protein	0		C:GO:0016021; C:GO:0016020		-
	-	0				-
Brugia malayi	hypothetical protein Bm1_34160 [Brugia malayi]	0		C:GO:0005737; C:GO:0016020		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	actin-binding rho activating	0				PTHR22739 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Homo sapiens	tissue inhibitor of metalloprotei-se 1	7	P:GO:0051045; P:GO:0043249; F:GO:0046872; F:GO:0005515; F:GO:0008191; P:GO:0008284; C:GO:0005578	-		-
Pongo abelii	family with sequence similarity member a	3	C:GO:0016021; C:GO:0005789; C:GO:0033116	-		IPR021999; PTHR13167 (PANTHER), PTHR13167:SF7 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	acid ceramidase precursor	5	P:GO:0006629; P:GO:0010033; C:GO:0005764; P:GO:0030324; F:GO:0017040	-	EC:3.5.1.23	SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	cadherin domain containing protein	0		P:GO:0007218; F:GO:0005509; P:GO:0007156; F:GO:0004930; P:GO:0007155; C:GO:0016021; C:GO:0016020; C:GO:0005886		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-tag-164 protein	0		C:GO:0016021		-
	-	0				-
Chlorocebus aethiops	heavy chain non-muscle	43	P:GO:0001525; C:GO:0030863; P:GO:0008360; C:GO:0031594; P:GO:0030048; F:GO:0030898; P:GO:0051295; C:GO:0005913; P:GO:0016337; F:GO:0043531; P:GO:0032796; P:GO:0015031; C:GO:0001772; P:GO:0050900; P:GO:0007229; C:GO:0005829; P:GO:0007520; F:GO:0000146; P:GO:0006509; P:GO:0043534; C:GO:0008305; C:GO:0005819; C:GO:0001726; P:GO:0007132; C:GO:0032154; P:GO:0000904; P:GO:0001768; F:GO:0043495;	-		-
	-	0				-

Ailuropoda melanoleuca	dynein light chain cytoplasmic	24	P:GO:0009653; P:GO:0006810; F:GO:0008022; C:GO:0005624; P:GO:0045019; C:GO:0005829; C:GO:0005874; F:GO:0003777; P:GO:0030036; P:GO:0042326; F:GO:0019904; F:GO:0030235; P:GO:0042133; P:GO:0007292; P:GO:0045449; F:GO:0042803; P:GO:0008633; C:GO:0005868; F:GO:0019899; P:GO:0007018; C:GO:0005886; F:GO:0004857; C:GO:0005634; C:GO:0005739	-		SignalP (SIGNALP)
Caenorhabditis elegans	serpentine class ab (class a-like) family member (srab-14)	4	P:GO:0007186; C:GO:0016021; P:GO:0007606; F:GO:0004888	-		IPR019408; SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Callithrix jacchus	nhp2 non-histone chromosome protein 2-like 1 (cerevisiae)	8	P:GO:0008380; C:GO:0031428; F:GO:0030515; C:GO:0005681; F:GO:0005515; P:GO:0042254; P:GO:0006397; P:GO:0007338	-		IPR004037; IPR004038; IPR018492; G3DSA:3.30.1330.30 (GENE3D), PTHR23105 (PANTHER), PTHR23105:SF11 (PANTHER), SSF55315 (SUPERFAMILY)
Caenorhabditis elegans	Hypothetical protein Y59E9AL.36 [Caenorhabditis elegans]	0		F:GO:0003676; F:GO:0000166; C:GO:0016020; P:GO:0055085; F:GO:0005215; P:GO:0006810		IPR000504; IPR012677; PTHR10432 (PANTHER), SignalP (SIGNALP), SSF54928 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	scavenger receptor class a- c-type lectin (agap009143-pa)	3	C:GO:0016020; F:GO:0005044; F:GO:0005488	-		IPR001190; IPR017448; G3DSA:3.10.250.10 (GENE3D), PTHR19331 (PANTHER), PTHR19331:SF24 (PANTHER)
	-	0				-

Caenorhabditis elegans	stress-activated protein ki-se jnk	10	P:GO:0007254; F:GO:0004705; P:GO:0031558; F:GO:0005524; P:GO:0010744; F:GO:0005515; P:GO:0010628; C:GO:0005654; P:GO:0046686; P:GO:0006468	-		IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF62 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		C:GO:0034703; P:GO:0055080; F:GO:0005261		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	ran-binding protein	1	F:GO:0005488	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				IPR001810; G3DSA:1.20.1280.50 (GENE3D)
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG15282 [Caenorhabditis briggsae]	0		F:GO:0016491; F:GO:0004867; F:GO:0005515		-
	-	0				-
	-	0				IPR000909; IPR017946; PTHR10336 (PANTHER), PTHR10336:SF7 (PANTHER)
	-	0				-
Brugia malayi	zinc finger r- binding protein	3	F:GO:0005488; C:GO:0043232; C:GO:0005634	-		IPR003604; IPR006561; IPR007087; IPR015880; IPR022755; PTHR10910 (PANTHER), PTHR10910:SF26 (PANTHER), SSF57667 (SUPERFAMILY)
Brugia malayi	zinc finger r- binding protein	3	F:GO:0005488; C:GO:0043232; C:GO:0005634	-		IPR003604; IPR006561; IPR007087; IPR015880; IPR022755; PTHR10910 (PANTHER), PTHR10910:SF26 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis elegans	uncoordi-ted family member (unc-49)	7	P:GO:0010171; F:GO:0004872; C:GO:0045211; C:GO:0030054; F:GO:0005230; P:GO:0006811; C:GO:0016021	-		IPR006029; IPR006201; G3DSA:1.20.120.370 (GENE3D), PTHR18945:SF8 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				PTHR13179 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-tag-149 protein	0				SignalP (SIGNALP)

Caenorhabditis briggsae	briggsae cbr-cht-1 protein	8	P:GO:0009792; C:GO:0005615; F:GO:0008843; P:GO:0006032; F:GO:0043169; P:GO:0009617; F:GO:0008061; P:GO:0006955	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	mitochondrial translatio-l release factor 1	3	F:GO:0003747; C:GO:0005739; P:GO:0006415	-		PTHR11075 (PANTHER), PTHR11075:SF11 (PANTHER), SSF75620 (SUPERFAMILY)
Caenorhabditis briggsae	solute carrier organic anion transporter member 4c1	3	P:GO:0006810; C:GO:0016020; F:GO:0005215	-		IPR001412; IPR004156; IPR016196; IPR020830; G3DSA:1.20.1250.20 (GENE3D), PTHR11388:SF10 (PANTHER), PS51465 (PROFILE)
	-	0				IPR004296
Loa loa	polymerase iii (d- directed) polypeptide 155kda	2	F:GO:0005488; F:GO:0016779	-	EC:2.7.7.0	-
Caenorhabditis elegans	3-oxoacyl-	2	F:GO:0016747; P:GO:0009058	-	EC:2.3.1.0	-
	-	0				SignalP (SIGNALP)
Loa loa	hypothetical protein LOAG_10658 [Loa loa]	0				IPR007145
Caenorhabditis elegans	pyrazi-midase and oti-midase family member (pnc-1)	1	F:GO:0003824	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	frizzled homolog 7b	6	P:GO:0048729; P:GO:0007166; F:GO:0005515; P:GO:0007369; C:GO:0016020; F:GO:0004888	-		IPR000539; IPR015526; IPR017981; IPR020067; PTHR11309:SF20 (PANTHER)
Brugia malayi	frizzled homolog 7b	3	P:GO:0007166; C:GO:0016020; F:GO:0004888	-		-
	-	0				-
Caenorhabditis elegans	homology domain containing protein	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-asp-5 protein	6	C:GO:0016021; P:GO:0008219; P:GO:0006508; F:GO:0004190; F:GO:0005515; P:GO:0040011	-	EC:3.4.23.0	-
Caenorhabditis briggsae	serine threonine protein	3	P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF19 (PANTHER)
	-	0				-
	-	0				-

Caenorhabditis elegans	protein-tyrosine phosphatase containing protein	1	F:GO:0004721	-	EC:3.1.3.16	IPR000242; IPR000387; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	bypass of response to pheromone in yeast family member (brp-1)	0		F:GO:0005515		-
Caenorhabditis elegans	bypass of response to pheromone in yeast family member (brp-1)	0		F:GO:0005515		-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG16145 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	kelch-like 18	0		F:GO:0003674; F:GO:0005515; C:GO:0005575		-
Brugia malayi	frizzled homolog 9	7	P:GO:0007186; F:GO:0004926; C:GO:0016021; P:GO:0007165; P:GO:0007275; P:GO:0016055; F:GO:0004930	-		IPR000539; IPR015526; PTHR11309:SF18 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Loa loa	cg10889 cg10889-pa	0		F:GO:0003676; F:GO:0003674; F:GO:0008270; C:GO:0005575		-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG01087 [Caenorhabditis briggsae]	0				-
Haemonchus contortus	aspartyl protease family member (asp-2)	4	P:GO:0008219; F:GO:0016787; F:GO:0005515; P:GO:0040011	-		IPR001461; IPR009007; IPR021109; PTHR13683:SF53 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis briggsae	coronin family member (cor-1)	2	F:GO:0008415; P:GO:0000003	-		IPR015049; IPR015505
	-	0				-
Caenorhabditis elegans	fibronectin 1b	8	P:GO:0018996; P:GO:0009792; P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		IPR003961; IPR008957; IPR013783
Haemonchus contortus	ornithine decarboxylase	2	P:GO:0006596; F:GO:0004586	-	EC:4.1.1.17	IPR009006; IPR022643; PTHR11482 (PANTHER)
	-	0				-

Ancylostoma ceylanicum	metalloprotease 1 precursor	2	F:GO:0046872; F:GO:0008237	-		IPR000859; IPR001506; IPR006026; IPR006210; IPR013032; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
Ancylostoma ceylanicum	metalloprotease 1 precursor	2	F:GO:0046872; F:GO:0008237	-		
Ancylostoma ceylanicum	metalloprotease 1 precursor	2	F:GO:0046872; F:GO:0008237	-		IPR000859; IPR001506; IPR006026; IPR006210; IPR013032; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
Ancylostoma ceylanicum	metalloprotease 1 precursor	2	F:GO:0046872; F:GO:0008237	-		IPR000859; IPR001506; IPR006026; IPR006210; IPR013032; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
Ancylostoma ceylanicum	metalloprotease 1 precursor	2	F:GO:0046872; F:GO:0008237	-		IPR000859; IPR001506; IPR006026; IPR006210; IPR013032; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
Ancylostoma ceylanicum	metalloprotease 1 precursor	2	F:GO:0046872; F:GO:0008237	-		
Ancylostoma ceylanicum	metalloprotease 1 precursor	2	F:GO:0046872; F:GO:0008237	-		IPR000859; IPR001506; IPR006026; IPR006210; IPR013032; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	P:GO:0040015; P:GO:0040010; P:GO:0040011	-		IPR000859; PTHR22991 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-

Homo sapiens	nucleoside diphosphate ki-se a	34	C:GO:0030027; P:GO:0002762; F:GO:0004550; P:GO:0006241; F:GO:0043015; C:GO:0005792; P:GO:0030819; F:GO:0005525; C:GO:0005882; C:GO:0005829; P:GO:0008285; P:GO:0006165; C:GO:0001726; F:GO:0042802; C:GO:0005813; P:GO:0045618; P:GO:0006897; P:GO:0006183; F:GO:0000287; P:GO:0006228; P:GO:0042493; P:GO:0051591; P:GO:0050679; F:GO:0004536; C:GO:0048471; P:GO:0007399;	-	EC:2.7.4.6	SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	wd repeat-containing protein 70	2	F:GO:0005515; F:GO:0016740	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR16017 (PANTHER)
Haemonchus contortus	glutamate dehydroge-se	6	F:GO:0004353; P:GO:0055114; P:GO:0000003; P:GO:0006520; F:GO:0005488; P:GO:0040010	-	EC:1.4.1.3	SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	intracister-l a particle-promoted polypeptide-like	1	F:GO:0005515	-		-
	-	0				-
	-	0				-
Loa loa	d--directed r- beta subunit family protein	9	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0003899; F:GO:0003677; P:GO:0006350; F:GO:0032549; P:GO:0040007; C:GO:0005634	-	EC:2.7.7.6	-
	-	0				-

Loa loa	trehalose 6-phosphate synthase	3	F:GO:0003825; P:GO:0034608; P:GO:0005992	-	EC:2.4.1.15	-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Bombyx mori	transposase [Bombyx mori]	0		P:GO:0045449; F:GO:0003677		PTHR23022 (PANTHER), PTHR23022:SF6 (PANTHER)
Caenorhabditis elegans	hypothetical protein K02D10.1 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	briggsae cbr-rpm-1 protein	0		F:GO:0046872; P:GO:0030071; C:GO:0005680; F:GO:0008270; F:GO:0005515; C:GO:0005622		PTHR12846 (PANTHER), PTHR12846:SF2 (PANTHER)
	-	0				-
Caenorhabditis elegans	nuclear receptor nhr-1	6	F:GO:0003700; F:GO:0043565; F:GO:0003707; C:GO:0005634; F:GO:0008270; P:GO:0006355	-		IPR008946; PTHR11865 (PANTHER), PTHR11865:SF218 (PANTHER)
Callithrix jacchus	60s ribosomal protein l21-like	4	F:GO:0003735; F:GO:0003723; C:GO:0022625; P:GO:0006414	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	wd repeat protein 39	0		F:GO:0005488; P:GO:0016226; C:GO:0005856; P:GO:0005975		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; PTHR22838 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG03790 [Caenorhabditis briggsae]	1	F:GO:0005515	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-rpy-1 protein	7	C:GO:0005856; C:GO:0045211; P:GO:0007268; C:GO:0030054; F:GO:0033130; P:GO:0019915; F:GO:0008270	-		PTHR10098 (PANTHER), PTHR10098:SF7 (PANTHER)
	-	0				-
Caenorhabditis elegans	yqy2_caeel ame: full=uncharacterized protein	0				-
	-	0				-
	-	0				-

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0016740; F:GO:0030246; C:GO:0016021; F:GO:0003700; C:GO:0005634; F:GO:0016758; F:GO:0016757; P:GO:0005975; P:GO:0030259; P:GO:0006355; P:GO:0008152; P:GO:0045449		SignalP (SIGNALP)
	-	0				-
Phytophthora infestans T30-4	copine-like protein	0				G3DSA:2.60.40.150 (GENE3D)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	homeobox domain containing protein	4	F:GO:0003700; F:GO:0043565; C:GO:0005634; P:GO:0006355	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		-
	-	0				-
Loa loa	hypothetical protein LOAG_06866 [Loa loa]	1	P:GO:0040010	-		IPR000436; IPR016060
Caenorhabditis elegans	protein-tyrosine phosphatase containing protein	1	F:GO:0016791	-	EC:3.1.3.0	IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	F:GO:0003824	-		IPR000718; IPR008753; IPR018497; G3DSA:3.40.390.10 (GENE3D), PTHR11733:SF15 (PANTHER), SignalP (SIGNALP), SSF55486 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	malate l-lactate dehydroge-se family protein	2	F:GO:0016491; P:GO:0055114	-		IPR003767; G3DSA:3.30.1370.60 (GENE3D)
Angiostrongylus cantonensis	protein mida mitochondrial precursor	0		C:GO:0005739; F:GO:0003674; P:GO:0008150		IPR003788; PTHR12049 (PANTHER), SSF53335 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Loa loa	regulatory-associated protein of mtor	1	F:GO:0005488	-		IPR004083; IPR011989; IPR016024; PTHR12848:SF2 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0006629; F:GO:0016787; F:GO:0004806		-
	-	0				-
Pan troglodytes	PREDICTED: hypothetical protein [Pan troglodytes]	0				-
Homo sapiens	eukaryotic translation elongation factor 1 delta	7	F:GO:0003746; F:GO:0004871; C:GO:0005853; F:GO:0005515; P:GO:0043123; C:GO:0005829; P:GO:0006414	-		SignalP (SIGNALP)

Brugia malayi	tbp-like factor	4	F:GO:0003677; F:GO:0003702; P:GO:0006367; P:GO:0006355	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	--k-cl cotransporter homolog family member (nkcc-1)	4	F:GO:0022891; P:GO:0055085; C:GO:0016021; F:GO:0022804	-		IPR000792; IPR004841; PTHR11827 (PANTHER), PTHR11827:SF8 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	solute carrier family 12 (sodium potassium chloride transporters) member 2	3	P:GO:0055085; P:GO:0006811; C:GO:0016021	-		-
Caenorhabditis elegans	--k-cl cotransporter homolog family member (nkcc-1)	4	F:GO:0022891; P:GO:0055085; C:GO:0016021; F:GO:0022804	-		IPR000792; IPR004841; PTHR11827 (PANTHER), PTHR11827:SF8 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	tubulointerstitial nephritis antigen	6	P:GO:0006955; F:GO:0030247; F:GO:0005044; P:GO:0006508; C:GO:0042600; F:GO:0004197	-	EC:3.4.22.0	-
	-	0				-
Caenorhabditis elegans	prolyl carboxy peptidase like family member (pcp-3)	0		P:GO:0006508; F:GO:0004180; F:GO:0008236; C:GO:0016021		IPR008758; PTHR11010:SF4 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	mechanosensory abnormality family member (mec-2)	1	C:GO:0016020	-		IPR001107; IPR001972; SignalP (SIGNALP), SSF117892 (SUPERFAMILY)
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
Heliconius melpomene	r--directed d- polymerase hmg-i and hmg- d--	4	F:GO:0004519; F:GO:0003723; F:GO:0003964; P:GO:0006278	-	EC:2.7.7.49	-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-tag-180 protein	1	C:GO:0016020	-		PTHR10166 (PANTHER), PTHR10166:SF4 (PANTHER)

Loa loa	26s protease regulatory subunit 8	22	P:GO:0008340; P:GO:0051437; P:GO:0040007; P:GO:0006310; F:GO:0031531; P:GO:0040017; P:GO:0051436; P:GO:0007091; C:GO:0005737; C:GO:0005730; P:GO:0009792; C:GO:0000502; P:GO:0002119; P:GO:0016481; F:GO:0016887; F:GO:0008233; P:GO:0031145; F:GO:0008134; F:GO:0005524; F:GO:0009378; P:GO:0040035; P:GO:0006281	-		IPR003593; IPR003959; IPR003960; IPR005937; G3DSA:1.10.8.60 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23073 (PANTHER), PTHR23073:SF12 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0003676; F:GO:0004523		G3DSA:3.30.420.10 (GENE3D)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				IPR001799; IPR008972; PTHR11304:SF23 (PANTHER), SignalP (SIGNALP)
Heligmosomoides polygyrus corsicum	cytochrome b	8	F:GO:0046872; F:GO:0016491; C:GO:0070469; F:GO:0009055; P:GO:0006810; C:GO:0016021; P:GO:0022904; C:GO:0005739	-		IPR016174; IPR016175; SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	expulsion defective family member (aex-3)	6	P:GO:0007618; P:GO:0007268; P:GO:0018991; C:GO:0005623; P:GO:0030421; F:GO:0017112	-		PTHR13008 (PANTHER)
Homo sapiens	immunoglobulin heavy chain variable region	0				IPR013783; PTHR23266 (PANTHER), PTHR23266:SF9 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-

	-	0				-
Homo sapiens	immunoglobulin heavy chain variable region	0				-
Caenorhabditis elegans	large subunit ribosomal protein 10	10	P:GO:0006412; P:GO:0040010; C:GO:0005840; P:GO:0006355; F:GO:0003735; P:GO:0000003; F:GO:0043565; P:GO:0002119; F:GO:0003700; P:GO:0009792	-	EC:3.6.5.3	-
Caenorhabditis elegans	l-lactate dehydroge-se	5	C:GO:0005737; F:GO:0005488; F:GO:0004459; P:GO:0055114; P:GO:0006096	-	EC:1.1.1.27	IPR001236; IPR001557; IPR016040; PTHR11540 (PANTHER), PTHR11540:SF3 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	F:GO:0010181; P:GO:0008152; F:GO:0016491	-		PTHR22893 (PANTHER), PTHR22893:SF6 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Loa loa	myosin xviiia	7	C:GO:0005730; C:GO:0016459; F:GO:0042802; P:GO:0006916; F:GO:0005524; F:GO:0003774; C:GO:0005794	-		-
	-	0				IPR014044; SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	P:GO:0009792; F:GO:0016818; F:GO:0005488; P:GO:0000003	-	EC:3.6.1.0	PTHR11472 (PANTHER), PTHR11472:SF5 (PANTHER)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	2	P:GO:0007186; C:GO:0016021	-		IPR000276; IPR017452; G3DSA:1.20.1070.10 (GENE3D), PTHR22751 (PANTHER), PTHR22751:SF8 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	F:GO:0005488; P:GO:0019915; P:GO:0007165	-		IPR000198; IPR008936; PTHR23178 (PANTHER), PTHR23178:SF4 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	F:GO:0005488; P:GO:0019915; P:GO:0007165	-		IPR000198; IPR008936; PTHR23178 (PANTHER), PTHR23178:SF4 (PANTHER)
	-	0				-
	-	0				-
Loa loa	hypothetical protein LOAG_02385 [Loa loa]	0				-
	-	0				-

Caenorhabditis briggsae	beta 2	0		F:GO:0046872; C:GO:0005739; F:GO:0003674; P:GO:0008152; F:GO:0016787; P:GO:0008150		G3DSA:3.60.15.10 (GENE3D), PTHR23131 (PANTHER), SSF56281 (SUPERFAMILY)
Caenorhabditis briggsae	endoplasmic reticulum metallopeptidase 1	5	F:GO:0008233; P:GO:0040011; C:GO:0016021; P:GO:0006508; C:GO:0005783	-		IPR007484; PTHR12147 (PANTHER)
	-	0				-
Callithrix jacchus	transmembrane 4 superfamily member 1	1	C:GO:0005887	-		-
Caenorhabditis briggsae	sterol regulatory element-binding protein cleavage-activating protein	2	P:GO:0009792; C:GO:0016020	-		IPR000731; PF12349 (PFAM)
Caenorhabditis elegans	briggsae cbr-hhat-1 protein	0				-
Caenorhabditis elegans	tho complex subunit 1	7	P:GO:0006396; P:GO:0006915; C:GO:0000445; F:GO:0005515; F:GO:0003711; C:GO:0005737; P:GO:0046784	-		IPR021861; PTHR13265 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	type i phosphodiesterase nucleotide pyrophosphatase family protein	3	P:GO:0008152; C:GO:0031674; C:GO:0055120	-		PTHR10151 (PANTHER), PTHR10151:SF10 (PANTHER)
Caenorhabditis elegans	uncoordi-ted family member (unc-89)	3	P:GO:0016310; F:GO:0004674; F:GO:0000166	-	EC:2.7.11.0	-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				G3DSA:3.40.50.300 (GENE3D), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
Brugia malayi	h aca ribonucleoprotein complex subunit 4	10	P:GO:0040010; F:GO:0003723; C:GO:0005730; P:GO:0006364; P:GO:0000003; P:GO:0002119; F:GO:0005515; P:GO:0001522; F:GO:0009982; C:GO:0030529	-	EC:5.4.99.12	IPR002478; IPR002501; IPR004521; IPR004802; IPR012960; IPR015947; IPR020103; G3DSA:2.30.130.10 (GENE3D), PTHR23127 (PANTHER)
Caenorhabditis elegans	nematode astacin protease protein 30	3	F:GO:0004222; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	IPR013032; PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER)

Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	6	P:GO:0002119; P:GO:0006468; F:GO:0005524; P:GO:0040011; P:GO:0040007; F:GO:0004674	-	EC:2.7.11.0	SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-casy-1 protein	9	P:GO:0009792; C:GO:0005615; P:GO:0007156; F:GO:0005515; C:GO:0032809; P:GO:0008355; C:GO:0043231; F:GO:0005509; C:GO:0016021	-		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Brugia malayi	ancient conserved domain protein	0		C:GO:0016021; C:GO:0016020; F:GO:0050660; P:GO:0006811; P:GO:0006810; P:GO:0055114; F:GO:0003824; P:GO:0040010; C:GO:0005886		PTHR12064 (PANTHER)
Caenorhabditis elegans	briggsae cbr-tag-165 protein	1	P:GO:0000003	-		-
	-	0				-
Brugia malayi	kelch motif family protein	0		C:GO:0019031; F:GO:0004252; C:GO:0016021; C:GO:0016020; F:GO:0008061; C:GO:0005576; F:GO:0003824; F:GO:0005044; P:GO:0006508; F:GO:0005515; P:GO:0006030		-
	-	0				-
	-	0				-
Loa loa	hypothetical protein LOAG_09109 [Loa loa]	0				IPR009027; IPR011320
	-	0				-
	-	0				IPR019515
Ailuropoda melanoleuca	translocase of outer mitochondrial membrane 5 homolog	4	P:GO:0006626; F:GO:0008565; C:GO:0005742; C:GO:0016021	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis elegans	briggsae cbr-efn-4 protein	0		P:GO:0007275; C:GO:0016020; C:GO:0031225; C:GO:0005886		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Brugia malayi	rap guanine nucleotide exchange factor 4	27	F:GO:0008603; C:GO:0001750; P:GO:0017157; P:GO:0019933; C:GO:0043197; F:GO:0005088; P:GO:0051056; P:GO:0007507; C:GO:0005624; P:GO:0017156; C:GO:0016323; C:GO:0005829; F:GO:0030552; P:GO:0001932; F:GO:0017016; C:GO:0060076; F:GO:0004692; C:GO:0005952; C:GO:0030424; P:GO:0030073; P:GO:0007186; F:GO:0032403; P:GO:0050805; C:GO:0001917; P:GO:0014911; C:GO:0016324; P:GO:0050773	-	EC:2.7.11.12	IPR001895; IPR008937; PTHR23113:SF25 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	serine threonine phosphatase	5	C:GO:0005737; F:GO:0004722; P:GO:0006470; P:GO:0019915; C:GO:0005634	-		IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF19 (PANTHER), SSF56300 (SUPERFAMILY)
	-	0				-
Homo sapiens	complement subcomponent c1s (ec) precursor	8	F:GO:0005509; P:GO:0006958; P:GO:0045087; P:GO:0010001; P:GO:0006508; F:GO:0004252; C:GO:0005576; P:GO:0051591	-	EC:3.4.21.0	IPR000859; PTHR19355 (PANTHER), PTHR19355:SF12 (PANTHER)
Caenorhabditis elegans	-d(+) adp-ribosyltransferase-3-like protein	0		F:GO:0003950; F:GO:0016740; P:GO:0006471		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF255 (PANTHER)

Loa loa	briggsae cbr-tag-246 protein	13	P:GO:0040010; P:GO:0007517; F:GO:0016251; P:GO:0040035; P:GO:0010171; P:GO:0007413; P:GO:0002119; C:GO:0035060; P:GO:0006898; F:GO:0003713; P:GO:0045893; P:GO:0009792; P:GO:0048813	-		IPR006569; IPR006903; IPR008942; PTHR15921 (PANTHER)
Caenorhabditis elegans	brg-1 associated factor	7	P:GO:0040035; P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040010; P:GO:0006898; P:GO:0007413	-		IPR003121; IPR019835; PTHR13844 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				IPR010916
Caenorhabditis elegans	tnni3 interacting ki-se	8	C:GO:0005737; P:GO:0006468; F:GO:0046872; F:GO:0005524; F:GO:0008022; C:GO:0005634; F:GO:0004674; F:GO:0031013	-	EC:2.7.11.0	-
Caenorhabditis briggsae	collagen alpha-5 chain	0		P:GO:0007155; C:GO:0005578; C:GO:0005576		IPR002035; G3DSA:3.40.50.410 (GENE3D), SSF53300 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	2	F:GO:0003824; P:GO:0008152	-		IPR002198; PTHR19410:SF18 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Paramecium tetraurelia strain d4-2	poly(adp-ribose) polymerase	9	C:GO:0005739; C:GO:0031981; F:GO:0046872; P:GO:0090304; P:GO:0006471; F:GO:0005515; P:GO:0065007; P:GO:0006974; F:GO:0003950	-	EC:2.4.2.30	IPR008893; IPR012317; G3DSA:3.90.228.10 (GENE3D), PTHR15447 (PANTHER)
	-	0				-

Caenorhabditis elegans	histone deacetylase 1	21	F:GO:0016566; F:GO:0004407; P:GO:0070932; F:GO:0042826; P:GO:0010552; C:GO:0016581; P:GO:0070933; P:GO:0045786; P:GO:0010832; C:GO:0005829; F:GO:0016563; P:GO:0043922; P:GO:0006916; P:GO:0008284; P:GO:0010553; F:GO:0042802; C:GO:0016580; P:GO:0006338; F:GO:0003700; P:GO:0010870; F:GO:0008134	-		IPR000286; IPR003084; SSF52768 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	alkaline ceramidase 2-like	3	P:GO:0006672; C:GO:0016021; F:GO:0017040	-	EC:3.5.1.23	IPR008901; PTHR12956 (PANTHER), PTHR12956:SF8 (PANTHER), SignalP (SIGNALP)
Caenorhabditis brenneri	hypothetical protein Cbre_JD20.006 [Caenorhabditis brenneri]	0				-
Brugia malayi	low density lipid receptor-related	30	P:GO:0010165; P:GO:0006898; C:GO:0031526; P:GO:0046879; P:GO:0031100; P:GO:0033280; C:GO:0005624; P:GO:0032526; P:GO:0006766; P:GO:0007568; P:GO:0008283; C:GO:0005615; F:GO:0005509; C:GO:0016021; P:GO:0030900; P:GO:0020028; C:GO:0005794; F:GO:0030492; C:GO:0005905; C:GO:0030139; P:GO:0016197; P:GO:0050789; P:GO:0042493; C:GO:0005768; P:GO:0045056; F:GO:0004872; C:GO:0005783;	-		IPR000152; IPR006210; IPR011042; IPR013032; G3DSA:2.10.25.10 (GENE3D), PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER), SSF57196 (SUPERFAMILY)
	-	0				-

Caenorhabditis elegans	laminin a	1	C:GO:0005578	-		IPR001791; IPR008985; IPR013320; PTHR10574 (PANTHER), PTHR10574:SF56 (PANTHER)
	-	0				-
Caenorhabditis elegans	and ph domain containing 6	0		F:GO:0005089; P:GO:0035023; F:GO:0005085; C:GO:0005737; F:GO:0008270; F:GO:0003674; P:GO:0050790; C:GO:0005575; C:GO:0005622; F:GO:0046872; P:GO:0008150; C:GO:0005856		IPR000219; IPR000306; IPR001849; IPR011011; IPR011993; IPR013083; IPR017455; PTHR12673 (PANTHER), SSF50729 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	uncoordi-ted protein isoform partially confirmed by transcript evidence	7	P:GO:0006629; F:GO:0005219; P:GO:0006816; P:GO:0006874; P:GO:0055085; F:GO:0005509; C:GO:0016021	-		-
Caenorhabditis elegans	amop domain containing protein	0		P:GO:0007160; C:GO:0016021		IPR003886
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	calcium-binding atopy-related autoantigen 1	2	C:GO:0016021; F:GO:0005509	-		-
Caenorhabditis briggsae	calcium-binding atopy-related autoantigen 1	2	C:GO:0016021; F:GO:0005509	-		IPR011992; IPR018247; IPR018249; PTHR12294 (PANTHER), PTHR12294:SF1 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	P:GO:0008340; P:GO:0040011	-		SignalP (SIGNALP)
Pongo abelii	cd81 antigen	9	P:GO:0046813; P:GO:0006661; P:GO:0043128; F:GO:0005515; P:GO:0008284; P:GO:0000187; P:GO:0008104; P:GO:0050731; C:GO:0005887	-		IPR000301; IPR018499; IPR018503; SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG08415 [Caenorhabditis briggsae]	0		F:GO:0005515		-
	-	0				-
Brugia malayi	n-acetyltransferase 10	2	F:GO:0008080; P:GO:0008152	-		PTHR10925 (PANTHER), PTHR10925:SF5 (PANTHER)
	-	0				-
	-	0				-
	-	0				-

Brugia malayi	pdz domain containing protein	0		P:GO:0000003; P:GO:0040035; P:GO:0002119; P:GO:0009792; P:GO:0040007; F:GO:0005515		IPR001478; G3DSA:2.30.42.10 (GENE3D)
Caenorhabditis elegans	asparagine synthase family protein	0		P:GO:0006529; F:GO:0004066		IPR014729; SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis briggsae	protein-tyrosine phosphatase containing protein	4	F:GO:0004725; P:GO:0006470; P:GO:0009792; F:GO:0008138	-	EC:3.1.3.48	IPR000242; IPR000387; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis briggsae	ribophorin i	2	C:GO:0030867; C:GO:0019718	-		IPR007676; SignalP (SIGNALP)
Caenorhabditis elegans	ribophorin i	4	C:GO:0008250; P:GO:0018279; F:GO:0005515; F:GO:0004579	-	EC:2.4.1.119	IPR007676
Caenorhabditis elegans	ribophorin i	3	C:GO:0019718; F:GO:0016740; C:GO:0030867	-		IPR007676; SignalP (SIGNALP)
Caenorhabditis elegans	ribophorin i	3	C:GO:0019718; F:GO:0016740; C:GO:0030867	-		IPR007676; SignalP (SIGNALP)
Caenorhabditis elegans	ribophorin i	3	C:GO:0019718; F:GO:0016740; C:GO:0030867	-		IPR007676; SignalP (SIGNALP)
Caenorhabditis elegans	apoptosis-inducing mitochondrion- 3	10	C:GO:0005829; P:GO:0006917; C:GO:0005743; F:GO:0008656; P:GO:0008635; P:GO:0051882; F:GO:0005515; C:GO:0005783; C:GO:0005634; C:GO:0005886	-		IPR001327; IPR004099; IPR013027; IPR016156; PR00411 (PRINTS), G3DSA:3.50.50.60 (GENE3D), PTHR22912 (PANTHER), PTHR22912:SF31 (PANTHER), SSF51905 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	zinc finger protein 534	3	F:GO:0008270; F:GO:0003676; C:GO:0005622	-		IPR007087; IPR013087; IPR015880; PTHR23223 (PANTHER), PTHR23223:SF25 (PANTHER), SSF57667 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Homo sapiens	proteasome (macropain) beta 8 (large multifunctio-l peptidase 7)	10	P:GO:0051436; P:GO:0051437; F:GO:0004298; P:GO:0031145; P:GO:0019882; F:GO:0005515; P:GO:0044419; C:GO:0005737; C:GO:0005839; C:GO:0005634	-	EC:3.4.25.0	-
Drosophila ananassae	atpase n2b	0		F:GO:0005524; F:GO:0000166		IPR005654

	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	matrilin 4	3	F:GO:0030414; F:GO:0005509; F:GO:0005515	-		IPR002035; PR00453 (PRINTS), G3DSA:3.40.50.410 (GENE3D), PTHR22992 (PANTHER), PTHR22992:SF12 (PANTHER), SSF53300 (SUPERFAMILY)
	-	0				-
	-	0				-
Brugia malayi	hypothetical protein Bm1_17960 [Brugia malayi]	0				-
Pan troglodytes	atp synthase subunit mitochondrial-like isoform 2	5	C:GO:0005753; F:GO:0022857; C:GO:0045263; P:GO:0042776; F:GO:0016887	-		-
Caenorhabditis elegans	briggsae cbr-rrf-3 protein	1	P:GO:0009792	-		SignalP (SIGNALP)
Caenorhabditis elegans	laminin a	1	C:GO:0005578	-		-
Ailuropoda melanoleuca	sodium potassium-transporting atpase subunit alpha-1	20	F:GO:0005515; P:GO:0045989; P:GO:0045822; F:GO:0003869; C:GO:0005792; C:GO:0016323; C:GO:0042470; F:GO:0046872; P:GO:0006754; C:GO:0042383; F:GO:0005391; P:GO:0045823; P:GO:0042493; P:GO:0031947; C:GO:0005890; P:GO:0006813; P:GO:0002026; F:GO:0005524; P:GO:0008217; P:GO:0006814	-	EC:3.1.3.41; EC:3.6.3.9	-
Caenorhabditis elegans	hypothetical protein T13H5.6 [Caenorhabditis elegans]	3	P:GO:0040007; P:GO:0006898; P:GO:0002119	-		IPR008516; SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; P:GO:0055085		-
	-	0				-
Loa loa	lps glycosyltransferase family protein	7	P:GO:0009103; P:GO:0040010; P:GO:0040035; F:GO:0016740; F:GO:0005515; P:GO:0040011; P:GO:0002009	-		-
	-	0				-
	-	0				-

	-	0				-
Caenorhabditis elegans	variable abnormal morphology family member (vab-10)	0				-
	-	0				-
Bombyx mori	endonuclease-reverse transcriptase	1	F:GO:0003824	-		-
	-	0				-
Loa loa	entric chromosome binding protein family member (hcp-6)	0		C:GO:0030117; F:GO:0005488; P:GO:0016192; P:GO:0006886; F:GO:0005515		-
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	hypothetical protein [Brugia malayi]	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				G3DSA:3.80.20.20 (GENE3D)
Homo sapiens	-dh dehydroge-se	4	P:GO:0006120; F:GO:0008137; P:GO:0006810; C:GO:0005747	-	EC:1.6.5.3	IPR007741; IPR012336; PTHR12878 (PANTHER)
	-	0				-
	-	0				-
Loa loa	zinc dhhc domain containing 17	0		P:GO:0043123; F:GO:0046872; C:GO:0016021; C:GO:0016020; C:GO:0030660; F:GO:0015095; F:GO:0004871; P:GO:0042953; C:GO:0000139; P:GO:0008152; C:GO:0005737; F:GO:0016409; C:GO:0031410; C:GO:0005794; F:GO:0008415; P:GO:0006811; P:GO:0006810; F:GO:0008270; F:GO:0019706; P:GO:0018345; F:GO:0016740; F:GO:0005515		SignalP (SIGNALP)
	-	0				-
	-	0				-

Angiostrongylus cantonensis	cg7484	0		F:GO:0004970; F:GO:0005216; C:GO:0016021; C:GO:0016020; C:GO:0045202; P:GO:0006811; P:GO:0006810; C:GO:0030054; F:GO:0005234; F:GO:0004872; P:GO:0045454; C:GO:0005886; C:GO:0045211		-
Loa loa	temporarily assigned gene -me family member (tag-53)	5	P:GO:0018991; C:GO:0016021; P:GO:0040010; F:GO:0005515; P:GO:0040011	-		PTHR10574 (PANTHER), PTHR10574:SF3 (PANTHER)
Homo sapiens	transmembrane protein isoform cra_c	1	C:GO:0016020	-		IPR005349; SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-smgl-1 protein	0				-
	-	0				-
	-	0				-
Camponotus floridanus	btb poz domain-containing protein 9	0		P:GO:0007155; F:GO:0005515		IPR000210; IPR011333; IPR013069; IPR013089; PTHR23230:SF181 (PANTHER)
	-	0				-
Loa loa	malonyl- synthase	1	F:GO:0003824	-		IPR000873; IPR020459; IPR020845; G3DSA:3.40.50.980 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF48 (PANTHER), SSF56801 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)

Chlorocebus aethiops	heavy chain non-muscle	43	C:GO:0030863; P:GO:0008360; C:GO:0031594; P:GO:0030048; F:GO:0030898; P:GO:0051295; C:GO:0005913; P:GO:0016337; F:GO:0043531; P:GO:0032796; P:GO:0015031; C:GO:0001772; P:GO:0050900; P:GO:0007229; C:GO:0005829; P:GO:0007520; F:GO:0000146; P:GO:0006509; P:GO:0043534; C:GO:0008305; C:GO:0005819; C:GO:0001726; P:GO:0007132; C:GO:0032154; P:GO:0000904; P:GO:0001768; F:GO:0043495;	-		-
Caenorhabditis briggsae	probable dimethyladenosine transferase	5	C:GO:0005737; C:GO:0005730; F:GO:0003723; P:GO:0000154; F:GO:0000179	-		IPR001737; G3DSA:3.40.50.150 (GENE3D), SSF53335 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	briggsae cbr-prx-2 protein	1	F:GO:0005488	-		-
Loa loa	hypothetical protein LOAG_05535 [Loa loa]	0				-
Loa loa	bromodomain containing protein	1	F:GO:0046872	-		-
	-	0				-
Caenorhabditis elegans	atp-dependent r-	4	F:GO:0003676; F:GO:0005524; F:GO:0005515; F:GO:0008026	-		PTHR18934 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0005515		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	audal c homolog family member (bcc-1)	0				-
	-	0				-
Caenorhabditis elegans	calcium binding egf domain containing protein	0		F:GO:0005509		IPR000859
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Brugia malayi	sh2 domain containing protein	4	P:GO:0006468; F:GO:0005515; F:GO:0004713; F:GO:0005524	-	EC:2.7.10.0	IPR000980
	-	0				-

Caenorhabditis briggsae	yms5_caeel ame: full=uncharacterized protein flags: precursor	0		P:GO:0007160; C:GO:0016021		IPR003886; SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0006355; F:GO:0043565; F:GO:0046983; F:GO:0003700		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG12331 [Caenorhabditis briggsae]	1	F:GO:0016791	-	EC:3.1.3.0	PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER)
Caenorhabditis elegans	hypothetical protein C43H6.7 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-sax-2 protein	11	F:GO:0005515; P:GO:0048601; P:GO:0016055; P:GO:0042052; P:GO:0008407; F:GO:0016563; P:GO:0045860; P:GO:0048800; P:GO:0035317; P:GO:0048814; C:GO:0005938	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	cytoplasmic intermediate filament protein	10	C:GO:0005737; P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0018991; F:GO:0005515; C:GO:0005882; P:GO:0040011; P:GO:0040007; F:GO:0005198	-		SignalP (SIGNALP)
	-	0				-
Loa loa	g protein pathway suppressor 1	4	P:GO:0000910; P:GO:0040035; F:GO:0005515; C:GO:0005634	-		IPR000717; IPR011991; IPR019585; PTHR14145 (PANTHER), PTHR14145:SF2 (PANTHER), SSF46785 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F43D9.1 [Caenorhabditis elegans]	0		C:GO:0016020; F:GO:0008158		SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-unc-8 protein	3	C:GO:0016020; F:GO:0005216; P:GO:0006811	-		SignalP (SIGNALP)
	-	0				-
	-	0				IPR003378; PTHR10811 (PANTHER), PTHR10811:SF1 (PANTHER)
	-	0				-
Homo sapiens	immunoglobulin kappa chain	3	C:GO:0005576; F:GO:0003823; P:GO:0006955	-		IPR013106; IPR013783; PTHR23267 (PANTHER), PTHR23267:SF33 (PANTHER), SSF48726 (SUPERFAMILY)

Homo sapiens	immunoglobulin kappa light chain vlj region	4	C:GO:0005576; F:GO:0005515; F:GO:0003823; P:GO:0006955	-		IPR013106; IPR013783; PTHR23267 (PANTHER), PTHR23267:SF33 (PANTHER), SSF48726 (SUPERFAMILY)
Homo sapiens	immunoglobulin kappa light chain vlj region	0				IPR003006; IPR003596; IPR003597; IPR007110; IPR013106; IPR013783; PTHR23267 (PANTHER), PTHR23267:SF33 (PANTHER), SSF48726 (SUPERFAMILY)
Homo sapiens	anti-tetanus toxoid immunoglobulin light chain variable region	0				IPR003596; IPR007110; IPR013106; IPR013783; PTHR23267 (PANTHER), PTHR23267:SF33 (PANTHER), SSF48726 (SUPERFAMILY)
Homo sapiens	ig kappa light chain	3	C:GO:0005576; F:GO:0003823; P:GO:0006955	-		IPR003596; IPR007110; IPR013106; IPR013783; PTHR23267 (PANTHER), PTHR23267:SF33 (PANTHER), SignalP (SIGNALP), SSF48726 (SUPERFAMILY)
Homo sapiens	immunoglobulin light chain variable region	3	C:GO:0005576; F:GO:0003823; P:GO:0006955	-		IPR003596; IPR007110; IPR013106; IPR013783; PTHR23267 (PANTHER), PTHR23267:SF33 (PANTHER), SSF48726 (SUPERFAMILY)
Homo sapiens	immunoglobulin kappa light chain vlj region	3	C:GO:0005576; F:GO:0003823; P:GO:0006955	-		IPR003596; IPR007110; IPR013106; IPR013783; PTHR23267 (PANTHER), PTHR23267:SF33 (PANTHER), SignalP (SIGNALP), SSF48726 (SUPERFAMILY)
Homo sapiens	immunoglobulin kappa light chain vlj region	4	C:GO:0005576; F:GO:0005515; F:GO:0003823; P:GO:0006955	-		IPR003006; IPR003596; IPR003597; IPR007110; IPR013106; IPR013783; PTHR23267 (PANTHER), PTHR23267:SF33 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis brenneri	hypothetical protein Cbre_JD15.003 [Caenorhabditis brenneri]	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis remanei	slo-2	6	C:GO:0016020; P:GO:0006813; P:GO:0008152; F:GO:0003824; F:GO:0015269; F:GO:0005488	-		PTHR10027 (PANTHER), PTHR10027:SF6 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	protein-tyrosine phosphatase containing protein	3	P:GO:0016311; F:GO:0004721; P:GO:0009792	-	EC:3.1.3.16	IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-dnj-2 protein	2	C:GO:0016021; F:GO:0031072	-		IPR001623; IPR015609; PTHR11821:SF43 (PANTHER), SignalP (SIGNALP)

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	9	P:GO:0055085; P:GO:0040010; P:GO:0009851; C:GO:0016021; F:GO:0042626; P:GO:0000003; F:GO:0005524; P:GO:0002119; P:GO:0016246	-		G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF82 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				PD035033 (PRODOM)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	duoxa_caeel ame: full=duoxa-like protein	0		C:GO:0005789; C:GO:0016021; P:GO:0015031		IPR018469; SignalP (SIGNALP)
Caenorhabditis elegans	tfiih basal transcription factor complex helicase subunit	4	F:GO:0008026; P:GO:0006139; F:GO:0003676; F:GO:0000166	-		-
	-	0				-
Homo sapiens	mitochondrial ribosomal protein s21	4	C:GO:0005763; C:GO:0005743; F:GO:0003735; P:GO:0006412	-	EC:3.6.5.3	IPR001911; PTHR21109 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	kelch-like 10	0		F:GO:0045480; P:GO:0055114; F:GO:0016491; F:GO:0005515		IPR006652; IPR013089; IPR015915; PTHR23230:SF184 (PANTHER), SSF117281 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-tag-180 protein	0		C:GO:0016020		PTHR10166 (PANTHER), PTHR10166:SF4 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-lam-3 protein	3	P:GO:0007155; P:GO:0050794; C:GO:0005604	-		-
Loa loa	hypothetical protein LOAG_08316 [Loa loa]	0				-
	-	0				-
Caenorhabditis elegans	Hypothetical protein Y55F3BL.4 [Caenorhabditis elegans]	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-cpin-1 protein	0		F:GO:0016787; F:GO:0016810		-
Caenorhabditis elegans	dynein heavy chain	5	P:GO:0007018; C:GO:0030286; F:GO:0016887; F:GO:0005524; F:GO:0003777	-		IPR004273; PTHR10676 (PANTHER), PTHR10676:SF28 (PANTHER)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG19874 [Caenorhabditis briggsae]	4	P:GO:0002119; P:GO:0040010; P:GO:0000003; P:GO:0006898	-		-
	-	0				SignalP (SIGNALP)

Pan troglodytes	cystatin c	44	P:GO:0010711; P:GO:0060548; P:GO:0010951; C:GO:0031982; C:GO:0031965; P:GO:0070301; C:GO:0005615; P:GO:0043067; C:GO:0005764; P:GO:0042747; P:GO:0014070; F:GO:0001540; P:GO:0010716; P:GO:0008284; P:GO:0007420; C:GO:0043025; P:GO:0001654; P:GO:0001666; P:GO:0048678; C:GO:0005771; P:GO:0006915; P:GO:0007566; P:GO:0051789; P:GO:0042493; P:GO:0060009; F:GO:0002020; C:GO:0048471;	-		-
Caenorhabditis briggsae	gamma-interferon-inducible lysosomal thiol reductase precursor	0				IPR004911; PTHR13234:SF3 (PANTHER)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG13928 [Caenorhabditis briggsae]	0		F:GO:0003951; P:GO:0008152; F:GO:0005515		-
	-	0				-
Caenorhabditis briggsae	family c54 u-ssigned peptidase (c54 family)	1	F:GO:0016787	-		IPR005078; PTHR22624:SF15 (PANTHER)
Caenorhabditis elegans	briggsae cbr-atm-1 protein	4	C:GO:0000785; F:GO:0005488; P:GO:0043581; F:GO:0016740	-		IPR000403; IPR011009; IPR015519; G3DSA:3.30.1010.10 (GENE3D), PTHR11139 (PANTHER)
Caenorhabditis sp. PS1010	elegans protein confirmed by transcript evidence	0				IPR011107
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	F:GO:0015269; C:GO:0016020	-		IPR011996; IPR015449; PTHR10153:SF6 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	polh (d- polymerase eta) homolog family member (polh-1)	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	kinesin family member 3a	15	C:GO:0035085; P:GO:0007224; P:GO:0048260; C:GO:0008021; P:GO:0007507; F:GO:0003774; F:GO:0005515; P:GO:0021904; F:GO:0000166; C:GO:0032391; P:GO:0001822; P:GO:0007368; P:GO:0042384; P:GO:0001701; P:GO:0009952	-		PTHR16012 (PANTHER), PTHR16012:SF160 (PANTHER)
	-	0				-
Caenorhabditis briggsae	nuclear receptor nhr-1	1	F:GO:0005515	-		-
	-	0				-
	-	0				-
Callithrix jacchus	peroxiredoxin 1	19	P:GO:0001501; P:GO:0032872; P:GO:0042744; P:GO:0034101; C:GO:0005759; P:GO:0042267; C:GO:0005719; F:GO:0020037; P:GO:0008283; C:GO:0042470; P:GO:0019430; F:GO:0008379; C:GO:0005730; C:GO:0005829; P:GO:0045454; P:GO:0042345; P:GO:0055114; F:GO:0042803; C:GO:0005782	-		IPR000866; IPR012335; IPR012336; PTHR10681 (PANTHER), PTHR10681:SF8 (PANTHER)
Angiostrongylus cantonensis	gamma-butyrobetaine dioxyge-se	7	C:GO:0005737; F:GO:0005506; C:GO:0043231; P:GO:0055114; F:GO:0016702; F:GO:0008336; P:GO:0045329	-	EC:1.13.11.0 ; EC:1.14.11.1	IPR022407; PTHR10696 (PANTHER), PTHR10696:SF3 (PANTHER)
Caenorhabditis elegans	calcitonin receptor	5	P:GO:0007186; C:GO:0016021; P:GO:0007165; C:GO:0005886; F:GO:0004930	-		IPR000832; PTHR12011 (PANTHER), PTHR12011:SF14 (PANTHER)
	-	0				IPR015418; PTHR13476 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	uncoordi-ted family member (unc-89)	0		F:GO:0004672; F:GO:0005524; P:GO:0006468; F:GO:0004674		IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF7 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	briggsae cbr-ztf-8 protein	0		F:GO:0003676; F:GO:0008270; F:GO:0005515; C:GO:0005622		-
	-	0				-
Ailuropoda melanoleuca	p4hb protein	12	F:GO:0003756; F:GO:0004656; C:GO:0005793; P:GO:0045454; C:GO:0009986; C:GO:0042470; C:GO:0005792; C:GO:0005788; F:GO:0005515; P:GO:0018401; C:GO:0005576; C:GO:0005886	-	EC:5.3.4.1; EC:1.14.11.2	IPR012335; IPR012336; IPR013766; PTHR18929 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	serotonin receptor	4	C:GO:0016021; P:GO:0007186; F:GO:0004930; P:GO:0007165	-		IPR000276; IPR017452; G3DSA:1.20.1070.10 (GENE3D), PTHR19266 (PANTHER), PTHR19266:SF85 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	temporarily assigned gene -me family member (tag-180)	1	C:GO:0016020	-		PTHR10166 (PANTHER), PTHR10166:SF4 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	F:GO:0046872	-		IPR001128; PTHR19383:SF176 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	endoplasmin precursor	13	C:GO:0016529; P:GO:0040010; P:GO:0030433; P:GO:0006457; C:GO:0044459; C:GO:0042470; F:GO:0005524; P:GO:0002119; C:GO:0005788; P:GO:0040011; F:GO:0051082; P:GO:0006898; P:GO:0006950	-		IPR001404; IPR003594; IPR015566; IPR019805; IPR020568; IPR020575; IPR020576; SignalP (SIGNALP), SSF110942 (SUPERFAMILY)

Caenorhabditis briggsae	endoplasmin precursor	13	C:GO:0016529; P:GO:0040010; P:GO:0030433; P:GO:0006457; C:GO:0044459; C:GO:0042470; F:GO:0005524; P:GO:0002119; C:GO:0005788; P:GO:0040011; F:GO:0051082; P:GO:0006898; P:GO:0006950	-		IPR001404; IPR003594; IPR015566; IPR019805; IPR020568; IPR020575; IPR020576; SignalP (SIGNALP), SSF110942 (SUPERFAMILY)
Caenorhabditis briggsae	endoplasmin precursor	13	C:GO:0016529; P:GO:0040010; P:GO:0030433; P:GO:0006457; C:GO:0044459; C:GO:0042470; F:GO:0005524; P:GO:0002119; C:GO:0005788; P:GO:0040011; F:GO:0051082; P:GO:0006898; P:GO:0006950	-		IPR001404; IPR003594; IPR015566; IPR019805; IPR020568; IPR020575; IPR020576; SignalP (SIGNALP), SSF110942 (SUPERFAMILY)
Caenorhabditis elegans	atp-binding domain-containing protein 3	13	P:GO:0006412; C:GO:0005829; P:GO:0034227; P:GO:0000302; P:GO:0048598; P:GO:0048599; P:GO:0007283; F:GO:0005524; F:GO:0016740; P:GO:0040025; P:GO:0002098; F:GO:0000049; P:GO:0006974	-	EC:3.6.5.3	PTHR11807 (PANTHER), PTHR11807:SF3 (PANTHER)
	-	0				-
Loa loa	acyltransferase family protein	0		F:GO:0008415; F:GO:0016740; P:GO:0008152		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	briggsae cbr-qui-1 protein	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein F46C5.6 [Caenorhabditis elegans]	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG09112 [Caenorhabditis briggsae]	0		F:GO:0003723; F:GO:0005488; P:GO:0006396; C:GO:0005622		IPR012340; IPR016027; IPR022967

Caenorhabditis briggsae	acyl-coa dehydroge-se	5	F:GO:0050660; P:GO:0009792; P:GO:0055114; F:GO:0003995; P:GO:0040010	-	EC:1.3.99.3	IPR006089; IPR006090; IPR006091; IPR006092; IPR009075; IPR009100; IPR013786; PTHR10909 (PANTHER), PTHR10909:SF10 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-acn-1 protein	12	P:GO:0040035; P:GO:0009792; F:GO:0008241; P:GO:0002119; P:GO:0040018; P:GO:0018991; P:GO:0018996; P:GO:0040010; P:GO:0040011; P:GO:0006508; C:GO:0016020; F:GO:0008237	-	EC:3.4.15.0	IPR001548; PTHR10514:SF7 (PANTHER)
Pongo abelii	alpha-actinin-1-like isoform 4	13	C:GO:0005829; C:GO:0030018; F:GO:0017166; F:GO:0005509; P:GO:0051271; C:GO:0005730; P:GO:0042981; P:GO:0048041; C:GO:0031143; C:GO:0005925; F:GO:0003779; C:GO:0015629; F:GO:0005178	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Angiostrongylus cantonensis	briggsae cbr-nhl-1 protein	3	F:GO:0005515; F:GO:0046872; P:GO:0006915	-		-
Caenorhabditis japonica	cpb1_caeja ame: full=cytoplasmic polyadenylation element-binding protein 1	0		F:GO:0003676; F:GO:0003723; P:GO:0030154; F:GO:0000166; P:GO:0007275; P:GO:0007283		-
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	polypeptide 1	9	F:GO:0003899; P:GO:0000910; P:GO:0040007; P:GO:0006260; P:GO:0040035; P:GO:0002119; F:GO:0005515; P:GO:0002009; P:GO:0009792	-	EC:2.7.7.6	IPR002755; IPR014052; G3DSA:3.90.920.10 (GENE3D), SSF56747 (SUPERFAMILY)

Loa loa	abnormal go-d development family member (gon-2)	6	P:GO:0007067; P:GO:0055085; P:GO:0006811; C:GO:0016021; P:GO:0008406; F:GO:0005216	-		PTHR13800 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Haemonchus contortus	ecdysone receptor isoform +	6	F:GO:0003700; F:GO:0043565; F:GO:0003707; C:GO:0005634; F:GO:0008270; P:GO:0006355	-		-
Caenorhabditis elegans	olfactory receptor 350	4	P:GO:0007186; C:GO:0016021; P:GO:0007165; F:GO:0004930	-		-
Caenorhabditis briggsae	rnp-1 like r--binding protein	4	F:GO:0003723; P:GO:0009792; P:GO:0006378; F:GO:0000166	-		IPR000504; IPR012677; IPR015465; PTHR10432 (PANTHER), SSF54928 (SUPERFAMILY)
Loa loa	ribonucleases p mrp protein subunit pop1 containing protein	0		P:GO:0001682; F:GO:0004526; P:GO:0006396		-
	-	0				-
Caenorhabditis briggsae	d- polymerase family b containing protein	0		F:GO:0003676; P:GO:0006139; P:GO:0006260; F:GO:0016779; F:GO:0003887; F:GO:0016740; F:GO:0000166; F:GO:0003677		-
	-	0				-
Brugia malayi	briggsae cbr-emb-30 protein	2	F:GO:0016787; F:GO:0005515	-		IPR015943
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	isoform c	6	P:GO:0043254; P:GO:0006355; F:GO:0005524; F:GO:0016887; F:GO:0008134; C:GO:0005634	-		IPR011704; G3DSA:3.40.50.300 (GENE3D), PTHR22908 (PANTHER), PTHR22908:SF13 (PANTHER)

Caenorhabditis elegans	proteasome-associated protein ecm29 homolog	10	C:GO:0000502; P:GO:0030433; C:GO:0030134; C:GO:0005813; C:GO:0005770; C:GO:0005769; P:GO:0007067; C:GO:0005802; C:GO:0005783; C:GO:0005634	-		PTHR23346 (PANTHER), PTHR23346:SF2 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Pongo abelii	transmembrane protein 219	0		C:GO:0016021; C:GO:0016020		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	hypothetical protein Y95B8A.11 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-cua-1 protein	7	F:GO:0046872; F:GO:0015662; F:GO:0046873; F:GO:0000166; P:GO:0008152; P:GO:0030001; C:GO:0016020	-		IPR001757; IPR006121; IPR006403; IPR017969; G3DSA:3.30.70.100 (GENE3D), PTHR11939:SF38 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	olfactory ing defective family member (olrn-1)	0				-
Caenorhabditis briggsae	Hypothetical protein CBG19593 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	phosphatidate phosphatase	2	F:GO:0016791; C:GO:0016021	-	EC:3.1.3.0	IPR000326; IPR016118; PTHR10165 (PANTHER), PTHR10165:SF22 (PANTHER)
Caenorhabditis briggsae	phosphatidate phosphatase	2	F:GO:0016791; C:GO:0016021	-	EC:3.1.3.0	IPR000326; IPR016118; PTHR10165 (PANTHER), PTHR10165:SF22 (PANTHER)
Caenorhabditis briggsae	phosphatidate phosphatase	2	F:GO:0016791; C:GO:0016021	-	EC:3.1.3.0	IPR000326; IPR016118; PTHR10165 (PANTHER), PTHR10165:SF22 (PANTHER)
Caenorhabditis briggsae	phosphatidate phosphatase	2	F:GO:0016791; C:GO:0016021	-	EC:3.1.3.0	IPR000326; IPR016118; PTHR10165 (PANTHER), PTHR10165:SF22 (PANTHER)
Caenorhabditis elegans	r- polymerase domain 2 family protein	3	C:GO:0005736; F:GO:0005515; F:GO:0016740	-		IPR000722; IPR015699; PTHR19376 (PANTHER), SSF64484 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	r- dependent r- polymerase family protein	1	F:GO:0005515	-		-
Caenorhabditis briggsae	hed family member (ptc-2)	0		C:GO:0016021; C:GO:0016020; F:GO:0008158		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	C:GO:0043229	-		-

	-	0				-
Loa loa	uncoordi-ted family member (unc-13)	8	F:GO:0005516; P:GO:0023034; F:GO:0046872; C:GO:0008021; C:GO:0043195; P:GO:0016082; C:GO:0045211; F:GO:0019992	-		IPR014772; IPR019558; PTHR10480 (PANTHER)
Caenorhabditis elegans	ypc4_caeel ame: full=uncharacterized protein	0		F:GO:0005515		-
Caenorhabditis briggsae	briggsae cbr-deg-1 protein	4	C:GO:0016021; F:GO:0005272; P:GO:0008219; P:GO:0006814	-		-
Caenorhabditis briggsae	yk84_caeel ame: full=uncharacterized protein	1	F:GO:0016787	-		-
Caenorhabditis elegans	calumenin isoform 1	14	P:GO:0010171; P:GO:0002119; C:GO:0016529; C:GO:0005788; C:GO:0005794; F:GO:0005515; P:GO:0018996; F:GO:0005509; P:GO:0000003; P:GO:0008340; P:GO:0040011; C:GO:0005576; P:GO:0040007; P:GO:0002009	-		IPR002048; IPR011992; IPR018247; IPR018249; PTHR10827 (PANTHER), SSF47473 (SUPERFAMILY)
Brugia malayi	regulator of g protein sig-ling domain containing protein	0		F:GO:0004871		-
Caenorhabditis briggsae	briggsae cbr-acc-1 protein	4	C:GO:0016021; C:GO:0045211; F:GO:0005230; P:GO:0006810	-		-
Caenorhabditis briggsae	Hypothetical protein CBG17315 [Caenorhabditis briggsae]	1	F:GO:0005488	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	protein-tyrosine phosphatase containing protein	1	F:GO:0016791	-	EC:3.1.3.0	IPR000242; IPR000387; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), SSF52799 (SUPERFAMILY)
Loa loa	elegans protein confirmed by transcript evidence	0		C:GO:0016021; C:GO:0016020; C:GO:0005829		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF283 (PANTHER)
Caenorhabditis briggsae	clc-type chloride channel family member (clh-2)	6	P:GO:0009792; F:GO:0005247; P:GO:0055085; P:GO:0000003; C:GO:0016021; P:GO:0006821	-		-
	-	0				-
	-	0				-

Caenorhabditis briggsae	plasminogen precursor	10	P:GO:0022617; F:GO:0004252; C:GO:0005615; P:GO:0051918; P:GO:0048856; P:GO:0010812; F:GO:0043498; P:GO:0051919; F:GO:0034185; C:GO:0031232	-	EC:3.4.21.0	-
	-	0				-
Caenorhabditis briggsae	lactate dehydroge-se d	4	F:GO:0016491; F:GO:0005515; C:GO:0016020; C:GO:0005739	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	- h exchanger family member (nhx-9)	2	P:GO:0006811; F:GO:0015297	-		-
	-	0				-
Caenorhabditis briggsae	protein ki-se domain containing protein	3	F:GO:0004672; P:GO:0000003; F:GO:0000166	-		IPR000719; IPR001245; IPR008266; IPR011009; IPR020685; IPR020764; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
	-	0				-
	-	0				-
Caenorhabditis briggsae	annexin b11 isoform a	2	F:GO:0005509; F:GO:0005544	-		IPR001464; IPR013286; IPR018252; IPR018502; PTHR10502:SF30 (PANTHER)
Caenorhabditis elegans	6-phosphofructo-2-ki-se fructose -bisphosphatase	4	F:GO:0003873; P:GO:0006003; F:GO:0016787; F:GO:0005524	-	EC:2.7.1.105	IPR001345; IPR003094; IPR013079; G3DSA:3.40.50.300 (GENE3D), PTHR10606:SF11 (PANTHER), SSF52540 (SUPERFAMILY), SSF53254 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Homo sapiens	lactotransferrin precursor	10	F:GO:0008199; P:GO:0042742; P:GO:0006879; P:GO:0006959; P:GO:0006826; F:GO:0005515; F:GO:0004252; F:GO:0008201; C:GO:0030141; C:GO:0005576	-	EC:3.4.21.0	-
	-	0				-
Apis mellifera	pantothe-te ki-se 4	8	P:GO:0009792; P:GO:0002119; P:GO:0015937; P:GO:0040010; F:GO:0005524; P:GO:0000003; P:GO:0008340; F:GO:0004594	-	EC:2.7.1.33	IPR011602; PTHR12280 (PANTHER)
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	hypothetical protein C35B8.3 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	aldehyde dehydroge-se	2	P:GO:0044237; F:GO:0016491	-		IPR012394; IPR015590; IPR016161; IPR016162
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	24-dehydrocholesterol reductase	10	P:GO:0009888; P:GO:0043154; F:GO:0050614; C:GO:0005789; P:GO:0006916; P:GO:0006695; F:GO:0042605; F:GO:0019899; C:GO:0005634; P:GO:0006979	-	EC:1.3.1.72	IPR006094; IPR016166; IPR016168; PTHR10801 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	24-dehydrocholesterol reductase	10	P:GO:0009888; P:GO:0043154; F:GO:0050614; C:GO:0005789; P:GO:0006916; P:GO:0006695; F:GO:0042605; F:GO:0019899; C:GO:0005634; P:GO:0006979	-	EC:1.3.1.72	IPR006094; IPR016166; IPR016168; PTHR10801 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				IPR012435; SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	gf19599- partial	0		C:GO:0016021; P:GO:0008218; F:GO:0004857; C:GO:0016020; P:GO:0018298; C:GO:0005578; C:GO:0005576; F:GO:0030414; F:GO:0005201; F:GO:0004867; F:GO:0005509		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG24940 [Caenorhabditis briggsae]	0				IPR000477
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-

Callithrix jacchus	class member 1	8	C:GO:0005625; F:GO:0004559; C:GO:0005764; P:GO:0006013; P:GO:0006517; F:GO:0008270; P:GO:0007611; F:GO:0005537	-	EC:3.2.1.24	IPR000602; IPR011330; PTHR11607 (PANTHER), PTHR11607:SF3 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Trichoplax adhaerens	fat tumor suppressor homolog 1	1	P:GO:0009987	-		IPR002126; IPR015919; PTHR10596 (PANTHER), PTHR10596:SF74 (PANTHER)
Caenorhabditis elegans	groundhog (hedgehog-like family) protein partially confirmed by transcript evidence	1	F:GO:0005515	-		IPR007284
	-	0				-
Ectocarpus siliculosus	hypothetical protein [Ectocarpus siliculosus]	0		F:GO:0005524; F:GO:0000166; F:GO:0017111; F:GO:0005515; C:GO:0005622; P:GO:0006810		PTHR10887 (PANTHER)
	-	0				-
Caenorhabditis elegans	neuro-l symmetry protein isoform b	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	dolichyl pyrophosphate man9 c2 alpha- -glucosyltransferase	2	P:GO:0000003; C:GO:0044425	-		IPR004856; SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	topoisomerase iii alpha	7	P:GO:0006268; P:GO:0007276; F:GO:0003917; P:GO:0007126; C:GO:0005694; P:GO:0006265; F:GO:0008270	-	EC:5.99.1.2	-
	-	0				-
Nasonia vitripennis	PREDICTED: similar to ENSANGP00000010363 [-sonia vitripennis]	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	sodium-bile acid cotransporter	2	F:GO:0008508; C:GO:0016021	-		IPR002657; SignalP (SIGNALP)
Caenorhabditis briggsae	serine threonine-protein phosphatase 5	11	C:GO:0005829; P:GO:0051291; C:GO:0043005; F:GO:0004871; P:GO:0016311; P:GO:0043123; C:GO:0043025; F:GO:0019904; F:GO:0004721; P:GO:0043278; C:GO:0005634	-	EC:3.1.3.16	IPR011990; IPR013026; IPR019734; PTHR22904 (PANTHER), PTHR22904:SF12 (PANTHER), SSF48452 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	hypothetical protein Y69A2AR.31 [Caenorhabditis elegans]	0				-

	-	0				-
	-	0				-
Caenorhabditis elegans	low density lipid receptor-related	3	F:GO:0004872; C:GO:0016021; F:GO:0005509	-		IPR011042
Caenorhabditis elegans	hypothetical kda protein in chromosome	1	F:GO:0005515	-		-
Caenorhabditis elegans	hypothetical protein Y71H2AM.15 [Caenorhabditis elegans]	0		P:GO:0008340; F:GO:0005515		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	u2af splicing factor family member (uaf-1)	7	P:GO:0008380; F:GO:0003723; F:GO:0005515; P:GO:0006397; C:GO:0030529; C:GO:0005634; F:GO:0000166	-		-
Loa loa	zinc c2h2 type family protein	0		F:GO:0046872; F:GO:0003676; F:GO:0003674; P:GO:0008150; F:GO:0008270; C:GO:0005575; C:GO:0005622		IPR007087; IPR013087; IPR015880; PTHR23224 (PANTHER), PTHR23224:SF209 (PANTHER), SSF57667 (SUPERFAMILY)
	-	0				-
Loa loa	pdz domain containing protein	0		P:GO:0000003; P:GO:0040035; P:GO:0002119; P:GO:0009792; P:GO:0040007; F:GO:0005515		-
	-	0				-
Caenorhabditis elegans	hypothetical protein Y71H2AM.13 [Caenorhabditis elegans]	0		F:GO:0016787		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Dictyocaulus viviparus	60s ribosomal protein l37a	8	P:GO:0000022; P:GO:0006412; P:GO:0040010; F:GO:0046872; F:GO:0003735; P:GO:0002119; P:GO:0009792; C:GO:0022625	-	EC:3.6.5.3	IPR002674; IPR011331; IPR011332; PTHR11517:SF1 (PANTHER)
Caenorhabditis briggsae	protein ki-se domain containing protein	3	F:GO:0004672; P:GO:0040011; F:GO:0000166	-		IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)

Loa loa	mutator family member (mut-7)	0		F:GO:0003676; P:GO:0006139; F:GO:0004527; F:GO:0005515; C:GO:0005622; F:GO:0008408		IPR002562; IPR012337; G3DSA:3.30.420.10 (GENE3D)
Caenorhabditis briggsae	hydroxypyruvate reductase	0		P:GO:0055114; F:GO:0016491		G3DSA:3.40.50.10180 (GENE3D), PTHR12227 (PANTHER), SignalP (SIGNALP), SSF82544 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-spon-1 protein	0				-
Caenorhabditis briggsae	Hypothetical protein CBG03199 [Caenorhabditis briggsae]	0		C:GO:0016021; P:GO:0007186		PTHR19264 (PANTHER), PTHR19264:SF286 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis briggsae	briggsae cbr-cdh-12 protein	1	C:GO:0016020	-		-
	-	0				-
Brugia malayi	golgi s-p receptor complex member 2	4	C:GO:0000139; C:GO:0005789; F:GO:0005515; P:GO:0016192	-		PTHR21230 (PANTHER), PTHR21230:SF1 (PANTHER), PF12352 (PFAM)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		C:GO:0016021; C:GO:0016020		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Ailuropoda melanoleuca	tripartite motif-containing 28	15	C:GO:0005654; P:GO:0000122; F:GO:0003714; F:GO:0008270; P:GO:0001837; P:GO:0046777; F:GO:0070087; C:GO:0005719; P:GO:0043193; F:GO:0004672; C:GO:0005730; F:GO:0003713; C:GO:0005720; F:GO:0043565; F:GO:0003700	-		-
Brugia malayi	protein-tyrosine phosphatase containing protein	4	P:GO:0016311; F:GO:0004721; P:GO:0009792; P:GO:0000003	-	EC:3.1.3.16	IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis elegans	thioredoxin-like protein	0		P:GO:0045454		-
	-	0				SignalP (SIGNALP)
Haemonchus contortus	microsomal aminopeptidase	3	C:GO:0016020; F:GO:0046872; F:GO:0070011	-		SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	timeless protein	8	P:GO:0042127; F:GO:0005515; P:GO:0007275; P:GO:0033261; P:GO:0048856; P:GO:0009628; P:GO:0016481; C:GO:0000790	-		IPR006906
Pan troglodytes	alpha-2-macroglobulin precursor	12	F:GO:0004867; F:GO:0043120; F:GO:0019966; P:GO:0001869; P:GO:0007584; C:GO:0005615; C:GO:0031093; F:GO:0019959; F:GO:0019899; P:GO:0010037; P:GO:0051384; P:GO:0006953	-		IPR011626; G3DSA:1.50.10.20 (GENE3D), PTHR11412 (PANTHER), PTHR11412:SF11 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	cd9 antigen	4	P:GO:0009987; C:GO:0016021; P:GO:0016043; C:GO:0005886	-		IPR000301; IPR008952; IPR018499; PTHR19282 (PANTHER), PTHR19282:SF14 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	cd9 antigen	4	P:GO:0009987; C:GO:0016021; P:GO:0007399; C:GO:0005886	-		IPR000301; IPR008952; IPR018499; PTHR19282 (PANTHER), PTHR19282:SF14 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein Y54G2A.29 [Caenorhabditis elegans]	0				IPR019326
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0000003; P:GO:0040011; C:GO:0016020; P:GO:0040010; P:GO:0002119; P:GO:0040007		-
	-	0				-
	-	0				SignalP (SIGNALP)
Schistosoma mansoni	inhibitor of growth family member 5	0		F:GO:0046872; F:GO:0008270; F:GO:0005515		-
	-	0				SignalP (SIGNALP)
	-	0				-
Homo sapiens	-dh dehydroge-se	4	P:GO:0006120; F:GO:0008137; P:GO:0006810; C:GO:0005747	-	EC:1.6.5.3	-
	-	0				-
Brugia malayi	nuclear receptor subfamily 2 group c member 2	3	P:GO:0045449; F:GO:0004872; F:GO:0005515	-		IPR001628; IPR008946; IPR013088; PR00350 (PRINTS), PTHR11865 (PANTHER), PTHR11865:SF147 (PANTHER), SignalP (SIGNALP), SSF57716 (SUPERFAMILY)

	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	astacin-like metalloendopeptidase (m12 family)	3	F:GO:0004222; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	IPR001506; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF64 (PANTHER), SSF55486 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	ck1 worm6 protein ki-se	4	P:GO:0007283; P:GO:0006468; F:GO:0004672; F:GO:0005524	-		IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Brugia malayi	nfrkb protein	0		F:GO:0002020; P:GO:0006366; F:GO:0003704; C:GO:0031011; C:GO:0005730; F:GO:0003677; P:GO:0006954; C:GO:0005634		-
Brugia malayi	nfrkb protein	0		F:GO:0002020; P:GO:0006366; F:GO:0003704; C:GO:0031011; C:GO:0005730; F:GO:0003677; P:GO:0006954; C:GO:0005634		-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	5	C:GO:0016021; F:GO:0015250; C:GO:0043025; C:GO:0005929; P:GO:0006833	-		IPR000425; PTHR19139:SF25 (PANTHER)
Caenorhabditis briggsae	tapt1_caeel ame: full=protein tapt1 homolog	1	P:GO:0009792	-		-
Caenorhabditis elegans	briggsae cbr-casy-1 protein	9	P:GO:0009792; C:GO:0005615; P:GO:0007156; F:GO:0005515; C:GO:0032809; P:GO:0008355; C:GO:0043231; F:GO:0005509; C:GO:0016021	-		-
	-	0				-
	-	0				-
Brugia malayi	adducin family member (add-1)	0		F:GO:0046872		PTHR10672 (PANTHER), PTHR10672:SF3 (PANTHER)
	-	0				-
Caenorhabditis elegans	hypothetical protein ZK973.1 [Caenorhabditis elegans]	0		P:GO:0006139; F:GO:0016788		IPR018974

Haematobia irritans irritans	cyclin-dependent ki-se (cdc2-like) 10	4	P:GO:0009987; C:GO:0005634; F:GO:0004674; F:GO:0000166	-	EC:2.7.11.0	IPR000719; IPR002290; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF86 (PANTHER)
	-	0				SignalP (SIGNALP)
Pongo abelii	tr- methyltransferase 112 homolog	4	C:GO:0043234; F:GO:0008276; F:GO:0005515; P:GO:0018364	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	5	P:GO:0009792; P:GO:0000003; P:GO:0040010; P:GO:0006810; P:GO:0002119	-		-
	-	0				-
	-	0				IPR003677; PTHR21593 (PANTHER)
Caenorhabditis elegans	sdad1 protein	5	C:GO:0005730; P:GO:0002119; P:GO:0006898; P:GO:0040007; P:GO:0051729	-		PTHR12730 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	transcription elongation factor a 2	6	F:GO:0030528; P:GO:0006357; F:GO:0003676; F:GO:0046872; F:GO:0005515; C:GO:0005654	-		IPR001222; IPR003618; IPR006289; IPR016492; IPR017890; IPR017923; G3DSA:2.20.25.10 (GENE3D), PTHR11477 (PANTHER), SSF57783 (SUPERFAMILY)
Nippostrongylus brasiliensis	globin	6	F:GO:0020037; C:GO:0005615; C:GO:0005737; F:GO:0005344; P:GO:0015671; F:GO:0019825	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	rn207_caeel ame: full=probable ring finger protein 207 homolog	1	F:GO:0046872	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		-
	-	0				-

	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	cytochrome family subfamily polypeptide 2	5	F:GO:0009055; F:GO:0004497; F:GO:0020037; P:GO:0055114; C:GO:0016020	-		IPR001128; IPR002403; PTHR19383:SF165 (PANTHER)
Danio rerio	alpha- -mannosylglycoprotein 6-beta-n-acetylglucosaminyltransferase a	4	C:GO:0000139; F:GO:0030144; P:GO:0006487; C:GO:0016021	-	EC:2.4.1.155	PTHR15075 (PANTHER)
Caenorhabditis elegans	collagen type iv alpha-3-binding protein	0		F:GO:0004674		IPR001849; IPR002913; IPR011993; G3DSA:3.30.530.20 (GENE3D), PTHR10219 (PANTHER), PTHR10219:SF3 (PANTHER), SSF50729 (SUPERFAMILY), SSF55961 (SUPERFAMILY)
	-	0				IPR000626; IPR019955; G3DSA:3.10.20.90 (GENE3D), SSF54236 (SUPERFAMILY)
	-	0				-
Schistosoma mansoni	-s13_caeel ame: full=zinc metalloprotei-se -s-13 ame: full=nematode astacin 13 flags: precursor	0		F:GO:0008233		IPR003582
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	F:GO:0005515; P:GO:0007600; P:GO:0007165	-		IPR011021; IPR014756; PTHR11188 (PANTHER), PTHR11188:SF13 (PANTHER)
Bos taurus	chaperonin containing subunit 3	5	C:GO:0005856; P:GO:0006457; C:GO:0005832; F:GO:0005524; F:GO:0051082	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				G3DSA:3.40.390.10 (GENE3D), PTHR10201 (PANTHER), PTHR10201:SF5 (PANTHER)
Caenorhabditis sp. PS1010	elegans protein partially confirmed by transcript evidence	8	P:GO:0002119; P:GO:0006468; P:GO:0040010; F:GO:0005524; P:GO:0019915; P:GO:0006898; P:GO:0006974; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	daf-16 foxo germline tumor affecting family member (dct-1)	8	F:GO:0002020; P:GO:0043065; F:GO:0003700; P:GO:0051726; P:GO:0008340; C:GO:0016021; F:GO:0042803; C:GO:0031966	-		-
Loa loa	chromaffin granule amine transporter	0				-
	-	0				-
	-	0				-

Caenorhabditis elegans	hot_caeel ame: full=probable hydroxyacid-oxoacid mitochondrial short=hot flags: precursor	7	F:GO:0047988; F:GO:0046872; P:GO:0015993; P:GO:0009073; P:GO:0055114; F:GO:0003856; C:GO:0005739	-	EC:1.1.99.24; EC:4.2.3.4	-
Pan troglodytes	eukaryotic translation elongation factor 1 beta 2	5	C:GO:0005829; F:GO:0003746; C:GO:0005853; F:GO:0005515; P:GO:0006414	-		IPR001326; IPR018940; PTHR11595 (PANTHER), PTHR11595:SF7 (PANTHER)
Caenorhabditis briggsae	2-hydroxyacyl- lyase 1	3	F:GO:0030976; F:GO:0000287; F:GO:0003824	-		-
	-	0				-
Brugia malayi	briggsae cbr-ctg-1 protein	0		F:GO:0005215; C:GO:0005622; P:GO:0006810		-
	-	0				-
	-	0				-
Caenorhabditis elegans	isoleucyl-tr- synthetase	6	C:GO:0005625; F:GO:0005515; P:GO:0006418; F:GO:0004822; C:GO:0005829; F:GO:0000166	-	EC:6.1.1.5	IPR002300; IPR002301; IPR009080; IPR013155; IPR014729; G3DSA:1.10.730.10 (GENE3D), PTHR11946 (PANTHER), SSF52374 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-acl-7 protein	0		F:GO:0008415		PTHR12563 (PANTHER), PTHR12563:SF3 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	i uaiaretic acid resistant family member (ndg-4)	3	P:GO:0009792; P:GO:0010171; P:GO:0040010	-		PTHR11161 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	serine threonine-protein	3	P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	-
	-	0				-
	-	0				-
Caenorhabditis briggsae	d- topoisomerase i	16	C:GO:0005703; C:GO:0005875; P:GO:0006268; P:GO:0030261; C:GO:0005730; F:GO:0003917; P:GO:0002168; P:GO:0007059; C:GO:0005665; C:GO:0005719; F:GO:0003918; P:GO:0048477; P:GO:0006265; P:GO:0008283; C:GO:0005737; P:GO:0009790	-	EC:5.99.1.2; EC:5.99.1.3	IPR001631; IPR009054; IPR011010; IPR013499; IPR013500; IPR014711; IPR014727; IPR018521; PTHR10290 (PANTHER)

	-	0				-
Caenorhabditis elegans	-+ k+-atpase alpha-subunit	2	P:GO:0006810; F:GO:0003824	-		IPR001757; G3DSA:3.40.1110.10 (GENE3D), PTHR11939:SF100 (PANTHER), SSF81660 (SUPERFAMILY)
Caenorhabditis briggsae	zinc finger transcription factor family member (ztf-19)	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		IPR020003
	-	0				-
Callithrix jacchus	polymerase ii (d- directed) polypeptide	10	F:GO:0003899; F:GO:0030528; F:GO:0008270; F:GO:0004672; P:GO:0006367; P:GO:0045449; P:GO:0008380; C:GO:0005665; F:GO:0003677; P:GO:0006368	-	EC:2.7.7.6	IPR001222; IPR001529; IPR003006; IPR019761; G3DSA:2.20.25.10 (GENE3D), PTHR11239 (PANTHER), PTHR11239:SF1 (PANTHER), SSF57783 (SUPERFAMILY)
	-	0				-
Canis familiaris	heat shock cog-te 71 kda	2	F:GO:0005524; P:GO:0006950	-		-
Pongo abelii	transcription elongation factor b polypeptide 1	10	C:GO:0005829; F:GO:0003746; P:GO:0006511; P:GO:0006357; F:GO:0004842; F:GO:0005515; F:GO:0003711; P:GO:0044419; C:GO:0005654; C:GO:0030891	-	EC:6.3.2.19	-
	-	0				-
Caenorhabditis elegans	briggsae cbr-coq-8 protein	0				-
Caenorhabditis elegans	antigenic determi-nt of reca protein homolog	13	P:GO:0040010; F:GO:0003690; F:GO:0046872; P:GO:0006260; P:GO:0000003; P:GO:0010171; P:GO:0002119; P:GO:0040011; P:GO:0010467; P:GO:0002009; P:GO:0009792; C:GO:0005634; P:GO:0006974	-		IPR019447; PTHR12805 (PANTHER)

Caenorhabditis elegans	antigenic determi-nt of reca protein homolog	13	P:GO:0040010; F:GO:0003690; F:GO:0046872; P:GO:0006260; P:GO:0000003; P:GO:0010171; P:GO:0002119; P:GO:0040011; P:GO:0010467; P:GO:0002009; P:GO:0009792; C:GO:0005634; P:GO:0006974	-		IPR019447; PTHR12805 (PANTHER)
Caenorhabditis elegans	antigenic determi-nt of reca protein homolog	13	P:GO:0040010; F:GO:0003690; F:GO:0046872; P:GO:0006260; P:GO:0000003; P:GO:0010171; P:GO:0002119; P:GO:0040011; P:GO:0010467; P:GO:0002009; P:GO:0009792; C:GO:0005634; P:GO:0006974	-		IPR019447; PTHR12805 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Anopheles gambiae str. PEST	secreted trypsin-like serine protease	0		P:GO:0006508; F:GO:0004252; F:GO:0008236; F:GO:0016787; F:GO:0003824; F:GO:0008233		IPR005514; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR19355 (PANTHER), PTHR19355:SF48 (PANTHER)
						-
	-	0				-
	-	0				PTHR21512 (PANTHER), PTHR21512:SF7 (PANTHER)
	-	0				-
	-	0				-
Loa loa	rn207_caebr ame: full=probable ring finger protein 207 homolog	0		F:GO:0046872; F:GO:0008270; F:GO:0005515; C:GO:0005622		-
Caenorhabditis briggsae	Hypothetical protein CBG02374 [Caenorhabditis briggsae]	0		F:GO:0005515		-
Ailuropoda melanoleuca	cytohesin 1	5	C:GO:0005737; P:GO:0030155; C:GO:0005886; F:GO:0005515; P:GO:0016192	-		IPR000904; G3DSA:1.10.1000.11 (GENE3D), PTHR10663 (PANTHER)
Caenorhabditis briggsae	sushi domain containing	2	C:GO:0016021; P:GO:0007160	-		IPR005533; PTHR13802 (PANTHER), PTHR13802:SF1 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein C46G7.1 [Caenorhabditis elegans]	0				-
Pongo abelii	PREDICTED: hypothetical protein LOC100437226 [Pongo abelii]	0				-

Caenorhabditis elegans	briggsae cbr-cav-1 protein	0		C:GO:0030141; C:GO:0016021; C:GO:0005901; C:GO:0016020; C:GO:0000139; C:GO:0030133; C:GO:0005794; C:GO:0009898; C:GO:0048471; P:GO:0040011; C:GO:0005938; P:GO:0007265; P:GO:0040010; C:GO:0005887; P:GO:0040007; C:GO:0005886; P:GO:0007126		IPR001612; PTHR10844:SF2 (PANTHER), SignalP (SIGNALP)
Ixodes scapularis	hexosaminidase domain-containing	0		F:GO:0004553; F:GO:0004563; P:GO:0005975; P:GO:0008152; F:GO:0016787; F:GO:0003824; F:GO:0016798; F:GO:0043169		-
Caenorhabditis elegans	mitochondrial 2-oxoglutarate malate carrier protein	5	F:GO:0005488; C:GO:0005743; P:GO:0055085; C:GO:0016021; F:GO:0005215	-		IPR001993; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF78 (PANTHER)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG02369 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	Hypothetical protein CBG02369 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	briggsae cbr-itx-1 protein	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-rpy-1 protein	7	C:GO:0005856; C:GO:0045211; P:GO:0007268; C:GO:0030054; F:GO:0033130; P:GO:0019915; F:GO:0008270	-		PTHR10098 (PANTHER), PTHR10098:SF7 (PANTHER)
Caenorhabditis briggsae	kinesin-like protein family member (klp-4)	5	P:GO:0007018; F:GO:0005515; F:GO:0005524; F:GO:0003777; C:GO:0005874	-		IPR022164; PTHR16012 (PANTHER), PTHR16012:SF65 (PANTHER)
	-	0				-
Taeniopygia guttata	rcg47273-like	1	C:GO:0016021	-		-
	-	0				SignalP (SIGNALP)

Callithrix jacchus	glutamine synthetase	10	C:GO:0005829; P:GO:0009749; C:GO:0005739; F:GO:0004351; F:GO:0042802; P:GO:0006542; F:GO:0005524; F:GO:0004356; P:GO:0008283; C:GO:0005794	-	EC:4.1.1.15; EC:6.3.1.2	IPR008146; IPR014746; PTHR20852 (PANTHER), PTHR20852:SF14 (PANTHER), SSF55931 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	dolichyl-phosphate mannosyltransferase polypeptide catalytic subunit	12	P:GO:0006506; P:GO:0019673; F:GO:0043178; F:GO:0005537; C:GO:0033185; P:GO:0035269; F:GO:0004582; C:GO:0005792; F:GO:0004169; F:GO:0005515; C:GO:0005789; P:GO:0019348	-	EC:2.4.1.83; EC:2.4.1.109	IPR001173; G3DSA:3.90.550.10 (GENE3D), PTHR10859 (PANTHER), SSF53448 (SUPERFAMILY)
Caenorhabditis briggsae	nudix hydrolase	3	F:GO:0030145; P:GO:0009132; F:GO:0016818	-	EC:3.6.1.0	IPR000059; IPR000086; PTHR12992 (PANTHER)
	-	0				-
Loa loa	c-termi-l binding protein 1	13	C:GO:0005829; F:GO:0003676; C:GO:0017053; P:GO:0050872; C:GO:0005667; F:GO:0016616; F:GO:0016564; P:GO:0000122; F:GO:0051287; F:GO:0003700; P:GO:0007030; F:GO:0008134; F:GO:0042803	-	EC:1.1.1.0	IPR006140; IPR016040; PTHR10996 (PANTHER), PTHR10996:SF11 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	tr- (5-methylaminomethyl-2-thiouridylate)-methyltransferase	1	F:GO:0005488	-		IPR004506; G3DSA:2.30.30.280 (GENE3D)
	-	0				-
Caenorhabditis briggsae	receptor protein tyrosine	2	F:GO:0004725; P:GO:0006470	-	EC:3.1.3.48	IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF35 (PANTHER), SignalP (SIGNALP), SSF52799 (SUPERFAMILY)
	-	0				-
Loa loa	surp module family protein	1	F:GO:0003676	-		IPR000061; IPR006569; PTHR23140 (PANTHER), SSF109905 (SUPERFAMILY)
	-	0				G3DSA:3.80.10.10 (GENE3D)
	-	0				SignalP (SIGNALP)

Caenorhabditis briggsae	Hypothetical protein CBG09112 [Caenorhabditis briggsae]	0		F:GO:0003723; F:GO:0005488; P:GO:0006396; C:GO:0005622		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG18297 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)
Caenorhabditis elegans	expulsion defective family member (exp-2)	5	C:GO:0008076; F:GO:0005249; F:GO:0005515; P:GO:0055085; P:GO:0006813	-		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		C:GO:0005789; P:GO:0040017; N:GO:0035545; P:GO:0032527; P:GO:0035418		-
Homo sapiens	milk fat globule-egf factor 8 protein variant	17	P:GO:0001525; P:GO:0006910; F:GO:0008429; C:GO:0009897; P:GO:0043627; P:GO:0050766; C:GO:0005615; P:GO:0006911; P:GO:0007155; F:GO:0005178; F:GO:0001786; C:GO:0031012; P:GO:0044419; P:GO:0008284; C:GO:0005737; C:GO:0019897; P:GO:0007338	-		-
	-	0				-
Caenorhabditis briggsae	protein-tyrosine phosphatase containing protein	5	P:GO:0009792; P:GO:0016311; F:GO:0004721; P:GO:0000003; P:GO:0043687	-	EC:3.1.3.16	IPR000242; IPR000387; IPR003595; IPR016130; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	dual specificity protein phosphatase 9	5	P:GO:0007254; P:GO:0000188; F:GO:0017017; C:GO:0005783; C:GO:0005634	-		-
Caenorhabditis elegans	dual specificity protein phosphatase 9	5	P:GO:0007254; P:GO:0000188; F:GO:0017017; C:GO:0005783; C:GO:0005634	-		-
Caenorhabditis briggsae	hypothetical kda protein in chromosome	4	P:GO:0009792; P:GO:0040010; F:GO:0005515; P:GO:0002119	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-

	-	0				-
Caenorhabditis elegans	dynein heavy chain	5	P:GO:0007018; C:GO:0030286; F:GO:0016887; F:GO:0005524; F:GO:0003777	-		IPR013594
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	met-10+ like-protein	0		F:GO:0004827; F:GO:0005524; P:GO:0006412; F:GO:0004812; C:GO:0005737; F:GO:0000166; P:GO:0006433; P:GO:0006418		-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-acr-6 protein	9	P:GO:0009792; F:GO:0004872; P:GO:0002119; C:GO:0005887; C:GO:0045211; C:GO:0030054; P:GO:0006811; P:GO:0040007; F:GO:0004889	-		-
Caenorhabditis elegans	briggsae cbr-cogc-1 protein	1	F:GO:0005515	-		-
Ailuropoda melanoleuca	eukaryotic translation initiation factor subunit 8	6	C:GO:0005852; F:GO:0005515; P:GO:0045948; F:GO:0003743; C:GO:0005829; F:GO:0043022	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Homo sapiens	ornithine decarboxylase antizyme 1	4	P:GO:0006596; F:GO:0008073; P:GO:0050790; F:GO:0005515	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Cooperia oncophora	latrophilin-like protein 2	6	P:GO:0007218; C:GO:0016021; P:GO:0007165; C:GO:0005886; F:GO:0005529; F:GO:0004930	-		IPR001304; IPR016186
Caenorhabditis elegans	msp-domain protein 1 variant	6	P:GO:0040018; C:GO:0031143; P:GO:0040017; P:GO:0000003; P:GO:0019915; C:GO:0044297	-		-
	-	0				SignalP (SIGNALP)

	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Ascaris suum	serine threonine phosphatase	2	P:GO:0000003; F:GO:0004721	-	EC:3.1.3.16	IPR004843; IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF19 (PANTHER), SSF56300 (SUPERFAMILY)
	-	0				-
Loa loa	briggsae cbr-ced-5 protein	7	F:GO:0005083; P:GO:0043652; C:GO:0005886; F:GO:0032403; F:GO:0019899; P:GO:0040039; F:GO:0017124	-		PTHR23317 (PANTHER), PTHR23317:SF16 (PANTHER)
Caenorhabditis elegans	laminin b2	5	C:GO:0005604; P:GO:0048598; P:GO:0009887; P:GO:0007155; P:GO:0009888	-		IPR000034; IPR002049; IPR007087; IPR008211; IPR013032; PR00011 (PRINTS), G3DSA:2.10.25.10 (GENE3D), G3DSA:2.60.120.260 (GENE3D), PTHR10574 (PANTHER), PTHR10574:SF48 (PANTHER), SignalP (SIGNALP), SSF57196 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Loa loa	phosphatidylcholine:ceramide cholinephosphotransferase	1	F:GO:0016740	-		PTHR21290 (PANTHER), PTHR21290:SF3 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	d- polymerase eta	1	P:GO:0006281	-		IPR001126; IPR017961; PTHR11076:SF11 (PANTHER), PF11799 (PFAM)
Caenorhabditis briggsae	briggsae cbr-aex-1 protein	0		F:GO:0004871; P:GO:0016079; P:GO:0030421; C:GO:0005622		-
Caenorhabditis elegans	hypothetical protein F55D12.5 [Caenorhabditis elegans]	0				IPR013032
	-	0				-
	-	0				-
	-	0				-
	-	0				IPR000233; PTHR10596 (PANTHER), PTHR10596:SF103 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-haf-9 protein	6	F:GO:0015197; F:GO:0042626; P:GO:0015833; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		IPR005829; IPR017940; G3DSA:1.20.1560.10 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF82 (PANTHER), SignalP (SIGNALP)
	-	0				-
Loa loa	hypothetical protein LOAG_00885 [Loa loa]	0				-
Loa loa	hypothetical protein LOAG_12685 [Loa loa]	0				-

Caenorhabditis elegans	kiaa0152 homolog precursor	4	F:GO:0030246; P:GO:0006496; C:GO:0016020; C:GO:0005783	-		IPR021720; PTHR13460 (PANTHER)
	-	0				-
Ancylostoma caninum	cytochrome c oxidase subunit i	9	P:GO:0009060; C:GO:0005743; C:GO:0070469; F:GO:0009055; F:GO:0020037; P:GO:0006810; C:GO:0016021; P:GO:0022900; F:GO:0004129	-	EC:1.9.3.1	IPR000883; SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	wd repeat-containing protein 47	1	F:GO:0005515	-		IPR001680; PTHR19863 (PANTHER), PTHR19863:SF2 (PANTHER)
	-	0				-
Caenorhabditis elegans	r- polymerase domain 2 family protein	4	F:GO:0003899; F:GO:0003677; P:GO:0006350; C:GO:0005634	-	EC:2.7.7.6	IPR000722; IPR007066; IPR015699; PTHR19376 (PANTHER), SSF64484 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Trichoplax adhaerens	loc495229 protein	0		P:GO:0008152; F:GO:0003824; F:GO:0016853		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	loc398543 protein	0		F:GO:0003676		-
Caenorhabditis elegans	myosin heavy chain	6	C:GO:0032982; F:GO:0003779; F:GO:0005524; F:GO:0003774; C:GO:0031672; P:GO:0007626	-		-
Tribolium castaneum	ccaat-binding transcription factor subunit a	3	F:GO:0043565; C:GO:0005634; P:GO:0006355	-		IPR003957; IPR003958; IPR009072; PTHR11064 (PANTHER)
	-	0				-
Caenorhabditis elegans	proteasome (macropain) activator subunit 4	0		F:GO:0005488; C:GO:0000502; C:GO:0005634		-
Brugia malayi	domain containing protein	0				IPR003582; PTHR21724 (PANTHER), SignalP (SIGNALP)
	-	0				-

Pongo abelii	keratin 7	10	P:GO:0006417; C:GO:0005730; P:GO:0051325; P:GO:0007010; P:GO:0006260; F:GO:0005515; C:GO:0045095; P:GO:0044419; F:GO:0005198; C:GO:0005737	-		SignalP (SIGNALP)
Esox lucius	mitochondrial precursor	3	F:GO:0003676; C:GO:0043231; F:GO:0004527	-		IPR012337; IPR013520; G3DSA:3.30.420.10 (GENE3D), PTHR11046 (PANTHER)
	-	0				-
Caenorhabditis elegans	let-23 fertility effector regulator family member (lfe-2)	1	F:GO:0008440	-	EC:2.7.1.127	-
	-	0				IPR003582; SignalP (SIGNALP)
Caenorhabditis briggsae	failed axon	0				PTHR12289 (PANTHER), PTHR12289:SF17 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Nasonia vitripennis	glycosyl group 2 family protein	0		F:GO:0016740; C:GO:0016021; C:GO:0016020; F:GO:0005529; C:GO:0005794; F:GO:0016757		IPR000772; IPR008997; G3DSA:2.80.10.50 (GENE3D)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0002119; C:GO:0005622		IPR001357; G3DSA:3.40.50.10190 (GENE3D)
	-	0				-
Caenorhabditis elegans	dis3 mitotic control homolog (cerevisiae)-like 2	2	F:GO:0004540; F:GO:0003723	-		IPR001900; PTHR23355 (PANTHER), PTHR23355:SF10 (PANTHER)
Caenorhabditis elegans	dis3 mitotic control homolog (cerevisiae)-like 2	2	F:GO:0004540; F:GO:0003723	-		IPR001900; PTHR23355 (PANTHER), PTHR23355:SF10 (PANTHER)
Loa loa	briggsae cbr-atf-2 protein	0		P:GO:0006355; F:GO:0043565; F:GO:0046983; F:GO:0005515; F:GO:0003677; F:GO:0003700; C:GO:0005634		-
	-	0				-
Teladorsagia circumcincta	l3b25 precusor	0				IPR003677
Caenorhabditis briggsae	briggsae cbr-fshr-1 protein	0		F:GO:0003735; P:GO:0006952; C:GO:0016021; P:GO:0006412; P:GO:0000003; P:GO:0009792; C:GO:0005840; C:GO:0005622; P:GO:0040010; P:GO:0007186; F:GO:0016500		-
	-	0				-
Caenorhabditis briggsae	ybri_caeel ame: full=uncharacterized protein	1	P:GO:0006898	-		-
	-	0				-

Caenorhabditis briggsae	activating sig-l cointegrator 1 complex subunit 3	4	F:GO:0008026; F:GO:0003677; C:GO:0005622; F:GO:0005524	-		IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR11752 (PANTHER), PTHR11752:SF8 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	: shorter than wild-type family member (dpy-27)	0		F:GO:0005515		IPR010935; PTHR18937 (PANTHER), PTHR18937:SF13 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	3	P:GO:0006032; P:GO:0016998; F:GO:0004568	-	EC:3.2.1.14	IPR000726; PTHR22595:SF6 (PANTHER)
	-	0				PTHR15286 (PANTHER), PTHR15286:SF2 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	class type 10a	7	C:GO:0016021; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0015914; F:GO:0000287; F:GO:0004012	-	EC:3.6.3.1	IPR001757; IPR005834; G3DSA:3.40.1110.10 (GENE3D), G3DSA:3.40.50.1000 (GENE3D), PTHR11939:SF14 (PANTHER), SSF56784 (SUPERFAMILY), SSF81660 (SUPERFAMILY), SSF81665 (SUPERFAMILY)
Brugia malayi	bax inhibitor 1	2	P:GO:0007283; P:GO:0030324	-		IPR001412; IPR006214; PTHR23291:SF4 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	cation efflux family protein	5	C:GO:0016021; P:GO:0000003; F:GO:0008324; P:GO:0006812; P:GO:0055085	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	hypothetical protein ZK154.5 [Caenorhabditis elegans]	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Homo sapiens	phosphofurin acidic cluster sorting protein isoform cra_b	5	C:GO:0030137; F:GO:0005515; P:GO:0000042; C:GO:0005829; P:GO:0044419	-		-
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis elegans	bone morphogenetic protein 1	10	P:GO:0030154; C:GO:0005615; F:GO:0008083; F:GO:0004222; P:GO:0001503; F:GO:0005125; F:GO:0005509; P:GO:0006508; F:GO:0008270; P:GO:0051216	-	EC:3.4.24.0	IPR001506; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF70 (PANTHER), SSF55486 (SUPERFAMILY)
Heliconius melpomene	endonuclease-reverse transcriptase -e01	0		F:GO:0003723; P:GO:0006278; F:GO:0004519; F:GO:0003964		-
	-	0				-
Caenorhabditis elegans	selenocysteine-specific translation elongation factor	3	F:GO:0003746; F:GO:0005525; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000795; G3DSA:3.40.50.300 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF25 (PANTHER), SSF52540 (SUPERFAMILY)
Brugia malayi	abc transporter family protein	5	F:GO:0042626; C:GO:0005886; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		IPR003439; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF96 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-tag-241 protein	0				-
Homo sapiens	granulin	8	C:GO:0005615; P:GO:0050679; F:GO:0008083; F:GO:0005125; P:GO:0007165; C:GO:0005739; P:GO:0007566; P:GO:0001835	-		IPR000118; PTHR12274 (PANTHER), SSF57277 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	copine family protein	1	F:GO:0016740	-		-
Brugia malayi	grip and coiled-coil domain-containing protein 1	0				PTHR23157 (PANTHER), PTHR23157:SF11 (PANTHER)
	-	0				-
Caenorhabditis briggsae	patched family protein	12	P:GO:0040025; F:GO:0008158; P:GO:0040018; P:GO:0018996; P:GO:0040002; P:GO:0006810; P:GO:0000003; P:GO:0008340; P:GO:0040011; C:GO:0016021; P:GO:0019915; F:GO:0005215	-		IPR001036; IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER), SignalP (SIGNALP), SSF82866 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein T19D12.10 [Caenorhabditis elegans]	1	P:GO:0006810	-		PTHR11662 (PANTHER), PTHR11662:SF17 (PANTHER)

Caenorhabditis briggsae	serine threonine protein ki-se	0		P:GO:0000003; F:GO:0004672; F:GO:0005524; F:GO:0000166; P:GO:0006468; P:GO:0009792; F:GO:0004674		-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Loa loa	scf complex protein cul-1	12	P:GO:0007050; C:GO:0005829; P:GO:0051437; C:GO:0019005; P:GO:0009887; P:GO:0008285; F:GO:0004842; P:GO:0008629; F:GO:0005515; P:GO:0000082; P:GO:0031146; C:GO:0005654	-	EC:6.3.2.19	IPR001373; IPR016159; G3DSA:1.20.1310.10 (GENE3D)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	fyve zinc finger family protein	3	F:GO:0046872; P:GO:0044237; P:GO:0044238	-		IPR002423; G3DSA:3.50.7.10 (GENE3D), PTHR11353:SF14 (PANTHER), SSF52029 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-rha-2 protein	7	P:GO:0040010; P:GO:0008340; P:GO:0000003; P:GO:0002119; P:GO:0006898; P:GO:0009792; P:GO:0016246	-		-
Harpegnathos saltator	histone-lysine n-methyltransferase setmar	0				SignalP (SIGNALP)
	-	0				-

Loa loa	polo-like ki-se	22	P:GO:0007098; P:GO:0031572; P:GO:0007077; C:GO:0000940; F:GO:0005515; P:GO:0007417; F:GO:0000166; P:GO:0035046; P:GO:0007052; P:GO:0007058; P:GO:0006911; P:GO:0007060; P:GO:0007067; F:GO:0004674; C:GO:0005813; P:GO:0007344; C:GO:0030496; P:GO:0007406; C:GO:0005634; C:GO:0000922; P:GO:0035044; P:GO:0000910	-	EC:2.7.11.0	IPR000719; IPR000959; IPR002290; IPR008271; IPR011009; IPR015728; IPR017441; IPR017442; IPR020636; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.1120.30 (GENE3D), G3DSA:3.30.200.20 (GENE3D), SSF82615 (SUPERFAMILY)
	-	0				-
Loa loa	polo-like ki-se	22	P:GO:0007098; P:GO:0031572; P:GO:0007077; C:GO:0000940; F:GO:0005515; P:GO:0007417; F:GO:0000166; P:GO:0035046; P:GO:0007052; P:GO:0007058; P:GO:0006911; P:GO:0007060; P:GO:0007067; F:GO:0004674; C:GO:0005813; P:GO:0007344; C:GO:0030496; P:GO:0007406; C:GO:0005634; C:GO:0000922; P:GO:0035044; P:GO:0000910	-	EC:2.7.11.0	IPR000719; IPR000959; IPR002290; IPR008271; IPR011009; IPR015728; IPR017441; IPR017442; IPR020636; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.1120.30 (GENE3D), G3DSA:3.30.200.20 (GENE3D), SSF82615 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-

Loa loa	polypyrimidine tract binding protein	13	P:GO:0007219; P:GO:0008103; P:GO:0008586; F:GO:0000166; F:GO:0000900; F:GO:0003730; C:GO:0005737; P:GO:0000398; P:GO:0008587; P:GO:0007319; F:GO:0008187; C:GO:0005634; C:GO:0030529	-		IPR012677; PTHR11546 (PANTHER), PTHR11546:SF4 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	chromatin modifying protein 4b	2	C:GO:0044444; P:GO:0006810	-		IPR005024; PTHR22761 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	8	F:GO:0004383; F:GO:0004674; C:GO:0016021; P:GO:0019932; F:GO:0008528; F:GO:0005524; P:GO:0006468; P:GO:0006182	-	EC:4.6.1.2; EC:2.7.11.0	IPR001054; PTHR11920 (PANTHER), PTHR11920:SF40 (PANTHER)
Brugia malayi	dehydroge-se reductase sdr family member 1	4	C:GO:0005794; P:GO:0040010; C:GO:0005634; C:GO:0005783	-		IPR002198; IPR016040; PTHR19410:SF32 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		C:GO:0005604; P:GO:0007155; C:GO:0031012; C:GO:0005578		IPR008985; IPR012679; IPR013320
	-	0				-

Bos taurus	nucleophosmin 1 isoform 1	39	F:GO:0042803; F:GO:0043024; F:GO:0051082; P:GO:0008284; P:GO:0000056; C:GO:0015934; C:GO:0015935; P:GO:0006884; F:GO:0043023; P:GO:0042273; C:GO:0005829; P:GO:0042274; P:GO:0016049; F:GO:0019843; P:GO:0007569; P:GO:0031328; P:GO:0010825; P:GO:0006916; P:GO:0010826; F:GO:0003713; C:GO:0031616; P:GO:0006886; P:GO:0051092; F:GO:0042393; P:GO:0048025; P:GO:0006407; P:GO:0044419; P:GO:0008285;	-		IPR004301; G3DSA:2.60.120.340 (GENE3D), PTHR22747:SF2 (PANTHER)
	-	0				-
Brugia malayi	u3 small nucleolar r--associated protein 6 homolog	0		F:GO:0005488; P:GO:0006364; P:GO:0006396; F:GO:0005515; C:GO:0005730; C:GO:0005634; C:GO:0005622		PTHR23271 (PANTHER), PTHR23271:SF1 (PANTHER)
Caenorhabditis elegans	cytoskeleton associated protein 5	1	P:GO:0009987	-		-
Caenorhabditis elegans	cytoskeleton associated protein 5	1	P:GO:0009987	-		-
Caenorhabditis briggsae	abhydrolase domain containing 14a	1	F:GO:0005515	-		G3DSA:3.40.50.1820 (GENE3D), PTHR10992 (PANTHER), PTHR10992:SF20 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	C:GO:0016021	-		IPR007237; SignalP (SIGNALP)
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Homo sapiens	ring finger protein 181	4	F:GO:0008270; F:GO:0016874; F:GO:0005515; P:GO:0008152	-		IPR001841; IPR013083; IPR018957; PTHR22763 (PANTHER), SSF57850 (SUPERFAMILY)

Caenorhabditis briggsae	nop16 nucleolar protein homolog	6	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0040002; P:GO:0040007; P:GO:0006898	-		IPR019002; PTHR13243 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-tag-180 protein	0		C:GO:0016020		PTHR10166 (PANTHER), PTHR10166:SF4 (PANTHER)
Caenorhabditis elegans	leucine rich repeat family protein	7	P:GO:0018996; C:GO:0016021; P:GO:0009792; P:GO:0040017; P:GO:0040007; F:GO:0005515; P:GO:0002119	-		-
Caenorhabditis briggsae	briggsae cbr-rgs-5 protein	0		F:GO:0004871		-
Caenorhabditis briggsae	ribosomal protein s6 ki-se alpha-5	17	P:GO:0007243; F:GO:0004674; P:GO:0016572; P:GO:0006355; P:GO:0040007; P:GO:0000003; P:GO:0042221; F:GO:0005524; P:GO:0002119; F:GO:0005515; F:GO:0000287; C:GO:0005654; P:GO:0009792; C:GO:0005737; P:GO:0006950; P:GO:0007173; P:GO:0009605	-	EC:2.7.11.0	IPR000719; IPR002290; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22985 (PANTHER), PTHR22985:SF82 (PANTHER)
Caenorhabditis elegans	ribosomal protein s6 ki-se alpha-5	16	P:GO:0007243; F:GO:0004674; P:GO:0016572; P:GO:0006355; P:GO:0040007; P:GO:0000003; P:GO:0042221; F:GO:0005524; P:GO:0002119; F:GO:0005515; F:GO:0000287; C:GO:0005654; P:GO:0009792; P:GO:0006950; P:GO:0007173; P:GO:0009605	-	EC:2.7.11.0	IPR000719; IPR000961; IPR002290; IPR008271; IPR011009; IPR017441; IPR017442; IPR017892; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22985 (PANTHER), PTHR22985:SF82 (PANTHER)
	-	0				-
	-	0				-

	-	0				-
Caenorhabditis elegans	Hypothetical protein T15B7.1 [Caenorhabditis elegans]	1	P:GO:0009792	-		-
Caenorhabditis elegans	cyclin-dependent ki-se 9	15	P:GO:0007049; P:GO:0006367; C:GO:0005730; F:GO:0008353; P:GO:0045449; C:GO:0008023; P:GO:0051301; F:GO:0003677; F:GO:0005524; F:GO:0005515; P:GO:0006368; F:GO:0004693; P:GO:0008283; F:GO:0017069; P:GO:0006468	-	EC:2.7.11.23 ; EC:2.7.11.22	IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF111 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0046872; F:GO:0003676; F:GO:0016787; P:GO:0008152; C:GO:0016021; F:GO:0003824		PTHR10151 (PANTHER), PTHR10151:SF28 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	ynx4_caeel ame: full=uncharacterized protein	0				-
Caenorhabditis elegans	programmed cell death 2	7	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0005488; P:GO:0040010; C:GO:0044464; P:GO:0006898	-		IPR007320; PTHR12298 (PANTHER), PTHR12298:SF4 (PANTHER)
Caenorhabditis briggsae	pla2g15 protein	2	P:GO:0019915; F:GO:0008415	-		IPR003386; G3DSA:3.40.50.1820 (GENE3D), PTHR11440:SF15 (PANTHER)
Branchiostoma floridae	protein n-termi-l glutamine amidohydrolase	0		C:GO:0005737; F:GO:0016787; C:GO:0005829; F:GO:0070773; C:GO:0005634; P:GO:0006464		IPR019161; IPR023128; PTHR13035 (PANTHER)
Caenorhabditis elegans	transmembrane protein 144	2	C:GO:0016020; P:GO:0002119	-		IPR012435
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-tag-241 protein	0				-
	-	0				SignalP (SIGNALP)

Pan troglodytes	interferon alpha-inducible protein	9	C:GO:0005737; C:GO:0005615; P:GO:0032020; F:GO:0031386; P:GO:0019941; F:GO:0005515; P:GO:0007267; P:GO:0009615; P:GO:0044419	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	11	C:GO:0005737; P:GO:0009792; F:GO:0004743; F:GO:0016830; P:GO:0006725; F:GO:0005515; F:GO:0030955; C:GO:0043231; F:GO:0000287; P:GO:0006096; F:GO:0000166	-	EC:2.7.1.40	-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	11	C:GO:0005737; P:GO:0009792; F:GO:0004743; F:GO:0016830; P:GO:0006725; F:GO:0005515; F:GO:0030955; C:GO:0043231; F:GO:0000287; P:GO:0006096; F:GO:0000166	-	EC:2.7.1.40	-
	-	0				-
	-	0				-
Caenorhabditis elegans	zinc c2h2 type family protein	3	F:GO:0008270; F:GO:0003676; C:GO:0005622	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Angiostrongylus cantonensis	ring finger protein	2	F:GO:0008270; F:GO:0005515	-		IPR001841; IPR013083; IPR018957; PTHR22663 (PANTHER), PTHR22663:SF10 (PANTHER), SSF57850 (SUPERFAMILY)
Homo sapiens	mhc class ib antigen	5	P:GO:0006955; F:GO:0032393; C:GO:0016021; P:GO:0002474; C:GO:0042612	-		IPR001039; IPR003597; IPR007110; IPR011161; IPR011162; IPR013783; PTHR16675 (PANTHER), PTHR16675:SF53 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-

Caenorhabditis briggsae	wnt-4 protein	55	C:GO:0009986; P:GO:0030237; P:GO:0045892; P:GO:0030501; F:GO:0004871; P:GO:0007223; P:GO:0072034; N:GO:0039018; P:GO:0071392; P:GO:0018345; P:GO:0045669; P:GO:0032349; N:GO:2000066; P:GO:0045836; P:GO:0009880; P:GO:0048599; P:GO:0001889; C:GO:0005615; N:GO:0061205; P:GO:0001837; P:GO:0045596; P:GO:0060126; P:GO:0090002; F:GO:0003714; P:GO:0006702; P:GO:0060748; P:GO:0090263;	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Brugia malayi	cdc73 domain protein	2	P:GO:0044260; P:GO:0044238	-		SignalP (SIGNALP)
Brugia malayi	cdc73 domain protein	2	P:GO:0044260; P:GO:0044238	-		SignalP (SIGNALP)
Nematostella vectensis	prokaryotic d- topoisomerase	6	P:GO:0006268; F:GO:0003917; P:GO:0000737; C:GO:0005694; P:GO:0006265; F:GO:0004520	-	EC:5.99.1.2	-
Brugia malayi	b-box zinc finger family protein	1	F:GO:0005488	-		IPR000408; IPR009091; PTHR12846 (PANTHER), PTHR12846:SF2 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-sma-4 protein	5	F:GO:0003700; F:GO:0005515; C:GO:0005667; P:GO:0006355; P:GO:0007179	-		-
	-	0				-
Ostertagia ostertagi	ancyclostoma-secreted protein	0		C:GO:0005576		IPR014044; SignalP (SIGNALP)

Caenorhabditis elegans	briggsae cbr-bub-1 protein	8	P:GO:0000910; P:GO:0040035; C:GO:0000776; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0002009; P:GO:0009792	-		IPR015661
Squalius cephalus	atp-binding cassette transporter 13-like	8	C:GO:0005887; F:GO:0042626; C:GO:0005624; P:GO:0042493; P:GO:0055085; P:GO:0055114; F:GO:0005524; F:GO:0032440	-	EC:1.3.1.74	IPR003439; G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF37 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	d- topoisomerase 2	0		F:GO:0003918; F:GO:0003916; P:GO:0006265; P:GO:0000910; C:GO:0005694; F:GO:0003700; P:GO:0006259; F:GO:0003677; F:GO:0000166; P:GO:0051301; F:GO:0005524; P:GO:0009792; P:GO:0006355; F:GO:0016853		-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	uroca-te hydratase	2	P:GO:0006548; F:GO:0016153	-	EC:4.2.1.49	-
	-	0				IPR020685; IPR020688; SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0003824	-		IPR000850; G3DSA:3.40.50.300 (GENE3D)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-sax-2 protein	1	F:GO:0005515	-		PTHR12295 (PANTHER), PTHR12295:SF6 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0008150; C:GO:0005575		IPR019132; PTHR16127 (PANTHER), PTHR16127:SF8 (PANTHER)
	-	0				-
Loa loa	hypothetical protein LOAG_01331 [Loa loa]	0		C:GO:0005737; C:GO:0016020		-
Caenorhabditis elegans	folate carrier	4	P:GO:0006810; P:GO:0040010; P:GO:0008340; C:GO:0016020	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF73 (PANTHER)
	-	0				-

Caenorhabditis elegans	pfkfb3 protein	4	F:GO:0003873; P:GO:0006003; F:GO:0005524; P:GO:0006796	-	EC:2.7.1.105	IPR003094; IPR013078; G3DSA:3.40.50.1240 (GENE3D), PTHR10606:SF11 (PANTHER), SSF53254 (SUPERFAMILY)
Caenorhabditis elegans	protein ki-se c	7	P:GO:0006468; F:GO:0046872; P:GO:0023034; F:GO:0019992; F:GO:0004698; F:GO:0005524; C:GO:0016020	-		-
Caenorhabditis elegans	cytochrome p450 family protein partially confirmed by transcript evidence	0		F:GO:0020037; F:GO:0005506; C:GO:0016021; F:GO:0009055; P:GO:0019915; P:GO:0055114; F:GO:0016491; P:GO:0008340; F:GO:0005515; F:GO:0046872; F:GO:0004497		IPR001128; PTHR19383:SF59 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Brugia malayi	hypothetical protein Bm1_33605 [Brugia malayi]	0				-
Caenorhabditis elegans	g elongation mitochondrial 1	11	F:GO:0016779; F:GO:0003746; P:GO:0040010; P:GO:0070125; C:GO:0005739; P:GO:0000003; P:GO:0002119; F:GO:0003924; P:GO:0006898; P:GO:0009792; F:GO:0005525	-	EC:2.7.7.0; EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR005517; IPR009000; IPR009022; IPR014721; IPR020568; G3DSA:2.40.30.10 (GENE3D), G3DSA:3.30.70.870 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF13 (PANTHER)
Mus musculus	isoform cra_d	15	P:GO:0006470; P:GO:0030324; C:GO:0005829; P:GO:0007049; C:GO:0005730; F:GO:0046872; F:GO:0042802; P:GO:0051301; C:GO:0005741; F:GO:0004722; P:GO:0046822; C:GO:0070688; P:GO:0005977; P:GO:0048754; F:GO:0008599	-		-
	-	0				-
	-	0				-
	-	0				IPR008160; PTHR10499 (PANTHER), PTHR10499:SF114 (PANTHER)

Caenorhabditis briggsae	- k 2cl co-transporter	0		F:GO:0015377; F:GO:0005215; F:GO:0008511; C:GO:0016021; C:GO:0016020; P:GO:0006814; P:GO:0006813; P:GO:0003333; F:GO:0015293; P:GO:0006811; P:GO:0006810; P:GO:0055085; F:GO:0015171; P:GO:0006821		-
Sus scrofa	protein tyrosine non-receptor type 20	1	F:GO:0016791	-	EC:3.1.3.0	IPR000242; IPR000387; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	C:GO:0016021; P:GO:0008340; F:GO:0008378	-		IPR002659; PTHR23033 (PANTHER), PTHR23033:SF1 (PANTHER)
	-	0				-
Brugia malayi	low-density lipoprotein receptor	0		P:GO:0042733; P:GO:0042074; C:GO:0016021; C:GO:0016020; P:GO:0009952; C:GO:0005739; P:GO:0060070; F:GO:0004872; P:GO:0060828; P:GO:0001702		IPR000033; IPR006210; IPR011042; IPR013032; G3DSA:2.10.25.10 (GENE3D), PTHR10529 (PANTHER), SignalP (SIGNALP), SSF57196 (SUPERFAMILY), SSF63825 (SUPERFAMILY)
Caenorhabditis briggsae	s-re domain containing protein	9	P:GO:0040010; P:GO:0040035; P:GO:0018996; P:GO:0002119; P:GO:0040011; P:GO:0006898; C:GO:0044464; P:GO:0009792; P:GO:0016246	-		IPR012890; IPR022783
	-	0				-
Caenorhabditis briggsae	myosin heavy chain	6	C:GO:0032982; F:GO:0003779; F:GO:0005524; F:GO:0003774; C:GO:0031672; P:GO:0007626	-		IPR015650; G3DSA:4.10.270.10 (GENE3D), PTHR13140 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-

Caenorhabditis briggsae	dead h (asp-glu-ala-asp his) box polypeptide 11	5	F:GO:0005488; P:GO:0007049; P:GO:0000003; F:GO:0004386; P:GO:0009792	-		PTHR11472 (PANTHER), PTHR11472:SF5 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				PTHR21749 (PANTHER)
Caenorhabditis elegans	briggsae cbr-cpt-6 protein	1	F:GO:0008415	-		-
Caenorhabditis briggsae	clathrin coat assembly protein	10	P:GO:0009792; P:GO:0010171; P:GO:0002119; F:GO:0005515; C:GO:0030117; F:GO:0008565; P:GO:0016192; P:GO:0000003; P:GO:0006886; P:GO:0040007	-		IPR000804; IPR011012; IPR016635; IPR022775; G3DSA:3.30.450.60 (GENE3D), PTHR11753 (PANTHER), PTHR11753:SF2 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	anion bicarbo-te porter family member (abts-3)	5	F:GO:0005452; P:GO:0006820; P:GO:0009401; F:GO:0005351; C:GO:0016021	-		-
Loa loa	coiled-coil domain-containing protein 75	0		F:GO:0003676; F:GO:0003674; P:GO:0008150; C:GO:0005575; C:GO:0005622		SignalP (SIGNALP)
Pan troglodytes	PREDICTED: hypothetical protein [Pan troglodytes]	0				-
Pongo abelii	midkine (neurite growth-promoting factor 2)	10	P:GO:0030154; F:GO:0008083; P:GO:0030325; P:GO:0009611; F:GO:0008201; P:GO:0016477; P:GO:0051781; P:GO:0007399; P:GO:0007165; C:GO:0005576	-		-
Caenorhabditis elegans	cleavage and polyadenylation specificity factor subunit 4	5	P:GO:0009792; P:GO:0002119; F:GO:0003676; P:GO:0000910; F:GO:0008270	-		IPR001878; IPR013084; PTHR23102 (PANTHER), PTHR23102:SF14 (PANTHER)
Caenorhabditis elegans	cleavage and polyadenylation specificity factor subunit 4	5	P:GO:0009792; P:GO:0002119; F:GO:0003676; P:GO:0000910; F:GO:0008270	-		IPR001878; IPR013084; PTHR23102 (PANTHER), PTHR23102:SF14 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	von willebrand factor type egf and pentraxin domain containing 1	1	F:GO:0003682	-		IPR000436; IPR016060; PTHR19325 (PANTHER), PTHR19325:SF40 (PANTHER)
	-	0				-

	-	0				-
Caenorhabditis elegans	pdz domain containing protein	5	P:GO:0009792; P:GO:0040007; P:GO:0040035; F:GO:0005515; P:GO:0002119	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR19964 (PANTHER), PTHR19964:SF5 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-lgc-2 protein	0				IPR006201; PTHR18945:SF55 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	ysyf_caeel ame: full=uncharacterized f-box protein	0				-
	-	0				-
Homo sapiens	carrier liver isoform t2 variant	7	P:GO:0006915; F:GO:0005515; P:GO:0055085; F:GO:0005471; C:GO:0005744; C:GO:0016021; P:GO:0044419	-		-
	-	0				-
	-	0				-
Onchocerca volvulus	thioredoxin	0		P:GO:0045454; F:GO:0016491; F:GO:0016209		IPR012335; PTHR13871 (PANTHER), PTHR13871:SF5 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Clostridium perfringens C str. JGS1495	conserved hypothetical protein [Clostridium perfringens C str. JGS1495]	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Homo sapiens	chloride intracellular channel 1	13	P:GO:0044070; F:GO:0005247; P:GO:0034765; C:GO:0005625; C:GO:0031965; C:GO:0005903; C:GO:0034707; C:GO:0005624; P:GO:0006821; F:GO:0005515; P:GO:0007165; C:GO:0005737; C:GO:0005886	-		IPR002946; IPR010987; PTHR11260 (PANTHER), PTHR11260:SF1 (PANTHER)

Ailuropoda melanoleuca	amyloid beta a4 isoform 4	54	C:GO:0043198; F:GO:0016504; C:GO:0019717; P:GO:0050885; F:GO:0008201; P:GO:0035235; F:GO:0004867; P:GO:0007176; P:GO:0050803; P:GO:0016358; C:GO:0031594; P:GO:0000085; F:GO:0046872; C:GO:0035253; P:GO:0040014; P:GO:0030900; P:GO:0001967; P:GO:0051402; P:GO:0010952; P:GO:0008542; C:GO:0030424; C:GO:0051233; P:GO:0016199; P:GO:0045944; P:GO:0007219; C:GO:0005887; C:GO:0048471;	-		SignalP (SIGNALP)
	-	0				-
Tribolium castaneum	histone deacetylase 11	1	F:GO:0016787	-		IPR000286; PTHR10625:SF9 (PANTHER), SSF52768 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	notch-like transmembrane receptor lin-12	1	F:GO:0005515	-		IPR002110; IPR020683; PTHR18958 (PANTHER)
Caenorhabditis elegans	camp-dependent protein ki-se catalytic	6	F:GO:0004872; P:GO:0006468; P:GO:0007224; F:GO:0005524; P:GO:0007165; F:GO:0004703	-	EC:2.7.11.16	-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein H24K24.4 [Caenorhabditis elegans]	0		F:GO:0000166; P:GO:0006396; F:GO:0008173		PTHR11061 (PANTHER), PTHR11061:SF2 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0006508; F:GO:0004181; F:GO:0008270	-	EC:3.4.17.0	G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), PTHR11705:SF12 (PANTHER)
Caenorhabditis briggsae	luc7-like protein 3	6	P:GO:0008380; F:GO:0003729; P:GO:0006915; F:GO:0005515; P:GO:0006950; C:GO:0005634	-		IPR004882; PTHR12375:SF17 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	Hypothetical protein F35D2.4 [Caenorhabditis elegans]	0				SignalP (SIGNALP)

	-	0				-
	-	0				SignalP (SIGNALP)
Methanobrevibacter smithii DSM 2374	conserved hypothetical protein [Methanobrevibacter smithii DSM 2374]	0				SignalP (SIGNALP)
Caenorhabditis briggsae	zinc c2h2 type family protein	5	C:GO:0016021; F:GO:0003676; P:GO:0009792; C:GO:0005622; F:GO:0008270	-		-
	-	0				-
	-	0				-
Brugia malayi	hypothetical protein Bm1_19380 [Brugia malayi]	0				-
Caenorhabditis elegans	hypothetical protein F13H6.5 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-acl-12 protein	1	P:GO:0019915	-		-
Loa loa	sec14l1 protein	3	C:GO:0005622; P:GO:0006810; F:GO:0005215	-		IPR001251; PTHR23324 (PANTHER), PTHR23324:SF8 (PANTHER)
	-	0				-
Caenorhabditis elegans	chondroitin sulfate proteoglycan 4	1	P:GO:0009792	-		-
Caenorhabditis elegans	mrp-4	4	F:GO:0016887; P:GO:0006810; F:GO:0000166; F:GO:0005215	-		IPR001140; IPR011527; IPR017940; PTHR19242 (PANTHER), PTHR19242:SF15 (PANTHER)
	-	0				-
Ancylostoma ceylanicum	metalloprotease 1 precursor	2	F:GO:0046872; F:GO:0008237	-		-
Caenorhabditis elegans	uncoordi-ted family member (unc-89)	0				-
Brugia malayi	l-aminoadipate-semialdehyde dehydroge-se-phosphopantetheinyl transferase	3	P:GO:0009792; P:GO:0040010; P:GO:0040011	-		IPR008278; PTHR12215 (PANTHER), PTHR12215:SF4 (PANTHER)
	-	0				-
	-	0				-
Mus musculus	ribosomal protein s15a	11	P:GO:0009615; F:GO:0003723; P:GO:0045787; C:GO:0005739; P:GO:0007420; F:GO:0003735; P:GO:0006414; C:GO:0022627; F:GO:0005515; P:GO:0008284; P:GO:0009790	-		IPR000630; G3DSA:3.30.1370.30 (GENE3D), G3DSA:3.30.1490.10 (GENE3D)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
	-	0				-

Homo sapiens	defender against cell death 1	8	C:GO:0008250; P:GO:0018279; C:GO:0016021; P:GO:0007584; P:GO:0006916; P:GO:0001824; P:GO:0042493; F:GO:0004579	-	EC:2.4.1.119	SignalP (SIGNALP)
	-	0				-
Strongylocentrotus purpuratus	flavin-containing monoamine oxidase aofh	1	C:GO:0044464	-		IPR002937; PR00419 (PRINTS), G3DSA:3.50.50.60 (GENE3D), PTHR10742 (PANTHER), SSF51905 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-unc-68 protein	8	F:GO:0004872; P:GO:0006629; F:GO:0005219; P:GO:0006816; P:GO:0006874; P:GO:0055085; F:GO:0005509; C:GO:0016021	-		IPR015925; PTHR13715:SF11 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG19102 [Caenorhabditis briggsae]	0		F:GO:0005524; F:GO:0004672; F:GO:0004713; P:GO:0006468		SignalP (SIGNALP)
Loa loa	ring finger protein 121	3	F:GO:0008270; F:GO:0005515; C:GO:0016020	-		PTHR13407 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein Y110A7A.21 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	coiled-coil domain containing 88a	15	F:GO:0035091; P:GO:0030032; C:GO:0030027; P:GO:0016044; P:GO:0031323; C:GO:0005794; C:GO:0005829; F:GO:0003779; P:GO:0032956; C:GO:0031410; F:GO:0043422; F:GO:0042803; C:GO:0005783; C:GO:0005886; P:GO:0016477	-		PTHR18947 (PANTHER)
	-	0				SignalP (SIGNALP)

Pan troglodytes	heavy chain vh1 region precursor	5	P:GO:0018298; P:GO:0006955; F:GO:0003823; C:GO:0005624; F:GO:0005515	-		PTHR23266 (PANTHER), PTHR23266:SF8 (PANTHER), SignalP (SIGNALP)
	-	0				-
Loa loa	de-etiolated homolog 1	0				IPR019138
Caenorhabditis briggsae	Hypothetical protein CBG08133 [Caenorhabditis briggsae]	0				IPR004012
	-	0				-
	-	0				-
Ixodes scapularis	elegans protein partially confirmed by transcript evidence	1	P:GO:0006898	-		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	Hypothetical protein Y110A2AL.12a [Caenorhabditis elegans]	0		P:GO:0006506; C:GO:0016021; F:GO:0016746		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	patched family protein	0		F:GO:0005215; C:GO:0016021; C:GO:0016020; P:GO:0040025; P:GO:0006810; P:GO:0000003; P:GO:0040018; F:GO:0008158; P:GO:0008340; P:GO:0040011; P:GO:0018996		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	4	C:GO:0016021; P:GO:0008152; F:GO:0003824; F:GO:0005488	-		PTHR10151 (PANTHER), PTHR10151:SF28 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	yms5_caeel ame: full=uncharacterized protein flags: precursor	0		P:GO:0007160; C:GO:0016021		-
	-	0				-
Caenorhabditis briggsae	golgi traffic protein	5	P:GO:0009792; P:GO:0002119; P:GO:0040010; P:GO:0008340; P:GO:0006898	-		IPR007305; IPR011691
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Brugia malayi	egf-like domain containing protein	3	P:GO:0035152; C:GO:0016324; F:GO:0005488	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)

Achlya klebsiana	heat shock cog-te 71 kda	3	F:GO:0005524; P:GO:0006950; F:GO:0016491	-		IPR001023; IPR013126; G3DSA:2.60.34.10 (GENE3D), PTHR19375:SF1 (PANTHER), SSF100920 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	wd repeat domain 39	3	C:GO:0005856; P:GO:0016226; F:GO:0005488	-		IPR001680; IPR015943; IPR017986; IPR019781; IPR019782; PTHR19920 (PANTHER)
Loa loa	hypothetical protein LOAG_04713 [Loa loa]	0		P:GO:0035158; P:GO:0007362; P:GO:0006548; P:GO:0035152; P:GO:0035151; F:GO:0004500; P:GO:0001838; P:GO:0008293; P:GO:0007424; P:GO:0006035; P:GO:0006031; P:GO:0008362		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Culex quinquefasciatus	atp-binding cassette transporter	4	F:GO:0042626; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF97 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	AC024790_6Hypothetical protein Y47D7A.14a [Caenorhabditis elegans]	0				IPR009357; SignalP (SIGNALP)
Caenorhabditis elegans	chch domain containing protein	1	F:GO:0005515	-		PTHR21622 (PANTHER)
Brugia malayi	spry domain containing protein	8	F:GO:0046872; P:GO:0040007; P:GO:0040027; P:GO:0040035; P:GO:0048096; F:GO:0005515; P:GO:0007474; C:GO:0005634	-		IPR001870; IPR003877; IPR008985; IPR018355; PTHR10598 (PANTHER)
Loa loa	d- polymerase epsilon catalytic subunit	16	P:GO:0055085; F:GO:0008270; F:GO:0003887; P:GO:0006260; P:GO:0040035; F:GO:0003677; F:GO:0046873; F:GO:0000166; P:GO:0040011; P:GO:0006997; F:GO:0004527; P:GO:0002009; P:GO:0009792; P:GO:0030001; C:GO:0016020; C:GO:0005634	-	EC:2.7.7.7	IPR012337; PTHR10670 (PANTHER)
	-	0				-

	-	0				-
Caenorhabditis elegans	uncoordi-ted family member (unc-89)	1	F:GO:0004674	-	EC:2.7.11.0	IPR003598; IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	serotonin octopamine receptor family member (ser-7)	0		F:GO:0004872; F:GO:0004930; C:GO:0016021; F:GO:0004871; P:GO:0007165; P:GO:0007186		-
	-	0				-
Pongo abelii	gipc pdz domain containing member 1	24	P:GO:0014047; C:GO:0043198; P:GO:0043542; C:GO:0012506; C:GO:0043197; F:GO:0005102; F:GO:0030165; P:GO:0031647; C:GO:0005624; P:GO:0006605; P:GO:0048167; F:GO:0017022; F:GO:0003779; C:GO:0030139; C:GO:0044445; P:GO:0032435; F:GO:0005096; C:GO:0005903; P:GO:0007186; C:GO:0008021; P:GO:0030511; F:GO:0042803; C:GO:0005625; C:GO:0005938	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR12259 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	t-complex protein 1 subunit delta	13	C:GO:0005737; P:GO:0009792; P:GO:0002119; P:GO:0006457; F:GO:0005524; P:GO:0000003; P:GO:0008340; F:GO:0016740; F:GO:0051082; P:GO:0040007; P:GO:0006898; P:GO:0040032; P:GO:0002009	-		IPR002194; IPR002423; IPR012717; IPR017998; G3DSA:1.10.560.10 (GENE3D), G3DSA:3.30.260.10 (GENE3D), SSF54849 (SUPERFAMILY)
Caenorhabditis elegans	-dh dehydroge-se	7	P:GO:0040010; P:GO:0008340; F:GO:0008137; C:GO:0005747; P:GO:0006120; P:GO:0002119; P:GO:0009792	-	EC:1.6.5.3	IPR006806; PTHR12653 (PANTHER)

Pan troglodytes	immunoglobulin heavy chain variable region	0				IPR013106; IPR013783; PTHR23266 (PANTHER), PTHR23266:SF10 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	7	P:GO:0009792; P:GO:0006139; F:GO:0003677; F:GO:0004003; F:GO:0005524; P:GO:0000003; C:GO:0005634	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0016788; P:GO:0006886; C:GO:0031227		SignalP (SIGNALP)
	-	0				-
	-	0				-
Xenopus (Silurana) tropicalis	protein phosphatase 1l	8	P:GO:0006470; P:GO:0000165; F:GO:0046872; C:GO:0008287; F:GO:0004722; F:GO:0005515; P:GO:0007178; C:GO:0005789	-		-
Caenorhabditis elegans	ryanodine receptor	11	P:GO:0055085; P:GO:0006629; C:GO:0005875; F:GO:0005509; C:GO:0016021; F:GO:0004872; P:GO:0006874; P:GO:0006816; C:GO:0005789; F:GO:0005219; P:GO:0006936	-		IPR013662; IPR015925; PTHR13715:SF11 (PANTHER)
	-	0				-
Brugia malayi	gtpase activating protein and vps9 domains 1	2	C:GO:0005622; P:GO:0050789	-		IPR001936; IPR008936; PTHR14149 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr--s-3 protein	2	F:GO:0046872; F:GO:0008237	-		PTHR10127 (PANTHER), PTHR10127:SF64 (PANTHER)
Caenorhabditis briggsae	#NAME?	7	P:GO:0015672; F:GO:0015077; F:GO:0015662; F:GO:0000166; P:GO:0008152; P:GO:0030001; C:GO:0016020	-		IPR001757; IPR006068; IPR006069; G3DSA:1.20.1110.10 (GENE3D), PTHR11939:SF23 (PANTHER), SSF81665 (SUPERFAMILY)
Caenorhabditis briggsae	solute carrier organic anion transporter member 5a1	4	C:GO:0016021; P:GO:0009792; P:GO:0055085; F:GO:0005215	-		IPR004156; PTHR11388:SF7 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)

	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	P:GO:0000003	-		IPR004245; IPR006061; IPR017849; PTHR10974:SF7 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	briggsae cbr-jph-1 protein	0				-
Caenorhabditis elegans	multidrug resistance protein	5	P:GO:0009792; F:GO:0042626; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		-
Caenorhabditis briggsae	cathepsin a	3	F:GO:0008233; C:GO:0043231; C:GO:0044444	-		IPR001563; G3DSA:3.40.50.1820 (GENE3D), PTHR11802:SF9 (PANTHER), SSF53474 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	yfef9_caeel ame: full=uncharacterized protein flags: precursor	0				-
Caenorhabditis elegans	multidrug resistance protein family member (mrp-3)	3	F:GO:0016887; P:GO:0006810; F:GO:0000166	-		SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; C:GO:0016020; F:GO:0008375		IPR003406; PTHR19297:SF3 (PANTHER)
Brugia malayi	transcription elongation factor spt6-like	14	P:GO:0040010; F:GO:0003723; P:GO:0006310; P:GO:0006281; P:GO:0006357; F:GO:0016788; P:GO:0002119; F:GO:0005515; F:GO:0003700; F:GO:0003711; P:GO:0009792; C:GO:0005737; P:GO:0006338; C:GO:0005634	-		IPR023097; PTHR10145 (PANTHER), PTHR10145:SF1 (PANTHER)
	-	0				-
Homo sapiens	cathepsin s	6	P:GO:0006955; C:GO:0005576; C:GO:0016020; C:GO:0005764; P:GO:0006508; F:GO:0004197	-	EC:3.4.22.0	SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	mip tip subfamily	4	F:GO:0015250; C:GO:0043025; C:GO:0005929; P:GO:0006833	-		IPR000425; PTHR19139:SF25 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-ric-3 protein	0		C:GO:0005789; C:GO:0016021; C:GO:0005783; C:GO:0016020; F:GO:0005515		SignalP (SIGNALP)

Caenorhabditis briggsae	cg12125 cg12125-pa	0		F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150; C:GO:0005575		IPR019392; PTHR21508 (PANTHER)
Loa loa	hemicentin 1	0		P:GO:0007601; P:GO:0050896; F:GO:0005509; C:GO:0005604; P:GO:0018298; C:GO:0005576; P:GO:0008218		IPR003598; IPR007110; IPR013151; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF8 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-itx-1 protein	0				IPR013320; PTHR10127 (PANTHER), PTHR10127:SF11 (PANTHER)
Mus musculus	proteophosphoglycan ppg4	0		F:GO:0005524; F:GO:0003674; P:GO:0006298; F:GO:0030983; C:GO:0005575		-
Pongo abelii	h+ lysosomal v0 subunit b	7	F:GO:0008553; C:GO:0016021; C:GO:0016471; P:GO:0015986; C:GO:0033179; C:GO:0005768; P:GO:0015991	-	EC:3.6.3.6	PTHR10263 (PANTHER)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	6	P:GO:0002119; P:GO:0006468; F:GO:0005524; P:GO:0040011; P:GO:0040007; F:GO:0004674	-	EC:2.7.11.0	IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
Loa loa	hypothetical protein LOAG_04940 [Loa loa]	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	F:GO:0022891; C:GO:0016021; P:GO:0055085	-		IPR005828; IPR005829; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11600 (PANTHER)
Caenorhabditis elegans	tr--dihydrouridine synthase 3-like	6	F:GO:0003676; P:GO:0055114; F:GO:0050660; F:GO:0008270; F:GO:0017150; P:GO:0008033	-		IPR001269; PTHR11082:SF8 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis sp. PS1010	heavy unconventio-l myosin protein 7	5	F:GO:0046872; C:GO:0016459; F:GO:0005524; P:GO:0007165; F:GO:0003774	-		IPR002219; G3DSA:3.30.60.20 (GENE3D), SSF57889 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	protein clec16a	0		P:GO:0008150; C:GO:0005575		IPR019155; PTHR21481 (PANTHER)

Aplysia californica	poly	13	F:GO:0047485; P:GO:0050789; P:GO:0006281; P:GO:0032869; C:GO:0005730; F:GO:0046872; C:GO:0005667; F:GO:0042802; P:GO:0006471; F:GO:0008134; C:GO:0005635; P:GO:0006366; F:GO:0003950	-	EC:2.4.2.30	IPR004102; PTHR15447 (PANTHER)
Aspergillus niger	hypothetical protein An03g03270 [Aspergillus niger]	0				-
	-	0				IPR017970
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	malonyl- decarboxylase	7	P:GO:0006085; C:GO:0005829; C:GO:0005777; C:GO:0005739; P:GO:0031998; F:GO:0005515; F:GO:0050080	-	EC:4.1.1.9	IPR007956
Caenorhabditis briggsae	Hypothetical protein CBG19103 [Caenorhabditis briggsae]	5	P:GO:0040007; F:GO:0005488; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		-
	-	0				-
	-	0				-
	-	0				-
						IPR003599; IPR007110; IPR010939; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF9 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	aspartyl aminopeptidase	0		F:GO:0046872; P:GO:0006508; F:GO:0008237; C:GO:0005773; F:GO:0004177; F:GO:0016787; F:GO:0008233; F:GO:0008270		IPR001948; G3DSA:2.30.250.10 (GENE3D), SSF101821 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	sy-pse-associated protein 1	0				-
Loa loa	hypothetical protein LOAG_04165 [Loa loa]	0				-
Brugia malayi	vacuolar protein sorting protein	0		C:GO:0005739; F:GO:0008270; F:GO:0005515		PTHR23323 (PANTHER), PTHR23323:SF25 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG02032 [Caenorhabditis briggsae]	0				-

Caenorhabditis briggsae	26s proteasome subunit s9	4	C:GO:0005875; C:GO:0008541; P:GO:0006508; F:GO:0004175	-		PTHR10678 (PANTHER), PTHR10678:SF2 (PANTHER)
Caenorhabditis briggsae	protein-tyrosine phosphatase containing protein	0		P:GO:0016311; F:GO:0016791; P:GO:0006470; F:GO:0016787; F:GO:0004725; F:GO:0005515; F:GO:0004721		IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	leucine rich repeat family protein	0		C:GO:0016021; P:GO:0040010; P:GO:0002119; P:GO:0040007; F:GO:0005515		PTHR23154 (PANTHER), PTHR23154:SF127 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	yo91_caeel ame: full=tpr repeat-containing protein	0		F:GO:0005488		-
Caenorhabditis briggsae	lim domain family member (lim-8)	1	F:GO:0005515	-		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	protein ki-se domain containing protein	2	F:GO:0016301; P:GO:0000003	-		IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
	-	0				-
	-	0				-
						IPR003599; IPR007110; IPR013098; IPR013783; PTHR19900 (PANTHER), PTHR19900:SF7 (PANTHER), SSF48726 (SUPERFAMILY)
Trichostrongylus vitrinus	atp synthase f0 subunit 6	5	F:GO:0015078; C:GO:0005743; C:GO:0016021; P:GO:0015986; C:GO:0045263	-		SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	r- dependent r- polymerase family protein	2	F:GO:0005515; P:GO:0009792	-		IPR007855
	-	0				-
	-	0				-
Caenorhabditis briggsae	ync9_caeel ame: full=uncharacterized protein flags: precursor	0				IPR012335; IPR012336
	-	0				-
Caenorhabditis elegans	amidinotransferase family protein	1	F:GO:0016787	-		IPR003198; G3DSA:3.75.10.10 (GENE3D), PTHR12737 (PANTHER), PTHR12737:SF1 (PANTHER), SSF55909 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				IPR013069
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	methylenetetrahydrofolate dehydroge-se (-dp+ dependent) methenyltetrahydrofolate formyltetrahydrofolate synthetase	8	P:GO:0040010; P:GO:0008340; F:GO:0004488; F:GO:0004477; P:GO:0008652; F:GO:0005515; P:GO:0009396; C:GO:0005737	-	EC:1.5.1.5; EC:3.5.4.9	-
Homo sapiens	glucose phosphate isomerase	10	P:GO:0001525; F:GO:0005125; C:GO:0005615; F:GO:0004347; P:GO:0006959; P:GO:0006096; P:GO:0007599; P:GO:0006094; C:GO:0005737; F:GO:0008083	-	EC:5.3.1.9	-
Caenorhabditis elegans	ypl1_caeel ame: full=protein yippee-like	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	gl actin (drosophila neuroligin-like) homolog family member (nrx-1)	0				IPR008985; IPR012680; IPR013320
	-	0				-
Loa loa	stromal antigen	1	F:GO:0005488	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	rho gtpase-activating protein 26	5	P:GO:0019915; F:GO:0005096; P:GO:0007165; C:GO:0005622; F:GO:0005515	-		-
Caenorhabditis elegans	rho gtpase-activating protein 26	4	F:GO:0005096; P:GO:0007165; C:GO:0005622; F:GO:0005515	-		-
	-	0				-
Pan troglodytes	l antigen member 3	1	F:GO:0005515	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	high incidence of males (increased x chromosome loss) family member (him-4)	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	follicle stimulating hormone receptor	10	P:GO:0009792; C:GO:0005840; P:GO:0006952; F:GO:0003735; P:GO:0040010; P:GO:0000003; P:GO:0007186; C:GO:0016021; F:GO:0016500; P:GO:0006412	-	EC:3.6.5.3	IPR002131; PTHR23154 (PANTHER), PTHR23154:SF24 (PANTHER)
	-	0				-

	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	williams-beuren syndrome chromosome region 16 protein	0		C:GO:0005739; P:GO:0008150; C:GO:0005575		IPR000408; IPR009091; PTHR22870 (PANTHER), PTHR22870:SF11 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-asp-6 protein	4	P:GO:0008219; F:GO:0005515; P:GO:0040011; F:GO:0008233	-		IPR001461; IPR009007; IPR021109; PTHR13683:SF53 (PANTHER)
	-	0				SignalP (SIGNALP)
Brugia malayi	zinc c2h2 type family protein	2	F:GO:0008270; C:GO:0005622	-		IPR015880
Loa loa	o-glycosyl hydrolase family 30 protein	6	P:GO:0005975; F:GO:0043169; P:GO:0006665; C:GO:0005764; F:GO:0004348; P:GO:0007040	-	EC:3.2.1.45	IPR001139; IPR013781; IPR017853
	-	0				-
	-	0				-
Caenorhabditis briggsae	ca++ type member 1	24	F:GO:0004871; F:GO:0030145; P:GO:0016339; C:GO:0005802; C:GO:0030133; P:GO:0008544; C:GO:0000139; P:GO:0030026; C:GO:0005792; F:GO:0015410; P:GO:0032468; F:GO:0005509; C:GO:0016021; P:GO:0006754; P:GO:0043123; P:GO:0032472; F:GO:0005388; P:GO:0070588; C:GO:0030141; P:GO:0031532; P:GO:0006200; C:GO:0005886; F:GO:0005524; P:GO:0006828	-	EC:3.6.3.35; EC:3.6.3.8	IPR001757; IPR004014; IPR008250; G3DSA:1.20.1110.10 (GENE3D), PTHR11939:SF87 (PANTHER), SignalP (SIGNALP), SSF81653 (SUPERFAMILY), SSF81665 (SUPERFAMILY)
Homo sapiens	ig kappa light chain	3	C:GO:0005576; F:GO:0003823; P:GO:0006955	-		IPR013783; PTHR23267 (PANTHER), PTHR23267:SF33 (PANTHER), SignalP (SIGNALP), SSF48726 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)

Rattus norvegicus	cold shock domain protein a	20	C:GO:0005921; P:GO:0000122; F:GO:0003714; C:GO:0005844; F:GO:0003730; P:GO:0031100; P:GO:0009566; P:GO:0007283; P:GO:0048642; P:GO:0008584; F:GO:0003697; C:GO:0005737; P:GO:0046622; F:GO:0003702; P:GO:0009409; F:GO:0003700; F:GO:0003690; C:GO:0005634; P:GO:0043066; P:GO:0001701	-		IPR001969
Ailuropoda melanoleuca	stress-induced phosphoprotein 1	9	P:GO:0046425; F:GO:0051087; P:GO:0045449; F:GO:0008022; C:GO:0008023; F:GO:0019901; P:GO:0006950; C:GO:0005794; F:GO:0030544	-		SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-ugt-58 protein	0		P:GO:0008152; F:GO:0016758		-
Caenorhabditis briggsae	olin-like family member (gsnl-1)	0		F:GO:0003779		-
Caenorhabditis elegans	mboat family protein	2	C:GO:0016020; P:GO:0010171	-		PTHR13906 (PANTHER), PTHR13906:SF2 (PANTHER)
Caenorhabditis briggsae	g-patch domain containing protein	7	P:GO:0040035; P:GO:0009792; P:GO:0002119; C:GO:0005622; F:GO:0005515; P:GO:0040011; P:GO:0040007	-		IPR000467; PTHR13288 (PANTHER), PTHR13288:SF8 (PANTHER)
Caenorhabditis briggsae	d- ligase	4	P:GO:0006259; F:GO:0016874; P:GO:0006974; F:GO:0000166	-		IPR012308; G3DSA:1.10.3260.10 (GENE3D), SSF117018 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG10557 [Caenorhabditis briggsae]	1	F:GO:0005515	-		-
Caenorhabditis briggsae	3 -phosphoadenosine 5 -phosphosulfate synthase 2	8	P:GO:0001501; F:GO:0004781; F:GO:0005515; F:GO:0005524; P:GO:0000003; P:GO:0008340; P:GO:0000103; F:GO:0004020	-	EC:2.7.7.4; EC:2.7.1.25	IPR002650; IPR014729; IPR015947; G3DSA:3.10.400.10 (GENE3D), PTHR11055 (PANTHER), PTHR11055:SF2 (PANTHER), SSF52374 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis elegans	hypothetical protein F25F6.1 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	macrophage-stimulating protein receptor	8	P:GO:0009615; C:GO:0016021; P:GO:0023052; C:GO:0001725; F:GO:0005515; P:GO:0050794; F:GO:0004714; C:GO:0005886	-	EC:2.7.10.1	IPR001245; IPR011009; IPR020685; IPR020739; G3DSA:1.10.510.10 (GENE3D)
	-	0				-
	-	0				-
Caenorhabditis elegans	r- helicase	4	F:GO:0003676; F:GO:0000166; F:GO:0004386; C:GO:0005634	-		-
Caenorhabditis elegans	r- helicase	4	F:GO:0003676; F:GO:0000166; F:GO:0004386; C:GO:0005634	-		-
Caenorhabditis elegans	leucine-rich ras-like ki-se family member (lrk-1)	0				G3DSA:3.80.10.10 (GENE3D), PS51450 (PROFILE)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG18375 [Caenorhabditis briggsae]	0		C:GO:0016020; F:GO:0008158		-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	phytanoyl- hydroxylase interacting	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Dictyocaulus viviparus	acetylcholinesterase 2	5	P:GO:0001507; F:GO:0003990; C:GO:0005623; P:GO:0040012; F:GO:0042803	-	EC:3.1.1.7	SignalP (SIGNALP)
Dictyocaulus viviparus	acetylcholinesterase 2	5	P:GO:0001507; F:GO:0003990; C:GO:0005623; P:GO:0040012; F:GO:0042803	-	EC:3.1.1.7	IPR000997; IPR002018; G3DSA:3.40.50.1820 (GENE3D), PTHR11559:SF33 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
Dictyocaulus viviparus	acetylcholinesterase 2	5	P:GO:0001507; F:GO:0003990; C:GO:0005623; P:GO:0040012; F:GO:0042803	-	EC:3.1.1.7	-
Dictyocaulus viviparus	acetylcholinesterase 2	5	P:GO:0001507; F:GO:0003990; C:GO:0005623; P:GO:0040012; F:GO:0042803	-	EC:3.1.1.7	-
Caenorhabditis elegans	briggsae cbr-hmr-1 protein	1	F:GO:0005515	-		-
Canis familiaris	actin-related protein 2 3 complex subunit 1b (arp2 3 complex 41 kda subunit) (p41-arc)	0				-

	-	0				-
	-	0				-
Loa loa	mef2c protein	25	P:GO:0035051; F:GO:0042826; P:GO:0002062; P:GO:0001649; P:GO:0003151; C:GO:0016607; F:GO:0019901; P:GO:0009952; P:GO:0001568; P:GO:0010552; C:GO:0005730; F:GO:0016563; F:GO:0003702; P:GO:0010553; P:GO:0045885; P:GO:0003211; P:GO:0007519; F:GO:0043565; F:GO:0003700; P:GO:0007399; P:GO:0007521; P:GO:0090073; P:GO:0001974; P:GO:0051145; P:GO:0001958	-		IPR002100; PTHR11945 (PANTHER), PTHR11945:SF24 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	uncoordi-ted family member (unc-62)	13	P:GO:0048645; F:GO:0005515; P:GO:0001752; P:GO:0010552; P:GO:0007383; P:GO:0007420; F:GO:0043565; P:GO:0007480; P:GO:0048735; F:GO:0003700; P:GO:0009954; C:GO:0005634; P:GO:0007476	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-mrp-6 protein	5	F:GO:0022857; F:GO:0016887; P:GO:0006810; C:GO:0016020; F:GO:0000166	-		IPR001140; IPR009147; IPR011527; IPR017940; G3DSA:1.20.1560.10 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF97 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-

Caenorhabditis briggsae	d- polymerase epsilon catalytic subunit	11	F:GO:0008270; F:GO:0003887; P:GO:0006260; P:GO:0040035; F:GO:0003677; F:GO:0000166; P:GO:0040011; P:GO:0006997; P:GO:0002009; P:GO:0009792; C:GO:0005634	-	EC:2.7.7.7	PTHR10670 (PANTHER)
Loa loa	transcription elongation factor b polypeptide 1	1	F:GO:0005488	-		IPR011333; IPR016073; PTHR20648 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	nuclear hormone receptor family member (nhr-1)	11	F:GO:0008270; P:GO:0006355; F:GO:0042802; F:GO:0043565; P:GO:0002119; P:GO:0040017; F:GO:0003700; F:GO:0003707; P:GO:0040018; P:GO:0032094; C:GO:0005634	-		IPR001628; IPR008946; IPR013088; PTHR11865 (PANTHER), PTHR11865:SF218 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis elegans	nuclear receptor nhr-1	11	F:GO:0008270; P:GO:0006355; F:GO:0042802; F:GO:0043565; P:GO:0002119; P:GO:0040017; F:GO:0003700; F:GO:0003707; P:GO:0040018; P:GO:0032094; C:GO:0005634	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	mpo-a protein	6	F:GO:0020037; P:GO:0055114; F:GO:0004666; F:GO:0004601; F:GO:0005509; P:GO:0006979	-	EC:1.14.99.1; EC:1.11.1.7	-
Caenorhabditis elegans	mgc83087 protein	1	F:GO:0005515	-		-
	-	0				SignalP (SIGNALP)

Brugia malayi	adaptor-related protein complex beta 1 subunit	9	P:GO:0009792; P:GO:0002119; F:GO:0005515; F:GO:0008565; P:GO:0000003; P:GO:0006886; P:GO:0040007; P:GO:0006898; C:GO:0030131	-		IPR002553; IPR011989; IPR016024; PTHR11134 (PANTHER), PTHR11134:SF3 (PANTHER)
	-	0				-
Homo sapiens	protein disulfide isomerase family member 3	11	F:GO:0004629; F:GO:0003756; P:GO:0043065; P:GO:0006606; P:GO:0045454; F:GO:0004197; C:GO:0042470; C:GO:0005788; F:GO:0005515; P:GO:0007165; P:GO:0006621	-	EC:5.3.4.1; EC:3.4.22.0	IPR012335; IPR012336
Caenorhabditis elegans	calcium alpha subunit family member (cca-1)	6	P:GO:0051899; P:GO:0045760; P:GO:0043051; P:GO:0006811; C:GO:0016021; F:GO:0008332	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-asp-6 protein	3	P:GO:0008219; F:GO:0016787; F:GO:0005515	-		IPR001461; IPR009007; IPR021109; PTHR13683:SF53 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	zo-1 mdck	6	P:GO:0070830; C:GO:0005923; C:GO:0031410; F:GO:0005515; P:GO:0071277; C:GO:0016323	-		-
Caenorhabditis briggsae	zo-1 mdck	6	P:GO:0070830; C:GO:0005923; C:GO:0031410; F:GO:0005515; P:GO:0071277; C:GO:0016323	-		IPR000906; PTHR13865 (PANTHER), PTHR13865:SF7 (PANTHER)
Caenorhabditis briggsae	zo-1 mdck	6	P:GO:0070830; C:GO:0005923; C:GO:0031410; F:GO:0005515; P:GO:0071277; C:GO:0016323	-		IPR000906; PTHR13865 (PANTHER), PTHR13865:SF7 (PANTHER)

Caenorhabditis briggsae	tight junction protein	0		F:GO:0004385; P:GO:0007391; P:GO:0035156; P:GO:0016337; P:GO:0007254; P:GO:0046328; P:GO:0035147; P:GO:0007163; C:GO:0005913; C:GO:0005912; C:GO:0005622; F:GO:0005515; P:GO:0042981		PTHR13865 (PANTHER), PTHR13865:SF7 (PANTHER)
Caenorhabditis briggsae	zo-1 mdck	6	P:GO:0070830; C:GO:0005923; C:GO:0031410; F:GO:0005515; P:GO:0071277; C:GO:0016323	-		IPR000906; PTHR13865 (PANTHER), PTHR13865:SF7 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Drosophila melanogaster	cg3603-pa	3	F:GO:0016491; P:GO:0055114; F:GO:0005488	-		-
Caenorhabditis briggsae	otu domain-containing protein 6b	0		C:GO:0016021; F:GO:0008233		-
Caenorhabditis elegans	met proto-oncogene precursor	43	P:GO:0033138; F:GO:0004674; P:GO:0006915; P:GO:0010552; F:GO:0005008; C:GO:0009925; C:GO:0014069; P:GO:0050775; P:GO:0030534; P:GO:0007420; P:GO:0048012; P:GO:0001889; C:GO:0005615; P:GO:0014812; P:GO:0014902; F:GO:0008013; P:GO:0045740; C:GO:0005737; P:GO:0051450; P:GO:0030317; C:GO:0005887; C:GO:0060076; P:GO:0001890; F:GO:0005524; C:GO:0045211; F:GO:0003723; F:GO:0043274;	-	EC:2.7.11.0	IPR000719; IPR001245; IPR011009; IPR020685; IPR020739; G3DSA:1.10.510.10 (GENE3D)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	hd domain-containing protein 3	1	F:GO:0003824	-		-

	-	0				-
Brugia malayi	fizzy-related protein	28	P:GO:0006930; C:GO:0016020; C:GO:0005814; P:GO:0007155; P:GO:0001752; P:GO:0030713; F:GO:0005525; C:GO:0008287; F:GO:0046872; P:GO:0007391; P:GO:0035099; C:GO:0005819; P:GO:0008347; P:GO:0007264; P:GO:0007067; P:GO:0007126; P:GO:0007455; P:GO:0030163; P:GO:0006470; P:GO:0010001; P:GO:0030718; F:GO:0019003; C:GO:0005811; F:GO:0003924; P:GO:0016476; P:GO:0046328; F:GO:0004722	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Strongylocentrotus purpuratus	mannose c type 1-like 1	0		F:GO:0005488; F:GO:0005529		IPR001304; IPR016186; IPR016187; PTHR22802 (PANTHER), PTHR22802:SF15 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	4	F:GO:0003700; F:GO:0043565; C:GO:0005634; P:GO:0006355	-		-
	-	0				-
Pongo abelii	mhc class ii antigen	3	P:GO:0006955; P:GO:0002504; C:GO:0042613	-		-
Pongo abelii	mhc class ii antigen	3	P:GO:0006955; P:GO:0002504; C:GO:0042613	-		PTHR19944 (PANTHER), PTHR19944:SF27 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		-
Caenorhabditis elegans	briggsae cbr-sel-2 protein	6	C:GO:0005737; P:GO:0008104; F:GO:0051018; P:GO:0042675; C:GO:0016020; C:GO:0005634	-		IPR000409; IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR13743 (PANTHER)
	-	0				-

Caenorhabditis elegans	recombi-tion factor ad54	13	P:GO:0006915; P:GO:0000711; P:GO:0010212; P:GO:0000003; P:GO:0051301; F:GO:0003677; F:GO:0005524; F:GO:0005515; P:GO:0007067; F:GO:0004386; P:GO:0006338; P:GO:0043150; C:GO:0005634	-		-
	-	0				-
Caenorhabditis elegans	hypothetical protein C37C3.12 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	adam metallopeptidase with thrombospondin type 1 7	4	F:GO:0004222; C:GO:0005578; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	-
	-	0				-
Pongo abelii	slc4a2 protein	6	C:GO:0016323; F:GO:0015108; F:GO:0005452; C:GO:0005624; C:GO:0016021; P:GO:0006821	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG07699 [Caenorhabditis briggsae]	0		F:GO:0005524; F:GO:0016874; P:GO:0008152; F:GO:0003824; F:GO:0009374; P:GO:0006633; F:GO:0003989		-
	-	0				-
Caenorhabditis elegans	isoform e	11	C:GO:0009353; P:GO:0040010; P:GO:0008340; C:GO:0031966; P:GO:0055114; P:GO:0006099; P:GO:0002119; P:GO:0006096; P:GO:0009792; F:GO:0004591; F:GO:0030976	-	EC:1.2.4.2	IPR011603

Brugia malayi	briggsae cbr-scc-3 protein	30	F:GO:0005515; P:GO:0006412; P:GO:0016045; P:GO:0007141; C:GO:0005576; C:GO:0005730; P:GO:0007286; F:GO:0003677; P:GO:0009253; C:GO:0005875; F:GO:0003735; P:GO:0045449; P:GO:0032494; P:GO:0008592; P:GO:0007379; C:GO:0005811; F:GO:0032500; P:GO:0006965; F:GO:0016019; C:GO:0005887; P:GO:0045087; C:GO:0035327; C:GO:0000922; C:GO:0005721; P:GO:0006260; C:GO:0008278; F:GO:0008745;	-	EC:3.6.5.3; EC:3.5.1.28	-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis briggsae	endothelin-converting protein 1	3	C:GO:0016021; F:GO:0004222; P:GO:0006508	-	EC:3.4.24.0	IPR000718; IPR018497; G3DSA:3.40.390.10 (GENE3D), PTHR11733:SF20 (PANTHER), SSF55486 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	patched family protein	7	P:GO:0018996; C:GO:0016021; P:GO:0008340; P:GO:0000003; P:GO:0040025; F:GO:0008158; P:GO:0040011	-		IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER)
	-	0				-

Ailuropoda melanoleuca	filamin alpha	28	F:GO:0004871; C:GO:0005802; P:GO:0043433; P:GO:0034394; C:GO:0015629; P:GO:0050821; P:GO:0051220; C:GO:0005576; C:GO:0005829; F:GO:0001948; P:GO:0051764; P:GO:0043123; F:GO:0051015; F:GO:0048365; P:GO:0045022; P:GO:0007195; F:GO:0042803; F:GO:0034989; P:GO:0031532; F:GO:0034988; C:GO:0005886; F:GO:0008134; P:GO:0042177; C:GO:0005634; P:GO:0042993; C:GO:0005938; P:GO:0043113	-		-
Loa loa	uncharacterized protein family upf0005 containing protein	0		C:GO:0016021; C:GO:0016020		IPR006214; PTHR23291:SF14 (PANTHER), SignalP (SIGNALP)
Loa loa	uncoordi-ted family member (unc-13)	0		F:GO:0046872		IPR010439; PTHR10480 (PANTHER)
Caenorhabditis elegans	trafficking protein particle complex	3	P:GO:0006182; F:GO:0020037; F:GO:0004383	-	EC:4.6.1.2	IPR007194; IPR011644; G3DSA:3.30.1380.20 (GENE3D), PTHR20902 (PANTHER)
Callithrix jacchus	b chain activator-bound structure of human pyruvate ki-se m2	11	F:GO:0004743; C:GO:0019861; F:GO:0005515; F:GO:0030955; F:GO:0005524; F:GO:0000287; P:GO:0006096; P:GO:0012501; C:GO:0005634; C:GO:0005829; C:GO:0005739	-	EC:2.7.1.40	IPR001697; IPR015793; IPR015813
Caenorhabditis elegans	ynp8_caeel ame: full=uncharacterized protein	0				-
Caenorhabditis briggsae	atp-binding sub-family c (cftr mrp) member 2	4	F:GO:0016887; P:GO:0006810; F:GO:0000166; F:GO:0005215	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				IPR016186; IPR016187
	-	0				-
	-	0				-

Caenorhabditis elegans	atp dependent d- ligase c termi-l region family protein	0		P:GO:0006260; F:GO:0005524; F:GO:0016874; P:GO:0006281; F:GO:0003910; P:GO:0006310; F:GO:0003677; C:GO:0005622		-
Caenorhabditis elegans	briggsae cbr-dep-1 protein	3	P:GO:0040026; P:GO:0040027; F:GO:0016787	-		-
Caenorhabditis briggsae	cleft lip and palate associated transmembrane protein	1	F:GO:0005515	-		IPR008429
	-	0				-
	-	0				IPR009003; G3DSA:2.40.10.10 (GENE3D)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0006952; P:GO:0008152; F:GO:0003824	-		IPR002198; IPR002347; IPR016040; PTHR19410:SF18 (PANTHER), SSF51735 (SUPERFAMILY)
Branchiostoma floridae	briggsae cbr-pan-1 protein	0		C:GO:0016021; C:GO:0016020; F:GO:0004930; P:GO:0007165; F:GO:0004872; F:GO:0005515; F:GO:0004871; P:GO:0007186; C:GO:0005886; F:GO:0016500		-
Caenorhabditis briggsae	dihydrolipoamide branched chain transacylase e2	12	F:GO:0008415; F:GO:0004674; C:GO:0042645; F:GO:0005524; F:GO:0043754; P:GO:0032436; C:GO:0005576; F:GO:0005179; P:GO:0009792; P:GO:0046949; F:GO:0048037; P:GO:0006468	-	EC:2.7.11.0; EC:2.3.1.168	IPR000089; IPR003016; IPR011053; IPR015761; G3DSA:2.40.50.100 (GENE3D), PTHR23151 (PANTHER)
	-	0				-
	-	0				IPR000095; SignalP (SIGNALP)
Caenorhabditis elegans	ataxia telangiectasia mutated	1	C:GO:0000785	-		PTHR11139 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	kinesin light chain family member (klc-2)	3	F:GO:0003777; F:GO:0005515; C:GO:0005871	-		-
	-	0				IPR002293; PTHR11785:SF76 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	briggsae cbr-tag-263 protein	3	C:GO:0016021; F:GO:0005272; P:GO:0006814	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)

	-	0				IPR004129; IPR017946; SignalP (SIGNALP)
Caenorhabditis elegans	cyclin-dependent ki-se family member (cdk-9)	4	P:GO:0006468; F:GO:0005524; F:GO:0004674; P:GO:0051301	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF111 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Angiostrongylus cantonensis	briggsae cbr-gbh-1 protein	5	F:GO:0005506; P:GO:0055114; F:GO:0016702; F:GO:0008336; P:GO:0045329	-	EC:1.13.11.0; EC:1.14.11.1	G3DSA:3.60.130.10 (GENE3D), PTHR10696 (PANTHER), PTHR10696:SF3 (PANTHER), SSF51197 (SUPERFAMILY)
Caenorhabditis briggsae	serine threonine-protein ki-se d3	2	F:GO:0046872; C:GO:0016021	-		IPR002219; G3DSA:3.30.60.20 (GENE3D), PTHR21119 (PANTHER), PTHR21119:SF1 (PANTHER), SSF57889 (SUPERFAMILY)
Loa loa	hypothetical protein LOAG_05011 [Loa loa]	0				IPR015633; SSF144074 (SUPERFAMILY)
Caenorhabditis briggsae	programmed cell death 6-interacting protein	0				G3DSA:1.20.140.50 (GENE3D), PTHR23030 (PANTHER), PTHR23030:SF11 (PANTHER)
Caenorhabditis briggsae	tfiie alpha subunit family protein	9	P:GO:0040010; F:GO:0008270; P:GO:0006367; P:GO:0045449; P:GO:0010171; P:GO:0040011; P:GO:0006898; P:GO:0002009; P:GO:0009792	-		IPR017919; PTHR13097 (PANTHER), PF02002 (PFAM)
	-	0				-
Caenorhabditis elegans	spartin	0		C:GO:0005737; F:GO:0031625; P:GO:0008219		IPR000169; IPR009686; PTHR21068 (PANTHER), PTHR21068:SF8 (PANTHER)
Loa loa	acl-8 protein	0				-
Caenorhabditis elegans	c-type lectin family member (clec-89)	0				-
Caenorhabditis elegans	briggsae cbr-imb-6 protein	0				PTHR15952 (PANTHER), PTHR15952:SF11 (PANTHER)
Caenorhabditis elegans	inositol -trisphosphate receptor	5	P:GO:0006816; F:GO:0005220; P:GO:0055085; C:GO:0016021; C:GO:0005783	-		IPR015925; PTHR13715:SF2 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-

Caenorhabditis elegans	protein	0		C:GO:0016023; C:GO:0016021; P:GO:0006950; C:GO:0005737; F:GO:0005524; F:GO:0031072; C:GO:0005788; P:GO:0009408; P:GO:0006457; F:GO:0046872; C:GO:0005886; F:GO:0051082		IPR001623; IPR015609; PTHR11821:SF22 (PANTHER)
Taeniopygia guttata	atp-binding sub-family a member 4	5	P:GO:0006649; F:GO:0042626; P:GO:0045494; F:GO:0004012; C:GO:0005887	-	EC:3.6.3.1	IPR003439; G3DSA:3.40.50.300 (GENE3D), PTHR19229 (PANTHER), PTHR19229:SF30 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	hypothetical protein Y75B7AR.1 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	hypothetical protein Y75B7AR.1 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	briggsae cbr-let-268 protein	6	F:GO:0031418; F:GO:0005506; P:GO:0055114; F:GO:0008475; C:GO:0016020; C:GO:0005783	-	EC:1.14.11.4	PTHR10730 (PANTHER), PTHR10730:SF1 (PANTHER)
Haemonchus contortus	acetylcholine receptor deg-3-like protein	4	C:GO:0016021; C:GO:0045211; P:GO:0006811; F:GO:0005230	-		IPR006029; IPR006201; G3DSA:1.20.120.370 (GENE3D), PTHR18945:SF55 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Heliconius melpomene	endonuclease-reverse transcriptase -e01	0		F:GO:0003723; P:GO:0006278; F:GO:0004519; F:GO:0003964		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	g in family member (glb-29)	3	F:GO:0020037; P:GO:0015671; F:GO:0019825	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	spectrin alpha chain	1	F:GO:0005509	-		-
Caenorhabditis briggsae	taf5 r- polymerase tata box binding protein -associated factor	12	F:GO:0016986; P:GO:0006367; C:GO:0005730; F:GO:0010843; C:GO:0033276; F:GO:0046983; C:GO:0015629; P:GO:0006368; F:GO:0003700; F:GO:0004402; C:GO:0005669; C:GO:0005737	-	EC:2.3.1.48	IPR001680; IPR011047; IPR015943; IPR017986; IPR019781; IPR019782; PTHR19879 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0055085		SignalP (SIGNALP)
	-	0				-
	-	0				IPR015880
Ectocarpus siliculosus	threonine dehydratase	3	F:GO:0030170; P:GO:0006520; F:GO:0004794	-	EC:4.3.1.19	IPR001926; G3DSA:3.40.50.1100 (GENE3D), PTHR10314 (PANTHER), PTHR10314:SF17 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	F:GO:0016491; P:GO:0055114	-		-
Homo sapiens	b chain activator-bound structure of human pyruvate ki-se m2	11	F:GO:0004743; C:GO:0019861; F:GO:0005515; F:GO:0030955; F:GO:0005524; F:GO:0000287; P:GO:0006096; P:GO:0012501; C:GO:0005634; C:GO:0005829; C:GO:0005739	-	EC:2.7.1.40	IPR001697; IPR015793; IPR015813; IPR018209
	-	0				-
Caenorhabditis briggsae	cell-cycle and apoptosis regulatory protein 1	4	P:GO:0040027; F:GO:0005515; P:GO:0040017; P:GO:0040010	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-deg-1 protein	3	C:GO:0016021; F:GO:0005272; P:GO:0006814	-		IPR001873; G3DSA:2.60.470.10 (GENE3D), PTHR11690:SF17 (PANTHER)
Bos taurus	amino-termi-l enhancer of split	11	P:GO:0040008; P:GO:0031668; P:GO:0060761; P:GO:0009887; P:GO:0032091; P:GO:0001501; P:GO:0010553; F:GO:0003714; P:GO:0090090; P:GO:0070555; C:GO:0005634	-		IPR005617; PTHR10814 (PANTHER)
	-	0				-
	-	0				-
Loa loa	elegans protein partially confirmed by transcript evidence	2	P:GO:0006810; C:GO:0016020	-		-
	-	0				-
Caenorhabditis elegans	briggsae cbr-acl-4 protein	0		F:GO:0008415; P:GO:0008152; C:GO:0016021		-
Caenorhabditis elegans	homeodomain interacting protein ki-se family member (hpk-1)	5	P:GO:0006468; F:GO:0003677; F:GO:0005524; P:GO:0008340; F:GO:0004674	-	EC:2.7.11.0	IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF117 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	yws1_caeel ame: full=uncharacterized protein	0		P:GO:0019915		SignalP (SIGNALP)

Caenorhabditis briggsae	fatty acid 2-hydroxylase	10	P:GO:0040010; P:GO:0006633; C:GO:0016021; P:GO:0055114; F:GO:0016491; P:GO:0002119; F:GO:0005515; F:GO:0020037; P:GO:0040018; C:GO:0005783	-		IPR001199; IPR006694; PTHR12863 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	d- chr erato doi isoform cra_a	0		F:GO:0003674; P:GO:0008150; C:GO:0005575		-
Caenorhabditis briggsae	zcchc4 protein	2	F:GO:0046872; F:GO:0016740	-		IPR019369
	-	0				SignalP (SIGNALP)
	-	0				-
Teladorsagia circumcincta	nicotinic acetylcholine receptor alpha subunit 38	6	F:GO:0004872; C:GO:0045211; C:GO:0030054; P:GO:0006811; C:GO:0016021; F:GO:0004889	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein Y37E11AM.2 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	hypothetical protein Y37E11AM.2 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)

Neovison vison	78 kda glucose-regulated protein precursor	30	P:GO:0030433; P:GO:0043154; F:GO:0051087; P:GO:0030512; P:GO:0021680; C:GO:0030176; P:GO:0021589; C:GO:0005788; P:GO:0031398; C:GO:0008303; P:GO:0060904; C:GO:0042470; F:GO:0043027; F:GO:0005509; F:GO:0043022; P:GO:0006983; C:GO:0005576; F:GO:0030674; P:GO:0006916; C:GO:0009986; F:GO:0031625; P:GO:0006987; P:GO:0040019; F:GO:0051082; P:GO:0042149; F:GO:0051787; C:GO:0048471;	-		-
Caenorhabditis elegans	hypothetical protein Y92H12A.5 [Caenorhabditis elegans]	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	olfactory ing defective family member (olrn-1)	0		F:GO:0005509		-
Brugia malayi	voltage gated chloride channel family protein	0		F:GO:0005216; C:GO:0005902; C:GO:0016021; C:GO:0016020; C:GO:0015629; C:GO:0005626; F:GO:0005254; F:GO:0005515; P:GO:0055085; F:GO:0005247; P:GO:0006821		IPR001807; IPR014743; PTHR11689:SF5 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				IPR006652; IPR015915
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F01F1.2 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	trpa cation channel homolog family member (trpa-1)	0				PTHR18958 (PANTHER), PTHR18958:SF250 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-ztf-9 protein	1	F:GO:0005515	-		IPR015880; SSF57667 (SUPERFAMILY)

Caenorhabditis elegans	briggsae cbr-ztf-9 protein	1	F:GO:0005515	-		IPR015880; SSF57667 (SUPERFAMILY)
Caenorhabditis elegans	lbp bpi cetp c-termi-l domain containing protein	1	F:GO:0008289	-		SignalP (SIGNALP)
	-	0				-
						IPR003598; IPR007110; IPR009134; IPR013098; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	lethal family member (let-2)	3	C:GO:0005587; F:GO:0030020; P:GO:0016043	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	major intrinsic protein	3	P:GO:0006810; C:GO:0016021; F:GO:0005215	-		IPR000425; PTHR19139:SF11 (PANTHER)
	-	0				-
Caenorhabditis elegans	retinoblastoma-binding protein 8	0		F:GO:0000014; F:GO:0003684; C:GO:0005634; P:GO:0006357; P:GO:0006281; F:GO:0005515; P:GO:0010792; P:GO:0001835; P:GO:0000075		IPR013882
	-	0				-
	-	0				SignalP (SIGNALP)
Ancylostoma duodenale	ancylostoma-secreted protein 1 precursor	0		C:GO:0005576		IPR001283; IPR014044; PTHR10334:SF2 (PANTHER)
	-	0				-
Caenorhabditis elegans	ras and ef-hand domain containing	10	P:GO:0006412; C:GO:0005840; F:GO:0005509; P:GO:0007264; F:GO:0003735; P:GO:0006913; F:GO:0005515; C:GO:0048471; P:GO:0006886; F:GO:0005525	-	EC:3.6.5.3	-
	-	0				IPR007087; IPR015880; PTHR12487 (PANTHER), PTHR12487:SF1 (PANTHER)
	-	0				-
Caenorhabditis briggsae	related to yeast vacuolar protein sorting factor family member (vps-39)	7	P:GO:0002009; P:GO:0008219; P:GO:0009792; P:GO:0000003; F:GO:0005083; P:GO:0010171; F:GO:0005515	-		PTHR12894 (PANTHER), PTHR12894:SF10 (PANTHER), SignalP (SIGNALP)
Cyathostominae sp. JM-2007a	temporarily assigned gene -me family member (tag-273)	2	F:GO:0008270; P:GO:0000003	-		-
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		C:GO:0016021; P:GO:0016042; P:GO:0006644		IPR013090; SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	F:GO:0003676; F:GO:0000166	-		IPR019363
	-	0				-
Caenorhabditis elegans	hla class iii protein dom3z	0		P:GO:0006353; P:GO:0006364; P:GO:0006350; P:GO:0006397; P:GO:0045449; C:GO:0005634		-
Ailuropoda melanoleuca	platelet	11	C:GO:0005625; F:GO:0046872; C:GO:0005945; F:GO:0003872; F:GO:0070095; F:GO:0005524; P:GO:0006002; F:GO:0005515; P:GO:0006096; P:GO:0051289; P:GO:0030388	-	EC:2.7.1.11	G3DSA:3.40.50.460 (GENE3D), PTHR13697 (PANTHER)
Caenorhabditis briggsae	ykad_caeel ame: full=uncharacterized protein	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Callithrix jacchus	40s ribosomal protein s25-like	7	F:GO:0003723; C:GO:0005730; F:GO:0003735; P:GO:0006414; C:GO:0022627; F:GO:0005515; P:GO:0000028	-		IPR004977; PTHR12850:SF4 (PANTHER)
Caenorhabditis elegans	d- topoisomerase 2-binding protein 1	6	P:GO:0009987; P:GO:0050896; F:GO:0005488; C:GO:0043232; C:GO:0044446; C:GO:0005634	-		IPR001357; G3DSA:3.40.50.10190 (GENE3D), PTHR13561 (PANTHER), PTHR13561:SF4 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	osm-9 and capsaicin receptor-related family member (ocr-3)	0				-
Ostertagia ostertagi	sxc2 protein	0				IPR003582
	-	0				SignalP (SIGNALP)
	-	0				IPR018073; SignalP (SIGNALP)
	-	0				-
	-	0				-

Caenorhabditis briggsae	isl lim homeobox 2	9	F:GO:0003700; F:GO:0043565; F:GO:0003702; F:GO:0005515; P:GO:0007275; C:GO:0005634; F:GO:0008270; P:GO:0006355; P:GO:0006091	-		-
Homo sapiens	cytochrome c oxidase subunit ii	57	F:GO:0004601; F:GO:0004129; P:GO:0042640; C:GO:0005901; F:GO:0008289; F:GO:0005507; P:GO:0030282; P:GO:0045429; P:GO:0090271; P:GO:0051384; C:GO:0043234; P:GO:0031394; P:GO:0031622; P:GO:0043065; P:GO:0010243; P:GO:0019371; P:GO:0010575; P:GO:0031915; P:GO:0051726; P:GO:0007613; C:GO:0005788; F:GO:0020037; P:GO:0008217; C:GO:0005792; P:GO:0006979; F:GO:0004666; P:GO:0010042; C:GO:0016021;	-	EC:1.11.1.7; EC:1.9.3.1; EC:1.14.99.1 ; EC:1.13.11.0	-
	-	0				-
Homo sapiens	histidine triad nucleotide-binding protein 1-like	6	C:GO:0005856; C:GO:0005737; F:GO:0016787; P:GO:0007165; C:GO:0005634; F:GO:0005080	-		SignalP (SIGNALP)
Caenorhabditis elegans	uncoordi-ted family member (unc-13)	10	C:GO:0030054; F:GO:0001566; P:GO:0006917; P:GO:0023034; F:GO:0046872; C:GO:0045202; P:GO:0007588; P:GO:0016082; P:GO:0007165; C:GO:0005794	-		IPR000008; IPR008973
	-	0				-
	-	0				-

Pan troglodytes	eukaryotic translation elongation factor 1 beta 2	5	C:GO:0005829; F:GO:0003746; C:GO:0005853; F:GO:0005515; P:GO:0006414	-		PTHR11595 (PANTHER), PTHR11595:SF7 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	r- dependent r- polymerase family protein	2	F:GO:0005515; P:GO:0009792	-		IPR000215; IPR007855
Caenorhabditis elegans	piwi domain containing protein	1	P:GO:0000003	-		IPR003165; IPR012337; PTHR22891 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Selaginella moellendorffii	-aladase ii protein	1	F:GO:0016787	-		IPR003137; G3DSA:3.50.30.30 (GENE3D), PTHR10404 (PANTHER), PTHR10404:SF15 (PANTHER), SSF52025 (SUPERFAMILY)
	-	0				-
Oryctolagus cuniculus	tropomyosin gamma isoform 8	11	C:GO:0002102; C:GO:0030863; P:GO:0006928; C:GO:0030426; P:GO:0006937; F:GO:0003779; C:GO:0005862; C:GO:0031941; C:GO:0032154; P:GO:0007420; C:GO:0001725	-		-
	-	0				-
Caenorhabditis briggsae	yqd7_caeel ame: full=uncharacterized protein	0				-
	-	0				-
Caenorhabditis briggsae	innexin family protein	3	P:GO:0019915; C:GO:0005921; F:GO:0008234	-		IPR000990
Caenorhabditis briggsae	d-amino acid oxidase	4	P:GO:0009792; P:GO:0055114; F:GO:0008445; F:GO:0047821	-	EC:1.4.3.1; EC:1.4.3.7	IPR016040; PTHR11530 (PANTHER)
Caenorhabditis elegans	bifunctio-l purine biosynthesis protein purh	4	F:GO:0004643; P:GO:0006188; F:GO:0003937; F:GO:0042803	-	EC:2.1.2.3; EC:3.5.4.10	IPR002695; IPR011607; IPR013982; IPR016193; G3DSA:1.10.287.440 (GENE3D), G3DSA:3.40.140.20 (GENE3D)
Caenorhabditis elegans	bifunctio-l purine biosynthesis protein purh	4	F:GO:0004643; P:GO:0006188; F:GO:0003937; F:GO:0042803	-	EC:2.1.2.3; EC:3.5.4.10	IPR002695; IPR011607; IPR013982; IPR016193; G3DSA:1.10.287.440 (GENE3D), G3DSA:3.40.140.20 (GENE3D)
Caenorhabditis briggsae	alkali metal ion proton exchanger 3	6	P:GO:0009792; F:GO:0015385; P:GO:0055085; P:GO:0006885; C:GO:0016021; P:GO:0006814	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)

Nasonia vitripennis	ubiquitin associated and sh3 domain-containing protein b	0		F:GO:0004619; F:GO:0004872; P:GO:0016070; F:GO:0003824; C:GO:0005622; F:GO:0016853		G3DSA:3.40.50.1240 (GENE3D), PTHR16469 (PANTHER), PTHR16469:SF8 (PANTHER)
Ailuropoda melanoleuca	filamin alpha	28	F:GO:0004871; C:GO:0005802; P:GO:0043433; P:GO:0034394; C:GO:0015629; P:GO:0050821; P:GO:0051220; C:GO:0005576; C:GO:0005829; F:GO:0001948; P:GO:0051764; P:GO:0043123; F:GO:0051015; F:GO:0048365; P:GO:0045022; P:GO:0007195; F:GO:0042803; F:GO:0034989; P:GO:0031532; F:GO:0034988; C:GO:0005886; F:GO:0008134; P:GO:0042177; C:GO:0005634; P:GO:0042993; C:GO:0005938; P:GO:0043113	-		IPR013783; IPR014756; IPR017868; PTHR11915 (PANTHER), PTHR11915:SF24 (PANTHER)
Caenorhabditis elegans	yms5_caeel ame: full=uncharacterized protein flags: precursor	2	C:GO:0016021; P:GO:0007160	-		PTHR13802 (PANTHER), PTHR13802:SF1 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	2	F:GO:0003700; P:GO:0045449	-		-
	-	0				IPR000887
	-	0				-
Caenorhabditis briggsae	phosphodiesterase cgmp-inhibited	13	P:GO:0043951; C:GO:0016020; P:GO:0006198; P:GO:0032869; P:GO:0050995; C:GO:0005792; F:GO:0004114; C:GO:0005794; F:GO:0046872; F:GO:0043422; C:GO:0032045; P:GO:0033629; C:GO:0005783	-	EC:3.1.4.17	-
Caenorhabditis elegans	multiple pdz domain protein family member (mpz-1)	2	F:GO:0005515; C:GO:0016021	-		PTHR19964 (PANTHER), PTHR19964:SF5 (PANTHER)

Brugia malayi	d--directed r- polymerase ii kda polypeptide	7	F:GO:0003899; F:GO:0030528; F:GO:0008270; P:GO:0045449; C:GO:0005665; F:GO:0003677; P:GO:0006366	-	EC:2.7.7.6	IPR001222; IPR001529; IPR019761; G3DSA:2.20.25.10 (GENE3D), PTHR11239 (PANTHER), PTHR11239:SF1 (PANTHER), SSF57783 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-hmr-1 protein	3	C:GO:0016020; P:GO:0007155; F:GO:0005515	-		SignalP (SIGNALP)
	-	0				-
	-	0				IPR019128
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein C26D10.6 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0016787; F:GO:0003824; F:GO:0008270		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	2	P:GO:0008152; F:GO:0016758	-	EC:2.4.1.0	SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein C06E7.2 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	briggsae cbr-fzo-1 protein	5	P:GO:0008053; F:GO:0005525; C:GO:0016021; C:GO:0005741; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001019; IPR001401; G3DSA:3.40.50.300 (GENE3D), PTHR10465 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	atp-dependent r- helicase ddx41	4	F:GO:0003676; F:GO:0005524; F:GO:0008270; F:GO:0008026	-		-
	-	0				-
Caenorhabditis elegans	briggsae cbr-casy-1 protein	9	P:GO:0009792; C:GO:0005615; P:GO:0007156; F:GO:0005515; C:GO:0032809; P:GO:0008355; C:GO:0043231; F:GO:0005509; C:GO:0016021	-		PTHR14139 (PANTHER)
	-	0				-
Caenorhabditis elegans	thump domain containing 3	0		F:GO:0003723; F:GO:0008168; F:GO:0003674; F:GO:0016740; P:GO:0008152; P:GO:0008150; F:GO:0005515; C:GO:0005575		IPR004114
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0007264; F:GO:0005085		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-

Ancylostoma ceylanicum	secreted protein asp-2	2	P:GO:0040011; P:GO:0006898	-		IPR001283; IPR002413; IPR014044; IPR018244; PTHR10334:SF11 (PANTHER), SignalP (SIGNALP)
	-	0				-
Ailuropoda melanoleuca	calponin 2	13	P:GO:0042060; P:GO:0031032; F:GO:0005516; P:GO:0030336; P:GO:0050765; P:GO:0030097; P:GO:0032970; C:GO:0001725; C:GO:0005911; F:GO:0003779; P:GO:0010628; P:GO:0042127; P:GO:0071260	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Pongo abelii	keratin 5	9	F:GO:0005200; P:GO:0050680; P:GO:0030855; P:GO:0031581; P:GO:0008544; F:GO:0005515; C:GO:0005829; C:GO:0005739; C:GO:0045095	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	nck adaptor protein 1	10	C:GO:0012506; P:GO:0030032; F:GO:0005102; P:GO:0042102; C:GO:0005829; P:GO:0008285; F:GO:0019904; P:GO:0007176; P:GO:0030838; P:GO:0016477	-		IPR001452; G3DSA:2.30.30.40 (GENE3D), PTHR22820 (PANTHER), PTHR22820:SF7 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	gtp-binding protein alpha g-o	4	P:GO:0007186; F:GO:0004871; P:GO:0007165; F:GO:0005525	-		IPR001019; G3DSA:3.40.50.300 (GENE3D), PTHR10218:SF63 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	had-superfamily subfamily variant 1 containing protein	4	P:GO:0009792; F:GO:0016787; P:GO:0040007; P:GO:0002119	-		G3DSA:3.40.50.1000 (GENE3D), PTHR12725 (PANTHER), PTHR12725:SF5 (PANTHER), SSF56784 (SUPERFAMILY)
Loa loa	uncoordi-ted protein isoform partially confirmed by transcript evidence	3	P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22971 (PANTHER)
	-	0				-

	-	0				-
	-	0				-
Saccoglossus kowalevskii	uncharacterized protein mitochondrial	2	F:GO:0003824; P:GO:0008152	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	spermatogenesis associated 20	1	F:GO:0005515	-		IPR004879; IPR008928; IPR012335; IPR012336; IPR012341; PTHR12145 (PANTHER)
Caenorhabditis briggsae	related to yeast vacuolar protein sorting factor family member (vps-41)	8	P:GO:0009792; P:GO:0002119; C:GO:0005773; F:GO:0005488; P:GO:0006624; P:GO:0040007; P:GO:0007034; P:GO:0043066	-		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	2	P:GO:0040010; F:GO:0005515	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	7	F:GO:0004386; P:GO:0007126; F:GO:0003916; F:GO:0005524; C:GO:0005634; P:GO:0006310; P:GO:0006281	-		IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR10799 (PANTHER), PTHR10799:SF66 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
Dictyocaulus viviparus	aba-1 allergen	1	F:GO:0019841	-		-
	-	0				-
Caenorhabditis briggsae	p70 ribosomal protein s6 ki-se	47	[illegible] P:GO:0014878; C:GO:0019717; P:GO:0032868; P:GO:0045948; P:GO:0033762; P:GO:0003009; P:GO:0007584; P:GO:0000082; P:GO:0043491; P:GO:0048015; C:GO:0005625; P:GO:0009749; P:GO:0009612; P:GO:0051384; C:GO:0005829; P:GO:0043201; P:GO:0014911; P:GO:0045471; P:GO:0032870; C:GO:0030054; P:GO:0033574; P:GO:0007568; P:GO:0009408; C:GO:0048471; P:GO:0043066; F:GO:0042277; F:GO:0005515;	-		IPR000719; IPR011009; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR22985 (PANTHER), PTHR22985:SF83 (PANTHER)
	-	0				-

Brugia malayi	suppressor of cytokine sig-ling 9	8	P:GO:0007482; P:GO:0045873; P:GO:0048072; P:GO:0008586; P:GO:0048802; P:GO:0042059; P:GO:0046426; P:GO:0030718	-		IPR000980; IPR001496; PTHR10385 (PANTHER), PTHR10385:SF9 (PANTHER), SSF55550 (SUPERFAMILY)
Brugia malayi	suppressor of cytokine sig-ling 9	9	P:GO:0007482; P:GO:0045873; P:GO:0048072; P:GO:0008586; P:GO:0048802; P:GO:0042059; F:GO:0005515; P:GO:0046426; P:GO:0030718	-		IPR000980; IPR001496; PTHR10385 (PANTHER), PTHR10385:SF9 (PANTHER), SSF55550 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
	-	0				-
Loa loa	dedicator of cytokinesis family protein	0		F:GO:0005525; F:GO:0051020; F:GO:0005085		PTHR23317 (PANTHER), PTHR23317:SF26 (PANTHER)
Loa loa	sentrin-specific protease 8	1	F:GO:0008233	-		SignalP (SIGNALP)
	-	0				-
Loa loa	uncoordi-ted family member (unc-13)	1	F:GO:0046872	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Loa loa	adam metallopeptidase with thrombospondin type 1 9	7	F:GO:0004222; P:GO:0007275; P:GO:0006516; P:GO:0006508; F:GO:0008270; C:GO:0005578; P:GO:0048070	-	EC:3.4.24.0	IPR010294; PTHR13723 (PANTHER), PTHR13723:SF36 (PANTHER)
Caenorhabditis elegans	lethal family member (let-805)	8	P:GO:0018996; P:GO:0009792; P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		PTHR19143 (PANTHER), PTHR19143:SF2 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-ndg-4 protein	3	P:GO:0009792; P:GO:0010171; P:GO:0040010	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	2	P:GO:0055085; C:GO:0016021	-		IPR011701; IPR016196; G3DSA:1.20.1250.20 (GENE3D), PTHR11662 (PANTHER), PTHR11662:SF17 (PANTHER), SignalP (SIGNALP)

Caenorhabditis elegans	statb_caeel ame: full=sig-l transducer and activator of transcription b ame: full=zinc finger protein stat-b	7	F:GO:0003700; F:GO:0004871; F:GO:0005515; F:GO:0005509; P:GO:0007165; C:GO:0005634; P:GO:0006355	-		-
Angiostrongylus cantonensis	elongation factor 1 beta	7	P:GO:0009792; P:GO:0002119; F:GO:0003746; C:GO:0005853; P:GO:0040010; P:GO:0006898; P:GO:0006414	-		IPR001326; IPR014038; IPR014717; IPR018940; PTHR11595 (PANTHER), PTHR11595:SF4 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	leucine-rich repeat ki-se	7	P:GO:0006468; F:GO:0005525; C:GO:0005622; F:GO:0005515; F:GO:0005524; F:GO:0004674; P:GO:0007264	-	EC:2.7.11.0	IPR001611; G3DSA:3.80.10.10 (GENE3D)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-folt-1 protein	8	F:GO:0004872; F:GO:0015234; C:GO:0005886; F:GO:0005542; P:GO:0055085; P:GO:0015888; F:GO:0008518; C:GO:0016021	-		-
Pongo abelii	interferon regulatory factor 2 binding protein 2	2	P:GO:0045449; C:GO:0005634	-		IPR022750
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein T20F7.6 [Caenorhabditis elegans]	0		P:GO:0008152; F:GO:0003824		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0005488; P:GO:0032012; F:GO:0005086; C:GO:0005622		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-

Homo sapiens	fibronectin 1	13	P:GO:0018149; P:GO:0016477; P:GO:0001525; P:GO:0008360; C:GO:0005793; C:GO:0031093; P:GO:0034446; F:GO:0005518; C:GO:0005577; F:GO:0008201; C:GO:0005578; F:GO:0005201; P:GO:0006953	-		IPR003961; IPR008957; IPR013783; PTHR19143 (PANTHER), PTHR19143:SF6 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	r- 3 -termi-l phosphate cyclase-like protein	2	F:GO:0003824; C:GO:0005634	-		IPR000228; IPR013792; IPR013796; IPR020719; PD397608 (PRODOM)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	4	F:GO:0016810; F:GO:0005524; F:GO:0003952; P:GO:0009435	-	EC:6.3.5.1	SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	tnni3 interacting ki-se	7	C:GO:0005737; P:GO:0006468; F:GO:0005524; F:GO:0008022; C:GO:0005634; F:GO:0004674; F:GO:0031013	-	EC:2.7.11.0	-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Squalus acanthias	beta tubulin	14	P:GO:0001764; C:GO:0005829; F:GO:0042277; C:GO:0005874; F:GO:0042288; P:GO:0042267; P:GO:0051258; P:GO:0007018; P:GO:0007067; F:GO:0003924; F:GO:0051082; F:GO:0005198; P:GO:0030182; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000217; IPR002453; IPR008280; IPR018316
Haemonchus contortus	microsomal aminopeptidase	10	C:GO:0005625; C:GO:0031983; P:GO:0006725; F:GO:0004177; C:GO:0012506; F:GO:0042277; C:GO:0016021; P:GO:0006508; F:GO:0008270; F:GO:0008237	-	EC:3.4.11.0	-

Caenorhabditis elegans	hypothetical protein Y54E10A.11 [Caenorhabditis elegans]	0		F:GO:0046872; F:GO:0005488; F:GO:0008270; F:GO:0005515		PTHR12389 (PANTHER)
Caenorhabditis briggsae	likely calmodulin	1	F:GO:0005488	-		IPR002048; IPR011992; IPR018247; IPR018249; PTHR23050 (PANTHER), PTHR23050:SF1 (PANTHER), SSF47473 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-gnrr-8 protein	2	P:GO:0007186; C:GO:0016021	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Homo sapiens	enoyl coenzyme a hydratase peroxisomal	7	C:GO:0005777; F:GO:0005515; P:GO:0006635; F:GO:0016853; C:GO:0005739; F:GO:0004300; P:GO:0006091	-	EC:4.2.1.17	IPR014748; SSF52096 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-ugt-63 protein	0		P:GO:0030259; F:GO:0030246; P:GO:0005975; C:GO:0016021; P:GO:0008152; F:GO:0016758		-
	-	0				-
Caenorhabditis briggsae	db module family protein	0				PTHR21679 (PANTHER)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				IPR008976
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-sbp-1 protein	1	F:GO:0005515	-		PTHR12565 (PANTHER), PTHR12565:SF3 (PANTHER)
Pongo abelii	stress-induced-phosphoprotein 1	9	P:GO:0046425; F:GO:0051087; P:GO:0045449; F:GO:0008022; C:GO:0008023; F:GO:0019901; P:GO:0006950; C:GO:0005794; F:GO:0030544	-		IPR001440; IPR011990; IPR013026; PTHR22904 (PANTHER), PTHR22904:SF14 (PANTHER)
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	kruppel-like factor 4	26	P:GO:0007500; C:GO:0000785; P:GO:0014067; F:GO:0008270; P:GO:0048662; P:GO:0031077; P:GO:0032526; P:GO:0048730; P:GO:0070373; F:GO:0035014; P:GO:0009913; P:GO:0045892; C:GO:0005730; F:GO:0016563; C:GO:0005667; P:GO:0019827; F:GO:0003702; F:GO:0043565; P:GO:0042325; P:GO:0050790; P:GO:0014740; F:GO:0003700; P:GO:0045944; F:GO:0003690; P:GO:0051898; F:GO:0016564	-		-
	-	0				-
Pongo abelii	type alpha 1	22	P:GO:0009314; P:GO:0018149; P:GO:0030168; P:GO:0048565; P:GO:0043206; C:GO:0005586; P:GO:0007229; P:GO:0050777; P:GO:0007507; P:GO:0007160; C:GO:0005615; F:GO:0046332; P:GO:0001501; F:GO:0048407; P:GO:0043588; P:GO:0030199; F:GO:0005178; P:GO:0007179; P:GO:0034097; P:GO:0032964; F:GO:0005201; P:GO:0001568	-		IPR000885; PTHR22687 (PANTHER), PS51461 (PROFILE)
Caenorhabditis elegans	lethal family member (let-805)	8	P:GO:0018996; P:GO:0009792; P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		-
	-	0				-

Caenorhabditis elegans	c-type lectin family member (clec-225)	2	C:GO:0016021; F:GO:0005488	-		-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	3	F:GO:0003951; P:GO:0008152; C:GO:0005739	-	EC:2.7.1.23	PS51257 (PROFILE)
	-	0				-
	-	0				-
Bos taurus	heat shock protein hsp 90-beta	13	C:GO:0005739; P:GO:0006457; F:GO:0030235; P:GO:0060334; P:GO:0001890; C:GO:0042470; F:GO:0005524; P:GO:0032435; F:GO:0030911; P:GO:0060338; F:GO:0051082; P:GO:0006986; P:GO:0045429	-		IPR001404; IPR020568; IPR020576
	-	0				-
	-	0				-
Caenorhabditis elegans	protein-tyrosine phosphatase containing protein	3	F:GO:0004721; P:GO:0009792; P:GO:0000003	-	EC:3.1.3.16	IPR000242; IPR000387; IPR016130; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
	-	0				-
Callithrix jacchus	myc-associated zinc finger protein	8	F:GO:0003723; P:GO:0006369; F:GO:0008270; P:GO:0006367; P:GO:0045449; F:GO:0003677; F:GO:0005515; C:GO:0005634	-		IPR007087; IPR013087; IPR015880; PTHR23228 (PANTHER), PTHR23228:SF28 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	C:GO:0016021	-		-
	-	0				-

Drosophila willistoni	importin 8	24	C:GO:0000790; P:GO:0042052; P:GO:0016321; P:GO:0006325; C:GO:0005700; P:GO:0007474; C:GO:0016456; F:GO:0008565; P:GO:0043524; F:GO:0035175; C:GO:0048471; P:GO:0045465; P:GO:0031936; F:GO:0005515; P:GO:0006468; P:GO:0007173; P:GO:0000189; P:GO:0008283; P:GO:0035311; P:GO:0016318; P:GO:0008586; P:GO:0042675; C:GO:0005938; P:GO:0048477	-			IPR001494; IPR011989; IPR016024; PTHR10997 (PANTHER), PTHR10997:SF18 (PANTHER)
	-	0					-
Caenorhabditis briggsae	briggsae cbr-dpf-6 protein	1	F:GO:0016787	-			SignalP (SIGNALP)
	-	0					SignalP (SIGNALP)
	-	0					-
	-	0					-
	-	0					SignalP (SIGNALP)
	-	0					SignalP (SIGNALP)
	-	0					-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	P:GO:0006541; F:GO:0004359	-		EC:3.5.1.2	IPR010916; IPR012338; IPR015868; G3DSA:1.10.1500.10 (GENE3D), PTHR12544:SF3 (PANTHER)
	-	0					-
	-	0					IPR018294; SignalP (SIGNALP), SSF52058 (SUPERFAMILY)
	-	0					-
	-	0					IPR008491; SignalP (SIGNALP)
Pan troglodytes	brain protein i3	9	P:GO:0012502; C:GO:0005765; C:GO:0016021; F:GO:0001540; C:GO:0005624; F:GO:0005524; C:GO:0048471; P:GO:0010977; C:GO:0005794	-			-
	-	0					-
	-	0					-
	-	0					-

Haemonchus contortus	aspartic protease	0		P:GO:0006508; C:GO:0016021; F:GO:0004190; F:GO:0016787; P:GO:0040011; F:GO:0008233; P:GO:0008219; F:GO:0005515		IPR001461; IPR009007; PTHR13683:SF53 (PANTHER)
	-	0				-
Loa loa	amp-activated protein gamma regulatory subunit	2	F:GO:0003824; P:GO:0008152	-		PTHR13780 (PANTHER)
	-	0				-
Caenorhabditis elegans	h+-atpase v-type subunit	6	F:GO:0046933; C:GO:0016021; P:GO:0015986; C:GO:0033179; C:GO:0045263; C:GO:0005774	-	EC:3.6.3.14	IPR000245; IPR002379; IPR011555; PTHR10263 (PANTHER)
Brugia malayi	cadherin domain containing protein	2	C:GO:0016020; P:GO:0007155	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0007600; P:GO:0007165; F:GO:0042802; F:GO:0005515		IPR014756; PTHR11188 (PANTHER), PTHR11188:SF13 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein R148.5 [Caenorhabditis elegans]	1	F:GO:0005515	-		-
	-	0				-
Caenorhabditis briggsae	membrane calcium atpase family member (mca-1)	5	F:GO:0005388; C:GO:0016021; P:GO:0006754; F:GO:0005524; P:GO:0006816	-	EC:3.6.3.8	SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	ras-related protein rab-	1	F:GO:0000166	-		-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0005488; C:GO:0016021		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	riken cd- 2700097o09	1	P:GO:0009792	-		-
	-	0				-
	-	0				-

Caenorhabditis elegans	atp-binding sub-family b (mdr tap) member isoform cra_a	6	P:GO:0055085; C:GO:0005739; C:GO:0016021; F:GO:0042626; F:GO:0005524; P:GO:0008152	-		IPR003439; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF62 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	chiti-se	8	F:GO:0004383; P:GO:0006032; P:GO:0016998; F:GO:0004672; F:GO:0005524; F:GO:0004568; P:GO:0006468; P:GO:0006182	-	EC:4.6.1.2; EC:3.2.1.14	IPR000726; G3DSA:1.10.530.10 (GENE3D), G3DSA:3.30.20.10 (GENE3D), PTHR22595:SF6 (PANTHER), SignalP (SIGNALP), SSF53955 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein C06E7.2 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	yip1 domain member 6	1	C:GO:0016020	-		IPR006977; PTHR21236 (PANTHER), PTHR21236:SF1 (PANTHER)
Loa loa	briggsae cbr-cpg-3 protein	0				SignalP (SIGNALP)
Loa loa	briggsae cbr-cpg-3 protein	0				SignalP (SIGNALP)
Loa loa	briggsae cbr-cpg-3 protein	0				-
Loa loa	briggsae cbr-cpg-3 protein	0				-
Loa loa	briggsae cbr-cpg-3 protein	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Loa loa	briggsae cbr-cpg-3 protein	0				SignalP (SIGNALP)
Loa loa	briggsae cbr-cpg-3 protein	0				SignalP (SIGNALP)
Caenorhabditis elegans	pyroglutamyl-peptidase 1	0		P:GO:0006508; F:GO:0016787; C:GO:0005575		IPR000816; IPR016125; PTHR23402:SF1 (PANTHER)
	-	0				-
	-	0				-
Pongo abelii	proteasome (macropain) beta 7	8	P:GO:0051436; P:GO:0051437; F:GO:0004298; P:GO:0031145; P:GO:0044419; C:GO:0005737; C:GO:0005839; C:GO:0005634	-	EC:3.4.25.0	-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-mab-10 protein	3	P:GO:0040035; F:GO:0005515; P:GO:0002009	-		-
	-	0				IPR000832; PTHR12011 (PANTHER), PTHR12011:SF56 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-

Caenorhabditis briggsae	heat shock 70kda protein 4	4	F:GO:0005515; P:GO:0006950; P:GO:0051085; F:GO:0000166	-		IPR001023; IPR013126; IPR018181; G3DSA:1.20.1270.10 (GENE3D), G3DSA:2.60.34.10 (GENE3D), G3DSA:3.30.30.30 (GENE3D), G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), PTHR19375:SF15 (PANTHER), SSF100920 (SUPERFAMILY), SSF100934 (SUPERFAMILY), SSF53067 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	immunoglobulin i-set domain containing protein	2	F:GO:0005509; F:GO:0003824	-		IPR002035; G3DSA:3.40.50.410 (GENE3D), PTHR22992 (PANTHER), SSF53300 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	6	C:GO:0016021; P:GO:0009792; P:GO:0000003; P:GO:0040010; P:GO:0055085; P:GO:0002119	-		IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR10074 (PANTHER), PTHR10074:SF22 (PANTHER), SignalP (SIGNALP)
	-	0				-
Homo sapiens	cd44 variant	30	F:GO:0005057; P:GO:0007160; P:GO:0070374; P:GO:0033138; P:GO:0001558; P:GO:0033189; F:GO:0051219; P:GO:0016337; C:GO:0016323; F:GO:0005540; P:GO:0043518; P:GO:0031175; P:GO:0001955; P:GO:0014070; P:GO:0001658; P:GO:0033031; P:GO:0060442; C:GO:0043234; C:GO:0009897; P:GO:0050731; F:GO:0004872; F:GO:0005518; C:GO:0005887; C:GO:0005634; P:GO:0002246; P:GO:0016477; P:GO:0043066;	-		IPR001231; PTHR10225 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Frankia sp. CcI3	nudix hydrolase	0		F:GO:0016787		IPR000086; IPR015797; PTHR13994 (PANTHER), PTHR13994:SF4 (PANTHER)

Caenorhabditis elegans	cathepsin a	3	F:GO:0004185; P:GO:0019915; P:GO:0006508	-	EC:3.4.16.0	IPR001563; IPR018202; G3DSA:3.40.50.1820 (GENE3D), PTHR11802:SF9 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	cathepsin a	3	F:GO:0004185; P:GO:0019915; P:GO:0006508	-	EC:3.4.16.0	IPR001563; IPR018202; G3DSA:3.40.50.1820 (GENE3D), PTHR11802:SF9 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
Loa loa	der1-like domain member 3	6	P:GO:0030433; C:GO:0030176; P:GO:0030968; P:GO:0030970; P:GO:0030307; P:GO:0008284	-		IPR007599; SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	hypothetical protein H05L14.1 [Caenorhabditis elegans]	0		F:GO:0004672; F:GO:0005524; F:GO:0000166; P:GO:0006468; F:GO:0004674		IPR000719; IPR017441; G3DSA:3.30.200.20 (GENE3D)
	-	0				-
Ailuropoda melanoleuca	high-mobility group box 1	67	F:GO:0003700; C:GO:0009986; P:GO:0000902; P:GO:0002053; P:GO:0032868; F:GO:0000401; P:GO:0010552; C:GO:0043005; F:GO:0008201; F:GO:0003690; F:GO:0003697; C:GO:0005625; P:GO:0009749; P:GO:0033151; P:GO:0031532; P:GO:0051384; P:GO:0008156; F:GO:0008301; P:GO:0014911; P:GO:0034341; F:GO:0070491; F:GO:0051861; F:GO:0008134; C:GO:0005615; P:GO:0001934; P:GO:0017055; P:GO:0002437; P:GO:0001654;	-		IPR000135; IPR000910; IPR009071; PTHR13711 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	patched family protein	7	P:GO:0040025; F:GO:0008158; P:GO:0040018; P:GO:0018996; P:GO:0040002; C:GO:0016021; P:GO:0019915	-		-

Caenorhabditis elegans	ipase c family member (plc-1)	9	F:GO:0005085; P:GO:0006629; F:GO:0004871; C:GO:0005622; F:GO:0004435; P:GO:0040010; F:GO:0005509; P:GO:0009566; P:GO:0007264	-	EC:3.1.4.11	IPR011992; IPR015359; PTHR10336 (PANTHER), PTHR10336:SF6 (PANTHER), SSF47473 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	mitochondrial ornithine transporter 1	2	P:GO:0055085; C:GO:0016020	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF53 (PANTHER)
Loa loa	fission 1 (mitochondrial outer membrane) homolog (cerevisiae)	6	C:GO:0005779; P:GO:0006915; F:GO:0005515; P:GO:0016559; P:GO:0000266; C:GO:0031307	-		IPR011990; PTHR13247 (PANTHER), SSF48452 (SUPERFAMILY)
Dictyocaulus viviparus	calcium-independent phospholipase a2 isoform a	2	P:GO:0016042; F:GO:0016787	-		-
Caenorhabditis elegans	protein ki-se domain containing protein	7	P:GO:0006468; P:GO:0040022; F:GO:0005515; F:GO:0005524; P:GO:0019915; P:GO:0051729; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
	-	0				IPR003582; SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-trpa-1 protein	0		C:GO:0016021; C:GO:0016020; P:GO:0055085; P:GO:0006811; F:GO:0005216; P:GO:0006810		-
Brugia malayi	wd repeat domain 36	0		C:GO:0032040; P:GO:0006364		-
Caenorhabditis briggsae	ipase c family member (plc-1)	15	P:GO:0007265; F:GO:0004435; P:GO:0006629; P:GO:0040010; P:GO:0045859; F:GO:0005509; F:GO:0004871; P:GO:0007186; F:GO:0017016; F:GO:0005085; P:GO:0009566; C:GO:0044444; P:GO:0009966; P:GO:0035466; P:GO:0043085	-	EC:3.1.4.11	-

Caenorhabditis briggsae	glutamine-oxaloacetic transami-se	6	F:GO:0030170; P:GO:0006536; P:GO:0006531; P:GO:0006103; P:GO:0009058; F:GO:0004069	-	EC:2.6.1.1	IPR000796; IPR004838; IPR004839; IPR015421; IPR015424
Caenorhabditis briggsae	glutamine-oxaloacetic transami-se	6	F:GO:0030170; P:GO:0006536; P:GO:0006531; P:GO:0006103; P:GO:0009058; F:GO:0004069	-	EC:2.6.1.1	IPR000796; IPR004838; IPR004839; IPR015421; IPR015424
Caenorhabditis briggsae	glutamine-oxaloacetic transami-se	6	F:GO:0030170; P:GO:0006536; P:GO:0006531; P:GO:0006103; P:GO:0009058; F:GO:0004069	-	EC:2.6.1.1	IPR000796; IPR004838; IPR004839; IPR015421; IPR015424
Caenorhabditis briggsae	glutamine-oxaloacetic transami-se	6	F:GO:0030170; P:GO:0006536; P:GO:0006531; P:GO:0006103; P:GO:0009058; F:GO:0004069	-	EC:2.6.1.1	IPR000796; IPR004838; IPR004839; IPR015421; IPR015424
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	P:GO:0019915	-		IPR010291; IPR016196; G3DSA:1.20.1250.20 (GENE3D), PTHR23294 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	wd repeat and fyve domain-containing protein 3	1	F:GO:0005488	-		-
	-	0				-
Caenorhabditis elegans	gns1 sur4 family protein	2	C:GO:0016021; P:GO:0007283	-		IPR002076
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Pongo abelii	calcium and integrin binding 1	10	C:GO:0016324; P:GO:0006915; C:GO:0005654; P:GO:0007229; F:GO:0005515; P:GO:0007155; P:GO:0006302; F:GO:0005509; C:GO:0030175; C:GO:0005783	-		IPR011992; IPR018247; IPR018249; PTHR23056 (PANTHER), PTHR23056:SF7 (PANTHER), SSF47473 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	sucrase- intesti-l	0		F:GO:0004553; F:GO:0030246; P:GO:0005975; F:GO:0003824		IPR000519

	-	0				-
	-	0				-
Loa loa	briggsae cbr-ctg-2 protein	0				-
Angiostrongylus cantonensis	ap1 gamma subunit binding protein 1	0		P:GO:0015031; C:GO:0016020; P:GO:0006897; P:GO:0006810; C:GO:0005737; C:GO:0030130; F:GO:0003674; C:GO:0005794; P:GO:0006886; C:GO:0030121; P:GO:0008150; F:GO:0005509		-
Caenorhabditis briggsae	briggsae cbr-vha-5 protein	0		F:GO:0015078; P:GO:0015986; C:GO:0033177		IPR002490; PTHR11629:SF23 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				PTHR11127 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-ocrl-1 protein	5	P:GO:0000003; P:GO:0007165; P:GO:0040013; C:GO:0005622; F:GO:0004437	-		G3DSA:3.60.10.10 (GENE3D), PTHR11200 (PANTHER), PTHR11200:SF26 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	vacuolar protein sorting 35	3	C:GO:0016021; P:GO:0006624; F:GO:0005515	-		IPR005378
Caenorhabditis elegans	carbonic anhydrase	4	P:GO:0044237; F:GO:0008270; F:GO:0004089; P:GO:0015976	-	EC:4.2.1.1	IPR001765
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	C:GO:0016021	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
	-	0				-
	-	0				-
Pongo abelii	hcls1 associated protein x-1	8	C:GO:0005625; F:GO:0019966; C:GO:0031965; C:GO:0016529; C:GO:0016023; F:GO:0047485; C:GO:0015629; C:GO:0005739	-		-
	-	0				-

Brugia malayi	riken cd- 2700097o09	0		F:GO:0003674; F:GO:0000062; F:GO:0008176; P:GO:0008150; P:GO:0009792; F:GO:0008757			G3DSA:3.40.50.150 (GENE3D)
Caenorhabditis elegans	myotubularin-related protein 9	1	F:GO:0005515	-			IPR010569; IPR017906; PTHR10807 (PANTHER), PTHR10807:SF9 (PANTHER), SignalP (SIGNALP), SSF52799 (SUPERFAMILY)
	-	0					SignalP (SIGNALP)
	-	0					-
	-	0					-
Brugia malayi	excision repair cross-complementing rodent repair complementation group 2	42	P:GO:0043249; P:GO:0001701; F:GO:0047485; F:GO:0008022; F:GO:0004003; P:GO:0030282; P:GO:0043588; P:GO:0021510; N:GO:0071817; F:GO:0008353; P:GO:0006283; P:GO:0048820; P:GO:0007059; P:GO:0009791; P:GO:0035264; P:GO:0006368; C:GO:0005675; P:GO:0001666; P:GO:0009650; P:GO:0000718; P:GO:0040016; P:GO:0006979; P:GO:0045944; P:GO:0007568; C:GO:0005737; C:GO:0019907; P:GO:0043066;	-	EC:2.7.11.23	IPR006554; IPR010614; IPR014013; G3DSA:3.40.50.300 (GENE3D), PTHR11472 (PANTHER), PTHR11472:SF1 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0					-
Caenorhabditis elegans	eps (human endocytosis) related family member (eps-8)	1	F:GO:0005515	-			-
	-	0					-
	-	0					-
Caenorhabditis elegans	atpase aaa domain containing 1	11	P:GO:0010171; P:GO:0002119; F:GO:0016887; F:GO:0005515; F:GO:0005524; C:GO:0016021; P:GO:0040007; C:GO:0005739; P:GO:0006310; F:GO:0009378; P:GO:0006281	-			IPR003959; G3DSA:3.40.50.300 (GENE3D), PTHR23074 (PANTHER), PTHR23074:SF20 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0					-

Ancylostoma duodenale	secreted protein 5 precursor	0		P:GO:0040011; P:GO:0006898; C:GO:0005576		IPR001283; IPR014044; SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical kda protein in chromosome	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-nlp-10 protein	0				-
	-	0				SignalP (SIGNALP)
	-	0				G3DSA:2.40.50.40 (GENE3D)
	-	0				SignalP (SIGNALP)
Angiostrongylus cantonensis	ef hand family protein	5	C:GO:0005625; F:GO:0005515; F:GO:0005509; C:GO:0005626; C:GO:0016020	-		IPR011992; IPR018247; IPR018248; IPR018249; PTHR23050 (PANTHER), PTHR23050:SF9 (PANTHER), SSF47473 (SUPERFAMILY)
Caenorhabditis elegans	-dp-dependent malic mitochondrial precursor	10	P:GO:0009060; F:GO:0046872; P:GO:0006090; F:GO:0051287; C:GO:0005759; F:GO:0016619; P:GO:0006108; P:GO:0055114; F:GO:0004473; P:GO:0006800	-	EC:1.1.1.38; EC:1.1.1.40	IPR001891; IPR012301; IPR012302; IPR015884; IPR016040; G3DSA:3.40.50.10380 (GENE3D), PTHR23406 (PANTHER), PTHR23406:SF2 (PANTHER), SSF51735 (SUPERFAMILY), SSF53223 (SUPERFAMILY)
	-	0				IPR006612; IPR007087; IPR015880
	-	0				IPR006612; IPR007087; IPR015880
Caenorhabditis elegans	briggsae cbr-twk-40 protein	3	C:GO:0016020; F:GO:0005216; P:GO:0006811	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Strongylocentrotus purpuratus	copine viii	0		F:GO:0003674; P:GO:0008150; C:GO:0005575		-
Caenorhabditis briggsae	briggsae cbr-ga--1 protein	3	P:GO:0005975; F:GO:0004553; F:GO:0043169	-	EC:3.2.1.0	-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis briggsae	briggsae cbr-npp-21 protein	0				-
Loa loa	twik (kcnk-like) family of potassium alpha subunit 5	0		F:GO:0005216; C:GO:0016021; F:GO:0004674; C:GO:0016020; P:GO:0006813; F:GO:0004672; F:GO:0005267; P:GO:0006811; P:GO:0006810; P:GO:0006468; F:GO:0005524		IPR013099; G3DSA:1.10.287.70 (GENE3D), PTHR11003 (PANTHER), PTHR11003:SF7 (PANTHER), SSF81324 (SUPERFAMILY)
	-	0				-

Homo sapiens	glutathione s-transferase kappa 1	5	C:GO:0005777; F:GO:0004364; F:GO:0015035; F:GO:0042802; C:GO:0030288	-	EC:2.5.1.18	-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Callithrix jacchus	coactosin-like 1	5	P:GO:0050832; C:GO:0005856; C:GO:0005737; F:GO:0003779; F:GO:0019899	-		-
Caenorhabditis elegans	hypothetical protein F55D10.4 [Caenorhabditis elegans]	0				G3DSA:1.20.1070.10 (GENE3D), PTHR19266 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-ltd-1 protein	1	F:GO:0008270	-		-
Caenorhabditis briggsae	-dh dehydroge-se	14	P:GO:0006810; F:GO:0051537; F:GO:0008137; C:GO:0005747; F:GO:0046872; P:GO:0040007; F:GO:0009055; F:GO:0051287; P:GO:0007399; P:GO:0006120; P:GO:0002119; F:GO:0005515; P:GO:0048738; P:GO:0009792	-	EC:1.6.5.3	IPR002023; IPR012335; IPR012336
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-lgc-30 protein	4	C:GO:0016021; C:GO:0045211; P:GO:0006811; F:GO:0005230	-		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG13418 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	Hypothetical protein CBG07809 [Caenorhabditis briggsae]	0		F:GO:0005198		IPR000535; IPR008962; PTHR22947 (PANTHER)
	-	0				-
	-	0				-

Caenorhabditis briggsae	cathepsin l-like cysteine protei-se	1	F:GO:0008234	-		IPR000668; IPR013128; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF26 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis briggsae	ferm domain (-ezrin-radixin-moesin) family member (frm-8)	1	F:GO:0005515	-		PTHR13436 (PANTHER), PTHR13436:SF1 (PANTHER)
Caenorhabditis elegans	briggsae cbr-ark-1 protein	0		F:GO:0016740; F:GO:0004674; P:GO:0040027; F:GO:0004672; F:GO:0000166; P:GO:0006468; F:GO:0005524; F:GO:0016301; P:GO:0009792; F:GO:0004713; P:GO:0042059; F:GO:0005515		-
Caenorhabditis elegans	- h exchanger family member (nhx-9)	6	P:GO:0009792; F:GO:0015385; P:GO:0055085; P:GO:0006885; C:GO:0016021; P:GO:0006814	-		-
Caenorhabditis briggsae	protein ki-se domain containing protein	3	P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	G3DSA:3.30.200.20 (GENE3D)
Caenorhabditis briggsae	tyrosylprotein sulfotransferase 2	0		F:GO:0008146; F:GO:0016740; C:GO:0016021; C:GO:0016020; C:GO:0000139; C:GO:0005794; F:GO:0008476; P:GO:0008152; C:GO:0005783		PTHR12788 (PANTHER)
Caenorhabditis elegans	f-box domain containing protein	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	briggsae cbr-tre-4 protein	0		P:GO:0005991; C:GO:0016021; F:GO:0003824; F:GO:0004555		-
Caenorhabditis briggsae	light protein	8	P:GO:0009792; P:GO:0002119; C:GO:0005773; F:GO:0005488; P:GO:0006624; P:GO:0040007; P:GO:0007034; P:GO:0043066	-		PTHR12616 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-rhr-1 protein	4	C:GO:0016021; P:GO:0009792; P:GO:0055085; F:GO:0008519	-		-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0005515		IPR000980

	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-mbk-1 protein	11	P:GO:0018108; F:GO:0004674; C:GO:0005730; C:GO:0016607; F:GO:0043621; F:GO:0005524; P:GO:0007399; P:GO:0001706; P:GO:0030100; P:GO:0046777; F:GO:0004715	-	EC:2.7.11.0; EC:2.7.10.2	IPR011009; G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF116 (PANTHER)
	-	0				-
Caenorhabditis briggsae	intermediate filament protein	4	C:GO:0005882; C:GO:0005737; F:GO:0005198; F:GO:0005515	-		IPR001664; IPR016044; PTHR23239:SF13 (PANTHER)
	-	0				-
Caenorhabditis elegans	ibromatosis homolog family member (nfm-1)	7	C:GO:0005737; C:GO:0005856; P:GO:0009792; C:GO:0005912; P:GO:0045197; C:GO:0019898; F:GO:0003779	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Loa loa	uncoordi-ted family member (unc-13)	1	F:GO:0046872	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Ostertagia ostertagi	elegans protein partially confirmed by transcript evidence	1	F:GO:0008233	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Homo sapiens	transmembrane protein 176b	4	C:GO:0031965; P:GO:0030154; P:GO:0009887; C:GO:0016021	-		IPR007237; IPR009281; PTHR15756:SF1 (PANTHER), SignalP (SIGNALP)

Caenorhabditis briggsae	laminin a	11	P:GO:0016477; P:GO:0007229; C:GO:0005615; P:GO:0034446; P:GO:0048513; F:GO:0005178; P:GO:0050794; C:GO:0043259; P:GO:0002009; P:GO:0009790; N:GO:0071842	-		IPR002049; IPR013032; PR00011 (PRINTS), G3DSA:2.10.25.10 (GENE3D), PTHR10574 (PANTHER), PTHR10574:SF56 (PANTHER), SSF57196 (SUPERFAMILY)
	-	0				-
	-	0				-
Ancylostoma ceylanicum	glutamate cysteine ligase	8	C:GO:0017109; F:GO:0004357; F:GO:0005515; F:GO:0005524; P:GO:0006974; C:GO:0005634; P:GO:0006750; C:GO:0048471	-	EC:6.3.2.2	IPR004308; SSF55931 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Loa loa	tk fer protein ki-se	14	F:GO:0004718; F:GO:0042393; P:GO:0035409; F:GO:0005102; C:GO:0016020; F:GO:0000166; P:GO:0042531; P:GO:0046777; P:GO:0060397; P:GO:0019221; P:GO:0030218; F:GO:0035401; P:GO:0042977; C:GO:0005634	-		IPR000719; IPR001245; IPR011009; IPR020685; IPR020764; G3DSA:3.30.200.20 (GENE3D)
Caenorhabditis elegans	acetyl- hydrolase transferase family protein	1	F:GO:0003824	-		IPR003702; G3DSA:3.40.1080.10 (GENE3D), PTHR21432:SF11 (PANTHER)
	-	0				SignalP (SIGNALP)

Ailuropoda melanoleuca	fn1 protein	22	P:GO:0042060; P:GO:0018149; F:GO:0045340; P:GO:0016477; P:GO:0001525; P:GO:0008360; C:GO:0005793; C:GO:0005604; P:GO:0007044; P:GO:0007160; C:GO:0031093; P:GO:0006916; F:GO:0002020; P:GO:0034446; F:GO:0005518; C:GO:0005577; C:GO:0016324; F:GO:0008201; F:GO:0005201; F:GO:0016504; P:GO:0006953; P:GO:0030198	-		IPR003961; IPR008957; IPR013783
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-emb-30 protein	0		P:GO:0016311; F:GO:0016791; P:GO:0006470; F:GO:0016787; F:GO:0008138; F:GO:0004725		-
Caenorhabditis elegans	nuclear hormone receptor family member (nhr-66)	5	P:GO:0040010; P:GO:0000003; P:GO:0002119; F:GO:0005515; P:GO:0009792	-		IPR000536; IPR008946; PTHR11865 (PANTHER), PTHR11865:SF235 (PANTHER)
	-	0				-
Caenorhabditis elegans	sy-ptotagmin i	7	P:GO:0006810; C:GO:0030659; C:GO:0008021; C:GO:0044425; F:GO:0005515; F:GO:0005215; C:GO:0030141	-		-
Loa loa	briggsae cbr-ugt-58 protein	2	C:GO:0005743; F:GO:0016757	-		IPR002213; G3DSA:3.40.50.2000 (GENE3D), PTHR11926:SF3 (PANTHER), SSF53756 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	mpv17-like protein 2	0		C:GO:0005739; F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150		-
Caenorhabditis briggsae	cytochrome c oxidase assembly protein cox11 containing protein	3	F:GO:0016787; F:GO:0008270; F:GO:0005507	-		IPR007533
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-

Ostertagia ostertagi	24 kda excretory secretory protein	1	P:GO:0040011	-		IPR001283; IPR002413; IPR014044; IPR018244; PTHR10334:SF11 (PANTHER)
	-	0				SignalP (SIGNALP)
Ostertagia ostertagi	two-domain activation associated secreted protein asp4 precursor	0		C:GO:0005576		IPR001283; IPR014044
Ostertagia ostertagi	venom-allergen-like protein family member (vap-1)	0		P:GO:0040011; P:GO:0006898; C:GO:0005576		IPR001283; IPR002413; IPR014044; IPR018244; PTHR10334:SF11 (PANTHER)
Ciona intestinalis	uncharacterized transposase-like protein	0		F:GO:0046872; P:GO:0055114; F:GO:0009055; F:GO:0016491; F:GO:0020037; F:GO:0005506; F:GO:0004497		IPR007087; IPR015880
	-	0				-
Caenorhabditis elegans	uncoordi-ted family member (unc-13)	17	F:GO:0047485; C:GO:0030054; C:GO:0043234; P:GO:0023034; F:GO:0046872; F:GO:0017075; P:GO:0006887; C:GO:0042734; P:GO:0007269; P:GO:0050435; P:GO:0016188; C:GO:0019717; F:GO:0019992; F:GO:0019904; F:GO:0046982; F:GO:0042803; C:GO:0005737	-		-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	cytochrome p450 family member (cyp-34a9)	0		F:GO:0020037; F:GO:0005506; C:GO:0016021; F:GO:0009055; P:GO:0055114; F:GO:0016491; P:GO:0008340; F:GO:0046872; F:GO:0004497		-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-lam-3 protein	5	C:GO:0005606; P:GO:0030334; P:GO:0045995; P:GO:0030155; F:GO:0005102	-		IPR000034; PTHR10574 (PANTHER), PTHR10574:SF38 (PANTHER)
	-	0				-
Caenorhabditis elegans	valyl-tr- synthetase	4	C:GO:0005737; P:GO:0006438; F:GO:0005524; F:GO:0004832	-	EC:6.1.1.9	-
	-	0				-

Caenorhabditis elegans	proteasome subunit alpha type-5	14	P:GO:0040022; P:GO:0008340; P:GO:0051436; P:GO:0051437; P:GO:0040007; P:GO:0040027; F:GO:0004298; P:GO:0031145; F:GO:0005515; P:GO:0040011; C:GO:0019773; P:GO:0009792; C:GO:0005737; C:GO:0005634	-	EC:3.4.25.0	IPR000426; IPR001353; G3DSA:3.60.20.10 (GENE3D), PTHR11599 (PANTHER), PTHR11599:SF14 (PANTHER), PS51475 (PROFILE), SSF56235 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-lam-3 protein	0		C:GO:0005606; F:GO:0005102; C:GO:0005604; P:GO:0045995; C:GO:0005578; P:GO:0030155; C:GO:0031012; P:GO:0030334; P:GO:0007155		-
Pongo abelii	aurora ki-se a-interacting protein	7	P:GO:0045862; C:GO:0005739; P:GO:0045839; F:GO:0005515; P:GO:0016310; F:GO:0016301; C:GO:0005634	-		-
Caenorhabditis elegans	ched related family member (ptr-23)	7	P:GO:0018996; C:GO:0016021; P:GO:0008340; P:GO:0000003; P:GO:0040025; F:GO:0008158; P:GO:0040011	-		IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER)
Caenorhabditis elegans	hypothetical protein Y53G8AL.1 [Caenorhabditis elegans]	0				IPR000253; IPR001412
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG08399 [Caenorhabditis briggsae]	2	P:GO:0007186; C:GO:0016021	-		G3DSA:1.20.1070.10 (GENE3D), PTHR22751 (PANTHER), PTHR22751:SF8 (PANTHER)
Caenorhabditis elegans	briggsae cbr-hex-2 protein	1	F:GO:0003824	-		-
	-	0				-
Caenorhabditis briggsae	uncoordi-ted family member (unc-89)	0				IPR013098; IPR013783; IPR020675; PTHR22964:SF5 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
Brugia malayi	mynd finger family protein	1	F:GO:0008270	-		G3DSA:2.170.270.10 (GENE3D), PTHR12197 (PANTHER), PTHR12197:SF9 (PANTHER)
Haemochus contortus	briggsae cbr-gst- protein	4	P:GO:0008340; F:GO:0004364; P:GO:0040010; F:GO:0005515	-	EC:2.5.1.18	-
	-	0				-

Caenorhabditis elegans	anten-pedia protein	6	F:GO:0003700; F:GO:0030528; F:GO:0043565; P:GO:0007275; C:GO:0005634; P:GO:0006355	-		IPR001356; IPR001827; IPR009057; IPR012287; IPR017995; PTHR19418 (PANTHER), PTHR19418:SF166 (PANTHER)
Oesophagostomum dentatum	fmrf-like peptide family member (flp-1)	1	P:GO:0007218	-		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				IPR010347; G3DSA:3.30.870.20 (GENE3D)
Loa loa	nematode astacin protease protein 30	1	F:GO:0008233	-		IPR013032; PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	- ca exchangers family member (ncx-2)	6	F:GO:0005432; P:GO:0006816; P:GO:0055085; P:GO:0040010; P:GO:0000003; C:GO:0016021	-		PTHR11878 (PANTHER), PTHR11878:SF4 (PANTHER)
Caenorhabditis briggsae	ubiquitin associated and sh3 domain-containing protein b	0		F:GO:0004619; P:GO:0016070; F:GO:0003824; C:GO:0005622; F:GO:0016853		G3DSA:3.40.50.1240 (GENE3D), PTHR16469 (PANTHER), PTHR16469:SF8 (PANTHER), SSF53254 (SUPERFAMILY)
	-	0				-
Macaca mulatta	epididymal secretory protein e1 precursor	11	P:GO:0042632; P:GO:0046836; C:GO:0005764; P:GO:0033344; P:GO:0032367; F:GO:0019899; C:GO:0005576; P:GO:0015914; P:GO:0009615; F:GO:0015485; P:GO:0019747	-		SignalP (SIGNALP)
Caenorhabditis elegans	atp-binding cassette sub-family b member mitochondrial precursor	4	F:GO:0042626; P:GO:0055085; C:GO:0016021; F:GO:0000166	-		IPR001140; IPR011527; IPR017940; G3DSA:1.20.1560.10 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF77 (PANTHER)
	-	0				-
Caenorhabditis briggsae	acyl- synthetase	2	F:GO:0016877; P:GO:0008152	-		IPR000873; G3DSA:2.30.38.10 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF43 (PANTHER), SSF56801 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0005515		-
Caenorhabditis briggsae	serine threonine-protein phosphatase 5	6	C:GO:0005737; P:GO:0000278; F:GO:0046872; F:GO:0004722; P:GO:0006470; C:GO:0005634	-		IPR006186; IPR013235; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF12 (PANTHER), SSF56300 (SUPERFAMILY)

						IPR003598; IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-gly-2 protein	0				PTHR15075 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG18923 [Caenorhabditis briggsae]	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein T19E7.6 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	laminin alpha chain	4	F:GO:0005488; P:GO:0007155; P:GO:0050794; C:GO:0005604	-		IPR001791; IPR008985; IPR012680; IPR013320
Caenorhabditis briggsae	fam108a1 protein	0		P:GO:0006508; F:GO:0008236; F:GO:0016787; C:GO:0005576		IPR005645; G3DSA:3.40.50.1820 (GENE3D), PTHR12277 (PANTHER), PTHR12277:SF8 (PANTHER), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	enhancer of polycomb homolog 1	12	P:GO:0008340; P:GO:0000003; P:GO:0040027; P:GO:0040010; P:GO:0006898; P:GO:0040018; P:GO:0040011; P:GO:0010468; P:GO:0006350; P:GO:0009792; P:GO:0050794; C:GO:0005634	-		IPR019542; PTHR14898 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	protein fam73a-like	0		C:GO:0016021; C:GO:0016020		IPR019392; PTHR21508 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Loa loa	myo-2	4	C:GO:0032982; F:GO:0003779; F:GO:0005524; F:GO:0003774	-		SignalP (SIGNALP)

	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	5	F:GO:0005097; C:GO:0005622; F:GO:0004222; P:GO:0006508; P:GO:0032313	-	EC:3.4.24.0	-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	5	F:GO:0005097; C:GO:0005622; F:GO:0004222; P:GO:0006508; P:GO:0032313	-	EC:3.4.24.0	-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	5	F:GO:0005097; C:GO:0005622; F:GO:0004222; P:GO:0006508; P:GO:0032313	-	EC:3.4.24.0	-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	5	F:GO:0005097; C:GO:0005622; F:GO:0004222; P:GO:0006508; P:GO:0032313	-	EC:3.4.24.0	-
	-	0				SignalP (SIGNALP)
Homo sapiens	pre-mr--processing-splicing factor 8	8	C:GO:0005682; P:GO:0050896; C:GO:0005681; F:GO:0003723; F:GO:0005515; C:GO:0016607; P:GO:0007601; P:GO:0000398	-		IPR012984; PTHR11140 (PANTHER)
Caenorhabditis elegans	a disintegrin and metalloprotei-se with thrombospondin motifs 20-like	9	P:GO:0009967; F:GO:0008270; C:GO:0005615; F:GO:0004222; P:GO:0006508; P:GO:0045636; C:GO:0005578; P:GO:0043066; P:GO:0030198	-	EC:3.4.24.0	-
	-	0				IPR012317
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR019363; PTHR13390 (PANTHER)
	-	0				-
Nippostrongylus brasiliensis	briggsae cbr-cpi-2 protein	2	F:GO:0004869; P:GO:0000003	-		-
Nippostrongylus brasiliensis	briggsae cbr-cpi-2 protein	2	F:GO:0004869; P:GO:0000003	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-trpa-1 protein	0		C:GO:0016021; C:GO:0016020; P:GO:0055085; P:GO:0006811; F:GO:0005216; P:GO:0006810		-
	-	0				SignalP (SIGNALP)

Ailuropoda melanoleuca	type alpha 1	31	P:GO:0043589; P:GO:0060351; P:GO:0001957; P:GO:0071363; P:GO:0007605; P:GO:0034505; P:GO:0042542; P:GO:0001649; P:GO:0009612; P:GO:0001568; P:GO:0060325; F:GO:0005201; C:GO:0005615; P:GO:0048706; P:GO:0015031; F:GO:0048407; C:GO:0005737; P:GO:0043434; P:GO:0071300; P:GO:0007601; P:GO:0010812; C:GO:0005584; F:GO:0042802; P:GO:0060346; P:GO:0032964; P:GO:0030199; P:GO:0051591; P:GO:0031960;	-		-
	-	0				SignalP (SIGNALP)
Loa loa	laminin alpha chain	5	C:GO:0005606; P:GO:0030334; P:GO:0045995; P:GO:0030155; F:GO:0005102	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	transformation transcription domain-associated protein	3	C:GO:0070461; F:GO:0005515; P:GO:0016573	-		-
Caenorhabditis briggsae	transformation transcription domain-associated protein	3	C:GO:0070461; F:GO:0005515; P:GO:0016573	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	uncharacterized protein c12orf4-like protein	0				IPR019311
Homo sapiens	eukaryotic translation initiation factor subunit structural gene x-linked	7	F:GO:0003743; C:GO:0005829; P:GO:0045948; P:GO:0006184; F:GO:0005515; F:GO:0003924; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	G3DSA:3.40.50.300 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF9 (PANTHER)
	-	0				-

Caenorhabditis briggsae	cd81 antigen	10	P:GO:0030307; P:GO:0043128; F:GO:0005515; P:GO:0046813; P:GO:0008104; P:GO:0050731; P:GO:0006661; C:GO:0005887; P:GO:0000187; P:GO:0030890	-		IPR000301; IPR018499; IPR018503; SignalP (SIGNALP)
Caenorhabditis sp. PS1010	tub family protein	0				IPR000007; IPR001680; IPR015943; IPR019782; PTHR16517 (PANTHER), PTHR16517:SF2 (PANTHER), SSF117289 (SUPERFAMILY)
Caenorhabditis sp. PS1010	tub family protein	0				IPR000007; PTHR16517 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Bos taurus	mitochondrial h+-transporting atp synthase f0 complex subunit c3	5	F:GO:0046933; C:GO:0016021; P:GO:0015986; F:GO:0008289; C:GO:0045263	-	EC:3.6.3.14	IPR000454; IPR002379; IPR020537; PTHR10031 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein H24K24.4 [Caenorhabditis elegans]	3	F:GO:0008173; P:GO:0006396; F:GO:0000166	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	twik (kcnk-like) family of potassium alpha subunit 45	4	C:GO:0016021; P:GO:0006813; F:GO:0005267; P:GO:0055085	-		IPR013099; IPR018723; G3DSA:1.10.287.70 (GENE3D), PTHR11003 (PANTHER), PTHR11003:SF7 (PANTHER), SignalP (SIGNALP), SSF81324 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein F46F11.7 [Caenorhabditis elegans]	0				PTHR11201 (PANTHER), PTHR11201:SF1 (PANTHER)
Caenorhabditis elegans	serine threonine protein ki-se	4	F:GO:0017111; P:GO:0050789; C:GO:0005622; F:GO:0000166	-	EC:3.6.1.15	IPR002078; G3DSA:3.40.50.300 (GENE3D), PTHR22908 (PANTHER), PTHR22908:SF13 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	protein ki-se protein	8	P:GO:0006468; F:GO:0004715; C:GO:0005886; F:GO:0005515; F:GO:0005524; F:GO:0000287; P:GO:0000003; F:GO:0004674	-	EC:2.7.10.2; EC:2.7.11.0	IPR000719; IPR001245; IPR008266; IPR011009; IPR015779; IPR020685; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
Caenorhabditis elegans	calmodulin-binding transcription	7	P:GO:0045449; F:GO:0043565; F:GO:0042803; P:GO:0016059; P:GO:0009792; C:GO:0005634; F:GO:0003702	-		SignalP (SIGNALP)

Caenorhabditis elegans	calmodulin-binding transcription	7	P:GO:0045449; F:GO:0043565; F:GO:0042803; P:GO:0016059; P:GO:0009792; C:GO:0005634; F:GO:0003702	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	endou_caeel ame: full=poly -specific endoribonuclease homolog ame: full=protein endou ame: full=uridylate-specific endoribonuclease homolog flags: precursor	2	F:GO:0004521; F:GO:0003723	-		-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG07002 [Caenorhabditis briggsae]	4	P:GO:0040035; P:GO:0002119; P:GO:0040007; P:GO:0006898	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0006508; F:GO:0004181; F:GO:0008270	-	EC:3.4.17.0	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), PTHR11705:SF12 (PANTHER), SSF53187 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-pqn-48 protein	0				IPR004911; PTHR13234:SF3 (PANTHER)
Caenorhabditis elegans	hypothetical protein Y73B6BL.1 [Caenorhabditis elegans]	0		F:GO:0046872; F:GO:0016491; P:GO:0008152		-
Caenorhabditis briggsae	sugar transporter	11	P:GO:0055085; P:GO:0009845; C:GO:0016021; F:GO:0005353; F:GO:0005355; P:GO:0009911; P:GO:0015758; C:GO:0009705; P:GO:0015755; P:GO:0009624; C:GO:0005886	-		IPR005828; IPR016196; PTHR11600 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	glucose transporter	3	F:GO:0022891; P:GO:0055085; C:GO:0016021	-		IPR003663; IPR005828; IPR005829; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11600 (PANTHER), PTHR11600:SF103 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-dve-1 protein	5	F:GO:0003700; F:GO:0043565; F:GO:0005515; C:GO:0005634; P:GO:0006355	-		PTHR15116 (PANTHER), PTHR15116:SF3 (PANTHER)
	-	0				IPR015650; PTHR13140 (PANTHER)
	-	0				-

Caenorhabditis briggsae	Hypothetical protein CBG18604 [Caenorhabditis briggsae]	0		F:GO:0046872; P:GO:0055114; F:GO:0009055; F:GO:0016491; F:GO:0020037; F:GO:0005506; F:GO:0004497		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0019915; P:GO:0009792; P:GO:0040010	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Trichostrongylus colubriformis	globin	6	F:GO:0020037; C:GO:0005615; C:GO:0005737; F:GO:0005344; P:GO:0015671; F:GO:0019825	-		IPR000971; IPR009050; IPR012085; IPR012292; SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				IPR003124
	-	0				IPR017956
Caenorhabditis elegans	ancient conserved domain protein	0				PTHR12064 (PANTHER), PTHR12064:SF6 (PANTHER)
	-	0				-
	-	0				-
Loa loa	elegans protein confirmed by transcript evidence	4	C:GO:0005794; P:GO:0006810; C:GO:0016020; F:GO:0005216	-		IPR015672; IPR022535
Caenorhabditis briggsae	cationic amino acid transporter	5	P:GO:0019915; C:GO:0016021; P:GO:0006865; F:GO:0015171; P:GO:0055085	-		IPR002293; IPR004841; IPR015606; SignalP (SIGNALP)
Loa loa	hypothetical protein LOAG_10588 [Loa loa]	0				IPR019387; PTHR13527 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	C:GO:0005578	-		-
	-	0				-
	-	0				-
Dracunculus medinensis	briggsae cbr-hmr-1 protein	4	C:GO:0016020; P:GO:0007156; F:GO:0005509; F:GO:0005515	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-mup-4 protein	1	F:GO:0005515	-		PTHR22992 (PANTHER), PTHR22992:SF12 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis elegans	d- polymerase epsilon catalytic subunit a	11	F:GO:0008270; F:GO:0003887; P:GO:0006260; P:GO:0040035; F:GO:0003677; F:GO:0000166; P:GO:0040011; P:GO:0006997; P:GO:0002009; P:GO:0009792; C:GO:0005634	-	EC:2.7.7.7	PTHR10670 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Macaca mulatta	high density lipoprotein binding protein isoform 8	9	C:GO:0005737; F:GO:0008289; C:GO:0005886; F:GO:0003723; F:GO:0005515; P:GO:0006869; P:GO:0008203; C:GO:0005634; C:GO:0034364	-		IPR004088; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR10627 (PANTHER), PTHR10627:SF9 (PANTHER), SSF54791 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	alpha- ulin (catenin vinculin related) family member (ctn-1)	5	C:GO:0016021; P:GO:0007155; F:GO:0005198; F:GO:0045296; C:GO:0015629	-		IPR006077; G3DSA:1.20.120.230 (GENE3D), PTHR18914 (PANTHER), PTHR18914:SF8 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0005524; C:GO:0005856; C:GO:0016459; F:GO:0003774		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG18470 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	abnormal go-d development family member (gon-2)	2	C:GO:0016020; P:GO:0006810	-		PTHR13800 (PANTHER)

Homo sapiens	mhc class ii antigen	14	C:GO:0005789; C:GO:0005769; C:GO:0042613; C:GO:0005771; C:GO:0005794; P:GO:0019886; F:GO:0005515; C:GO:0009897; C:GO:0005765; C:GO:0016021; F:GO:0032395; C:GO:0010008; P:GO:0006955; F:GO:0042605	-		IPR003006; IPR013783; PTHR19944 (PANTHER), PTHR19944:SF26 (PANTHER)
	-	0				IPR001368; G3DSA:2.10.50.10 (GENE3D), SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	hr1 repeat family protein	5	P:GO:0006468; C:GO:0005622; F:GO:0005524; P:GO:0007165; F:GO:0004674	-	EC:2.7.11.0	-
Homo sapiens	complement component 3	16	F:GO:0048037; P:GO:0006957; F:GO:0005102; P:GO:0010951; P:GO:0050766; P:GO:0045766; C:GO:0005615; P:GO:0001798; P:GO:0007596; P:GO:0007165; P:GO:0010575; P:GO:0006935; P:GO:0007186; P:GO:0006958; F:GO:0004866; P:GO:0001970	-		-
Homo sapiens	tyrosine 3 tryptophan 5 -monooxyge-se activation zeta polypeptide-like	15	C:GO:0043234; C:GO:0005625; C:GO:0005739; F:GO:0032403; P:GO:0006626; P:GO:0002553; P:GO:0006916; F:GO:0004497; C:GO:0042470; F:GO:0019904; P:GO:0007165; F:GO:0008134; P:GO:0042493; C:GO:0014069; C:GO:0005634	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)

Caenorhabditis briggsae	r- polymerase domain 2 family protein	8	F:GO:0003899; C:GO:0032991; F:GO:0046872; C:GO:0043232; F:GO:0003677; F:GO:0005515; C:GO:0005654; P:GO:0006350	-	EC:2.7.7.6	IPR007080; IPR015699; PTHR19376 (PANTHER), SSF64484 (SUPERFAMILY)
Caenorhabditis briggsae	cathepsin a	2	P:GO:0019915; P:GO:0006508	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	uncoordi-ted family member (unc-52)	2	P:GO:0030239; C:GO:0005578	-		IPR003599; IPR007110; IPR013098; IPR013783; PTHR10574 (PANTHER), PTHR10574:SF20 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Homo sapiens	tyrosine ki-se binding protein	7	F:GO:0005057; C:GO:0005887; P:GO:0023034; F:GO:0016301; F:GO:0005515; P:GO:0007165; P:GO:0006968	-		-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-let-2 protein	4	C:GO:0005587; F:GO:0005488; F:GO:0030020; P:GO:0016043	-		IPR008160; PTHR10499 (PANTHER), PTHR10499:SF114 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	asparaginyl-tr- synthetase	3	F:GO:0016874; F:GO:0005488; P:GO:0006412	-	EC:3.6.5.3	IPR004364; IPR018150; G3DSA:3.30.930.10 (GENE3D), PTHR22594:SF6 (PANTHER), SSF55681 (SUPERFAMILY)
						-
Homo sapiens	adam metallopeptidase domain 15	12	P:GO:0001525; F:GO:0008270; C:GO:0005912; C:GO:0016021; P:GO:0007160; F:GO:0004222; P:GO:0006508; C:GO:0001669; C:GO:0012505; C:GO:0019861; P:GO:0030574; F:GO:0017124	-	EC:3.4.24.0	PTHR11905 (PANTHER), PTHR11905:SF16 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-

Heterotropus senex	carbamoylphosphate synthase	4	P:GO:0006541; F:GO:0004086; F:GO:0005524; P:GO:0009058	-		-
Ailuropoda melanoleuca	proteasome activator complex subunit 2-like	6	P:GO:0019884; P:GO:0051436; P:GO:0051437; C:GO:0008537; P:GO:0031145; N:GO:0061133	-		IPR003186; IPR009077; PTHR10660:SF6 (PANTHER)
	-	0				-
Pongo abelii	glycosyl hydrolase family catalytic domain containing protein	22	P:GO:0001501; C:GO:0001669; P:GO:0006689; P:GO:0007605; P:GO:0007626; C:GO:0016020; P:GO:0006874; P:GO:0007040; P:GO:0031323; F:GO:0004563; P:GO:0044267; C:GO:0005764; P:GO:0008049; P:GO:0019915; P:GO:0030203; P:GO:0050885; P:GO:0048477; F:GO:0042803; P:GO:0042552; P:GO:0009313; P:GO:0008654; P:GO:0007341	-	EC:3.2.1.52	IPR001540; IPR005829; IPR013781; IPR015882; IPR015883; IPR017853; G3DSA:3.30.379.10 (GENE3D), SSF55545 (SUPERFAMILY)
Necator americanus	surface-associated antigen 2	0				IPR003677
Caenorhabditis elegans	protein strawberry notch homolog 1	3	F:GO:0005524; F:GO:0004386; F:GO:0003677	-		PTHR12706 (PANTHER)
Caenorhabditis elegans	protein strawberry notch homolog 1	3	F:GO:0005524; F:GO:0004386; F:GO:0003677	-		PTHR12706 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	protein strawberry notch homolog 1	3	F:GO:0005524; F:GO:0004386; F:GO:0003677	-		PTHR12706 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	protein strawberry notch homolog 1	3	F:GO:0005524; F:GO:0004386; F:GO:0003677	-		PTHR12706 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				IPR015313
	-	0				-
	-	0				-
	-	0				IPR006162; SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein ZK84.1 [Caenorhabditis elegans]	0				SignalP (SIGNALP)

Caenorhabditis briggsae	adenylate ki-se 1	10	P:GO:0007050; P:GO:0046939; F:GO:0004017; P:GO:0046034; C:GO:0043005; C:GO:0005739; P:GO:0009165; F:GO:0005524; C:GO:0048471; C:GO:0005886	-	EC:2.7.4.3	IPR000850; G3DSA:3.40.50.300 (GENE3D), PTHR23359:SF23 (PANTHER)
Caenorhabditis elegans	long-chain acyl- synthetase	3	C:GO:0016020; P:GO:0001676; F:GO:0004467	-	EC:6.2.1.3	IPR000873; IPR020459; IPR020845; G3DSA:3.40.50.980 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF8 (PANTHER), SSF56801 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	pdz exchange factor family member (pxf-1)	7	P:GO:0051056; F:GO:0046582; F:GO:0004871; C:GO:0005622; F:GO:0005515; F:GO:0017034; C:GO:0016020	-		IPR000159; IPR000595; IPR000651; IPR001478; IPR001895; IPR008937; IPR014710; IPR018490; IPR019804; G3DSA:1.20.870.10 (GENE3D), G3DSA:2.30.42.10 (GENE3D), PTHR23113:SF21 (PANTHER), SSF54236 (SUPERFAMILY)
Brugia malayi	sec14-like 2 (cerevisiae)	0		F:GO:0005215; F:GO:0016765; C:GO:0005634; P:GO:0006810; C:GO:0005737; P:GO:0045542; P:GO:0050790; F:GO:0008289; F:GO:0008047; C:GO:0005622; P:GO:0006350; C:GO:0005829; P:GO:0045449		SignalP (SIGNALP)
Caenorhabditis elegans	serine threonine protein ki-se	4	F:GO:0017111; P:GO:0050789; C:GO:0005622; F:GO:0000166	-	EC:3.6.1.15	IPR000523; G3DSA:3.40.50.300 (GENE3D), PTHR22908 (PANTHER), PTHR22908:SF13 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Brugia malayi	20s rr- homolog	3	C:GO:0005730; F:GO:0005515; P:GO:0042255	-		IPR007034; PTHR12858 (PANTHER), PTHR12858:SF1 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-unc- protein	0				SignalP (SIGNALP)
Caenorhabditis elegans	phosphatidylinositol 3- and 4-ki-se family protein	1	F:GO:0016772	-		IPR000403; PTHR12865 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	set (trithorax polycomb) domain containing family member (set-18)	1	F:GO:0005515	-		-
	-	0				-
	-	0				-
Brugia malayi	hypothetical kda protein in chromosome	0				-
	-	0				-

Caenorhabditis briggsae	translocase of outer membrane 34	1	F:GO:0005488	-		IPR011989; IPR016024
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0008152; C:GO:0016021; F:GO:0003824		-
	-	0				-
	-	0				SignalP (SIGNALP)
Teladorsagia circumcincta	nicotinic acetylcholine receptor non-alpha subunit	6	F:GO:0004872; C:GO:0045211; C:GO:0030054; P:GO:0006811; C:GO:0016021; F:GO:0004889	-		IPR006201; IPR006202; IPR018000; PTHR18945:SF72 (PANTHER)
	-	0				-
Caenorhabditis elegans	patched family protein	3	P:GO:0018996; P:GO:0040018; P:GO:0040011	-		IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER)
Caenorhabditis elegans	briggsae cbr-gei-15 protein	0				-
Loa loa	smc c-termi-l domain containing protein	0		C:GO:0005694; F:GO:0005524; P:GO:0051276; F:GO:0005515		PTHR18937 (PANTHER), PTHR18937:SF12 (PANTHER)
	-	0				-
	-	0				-
Loa loa	nima (never in mitosis gene a)-related ki-se 7	10	C:GO:0005737; P:GO:0040035; P:GO:0006468; F:GO:0046872; F:GO:0005515; P:GO:0040010; F:GO:0005524; P:GO:0040011; F:GO:0004674; P:GO:0002009	-	EC:2.7.11.0	G3DSA:1.10.510.10 (GENE3D)
Caenorhabditis elegans	yqk4_caeel ame: full=uncharacterized protein flags: precursor	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-unc-45 protein	1	F:GO:0005488	-		-
Homo sapiens	diazepam-binding protein	5	F:GO:0030156; C:GO:0016021; C:GO:0005739; P:GO:0006810; F:GO:0000062	-		IPR000582; IPR014352; IPR022408; PTHR23310:SF12 (PANTHER)
	-	0				-
	-	0				-
	-	0				IPR013032
Caenorhabditis elegans	lethal family member (let-805)	8	P:GO:0018996; P:GO:0009792; P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		-
Caenorhabditis briggsae	peptidylprolyl isomerase d	2	P:GO:0009792; P:GO:0019915	-		-
Caenorhabditis elegans	lipb_caeel ame: full=liprin-beta ame: full=lar-interacting protein beta	0				-

	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	patched family protein	2	F:GO:0008158; C:GO:0016021	-		IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	choline ki-se a family member (cka-1)	6	C:GO:0005887; F:GO:0019904; C:GO:0005938; F:GO:0005069; F:GO:0005080; P:GO:0006612	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	small g protein sig-ling modulator 1	3	F:GO:0005097; C:GO:0005622; P:GO:0032313	-		IPR000195; G3DSA:1.10.8.270 (GENE3D), PTHR22957 (PANTHER), PTHR22957:SF35 (PANTHER)
Caenorhabditis elegans	udp-n-acetylglucosamine-dolichyl-phosphate n-acetylglucosaminephosphotransferase	7	P:GO:0006487; C:GO:0016021; P:GO:0019408; C:GO:0005792; F:GO:0003975; C:GO:0005789; P:GO:0007040	-	EC:2.7.8.15	IPR000715; PTHR10571 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	cathepsin b-like cysteine protei-se	9	P:GO:0009792; P:GO:0002119; F:GO:0005515; P:GO:0040011; F:GO:0004197; P:GO:0040007; P:GO:0006898; P:GO:0006508; P:GO:0050790	-	EC:3.4.22.0	IPR000169; IPR000668; IPR013128; IPR015643; G3DSA:3.90.70.10 (GENE3D), SSF54001 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	F:GO:0016787	-		IPR015868; PTHR12544:SF3 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	uncoordi-ted family member (unc-89)	0				-
Caenorhabditis elegans	calcium atpase	5	F:GO:0005388; C:GO:0016021; P:GO:0006754; F:GO:0005524; P:GO:0006816	-	EC:3.6.3.8	IPR006068; G3DSA:1.20.1110.10 (GENE3D), SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein Y71H2AM.7 [Caenorhabditis elegans]	0				-
synthetic construct	defender against cell death 1	8	C:GO:0008250; P:GO:0018279; C:GO:0016021; P:GO:0007584; P:GO:0006916; P:GO:0001824; P:GO:0042493; F:GO:0004579	-	EC:2.4.1.119	-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	cwf19-like cell cycle control (pombe)	0		F:GO:0003674; F:GO:0003824; P:GO:0008150		IPR006768; PTHR12072 (PANTHER)
Loa loa	hypothetical protein LOAG_05100 [Loa loa]	0				-

	-	0				SignalP (SIGNALP)
Bos taurus	hydroxysteroid (17-beta) dehydroge-se 11	8	C:GO:0005737; P:GO:0006694; F:GO:0005488; F:GO:0004303; P:GO:0055114; C:GO:0005576; C:GO:0005634; P:GO:0006710	-	EC:1.1.1.62	IPR002198; IPR016040; PTHR19410:SF36 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis briggsae	atp-dependent r- helicase	5	F:GO:0003676; F:GO:0005524; C:GO:0005622; F:GO:0008270; F:GO:0008026	-		-
Caenorhabditis briggsae	prolyl 4-hydroxylase	6	F:GO:0031418; F:GO:0005506; F:GO:0004656; P:GO:0055114; F:GO:0016702; C:GO:0005783	-	EC:1.14.11.2 ; EC:1.13.11.0	PTHR10869 (PANTHER), PTHR10869:SF13 (PANTHER)
Caenorhabditis briggsae	tetratricopeptide repeat protein 39b	1	F:GO:0005488	-		IPR019412
Brugia malayi	sphingosine ki-se 1	4	F:GO:0005488; P:GO:0006665; P:GO:0016310; F:GO:0017050	-		PTHR12358 (PANTHER), PTHR12358:SF9 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	smooth muscle myosin heavy chain 11 isoform sm1-like isoform 1	0				IPR019348; PTHR21448 (PANTHER)
	-	0				-
	-	0				-
Homo sapiens	protein s100-a10	5	C:GO:0005783; P:GO:0007165; F:GO:0005102; F:GO:0005509; P:GO:0045595	-		SignalP (SIGNALP)
	-	0				IPR001304; IPR016186; IPR016187; PTHR22802 (PANTHER), PTHR22802:SF7 (PANTHER)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	3	P:GO:0006637; F:GO:0016290; F:GO:0005515	-	EC:3.1.2.2	IPR014940; G3DSA:3.40.50.1820 (GENE3D), SSF53474 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				IPR001304; IPR016186; IPR016187; PTHR10499 (PANTHER), PTHR10499:SF13 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-

Pongo abelii	t-complex protein 1 subunit epsilon	7	C:GO:0005730; P:GO:0006457; C:GO:0005815; C:GO:0005832; F:GO:0005524; F:GO:0051082; P:GO:0009615	-		IPR002423; IPR012718; G3DSA:3.30.260.10 (GENE3D), SSF54849 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	ef hand family protein	0		F:GO:0005509; P:GO:0009792		SignalP (SIGNALP)
Macaca mulatta	acidic coiled-coil containing protein 3	11	P:GO:0030953; P:GO:0021987; P:GO:0051726; P:GO:0022008; P:GO:0030097; P:GO:0022027; C:GO:0005813; P:GO:0042994; P:GO:0032886; F:GO:0019904; P:GO:0006950	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	F:GO:0003723; P:GO:0001522; F:GO:0009982	-	EC:5.4.99.12	-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	integrator complex	6	P:GO:0016180; P:GO:0002119; F:GO:0005515; C:GO:0032039; P:GO:0040011; P:GO:0040015	-		-
Pongo abelii	ras-related protein rab-1a	10	C:GO:0005625; F:GO:0005525; C:GO:0005794; P:GO:0032482; P:GO:0006886; C:GO:0005626; P:GO:0006888; C:GO:0005783; C:GO:0043025; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR013753; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF302 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Angiostrongylus cantonensis	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	mgc80946 protein	10	F:GO:0004872; F:GO:0004715; P:GO:0016032; F:GO:0005515; P:GO:0018108; F:GO:0005524; C:GO:0016021; C:GO:0019028; F:GO:0004674; F:GO:0005198	-	EC:2.7.10.2; EC:2.7.11.0	IPR000719; IPR001245; IPR008266; IPR011009; IPR020685; IPR020764; G3DSA:1.10.510.10 (GENE3D)

	-	0				SignalP (SIGNALP)
Loa loa	elegans protein confirmed by transcript evidence	0		C:GO:0016021; P:GO:0055085; P:GO:0019915; P:GO:0006810		PTHR11662 (PANTHER), PTHR11662:SF17 (PANTHER), SignalP (SIGNALP)
	-	0				IPR003094; IPR013079; G3DSA:3.40.50.300 (GENE3D), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	pmr-type golgi atpase family member (pmr-1)	16	F:GO:0004871; F:GO:0030145; P:GO:0016339; C:GO:0005802; P:GO:0008544; C:GO:0000139; P:GO:0030026; F:GO:0015410; P:GO:0032468; F:GO:0005509; P:GO:0043123; P:GO:0032472; F:GO:0005388; P:GO:0031532; F:GO:0005524; P:GO:0006828	-	EC:3.6.3.35; EC:3.6.3.8	IPR001757; IPR005834; IPR006069; IPR018303; G3DSA:3.40.1110.10 (GENE3D), G3DSA:3.40.50.1000 (GENE3D), PTHR11939:SF87 (PANTHER), SSF56784 (SUPERFAMILY), SSF81660 (SUPERFAMILY)
Brugia malayi	integrator complex subunit 6	0				PTHR12957 (PANTHER), PTHR12957:SF2 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Loa loa	helicase conserved c-termi-l domain containing protein	0		P:GO:0006260; F:GO:0003676; F:GO:0004386; F:GO:0005524; F:GO:0003887; F:GO:0016787; F:GO:0003677; F:GO:0008026		PTHR11752 (PANTHER), PTHR11752:SF3 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0003723; F:GO:0008168; P:GO:0006396; F:GO:0008173; F:GO:0005515		IPR003582; PTHR21724 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	glycosylation related family member (gly-11)	4	C:GO:0016021; C:GO:0005794; F:GO:0016757; F:GO:0005529	-		IPR001173; G3DSA:3.90.550.10 (GENE3D), PTHR11675 (PANTHER), SSF53448 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis elegans	steroid receptor-interacting snf2 domain	5	F:GO:0004386; F:GO:0003677; F:GO:0005515; F:GO:0005524; C:GO:0016021	-		IPR000330; PTHR10799 (PANTHER), PTHR10799:SF51 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Homo sapiens	phosphohistidine phosphatase 1	4	P:GO:0016311; F:GO:0004721; C:GO:0005829; F:GO:0008969	-	EC:3.1.3.16	IPR007702; SSF143724 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-bch-1 protein	3	F:GO:0008026; F:GO:0000166; P:GO:0010569	-		IPR002464; IPR010614; IPR014013; PTHR11472 (PANTHER), PTHR11472:SF4 (PANTHER)
	-	0				-
	-	0				-
Loa loa	tnni3 interacting ki-se	2	F:GO:0005488; F:GO:0016301	-		IPR002110; IPR020683; PTHR23257 (PANTHER), PTHR23257:SF6 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F40H3.1 [Caenorhabditis elegans]	1	F:GO:0005515	-		-
	-	0				-
Caenorhabditis elegans	ferm domain (-ezrin-radixin-moesin) family member (frm-8)	1	F:GO:0005515	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR13436 (PANTHER), PTHR13436:SF6 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-rev-1 protein	4	P:GO:0009792; P:GO:0040010; P:GO:0006898; P:GO:0006974	-		IPR001126; IPR017963; PTHR11076:SF13 (PANTHER)
	-	0				-
Macaca mulatta	heterogeneous nuclear ribonucleoprotein a3	12	C:GO:0005737; C:GO:0005730; P:GO:0008380; C:GO:0030530; F:GO:0003729; F:GO:0051033; C:GO:0005681; F:GO:0005515; P:GO:0055085; P:GO:0051028; P:GO:0006397; F:GO:0000166	-		PTHR10432 (PANTHER), PTHR10432:SF13 (PANTHER)
Caenorhabditis briggsae	spingomyelin synthetase	2	F:GO:0016740; C:GO:0016021	-		PTHR21290 (PANTHER), PTHR21290:SF4 (PANTHER), SignalP (SIGNALP)

Loa loa	condensin-2 complex subunit h2	0		C:GO:0005694; P:GO:0030261; F:GO:0003674; C:GO:0005634; C:GO:0005575		IPR009378
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	inositol triphosphate receptor family member (itr-1)	4	F:GO:0004872; F:GO:0005262; P:GO:0006811; C:GO:0016020	-		-
Brugia malayi	leucyl-tr- synthetase	3	F:GO:0004812; P:GO:0006418; F:GO:0000166	-		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Xenopus (Silurana) tropicalis	heavy chain non-muscle	44	F:GO:0001525; C:GO:0030863; P:GO:0008360; C:GO:0031594; P:GO:0030048; F:GO:0030898; P:GO:0051295; C:GO:0005913; P:GO:0016337; F:GO:0043531; P:GO:0032796; P:GO:0015031; C:GO:0001772; P:GO:0050900; P:GO:0007229; C:GO:0005829; P:GO:0007520; F:GO:0000146; P:GO:0006509; P:GO:0043534; C:GO:0008305; C:GO:0005819; C:GO:0001726; P:GO:0007132; F:GO:0005391; C:GO:0032154; P:GO:0000904; P:GO:0001768;	-	EC:3.6.3.9	-

Caenorhabditis briggsae	interferon-induced helicase c domain-containing protein 1	0		F:GO:0004386; P:GO:0009615; F:GO:0003723; F:GO:0016787; F:GO:0003677; C:GO:0005634; F:GO:0003676; F:GO:0005524; F:GO:0046872; P:GO:0044419; P:GO:0042981; F:GO:0000166; C:GO:0005737; F:GO:0043021; F:GO:0008270; C:GO:0005622; F:GO:0005515; F:GO:0008026; P:GO:0045087		IPR021673; PTHR14074 (PANTHER)
Macaca mulatta	polymerase ii (d- directed) polypeptide	12	F:GO:0003899; F:GO:0030275; F:GO:0004672; P:GO:0006367; P:GO:0008380; C:GO:0005665; F:GO:0003677; F:GO:0046983; P:GO:0006368; P:GO:0051056; C:GO:0005666; F:GO:0005096	-	EC:2.7.7.6	-
	-	0				-
	-	0				-
	-	0				-
	-	0				G3DSA:2.40.10.10 (GENE3D)
	-	0				-
	-	0				IPR008906; IPR012337
Homo sapiens	-dh dehydroge-se	14	C:GO:0005654; P:GO:0017148; F:GO:0005515; F:GO:0008137; P:GO:0030262; C:GO:0016021; P:GO:0045892; P:GO:0022900; P:GO:0008624; C:GO:0005747; P:GO:0030308; P:GO:0006606; F:GO:0005524; P:GO:0006800	-	EC:1.6.5.3	IPR009346
Caenorhabditis elegans	trp (transient receptor potential) channel family member (trp-2)	5	C:GO:0016021; F:GO:0005262; P:GO:0006816; F:GO:0005515; P:GO:0055085	-		IPR002153; IPR005821; PTHR10117 (PANTHER), PTHR10117:SF10 (PANTHER)
	-	0				-
Caenorhabditis elegans	immunogenic protein 3	0				SignalP (SIGNALP)

	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-dhs-7 protein	3	P:GO:0008152; F:GO:0005488; F:GO:0003824	-		IPR002198; IPR002347; IPR016040; PTHR19410:SF99 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	d- repair and recombi-tion protein rad54-like	5	P:GO:0006915; P:GO:0033554; F:GO:0003676; P:GO:0000003; F:GO:0005515	-		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	cadherin domain containing protein	6	P:GO:0007218; C:GO:0016021; P:GO:0007156; F:GO:0005509; C:GO:0005886; F:GO:0004930	-		IPR002126; IPR015919; IPR020894; PTHR10596 (PANTHER), PTHR10596:SF73 (PANTHER)
Caenorhabditis elegans	hypothetical protein C29A12.6 [Caenorhabditis elegans]	0				G3DSA:3.40.50.410 (GENE3D)
	-	0				-
Homo sapiens	calmodulin 2	22	P:GO:0060316; C:GO:0005654; P:GO:0010880; F:GO:0031996; F:GO:0031997; P:GO:0060315; P:GO:0051592; P:GO:0018298; F:GO:0005509; P:GO:0006936; P:GO:0032465; P:GO:0006091; C:GO:0005576; C:GO:0005829; F:GO:0019904; C:GO:0005813; F:GO:0031432; P:GO:0007186; C:GO:0005876; C:GO:0005886; C:GO:0000922; P:GO:0008218	-		IPR002048; IPR011992; IPR018247; IPR018248; IPR018249; PTHR23050 (PANTHER), PTHR23050:SF20 (PANTHER), SSF47473 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	ribonucleases p mrp protein subunit pop1 containing protein	7	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040010; P:GO:0000003; P:GO:0006898; P:GO:0006396	-		IPR009723

	-	0				-
Caenorhabditis elegans	briggsae cbr-pqn-39 protein	0				-
Homo sapiens	cathepsin d	9	P:GO:0000045; C:GO:0005615; C:GO:0031012; C:GO:0005764; F:GO:0004190; C:GO:0042470; P:GO:0008219; P:GO:0006508; C:GO:0005739	-	EC:3.4.23.0	IPR012848
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	cleavage stimulation factor subunit 2 tau variant-like	4	C:GO:0005622; P:GO:0009792; F:GO:0000166; F:GO:0003723	-		IPR000504; IPR012677; IPR015465; PTHR10432 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	g in family member (glb-26)	0		F:GO:0005344; F:GO:0020037; F:GO:0019825; P:GO:0015671; F:GO:0005506; P:GO:0006810		IPR012292
	-	0				-
Homo sapiens	alpha-2-macroglobulin precursor	12	F:GO:0004867; F:GO:0043120; F:GO:0019966; P:GO:0001869; P:GO:0007584; C:GO:0005615; C:GO:0031093; F:GO:0019959; F:GO:0019899; P:GO:0010037; P:GO:0051384; P:GO:0006953	-		-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	4	F:GO:0008270; C:GO:0005622; F:GO:0005515; F:GO:0003677	-		-

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	4	F:GO:0008270; C:GO:0005622; F:GO:0005515; F:GO:0003677	-		-
Caenorhabditis elegans	hypothetical kda protein in chromosome	0				IPR019384; PTHR21705 (PANTHER)
	-	0				-
Brugia malayi	family protein	0		P:GO:0006281; F:GO:0003684; F:GO:0003887		-
	-	0				-
Caenorhabditis elegans	ke (drosophila actin-binding) homolog family member (ketn-1)	1	P:GO:0000003	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	solute carrier family member 9	1	C:GO:0016021	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	d- polymerase alpha catalytic subunit	7	F:GO:0016779; P:GO:0006281; C:GO:0044427; P:GO:0006261; P:GO:0030154; F:GO:0005515; C:GO:0044428	-	EC:2.7.7.0	IPR004578; IPR006133; IPR006134; IPR006172; IPR012337; G3DSA:3.30.420.10 (GENE3D), G3DSA:3.90.1600.10 (GENE3D), PTHR10322 (PANTHER), PTHR10322:SF3 (PANTHER), PF12254 (PFAM), SSF56672 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	uncoordi-ted family member (unc-22)	3	P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR003961; IPR008957; IPR013783; PR00014 (PRINTS), PTHR19900 (PANTHER), PTHR19900:SF7 (PANTHER)
	-	0				IPR000782
Danio rerio	selenocysteine-specific elongation factor	3	F:GO:0003924; F:GO:0003746; F:GO:0000166	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Homo sapiens	gamma-secretase subunit pen-2	14	C:GO:0032580; F:GO:0004175; P:GO:0006509; P:GO:0007219; P:GO:0031293; F:GO:0005515; P:GO:0007220; P:GO:0042987; P:GO:0008624; P:GO:0016485; P:GO:0043066; C:GO:0005789; P:GO:0043085; C:GO:0005887	-		-

Loa loa	histidine acid phosphatase family protein	0		C:GO:0030141; P:GO:0016311; C:GO:0016020; C:GO:0005771; F:GO:0016787; C:GO:0045177; F:GO:0003993; C:GO:0005765; C:GO:0005764; C:GO:0005576; F:GO:0033265; P:GO:0008152; C:GO:0031985		IPR000560; G3DSA:3.40.50.1240 (GENE3D), PTHR11567 (PANTHER), PTHR11567:SF18 (PANTHER), SSF53254 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Pongo abelii	glutamate n-methyl d-asparate-associated protein 1 (glutamate binding) isoform cra_a	3	C:GO:0016021; F:GO:0005261; F:GO:0004872	-		-
Caenorhabditis elegans	briggsae cbr-lnp-1 protein	3	P:GO:0032501; P:GO:0009987; C:GO:0016020	-		IPR019273; PTHR22166 (PANTHER), PTHR22166:SF4 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	leucine rich repeat family protein	1	P:GO:0009792	-		G3DSA:3.80.10.10 (GENE3D)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Eubacterium ventriosum ATCC 27560	pg1 homology to homo sapiens	4	F:GO:0008686; F:GO:0046872; P:GO:0009231; F:GO:0016853	-	EC:4.1.99.12	SignalP (SIGNALP)
Pan troglodytes	ribosomal protein s17	7	P:GO:0006413; F:GO:0003735; P:GO:0006364; C:GO:0022627; P:GO:0042274; P:GO:0034101; P:GO:0006414	-		IPR001210; IPR018273; SSF116820 (SUPERFAMILY)
Caenorhabditis elegans	copine domain atypical protein isoform partially confirmed by transcript evidence	0				-
Sorghum bicolor	10 kda secreted protein	0				-
	-	0				-
	-	0				-
	-	0				-

Homo sapiens	prolyl 4- beta polypeptide	12	F:GO:0003756; F:GO:0004656; C:GO:0005793; P:GO:0045454; C:GO:0009986; C:GO:0042470; C:GO:0005792; C:GO:0005788; F:GO:0005515; P:GO:0018401; C:GO:0005576; C:GO:0005886	-	EC:5.3.4.1; EC:1.14.11.2	IPR012335; IPR012336; IPR013766; IPR017936; IPR017937; PTHR18929 (PANTHER)
Caenorhabditis briggsae	tr- (guanine-n -)-methyltransferase	5	P:GO:0009792; P:GO:0006400; F:GO:0008176; C:GO:0005634; F:GO:0000049	-	EC:2.1.1.33	IPR003358; PTHR23417 (PANTHER)
	-	0				-
Macaca mulatta	adenylate ki-se 2	6	C:GO:0005758; F:GO:0004017; C:GO:0005743; P:GO:0009165; F:GO:0005524; P:GO:0046083	-	EC:2.7.4.3	IPR000850; G3DSA:3.40.50.300 (GENE3D), PTHR23359:SF22 (PANTHER)
	-	0				-
	-	0				-
Onchocerca volvulus	intermediate filament protein	7	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0018991; F:GO:0005515; P:GO:0040011; P:GO:0040007	-		IPR001322; IPR001664; G3DSA:1.20.5.170 (GENE3D), G3DSA:2.60.40.1260 (GENE3D), PTHR23239:SF13 (PANTHER), SSF74853 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG10738 [Caenorhabditis briggsae]	3	P:GO:0009792; P:GO:0000003; P:GO:0008340	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Homo sapiens	granulin	8	C:GO:0005615; P:GO:0050679; F:GO:0008083; F:GO:0005125; P:GO:0007165; C:GO:0005739; P:GO:0007566; P:GO:0001835	-		PTHR12274 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-cdh-1 protein	5	P:GO:0002119; P:GO:0007155; P:GO:0040010; P:GO:0040011; C:GO:0016020	-		-
	-	0				-
	-	0				-

Caenorhabditis elegans	protein	5	C:GO:0016021; C:GO:0030054; C:GO:0045211; F:GO:0005230; P:GO:0006811	-		IPR006201; IPR006202; PTHR18945:SF9 (PANTHER)
Caenorhabditis elegans	inositol triphosphate receptor family member (itr-1)	12	P:GO:0055085; C:GO:0030659; F:GO:0005488; C:GO:0043234; C:GO:0016021; F:GO:0005220; C:GO:0043232; C:GO:0071212; P:GO:0032501; P:GO:0006816; C:GO:0005635; C:GO:0005783	-		-
Caenorhabditis elegans	6-phosphogluco-te decarboxylating	15	C:GO:0005625; P:GO:0055114; P:GO:0019322; P:GO:0018996; C:GO:0005792; P:GO:0002119; P:GO:0019521; P:GO:0009051; F:GO:0031406; F:GO:0005515; F:GO:0004616; F:GO:0050661; P:GO:0009792; C:GO:0005737; F:GO:0005529	-	EC:1.1.1.44	-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	7	P:GO:0009792; P:GO:0010171; F:GO:0005267; P:GO:0040011; P:GO:0006813; C:GO:0016021; P:GO:0019915	-		-
	-	0				-
Brugia malayi	pdz domain containing protein	5	P:GO:0009792; P:GO:0040007; P:GO:0040035; F:GO:0005515; P:GO:0002119	-		-
Caenorhabditis elegans	briggsae cbr-acy-3 protein	2	P:GO:0009190; F:GO:0016849	-		PTHR11920 (PANTHER), PTHR11920:SF6 (PANTHER), SignalP (SIGNALP)

Macaca mulatta	transcription intermediary factor 1-beta	15	C:GO:0005654; P:GO:0000122; F:GO:0003714; F:GO:0008270; P:GO:0001837; P:GO:0046777; F:GO:0070087; C:GO:0005719; P:GO:0043193; F:GO:0004672; C:GO:0005730; F:GO:0003713; C:GO:0005720; F:GO:0043565; F:GO:0003700	-		PTHR13712 (PANTHER), PTHR13712:SF18 (PANTHER)
Loa loa	eukaryotic translation initiation factor subunit structural gene x-linked	14	F:GO:0003743; C:GO:0005829; P:GO:0040010; P:GO:0045948; P:GO:0000003; P:GO:0006184; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0040011; F:GO:0003924; P:GO:0009792; P:GO:0040018; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR004161; IPR009000; IPR009001; IPR015256; G3DSA:2.40.30.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF9 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	rhodanese-like domain containing protein	0				IPR001763; PTHR11364 (PANTHER)
Caenorhabditis elegans	endonuclease v	1	F:GO:0016787	-		IPR007581; IPR016040
Caenorhabditis briggsae	mboat family protein	2	C:GO:0016020; F:GO:0016747	-	EC:2.3.1.0	PTHR13906 (PANTHER), PTHR13906:SF5 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	phosphatidylinositol 4-ki-se alpha	7	F:GO:0004428; F:GO:0016773; P:GO:0035118; P:GO:0046854; P:GO:0000003; P:GO:0008219; P:GO:0048015	-	EC:2.7.1.0	-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	protein o-fucosyltransferase 1	0		F:GO:0008417; P:GO:0006493		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-

	-	0				-
	-	0				IPR013069
	-	0				-
Caenorhabditis sp. PS1010	cg12324 protein	7	P:GO:0000022; F:GO:0003676; F:GO:0003735; C:GO:0005811; F:GO:0005515; C:GO:0022627; P:GO:0006412	-	EC:3.6.5.3	-
Drosophila melanogaster	cg12324 protein	8	P:GO:0000022; F:GO:0003676; F:GO:0003735; C:GO:0005811; P:GO:0045454; F:GO:0005515; C:GO:0022627; P:GO:0006412	-	EC:3.6.5.3	IPR000630; G3DSA:3.30.1370.30 (GENE3D), G3DSA:3.30.1490.10 (GENE3D)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR001534; SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-crp-1 protein	0		F:GO:0005525; P:GO:0007264; F:GO:0000166; C:GO:0016020; C:GO:0005622		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	son of sevenless homolog 2	2	F:GO:0005085; P:GO:0051056	-		IPR000219
	-	0				-
	-	0				-
Caenorhabditis elegans	elmd3_caeel ame: full=elmo domain-containing protein	0		C:GO:0005856; P:GO:0006909		-
	-	0				-
	-	0				-
Caenorhabditis elegans	domain containing protein	0				PTHR15854 (PANTHER)
Loa loa	briggsae cbr-lgc-26 protein	4	C:GO:0016021; C:GO:0045211; P:GO:0006811; F:GO:0005230	-		-
Xenopus (Silurana) tropicalis	a chain crystal structures of hsc70bag1 in complex with small molecule inhibitors	11	P:GO:0006457; P:GO:0006892; F:GO:0042623; C:GO:0009986; P:GO:0016044; C:GO:0042470; F:GO:0005524; F:GO:0005515; C:GO:0030529; P:GO:0006986; P:GO:0044419	-		IPR001023; IPR013126; G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), PTHR19375:SF1 (PANTHER), SSF53067 (SUPERFAMILY)
Caenorhabditis briggsae	isochorismatase family protein	1	F:GO:0042802	-		IPR000868; PTHR14119 (PANTHER)
Caenorhabditis briggsae	expulsion defective family member (exp-2)	5	C:GO:0008076; F:GO:0005249; F:GO:0005515; P:GO:0055085; P:GO:0006813	-		-

	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	hypothetical zinc metalloprotei-se	3	C:GO:0016021; F:GO:0004222; P:GO:0006508	-	EC:3.4.24.0	IPR000718; PTHR11733:SF20 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	required for meiotic nuclear division protein 1 homolog	0		C:GO:0005739; P:GO:0008150; C:GO:0005575		IPR003734
	-	0				-
Stylochus zebra	transposase	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG22281 [Caenorhabditis briggsae]	0				-
Ostertagia ostertagi	hypothetical kda protein in plb1-hxt2 intergenic	5	P:GO:0009792; F:GO:0046872; P:GO:0019509; P:GO:0055114; F:GO:0051213	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	xanthine dehydroge-se	8	F:GO:0004855; F:GO:0009055; F:GO:0005506; F:GO:0004854; P:GO:0055114; P:GO:0008340; F:GO:0051537; F:GO:0050660	-	EC:1.17.3.2; EC:1.17.1.4	IPR000674; PTHR11908 (PANTHER), PTHR11908:SF9 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	dipeptidyl peptidase four family member (dpf-6)	1	F:GO:0008236	-		-
Macaca mulatta	myosin regulatory light chain smooth muscle isoform	4	C:GO:0016459; F:GO:0005509; F:GO:0003774; F:GO:0005515	-		IPR011992; IPR018247; IPR018248; IPR018249; PTHR23049 (PANTHER), PTHR23049:SF6 (PANTHER), SSF47473 (SUPERFAMILY)
	-	0				-

Callithrix jacchus	cytochrome p450 2c18	0		F:GO:0020037; F:GO:0005506; P:GO:0006082; C:GO:0016020; F:GO:0009055; P:GO:0017144; F:GO:0034875; P:GO:0055114; F:GO:0070330; C:GO:0005792; F:GO:0016491; P:GO:0070989; P:GO:0042738; C:GO:0005783; F:GO:0046872; F:GO:0004497		IPR001128; IPR002401; IPR017972; PTHR19383:SF88 (PANTHER)
Ailuropoda melanoleuca	b chain activator-bound structure of human pyruvate ki-se m2	9	F:GO:0004743; F:GO:0005515; F:GO:0030955; F:GO:0005524; F:GO:0000287; P:GO:0006096; P:GO:0012501; C:GO:0005634; C:GO:0005829	-	EC:2.7.1.40	IPR001697; IPR015793; IPR015806; IPR015813
	-	0				-
	-	0				IPR001283; IPR014044; PTHR10334:SF2 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				SSF57501 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Angiostrongylus cantonensis	pap 25a associated domain containing protein	3	C:GO:0005622; F:GO:0005515; F:GO:0003725	-		IPR002934; G3DSA:3.30.460.10 (GENE3D), SSF81301 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	rap ran-gap family protein	5	F:GO:0005099; C:GO:0005622; P:GO:0051056; F:GO:0005515; P:GO:0007265	-		IPR000331; PTHR15711 (PANTHER), SSF111347 (SUPERFAMILY)
	-	0				-
Ancylostoma caninum	ribosomal protein l36	5	C:GO:0005730; F:GO:0003735; F:GO:0005515; C:GO:0022625; P:GO:0006414	-		-

Brugia malayi	elegans protein partially confirmed by transcript evidence	13	P:GO:0009792; P:GO:0002119; F:GO:0008158; P:GO:0040018; P:GO:0001703; P:GO:0018996; P:GO:0000910; P:GO:0006810; P:GO:0040010; P:GO:0000003; P:GO:0040011; C:GO:0016021; F:GO:0005215	-		IPR000731; IPR003392; PTHR10796 (PANTHER), PTHR10796:SF32 (PANTHER), SSF82866 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	sodium-coupled neutral amino acid transporter 9	2	C:GO:0016021; P:GO:0006810	-		IPR013057; SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	a in (actin filament binding protein) homolog family member (afd-1)	2	P:GO:0040010; F:GO:0005515	-		-
Caenorhabditis elegans	a in (actin filament binding protein) homolog family member (afd-1)	2	P:GO:0040010; F:GO:0005515	-		-
	-	0				SignalP (SIGNALP)
Loa loa	cathepsin b	1	F:GO:0008233	-		IPR000169; IPR000668; IPR013128; IPR015643; G3DSA:3.90.70.10 (GENE3D), SSF54001 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	neuro-l igcam family member (rig-6)	4	C:GO:0016021; P:GO:0040018; P:GO:0000003; F:GO:0005488	-		IPR013783; PTHR10489 (PANTHER), PTHR10489:SF38 (PANTHER)
	-	0				IPR000718; PTHR11733:SF23 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	poly(adp-ribose) metabolism enzyme family member (pme-5)	0				PTHR18958 (PANTHER), PTHR18958:SF255 (PANTHER)
	-	0				IPR004296
	-	0				-
Caenorhabditis elegans	clc-type chloride channel family member (clh-2)	7	P:GO:0009792; F:GO:0005247; C:GO:0005886; P:GO:0055085; P:GO:0000003; C:GO:0016021; P:GO:0006821	-		IPR001807; IPR014743; PTHR11689:SF5 (PANTHER), SignalP (SIGNALP)

Caenorhabditis briggsae	probable e3 ubiquitin-protein ligase mycbp2	10	C:GO:0015630; C:GO:0030424; F:GO:0008270; P:GO:0021785; P:GO:0051493; P:GO:0032880; P:GO:0021952; P:GO:0030071; F:GO:0042803; C:GO:0005680	-		IPR012983; PTHR12846 (PANTHER), PTHR12846:SF2 (PANTHER)
Steinernema feltiae	glycogen synthase	7	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0005978; F:GO:0005515; F:GO:0004373; P:GO:0040011	-	EC:2.4.1.11	IPR008631
Caenorhabditis briggsae	briggsae cbr-twk-25 protein	3	C:GO:0016021; P:GO:0006813; F:GO:0005267	-		IPR013099; G3DSA:1.10.287.70 (GENE3D), PTHR11003 (PANTHER), SSF81324 (SUPERFAMILY)
Haemonchus contortus	multidrug resistance protein 1	5	F:GO:0042626; C:GO:0005886; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF96 (PANTHER), SSF52540 (SUPERFAMILY)
Brugia malayi	mediator of r- polymerase ii subunit 19 homolog	7	P:GO:0045449; P:GO:0040035; P:GO:0002119; F:GO:0005515; C:GO:0016592; P:GO:0048477; P:GO:0040018	-		IPR019403; PTHR22536 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG10706 [Caenorhabditis briggsae]	0				-
	-	0				-
Pongo abelii	proteasome (macropain) beta 2	10	P:GO:0010243; P:GO:0051436; P:GO:0051437; F:GO:0004298; P:GO:0031145; P:GO:0014070; P:GO:0044419; C:GO:0005737; C:GO:0005839; C:GO:0005634	-	EC:3.4.25.0	IPR001353; G3DSA:3.60.20.10 (GENE3D), PTHR11599 (PANTHER), PTHR11599:SF6 (PANTHER), PS51476 (PROFILE), SSF56235 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	cathepsin z	2	F:GO:0004197; P:GO:0006508	-	EC:3.4.22.0	IPR000169; IPR000668; IPR013128; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF14 (PANTHER), SignalP (SIGNALP), SSF54001 (SUPERFAMILY)
	-	0				-

Ixodes scapularis	protein-tyrosine phosphatase	0		F:GO:0016740; F:GO:0004725; C:GO:0016021; P:GO:0016311; C:GO:0016020; F:GO:0016791; F:GO:0004721; F:GO:0016787; P:GO:0006470; P:GO:0007507; P:GO:0007165; F:GO:0050254; F:GO:0004872; P:GO:0001570		SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG21816 [Caenorhabditis briggsae]	0		P:GO:0008152; F:GO:0008080		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Callithrix jacchus	actin binding 1a	26	C:GO:0030670; P:GO:0043029; F:GO:0043548; P:GO:0030217; C:GO:0030027; P:GO:0008360; P:GO:0048873; F:GO:0008022; C:GO:0031941; C:GO:0001891; P:GO:0050918; P:GO:0006816; P:GO:0051126; P:GO:0032796; P:GO:0001845; P:GO:0042102; C:GO:0001772; P:GO:0034097; P:GO:0031589; F:GO:0051015; F:GO:0042803; C:GO:0030864; P:GO:0030335; P:GO:0045087; C:GO:0005634; P:GO:0030595	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Ornithorhynchus anatinus	atp synthase subunit mitochondrial	4	F:GO:0015078; C:GO:0000276; P:GO:0042776; F:GO:0016887	-		SignalP (SIGNALP)
Caenorhabditis elegans	l-carnitine dehydratase bile acid-inducible protein f	2	P:GO:0008152; F:GO:0003824	-		-
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	briggsae cbr-odd-2 protein	8	F:GO:0003676; P:GO:0000003; P:GO:0043050; C:GO:0005622; P:GO:0040010; F:GO:0008270; P:GO:0002119; P:GO:0040011	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	cytosolic iron-sulfur protein assembly 1 homolog (cerevisiae)	1	P:GO:0016226	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR19920 (PANTHER)
	-	0				SignalP (SIGNALP)
Loa loa	spc-1	2	F:GO:0004725; F:GO:0005509	-	EC:3.1.3.48	IPR002017; IPR018159; G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF6 (PANTHER), SSF46966 (SUPERFAMILY)
Loa loa	hypothetical protein LOAG_10587 [Loa loa]	5	P:GO:0040007; F:GO:0005488; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	btb poz domain containing protein	0		F:GO:0005515		-
Caenorhabditis elegans	btb poz domain containing protein	0		F:GO:0005515		-
	-	0				SignalP (SIGNALP)
	-	0				-
Brugia malayi	d--directed r- beta subunit family protein	9	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0003899; F:GO:0003677; P:GO:0006350; F:GO:0032549; P:GO:0040007; C:GO:0005634	-	EC:2.7.7.6	-
	-	0				PTHR10127 (PANTHER), PTHR10127:SF2 (PANTHER), SignalP (SIGNALP)
Loa loa	ubiquitin-conjugating enzyme e2 h	6	P:GO:0006511; F:GO:0005524; P:GO:0070936; F:GO:0004842; P:GO:0051246; P:GO:0070979	-	EC:6.3.2.19	-
Loa loa	ubiquitin-conjugating enzyme e2 h	6	P:GO:0006511; F:GO:0005524; P:GO:0070936; F:GO:0004842; P:GO:0051246; P:GO:0070979	-	EC:6.3.2.19	-

Caenorhabditis briggsae	cadherin domain containing protein	2	C:GO:0016020; P:GO:0007155	-		IPR008985; IPR012680; IPR013320
Drosophila ananassae	GF22278 [Drosophila a--ssae]	0		F:GO:0003676		IPR012337
	-	0				-
	-	0				-
Trichoplax adhaerens	xylulose ki-se	2	F:GO:0016773; P:GO:0005975	-	EC:2.7.1.0	IPR000577; PTHR10196:SF5 (PANTHER)
Homo sapiens	ribonuclease inhibitor	11	C:GO:0032311; F:GO:0003723; C:GO:0005739; P:GO:0006264; F:GO:0008428; P:GO:0006402; F:GO:0000287; F:GO:0004523; P:GO:0045765; F:GO:0042803; C:GO:0005634	-	EC:3.1.26.4	-
Caenorhabditis briggsae	sy-ptojanin 1 isoform a	20	P:GO:0016082; P:GO:0046856; F:GO:0008022; F:GO:0000166; P:GO:0016191; P:GO:0032526; P:GO:0007612; C:GO:0019717; F:GO:0017120; P:GO:0034097; F:GO:0004445; P:GO:0007420; P:GO:0048260; P:GO:0014015; F:GO:0003723; F:GO:0004439; F:GO:0032403; C:GO:0030118; F:GO:0017124; P:GO:0048015	-	EC:3.1.3.56; EC:3.1.3.36	SignalP (SIGNALP)
	-	0				-
Rattus norvegicus	h+ v0 subunit b isoform cra_c	2	C:GO:0016021; C:GO:0005768	-		-
	-	0				-
	-	0				-
Nematostella vectensis	ubiquitin-conjugating enzyme e2o	0		F:GO:0005524; P:GO:0051246; P:GO:0043687; F:GO:0000166; F:GO:0019787; F:GO:0004842; P:GO:0016567		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				IPR002198; PTHR19410:SF18 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				-

Loa loa	cubilin (intrinsic factor-cobalamin receptor)	7	P:GO:0006810; C:GO:0043231; F:GO:0046872; C:GO:0044459; C:GO:0044444; F:GO:0042803; F:GO:0016787	-		IPR000859; PTHR10127 (PANTHER), PTHR10127:SF22 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Angiostrongylus cantonensis	zyg-11 homolog b	1	F:GO:0005515	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				PS51257 (PROFILE)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Pongo abelii	peroxiredoxin 5	11	P:GO:0006954; C:GO:0005777; P:GO:0045454; C:GO:0044445; P:GO:0055114; F:GO:0004601; F:GO:0043027; F:GO:0051920; P:GO:0034614; P:GO:0043066; C:GO:0005739	-	EC:1.11.1.7; EC:1.11.1.15	IPR012335; IPR012336; IPR013740; PTHR10430 (PANTHER), PTHR10430:SF3 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0016888		-
Caenorhabditis elegans	phosphatase and actin regulator 2	2	F:GO:0003779; F:GO:0004864	-		IPR019775
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0008168; P:GO:0008152; P:GO:0009792		-
	-	0				-
Caenorhabditis elegans	glycerol ki-se	13	C:GO:0005829; F:GO:0042393; C:GO:0005625; C:GO:0005739; P:GO:0045471; F:GO:0004370; P:GO:0009409; P:GO:0006072; F:GO:0000166; P:GO:0016310; P:GO:0042493; C:GO:0016020; C:GO:0005634	-	EC:2.7.1.30	IPR018484; G3DSA:3.30.420.40 (GENE3D), SSF53067 (SUPERFAMILY)
	-	0				IPR002129; IPR015421
	-	0				-

Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				IPR002018; G3DSA:3.40.50.1820 (GENE3D), PTHR11559:SF15 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0016301; F:GO:0004672; F:GO:0005524; F:GO:0016740; F:GO:0000166; F:GO:0004713; P:GO:0006468; F:GO:0005515		-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	zinc carboxypeptidase family protein	0		P:GO:0006508; F:GO:0004181; F:GO:0004180; F:GO:0008270		IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), PTHR11705:SF12 (PANTHER), SSF53187 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				PTHR13056 (PANTHER)
Hydra magnipapillata	transposase homolog	1	P:GO:0006259	-		PTHR23022 (PANTHER), PTHR23022:SF10 (PANTHER)
	-	0				-
Loa loa	paz domain containing protein	0		F:GO:0003676		-
Teladorsagia circumcincta	elegans protein confirmed by transcript evidence	3	C:GO:0005576; P:GO:0007218; C:GO:0016021	-		IPR002544; PTHR20986 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				PTHR10566 (PANTHER), PTHR10566:SF6 (PANTHER)
Caenorhabditis briggsae	legumain	9	P:GO:0009792; P:GO:0040015; C:GO:0045177; C:GO:0043231; C:GO:0044444; P:GO:0000003; P:GO:0006508; F:GO:0004674; F:GO:0008234	-	EC:2.7.11.0	IPR001096; PTHR12000:SF4 (PANTHER), SignalP (SIGNALP)
Ailuropoda melanoleuca	h2a histone member y	8	P:GO:0016568; C:GO:0000786; F:GO:0003677; P:GO:0006334; F:GO:0003682; P:GO:0007549; C:GO:0001740; C:GO:0000793	-		G3DSA:3.40.220.10 (GENE3D), SSF52949 (SUPERFAMILY)

	-	0				-
	-	0				-
	-	0				-
	-	0				-
Ailuropoda melanoleuca	mitogen-activated protein ki-se ki-se 7	10	F:GO:0004708; P:GO:0051403; F:GO:0004674; F:GO:0005524; F:GO:0004713; F:GO:0000287; F:GO:0019901; C:GO:0005737; C:GO:0005634; P:GO:0006468	-	EC:2.7.11.0; EC:2.7.10.0	-
Brugia malayi	briggsae cbr-grh-1 protein	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	protein	1	P:GO:0065007	-		IPR000716; PTHR14093 (PANTHER), PTHR14093:SF5 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	-d-dependent epimerase dehydratase	7	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0000003; P:GO:0040011; P:GO:0008152; F:GO:0003824	-		IPR002225; IPR016040; PTHR10366 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	P:GO:0007155; C:GO:0005604	-		IPR010307
Caenorhabditis brenneri	briggsae cbr-nlp-3 protein	0				-
Caenorhabditis elegans	fibronectin type-iii domain-containing protein c4orf31 homolog precursor	0		F:GO:0008201; P:GO:0019800; P:GO:0030198; C:GO:0031012; F:GO:0005539; C:GO:0005576		IPR019326
Caenorhabditis briggsae	Hypothetical protein CBG14163 [Caenorhabditis briggsae]	1	P:GO:0040010	-		-
	-	0				-
Loa loa	uncoordi-ted family member (unc-89)	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	filamin abp280 repeat family protein	8	P:GO:0009792; P:GO:0010171; C:GO:0005840; F:GO:0003735; F:GO:0003779; P:GO:0007126; P:GO:0000003; P:GO:0006412	-	EC:3.6.5.3	IPR013783; IPR014756; IPR017868; PTHR11915 (PANTHER), PTHR11915:SF24 (PANTHER)
Caenorhabditis elegans	briggsae cbr-pgp-11 protein	5	F:GO:0015440; F:GO:0008559; P:GO:0055085; F:GO:0005524; C:GO:0016021	-	EC:3.6.3.43; EC:3.6.3.44	-
Caenorhabditis briggsae	uncharacterized transposase-like protein	1	F:GO:0046872	-		-

Harpegnathos saltator	proclotting enzyme	0		P:GO:0006508; F:GO:0004252; F:GO:0008236; F:GO:0016787; F:GO:0003824; F:GO:0008233		IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR19355 (PANTHER), PTHR19355:SF126 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0016740; F:GO:0030246; C:GO:0016021; F:GO:0016758; F:GO:0016757; P:GO:0019915; P:GO:0005975; P:GO:0030259; P:GO:0008152		IPR002213; PTHR11926:SF3 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG11187 [Caenorhabditis briggsae]	7	P:GO:0006468; F:GO:0005515; F:GO:0004713; P:GO:0040010; F:GO:0005524; C:GO:0016021; F:GO:0004674	-	EC:2.7.10.0; EC:2.7.11.0	-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0005525; P:GO:0007264; F:GO:0000166; C:GO:0005622; P:GO:0015031		-
	-	0				-
	-	0				-
Callithrix jacchus	chromosome 19 open reading frame 43	0		F:GO:0003674; P:GO:0008150		-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	myg1 protein	1	P:GO:0043473	-		IPR003226
Callithrix jacchus	h aca ribonucleoprotein complex subunit 2	6	C:GO:0005730; C:GO:0015030; F:GO:0030515; P:GO:0031118; C:GO:0005732; F:GO:0005515	-		IPR004038; IPR018492; G3DSA:3.30.1330.30 (GENE3D), PTHR23105 (PANTHER), PTHR23105:SF12 (PANTHER), SSF55315 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)

Branchiostoma floridae	domain containing protein	0		P:GO:0007422; P:GO:0008360; P:GO:0007111; P:GO:0051225; P:GO:0007110; C:GO:0005634; P:GO:0007155; P:GO:0000915; P:GO:0035023; F:GO:0005089; P:GO:0000910; P:GO:0050770; F:GO:0005085; P:GO:0008078; P:GO:0045184; P:GO:0007443; P:GO:0007399; P:GO:0007509; P:GO:0023034; C:GO:0005622		IPR001357; G3DSA:3.40.50.10190 (GENE3D), PTHR16777 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-hsr-9 protein	5	P:GO:0002009; P:GO:0019915; P:GO:0040007; P:GO:0040035; P:GO:0002119	-		-
	-	0				-
	-	0				-
	-	0				-
Callithrix jacchus	ergic and golgi 3	6	C:GO:0005789; C:GO:0005794; F:GO:0005515; P:GO:0016192; C:GO:0016021; C:GO:0033116	-		IPR012936; PTHR10984 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	pab-dependent poly -specific ribonuclease subunit	0		F:GO:0004221; P:GO:0006397; F:GO:0016787; F:GO:0004535; F:GO:0003676; C:GO:0005737; F:GO:0004527; P:GO:0006511; C:GO:0005622; F:GO:0004518		PTHR15728 (PANTHER)
Caenorhabditis briggsae	sig-l transducing adaptor molecule (sh3 domain and itam motif) 2	5	C:GO:0005768; P:GO:0043409; C:GO:0044441; P:GO:0048013; F:GO:0005515	-		-

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0019915		IPR000626; IPR019955; G3DSA:3.10.20.90 (GENE3D), SSF54236 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	bardet-biedl syndrome 7	4	C:GO:0043005; F:GO:0005515; P:GO:0035058; P:GO:0045444	-		-
	-	0				-
	-	0				-
Clostridium botulinum D str. 1873	pyrroline-5-carboxylate reductase	4	F:GO:0005488; F:GO:0004735; P:GO:0055114; P:GO:0006561	-	EC:1.5.1.2	IPR000304; IPR008927
	-	0				-
	-	0				-
Caenorhabditis elegans	lim and sh3 domain protein	2	F:GO:0008270; P:GO:0000003	-		-
Caenorhabditis elegans	member ras oncogene partial	8	F:GO:0005525; F:GO:0005515; P:GO:0006913; F:GO:0005509; P:GO:0006886; C:GO:0005634; P:GO:0007264; C:GO:0048471	-		-
Heliconius melpomene	r--directed d- polymerase hmg-i and hmg- d--	4	F:GO:0004519; F:GO:0003723; F:GO:0003964; P:GO:0006278	-	EC:2.7.7.49	-
Caenorhabditis elegans	receptor protein tyrosine	3	F:GO:0004725; F:GO:0008238; P:GO:0006470	-	EC:3.1.3.48	IPR000242; IPR000387; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF35 (PANTHER), SSF52799 (SUPERFAMILY)
	-	0				-
	-	0				-
Brugia malayi	protein-tyrosine phosphatase containing protein	2	F:GO:0004725; P:GO:0006470	-	EC:3.1.3.48	-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-tag-273 protein	2	F:GO:0046872; P:GO:0000003	-		IPR001781
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	calcium calmodulin-dependent protein ki-se type 1	2	F:GO:0016301; F:GO:0005515	-		-
Caenorhabditis elegans	suppressor of activated let-60 ras family member (sur-2)	0		P:GO:0006350; P:GO:0045449; C:GO:0005634		-
Caenorhabditis briggsae	briggsae cbr-exoc-8 protein	6	P:GO:0009792; P:GO:0040018; P:GO:0000003; P:GO:0010171; P:GO:0002119; P:GO:0040011	-		PTHR21426 (PANTHER), PTHR21426:SF9 (PANTHER)
	-	0				-

	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	endonuclease exonuclease phosphatase family protein	1	F:GO:0016788	-		IPR005135; G3DSA:3.60.10.10 (GENE3D), PTHR11200 (PANTHER), PTHR11200:SF20 (PANTHER), SignalP (SIGNALP)
Monodelphis domestica	tpa_exp: ngep	2	C:GO:0005886; P:GO:0006811	-		IPR007632
Caenorhabditis elegans	Hypothetical protein W10D9.6 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	briggsae cbr-gur-4 protein	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
	-	0				IPR003953; G3DSA:3.50.50.60 (GENE3D), PTHR11632 (PANTHER), PTHR11632:SF3 (PANTHER), SignalP (SIGNALP), SSF51905 (SUPERFAMILY)
Homo sapiens	cartilage oligomeric matrix protein	11	P:GO:0060173; C:GO:0005615; F:GO:0008201; F:GO:0005518; F:GO:0005201; P:GO:0007155; F:GO:0005509; F:GO:0043395; P:GO:0006916; C:GO:0005578; P:GO:0003417	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Bombyx mori	endonuclease-reverse transcriptase	0		F:GO:0003723; P:GO:0006278; F:GO:0004519; F:GO:0003964		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	fructose- -bisphosphatase	3	P:GO:0016051; C:GO:0005737; F:GO:0042132	-	EC:3.1.3.11	IPR000146; IPR000408; IPR020548; G3DSA:3.30.540.10 (GENE3D), G3DSA:3.40.190.80 (GENE3D), SSF56655 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	yqy2_caeel ame: full=uncharacterized protein	1	F:GO:0004871	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis briggsae	s-phase ki-se-associated protein 1	18	P:GO:0008340; C:GO:0005654; F:GO:0016301; P:GO:0016246; F:GO:0005515; P:GO:0051437; P:GO:0040010; P:GO:0006898; P:GO:0040011; P:GO:0016310; C:GO:0005829; C:GO:0019005; P:GO:0009792; P:GO:0002009; F:GO:0004842; P:GO:0002119; P:GO:0031146; P:GO:0040035	-	EC:6.3.2.19	-
Ciona intestinalis	briggsae cbr-opt-1 protein	0		F:GO:0015198; P:GO:0006857; C:GO:0016021; C:GO:0016020; F:GO:0005215; P:GO:0006810		IPR000109; PTHR11654 (PANTHER), PTHR11654:SF13 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	ain family member (clp-1)	4	P:GO:0008219; C:GO:0005622; P:GO:0006508; F:GO:0004198	-		G3DSA:3.90.70.10 (GENE3D), PTHR10183 (PANTHER), PTHR10183:SF45 (PANTHER)
	-	0				-
	-	0				-
Branchiostoma floridae	tbc1 domain family member 30	0		P:GO:0032313; F:GO:0005097; C:GO:0005622		IPR000195; G3DSA:1.10.8.270 (GENE3D), PTHR22957 (PANTHER), PTHR22957:SF20 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	atp-binding cassette transporter 13-like	0		F:GO:0042626; F:GO:0005215; C:GO:0016021; P:GO:0006810; F:GO:0000166; F:GO:0017111; F:GO:0005524; F:GO:0016887; P:GO:0055085		-
Caenorhabditis briggsae	phosphatidate cytidylyltransferase	12	P:GO:0016056; P:GO:0008340; C:GO:0016021; P:GO:0040007; P:GO:0007602; P:GO:0000003; P:GO:0043052; P:GO:0002119; F:GO:0004605; C:GO:0005635; C:GO:0005790; C:GO:0005886	-	EC:2.7.7.41	IPR000374; PTHR13773 (PANTHER)

Caenorhabditis briggsae	phosphatidate cytidylyltransferase	12	P:GO:0016056; P:GO:0008340; C:GO:0016021; P:GO:0040007; P:GO:0007602; P:GO:0000003; P:GO:0043052; P:GO:0002119; F:GO:0004605; C:GO:0005635; C:GO:0005790; C:GO:0005886	-	EC:2.7.7.41	IPR000374; PTHR13773 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Heligmosomoides polygyrus	glutathione s-transferase	2	F:GO:0016740; P:GO:0008340	-		IPR004045; IPR012335; IPR012336; PTHR11571 (PANTHER), PTHR11571:SF7 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	peptidylglycine alpha-amidating monooxyge-se	19	P:GO:0044260; P:GO:0007595; P:GO:0060173; F:GO:0005515; F:GO:0004598; P:GO:0007417; P:GO:0007507; C:GO:0005624; P:GO:0009268; C:GO:0005615; P:GO:0051384; P:GO:0046688; P:GO:0044238; P:GO:0042493; F:GO:0004504; C:GO:0030141; F:GO:0005507; P:GO:0032355; C:GO:0043204	-	EC:4.3.2.5; EC:1.14.17.3	IPR000720; IPR001258; IPR011042; IPR013017; PTHR10680 (PANTHER), SSF63829 (SUPERFAMILY)

Pongo abelii	notch partial	26	P:GO:0030097; P:GO:0007219; F:GO:0005515; P:GO:0042246; P:GO:0006355; F:GO:0005509; P:GO:0030326; F:GO:0003706; P:GO:0002011; C:GO:0005576; C:GO:0005737; P:GO:0008285; P:GO:0006916; P:GO:0007050; C:GO:0009986; P:GO:0019827; P:GO:0006917; P:GO:0001709; P:GO:0046579; P:GO:0009887; P:GO:0007368; P:GO:0007399; P:GO:0016049; F:GO:0004872; C:GO:0005887; C:GO:0005634	-		IPR000742; IPR006210; IPR013032; IPR013111; G3DSA:2.10.25.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF199 (PANTHER), SSF57196 (SUPERFAMILY)
	-	0				-
Homo sapiens	wd repeat-containing protein 1 isoform 1 variant	5	C:GO:0005856; C:GO:0005576; C:GO:0005829; F:GO:0003779; P:GO:0007605	-		-
	-	0				-
	-	0				-

Caenorhabditis elegans	aldehyde dehydroge-se	35	P:GO:0030324; P:GO:0010628; P:GO:0031016; F:GO:0004028; P:GO:0051289; P:GO:0048566; P:GO:0048384; F:GO:0018479; P:GO:0035115; P:GO:0009952; P:GO:0001568; P:GO:0030902; P:GO:0014032; P:GO:0030900; P:GO:0009855; P:GO:0060324; C:GO:0005829; P:GO:0001936; P:GO:0008284; F:GO:0005497; P:GO:0042904; F:GO:0016918; F:GO:0042802; F:GO:0047113; F:GO:0004029; F:GO:0001758; P:GO:0031076;	-	EC:1.2.1.28; EC:1.2.99.3; EC:1.2.1.3; EC:1.2.1.36	IPR015590; IPR016161; IPR016163; PTHR11699:SF46 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	carboxypeptidase b1	0		F:GO:0004181; F:GO:0004180; P:GO:0030030; C:GO:0014704; C:GO:0030018; F:GO:0046872; F:GO:0008237; C:GO:0016020; C:GO:0030863; F:GO:0008233; C:GO:0008290; C:GO:0030027; P:GO:0008152; P:GO:0008150; P:GO:0006508; C:GO:0005737; F:GO:0003779; P:GO:0051693; F:GO:0008270; C:GO:0005856; P:GO:0030036; C:GO:0005576; C:GO:0005575; P:GO:0030032		IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SSF53187 (SUPERFAMILY)
	-	0				-

Caenorhabditis elegans	gei-4 interacting protein family member (gfi-2)	8	P:GO:0040035; P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040018; P:GO:0040010; P:GO:0008340; P:GO:0006898	-		-
Caenorhabditis elegans	gei-4 interacting protein family member (gfi-2)	8	P:GO:0040035; P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040018; P:GO:0040010; P:GO:0008340; P:GO:0006898	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	excitatory amino acid transporter 5-like	3	P:GO:0006835; F:GO:0017153; C:GO:0016021	-		IPR001991; PTHR11958:SF17 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	fat tumor suppressor homolog 3	0		C:GO:0016021; C:GO:0016020; F:GO:0003674; P:GO:0007275; C:GO:0005575; C:GO:0005886; P:GO:0007156; F:GO:0005509; P:GO:0007155		IPR002126; IPR015919; IPR020894; PTHR10596 (PANTHER), PTHR10596:SF116 (PANTHER)
Caenorhabditis briggsae	g protein-coupled receptor ki-se 4	5	F:GO:0004872; P:GO:0006468; F:GO:0005524; P:GO:0007165; F:GO:0004703	-	EC:2.7.11.16	IPR000239; IPR000719; IPR000961; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22985 (PANTHER), PTHR22985:SF101 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	atp-binding cassette subfamily member 1	10	P:GO:0055114; P:GO:0045329; P:GO:0033539; F:GO:0070991; F:GO:0042802; P:GO:0051793; P:GO:0019915; C:GO:0005759; P:GO:0019254; F:GO:0050660	-		IPR006089; IPR006091; IPR006092; IPR009100; IPR013786; PTHR10909 (PANTHER), PTHR10909:SF10 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	suppressor of activated let-60 ras family member (sur-2)	0		P:GO:0006350; P:GO:0045449; C:GO:0005634		-

Loa loa	negative elongation factor c d	3	F:GO:0003746; C:GO:0017053; P:GO:0007070	-		IPR006942
Caenorhabditis briggsae	briggsae cbr-tgt-2 protein	0		F:GO:0046872; F:GO:0008479; P:GO:0006400; P:GO:0008033; F:GO:0016740; P:GO:0008616; F:GO:0016757		-
Caenorhabditis elegans	neutral endopeptidase	1	F:GO:0008237	-		IPR000718; IPR008753; G3DSA:3.40.390.10 (GENE3D), PTHR11733:SF24 (PANTHER), SSF55486 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	binding protein family member (pab-1)	3	P:GO:0009792; F:GO:0000166; F:GO:0003723	-		-
Caenorhabditis briggsae	binding protein family member (pab-1)	3	P:GO:0009792; F:GO:0000166; F:GO:0003723	-		-
Caenorhabditis elegans	binding protein family member (pab-1)	3	P:GO:0009792; F:GO:0000166; F:GO:0003723	-		SignalP (SIGNALP)
Caenorhabditis elegans	binding protein family member (pab-1)	3	P:GO:0009792; F:GO:0000166; F:GO:0003723	-		SignalP (SIGNALP)
Ancylostoma ceylanicum	tpa_inf: eukaryotic translation elongation factor 1a	8	C:GO:0005737; P:GO:0009792; P:GO:0002119; P:GO:0007276; F:GO:0003746; F:GO:0005525; P:GO:0006414; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000795; IPR004160; IPR004161; IPR004539; IPR009000; IPR009001; G3DSA:2.40.30.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF37 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	microtubule binding protein	2	P:GO:0009987; F:GO:0005515	-		IPR000048; IPR001715; SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	microtubule binding protein	2	P:GO:0009987; F:GO:0005515	-		IPR000048; IPR001715; SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	microtubule binding protein	2	P:GO:0009987; F:GO:0005515	-		IPR000048; IPR001715; SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	microtubule binding protein	2	P:GO:0009987; F:GO:0005515	-		IPR000048; IPR001715; SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	zinc finger in meiosis family member (zim-3)	0		F:GO:0008270; C:GO:0005622		IPR007087; IPR015880
Loa loa	hypothetical protein LOAG_02027 [Loa loa]	0		F:GO:0005525; F:GO:0051020; F:GO:0005085		-

Ectocarpus siliculosus	protein	9	F:GO:0004674; C:GO:0005874; F:GO:0031625; C:GO:0005813; P:GO:0051301; F:GO:0005524; P:GO:0007067; C:GO:0005819; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017442; IPR020636; IPR020663; G3DSA:1.10.510.10 (GENE3D)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG11218 [Caenorhabditis briggsae]	0		F:GO:0003723; F:GO:0005488; P:GO:0006396; F:GO:0008173		-
	-	0				-
Caenorhabditis briggsae	ybri_caeel ame: full=uncharacterized protein	0		P:GO:0006898		-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Macaca mulatta	PREDICTED: hypothetical protein LOC100427666 [Macaca mulatta]	0				SignalP (SIGNALP)
Caenorhabditis briggsae	serine threonine-protein ki-se sbk1	5	P:GO:0018107; P:GO:0018105; F:GO:0005524; P:GO:0007420; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF19 (PANTHER)
	-	0				-
	-	0				-
Loa loa	voltage-gated ion channel	4	C:GO:0016021; F:GO:0005216; P:GO:0006811; P:GO:0055085	-		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	r--dependent r- polymerase family family member (rrf-1)	0				-
Caenorhabditis briggsae	mgc26979 protein	8	C:GO:0030659; P:GO:0030433; C:GO:0060170; C:GO:0005813; P:GO:0010826; F:GO:0051082; P:GO:0042384; C:GO:0005789	-		IPR019170; PTHR21274 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	patched family protein	8	P:GO:0040025; F:GO:0008158; P:GO:0040018; P:GO:0018996; P:GO:0040002; P:GO:0040011; C:GO:0016021; P:GO:0019915	-		IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	reti-l pigment epithelium-specific protein b	1	F:GO:0005515	-		IPR004294; PTHR10543:SF4 (PANTHER)
	-	0				SignalP (SIGNALP)

	-	0				-
Ostertagia ostertagi	metalloprotease 1 precursor	2	F:GO:0004222; P:GO:0006508	-	EC:3.4.24.0	IPR013032; PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER)
	-	0				-
Caenorhabditis elegans	quiescin q6 sulfhydryl oxidase 2	5	P:GO:0040010; C:GO:0043231; F:GO:0016491; P:GO:0040017; C:GO:0016020	-		IPR005746; IPR012335; IPR012336; IPR013766; IPR017936; PTHR18929 (PANTHER), SignalP (SIGNALP)
Homo sapiens	cytochrome b5 reductase 3	7	F:GO:0004128; C:GO:0005789; P:GO:0008015; C:GO:0005833; P:GO:0055114; P:GO:0006695; C:GO:0005741	-	EC:1.6.2.2	IPR001433; G3DSA:3.40.50.80 (GENE3D), PTHR19370 (PANTHER), PTHR19370:SF3 (PANTHER), SSF52343 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	arch_caebr ame: full=protein archease-like	0				IPR002804; PD012969 (PRODOM), PTHR12682:SF8 (PANTHER)
	-	0				-
Caenorhabditis elegans	glycerol uptake facilitator	0		F:GO:0005215; C:GO:0005929; C:GO:0016021; C:GO:0016020; P:GO:0006810; C:GO:0043025; P:GO:0006833; P:GO:0055085; F:GO:0015250		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	cuticular collagen	3	C:GO:0016021; P:GO:0010171; F:GO:0005515	-		PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG13503 [Caenorhabditis briggsae]	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	preg-ncy-induced growth inhibitor	0		P:GO:0007281; F:GO:0003674; F:GO:0005488; P:GO:0008152; F:GO:0003824; P:GO:0008150; P:GO:0007126; C:GO:0005575		G3DSA:3.50.50.60 (GENE3D), SSF51905 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	3-oxoacyl-	2	F:GO:0016747; P:GO:0009058	-	EC:2.3.1.0	IPR000794; IPR014031; IPR016038; IPR016039; PTHR11712:SF23 (PANTHER)
Caenorhabditis elegans	briggsae cbr-hhat-1 protein	0				SignalP (SIGNALP)
	-	0				-

Brugia malayi	plasma glutamate carboxypeptidase	0		F:GO:0003674; F:GO:0008237; C:GO:0005576; C:GO:0005575; F:GO:0008233; P:GO:0006508; F:GO:0046872; P:GO:0008150; F:GO:0004180; F:GO:0004177		IPR007484; G3DSA:3.40.630.10 (GENE3D), PTHR12053 (PANTHER), PTHR12053:SF2 (PANTHER), SSF53187 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	atpase type 13a1	5	C:GO:0016021; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0006812	-		IPR001757; PTHR11939:SF48 (PANTHER)
Caenorhabditis elegans	c2 domain containing protein	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	serine threonine-protein phosphatase pp1-alpha catalytic subunit	1	F:GO:0016787	-		IPR004843; IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF19 (PANTHER), SSF56300 (SUPERFAMILY)
	-	0				-
Caenorhabditis remanei	elegans protein confirmed by transcript evidence	3	P:GO:0006508; F:GO:0004181; F:GO:0008270	-	EC:3.4.17.0	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), PTHR11705:SF12 (PANTHER), SSF53187 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F07C3.2 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	obg-like atpase 1	10	C:GO:0016021; P:GO:0006200; P:GO:0015684; F:GO:0015093; F:GO:0005524; F:GO:0005515; P:GO:0009792; C:GO:0005737; F:GO:0016787; F:GO:0005525	-		-
Caenorhabditis elegans	obg-like atpase 1	10	C:GO:0016021; P:GO:0006200; P:GO:0015684; F:GO:0015093; F:GO:0005524; F:GO:0005515; P:GO:0009792; C:GO:0005737; F:GO:0016787; F:GO:0005525	-		-
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	lbp bpi cetp n-termi-l domain containing protein	0		F:GO:0008289		IPR017943; G3DSA:3.15.10.10 (GENE3D), PTHR10504 (PANTHER), PTHR10504:SF19 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Macaca mulatta	transcription factor dp-1	11	P:GO:0000084; P:GO:0006357; P:GO:0006915; C:GO:0005667; P:GO:0008544; F:GO:0003677; F:GO:0003700; F:GO:0019904; F:GO:0003713; P:GO:0045893; P:GO:0008283	-		-
	-	0				-
Caenorhabditis elegans	briggsae cbr-fer-1 protein	0		C:GO:0016021		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-tim-1 protein	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis remanei	briggsae cbr-tag-151 protein	6	P:GO:0009792; F:GO:0005515; P:GO:0042254; P:GO:0040010; P:GO:0040011; C:GO:0005634	-		IPR012948
Loa loa	hypothetical protein LOAG_04123 [Loa loa]	0				SignalP (SIGNALP)
Caenorhabditis elegans	megf11 protein	13	P:GO:0012501; P:GO:0043652; P:GO:0008340; C:GO:0030670; P:GO:0042742; P:GO:0034620; P:GO:0031532; P:GO:0045184; P:GO:0043654; C:GO:0031260; C:GO:0009986; F:GO:0005515; P:GO:0001845	-		IPR000742; IPR002049; IPR006210; IPR009030; IPR011489; IPR013032; PD936484 (PRODOM), PR00011 (PRINTS), G3DSA:2.170.300.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF221 (PANTHER), SignalP (SIGNALP), SSF57196 (SUPERFAMILY)
	-	0				-
	-	0				-

Selaginella moellendorffii	d-2-like helicase	11	C:GO:0005654; F:GO:0016890; P:GO:0043137; F:GO:0017108; F:GO:0004386; P:GO:0006284; P:GO:0006264; F:GO:0016887; P:GO:0045740; C:GO:0005760; F:GO:0005488	-	EC:3.1.25.0	PTHR10887 (PANTHER)
	-	0				-
	-	0				-
Loa loa	briggsae cbr-nex-3 protein	0		F:GO:0005509; F:GO:0005544; F:GO:0005515		-
	-	0				-
Brugia malayi	sodium:neurotransmitter symporter family protein	3	C:GO:0005887; F:GO:0005328; P:GO:0006836	-		IPR000175; PTHR11616:SF20 (PANTHER), SignalP (SIGNALP)
						SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	rt14 protein	1	F:GO:0005515	-		IPR015362; PTHR22959 (PANTHER)
Caenorhabditis briggsae	within the bgcn gene intron protein	5	C:GO:0035145; F:GO:0043022; P:GO:0045727; F:GO:0005515; P:GO:0000184	-		IPR015362; PTHR22959 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	dystrobrevin beta	12	F:GO:0005277; P:GO:0015870; F:GO:0008270; F:GO:0005509; C:GO:0045202; P:GO:0007271; F:GO:0005515; P:GO:0007529; P:GO:0046716; P:GO:0040017; C:GO:0016010; C:GO:0005737	-		IPR000433; PTHR11915 (PANTHER), PTHR11915:SF16 (PANTHER)
	-	0				PS51257 (PROFILE)
Strongylocentrotus purpuratus	endonuclease-reverse transcriptase	0		F:GO:0003723; P:GO:0006278; F:GO:0008270; F:GO:0004519; C:GO:0005622; F:GO:0003964		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	briggsae cbr-ptr-16 protein	5	P:GO:0018996; C:GO:0016021; P:GO:0040018; F:GO:0008158; P:GO:0040011	-		-
	-	0				-
	-	0				-

	-	0				-
	-	0				-
	-	0				PTHR14790 (PANTHER), PTHR14790:SF3 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-rbc-2 protein	1	P:GO:0006508	-		IPR015943; PTHR22847 (PANTHER), PTHR22847:SF4 (PANTHER)
Caenorhabditis remanei	tryptophan -dioxyge-se	53	P:GO:0006006; P:GO:0045892; P:GO:0008595; P:GO:0035289; P:GO:0006357; P:GO:0035071; P:GO:0035224; P:GO:0050770; P:GO:0019441; P:GO:0008348; P:GO:0006911; P:GO:0007418; F:GO:0020037; F:GO:0008134; P:GO:0007377; P:GO:0046843; P:GO:0007388; P:GO:0007464; P:GO:0040010; P:GO:0007486; P:GO:0007367; P:GO:0007254; F:GO:0004558; P:GO:0007485; C:GO:0005737; F:GO:0004833; P:GO:0048099;	-	EC:3.2.1.20; EC:1.13.11.11	IPR004981; SSF140959 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	cubn_caeel ame: full=probable cubilin flags: precursor	0		F:GO:0005509		-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0003676		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0003676		IPR003034; G3DSA:1.10.720.30 (GENE3D), PTHR15683 (PANTHER), SSF68906 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0003676		IPR003034; G3DSA:1.10.720.30 (GENE3D), PTHR15683 (PANTHER), SSF68906 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	Hypothetical protein R12B2.2 [Caenorhabditis elegans]	0				-
Loa loa	methyltransferase type 11	0		P:GO:0008610; F:GO:0008168; F:GO:0016740; P:GO:0008152		IPR013216; G3DSA:3.40.50.150 (GENE3D), PTHR10108 (PANTHER), PTHR10108:SF10 (PANTHER), SSF53335 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)

	-	0				-
Caenorhabditis elegans	cral trio domain containing protein	0		P:GO:0040010		PTHR23324 (PANTHER), PTHR23324:SF3 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG20802 [Caenorhabditis briggsae]	0				-
	-	0				IPR010916; PS51450 (PROFILE)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	sodium-independent organic anion transporter family protein	2	P:GO:0055085; C:GO:0016021	-		IPR004156; PTHR11388:SF5 (PANTHER), SignalP (SIGNALP)
Drosophila willistoni	protein phosphatase 2c	1	F:GO:0003824	-		IPR001932; IPR014045; IPR015655
Loa loa	transcription elongation factor	12	C:GO:0000176; P:GO:0032968; C:GO:0005703; F:GO:0008415; C:GO:0005705; P:GO:0040007; P:GO:0040035; P:GO:0007052; P:GO:0002119; F:GO:0003711; C:GO:0005576; P:GO:0009792	-		IPR005100; IPR005824; IPR006645; IPR008991; PTHR11125 (PANTHER)
Loa loa	transcription elongation factor	12	C:GO:0000176; P:GO:0032968; C:GO:0005703; F:GO:0008415; C:GO:0005705; P:GO:0040007; P:GO:0040035; P:GO:0007052; P:GO:0002119; F:GO:0003711; C:GO:0005576; P:GO:0009792	-		IPR005100; IPR005824; IPR006645; IPR008991; IPR022581; PTHR11125 (PANTHER)
Loa loa	transcription elongation factor	12	C:GO:0000176; P:GO:0032968; C:GO:0005703; F:GO:0008415; C:GO:0005705; P:GO:0040007; P:GO:0040035; P:GO:0007052; P:GO:0002119; F:GO:0003711; C:GO:0005576; P:GO:0009792	-		IPR005100; IPR005824; IPR006645; IPR008991; IPR022581; PTHR11125 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-

	-	0				-
Saccoglossus kowalevskii	n -(beta-n-acetylglucosaminyl)-l-asparagi-se	0		C:GO:0005764; F:GO:0003674; F:GO:0003948; F:GO:0016787; P:GO:0008150; C:GO:0005575		-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-tfg-1 protein	0		F:GO:0005515		IPR000270; G3DSA:3.10.20.240 (GENE3D), PTHR15335 (PANTHER), PTHR15335:SF3 (PANTHER), SSF54277 (SUPERFAMILY)
Caenorhabditis elegans	d- polymerase zeta catalytic subunit	5	F:GO:0003887; P:GO:0006260; F:GO:0003677; F:GO:0008408; F:GO:0000166	-	EC:2.7.7.7	IPR006134; IPR017964; PTHR10322 (PANTHER), PTHR10322:SF5 (PANTHER), SSF56672 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-tfg-1 protein	0		F:GO:0005515		IPR000270; G3DSA:3.10.20.240 (GENE3D), PTHR15335 (PANTHER), PTHR15335:SF3 (PANTHER), SSF54277 (SUPERFAMILY)
	-	0				-
Caenorhabditis remanei	carbamoyl-phosphate small subunit	15	P:GO:0006468; P:GO:0006541; F:GO:0005515; F:GO:0004070; F:GO:0016597; F:GO:0004516; C:GO:0005737; F:GO:0004086; P:GO:0060041; F:GO:0003677; P:GO:0006915; F:GO:0016812; F:GO:0004518; P:GO:0006207; F:GO:0005524	-	EC:2.1.3.2; EC:2.4.2.11; EC:3.5.2.0	IPR002474; G3DSA:3.50.30.20 (GENE3D), PTHR11405 (PANTHER), PTHR11405:SF3 (PANTHER)
Caenorhabditis elegans	twik family of potassium channels-related	3	C:GO:0016020; F:GO:0005216; P:GO:0006811	-		IPR013099; G3DSA:1.10.287.70 (GENE3D), PTHR11003 (PANTHER), PTHR11003:SF7 (PANTHER), SignalP (SIGNALP), SSF81324 (SUPERFAMILY)
	-	0				-
	-	0				-
Loa loa	translocase of outer membrane 34	1	F:GO:0005488	-		IPR011989; PTHR22904 (PANTHER), PTHR22904:SF28 (PANTHER), PF11701 (PFAM)
Caenorhabditis elegans	hypothetical protein T19D12.6 [Caenorhabditis elegans]	0				IPR008985; IPR012680; IPR013320
Caenorhabditis sp. PS1010	elegans protein confirmed by transcript evidence	3	P:GO:0006810; C:GO:0016020; F:GO:0005337	-		IPR002259; PTHR10332:SF6 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-

	-	0				-
Loa loa	sh2 domain binding protein	4	C:GO:0016593; P:GO:0010390; P:GO:0033523; F:GO:0042169	-		PTHR14027 (PANTHER), PTHR14027:SF2 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	2	F:GO:0005488; P:GO:0033036	-		IPR001680; IPR011046; IPR015943; PTHR23287 (PANTHER), PTHR23287:SF2 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	2	F:GO:0005488; P:GO:0033036	-		IPR001680; IPR011046; IPR015943; PTHR23287 (PANTHER), PTHR23287:SF2 (PANTHER)
Pongo abelii	c-x-c chemokine receptor 4	32	P:GO:0009615; P:GO:0001764; P:GO:0008354; C:GO:0016023; C:GO:0030426; P:GO:0001667; F:GO:0015026; P:GO:0007204; P:GO:0030334; P:GO:0050920; F:GO:0016493; F:GO:0016494; C:GO:0016021; F:GO:0043130; C:GO:0009986; C:GO:0031252; F:GO:0003779; P:GO:0007420; F:GO:0032027; P:GO:0008045; F:GO:0031625; P:GO:0001666; P:GO:0006915; P:GO:0007281; P:GO:0007186; P:GO:0006954;	-		PTHR19264 (PANTHER), PTHR19264:SF206 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	ys31_caeel ame: full=uncharacterized protein	0				-
	-	0				-
Caenorhabditis elegans	low density lipoprotein receptor associated protein (kd)	0		F:GO:0008201; F:GO:0050750; C:GO:0005783		SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		-
	-	0				-
	-	0				-
	-	0				-

Ailuropoda melanoleuca	eukaryotic translation initiation factor 3 subunit c	6	C:GO:0005852; F:GO:0005515; P:GO:0045948; F:GO:0003743; C:GO:0005829; F:GO:0043022	-		-
	-	0				SignalP (SIGNALP)
Loa loa	jumonji domain containing 5	7	F:GO:0051864; P:GO:0000086; F:GO:0016740; P:GO:0070544; P:GO:0045893; F:GO:0003682; C:GO:0005634	-	EC:1.14.11.27	IPR003347; PTHR12461 (PANTHER), PTHR12461:SF3 (PANTHER), SSF51197 (SUPERFAMILY)
Caenorhabditis elegans	histidine acid phosphatase family protein	5	P:GO:0009792; P:GO:0002119; P:GO:0000003; P:GO:0040007; P:GO:0006898	-		IPR000560; G3DSA:3.40.50.1240 (GENE3D), PTHR11567 (PANTHER), PTHR11567:SF17 (PANTHER), SSF53254 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein F44E7.2 [Caenorhabditis elegans]	2	P:GO:0008152; F:GO:0016791	-	EC:3.1.3.0	PTHR19288 (PANTHER), PTHR19288:SF11 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis remanei	leukotriene a4 hydrolase	5	P:GO:0006954; P:GO:0019370; P:GO:0006508; F:GO:0008270; F:GO:0008237	-		IPR001930; IPR014782; PTHR11533:SF4 (PANTHER), SSF63737 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Loa loa	transcription factor e2f3	0		P:GO:0006355; C:GO:0005667; P:GO:0006350; P:GO:0045449; F:GO:0003677; F:GO:0003700; C:GO:0005634		-
Caenorhabditis elegans	hypothetical protein F35H10.5 [Caenorhabditis elegans]	1	P:GO:0040011	-		IPR018552
Caenorhabditis elegans	e75 nuclear receptor	8	F:GO:0008270; P:GO:0006355; P:GO:0043053; F:GO:0004887; F:GO:0043565; F:GO:0003700; F:GO:0003707; C:GO:0005634	-		IPR001628; IPR008946; IPR013088; PR00350 (PRINTS), PTHR11865 (PANTHER), PTHR11865:SF172 (PANTHER), SSF57716 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)

	-	0				-
	-	0				-
Rattus norvegicus	kdel (lys-asp-glu-leu) endoplasmic reticulum protein retention receptor 1	11	F:GO:0004872; C:GO:0005789; C:GO:0005793; C:GO:0005624; P:GO:0006621; F:GO:0005515; F:GO:0005046; P:GO:0016192; P:GO:0006886; P:GO:0007165; C:GO:0016021	-		-
	-	0				-
Caenorhabditis briggsae	zinc c2h2 type family protein	0		F:GO:0008270; C:GO:0005622		IPR015880
Caenorhabditis briggsae	zinc c2h2 type family protein	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		IPR015880
	-	0				-
	-	0				-
	-	0				IPR007151
	-	0				-
	-	0				-
Pongo abelii	histone-lysine n-methyltransferase setmar	5	F:GO:0046872; P:GO:0006313; F:GO:0016787; F:GO:0008168; F:GO:0004803	-	EC:2.1.1.0	-
	-	0				IPR001372
Caenorhabditis elegans	major facilitator superfamily protein	4	C:GO:0016021; P:GO:0040010; P:GO:0055085; F:GO:0005215	-		PTHR11360 (PANTHER), PTHR11360:SF3 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	syntaxin 16-like isoform 2	2	P:GO:0040010; C:GO:0016020	-		IPR000727; IPR006011; IPR010989; G3DSA:1.20.58.70 (GENE3D), PTHR19957 (PANTHER), PTHR19957:SF5 (PANTHER)
	-	0				-
Caenorhabditis remanei	kinesin family member 13b	5	P:GO:0007018; F:GO:0005515; F:GO:0005524; F:GO:0003777; C:GO:0005874	-		IPR001752; IPR019821; PTHR16012 (PANTHER), PTHR16012:SF65 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	clc-type chloride channel family member (clh-2)	6	P:GO:0009792; F:GO:0005247; P:GO:0055085; P:GO:0000003; C:GO:0016021; P:GO:0006821	-		-

Caenorhabditis remanei	40s ribosomal protein s12	9	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040017; P:GO:0040010; C:GO:0044444; P:GO:0000003; C:GO:0043229; C:GO:0030529	-		SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Homo sapiens	-like protein 2-like	0		F:GO:0003674; P:GO:0008150		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-cpg-4 protein	0		P:GO:0040010		-
	-	0				-
Loa loa	rhomboid family protein	0		F:GO:0004252; F:GO:0005509; C:GO:0016021; P:GO:0007165		SignalP (SIGNALP)
Ascaris suum	hypothetical protein [Ascaris suum]	0		F:GO:0005488		IPR001304; IPR016186; IPR016187; PTHR22802 (PANTHER), PTHR22802:SF17 (PANTHER)
Caenorhabditis elegans	ipase c family member (plc-1)	9	F:GO:0005085; P:GO:0006629; F:GO:0004871; C:GO:0005622; F:GO:0004435; P:GO:0040010; F:GO:0005509; P:GO:0009566; P:GO:0007264	-	EC:3.1.4.11	IPR000159; PTHR10336 (PANTHER), PTHR10336:SF6 (PANTHER), SSF54236 (SUPERFAMILY)

Bos taurus	heat shock 70kda protein 5	30	C:GO:0005793; P:GO:0030433; P:GO:0043154; F:GO:0051087; P:GO:0030512; P:GO:0021680; C:GO:0030176; P:GO:0021589; C:GO:0005788; P:GO:0031398; C:GO:0008303; P:GO:0060904; C:GO:0042470; F:GO:0043027; F:GO:0005509; F:GO:0043022; P:GO:0006983; C:GO:0005576; F:GO:0030674; P:GO:0006916; C:GO:0009986; F:GO:0031625; P:GO:0006987; P:GO:0040019; F:GO:0051082; P:GO:0042149; F:GO:0051787; C:GO:0048471;	-		SignalP (SIGNALP)
Loa loa	elegans protein confirmed by transcript evidence	5	C:GO:0000139; F:GO:0005244; P:GO:0006811; C:GO:0016021; P:GO:0015031	-		IPR015672; PF12430 (PFAM)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein R06A10.4 [Caenorhabditis elegans]	3	P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR020636; PTHR22982:SF12 (PANTHER)
Loa loa	hypothetical protein LOAG_08965 [Loa loa]	0				-
	-	0				-
Caenorhabditis elegans	family with sequence similarity member a	0		P:GO:0007275		PTHR14592 (PANTHER)
Caenorhabditis elegans	family with sequence similarity member a	0		P:GO:0007275		PTHR14592 (PANTHER)
Caenorhabditis elegans	briggsae cbr-lpr-2 protein	2	C:GO:0016021; F:GO:0005488	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-smg-5 protein	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis remanei	elegans protein partially confirmed by transcript evidence	1	C:GO:0016020	-		-
	-	0				-

Callithrix jacchus	valosin-containing protein	27	C:GO:0000785; P:GO:0030433; P:GO:0006919; C:GO:0005792; F:GO:0031593; P:GO:0006302; C:GO:0005730; C:GO:0005829; P:GO:0032436; F:GO:0019904; P:GO:0016567; F:GO:0042802; C:GO:0000502; F:GO:0019903; P:GO:0006888; F:GO:0008289; P:GO:0030970; P:GO:0070842; F:GO:0032403; F:GO:0016887; P:GO:0051260; C:GO:0005783; P:GO:0006200; C:GO:0035101; P:GO:0030968; F:GO:0005524; P:GO:0034214	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	nicotinic acetylcholine receptor alpha subunit 63b	9	P:GO:0009792; F:GO:0004872; P:GO:0002119; C:GO:0045211; C:GO:0030054; P:GO:0006811; C:GO:0016021; P:GO:0040007; F:GO:0004889	-		IPR006201; IPR006202; PTHR18945:SF62 (PANTHER)
	-	0				-
Caenorhabditis remanei	hypothetical protein CRE_25481 [Caenorhabditis remanei]	0				-
Ailuropoda melanoleuca	10 kda heat shock mitochondrial-like	7	P:GO:0006457; F:GO:0051087; F:GO:0005524; C:GO:0005759; F:GO:0051082; P:GO:0006986; P:GO:0006919	-		IPR011032; IPR020818
Caenorhabditis elegans	hypothetical protein R148.5 [Caenorhabditis elegans]	1	F:GO:0005515	-		-
Caenorhabditis remanei	variable abnormal morphology family member (vab-10)	0				-
Macaca mulatta	polyglutamine binding protein 1	5	C:GO:0005737; F:GO:0003713; C:GO:0005730; F:GO:0003677; P:GO:0006355	-		PTHR21737 (PANTHER), PTHR21737:SF3 (PANTHER)
	-	0				-
Loa loa	variant sh3 domain containing protein	1	F:GO:0005515	-		-

Caenorhabditis briggsae	Hypothetical protein CBG02977 [Caenorhabditis briggsae]	0		C:GO:0016021; C:GO:0016020; P:GO:0055085; P:GO:0009792; P:GO:0002119; P:GO:0040007; F:GO:0005215; P:GO:0006810		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0005488	-		IPR001079; IPR008985; IPR013320; PTHR11346:SF2 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis remanei	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	cell death abnormality family member (ced-4)	13	C:GO:0005829; P:GO:0043281; P:GO:0043065; C:GO:0005625; C:GO:0005739; F:GO:0051434; C:GO:0005624; P:GO:0008361; F:GO:0005524; F:GO:0051432; C:GO:0048471; P:GO:0043066; C:GO:0005634	-		IPR002182
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	d- topoisomerase ii	8	F:GO:0003700; F:GO:0016491; F:GO:0003918; P:GO:0055114; F:GO:0005524; C:GO:0005694; P:GO:0006265; P:GO:0006355	-	EC:5.99.1.3	IPR001241; IPR003594; PTHR10169 (PANTHER), PTHR10169:SF2 (PANTHER)
Loa loa	acetyltransferase [Loa loa]	0				PTHR12461 (PANTHER), PTHR12461:SF3 (PANTHER), SignalP (SIGNALP)
Pongo abelii	transmembrane channel-like protein 6	2	C:GO:0016021; C:GO:0005789	-		PTHR23302 (PANTHER), PTHR23302:SF4 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-

Harpegnathos saltator	s-adenosylmethionine synthetase	12	P:GO:0040010; P:GO:0008340; F:GO:0004478; P:GO:0000003; P:GO:0006556; P:GO:0006730; F:GO:0005524; F:GO:0000287; P:GO:0040011; C:GO:0005737; P:GO:0040015; P:GO:0040018	-	EC:2.5.1.6	IPR002133; IPR022628; IPR022636; G3DSA:3.30.300.10 (GENE3D)
Caenorhabditis elegans	s-adenosylmethionine synthetase	17	P:GO:0040010; P:GO:0008340; C:GO:0016021; F:GO:0004478; P:GO:0040035; P:GO:0032940; P:GO:0006556; P:GO:0006730; F:GO:0005524; P:GO:0019915; P:GO:0002119; F:GO:0000287; P:GO:0040017; P:GO:0002009; C:GO:0005737; P:GO:0040015; P:GO:0040018	-	EC:2.5.1.6	IPR002133; IPR022628; IPR022629; IPR022630; IPR022631; IPR022636; G3DSA:3.30.300.10 (GENE3D)
Caenorhabditis elegans	s-adenosylmethionine synthetase	17	P:GO:0040010; P:GO:0008340; C:GO:0016021; F:GO:0004478; P:GO:0040035; P:GO:0032940; P:GO:0006556; P:GO:0006730; F:GO:0005524; P:GO:0019915; P:GO:0002119; F:GO:0000287; P:GO:0040017; P:GO:0002009; C:GO:0005737; P:GO:0040015; P:GO:0040018	-	EC:2.5.1.6	IPR002133; IPR022628; IPR022629; IPR022630; IPR022631; IPR022636; G3DSA:3.30.300.10 (GENE3D)

Caenorhabditis elegans	s-adenosylmethionine synthetase	17	P:GO:0040010; P:GO:0008340; C:GO:0016021; F:GO:0004478; P:GO:0040035; P:GO:0032940; P:GO:0006556; P:GO:0006730; F:GO:0005524; P:GO:0019915; P:GO:0002119; F:GO:0000287; P:GO:0040017; P:GO:0002009; C:GO:0005737; P:GO:0040015; P:GO:0040018	-	EC:2.5.1.6	IPR002133; IPR022628; IPR022629; IPR022630; IPR022631; IPR022636; G3DSA:3.30.300.10 (GENE3D)
Caenorhabditis elegans	s-adenosylmethionine synthetase	17	P:GO:0040010; P:GO:0008340; C:GO:0016021; F:GO:0004478; P:GO:0040035; P:GO:0032940; P:GO:0006556; P:GO:0006730; F:GO:0005524; P:GO:0019915; P:GO:0002119; F:GO:0000287; P:GO:0040017; P:GO:0002009; C:GO:0005737; P:GO:0040015; P:GO:0040018	-	EC:2.5.1.6	IPR002133; IPR022628; IPR022629; IPR022630; IPR022631; IPR022636; G3DSA:3.30.300.10 (GENE3D)
	-	0				-
	-	0				PTHR16012 (PANTHER), PTHR16012:SF14 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis remanei	hypothetical protein CRE_01961 [Caenorhabditis remanei]	0				IPR008559; SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	vacuolar proton	4	F:GO:0015078; C:GO:0033177; P:GO:0015986; F:GO:0016787	-		IPR002490; PTHR11629:SF1 (PANTHER)
	-	0				-
	-	0				IPR001254; G3DSA:2.40.10.10 (GENE3D)

Homo sapiens	n-termi-l ki-se-like protein	12	C:GO:0005815; C:GO:0030126; P:GO:0006890; C:GO:0005793; P:GO:0045449; F:GO:0003677; F:GO:0004713; F:GO:0005524; F:GO:0005515; C:GO:0005801; C:GO:0005634; P:GO:0006468	-	EC:2.7.10.0	SignalP (SIGNALP)
Brugia malayi	hypothetical protein Bm1_43075 [Brugia malayi]	0				-
Caenorhabditis remanei	suclg2 protein	4	P:GO:0009792; P:GO:0008152; F:GO:0005524; F:GO:0003824	-		IPR005809; IPR013650; SSF56059 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	phosphatidylglycerophosphate synthase 1	2	F:GO:0016740; C:GO:0005783	-		G3DSA:3.30.870.10 (GENE3D), PTHR12586 (PANTHER)
	-	0				-
Caenorhabditis remanei	hypothetical protein CRE_01767 [Caenorhabditis remanei]	4	F:GO:0020037; P:GO:0055114; F:GO:0004601; P:GO:0006979	-	EC:1.11.1.7	IPR002007; IPR010255; PTHR11475 (PANTHER), PTHR11475:SF6 (PANTHER)
Loa loa	family protein	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein C27A12.9 [Caenorhabditis elegans]	0		P:GO:0008152; F:GO:0003824		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	prolyl 4-hydroxylase	6	F:GO:0031418; F:GO:0005506; F:GO:0004656; P:GO:0055114; F:GO:0016702; C:GO:0005783	-	EC:1.14.11.2 ; EC:1.13.11.0	PTHR10869 (PANTHER), PTHR10869:SF13 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	2	C:GO:0005622; F:GO:0005525	-		-
Caenorhabditis remanei	elegans protein partially confirmed by transcript evidence	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-sas-6 protein	0		C:GO:0005737; P:GO:0007049; C:GO:0005856; P:GO:0007275; F:GO:0005515; C:GO:0005814		-
Angiostrongylus cantonensis	15 kda selenoprotein	0		C:GO:0005788; C:GO:0005783		-
Monodelphis domestica	protein	0				-
	-	0				-
	-	0				-

Caenorhabditis remanei	elegans protein confirmed by transcript evidence	3	F:GO:0003951; F:GO:0005515; P:GO:0008152	-	EC:2.7.1.23	SignalP (SIGNALP)
Caenorhabditis remanei	elegans protein partially confirmed by transcript evidence	1	P:GO:0044238	-		IPR002213; G3DSA:3.40.50.2000 (GENE3D), PTHR11926:SF3 (PANTHER), SSF53756 (SUPERFAMILY)
Caenorhabditis briggsae	methuselah-like protein mth-2	2	P:GO:0007218; C:GO:0016020	-		IPR010916
Caenorhabditis elegans	cre-npr-19 protein	2	P:GO:0007186; C:GO:0016021	-		IPR000276; IPR017452; G3DSA:1.20.1070.10 (GENE3D), PTHR22718 (PANTHER), PTHR22718:SF8 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	guanylyl cyclase family member (gcy-5)	0		C:GO:0016021; F:GO:0004674; F:GO:0004383; F:GO:0004672; P:GO:0009190; P:GO:0006182; P:GO:0023034; P:GO:0006468; F:GO:0000166; F:GO:0005524; F:GO:0016829; F:GO:0016849		-
Caenorhabditis remanei	hypothetical protein CRE_01591 [Caenorhabditis remanei]	0				-
Caenorhabditis briggsae	-d dependent epimerase dehydratase	4	F:GO:0050662; P:GO:0051246; F:GO:0019787; P:GO:0043687	-		IPR001509; IPR016040; PTHR10366 (PANTHER), PTHR10366:SF25 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis briggsae	-d dependent epimerase dehydratase	4	F:GO:0050662; P:GO:0051246; F:GO:0019787; P:GO:0043687	-		IPR001509; IPR016040; PTHR10366 (PANTHER), PTHR10366:SF25 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				-
Brugia malayi	iq calmodulin-binding motif family protein	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	serpentine class ab (class a-like) family member (srab-14)	3	C:GO:0016021; P:GO:0007606; F:GO:0004888	-		SignalP (SIGNALP)
Caenorhabditis elegans	7 transmembrane	0		F:GO:0016740; F:GO:0004872; F:GO:0004871; F:GO:0004930; C:GO:0016021; P:GO:0007165; F:GO:0050254; P:GO:0007186		-

Homo sapiens	mutant truncated midkine b	9	P:GO:0030154; F:GO:0008083; P:GO:0030325; P:GO:0009611; F:GO:0008201; P:GO:0051781; P:GO:0007399; P:GO:0007165; C:GO:0005576	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	P:GO:0040011; P:GO:0040018	-		IPR000615
Brugia malayi	hepatocellular carcinoma-associated antigen 66	0				IPR013949; PTHR23271 (PANTHER), PTHR23271:SF1 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR001534; SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR19355 (PANTHER), PTHR19355:SF90 (PANTHER)
Caenorhabditis remanei	elegans protein confirmed by transcript evidence	0		C:GO:0016021		-
	-	0				-
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0		F:GO:0008270; C:GO:0005622		-
Caenorhabditis briggsae	adp-ribosylation factor 6	27	P:GO:0016358; C:GO:0055037; P:GO:0031529; P:GO:0007155; F:GO:0031996; P:GO:0040010; C:GO:0005624; P:GO:0006928; F:GO:0005525; C:GO:0005794; P:GO:0006886; C:GO:0001726; P:GO:0009792; P:GO:0006915; C:GO:0005769; P:GO:0048261; P:GO:0007186; P:GO:0035020; C:GO:0012505; P:GO:0030838; P:GO:0001889; F:GO:0003924; P:GO:0030866; C:GO:0005886; C:GO:0005634; C:GO:0010008; C:GO:0005938	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR005225; IPR006688; IPR006689; G3DSA:3.40.50.300 (GENE3D), PTHR11711:SF30 (PANTHER), PS51417 (PROFILE), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)

	-	0				-
Caenorhabditis remanei	hypothetical protein CRE_07374 [Caenorhabditis remanei]	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	related to the icc protein	0		F:GO:0003674; F:GO:0016787; P:GO:0008150; C:GO:0005575		PTHR12905 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	- ca exchangers family member (ncx-2)	12	P:GO:0055085; F:GO:0005432; P:GO:0040010; C:GO:0016021; P:GO:0001947; P:GO:0000003; P:GO:0006816; P:GO:0007368; P:GO:0007154; P:GO:0009792; P:GO:0051480; P:GO:0042044	-		PTHR11878 (PANTHER), PTHR11878:SF4 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	methyltransferase-like protein 13	2	F:GO:0005515; F:GO:0003824	-		IPR001045; G3DSA:3.40.50.150 (GENE3D), PTHR12176 (PANTHER), SSF53335 (SUPERFAMILY)
	-	0				IPR002619
	-	0				-
Caenorhabditis remanei	hypothetical protein CRE_04697 [Caenorhabditis remanei]	0		P:GO:0016311; F:GO:0016791; F:GO:0016787; P:GO:0006470; F:GO:0004725; F:GO:0008138; P:GO:0009792; F:GO:0004721		IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER)
	-	0				-
Homo sapiens	major histocompatibility class dq beta 1	14	C:GO:0005789; C:GO:0005769; C:GO:0042613; C:GO:0005771; C:GO:0005794; P:GO:0019886; F:GO:0005515; C:GO:0009897; C:GO:0005765; C:GO:0016021; F:GO:0032395; C:GO:0010008; P:GO:0006955; F:GO:0042605	-		PTHR19944 (PANTHER), PTHR19944:SF26 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	sluggish isoform e	5	F:GO:0004657; P:GO:0006537; P:GO:0042331; C:GO:0005759; P:GO:0006562	-	EC:1.5.99.8	-

Caenorhabditis elegans	periodic tryptophan protein 2 homolog	0		F:GO:0004252; C:GO:0016021; C:GO:0016020; C:GO:0005634; P:GO:0007165; C:GO:0005730; P:GO:0006508; F:GO:0004871; P:GO:0055085		IPR007148; PTHR19858 (PANTHER)
	-	0				-
Ancylostoma caninum	metalloprotease 1 precursor	0		F:GO:0046872; P:GO:0006508; F:GO:0008237; F:GO:0016787; F:GO:0004222; F:GO:0008233; F:GO:0008270		-
	-	0				-
Danio rerio	desmocollin 2-like	0		F:GO:0004872; C:GO:0016021; P:GO:0007596		PTHR14360 (PANTHER), PTHR14360:SF2 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	-dph:adrenodoxin mitochondrial	1	P:GO:0008152	-		IPR016040; PTHR11938 (PANTHER), PTHR11938:SF4 (PANTHER)
Caenorhabditis remanei	alpha 1	15	P:GO:0030155; P:GO:0060441; P:GO:0060445; P:GO:0045198; C:GO:0005608; P:GO:0045995; C:GO:0005606; P:GO:0031175; P:GO:0002011; F:GO:0043208; C:GO:0005615; P:GO:0030334; F:GO:0005102; F:GO:0005201; P:GO:0007166	-		IPR008211; PTHR10574 (PANTHER), PTHR10574:SF38 (PANTHER)
Caenorhabditis briggsae	lethal family member (let-805)	0		P:GO:0000003; P:GO:0018996; P:GO:0040011; P:GO:0006898; P:GO:0002119; P:GO:0008340; P:GO:0009792; F:GO:0005515		PTHR19143 (PANTHER), PTHR19143:SF2 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	amop domain containing protein	2	C:GO:0016021; P:GO:0007160	-		IPR003886; PTHR13802 (PANTHER), PTHR13802:SF2 (PANTHER)
Caenorhabditis elegans	hypothetical protein T23B12.11 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0008152; F:GO:0003824		SignalP (SIGNALP)

Brugia malayi	eb module family protein	0		F:GO:0004674; F:GO:0016810; F:GO:0004672; P:GO:0006468; F:GO:0000166; F:GO:0005524; P:GO:0005975; F:GO:0003824; F:GO:0005488		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Homo sapiens	immunoglobulin lambda light chain variable region vl3	0				IPR013783; PTHR23267 (PANTHER), PTHR23267:SF14 (PANTHER), SignalP (SIGNALP), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	carbamoyl-phosphate synthetase	7	P:GO:0006541; F:GO:0016812; F:GO:0016597; F:GO:0004086; F:GO:0005524; P:GO:0006207; F:GO:0004070	-	EC:3.5.2.0; EC:2.1.3.2	-
	-	0				IPR021843
Caenorhabditis briggsae	Hypothetical protein CBG19248 [Caenorhabditis briggsae]	1	F:GO:0008289	-		SignalP (SIGNALP)
Homo sapiens	cytochrome b5 reductase 3	7	F:GO:0004128; C:GO:0005789; P:GO:0008015; C:GO:0005833; P:GO:0055114; P:GO:0006695; C:GO:0005741	-	EC:1.6.2.2	G3DSA:3.40.50.80 (GENE3D), PTHR19370 (PANTHER), PTHR19370:SF4 (PANTHER), SSF52343 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	solute carrier family 25 (mitochondrial carrier phosphate carrier) member 23	9	C:GO:0005743; P:GO:0055085; P:GO:0055114; F:GO:0005509; P:GO:0007165; C:GO:0016021; C:GO:0005578; F:GO:0032440; F:GO:0005215	-	EC:1.3.1.74	IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF34 (PANTHER)
	-	0				-
Homo sapiens	-dh dehydroge-se	5	P:GO:0006120; P:GO:0007605; F:GO:0008137; P:GO:0006810; C:GO:0005747	-	EC:1.6.5.3	PTHR12868 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)

Loa loa	briggsae cbr-cdh-1 protein	0		C:GO:0016021; C:GO:0016020; P:GO:0002119; P:GO:0040011; P:GO:0040010; F:GO:0005509; C:GO:0005886; P:GO:0007156; P:GO:0007155		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	c termi-l region family protein	9	F:GO:0046872; P:GO:0006457; P:GO:0007224; F:GO:0031072; F:GO:0005113; F:GO:0005524; F:GO:0051082; C:GO:0005829; P:GO:0009408	-		IPR001305; IPR001623; IPR001878; IPR002939; IPR003095; IPR008971; IPR015609; IPR018253; G3DSA:2.60.260.20 (GENE3D), PTHR11821:SF80 (PANTHER)
	-	0				IPR019265; PTHR15924 (PANTHER), PTHR15924:SF9 (PANTHER)
	-	0				IPR001245; G3DSA:3.30.200.20 (GENE3D)
Pan troglodytes	chromosome 1 open reading frame 43	3	F:GO:0016491; C:GO:0016021; F:GO:0050662	-		IPR010876
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0055114; F:GO:0005488; F:GO:0016491; P:GO:0008152; F:GO:0003824		IPR002198; PTHR19410:SF18 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	kiaa1143 homolog	0		F:GO:0003674; P:GO:0008150		-
Caenorhabditis briggsae	kiaa1143 homolog	0		F:GO:0003674; P:GO:0008150		-
	-	0				-
	-	0				-
Brugia malayi	mast c-terminus family protein	1	F:GO:0005488	-		PTHR21567 (PANTHER), PTHR21567:SF10 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis remanei	- h exchanger family member (nhx-9)	6	P:GO:0009792; F:GO:0015385; P:GO:0055085; P:GO:0006885; C:GO:0016021; P:GO:0006814	-		IPR006153; IPR018416; IPR018422; SignalP (SIGNALP)

Caenorhabditis elegans	malate dehydroge-se	4	P:GO:0018991; P:GO:0008152; F:GO:0016491; P:GO:0040011	-		IPR018486; SignalP (SIGNALP)
Ancylostoma caninum	secreted protein 4 precursor	0		C:GO:0005576		IPR001283; IPR014044; PTHR10334:SF11 (PANTHER), SignalP (SIGNALP)
Homo sapiens	kallikrein related-peptidase 6 precursor	17	P:GO:0042552; P:GO:0007417; P:GO:0042445; C:GO:0005739; C:GO:0005730; P:GO:0042982; P:GO:0016540; P:GO:0006508; C:GO:0005792; F:GO:0005515; P:GO:0045745; P:GO:0010975; F:GO:0004252; C:GO:0005576; P:GO:0030574; C:GO:0005783; P:GO:0042246	-	EC:3.4.21.0	-
	-	0				-
Loa loa	histone deacetylase complex subunit	8	C:GO:0071011; P:GO:0032582; P:GO:0000122; P:GO:0006342; F:GO:0003714; P:GO:0000398; C:GO:0071013; C:GO:0016580	-		-

Loa loa	egf-like domain containing protein	0		P:GO:0030718; P:GO:0008360; P:GO:0016477; P:GO:0007517; P:GO:0016339; P:GO:0007157; C:GO:0016021; P:GO:0007608; P:GO:0007155; C:GO:0016020; P:GO:0035160; P:GO:0008340; P:GO:0007494; C:GO:0005925; F:GO:0050839; F:GO:0004872; P:GO:0007275; P:GO:0007417; P:GO:0035099; F:GO:0005488; P:GO:0016340; P:GO:0007475; P:GO:0016203; P:GO:0007411; P:GO:0007160; P:GO:0007229; P:GO:0007391;		IPR001169; PTHR10082:SF5 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	4	C:GO:0016021; F:GO:0008271; P:GO:0008272; P:GO:0055085	-		IPR011547; PTHR11814 (PANTHER), PTHR11814:SF25 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis remanei	elegans protein partially confirmed by transcript evidence	2	F:GO:0005506; P:GO:0040010	-		IPR001128; PTHR19383:SF176 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	ysyf_caeel ame: full=uncharacterized f-box protein	0				-
	-	0				-
Caenorhabditis briggsae	n -(beta-n-acetylglucosaminyl)-l-asparagi-se	1	F:GO:0016787	-		IPR000246; PTHR10188:SF6 (PANTHER), SignalP (SIGNALP), SSF56235 (SUPERFAMILY)
	-	0				-
Cooperia punctata	af352702_1activation associated secreted protein	0		C:GO:0005576		-
	-	0				-
	-	0				-
Strongylocentrotus purpuratus	lipase maturation factor 2	1	C:GO:0016020	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis remanei	fumarylacetoacetate hydrolase domain containing 1	6	P:GO:0009792; P:GO:0002119; C:GO:0005743; P:GO:0008152; P:GO:0040007; F:GO:0003824	-		IPR002529; IPR011234; PTHR11820 (PANTHER), PTHR11820:SF7 (PANTHER)
Homo sapiens	endoglin	37	P:GO:0001300; F:GO:0042803; P:GO:0010552; P:GO:0030512; F:GO:0005114; P:GO:0070278; P:GO:0048745; P:GO:0030513; P:GO:0051001; F:GO:0005534; P:GO:0010862; C:GO:0005615; P:GO:0001947; P:GO:0003084; F:GO:0005539; P:GO:0031960; P:GO:0042060; P:GO:0001937; P:GO:0030155; P:GO:0048844; P:GO:0031953; C:GO:0009897; P:GO:0022617; F:GO:0005024; P:GO:0001569; C:GO:0070022; F:GO:0050431;	-		PTHR14002 (PANTHER), PTHR14002:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	serine threonine protein ki-se	1	F:GO:0005488	-		G3DSA:3.40.50.300 (GENE3D), PTHR22908 (PANTHER), PTHR22908:SF13 (PANTHER)
	-	0				-
Ciona intestinalis	eukaryotic translation initiation factor subunit 10	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Loa loa	briggsae cbr-sec-3 protein	0		P:GO:0000003; P:GO:0040011; P:GO:0040010; F:GO:0005515; P:GO:0007126		IPR019160
	-	0				-
Loa loa	hypothetical protein LOAG_07407 [Loa loa]	0				-
Bombyx mori	endonuclease-reverse transcriptase	0		F:GO:0003723; P:GO:0006278; F:GO:0004519; F:GO:0003964		-

Homo sapiens	complement c1r subcomponent precursor	6	F:GO:0004252; P:GO:0045087; F:GO:0005509; P:GO:0006958; C:GO:0005576; P:GO:0006508	-	EC:3.4.21.0	-
Caenorhabditis elegans	glutamyl-tr- amidotransferase subunit a	4	P:GO:0019915; P:GO:0006412; F:GO:0050567; F:GO:0016740	-	EC:3.6.5.3; EC:6.3.5.7	IPR000120; PTHR11895:SF7 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Loa loa	olfactomedin-like domain containing protein	0				PTHR23192 (PANTHER), PTHR23192:SF6 (PANTHER)
Brugia malayi	hypothetical kda protein in chromosome	0				-
	-	0				-
Caenorhabditis elegans	mgc80013 protein	0				PTHR22774 (PANTHER), PTHR22774:SF5 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	adenylate cyclase type	12	P:GO:0006952; P:GO:0008219; C:GO:0016021; F:GO:0004016; P:GO:0007188; P:GO:0009190; P:GO:0042221; P:GO:0002119; P:GO:0040017; F:GO:0000166; C:GO:0005886; P:GO:0030431	-	EC:4.6.1.1	IPR001054; PTHR11920 (PANTHER), PTHR11920:SF10 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-rhr-1 protein	0		C:GO:0016021; C:GO:0016020; F:GO:0008519; P:GO:0055085; P:GO:0009792; P:GO:0006810		IPR001905; G3DSA:1.10.3430.10 (GENE3D), PTHR11883 (PANTHER), PTHR11883:SF6 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	zinc c2h2 type family protein	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		IPR007087; IPR013087; IPR015880
Caenorhabditis elegans	related to yeast vacuolar protein sorting factor family member (vps-41)	13	C:GO:0005829; C:GO:0030897; P:GO:0007034; P:GO:0040007; P:GO:0006624; C:GO:0005624; P:GO:0002119; F:GO:0005515; P:GO:0048193; P:GO:0009792; P:GO:0043066; C:GO:0005798; P:GO:0015031	-		IPR011990; IPR016024; IPR019453; PTHR12616 (PANTHER), PF00637 (PFAM)
	-	0				-
	-	0				-

Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		SignalP (SIGNALP)
Homo sapiens	transmembrane protein 66	1	C:GO:0016021	-		IPR009567
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Pongo abelii	heterogeneous nuclear ribonucleoprotein l	9	C:GO:0005737; P:GO:0008380; C:GO:0030530; C:GO:0005654; C:GO:0045120; F:GO:0003723; F:GO:0005515; P:GO:0006397; F:GO:0000166	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	enhancer of unc-40 ventral axon guidance defects family member (eva-1)	0		F:GO:0005529		-
Caenorhabditis elegans	enhancer of unc-40 ventral axon guidance defects family member (eva-1)	0		F:GO:0005529		-
Caenorhabditis remanei	integrin alpha-8 precursor	11	P:GO:0009792; F:GO:0004872; P:GO:0002119; P:GO:0007229; P:GO:0018991; P:GO:0032940; P:GO:0007155; P:GO:0040007; P:GO:0006898; P:GO:0040039; C:GO:0008305	-		PTHR23220 (PANTHER), PTHR23220:SF11 (PANTHER)
	-	0				-
Caenorhabditis elegans	paps (adenosine 3 -phosphate 5 -phosphosulfate) transporter family member (pst-1)	2	P:GO:0055085; C:GO:0016021	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				IPR006210; IPR013032; G3DSA:2.10.25.10 (GENE3D)
Homo sapiens	lysosomal multispanning membrane protein 5	3	C:GO:0005887; C:GO:0005765; P:GO:0006810	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		-
Caenorhabditis elegans	briggsae cbr-hhat-1 protein	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F43D9.1 [Caenorhabditis elegans]	2	F:GO:0008158; C:GO:0016020	-		PTHR10796 (PANTHER), PTHR10796:SF13 (PANTHER)
	-	0				-

Ancylostoma caninum	activin a type i	26	P:GO:0006468; P:GO:0048332; F:GO:0005515; P:GO:0046588; P:GO:0009952; P:GO:0035124; P:GO:0048264; P:GO:0001944; P:GO:0035162; C:GO:0070724; P:GO:0051216; F:GO:0005024; P:GO:0042475; P:GO:0003230; P:GO:0001947; P:GO:0060030; P:GO:0007420; P:GO:0007368; P:GO:0021556; P:GO:0051260; P:GO:0001889; P:GO:0003146; F:GO:0005524; P:GO:0030510; P:GO:0048368; C:GO:0005938	-		-
	-	0				-
	-	0				-
Caenorhabditis remanei	nuclear hormone receptor family member (nhr-105)	7	F:GO:0042802; F:GO:0003700; F:GO:0043565; F:GO:0003707; C:GO:0005634; F:GO:0008270; P:GO:0006355	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Micromonas pusilla CCMP1545	protein	0				-
Caenorhabditis briggsae	Hypothetical protein CBG00701 [Caenorhabditis briggsae]	0				-
Brugia malayi	3 5 -cyclic nucleotide phosphodiesterase family protein	1	F:GO:0016787	-		-
Caenorhabditis elegans	kelch domain containing 10	0		F:GO:0003674; F:GO:0005515; C:GO:0005575		IPR006652; IPR015915; PTHR23244 (PANTHER), PTHR23244:SF35 (PANTHER), SSF117281 (SUPERFAMILY)

Caenorhabditis briggsae	laminin a	12	P:GO:0007411; P:GO:0016321; P:GO:0007498; P:GO:0031987; P:GO:0050789; P:GO:0001964; P:GO:0048854; P:GO:0007507; C:GO:0005605; P:GO:0007155; P:GO:0002121; P:GO:0009790	-		IPR002049; IPR013032; G3DSA:2.10.25.10 (GENE3D), PTHR10574 (PANTHER), PTHR10574:SF56 (PANTHER), SSF57196 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-haf-6 protein	4	F:GO:0042626; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		PTHR19242 (PANTHER), PTHR19242:SF77 (PANTHER), SignalP (SIGNALP)
	-	0				-
Loa loa	cleavage and polyadenylation specific factor 73kda	0		F:GO:0016787		IPR021718; PTHR11203 (PANTHER), PTHR11203:SF11 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	pyruvate carboxylase	10	P:GO:0006107; F:GO:0004736; C:GO:0005625; C:GO:0005743; F:GO:0009374; P:GO:0009252; F:GO:0005524; P:GO:0006094; C:GO:0005759; F:GO:0008716	-	EC:6.4.1.1; EC:6.3.2.4	IPR000089; IPR011053; G3DSA:2.40.50.100 (GENE3D), G3DSA:3.10.600.10 (GENE3D), PTHR18866 (PANTHER), PTHR18866:SF10 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	c2 domain containing protein	0		F:GO:0003674; C:GO:0008021; C:GO:0016020; P:GO:0008150; F:GO:0005215; P:GO:0006810		-
	-	0				-
	-	0				-
	-	0				-
Pinus koraiensis	ORF124 [Pinus koraiensis]	1	C:GO:0009507	-		-
	-	0				-
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	2	F:GO:0008270; F:GO:0005515	-		IPR000253; IPR008984; IPR013083; SSF57850 (SUPERFAMILY)
	-	0				IPR000253; IPR008984
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	2	F:GO:0008270; F:GO:0005515	-		IPR000253; IPR008984; IPR013083; SSF57850 (SUPERFAMILY)
Angiostrongylus cantonensis	si:dkey- protein	1	F:GO:0046872	-		-
	-	0				IPR000253; IPR008984

Caenorhabditis briggsae	polymerase (d- directed) alpha 2 (70kd subunit)	6	P:GO:0040007; P:GO:0002119; F:GO:0005515; C:GO:0044428; P:GO:0002009; P:GO:0009792	-		-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0008152; F:GO:0003824		G3DSA:3.40.50.980 (GENE3D)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis remanei	der1-like domain member 2	6	P:GO:0030433; C:GO:0030176; P:GO:0030968; P:GO:0030970; P:GO:0030307; P:GO:0008284	-		-
Caenorhabditis elegans	hed family member (ptc-3)	7	P:GO:0018996; C:GO:0016020; P:GO:0009792; P:GO:0040018; P:GO:0000003; P:GO:0002119; P:GO:0040011	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis brenneri	elegans protein confirmed by transcript evidence	0				-
Schizosaccharomyces japonicus yFS275	cysteine string protein	4	P:GO:0006457; F:GO:0046872; F:GO:0051082; F:GO:0031072	-		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	7	P:GO:0040035; P:GO:0009792; P:GO:0018991; F:GO:0005515; C:GO:0016607; P:GO:0040011; P:GO:0006898	-		IPR018482
Caenorhabditis briggsae	tata-binding protein-associated factor mot1	0		F:GO:0004386; F:GO:0003676; F:GO:0005524; F:GO:0005488; F:GO:0003677		IPR000330; PTHR10799 (PANTHER), PTHR10799:SF72 (PANTHER)
Caenorhabditis remanei	aldo keto reductase family protein	6	P:GO:0009792; P:GO:0055114; F:GO:0016491; P:GO:0040010; P:GO:0002119; P:GO:0040011	-		IPR001395; IPR018170; IPR020471; IPR023210; PTHR11732:SF34 (PANTHER)
	-	0				-
Caenorhabditis remanei	briggsae cbr-sqv-8 protein	0		F:GO:0016740; C:GO:0016020; F:GO:0015018; F:GO:0016757		-

Homo sapiens	protein tyrosine receptor f	22	P:GO:0050775; P:GO:0001960; P:GO:0007185; P:GO:0042059; P:GO:0050803; C:GO:0030426; F:GO:0005001; F:GO:0030971; C:GO:0005792; P:GO:0043525; F:GO:0042301; P:GO:0008285; C:GO:0043025; P:GO:0007156; C:GO:0060076; P:GO:0051387; C:GO:0005768; P:GO:0006470; P:GO:0046627; C:GO:0005887; P:GO:0031345; F:GO:0005158	-		-
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	hypothetical protein Bm1_26975 [Brugia malayi]	0				-
Caenorhabditis elegans	calmodulin	1	F:GO:0005509	-		IPR011992; PTHR23050 (PANTHER), PTHR23050:SF7 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	leucyl tr- synthetase family member (lrs-2)	2	F:GO:0016874; P:GO:0006412	-	EC:3.6.5.3	IPR002302; PTHR11946 (PANTHER)
	-	0				-
	-	0				PTHR14167 (PANTHER), PTHR14167:SF2 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	mitochondrial 28s ribosomal protein s28	1	P:GO:0000003	-		-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				PTHR12187 (PANTHER), PTHR12187:SF2 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis remanei	elegans protein confirmed by transcript evidence	1	P:GO:0019915	-		-
Caenorhabditis elegans	hypothetical protein Y69A2AR.16 [Caenorhabditis elegans]	0		P:GO:0055114; F:GO:0005488; F:GO:0016491		PTHR12596 (PANTHER), PTHR12596:SF3 (PANTHER), SignalP (SIGNALP)

Brugia malayi	integrator complex subunit 5	0		F:GO:0005215; C:GO:0016021; C:GO:0016020; P:GO:0016180; C:GO:0032039; P:GO:0006810; F:GO:0003674; C:GO:0005575; P:GO:0055085; P:GO:0008150		-
Brugia malayi	integrator complex subunit 5	0		F:GO:0005215; C:GO:0016021; C:GO:0016020; P:GO:0016180; C:GO:0032039; P:GO:0006810; F:GO:0003674; C:GO:0005575; P:GO:0055085; P:GO:0008150		-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG12852 [Caenorhabditis briggsae]	0		P:GO:0006412; P:GO:0009408		-
Caenorhabditis briggsae	feline leukemia virus subgroup c receptor-related protein 1	4	P:GO:0055085; P:GO:0040011; C:GO:0016021; P:GO:0007413	-		-
	-	0				-
Caenorhabditis remanei	noc3l_caeel ame: full=nucleolar complex protein 3 homolog short=noc3 protein homolog ame: full=noc3-like protein ame: full=nucleolar complex-associated protein 3-like protein	0		C:GO:0005634; C:GO:0005730		-
Nyctotherus ovalis	adp atp translocase	5	F:GO:0005488; C:GO:0005743; P:GO:0055085; C:GO:0016021; F:GO:0005215	-		-
Caenorhabditis elegans	myosin heavy chain	4	C:GO:0032982; F:GO:0003779; F:GO:0005524; F:GO:0003774	-		IPR015650; PTHR13140 (PANTHER)
	-	0				-
	-	0				-
						IPR003961; IPR008957; IPR013783; PR00014 (PRINTS), PTHR19900 (PANTHER), PTHR19900:SF7 (PANTHER)
	-	0				SignalP (SIGNALP)
NADP, mitochondrial isoform 3	isocitrate dehydroge-se	9	P:GO:0006097; P:GO:0006103; C:GO:0005743; P:GO:0055114; P:GO:0006099; F:GO:0051287; F:GO:0004450; F:GO:0000287; P:GO:0006102	-	EC:1.1.1.42	-
	-	0				-

	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	ck1 ttbk protein ki-se	0				IPR017441
	-	0				IPR015880; PTHR10071 (PANTHER), PTHR10071:SF5 (PANTHER)
Homo sapiens	lysosomal-associated membrane protein 1	9	C:GO:0005887; C:GO:0005624; C:GO:0005771; C:GO:0042383; C:GO:0042470; C:GO:0009897; C:GO:0005765; C:GO:0010008; P:GO:0006914	-		-
Caenorhabditis briggsae	abc1 protein	0				PTHR10566 (PANTHER)
Caenorhabditis briggsae	heat shock protein family member (hsp-)	26	P:GO:0006457; P:GO:0042542; C:GO:0032432; P:GO:0043010; C:GO:0000267; C:GO:0015630; P:GO:0007568; P:GO:0006936; C:GO:0005794; P:GO:0006916; C:GO:0009986; P:GO:0031109; C:GO:0031674; F:GO:0008017; P:GO:0030308; P:GO:0006006; F:GO:0051082; P:GO:0019222; P:GO:0032387; F:GO:0042803; P:GO:0051260; C:GO:0005634; P:GO:0032355; P:GO:0006800; P:GO:0051403; F:GO:0005212	-		IPR001436; IPR002068; IPR008978; G3DSA:2.60.40.790 (GENE3D), PTHR11527 (PANTHER), PTHR11527:SF34 (PANTHER)
	-	0				-
	-	0				-
Brugia malayi	ccr4-not transcription complex	1	P:GO:0048731	-		PTHR13162 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	4	P:GO:0055114; P:GO:0006952; F:GO:0016491; F:GO:0005488	-		IPR002198; IPR016040; PTHR19410:SF18 (PANTHER), SSF51735 (SUPERFAMILY)

Homo sapiens	milk fat globule-egf factor 8 protein	17	P:GO:0001525; P:GO:0006910; F:GO:0008429; C:GO:0009897; P:GO:0043627; P:GO:0050766; C:GO:0005615; P:GO:0006911; P:GO:0007155; F:GO:0005178; F:GO:0001786; C:GO:0031012; P:GO:0044419; P:GO:0008284; C:GO:0005737; C:GO:0019897; P:GO:0007338	-		IPR000421; IPR008979; G3DSA:2.60.120.260 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF28 (PANTHER)
Brugia malayi	expressed sequence ai841794-like	0		P:GO:0030510; F:GO:0005515; C:GO:0005886		IPR001611; IPR003591; G3DSA:3.80.10.10 (GENE3D), PTHR23154 (PANTHER), PTHR23154:SF134 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)
Caenorhabditis briggsae	udp-xylose and udp-n-acetylglucosamine transporter	6	F:GO:0005464; C:GO:0005794; P:GO:0015790; P:GO:0015788; C:GO:0016020; F:GO:0005462	-		IPR013657; PTHR10778 (PANTHER), PTHR10778:SF4 (PANTHER), SignalP (SIGNALP)
Caenorhabditis remanei	elegans protein partially confirmed by transcript evidence	3	F:GO:0004725; P:GO:0006470; F:GO:0008138	-	EC:3.1.3.48	-
	-	0				-
Caenorhabditis elegans	atpase h+ transporting v0 subunit	8	F:GO:0015078; F:GO:0042625; P:GO:0016049; C:GO:0016021; P:GO:0015986; C:GO:0033179; P:GO:0007035; P:GO:0015991	-		IPR008389
						IPR003961; IPR008957; IPR013783; PTHR19900 (PANTHER), PTHR19900:SF7 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	phosphoserine aminotransferase	5	F:GO:0030170; F:GO:0004648; P:GO:0051188; P:GO:0006564; P:GO:0008615	-	EC:2.6.1.52	IPR015421; IPR015424; PTHR21152 (PANTHER), PTHR21152:SF1 (PANTHER)
	-	0				-
	-	0				-
Angiostrongylus cantonensis	briggsae cbr-nhl-1 protein	3	F:GO:0008270; F:GO:0005515; P:GO:0006915	-		PTHR13712 (PANTHER), PTHR13712:SF9 (PANTHER)
	-	0				-

Gorilla gorilla	-dh dehydroge-se	4	P:GO:0006120; F:GO:0008137; P:GO:0006810; C:GO:0005747	-	EC:1.6.5.3	-
	-	0				-
Ascaris suum	disorganized muscle protein 1	4	P:GO:0007498; C:GO:0030018; F:GO:0008307; F:GO:0005515	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-fshr-1 protein	10	P:GO:0009792; C:GO:0005840; P:GO:0006952; F:GO:0003735; P:GO:0040010; P:GO:0000003; P:GO:0007186; C:GO:0016021; F:GO:0016500; P:GO:0006412	-	EC:3.6.5.3	SignalP (SIGNALP)
Caenorhabditis briggsae	spc-1	1	F:GO:0005509	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis remanei	egg laying defective protein isoform confirmed by transcript evidence	4	P:GO:0048675; P:GO:0006355; F:GO:0003700; C:GO:0005634	-		-
Ailuropoda melanoleuca	t-complex protein 1 subunit gamma-like isoform 2	5	C:GO:0005856; P:GO:0006457; C:GO:0005832; F:GO:0005524; F:GO:0051082	-		-
	-	0				-
Caenorhabditis elegans	peroxisomal biogenesis factor 19	4	C:GO:0005777; F:GO:0005515; P:GO:0007031; C:GO:0044425	-		IPR006708
Homo sapiens	transporter atp-binding sub-family b (mdr tap)	19	F:GO:0046979; C:GO:0042825; P:GO:0019060; F:GO:0015197; C:GO:0005792; P:GO:0042270; F:GO:0043531; C:GO:0005829; F:GO:0046982; F:GO:0046978; P:GO:0046967; P:GO:0015833; F:GO:0042626; P:GO:0019885; P:GO:0055085; F:GO:0042605; F:GO:0042803; F:GO:0005524; C:GO:0005739	-		G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF79 (PANTHER), SSF52540 (SUPERFAMILY)

Loa loa	adam metallopeptidase with thrombospondin type 1 9	4	F:GO:0004222; C:GO:0005578; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	-
	-	0				-
	-	0				IPR001283; IPR014044; PTHR10334:SF2 (PANTHER)
Caenorhabditis elegans	db module family protein	0				IPR002602; PTHR12974 (PANTHER), PTHR12974:SF2 (PANTHER)
Caenorhabditis briggsae	patched family protein	12	P:GO:0040025; F:GO:0008158; P:GO:0040018; P:GO:0018996; P:GO:0040002; P:GO:0006810; P:GO:0000003; P:GO:0008340; P:GO:0040011; C:GO:0016021; P:GO:0019915; F:GO:0005215	-		IPR000731; IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	zinc carboxypeptidase family protein	3	P:GO:0006508; F:GO:0004181; F:GO:0008270	-	EC:3.4.17.0	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), PTHR11705:SF12 (PANTHER), SSF53187 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Heligmosomoides polygyrus	calreticulin precursor	5	F:GO:0005529; P:GO:0006457; C:GO:0005788; F:GO:0005509; F:GO:0051082	-		IPR001580; IPR008985; IPR009169; IPR013320; IPR018124; SignalP (SIGNALP)
Heligmosomoides polygyrus	calreticulin	5	F:GO:0005529; P:GO:0006457; C:GO:0005788; F:GO:0005509; F:GO:0051082	-		IPR001580; IPR009033; IPR009169
Caenorhabditis elegans	isoform b	3	P:GO:0009987; F:GO:0005515; C:GO:0044424	-		IPR000504; IPR002075; IPR012677; IPR018222; G3DSA:3.10.450.50 (GENE3D), PTHR10693 (PANTHER), SSF54427 (SUPERFAMILY), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF65 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-osm-12 protein	3	C:GO:0043005; F:GO:0005515; P:GO:0035058	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-

Brugia malayi	heparan 6-o sulfotransferase hst-6	5	C:GO:0016021; P:GO:0048048; P:GO:0016051; F:GO:0017095; P:GO:0001569	-		IPR005331; IPR010635
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	2	F:GO:0016491; P:GO:0055114	-		IPR023210
Homo sapiens	pctaire protein ki-se 1	4	P:GO:0006468; F:GO:0005515; F:GO:0005524; F:GO:0004693	-	EC:2.7.11.22	IPR000719; IPR011009; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF104 (PANTHER)
Caenorhabditis remanei	ceramide ki-se	2	P:GO:0007205; F:GO:0004143	-	EC:2.7.1.107	-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Ailuropoda melanoleuca	guanine nucleotide binding protein (g protein) beta polypeptide 1	13	P:GO:0007603; P:GO:0007265; F:GO:0004871; P:GO:0007213; C:GO:0001750; P:GO:0050909; P:GO:0007200; P:GO:0007204; C:GO:0005834; P:GO:0009755; F:GO:0003924; F:GO:0031702; P:GO:0008283	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
	-	0				-
Brugia malayi	sh3 adapter protein spin90	0		F:GO:0005488		-
	-	0				-
Caenorhabditis elegans	voltage-gated potassium channel	5	C:GO:0008076; C:GO:0030659; F:GO:0005249; P:GO:0055085; P:GO:0006813	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		IPR007087; IPR015880; PTHR10032 (PANTHER), PTHR10032:SF32 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	2	P:GO:0055085; C:GO:0016021	-		IPR011701; IPR016196; G3DSA:1.20.1250.20 (GENE3D), PTHR11662 (PANTHER), PTHR11662:SF17 (PANTHER)
Caenorhabditis briggsae	cathepsin a	2	F:GO:0004185; P:GO:0006508	-	EC:3.4.16.0	-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	2	P:GO:0006629; F:GO:0004806	-	EC:3.1.1.3	IPR002921; G3DSA:3.40.50.1820 (GENE3D), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	exosome complex exonuclease rrp45	5	P:GO:0009792; P:GO:0002119; F:GO:0004527; P:GO:0040010; P:GO:0000003	-		IPR020568
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	pp2c-like domain-containing protein cg9801	1	F:GO:0003824	-		IPR001932; IPR010822; PTHR21586 (PANTHER)
Mus musculus	lipoprotein receptor-related protein	0				-
	-	0				-
Homo sapiens	protein cornichon homolog 4	4	P:GO:0023034; C:GO:0016021; C:GO:0005783; F:GO:0005515	-		IPR003377; PTHR12290 (PANTHER), PTHR12290:SF4 (PANTHER), SignalP (SIGNALP)
Homo sapiens	apoptosis-associated speck-like protein containing a card	13	F:GO:0004197; C:GO:0008385; P:GO:0050718; P:GO:0006919; C:GO:0005576; P:GO:0033209; P:GO:0006917; P:GO:0006954; P:GO:0006508; F:GO:0042803; P:GO:0051092; F:GO:0032090; F:GO:0008656	-	EC:3.4.22.0	-
	-	0				-
Pongo abelii	protein inhibitor of activated 3	15	F:GO:0047485; P:GO:0009725; F:GO:0008270; F:GO:0003676; C:GO:0030425; P:GO:0045449; F:GO:0008022; C:GO:0045202; C:GO:0016607; F:GO:0015459; P:GO:0033235; F:GO:0019899; P:GO:0010628; F:GO:0019789; P:GO:0045838	-		-
Caenorhabditis remanei	briggsae cbr-nhr-22 protein	0		F:GO:0043565; F:GO:0003700; F:GO:0003677; C:GO:0005634; F:GO:0004879; F:GO:0008270; P:GO:0006355; F:GO:0004872; F:GO:0005515; F:GO:0046872; P:GO:0006350; F:GO:0003707; P:GO:0045449		-

Streptomyces sp. ACTE	aldehyde dehydroge-se	15	F:GO:0004028; P:GO:0008284; P:GO:0014070; F:GO:0004029; P:GO:0007584; P:GO:0042493; F:GO:0008106; P:GO:0007568; P:GO:0055114; P:GO:0051384; P:GO:0001666; C:GO:0005829; P:GO:0006081; C:GO:0005783; P:GO:0051591	-	EC:1.2.1.3; EC:1.1.1.2	-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Brugia malayi	tyrosyl-d- phosphodiesterase 1	4	F:GO:0008081; F:GO:0043566; P:GO:0006281; C:GO:0044424	-	EC:3.1.4.0	IPR001736; IPR010347; IPR010916; G3DSA:3.30.870.10 (GENE3D), SSF56024 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Pongo abelii	nuclear factor of kappa light polypeptide gene enhancer in b-cells alpha	28	F:GO:0008139; P:GO:0045746; P:GO:0010745; P:GO:0032270; P:GO:0007253; P:GO:0070427; P:GO:0045638; P:GO:0042127; P:GO:0034142; P:GO:0010552; P:GO:0010875; P:GO:0031663; P:GO:0070431; C:GO:0005829; P:GO:0006916; P:GO:0032088; F:GO:0031072; F:GO:0031625; F:GO:0042802; P:GO:0000060; P:GO:0010888; F:GO:0051059; P:GO:0032495; F:GO:0032403; C:GO:0005634; P:GO:0043330; P:GO:0044419	-		IPR002110; IPR015681; IPR020683; PTHR18958 (PANTHER)

Loa loa	abc transporter	0		F:GO:0042626; C:GO:0016021; C:GO:0016020; F:GO:0016787; C:GO:0005739; P:GO:0006810; F:GO:0008559; F:GO:0000166; F:GO:0017111; F:GO:0005524; F:GO:0016887; P:GO:0055085		G3DSA:3.40.50.300 (GENE3D), PTHR11384 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	major facilitator superfamily protein	3	P:GO:0055085; C:GO:0016021; F:GO:0005215	-		IPR005828; PTHR11600 (PANTHER), PTHR11600:SF99 (PANTHER), SignalP (SIGNALP)
Caenorhabditis remanei	udp-galactose transporter	6	C:GO:0000139; P:GO:0007275; P:GO:0055085; F:GO:0046964; P:GO:0046963; C:GO:0016021	-		IPR013657; PTHR10778 (PANTHER), PTHR10778:SF8 (PANTHER)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG07050 [Caenorhabditis briggsae]	0		F:GO:0005515		-
Caenorhabditis elegans	son of sevenless homolog 2	5	F:GO:0005085; P:GO:0006915; F:GO:0005488; C:GO:0005622; P:GO:0007264	-		IPR001895; IPR008937; IPR015759
Homo sapiens	proteasome (macropain) 26s non- 4	10	P:GO:0006281; C:GO:0000502; F:GO:0008270; P:GO:0051436; P:GO:0051437; P:GO:0045449; P:GO:0031145; F:GO:0005515; C:GO:0005737; P:GO:0042044	-		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	4	F:GO:0005488; F:GO:0005086; P:GO:0032012; C:GO:0005622	-		-
	-	0				-
	-	0				-

Mus musculus	cubilin precursor	0		P:GO:0030154; F:GO:0004872; C:GO:0005887; C:GO:0005886; C:GO:0030666; C:GO:0045177; P:GO:0006898; P:GO:0006897; C:GO:0016021; C:GO:0016020; P:GO:0042742; P:GO:0001701; C:GO:0005783; P:GO:0006766; C:GO:0010008; P:GO:0007584; C:GO:0005624; F:GO:0005044; F:GO:0031419; P:GO:0020028; F:GO:0005041; P:GO:0007165; C:GO:0009897; F:GO:0030492; F:GO:0042803; P:GO:0015031; P:GO:0050793;		IPR000742; IPR013032; IPR013111; G3DSA:2.10.25.10 (GENE3D)
Caenorhabditis briggsae	solute carrier family 2 (facilitated glucose transporter) member 9 isoform 2	3	C:GO:0016020; P:GO:0006810; F:GO:0005215	-		IPR005828; IPR020846; PTHR11600 (PANTHER), PTHR11600:SF98 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR015395
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Strongylocentrotus purpuratus	btb domain containing 9	0		P:GO:0007155; F:GO:0005515		-
Caenorhabditis briggsae	db module family protein	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	sulfate transporter	3	C:GO:0016020; P:GO:0006810; F:GO:0005215	-		IPR011547; PTHR11814 (PANTHER), PTHR11814:SF25 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-

	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	o- c selective n-acetyl-beta-d-glucosaminidase (o- case) family member (oga-1)	0		F:GO:0004415; P:GO:0008152; F:GO:0016787; F:GO:0008080; F:GO:0016798		-
	-	0				-
	-	0				-
Caenorhabditis remanei	sy-ptotagmin 1	8	C:GO:0030054; P:GO:0016079; F:GO:0005509; F:GO:0000149; P:GO:0045955; F:GO:0035005; C:GO:0030285; F:GO:0005215	-	EC:2.7.1.154	IPR000008; IPR001565; IPR008973; IPR018029; G3DSA:2.60.40.150 (GENE3D), PTHR10024 (PANTHER), PTHR10024:SF40 (PANTHER)
Caenorhabditis elegans	briggsae cbr-gop-1 protein	0				IPR019155; PTHR21481 (PANTHER)
Loa loa	hypothetical protein LOAG_05911 [Loa loa]	0				-
Pan troglodytes	hmg-17 protein	0				IPR000079; PTHR23087:SF2 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0004568; C:GO:0016021; F:GO:0004674; F:GO:0004383; F:GO:0004672; P:GO:0009190; P:GO:0006182; P:GO:0016998; P:GO:0023034; P:GO:0006468; F:GO:0000166; F:GO:0005524; F:GO:0016829; P:GO:0006032; F:GO:0016849		-
Caenorhabditis briggsae	sulfate transporter	3	P:GO:0055085; C:GO:0016021; F:GO:0005215	-		-

Caenorhabditis elegans	cell division control protein 42 homolog precursor	28	P:GO:0030225; P:GO:0040027; P:GO:0040007; F:GO:0031996; P:GO:0006898; C:GO:0005626; P:GO:0031274; C:GO:0030175; P:GO:0000132; F:GO:0005525; P:GO:0040002; P:GO:0015031; C:GO:0016021; P:GO:0032970; C:GO:0005829; P:GO:0040039; P:GO:0030036; P:GO:0007264; P:GO:0009792; P:GO:0031333; C:GO:0005813; P:GO:0010171; C:GO:0048471; F:GO:0003924; C:GO:0005886; P:GO:0040035; C:GO:0005938; P:GO:0000910	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001806; IPR003578; IPR005225; IPR013753; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF286 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	adam metallopeptidase with thrombospondin type 1 9	9	P:GO:0009967; F:GO:0008270; C:GO:0005615; F:GO:0004222; P:GO:0006508; P:GO:0045636; C:GO:0005578; P:GO:0043066; P:GO:0030198	-	EC:3.4.24.0	-
Caenorhabditis elegans	ck1 worm6 protein ki-se	6	P:GO:0006468; F:GO:0005524; P:GO:0000003; P:GO:0040011; P:GO:0019915; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG22251 [Caenorhabditis briggsae]	0				-
	-	0				-
Caenorhabditis briggsae	multiple pdz domain protein family member (mpz-1)	1	C:GO:0016021	-		-
	-	0				IPR008160; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER)

Homo sapiens	fibronectin 1	13	P:GO:0018149; P:GO:0016477; P:GO:0001525; P:GO:0008360; C:GO:0005793; C:GO:0031093; P:GO:0034446; F:GO:0005518; C:GO:0005577; F:GO:0008201; C:GO:0005578; F:GO:0005201; P:GO:0006953	-		SignalP (SIGNALP)
	-	0				IPR019809
	-	0				-
Caenorhabditis briggsae	u4 u6 small nuclear ribonucleoprotein prp4	10	P:GO:0040010; P:GO:0040035; P:GO:0008380; P:GO:0002119; F:GO:0005515; P:GO:0040011; C:GO:0030529; P:GO:0009792; P:GO:0001703; C:GO:0005634	-		IPR001680; IPR011046; IPR014906; IPR015943; PTHR19846 (PANTHER)
Homo sapiens	PREDICTED: similar to hCG2040253 [Homo sapiens]	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis remanei	temporarily assigned gene -me family member (tag-308)	0				-
Caenorhabditis elegans	fad-binding protein	2	F:GO:0016491; F:GO:0050660	-		IPR004113; IPR016164; IPR016171; PTHR11748 (PANTHER), PTHR11748:SF7 (PANTHER)
	-	0				-
Caenorhabditis remanei	transmembrane protein 16h	0				-
Caenorhabditis remanei	elegans protein confirmed by transcript evidence	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Ixodes scapularis	snf2 super family	3	F:GO:0046872; F:GO:0003676; F:GO:0003824	-		IPR001650; PTHR10799 (PANTHER), PTHR10799:SF59 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	patched family protein	13	P:GO:0009792; P:GO:0002119; F:GO:0008158; P:GO:0040018; P:GO:0001703; P:GO:0018996; P:GO:0000910; P:GO:0006810; P:GO:0040010; P:GO:0000003; P:GO:0040011; C:GO:0016021; F:GO:0005215	-		IPR003392; PTHR10796 (PANTHER), PTHR10796:SF32 (PANTHER), SignalP (SIGNALP)

Caenorhabditis elegans	patched family protein	12	P:GO:0009792; P:GO:0002119; F:GO:0008158; P:GO:0040018; P:GO:0001703; P:GO:0018996; P:GO:0000910; P:GO:0006810; P:GO:0040010; P:GO:0000003; P:GO:0040011; C:GO:0016021	-		IPR000731; IPR001036; IPR003392; PTHR10796 (PANTHER), PTHR10796:SF32 (PANTHER), SignalP (SIGNALP), SSF82866 (SUPERFAMILY)
Caenorhabditis briggsae	patched family protein	12	P:GO:0009792; P:GO:0002119; F:GO:0008158; P:GO:0040018; P:GO:0001703; P:GO:0018996; P:GO:0000910; P:GO:0006810; P:GO:0040010; P:GO:0000003; P:GO:0040011; C:GO:0016021	-		IPR000731; IPR001036; IPR003392; PTHR10796 (PANTHER), PTHR10796:SF32 (PANTHER), SSF82866 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0005515		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis remanei	briggsae cbr-ced-11 protein	3	P:GO:0043068; P:GO:0006915; F:GO:0016787	-		-
Caenorhabditis elegans	cg12581 cg12581-pa	1	F:GO:0005515	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	briggsae cbr-cpg-3 protein	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Loa loa	protein-tyrosine phosphatase containing protein	0		P:GO:0016311; F:GO:0016791; P:GO:0006470; F:GO:0016787; F:GO:0004725; F:GO:0004721		IPR000242; IPR000387; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF29 (PANTHER), SSF52799 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Loa loa	hypothetical protein LOAG_04772 [Loa loa]	2	P:GO:0040039; P:GO:0000003	-		IPR002049; IPR013032; G3DSA:2.10.25.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF148 (PANTHER)
Brugia malayi	chromaffin granule amine transporter	0		F:GO:0015520; P:GO:0046677; C:GO:0016021; P:GO:0055085; P:GO:0015904		IPR016196; G3DSA:1.20.1250.20 (GENE3D), PTHR10074 (PANTHER), PTHR10074:SF32 (PANTHER), SignalP (SIGNALP)

Caenorhabditis remanei	fyve finger-containing phosphoinositide ki-se	12	P:GO:0042147; C:GO:0031901; P:GO:0046488; P:GO:0044267; F:GO:0008270; P:GO:0034504; C:GO:0031982; F:GO:0016308; F:GO:0005524; F:GO:0005515; C:GO:0045121; P:GO:0006898	-	EC:2.7.1.68	-
Caenorhabditis remanei	hypothetical protein CRE_06660 [Caenorhabditis remanei]	0				-
Loa loa	hypothetical protein LOAG_15135 [Loa loa]	0				-
	-	0				-
Loa loa	tmem16d protein	1	C:GO:0016020	-		IPR000418; IPR007632
	-	0				-
	-	0				-
Pongo abelii	filamin a	28	[illegible] F:GO:0004871; C:GO:0005802; P:GO:0043433; P:GO:0034394; C:GO:0015629; P:GO:0050821; P:GO:0051220; C:GO:0005576; C:GO:0005829; F:GO:0001948; P:GO:0051764; P:GO:0043123; F:GO:0051015; F:GO:0048365; P:GO:0045022; P:GO:0007195; F:GO:0042803; F:GO:0034989; P:GO:0031532; F:GO:0034988; C:GO:0005886; F:GO:0008134; P:GO:0042177; C:GO:0005634; P:GO:0042993; C:GO:0005938; P:GO:0043113	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	sy-ptosomal associated protein	1	C:GO:0019717	-		IPR000727; G3DSA:1.20.5.110 (GENE3D), PTHR19305 (PANTHER)

Caenorhabditis elegans	structural mainte-nce of chromosomes 1a	13	P:GO:0009314; P:GO:0000075; P:GO:0006281; P:GO:0007126; P:GO:0042770; P:GO:0051276; P:GO:0051301; F:GO:0005524; C:GO:0000776; F:GO:0005515; P:GO:0007067; F:GO:0003682; C:GO:0005634	-		PTHR18937 (PANTHER), PTHR18937:SF12 (PANTHER)
	-	0				-
Caenorhabditis remanei	uncoordi-ted family member (unc-89)	0				IPR013098; IPR013783; SSF48726 (SUPERFAMILY)
	-	0				-
Caenorhabditis brenneri	briggsae cbr-casy-1 protein	7	C:GO:0043231; C:GO:0032809; C:GO:0005615; P:GO:0007155; F:GO:0005515; P:GO:0008355; P:GO:0009792	-		PTHR14139 (PANTHER)
Loa loa	spen transcriptio-l regulator	3	F:GO:0030528; F:GO:0003676; P:GO:0045449	-		IPR000504; IPR012677; PTHR23189 (PANTHER), PTHR23189:SF9 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-amx-2 protein	0				PTHR10742 (PANTHER), PTHR10742:SF6 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	cx module family protein	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	membrane calcium atpase family member (mca-1)	6	F:GO:0015662; F:GO:0015085; F:GO:0000166; P:GO:0008152; P:GO:0006812; C:GO:0016020	-		IPR001757; IPR010916; PTHR11939:SF75 (PANTHER)
	-	0				-
Caenorhabditis remanei	elegans protein confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	C:GO:0016020; F:GO:0016757	-		IPR003406; PTHR19297:SF4 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-hmr-1 protein	1	F:GO:0005515	-		-
	-	0				-

Caenorhabditis remanei	protein prenyltransferase alpha subunit repeat containing protein	8	P:GO:0009792; P:GO:0002119; P:GO:0040010; P:GO:0008340; P:GO:0040011; P:GO:0008219; F:GO:0016740; P:GO:0002009	-		IPR002088; IPR008940; PTHR11129 (PANTHER), PTHR11129:SF1 (PANTHER), SSF48439 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	x-ray repair complementing defective repair in chinese hamster cells 6	1	P:GO:0006950	-		IPR016194; G3DSA:3.40.50.410 (GENE3D), PTHR12604 (PANTHER), PTHR12604:SF2 (PANTHER)
Callithrix jacchus	eukaryotic translation initiation factor subunit e	9	F:GO:0003743; C:GO:0005829; F:GO:0047485; P:GO:0045948; C:GO:0005852; C:GO:0000785; C:GO:0016605; P:GO:0045947; P:GO:0000184	-		IPR019010; PTHR10317 (PANTHER)
Loa loa	tk fer protein ki-se	0		F:GO:0016740; C:GO:0016021; C:GO:0016020; F:GO:0004674; F:GO:0004672; P:GO:0006468; F:GO:0000166; F:GO:0005524; F:GO:0016301; F:GO:0004713; F:GO:0004872; F:GO:0005515; F:GO:0005509; F:GO:0005488		-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Homo sapiens	cathepsin d	10	F:GO:0042277; C:GO:0005764; C:GO:0005739; P:GO:0008219; C:GO:0005615; P:GO:0000045; P:GO:0006508; C:GO:0042470; F:GO:0004190; C:GO:0031012	-	EC:3.4.23.0	IPR001461; IPR009007; IPR021109; PTHR13683:SF84 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-

Caenorhabditis elegans	protein ki-se iota	30	P:GO:0006468; P:GO:0007369; F:GO:0008270; P:GO:0032869; C:GO:0005624; P:GO:0048194; P:GO:0006612; F:GO:0005543; P:GO:0045197; P:GO:0007506; C:GO:0005829; P:GO:0006916; F:GO:0019904; P:GO:0035089; P:GO:0007015; P:GO:0042462; P:GO:0090004; C:GO:0000133; P:GO:0070555; C:GO:0005923; C:GO:0030864; C:GO:0005625; C:GO:0005634; F:GO:0005524; P:GO:0046903; P:GO:0045216;	-	EC:2.7.11.13	IPR000270; IPR000719; IPR002219; IPR002290; IPR008271; IPR011009; IPR015745; IPR017441; IPR017442; IPR020454; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.10.20.240 (GENE3D), G3DSA:3.30.200.20 (GENE3D), G3DSA:3.30.60.20 (GENE3D), PTHR22985 (PANTHER), SSF54277 (SUPERFAMILY), SSF57889 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0005488	-		PTHR13986 (PANTHER), PTHR13986:SF1 (PANTHER)
Caenorhabditis briggsae	ophagy (yeast atg homolog) family member (atg-)	2	P:GO:0006810; F:GO:0008233	-		-
Caenorhabditis remanei	nematode astacin protease family member (-s-9)	5	P:GO:0009792; P:GO:0040010; P:GO:0006508; F:GO:0008270; F:GO:0008237	-		IPR001506; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF66 (PANTHER)
	-	0				-
	-	0				PTHR11521 (PANTHER), PTHR11521:SF1 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-

Pongo abelii	annexin a5	16	P:GO:0043065; P:GO:0050819; C:GO:0014704; F:GO:0005509; F:GO:0005544; P:GO:0051260; F:GO:0043499; P:GO:0006916; C:GO:0042995; P:GO:0007165; F:GO:0030971; C:GO:0042383; C:GO:0005737; F:GO:0004859; P:GO:0007596; P:GO:0010033	-		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-fer-1 protein	0		C:GO:0016021		PTHR12546 (PANTHER), PTHR12546:SF5 (PANTHER)
	-	0				-
Salmo salar	3-oxo-5-alpha-steroid 4-dehydroge-se 2	6	C:GO:0016021; F:GO:0003865; P:GO:0055114; C:GO:0005737; P:GO:0008202; F:GO:0005515	-	EC:1.3.99.5	IPR001104; PTHR10556 (PANTHER), PTHR10556:SF5 (PANTHER)
Macaca mulatta	moesin	20	P:GO:0022614; F:GO:0030674; C:GO:0019898; C:GO:0009898; C:GO:0031527; C:GO:0005856; C:GO:0005625; C:GO:0005730; C:GO:0009986; P:GO:0050900; F:GO:0005102; C:GO:0001931; F:GO:0050839; F:GO:0003779; C:GO:0030667; P:GO:0007159; F:GO:0005200; C:GO:0016324; C:GO:0031528; C:GO:0016323	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Sorghum bicolor	dehydroge-se reductase sdr family member 2	3	F:GO:0016491; P:GO:0055114; F:GO:0005488	-		IPR002198; IPR016040; PTHR19410:SF67 (PANTHER), SSF51735 (SUPERFAMILY)

Ornithorhynchus anatinus	tmprss11a protein	0		P:GO:0006508; F:GO:0004252; F:GO:0008236; F:GO:0016787; F:GO:0003824; F:GO:0008233		IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR19355 (PANTHER), PTHR19355:SF168 (PANTHER)
	-	0				-
Loa loa	akirin 1	2	P:GO:0048518; P:GO:0050794	-		PTHR13293 (PANTHER), PTHR13293:SF6 (PANTHER)
Homo sapiens	mhc class ii antigen	9	C:GO:0005789; C:GO:0005887; C:GO:0042613; C:GO:0005794; P:GO:0002504; C:GO:0005765; F:GO:0032395; C:GO:0010008; P:GO:0006955	-		IPR001003; IPR003597; IPR007110; IPR011162; IPR013783; IPR014745; PTHR19944 (PANTHER), PTHR19944:SF27 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
	-	0				-
Ailuropoda melanoleuca	protein fat-free homolog	5	P:GO:0006869; P:GO:0015031; C:GO:0016021; C:GO:0005794; C:GO:0005634	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	major facilitator superfamily expressed	1	C:GO:0005886	-		IPR008509; IPR016196; G3DSA:1.20.1250.20 (GENE3D), SignalP (SIGNALP)
Caenorhabditis elegans	map ki-se activated protein ki-se family member (mak-2)	6	P:GO:0008360; P:GO:0006468; F:GO:0005515; P:GO:0007155; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017442; IPR020636; IPR020646; G3DSA:1.10.510.10 (GENE3D), G3DSA:4.10.1170.10 (GENE3D)
Homo sapiens	lipopolysaccharide-induced tnf factor	10	C:GO:0005765; P:GO:0006357; P:GO:0006915; F:GO:0004871; C:GO:0005813; P:GO:0043123; C:GO:0005576; F:GO:0050699; C:GO:0005794; F:GO:0003702	-		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	eating: abnormal pharyngeal pumping family member (eat-18)	0				-
	-	0				-
Homo sapiens	adp-ribosylation-like factor 6 interacting protein 4	2	C:GO:0005634; P:GO:0008380	-		-

	-	0				-
Caenorhabditis briggsae	ester hydrolase c11orf54 homolog	3	F:GO:0016788; C:GO:0005634; F:GO:0008270	-		-
	-	0				SignalP (SIGNALP)
Brugia malayi	rap ran-gap family protein	0		F:GO:0005096; P:GO:0051056; F:GO:0005488; C:GO:0005622; P:GO:0043547		IPR000331; PTHR10063 (PANTHER), SignalP (SIGNALP), SSF111347 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis remanei	elegans protein partially confirmed by transcript evidence	1	F:GO:0005488	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	cortactin	6	C:GO:0005625; C:GO:0030027; F:GO:0005515; C:GO:0001726; C:GO:0005938; P:GO:0006898	-		IPR001452; IPR003134; IPR008162; IPR015503; G3DSA:2.30.30.40 (GENE3D), PTHR10829 (PANTHER), SignalP (SIGNALP)
Tribolium castaneum	xylulose ki-se	3	P:GO:0005975; F:GO:0016773; P:GO:0006091	-	EC:2.7.1.0	IPR000577; PTHR10196:SF5 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Callithrix jacchus	angio-associated migratory cell protein	8	C:GO:0005737; P:GO:0030154; C:GO:0009986; P:GO:0045766; P:GO:0010595; F:GO:0008201; C:GO:0005886; P:GO:0014909	-		SignalP (SIGNALP)
Caenorhabditis elegans	beta- -galactosyltransferase 6	7	P:GO:0007411; P:GO:0006024; C:GO:0005797; P:GO:0007608; P:GO:0006486; F:GO:0008499; C:GO:0016020	-		IPR002659; PTHR11214:SF10 (PANTHER), SignalP (SIGNALP)

Homo sapiens	ywhaz protein	14	C:GO:0043234; C:GO:0005625; C:GO:0005739; F:GO:0032403; P:GO:0006626; P:GO:0002553; P:GO:0006916; C:GO:0042470; F:GO:0019904; P:GO:0007165; F:GO:0008134; P:GO:0042493; C:GO:0014069; C:GO:0005634	-		IPR000308
	-	0				IPR002259; PTHR10332:SF6 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR001810; IPR022364; G3DSA:1.20.1280.50 (GENE3D)
Caenorhabditis briggsae	major intrinsic protein	7	C:GO:0016323; P:GO:0045087; P:GO:0008340; P:GO:0050829; C:GO:0016021; P:GO:0015793; F:GO:0022838	-		-
Homo sapiens	af220047_1uncharacterized hematopoietic stem progenitor cells protein mds027	2	C:GO:0005856; C:GO:0005737	-		-
Callithrix jacchus	phosphatidylethanolamine-binding protein 1	40	C:GO:0019717; C:GO:0005791; P:GO:0001933; P:GO:0060409; C:GO:0005625; P:GO:0007420; P:GO:0051602; F:GO:0004867; F:GO:0005102; P:GO:0010243; C:GO:0043679; C:GO:0005615; P:GO:0045471; P:GO:0043409; F:GO:0008429; P:GO:0002026; P:GO:0051592; P:GO:0006979; P:GO:0007568; P:GO:0009408; P:GO:0007286; C:GO:0005794; P:GO:0051412; P:GO:0014823; P:GO:0042755; F:GO:0005524; P:GO:0010951;	-		IPR008914; PTHR11362 (PANTHER)

Brugia malayi	pr domain containing with znf domain	15	P:GO:0040010; P:GO:0008340; F:GO:0008270; F:GO:0003676; P:GO:0006915; C:GO:0005622; P:GO:0040035; P:GO:0000122; P:GO:0010171; P:GO:0019915; P:GO:0002119; F:GO:0003700; P:GO:0040011; P:GO:0002009; P:GO:0040018	-		IPR001214; G3DSA:2.170.270.10 (GENE3D)
Caenorhabditis remanei	cre-klf-1 protein	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Ixodes scapularis	delta-like 4 protein	0		P:GO:0008595; P:GO:0000003; P:GO:0060325; P:GO:0009953; P:GO:0040028; P:GO:0030154; P:GO:0046331; P:GO:0060351; F:GO:0003674; P:GO:0001889; P:GO:0016331; C:GO:0016021; C:GO:0016020; P:GO:0031016; P:GO:0007154; P:GO:0009792; P:GO:0007219; F:GO:0005509; F:GO:0030414; P:GO:0007275; P:GO:0001525; P:GO:0009880; P:GO:0043537; F:GO:0005112; F:GO:0005515		IPR001774; PTHR11201 (PANTHER), PTHR11201:SF192 (PANTHER), SignalP (SIGNALP)
Loa loa	prp39 pre-mr- processing factor 39 homolog	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-

Caenorhabditis remanei	calcium alpha subunit family member (cca-1)	7	P:GO:0051899; P:GO:0045760; P:GO:0043051; P:GO:0006816; P:GO:0055085; C:GO:0005891; F:GO:0008332	-		IPR005445; IPR005821; PTHR10037 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0000003; P:GO:0040010		-
	-	0				-
Caenorhabditis briggsae	uncoordi-ted family member (unc-22)	3	P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR003961; IPR013783
Brugia malayi	lem domain containing 3	4	P:GO:0090101; F:GO:0005488; C:GO:0016021; C:GO:0005637	-		-
Caenorhabditis briggsae	inner nuclear membrane protein man1	7	P:GO:0030514; P:GO:0032926; P:GO:0030512; C:GO:0016021; C:GO:0005624; F:GO:0005515; C:GO:0005637	-		-
	-	0				-
Brugia malayi	g protein-coupled receptor ki-se 4	10	C:GO:0005829; P:GO:0002031; F:GO:0050254; C:GO:0030425; F:GO:0004872; F:GO:0004703; F:GO:0005524; C:GO:0043025; P:GO:0007165; P:GO:0006468	-	EC:2.7.11.14; EC:2.7.11.16	-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis remanei	high incidence of males (increased x chromosome loss) family member (him-4)	1	F:GO:0005509	-		-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	P:GO:0007155; C:GO:0005604	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	f-box protein 42	0		F:GO:0003674; P:GO:0008150; F:GO:0005515; C:GO:0005575		IPR001810; IPR015915; IPR018229; PTHR23244 (PANTHER), PTHR23244:SF7 (PANTHER), SSF117281 (SUPERFAMILY)
	-	0				PS51257 (PROFILE)
Caenorhabditis elegans	briggsae cbr-pho-1 protein	0		F:GO:0003993		-
Caenorhabditis elegans	briggsae cbr-hmr-1 protein	3	C:GO:0016020; P:GO:0007155; F:GO:0005515	-		IPR002126
	-	0				-
	-	0				-
Apis mellifera	atg2 autophagy related 2 homolog b	0				PTHR13190 (PANTHER), PTHR13190:SF9 (PANTHER)

	-	0				-
Caenorhabditis elegans	briggsae cbr-spe-10 protein	1	F:GO:0046872	-		-
Homo sapiens	galactoside- 3 binding protein	9	F:GO:0005044; C:GO:0005615; F:GO:0005515; P:GO:0007155; P:GO:0007165; C:GO:0016020; C:GO:0005634; C:GO:0005578; P:GO:0006968	-		PTHR19331 (PANTHER), PTHR19331:SF8 (PANTHER)
Pongo abelii	nodal modulator 1	5	C:GO:0005789; F:GO:0004180; F:GO:0030246; F:GO:0005515; C:GO:0016021	-		PTHR23303 (PANTHER), PTHR23303:SF2 (PANTHER)
Culex quinquefasciatus	conserved hypothetical protein [Culex quinquefasciatus]	0		F:GO:0008270; C:GO:0005622		IPR007087; IPR015880
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
synthetic construct	monocyte differentiation antigen cd14	18	F:GO:0070891; P:GO:0006915; P:GO:0006954; P:GO:0006909; P:GO:0071223; P:GO:0032760; C:GO:0005615; P:GO:0045087; P:GO:0009408; F:GO:0001530; C:GO:0045121; F:GO:0001847; C:GO:0031225; C:GO:0046696; P:GO:0007166; P:GO:0071222; F:GO:0016019; C:GO:0005886	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	uncoordi-ted family member (unc-22)	6	C:GO:0030018; P:GO:0006468; F:GO:0008307; P:GO:0007498; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR013098; IPR013783; SSF48726 (SUPERFAMILY)
	-	0				-
Brugia malayi	-d-dependent malic mitochondrial precursor	8	F:GO:0046872; P:GO:0006090; F:GO:0051287; C:GO:0005759; F:GO:0016619; P:GO:0006108; P:GO:0055114; F:GO:0004473	-	EC:1.1.1.38; EC:1.1.1.40	-

	-	0				-
	-	0				IPR007834
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Haemonchus contortus	serine protease	3	P:GO:0006508; F:GO:0008236; F:GO:0004180	-		IPR008758; PTHR11010:SF4 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-oct-2 protein	3	P:GO:0055085; C:GO:0016021; F:GO:0005215	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	vacuolar atp synthase subunit h	17	F:GO:0046961; P:GO:0008340; F:GO:0005515; F:GO:0008553; P:GO:0040007; P:GO:0033227; P:GO:0040011; P:GO:0040002; P:GO:0018996; C:GO:0005829; P:GO:0050690; P:GO:0009792; P:GO:0015986; P:GO:0006897; P:GO:0002119; C:GO:0000221; C:GO:0005886	-	EC:3.6.3.14; EC:3.6.3.6	IPR004908; IPR011989; IPR016024
Caenorhabditis elegans	vacuolar atp synthase subunit h	14	F:GO:0046961; P:GO:0008340; F:GO:0008553; P:GO:0040007; P:GO:0033227; P:GO:0040011; P:GO:0040002; P:GO:0018996; P:GO:0009792; P:GO:0015986; P:GO:0002119; C:GO:0000221; C:GO:0005886; F:GO:0005488	-	EC:3.6.3.14; EC:3.6.3.6	IPR004908; IPR011987; IPR011989; IPR016024

Caenorhabditis elegans	vacuolar atp synthase subunit h	14	F:GO:0046961; P:GO:0008340; F:GO:0008553; P:GO:0040007; P:GO:0033227; P:GO:0040011; P:GO:0040002; P:GO:0018996; P:GO:0009792; P:GO:0015986; P:GO:0002119; C:GO:0000221; C:GO:0005886; F:GO:0005488	-	EC:3.6.3.14; EC:3.6.3.6	IPR004908; IPR011987; IPR011989; IPR016024
Caenorhabditis elegans	vacuolar atp synthase subunit h	14	F:GO:0046961; P:GO:0008340; F:GO:0008553; P:GO:0040007; P:GO:0033227; P:GO:0040011; P:GO:0040002; P:GO:0018996; P:GO:0009792; P:GO:0015986; P:GO:0002119; C:GO:0000221; C:GO:0005886; F:GO:0005488	-	EC:3.6.3.14; EC:3.6.3.6	IPR004908; IPR011987; IPR011989; IPR016024
Caenorhabditis elegans	tetraspanin family protein	1	C:GO:0016021	-		IPR008952; IPR018499; PTHR19282 (PANTHER), PTHR19282:SF65 (PANTHER), SignalP (SIGNALP)
Caenorhabditis remanei	hypothetical protein CRE_21280 [Caenorhabditis remanei]	0				IPR015063
	-	0				-
Caenorhabditis elegans	olin-like family member (gsnl-1)	0		F:GO:0003779		IPR007122; PTHR11977:SF8 (PANTHER)
	-	0				-
	-	0				-
Homo sapiens	hCG2042149 [Homo sapiens]	0				-
Caenorhabditis briggsae	mboat family protein	1	P:GO:0010171	-		PTHR13906 (PANTHER), PTHR13906:SF2 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	abhydrolase domain containing 4	2	P:GO:0040011; P:GO:0008152	-		G3DSA:3.40.50.1820 (GENE3D), PTHR10992 (PANTHER), PTHR10992:SF19 (PANTHER), SSF53474 (SUPERFAMILY)
Brugia malayi	zinc zz type family protein	0		P:GO:0015870; F:GO:0008270; P:GO:0046716; C:GO:0016010; P:GO:0040017; P:GO:0007271; P:GO:0007529; F:GO:0005515; F:GO:0005509; F:GO:0005277		-

Caenorhabditis elegans	briggsae cbr-crp-1 protein	0		F:GO:0005525; P:GO:0007264; F:GO:0000166; C:GO:0016020; C:GO:0005622		-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein T20B5.2 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				-
Ailuropoda melanoleuca	structure specific recognition protein 1	9	C:GO:0005737; P:GO:0006260; F:GO:0030528; C:GO:0005654; F:GO:0003677; P:GO:0045449; F:GO:0005515; C:GO:0005694; P:GO:0006281	-		IPR000969; PTHR13711 (PANTHER), PTHR13711:SF2 (PANTHER), SSF50729 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF284 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis remanei	briggsae cbr-ocr-2 protein	4	C:GO:0016021; F:GO:0005216; P:GO:0006811; P:GO:0055085	-		IPR020683; PTHR10582 (PANTHER), PTHR10582:SF2 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	scp-2 sterol transfer family protein	0		F:GO:0032934; C:GO:0016020		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	vacuolar protein sorting 13d	0		P:GO:0008104		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Branchiostoma floridae	-dh-cytochrome b5 reductase 3	0		P:GO:0055114; F:GO:0016491; F:GO:0020037		G3DSA:3.40.50.80 (GENE3D), PTHR19370 (PANTHER), PTHR19370:SF1 (PANTHER)
Caenorhabditis briggsae	aldo-keto reductase	4	P:GO:0009792; P:GO:0040010; P:GO:0002119; P:GO:0040011	-		IPR001395; IPR023210; PTHR11732:SF34 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-glr-4 protein	0		F:GO:0004970; F:GO:0005234; C:GO:0016020; F:GO:0005215; P:GO:0006810; C:GO:0030288		IPR015683; G3DSA:3.40.190.10 (GENE3D), PTHR18966:SF39 (PANTHER)
	-	0				-

	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-rpm-1 protein	0		F:GO:0046872; P:GO:0030071; C:GO:0005680; F:GO:0008270; F:GO:0005515; C:GO:0005622		-
Ailuropoda melanoleuca	homer protein homolog 3-like	8	C:GO:0005737; C:GO:0045211; F:GO:0019904; C:GO:0030054; P:GO:0006605; C:GO:0014069; F:GO:0008022; P:GO:0007216	-		SignalP (SIGNALP)
Caenorhabditis briggsae	amino acid transporter family member (aat-5)	3	C:GO:0016020; C:GO:0009986; P:GO:0006810	-		IPR002293; PTHR11785:SF76 (PANTHER)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	5	F:GO:0008667; P:GO:0009239; P:GO:0055114; F:GO:0050662; F:GO:0005515	-	EC:1.3.1.28	-
	-	0				-
Loa loa	uridine cytidine ki-se	0		F:GO:0016740; P:GO:0009058; F:GO:0004386; F:GO:0003677; F:GO:0016757; F:GO:0003676; F:GO:0000166; F:GO:0004849; F:GO:0005524; F:GO:0016301; F:GO:0004845; C:GO:0005575; P:GO:0006777; P:GO:0009116; P:GO:0008152; F:GO:0016773; P:GO:0001906		G3DSA:3.40.50.300 (GENE3D), PF03205 (PFAM), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	fk506-binding protein	4	P:GO:0006457; F:GO:0016887; F:GO:0005524; F:GO:0003755	-	EC:5.2.1.8	IPR001179; G3DSA:3.10.50.40 (GENE3D), PTHR10516:SF29 (PANTHER), SSF54534 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	3	P:GO:0006541; F:GO:0005509; F:GO:0004359	-	EC:3.5.1.2	-
Caenorhabditis elegans	ankyrin repeat-containing protein	0				IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF113 (PANTHER)

Caenorhabditis remanei	phytanoyl- 2-hydroxylase	0		P:GO:0008150; C:GO:0005575		PTHR21308 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-rad-54 protein	5	P:GO:0006915; P:GO:0033554; F:GO:0003676; P:GO:0000003; F:GO:0005515	-		-
Caenorhabditis remanei	myb-like d--binding domain containing protein	0		F:GO:0003677		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis remanei	uncoordi-ted protein isoform partially confirmed by transcript evidence	8	F:GO:0004872; P:GO:0006629; F:GO:0005219; P:GO:0006816; P:GO:0006874; P:GO:0055085; F:GO:0005509; C:GO:0016021	-		IPR000699; IPR015925; PTHR13715:SF11 (PANTHER)
	-	0				SignalP (SIGNALP)
Teladorsagia circumcincta	class 3 lipase protein	2	P:GO:0006629; F:GO:0004806	-	EC:3.1.1.3	-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Angiostrongylus cantonensis	briggsae cbr-cpi-1 protein	0		F:GO:0004869		SignalP (SIGNALP)
Xenopus (Silurana) tropicalis	protein tyrosine receptor f	22	P:GO:0050775; P:GO:0001960; P:GO:0007185; P:GO:0042059; P:GO:0050803; C:GO:0030426; F:GO:0005001; F:GO:0030971; C:GO:0005792; P:GO:0043525; F:GO:0042301; P:GO:0008285; C:GO:0043025; P:GO:0007156; C:GO:0060076; P:GO:0051387; C:GO:0005768; P:GO:0006470; P:GO:0046627; C:GO:0005887; P:GO:0031345; F:GO:0005158	-		IPR000242; IPR000387; IPR016130; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF48 (PANTHER), SSF52799 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis remanei	cation efflux family protein	2	C:GO:0016020; P:GO:0006810	-		G3DSA:1.20.1510.10 (GENE3D), SignalP (SIGNALP)

	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	- ca exchangers family member (ncx-2)	15	P:GO:0002026; P:GO:0055085; C:GO:0030315; F:GO:0005432; P:GO:0040010; F:GO:0031072; F:GO:0005516; C:GO:0016021; C:GO:0005901; P:GO:0051924; P:GO:0000003; P:GO:0002028; C:GO:0005624; P:GO:0007204; P:GO:0007154	-		IPR004837; PTHR11878 (PANTHER), PTHR11878:SF4 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG03789 [Caenorhabditis briggsae]	0		P:GO:0009058; F:GO:0016740; P:GO:0008152; F:GO:0003824		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Pongo abelii	lamin a c	13	C:GO:0005626; C:GO:0016363; P:GO:0006998; P:GO:0035105; C:GO:0005638; P:GO:0007517; P:GO:0007283; N:GO:0090343; P:GO:0055015; F:GO:0005515; C:GO:0048471; C:GO:0005635; F:GO:0005198	-		-
Pongo abelii	insulin-like growth factor binding protein 7	13	P:GO:0051414; P:GO:0050810; P:GO:0007566; P:GO:0001558; C:GO:0005615; P:GO:0009408; P:GO:0008285; P:GO:0007155; P:GO:0032870; P:GO:0014070; F:GO:0005520; P:GO:0032526; C:GO:0031012	-		SignalP (SIGNALP)

Caenorhabditis briggsae	i-d-like protein	9	P:GO:0040022; F:GO:0005488; P:GO:0045132; P:GO:0040007; P:GO:0002119; P:GO:0042127; P:GO:0008406; C:GO:0005737; P:GO:0040020	-		-
Caenorhabditis briggsae	i-d-like protein	9	P:GO:0040022; F:GO:0005488; P:GO:0045132; P:GO:0040007; P:GO:0002119; P:GO:0042127; P:GO:0008406; C:GO:0005737; P:GO:0040020	-		-
	-	0				-
Pongo abelii	glutamate n-methyl d-asparate-associated protein 1 (glutamate binding) isoform cra_a	1	C:GO:0016021	-		SignalP (SIGNALP)
Acyrthosiphon pisum	protein	0		F:GO:0016597; P:GO:0008152; F:GO:0003824; F:GO:0030170; F:GO:0004794		IPR001926; G3DSA:3.40.50.1100 (GENE3D), PTHR10314 (PANTHER), PTHR10314:SF17 (PANTHER)
	-	0				-
Caenorhabditis briggsae	major facilitator superfamily protein	2	P:GO:0055085; C:GO:0016021	-		-
	-	0				SignalP (SIGNALP)
Homo sapiens	transformation-related protein	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-vit-2 protein	4	P:GO:0009792; P:GO:0008340; P:GO:0040010; F:GO:0005515	-		IPR011030; IPR015255; PTHR23345 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-lact-6 protein	4	P:GO:0009792; P:GO:0008340; P:GO:0040010; F:GO:0005515	-		IPR015255; IPR015817; IPR015819; PTHR23345 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-vit-2 protein	4	P:GO:0009792; F:GO:0005515; P:GO:0040010; P:GO:0008340	-		IPR011030; IPR015255; IPR015817; IPR015819; PTHR23345 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-nrf-5 protein	0		F:GO:0008289		IPR017942; IPR017943; G3DSA:3.15.10.10 (GENE3D)
Caenorhabditis elegans	kelch-like 18	1	F:GO:0005515	-		-
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis remanei	briggsae cbr-acy-1 protein	11	P:GO:0006952; P:GO:0008219; C:GO:0016021; F:GO:0004016; P:GO:0007188; P:GO:0009190; P:GO:0042221; P:GO:0002119; P:GO:0040017; C:GO:0005886; P:GO:0030431	-	EC:4.6.1.1	-
	-	0				-
Caenorhabditis elegans	hypothetical protein M03F8.4 [Caenorhabditis elegans]	0				-
Pongo abelii	glycosyltransferase-like 1b	5	C:GO:0000139; F:GO:0016757; C:GO:0016021; P:GO:0008152; P:GO:0046716	-		PTHR12270 (PANTHER), PTHR12270:SF6 (PANTHER)
Brugia malayi	briggsae cbr-cln- protein	4	C:GO:0016020; C:GO:0005737; P:GO:0008340; P:GO:0046662	-		IPR003492
Ceratitis capitata	histone-lysine n-methyltransferase setmar	0				-
Caenorhabditis briggsae	nuclear receptor nhr-1	12	F:GO:0008270; P:GO:0006355; F:GO:0042802; F:GO:0043565; P:GO:0019915; P:GO:0002119; P:GO:0040017; F:GO:0003700; F:GO:0003707; P:GO:0040018; P:GO:0032094; C:GO:0005634	-		IPR001628; IPR008946; IPR013088; PR00350 (PRINTS), PTHR11865 (PANTHER), PTHR11865:SF218 (PANTHER), SSF57716 (SUPERFAMILY)
Callithrix jacchus	proteasome activator complex subunit 2-like	6	P:GO:0019884; P:GO:0051436; P:GO:0051437; C:GO:0008537; P:GO:0031145; N:GO:0061133	-		SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Pan troglodytes	coiled-coil-helix-coiled-coil-helix domain-containing protein mitochondrial-like	1	C:GO:0005739	-		IPR010625; PTHR13523 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-asd-2 protein	0		F:GO:0003723		-
	-	0				-
Homo sapiens	gpi transamidase component pig-t	7	C:GO:0042765; P:GO:0016255; C:GO:0016023; F:GO:0005515; P:GO:0051402; P:GO:0030182; F:GO:0003923	-		-

Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				G3DSA:2.40.30.10 (GENE3D), PTHR19370 (PANTHER), PTHR19370:SF1 (PANTHER)
Ancylostoma caninum	secreted protein asp-2	0		P:GO:0040011; C:GO:0005576		IPR001283; IPR014044; PTHR10334:SF11 (PANTHER)
Ancylostoma caninum	secreted protein asp-2	0		P:GO:0040011; C:GO:0005576		IPR001283; IPR014044; PTHR10334:SF11 (PANTHER), SignalP (SIGNALP)
Ancylostoma caninum	secreted protein asp-2	0		P:GO:0040011; C:GO:0005576		IPR001283; IPR014044; PTHR10334:SF11 (PANTHER)
Branchiostoma floridae	set binding factor 1	12	F:GO:0008239; P:GO:0006470; C:GO:0016021; F:GO:0046872; P:GO:0001558; P:GO:0007283; P:GO:0006508; F:GO:0008138; F:GO:0008235; F:GO:0016805; C:GO:0005634; F:GO:0001691	-	EC:3.4.13.0	IPR017906; PTHR10807 (PANTHER), PTHR10807:SF4 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis briggsae	ankyrin repeats- partial	4	C:GO:0016021; F:GO:0005216; P:GO:0006811; P:GO:0055085	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0045449; F:GO:0003700; C:GO:0005634; F:GO:0003677		IPR008895
Caenorhabditis remanei	d-2-hydroxyglutarate mitochondrial precursor	3	F:GO:0016491; C:GO:0016020; F:GO:0050660	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	c2 domain containing protein	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis remanei	rte-1 element	0		F:GO:0003723; P:GO:0006278; F:GO:0004519; F:GO:0003964		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-dep-1 protein	5	F:GO:0004725; P:GO:0040026; P:GO:0040027; P:GO:0006470; C:GO:0016021	-	EC:3.1.3.48	-

	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	ribosome biogenesis protein brx1 homolog	6	P:GO:0009987; P:GO:0040010; F:GO:0005488; P:GO:0040035; P:GO:0002119; P:GO:0009792	-		IPR004154; IPR007109; PTHR13634 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis remanei	briggsae cbr-rhgf-1 protein	5	F:GO:0046872; F:GO:0005089; C:GO:0005622; F:GO:0005515; P:GO:0035023	-		IPR002219; G3DSA:3.30.60.20 (GENE3D), SSF57889 (SUPERFAMILY)
Gibberella zeae PH-1	histone acetyltransferase myst2	0		F:GO:0016740; C:GO:0000785; F:GO:0003682; F:GO:0003700; C:GO:0005634; F:GO:0003677; P:GO:0006333; F:GO:0008270; P:GO:0006355; F:GO:0016747; C:GO:0005622; F:GO:0005515; F:GO:0046872; P:GO:0045449		IPR002717; IPR016181; PTHR10615 (PANTHER), PTHR10615:SF28 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Ascaris suum	translation elongation factor tu	8	C:GO:0005737; P:GO:0009792; F:GO:0003746; F:GO:0005525; P:GO:0040010; P:GO:0000003; P:GO:0006414; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000795; IPR004541; G3DSA:3.40.50.300 (GENE3D), PTHR23115 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	hypothetical protein F08A10.1 [Caenorhabditis elegans]	2	F:GO:0005267; C:GO:0016020	-		-
	-	0				SignalP (SIGNALP)
Homo sapiens	slc2a4 regulator	6	C:GO:0005737; F:GO:0003700; F:GO:0003677; C:GO:0005634; F:GO:0008270; P:GO:0006355	-		PTHR13006 (PANTHER)

Saccoglossus kowalevskii	sphk1 (sphingosine ki-se 1) d-erythro-sphingosine ki-se diacylglycerol ki-se sphinganine ki-se	0		F:GO:0016740; C:GO:0005773; F:GO:0004143; P:GO:0009845; P:GO:0009737; C:GO:0009705; F:GO:0016301; F:GO:0008481; F:GO:0017050; P:GO:0007205		-
Caenorhabditis elegans	hypothetical protein R01H2.7 [Caenorhabditis elegans]	0				-
Ciona intestinalis	sp4 protein	0				-
Caenorhabditis elegans	aldehyde dehydroge-se family member (alh-4)	7	F:GO:0004030; C:GO:0005811; P:GO:0008218; P:GO:0055114; C:GO:0016021; P:GO:0006081; C:GO:0005739	-	EC:1.2.1.5	-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	8	P:GO:0055085; C:GO:0016021; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0015914; F:GO:0000287; F:GO:0004012	-	EC:3.6.3.1	IPR001757; IPR008250; G3DSA:2.70.150.10 (GENE3D), PTHR11939:SF18 (PANTHER), SSF81653 (SUPERFAMILY), SSF81665 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Homo sapiens	af061732_1my029 protein	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	clc-type chloride channel family member (clh-3)	7	C:GO:0005902; C:GO:0005886; F:GO:0005515; F:GO:0005254; C:GO:0005626; C:GO:0015629; P:GO:0006821	-		-
	-	0				-
Caenorhabditis remanei	troponin i	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-rgs-6 protein	0		F:GO:0004871		PTHR10845 (PANTHER), PTHR10845:SF14 (PANTHER)
Caenorhabditis elegans	kiaa0975 protein	4	P:GO:0009987; C:GO:0005829; F:GO:0005515; C:GO:0005886	-		IPR001611; PR00019 (PRINTS), G3DSA:3.80.10.10 (GENE3D), PTHR15454 (PANTHER), PTHR15454:SF6 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	P:GO:0019915	-		IPR010291; PTHR23294 (PANTHER)
	-	0				SignalP (SIGNALP)

Brugia malayi	nodal modulator 2	4	C:GO:0016021; P:GO:0000003; F:GO:0030246; F:GO:0004180	-		-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0007155; C:GO:0016021; C:GO:0016020		IPR002159; PTHR11923:SF6 (PANTHER)
Caenorhabditis elegans	briggsae cbr-wrs-2 protein	0		F:GO:0016874; P:GO:0006418; F:GO:0004830; F:GO:0000166; C:GO:0005737; P:GO:0006412; F:GO:0008270; F:GO:0005524; P:GO:0006436; P:GO:0007031; F:GO:0005515; F:GO:0004812; F:GO:0046872; C:GO:0005778		IPR013090
Caenorhabditis briggsae	Hypothetical protein CBG12847 [Caenorhabditis briggsae]	0				-
Caenorhabditis remanei	cre-nhr-62 protein	0				-
Caenorhabditis briggsae	mitochondrial ribosomal protein l24	11	P:GO:0006412; C:GO:0005840; C:GO:0005739; P:GO:0040007; F:GO:0003735; P:GO:0000003; P:GO:0002119; F:GO:0005515; P:GO:0006898; P:GO:0009792; P:GO:0016246	-	EC:3.6.5.3	IPR003256; IPR005824; IPR005825; IPR008991; IPR014723; IPR020894
	-	0				-
Caenorhabditis elegans	uncoordi-ted family member (unc-22)	3	P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	PTHR19900 (PANTHER), PTHR19900:SF7 (PANTHER)
Anthopleura elegantissima	plasma glutamate carboxypeptidase precursor	7	C:GO:0005615; F:GO:0046872; F:GO:0004180; F:GO:0004177; P:GO:0006508; F:GO:0008237; P:GO:0042246	-	EC:3.4.11.0	IPR007484; G3DSA:3.40.630.10 (GENE3D), PTHR12053 (PANTHER), PTHR12053:SF1 (PANTHER), SSF53187 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				IPR000615
	-	0				-
	-	0				-
Caenorhabditis briggsae	germi-l center ki-se family member (gck-1)	4	P:GO:0006468; F:GO:0005515; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF95 (PANTHER)
						-
	-	0				SignalP (SIGNALP)

Monodelphis domestica	chkb protein	0				IPR002573; G3DSA:3.90.1200.10 (GENE3D), PTHR22603:SF7 (PANTHER)
	-	0				SignalP (SIGNALP)
Rattus norvegicus	isoform cra_b	12	C:GO:0005737; C:GO:0005730; P:GO:0008380; C:GO:0030530; C:GO:0005654; C:GO:0005681; F:GO:0003723; F:GO:0005515; F:GO:0003697; P:GO:0006397; P:GO:0007165; P:GO:0044419	-		PTHR10288 (PANTHER), PTHR10288:SF38 (PANTHER)
Caenorhabditis elegans	abhydrolase domain-containing protein fam108a precursor	0		P:GO:0006508; F:GO:0003674; F:GO:0008236; P:GO:0008152; F:GO:0016787; P:GO:0008150; C:GO:0005576; C:GO:0005575		G3DSA:3.40.50.1820 (GENE3D), PTHR12277 (PANTHER), PTHR12277:SF8 (PANTHER)
Brugia malayi	dedicator of cytokinesis protein 6	2	P:GO:0008152; F:GO:0005488	-		PTHR23317 (PANTHER), PTHR23317:SF27 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	aspartyl protease family member (asp-2)	3	P:GO:0008219; F:GO:0005515; F:GO:0008233	-		-
Steinernema carpocapsae	briggsae cbr-asp-2 protein	4	P:GO:0008219; P:GO:0006508; F:GO:0004190; F:GO:0005515	-	EC:3.4.23.0	-
	-	0				-
	-	0				-
Caenorhabditis elegans	eb module family protein	0		F:GO:0008061; P:GO:0006030; P:GO:0005975; F:GO:0016810; F:GO:0003824; C:GO:0005576		-
Caenorhabditis briggsae	ufsp_caebr ame: full=probable ufm1-specific protease short=	0		F:GO:0016787; F:GO:0008234; F:GO:0008233		-
Loa loa	protein ki-se domain containing protein	11	P:GO:0006468; C:GO:0005929; C:GO:0030425; F:GO:0005515; P:GO:0034606; F:GO:0004713; C:GO:0030424; P:GO:0034608; F:GO:0005524; C:GO:0043025; F:GO:0004674	-	EC:2.7.10.0; EC:2.7.11.0	IPR000719; IPR001245; IPR008266; IPR011009; IPR020685; IPR020764; G3DSA:1.10.510.10 (GENE3D)

Caenorhabditis remanei	briggsae cbr-spo-11 protein	5	P:GO:0006259; F:GO:0003677; F:GO:0005524; C:GO:0005694; F:GO:0003824	-		IPR002815; G3DSA:3.40.1360.10 (GENE3D)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0032313; F:GO:0005097; C:GO:0005622		-
	-	0				-
	-	0				-
Caenorhabditis elegans	xylulose ki-se	1	F:GO:0016773	-	EC:2.7.1.0	IPR000577; PTHR10196:SF5 (PANTHER)
Homo sapiens	clu protein	20	P:GO:0009615; P:GO:0051788; P:GO:0048812; C:GO:0034366; P:GO:0045597; P:GO:0032463; P:GO:0043691; P:GO:0031018; C:GO:0016235; P:GO:0006916; P:GO:0008284; P:GO:0006629; P:GO:0006958; F:GO:0051787; C:GO:0048471; P:GO:0001836; P:GO:0045087; P:GO:0006979; C:GO:0031012; C:GO:0005739	-		SignalP (SIGNALP)
Caenorhabditis briggsae	acase_caebr ame: full=alkaline ceramidase short= ase ame: full=alkaline n-acylsphingosine amidohydrolase ame: full=alkaline acylsphingosine deacylase	3	P:GO:0006672; C:GO:0016021; F:GO:0017040	-	EC:3.5.1.23	-
	-	0				SignalP (SIGNALP)
Homo sapiens	protein yif1a	6	C:GO:0000139; C:GO:0005789; C:GO:0005793; P:GO:0016192; C:GO:0016021; P:GO:0015031	-		IPR005578
Caenorhabditis briggsae	briggsae cbr-tat- protein	8	F:GO:0008270; C:GO:0016021; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0015914; F:GO:0000287; F:GO:0004012	-	EC:3.6.3.1	IPR001757; G3DSA:2.70.150.10 (GENE3D), PTHR11939:SF14 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)

Callithrix jacchus	ribosomal protein l9	5	C:GO:0005730; F:GO:0003735; C:GO:0022625; F:GO:0019843; P:GO:0006414	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis remanei	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	calponin homolog	1	F:GO:0005515	-		IPR000557; PTHR18959 (PANTHER), PTHR18959:SF6 (PANTHER)
Caenorhabditis elegans	calponin homolog	1	F:GO:0005515	-		-
	-	0				-
	-	0				IPR015880
	-	0				IPR020683
	-	0				IPR013098; IPR013783
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis remanei	hypothetical protein CRE_11978 [Caenorhabditis remanei]	1	P:GO:0008104	-		PTHR16166 (PANTHER), PTHR16166:SF24 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elongation factor 1 beta	7	P:GO:0009792; P:GO:0002119; F:GO:0003746; C:GO:0005853; P:GO:0040010; P:GO:0006898; P:GO:0006414	-		IPR001326; IPR014038; IPR014717; IPR018940; PTHR11595 (PANTHER), PTHR11595:SF4 (PANTHER)
Angiostrongylus cantonensis	elongation factor 1 beta	7	P:GO:0009792; P:GO:0002119; F:GO:0003746; C:GO:0005853; P:GO:0040010; P:GO:0006898; P:GO:0006414	-		IPR001326; IPR014038; IPR014717; IPR018940; PTHR11595 (PANTHER), PTHR11595:SF4 (PANTHER)
Pongo abelii	adam metallopeptidase domain 15	12	P:GO:0001525; F:GO:0008270; C:GO:0005912; C:GO:0016021; P:GO:0007160; F:GO:0004222; P:GO:0006508; C:GO:0001669; C:GO:0012505; C:GO:0019861; P:GO:0030574; F:GO:0017124	-	EC:3.4.24.0	-
Loa loa	hypothetical protein LOAG_09255 [Loa loa]	0		F:GO:0005488		-
Homo sapiens	un-med protein product [Homo sapiens]	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis elegans	briggsae cbr-nhl-1 protein	0		F:GO:0046872; P:GO:0006915; F:GO:0008270; F:GO:0005515		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				IPR004988
Caenorhabditis briggsae	Hypothetical protein CBG12847 [Caenorhabditis briggsae]	0				-
	-	0				-
Caenorhabditis remanei	briggsae cbr-mup-2 protein	0		P:GO:0040017; P:GO:0040011		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Xenopus (Silurana) tropicalis	tp53-regulating ki-se	0		F:GO:0004674; C:GO:0016020; P:GO:0009103; F:GO:0004672; C:GO:0005634; P:GO:0006468; F:GO:0005524; F:GO:0016301; F:GO:0004713; F:GO:0002039; F:GO:0003824; F:GO:0005515; F:GO:0016773		-
	-	0				-
Caenorhabditis elegans	l2hdh_caeel ame: full=l-2-hydroxyglutarate mitochondrial flags: precursor	4	P:GO:0055114; C:GO:0005739; F:GO:0005488; F:GO:0047545	-	EC:1.1.99.2	IPR006076; G3DSA:3.50.50.60 (GENE3D), PTHR13847 (PANTHER), PTHR13847:SF23 (PANTHER), SSF51905 (SUPERFAMILY)
	-	0				IPR000276
	-	0				-
Caenorhabditis elegans	hypothetical protein W03G9.5 [Caenorhabditis elegans]	0		F:GO:0004672; F:GO:0005524; P:GO:0006468; F:GO:0004674		-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-nol-10 protein	0		P:GO:0000003; P:GO:0040010; P:GO:0009792; P:GO:0002119; P:GO:0040007; P:GO:0018991; C:GO:0005634		IPR012580; PTHR14927 (PANTHER)
Loa loa	amino acids transporter	3	P:GO:0019915; P:GO:0006810; C:GO:0005886	-		IPR002293; PTHR11785:SF74 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis remanei	alpha-tubulin	6	P:GO:0007018; F:GO:0005525; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000217; IPR002452; IPR003008; IPR008280

Caenorhabditis briggsae	mitochondrial carrier protein	6	F:GO:0005488; C:GO:0005743; P:GO:0055085; C:GO:0016021; P:GO:0019915; F:GO:0005215	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF75 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-lap-1 protein	2	C:GO:0005622; F:GO:0042802	-		IPR000819; IPR011356; G3DSA:3.40.50.10590 (GENE3D), G3DSA:3.40.630.10 (GENE3D), PTHR11963 (PANTHER), PTHR11963:SF4 (PANTHER), SSF53187 (SUPERFAMILY)
Caenorhabditis remanei	amp-binding enzyme family protein	2	F:GO:0003824; P:GO:0008152	-		-
Homo sapiens	-scent polypeptide-associated complex subunit alpha	7	F:GO:0003677; P:GO:0006350; C:GO:0005854; C:GO:0005634; P:GO:0006412; P:GO:0044419; P:GO:0015031	-	EC:3.6.5.3	IPR002715
	-	0				-
Caenorhabditis remanei	cre-dsc-4 protein	0		P:GO:0040011		-
	-	0				-
	-	0				-
	-	0				-
Callithrix jacchus	heterogeneous nuclear ribonucleoprotein a2 b1	11	C:GO:0005737; C:GO:0005730; P:GO:0050658; C:GO:0030530; C:GO:0005654; C:GO:0005681; F:GO:0003723; F:GO:0005515; F:GO:0043047; P:GO:0000398; F:GO:0000166	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	gamma-interferon inducible lysosomal thiol	0		C:GO:0005576		IPR004911; PTHR13234:SF2 (PANTHER)
Caenorhabditis remanei	briggsae cbr-psr-1 protein	0		F:GO:0070815; C:GO:0005634; F:GO:0016702; P:GO:0055114; P:GO:0016568; F:GO:0016491; P:GO:0018395; F:GO:0005515; F:GO:0046872; P:GO:0006350; P:GO:0045449		-
	-	0				-

Caenorhabditis remanei	briggsae cbr-cdh-1 protein	0		C:GO:0016021; C:GO:0016020; P:GO:0002119; P:GO:0040011; P:GO:0040010; F:GO:0005509; C:GO:0005886; P:GO:0007156; P:GO:0007155		IPR002126; IPR015919; PTHR10596 (PANTHER), PTHR10596:SF77 (PANTHER)
	-	0				SignalP (SIGNALP)
Trichostrongylus vitrinus	serine or cysteine protease inhibitor	2	F:GO:0004867; F:GO:0008233	-		IPR000215; G3DSA:3.30.497.10 (GENE3D)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Tetraodon nigroviridis	translocase of outer mitochondrial membrane 70 homolog a	1	C:GO:0044464	-		IPR011990; IPR013026; IPR019734; PTHR22904 (PANTHER), PTHR22904:SF32 (PANTHER), SSF48452 (SUPERFAMILY)
Tetraodon nigroviridis	translocase of outer mitochondrial membrane 70 homolog a	1	C:GO:0044464	-		IPR011990; IPR013026; IPR019734; PTHR22904 (PANTHER), PTHR22904:SF32 (PANTHER), SSF48452 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Loa loa	rb13-6 antigen	0		C:GO:0016021; C:GO:0016020; F:GO:0016787; F:GO:0003674; F:GO:0004528; F:GO:0003824; C:GO:0005575; F:GO:0004551; P:GO:0008152; P:GO:0008150		IPR017849; IPR017850; PTHR10151 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-cdh-1 protein	1	C:GO:0016020	-		-
Caenorhabditis elegans	dtdp-glucose -dehydratase	9	P:GO:0002119; P:GO:0006694; F:GO:0003854; P:GO:0018991; P:GO:0045226; P:GO:0040011; F:GO:0050662; P:GO:0040007; F:GO:0008831	-	EC:1.1.1.145; EC:1.1.1.133	IPR001509; G3DSA:3.90.25.10 (GENE3D), PTHR10366 (PANTHER), PTHR10366:SF41 (PANTHER)

Caenorhabditis elegans	dihydrolipoamide s-acetyltransferase (e2 component of pyruvate dehydroge-se complex)	10	P:GO:0040010; F:GO:0004742; P:GO:0000003; F:GO:0005515; P:GO:0006096; P:GO:0006898; C:GO:0005967; P:GO:0010510; P:GO:0009792; P:GO:0030431	-	EC:2.3.1.12	IPR001078; G3DSA:3.30.559.10 (GENE3D), PTHR23151 (PANTHER), PTHR23151:SF9 (PANTHER), SSF52777 (SUPERFAMILY)
Cooperia oncophora	latrophilin-like protein 2	6	P:GO:0007218; C:GO:0016021; P:GO:0007165; C:GO:0005886; F:GO:0005529; F:GO:0004930	-		-
Ailuropoda melanoleuca	lysyl oxidase-like 1	7	F:GO:0005507; C:GO:0005615; P:GO:0055114; F:GO:0016641; C:GO:0005578; P:GO:0018277; F:GO:0005515	-	EC:1.4.3.0	-
	-	0				-
Caenorhabditis briggsae	atp-dependent d- helicase recq	5	F:GO:0008026; F:GO:0003676; F:GO:0005524; P:GO:0006974; P:GO:0006310	-		IPR004589; PTHR13710:SF6 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	sh3-domain grb2-like endophilin b2	4	P:GO:0007126; P:GO:0009792; C:GO:0005737; F:GO:0005515	-		G3DSA:2.30.30.40 (GENE3D), PTHR10661 (PANTHER), PTHR10661:SF12 (PANTHER)
	-	0				-
Brugia malayi	d- excision repair protein ercc-6	3	F:GO:0005524; F:GO:0004386; F:GO:0003677	-		IPR000330; IPR014021; PTHR10799 (PANTHER), PTHR10799:SF67 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	neuro-l igcam family member (rig-6)	0		P:GO:0000003; F:GO:0005488; C:GO:0016021; P:GO:0040018		PTHR10489 (PANTHER), PTHR10489:SF38 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	7	P:GO:0009792; P:GO:0002119; P:GO:0055085; P:GO:0040010; P:GO:0000003; P:GO:0042221; C:GO:0016021	-		IPR020846; PTHR10074 (PANTHER), PTHR10074:SF22 (PANTHER), SignalP (SIGNALP)
Loa loa	alg3 protein	5	P:GO:0006487; F:GO:0004584; F:GO:0046527; C:GO:0016021; C:GO:0005783	-	EC:2.4.1.130	-

	-	0				-
	-	0				-
	-	0				IPR013032
Caenorhabditis remanei	ifa-1	4	C:GO:0005882; C:GO:0005737; F:GO:0005198; F:GO:0005515	-		IPR001664; PTHR23239:SF13 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis remanei	elegans protein partially confirmed by transcript evidence	2	P:GO:0055085; C:GO:0016021	-		PTHR11662 (PANTHER), PTHR11662:SF21 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis remanei	briggsae cbr-sulp-3 protein	4	C:GO:0016021; F:GO:0008271; P:GO:0008272; P:GO:0055085	-		IPR011547; PTHR11814 (PANTHER), PTHR11814:SF26 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	zinc carboxypeptidase	3	P:GO:0006508; F:GO:0004181; F:GO:0008270	-	EC:3.4.17.0	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SSF53187 (SUPERFAMILY)
	-	0				-
	-	0				IPR020683; PTHR18958 (PANTHER), PTHR18958:SF271 (PANTHER)
Caenorhabditis elegans	cathepsin a	4	F:GO:0004185; P:GO:0002119; P:GO:0040007; P:GO:0006508	-	EC:3.4.16.0	IPR001563; G3DSA:3.40.50.1820 (GENE3D), PTHR11802:SF9 (PANTHER), SSF53474 (SUPERFAMILY)
Caenorhabditis remanei	alpha-methylacyl- racemase	2	F:GO:0003824; P:GO:0008152	-		-
Caenorhabditis elegans	spondin 1a	0		F:GO:0004867		IPR009465; PTHR11311 (PANTHER), PTHR11311:SF2 (PANTHER), PF06468 (PFAM)
Mus musculus	type i ii iii v alpha	0		P:GO:0007218; F:GO:0003674; F:GO:0004872; F:GO:0004871; C:GO:0016020; F:GO:0008270; P:GO:0008150; C:GO:0005622		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis remanei	hypothetical protein CRE_15394 [Caenorhabditis remanei]	0				-
	-	0				-

Caenorhabditis elegans	rac serine threonine ki-se	10	P:GO:0008286; P:GO:0040010; F:GO:0005516; P:GO:0008340; F:GO:0004674; C:GO:0005622; P:GO:0043053; F:GO:0005524; P:GO:0019915; P:GO:0006468	-	EC:2.7.11.0	-
Caenorhabditis elegans	hypothetical protein K01A2.10 [Caenorhabditis elegans]	1	F:GO:0005515	-		-
	-	0				-
Nematostella vectensis	predicted protein [Nematostella vectensis]	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0008299; F:GO:0016740; P:GO:0002119; P:GO:0009792; P:GO:0040007		IPR008949; PTHR11525 (PANTHER)
Macaca mulatta	programmed cell death 6 interacting protein	10	C:GO:0005815; P:GO:0006915; F:GO:0046983; C:GO:0042470; P:GO:0007049; F:GO:0048306; C:GO:0005829; P:GO:0051301; P:GO:0044419; P:GO:0015031	-		PTHR23030 (PANTHER), PTHR23030:SF11 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-ttr-7 protein	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis remanei	hypothetical protein CRE_05993 [Caenorhabditis remanei]	0				-
Salmo salar	granulin	4	C:GO:0005737; F:GO:0008083; C:GO:0043231; P:GO:0050794	-		IPR000118; PTHR12274 (PANTHER), SignalP (SIGNALP), SSF57277 (SUPERFAMILY)
Saccoglossus kowalevskii	granulins precursor	6	C:GO:0005737; F:GO:0008083; P:GO:0007275; C:GO:0043231; P:GO:0007165; C:GO:0005576	-		IPR000118; PTHR12274 (PANTHER), SignalP (SIGNALP), SSF57277 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis remanei	ubiquitin-conjugating enzyme family protein	9	P:GO:0060711; P:GO:0008284; C:GO:0005624; P:GO:0060712; F:GO:0005515; P:GO:0016567; P:GO:0006916; P:GO:0051246; F:GO:0019787	-		IPR000608; IPR016135; PTHR11621 (PANTHER), PTHR11621:SF9 (PANTHER)
Caenorhabditis remanei	elegans protein confirmed by transcript evidence	2	F:GO:0005515; F:GO:0003677	-		IPR006578
Caenorhabditis elegans	sy-ptotagmin i	4	C:GO:0016020; C:GO:0008021; P:GO:0006810; F:GO:0005215	-		IPR000008; IPR008973; IPR018029; G3DSA:2.60.40.150 (GENE3D), PTHR10024 (PANTHER), PTHR10024:SF40 (PANTHER)
Ancylostoma caninum	briggsae cbr-jnk-1 protein	6	F:GO:0004707; P:GO:0030050; P:GO:0007254; F:GO:0005524; F:GO:0005515; P:GO:0006468	-	EC:2.7.11.24	SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0000166		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein Y119C1A.1 [Caenorhabditis elegans]	0		F:GO:0005515		IPR001876
Caenorhabditis elegans	hypothetical protein Y119C1A.1 [Caenorhabditis elegans]	0		F:GO:0005515		IPR001876
Caenorhabditis elegans	hypothetical protein Y119C1A.1 [Caenorhabditis elegans]	0		F:GO:0005515		IPR001876
	-	0				-
	-	0				-
Caenorhabditis briggsae	ptprf interacting binding protein 1 (liprin beta 1)	0				IPR011510; PTHR12587 (PANTHER), PTHR12587:SF1 (PANTHER)
	-	0				-
	-	0				-

Pongo abelii	type alpha 1 (ehlers-danlos syndrome type autosomal domi-nt) isoform cra_b	22	P:GO:0009314; P:GO:0018149; P:GO:0030168; P:GO:0048565; P:GO:0043206; C:GO:0005586; P:GO:0007229; P:GO:0050777; P:GO:0007507; P:GO:0007160; C:GO:0005615; F:GO:0046332; P:GO:0001501; F:GO:0048407; P:GO:0043588; P:GO:0030199; F:GO:0005178; P:GO:0007179; P:GO:0034097; P:GO:0032964; F:GO:0005201; P:GO:0001568	-		IPR000885; PTHR10499 (PANTHER), PTHR10499:SF71 (PANTHER), PS51461 (PROFILE)
	-	0				IPR007087; IPR015880; SSF57667 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Oscheius sp. (strain CEW1)	briggsae cbr-vit-6 protein	3	P:GO:0006810; F:GO:0022892; P:GO:0033036	-		-
	-	0				-
Caenorhabditis briggsae	tryptophan -dioxyge-se	11	C:GO:0005829; P:GO:0040010; C:GO:0005625; P:GO:0019441; P:GO:0055114; F:GO:0042802; F:GO:0019825; F:GO:0004833; F:GO:0020037; F:GO:0016597; P:GO:0019442	-	EC:1.13.11.11	IPR004981; SSF140959 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein Y71F9AL.1 [Caenorhabditis elegans]	0		F:GO:0003676; F:GO:0008168; P:GO:0032259		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG05371 [Caenorhabditis briggsae]	0		P:GO:0016311; F:GO:0016791; P:GO:0006470; F:GO:0016787; F:GO:0004725; F:GO:0004721		IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis elegans	atp binding domain 4	0		F:GO:0003674; P:GO:0008150; C:GO:0005575		IPR002761; G3DSA:3.90.1490.10 (GENE3D), PTHR12196 (PANTHER), SSF52402 (SUPERFAMILY)
	-	0				-

Homo sapiens	procollagen- -oxoglutarate 5-dioxyge-se 1 precursor	11	P:GO:0001666; P:GO:0055114; P:GO:0008544; F:GO:0016702; F:GO:0008475; F:GO:0031418; C:GO:0030867; F:GO:0042803; F:GO:0005506; P:GO:0046947; P:GO:0006464	-	EC:1.13.11.0; EC:1.14.11.4	IPR001006; PTHR10730 (PANTHER), PTHR10730:SF1 (PANTHER)
Loa loa	elegans protein partially confirmed by transcript evidence	0		F:GO:0003676; P:GO:0002119		IPR003100; IPR003165; IPR012337; G3DSA:2.170.260.10 (GENE3D), PTHR22891 (PANTHER), SSF101690 (SUPERFAMILY)
Loa loa	elegans protein partially confirmed by transcript evidence	0		F:GO:0003676; P:GO:0002119		-
Caenorhabditis briggsae	probable inner membrane protein oxa1l2	2	P:GO:0051205; C:GO:0016021	-		-
Caenorhabditis briggsae	neurotransmitter-gated ion-channel ligand binding domain containing protein	5	C:GO:0016021; C:GO:0030054; C:GO:0045211; F:GO:0005230; P:GO:0006811	-		IPR006201; PTHR18945:SF13 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-dyci-1 protein	12	C:GO:0043234; C:GO:0015630; P:GO:0040007; P:GO:0035046; P:GO:0000226; P:GO:0002119; P:GO:0030154; F:GO:0005515; P:GO:0046907; P:GO:0006898; P:GO:0009653; C:GO:0044430	-		PTHR12442 (PANTHER), PTHR12442:SF22 (PANTHER)
Caenorhabditis elegans	epoxide hydrolase	2	F:GO:0016787; C:GO:0016021	-		G3DSA:3.40.50.1820 (GENE3D), PTHR10992 (PANTHER), PTHR10992:SF22 (PANTHER), SSF53474 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				IPR002717; IPR016181; PTHR10615 (PANTHER), PTHR10615:SF24 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Loa loa	leucine rich repeat family protein	1	P:GO:0009792	-		-

Loa loa	ck1 ttbkl protein ki-se	4	F:GO:0004672; P:GO:0019915; P:GO:0006898; P:GO:0006974	-		IPR000719; IPR011009; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
Homo sapiens	deoxyguanosine ki-se	8	C:GO:0005829; C:GO:0005739; F:GO:0016773; F:GO:0005524; F:GO:0004138; P:GO:0046070; P:GO:0008617; P:GO:0006468	-	EC:2.7.1.0; EC:2.7.1.113	-
	-	0				-
Strongylocentrotus purpuratus	reverse ribonuclease integrase	0		F:GO:0003677; F:GO:0003676; F:GO:0005524; F:GO:0003964; F:GO:0008270; F:GO:0003723; P:GO:0015074; P:GO:0006281; P:GO:0006278; C:GO:0005622; F:GO:0004519; F:GO:0046872; F:GO:0004518		-
Caenorhabditis briggsae	briggsae cbr-dct-10 protein	0		F:GO:0046872; F:GO:0003676; F:GO:0008270		IPR005162
Caenorhabditis elegans	nonsense-mediated mr- decay protein 1	0		F:GO:0004386; F:GO:0016787; F:GO:0003677; F:GO:0000166; C:GO:0005737; F:GO:0017111; F:GO:0008270; F:GO:0005524; P:GO:0000184		-
Caenorhabditis elegans	nonsense-mediated mr- decay protein 1	0		F:GO:0004386; F:GO:0016787; F:GO:0003677; F:GO:0000166; C:GO:0005737; F:GO:0017111; F:GO:0008270; F:GO:0005524; P:GO:0000184		G3DSA:3.40.50.300 (GENE3D), PTHR10887 (PANTHER), SSF52540 (SUPERFAMILY)
Ajellomyces dermatitidis ER-3	conserved hypothetical protein [Ajellomyces dermatitidis ER-3]	0		F:GO:0003676; F:GO:0008270		-
Caenorhabditis elegans	nonsense-mediated mr- decay protein 1	0		F:GO:0004386; F:GO:0016787; F:GO:0003677; F:GO:0000166; C:GO:0005737; F:GO:0017111; F:GO:0008270; F:GO:0005524; P:GO:0000184		G3DSA:3.40.50.300 (GENE3D), PTHR10887 (PANTHER), SSF52540 (SUPERFAMILY)

Caenorhabditis briggsae	briggsae cbr-dct-10 protein	0		F:GO:0046872; F:GO:0003676; F:GO:0008270		IPR005162
	-	0				-
Caenorhabditis briggsae	briggsae cbr-dct-10 protein	0		F:GO:0003676; P:GO:0015074; F:GO:0003682; C:GO:0000785; P:GO:0006333; F:GO:0003677; C:GO:0005634		IPR001878; IPR013084
Caenorhabditis elegans	nonsense-mediated mr- decay protein 1	0		F:GO:0004386; F:GO:0016787; F:GO:0003677; F:GO:0000166; C:GO:0005737; F:GO:0017111; F:GO:0008270; F:GO:0005524; P:GO:0000184		G3DSA:3.40.50.300 (GENE3D), PTHR10887 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-dct-10 protein	0		F:GO:0046872; F:GO:0003676; F:GO:0008270		IPR005162
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	ribose-5-phosphate isomerase	7	P:GO:0009052; F:GO:0005529; C:GO:0000267; P:GO:0040011; F:GO:0004751; P:GO:0019915; C:GO:0005829	-	EC:5.3.1.6	IPR004788; G3DSA:3.30.70.260 (GENE3D), G3DSA:3.40.50.1360 (GENE3D), SSF100950 (SUPERFAMILY), SSF75445 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	beta lysosomal	1	F:GO:0003824	-		IPR013781; PTHR10066 (PANTHER), PTHR10066:SF12 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	tetraspanin family protein	0		F:GO:0046872; C:GO:0016021; C:GO:0016020; P:GO:0030001		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	C:GO:0016021; F:GO:0005488	-		-
Caenorhabditis briggsae	uncoordi-ted family member (unc-89)	0		F:GO:0004672; F:GO:0005524; F:GO:0000166; P:GO:0006468; F:GO:0004674		IPR013098; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)
Brugia malayi	map ki-se ki-se	2	F:GO:0016301; P:GO:0016246	-		IPR000719; IPR001245; IPR011009; G3DSA:1.10.510.10 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF28 (PANTHER)
Caenorhabditis elegans	hypothetical protein F28B4.3 [Caenorhabditis elegans]	0				-
	-	0				-

Angiostrongylus cantonensis	elegans protein confirmed by transcript evidence	3	F:GO:0005515; P:GO:0000003; F:GO:0005529	-		IPR001079; IPR008985; IPR013320; PTHR11346:SF4 (PANTHER)
Ailuropoda melanoleuca	mgc81609 protein	0		C:GO:0016021; C:GO:0016020; P:GO:0050873; C:GO:0005737; F:GO:0003674; C:GO:0005575; C:GO:0005783; P:GO:0008150; C:GO:0005886		PTHR21650 (PANTHER), PTHR21650:SF3 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Callithrix jacchus	protein	0		P:GO:0006412; F:GO:0005488; F:GO:0004045; P:GO:0008152; F:GO:0003824; F:GO:0008270		-
Caenorhabditis sp. PS1010	elegans protein confirmed by transcript evidence	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		C:GO:0016021; P:GO:0016042; P:GO:0006644		SignalP (SIGNALP)
Caenorhabditis elegans	ras-related c3 botulinum toxin substrate 1 (rho small gtp binding protein rac1)	57	F:GO:0005525; P:GO:0006954; P:GO:0030334; P:GO:0030838; P:GO:0050885; P:GO:0048261; P:GO:0007160; C:GO:0030426; P:GO:0043652; C:GO:0005625; P:GO:0031103; P:GO:0048846; P:GO:0016358; C:GO:0030027; C:GO:0005829; P:GO:0043552; P:GO:0040039; P:GO:0008624; P:GO:0033563; C:GO:0009898; C:GO:0000139; P:GO:0045740; P:GO:0035025; P:GO:0007520; P:GO:0016601; P:GO:0031529;	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001806; IPR003578; IPR005225; IPR013753; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF285 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG16894 [Caenorhabditis briggsae]	0				-
	-	0				-
	-	0				-

Caenorhabditis elegans	Hypothetical protein C01B10.11 [Caenorhabditis elegans]	0		P:GO:0040011		-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				G3DSA:2.40.10.10 (GENE3D)
	-	0				-
Brugia malayi	hypothetical protein [Brugia malayi]	0		F:GO:0000166		-
Caenorhabditis elegans	lethal family member (let-805)	8	P:GO:0018996; P:GO:0009792; P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		-
Loa loa	homeodomain interacting protein ki-se family member (hpk-1)	4	P:GO:0006468; F:GO:0005524; P:GO:0008340; F:GO:0004674	-	EC:2.7.11.0	G3DSA:1.10.510.10 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF117 (PANTHER)
Caenorhabditis elegans	uncoordi-ted family member (unc-26)	19	P:GO:0016082; P:GO:0046856; F:GO:0008022; F:GO:0000166; P:GO:0016191; P:GO:0032526; P:GO:0007612; C:GO:0019717; F:GO:0017120; P:GO:0034097; P:GO:0048260; P:GO:0014015; F:GO:0003723; F:GO:0004439; F:GO:0004518; F:GO:0032403; C:GO:0030118; F:GO:0017124; P:GO:0048015	-	EC:3.1.3.36	IPR005135; G3DSA:3.60.10.10 (GENE3D), PTHR11200 (PANTHER), PTHR11200:SF10 (PANTHER)
	-	0				-
Tetraodon nigroviridis	elegans protein confirmed by transcript evidence	5	C:GO:0005743; F:GO:0005515; F:GO:0004458; P:GO:0055114; F:GO:0050660	-	EC:1.1.2.4	IPR006094; IPR016166; IPR016168; PTHR11748 (PANTHER), PTHR11748:SF6 (PANTHER)
Caenorhabditis remanei	cerebral endothelial cell adhesion molecule	6	P:GO:0040035; P:GO:0009103; F:GO:0005515; P:GO:0040010; P:GO:0040011; P:GO:0002009	-		IPR002654; PTHR10730 (PANTHER)
Caenorhabditis remanei	uridine nucleosidase	0		P:GO:0008152; F:GO:0016787; F:GO:0016798; F:GO:0045437		IPR001910; IPR023186
	-	0				-

Ailuropoda melanoleuca	secreted frizzled-related protein 2	53	P:GO:0008284; P:GO:0007584; N:GO:2000041; P:GO:0050680; P:GO:0032582; P:GO:0045669; P:GO:0003214; P:GO:0030336; P:GO:0002063; P:GO:0043065; P:GO:0031668; P:GO:0045766; P:GO:0030199; F:GO:0005178; P:GO:0048546; C:GO:0005615; N:GO:2000035; P:GO:0090179; P:GO:0060349; P:GO:0043154; P:GO:0043508; F:GO:0001968; P:GO:0003151; P:GO:0061056; P:GO:0090263; F:GO:0017147; P:GO:0042733;	-		IPR001134; IPR015526; IPR018933; PTHR11309:SF10 (PANTHER)
Caenorhabditis remanei	elegans protein partially confirmed by transcript evidence	2	F:GO:0004867; C:GO:0016021	-		IPR002223
Loa loa	ubiquitin c	2	C:GO:0005634; C:GO:0005737	-		-
Loa loa	ubiquitin	5	C:GO:0005737; P:GO:0000003; P:GO:0040007; C:GO:0005634; P:GO:0002119	-		IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), PTHR10666:SF9 (PANTHER), SSF54236 (SUPERFAMILY)
	-	0				-
Caenorhabditis remanei	pyruvate carboxylase	6	F:GO:0004736; P:GO:0009252; F:GO:0005524; P:GO:0006094; C:GO:0005737; F:GO:0008716	-	EC:6.4.1.1; EC:6.3.2.4	IPR005479; IPR013816; PTHR18866 (PANTHER), PTHR18866:SF10 (PANTHER)
Homo sapiens	ig kappa light chain	3	C:GO:0005576; F:GO:0003823; P:GO:0006955	-		IPR013783; PTHR23267 (PANTHER), PTHR23267:SF33 (PANTHER), SignalP (SIGNALP)
Ailuropoda melanoleuca	wd repeat-containing protein 1 isoform 2	6	C:GO:0005856; C:GO:0005576; C:GO:0005829; F:GO:0003779; F:GO:0003824; P:GO:0007605	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis remanei	g-protein coupled receptor	0		F:GO:0004872; C:GO:0016021; P:GO:0007186		-

Homo sapiens	chromosome 19 open reading frame 6	4	P:GO:0050873; C:GO:0016021; C:GO:0005783; C:GO:0005886	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F43D9.1 [Caenorhabditis elegans]	0		C:GO:0016020; F:GO:0008158		SignalP (SIGNALP)
Caenorhabditis elegans	guanosine monophosphate reductase	8	P:GO:0009792; P:GO:0002119; F:GO:0046872; P:GO:0009409; F:GO:0003920; P:GO:0055114; P:GO:0040007; P:GO:0009117	-	EC:1.7.1.7	IPR001093; IPR013785; IPR015875; PTHR11911 (PANTHER), PTHR11911:SF7 (PANTHER), SSF51412 (SUPERFAMILY)
Loa loa	four domain-type voltage-gated ion channel alpha-1 subunit	4	C:GO:0016021; F:GO:0005216; P:GO:0006811; P:GO:0055085	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	gns1 sur4 family protein	1	C:GO:0016021	-		-
Loa loa	plasma glutamate carboxypeptidase	0		F:GO:0003674; F:GO:0008237; C:GO:0005576; C:GO:0005575; F:GO:0008233; P:GO:0006508; F:GO:0046872; F:GO:0004180; P:GO:0008150; F:GO:0004177		IPR003137; PTHR12053 (PANTHER), PTHR12053:SF1 (PANTHER)
Pongo abelii	complement component q subcomponent binding protein	6	C:GO:0005886; C:GO:0005759; F:GO:0001849; C:GO:0005634; P:GO:0006955; P:GO:0044419	-		IPR003428; PTHR10826 (PANTHER), PTHR10826:SF3 (PANTHER)
Caenorhabditis elegans	mboat family protein	2	C:GO:0016020; P:GO:0010171	-		IPR004299; PTHR13906 (PANTHER), PTHR13906:SF2 (PANTHER)
	-	0				-
	-	0				IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF181 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG04065 [Caenorhabditis briggsae]	1	P:GO:0040027	-		SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG04065 [Caenorhabditis briggsae]	1	P:GO:0040027	-		SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG04065 [Caenorhabditis briggsae]	1	P:GO:0040027	-		SignalP (SIGNALP)
Caenorhabditis briggsae	uncoordi-ted family member (unc-32)	6	F:GO:0015078; C:GO:0033177; C:GO:0016021; P:GO:0015986; P:GO:0040013; C:GO:0016023	-		IPR002490; PTHR11629:SF23 (PANTHER)
	-	0				-

Caenorhabditis briggsae	probable dimethyladenosine transferase	5	C:GO:0005737; C:GO:0005730; P:GO:0031167; F:GO:0003723; F:GO:0000179	-		IPR001737; IPR020596; G3DSA:3.40.50.150 (GENE3D), SSF53335 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein T06D8.1 [Caenorhabditis elegans]	0		F:GO:0008061; P:GO:0006030; C:GO:0005576		-
Loa loa	briggsae cbr-lact-2 protein	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	26s proteasome regulatory subunit	3	C:GO:0000502; F:GO:0005515; P:GO:0000003	-		IPR000555; G3DSA:3.40.140.10 (GENE3D), PTHR10410 (PANTHER), PTHR10410:SF5 (PANTHER), SignalP (SIGNALP), SSF102712 (SUPERFAMILY)
	-	0				-
Caenorhabditis remanei	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis elegans	eb module family protein	4	P:GO:0018991; P:GO:0040010; P:GO:0040035; P:GO:0040011	-		IPR006149
	-	0				-
	-	0				-
Callithrix jacchus	heterogeneous nuclear ribonucleoprotein a0	5	P:GO:0008380; C:GO:0030530; F:GO:0003723; P:GO:0006397; F:GO:0000166	-		-
Caenorhabditis remanei	elegans protein confirmed by transcript evidence	2	P:GO:0007155; C:GO:0005604	-		-
Loa loa	elegans protein partially confirmed by transcript evidence	5	P:GO:0006468; F:GO:0005515; F:GO:0004713; F:GO:0005524; F:GO:0004674	-	EC:2.7.10.0; EC:2.7.11.0	-
	-	0				-
Loa loa	egg laying defective family member (egl-15)	7	P:GO:0006468; P:GO:0008543; P:GO:0008284; F:GO:0005515; F:GO:0005007; F:GO:0005524; C:GO:0016021	-		IPR000719; IPR001245; IPR011009; IPR020685; IPR020725; G3DSA:1.10.510.10 (GENE3D)
Caenorhabditis elegans	vab-10b protein	0				-
Caenorhabditis remanei	briggsae cbr-nrx-1 protein	0				-
	-	0				-
Loa loa	beta- -galactosyltransferase 6	2	F:GO:0016757; C:GO:0044464	-		-
Anopheles gambiae str. PEST	proclotting enzyme	0		P:GO:0006508; F:GO:0004252; F:GO:0008236; F:GO:0016787; F:GO:0003824; F:GO:0008233		IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR19355 (PANTHER), PTHR19355:SF126 (PANTHER)

	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	ryanodine receptor homologue	10	P:GO:0055085; P:GO:0006629; C:GO:0005875; F:GO:0005509; C:GO:0016021; F:GO:0004872; P:GO:0006874; P:GO:0006816; F:GO:0005219; P:GO:0006936	-		IPR015925; PTHR13715:SF11 (PANTHER)
Loa loa	elegans protein confirmed by transcript evidence	0				IPR001534
	-	0				-
Hydra magnipapillata	haloacid dehaloge-se-like hydrolase family protein	0		F:GO:0003674; F:GO:0016787; P:GO:0008152; F:GO:0003824; P:GO:0008150; C:GO:0005575		G3DSA:3.40.50.1000 (GENE3D), PTHR18901 (PANTHER), SSF56784 (SUPERFAMILY)
Hydra magnipapillata	haloacid dehaloge-se-like hydrolase family protein	0		F:GO:0003674; F:GO:0016787; P:GO:0008152; F:GO:0003824; P:GO:0008150; C:GO:0005575		G3DSA:3.40.50.1000 (GENE3D), PTHR18901 (PANTHER), SSF56784 (SUPERFAMILY)
Hydra magnipapillata	haloacid dehaloge-se-like hydrolase family protein	0		F:GO:0003674; F:GO:0016787; P:GO:0008152; F:GO:0003824; P:GO:0008150; C:GO:0005575		G3DSA:3.40.50.1000 (GENE3D), PTHR18901 (PANTHER), SSF56784 (SUPERFAMILY)
Homo sapiens	fibronectin 1 protein	18	P:GO:0042060; P:GO:0018149; P:GO:0016477; P:GO:0001525; P:GO:0008360; C:GO:0005793; C:GO:0005604; P:GO:0007044; P:GO:0007160; C:GO:0031093; P:GO:0034446; F:GO:0005518; C:GO:0005577; C:GO:0016324; F:GO:0008201; F:GO:0005201; F:GO:0016504; P:GO:0006953	-		IPR003961; IPR008957; IPR013783; PTHR19143 (PANTHER)
	-	0				-
	-	0				-

Loa loa	polymerase iii (d- directed) polypeptide 155kda	8	F:GO:0003899; F:GO:0008270; P:GO:0032728; P:GO:0045087; F:GO:0003677; F:GO:0032549; P:GO:0006351; C:GO:0005666	-	EC:2.7.7.6	IPR007066; IPR015700; PTHR19376 (PANTHER), SSF64484 (SUPERFAMILY)
Caenorhabditis remanei	hypothetical protein CRE_22505 [Caenorhabditis remanei]	0				-
Pan troglodytes	nicoti-mide n-methyltransferase	7	C:GO:0005737; C:GO:0005625; P:GO:0042493; P:GO:0010243; F:GO:0008112; P:GO:0031100; P:GO:0032259	-	EC:2.1.1.1	IPR000940; G3DSA:3.40.50.150 (GENE3D), PTHR10867:SF5 (PANTHER)
Caenorhabditis remanei	cre-npr-13 protein	0				-
	-	0				IPR013032
	-	0				G3DSA:3.80.10.10 (GENE3D)
Caenorhabditis briggsae	ester hydrolase c11orf54 homolog	0		F:GO:0046872; F:GO:0016788; F:GO:0016787; F:GO:0008270; C:GO:0005634		IPR015021; SSF117856 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-ucr- protein	4	P:GO:0009792; P:GO:0000003; P:GO:0040019; P:GO:0040011	-		IPR007863; IPR011237; IPR011249; IPR011765; PTHR11851 (PANTHER), PTHR11851:SF59 (PANTHER)
Caenorhabditis elegans	briggsae cbr-ucr- protein	4	P:GO:0009792; P:GO:0000003; P:GO:0040019; P:GO:0040011	-		IPR007863; IPR011237; IPR011249; IPR011765; PTHR11851 (PANTHER), PTHR11851:SF59 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		IPR004202; G3DSA:4.10.49.10 (GENE3D), SSF81427 (SUPERFAMILY)
Pan troglodytes	fc fragment of alpha	8	P:GO:0006955; P:GO:0019882; F:GO:0030881; C:GO:0016021; F:GO:0019864; F:GO:0004872; P:GO:0007565; C:GO:0042612	-		-
Macaca mulatta	major vault protein	8	C:GO:0005737; C:GO:0005643; P:GO:0042493; F:GO:0005515; P:GO:0055085; P:GO:0051028; C:GO:0030529; P:GO:0015031	-		-
	-	0				-
Caenorhabditis remanei	matrixin family protein	2	F:GO:0046872; P:GO:0008152	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Brugia malayi	sea domain containing protein	0				-

	-	0				-
Angiostrongylus cantonensis	rab interacting factor	6	P:GO:0040035; F:GO:0005085; P:GO:0009792; P:GO:0040010; P:GO:0040011; P:GO:0007264	-		-
Angiostrongylus cantonensis	rab interacting factor	6	P:GO:0040035; F:GO:0005085; P:GO:0009792; P:GO:0040010; P:GO:0040011; P:GO:0007264	-		-
Caenorhabditis elegans	lethal family member (let-805)	8	P:GO:0018996; P:GO:0009792; P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		IPR003961; IPR008957; IPR013783
	-	0				IPR000560; G3DSA:3.40.50.1240 (GENE3D), SignalP (SIGNALP)
Caenorhabditis remanei	nnmt pnmt temt family protein	1	F:GO:0008168	-	EC:2.1.1.0	IPR000940; PTHR10867:SF3 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	small g protein rab	3	P:GO:0015031; F:GO:0005525; P:GO:0007264	-		IPR013753; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF264 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis remanei	oxidase peroxidase	4	F:GO:0020037; P:GO:0055114; F:GO:0004601; P:GO:0006979	-	EC:1.11.1.7	IPR002007; IPR010255; PTHR11475 (PANTHER), PTHR11475:SF9 (PANTHER)
Caenorhabditis elegans	methylmalonyl epimerase	2	P:GO:0046491; C:GO:0005739	-		-
Ailuropoda melanoleuca	otu ubiquitin aldehyde binding 1	5	C:GO:0005737; F:GO:0004843; P:GO:0071108; F:GO:0019784; F:GO:0043130	-		IPR019400; PTHR12931 (PANTHER), PTHR12931:SF6 (PANTHER), SSF54001 (SUPERFAMILY)
Brugia malayi	short-chain dehydroge-se reductase sdr	2	P:GO:0008152; F:GO:0016491	-		IPR002198; IPR016040; PTHR19410:SF85 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Pongo abelii	PREDICTED: hypothetical protein LOC100447004 [Pongo abelii]	0				-
	-	0				-
	-	0				-
	-	0				IPR013930
	-	0				-
	-	0				-

Caenorhabditis elegans	amp-activated protein ki-se gamma subunit	3	P:GO:0015758; F:GO:0003824; P:GO:0005978	-		IPR000644; IPR013785; PTHR13780 (PANTHER), SSF54631 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	hypothetical protein F48E3.2 [Caenorhabditis elegans]	0		C:GO:0016021; C:GO:0016020; P:GO:0055085; P:GO:0009792; F:GO:0005215; P:GO:0006810		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	protein ki-se domain containing protein	8	P:GO:0006468; P:GO:0030154; P:GO:0009103; F:GO:0005515; F:GO:0005524; F:GO:0000287; C:GO:0016020; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017442; IPR020636; IPR020659; G3DSA:1.10.510.10 (GENE3D)
Caenorhabditis briggsae	tbc1 domain member 17	2	C:GO:0005622; F:GO:0005096	-		IPR006162; IPR021935
Caenorhabditis briggsae	tbc1 domain member 17	2	C:GO:0005622; F:GO:0005096	-		IPR006162; IPR021935
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG19249 [Caenorhabditis briggsae]	5	C:GO:0008076; F:GO:0005249; F:GO:0005515; P:GO:0055085; P:GO:0006813	-		-
	-	0				-
Caenorhabditis elegans	hypothetical protein F43C9.2 [Caenorhabditis elegans]	1	F:GO:0005509	-		IPR011992; IPR018247; IPR018249; PTHR23050 (PANTHER), PTHR23050:SF5 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Ailuropoda melanoleuca	eif3b protein	7	C:GO:0005852; F:GO:0003723; P:GO:0045948; F:GO:0032947; F:GO:0003743; C:GO:0005829; F:GO:0000166	-		IPR011400; IPR013979
Caenorhabditis elegans	short-chain dehydroge-se	5	C:GO:0005875; P:GO:0055114; F:GO:0016491; F:GO:0032934; C:GO:0005811	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-

	-	0				-
	-	0				IPR000615; IPR021134; SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	man-n-binding lectin serine protease 1	1	F:GO:0008233	-		IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR19355 (PANTHER), PTHR19355:SF82 (PANTHER)
Caenorhabditis briggsae	phosphatidate cytidylyltransferase	13	P:GO:0016056; P:GO:0016024; P:GO:0007430; P:GO:0008340; P:GO:0040007; P:GO:0007602; P:GO:0000003; P:GO:0043052; P:GO:0002119; F:GO:0004605; C:GO:0005635; C:GO:0005887; C:GO:0005790	-	EC:2.7.7.41	IPR000374; PTHR13773 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-ltd-1 protein	1	F:GO:0008270	-		-
Caenorhabditis briggsae	kynurenine 3-monooxyge-se (kynurenine 3-hydroxylase)	14	P:GO:0019363; F:GO:0016174; C:GO:0005829; P:GO:0009651; C:GO:0016021; C:GO:0005743; P:GO:0019441; P:GO:0055114; F:GO:0009055; C:GO:0005741; P:GO:0019674; F:GO:0004502; F:GO:0050660; P:GO:0070189	-	EC:1.6.3.1; EC:1.14.13.9	-
	-	0				-
	-	0				-

Macaca mulatta	annexin a1	25	P:GO:0018149; P:GO:0006629; F:GO:0030674; P:GO:0006954; P:GO:0007049; F:GO:0005509; P:GO:0030216; F:GO:0005544; P:GO:0006916; F:GO:0005102; P:GO:0050482; C:GO:0005929; F:GO:0019834; P:GO:0006928; P:GO:0042127; P:GO:0007165; C:GO:0042383; C:GO:0016323; C:GO:0005576; F:GO:0005198; P:GO:0007166; C:GO:0005737; P:GO:0031340; C:GO:0001533; C:GO:0005634	-		IPR001464; IPR018502; PTHR10502:SF17 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Ancylostoma ceylanicum	venom-allergen-like protein family member (vap-1)	1	P:GO:0040011	-		IPR001283; IPR014044; SignalP (SIGNALP)
Caenorhabditis remanei	r- dependent r- polymerase family protein	1	F:GO:0005515	-		IPR007855
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis remanei	major facilitator superfamily protein	3	P:GO:0055085; C:GO:0016021; F:GO:0005215	-		-
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	ync3_caeel ame: full= zinc finger protein	0		F:GO:0008270; C:GO:0005622		-
Loa loa	diacylglycerol ki-se	13	F:GO:0004143; F:GO:0008270; F:GO:0003676; P:GO:0023034; P:GO:0006355; F:GO:0005515; F:GO:0003700; F:GO:0000166; F:GO:0019992; P:GO:0007165; F:GO:0003707; P:GO:0007205; C:GO:0005634	-	EC:2.7.1.107	-
	-	0				SignalP (SIGNALP)

Loa loa	prp31 pre-mr- processing factor 31 homolog	12	C:GO:0005687; F:GO:0070990; C:GO:0071339; C:GO:0015030; C:GO:0016607; P:GO:0040035; P:GO:0018996; P:GO:0040011; C:GO:0046540; P:GO:0002009; P:GO:0001703; P:GO:0000244	-		IPR002687; IPR012976; PTHR13904 (PANTHER), SSF89124 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis remanei	briggsae cbr-rhgf-2 protein	1	P:GO:0009792	-		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis remanei	glucose transporter 1 transcript	3	P:GO:0055085; C:GO:0016021; F:GO:0005215	-		-
Caenorhabditis elegans	lethal family member (let-805)	8	P:GO:0018996; P:GO:0009792; P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		-
Loa loa	will die slowly	5	C:GO:0071339; F:GO:0042800; P:GO:0045449; P:GO:0051568; F:GO:0005515	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Ostreococcus tauri	un-med protein product [Ostreococcus tauri]	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	est2_caeel ame: full=esterase cm06b1	1	F:GO:0016787	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-pis-1 protein	2	P:GO:0040018; P:GO:0000003	-		IPR001357; G3DSA:3.40.50.10190 (GENE3D), PTHR23196 (PANTHER), PTHR23196:SF1 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Saccoglossus kowalevskii	endonuclease-reverse partial	0				-

	-	0				-
	-	0				SignalP (SIGNALP)
Homo sapiens	atp synthase f0 subunit 6	6	F:GO:0015078; C:GO:0000276; C:GO:0016021; P:GO:0042776; F:GO:0016887; P:GO:0055093	-		SignalP (SIGNALP)
Homo sapiens	atp synthase f0 subunit 6	6	F:GO:0015078; C:GO:0000276; C:GO:0016021; P:GO:0042776; F:GO:0016887; P:GO:0055093	-		-
Homo sapiens	cytochrome oxydase subunit iii	0				SignalP (SIGNALP)
Homo sapiens	cytochrome oxydase subunit iii	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis remanei	solute carrier family 20 (phosphate transporter) member 1	7	F:GO:0004871; P:GO:0006796; F:GO:0005315; P:GO:0043123; F:GO:0005436; C:GO:0005887; P:GO:0006817	-		IPR001204; PTHR11101:SF12 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	immunoglobulin i-set domain containing protein	0				PTHR10489 (PANTHER), PTHR10489:SF39 (PANTHER)
Caenorhabditis briggsae	eb module family protein	4	P:GO:0018991; P:GO:0040010; P:GO:0040035; P:GO:0040011	-		IPR006149
	-	0				-
Angiostrongylus cantonensis	mida_caeel ame: full=protein mida mitochondrial	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				IPR006162
Homo sapiens	6-pyruvoyl tetrahydropterin synthase	5	F:GO:0046872; F:GO:0003874; P:GO:0006729; C:GO:0005739; F:GO:0042803	-	EC:4.2.3.12	-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	F:GO:0003676; F:GO:0016788	-		-
Ostertagia ostertagi	hypothetical protein [Ostertagia ostertagi]	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-

Homo sapiens	vitamin k epoxide reductase complex subunit 1	12	F:GO:0047057; P:GO:0046677; P:GO:0010243; C:GO:0016021; F:GO:0047058; P:GO:0030193; P:GO:0055114; P:GO:0042371; C:GO:0005792; P:GO:0050820; P:GO:0014070; C:GO:0005789	-	EC:1.1.4.1; EC:1.1.4.2	IPR012932; PTHR14519 (PANTHER)
Caenorhabditis elegans	ephrin b2	1	C:GO:0016020	-		IPR001799; IPR008972; PTHR11304:SF21 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	tr- pseudouridine synthase a	4	F:GO:0003723; P:GO:0001522; F:GO:0009982; P:GO:0008033	-	EC:5.4.99.12	IPR001406; IPR020095; IPR020103
Caenorhabditis elegans	briggsae cbr-hmr-1 protein	12	C:GO:0005911; P:GO:0016339; F:GO:0005515; P:GO:0007412; P:GO:0050774; P:GO:0007156; P:GO:0048676; P:GO:0031290; P:GO:0045467; P:GO:0016318; P:GO:0045463; P:GO:0048841	-		IPR002126; IPR015919; IPR020894; PTHR10596 (PANTHER), PTHR10596:SF114 (PANTHER)
Caenorhabditis remanei	briggsae cbr-dyb-1 protein	10	F:GO:0005277; P:GO:0015870; F:GO:0008270; F:GO:0005509; P:GO:0007271; F:GO:0005515; P:GO:0007529; P:GO:0046716; P:GO:0040017; C:GO:0016010	-		-
Caenorhabditis remanei	tubulin beta-2c chain	6	P:GO:0007018; F:GO:0005525; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000217; IPR002453; IPR003008
Caenorhabditis elegans	hypothetical protein T23F4.2 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	db module family protein	0				-
	-	0				-
	-	0				-
Loa loa	exosome component 7	4	F:GO:0005515; F:GO:0004518; P:GO:0016070; C:GO:0044424	-		SignalP (SIGNALP)

Loa loa	exosome component 7	4	F:GO:0005515; F:GO:0004518; P:GO:0016070; C:GO:0044424	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis remanei	phospholipase c gamma	5	F:GO:0004871; F:GO:0005515; F:GO:0004435; P:GO:0009395; P:GO:0007165	-	EC:3.1.4.11	IPR000008; IPR008973; IPR018029; G3DSA:2.60.40.150 (GENE3D), PTHR10336 (PANTHER), PTHR10336:SF22 (PANTHER)
Ailuropoda melanoleuca	secreted frizzled-related protein 2	53	P:GO:0008284; P:GO:0007584; N:GO:2000041; P:GO:0050680; P:GO:0032582; P:GO:0045669; P:GO:0003214; P:GO:0030336; P:GO:0002063; P:GO:0043065; P:GO:0031668; P:GO:0045766; P:GO:0030199; F:GO:0005178; P:GO:0048546; C:GO:0005615; N:GO:2000035; P:GO:0090179; P:GO:0060349; P:GO:0043154; P:GO:0043508; F:GO:0001968; P:GO:0003151; P:GO:0061056; P:GO:0090263; F:GO:0017147; P:GO:0042733;	-		IPR015526; IPR020067; PTHR11309:SF3 (PANTHER)
Caenorhabditis elegans	briggsae cbr-rpm-1 protein	0		F:GO:0046872; P:GO:0030071; C:GO:0005680; F:GO:0008270; F:GO:0005515; C:GO:0005622		PTHR12846 (PANTHER), PTHR12846:SF2 (PANTHER)
	-	0				PTHR23022 (PANTHER), PTHR23022:SF3 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				IPR013083
	-	0				-
Caenorhabditis briggsae	myosin heavy chain	6	C:GO:0032982; F:GO:0003779; F:GO:0005524; F:GO:0003774; C:GO:0031672; P:GO:0007626	-		-

	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Tetraodon nigroviridis	acyl- synthetase long-chain family member 5	0		P:GO:0046320; C:GO:0005829; C:GO:0005886; P:GO:0006641; P:GO:0009749; F:GO:0003987; P:GO:0008152; C:GO:0016021; P:GO:0010747; P:GO:0009744; C:GO:0016020; C:GO:0005789; P:GO:0034201; P:GO:0070723; C:GO:0005783; F:GO:0003824; P:GO:0007584; C:GO:0005625; P:GO:0015908; P:GO:0010033; P:GO:0010867; P:GO:0006631; F:GO:0005524; C:GO:0005778; C:GO:0005777; C:GO:0005743; P:GO:0008654; C:GO:0005741;		PTHR11968 (PANTHER), PTHR11968:SF8 (PANTHER), SSF56801 (SUPERFAMILY)
	-	0				-
Meloidogyne artiellia	briggsae cbr-lys- protein	4	P:GO:0005975; F:GO:0003824; P:GO:0043170; P:GO:0009056	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Callithrix jacchus	tr- (cytosine-5-)-methyltransferase	6	F:GO:0003676; F:GO:0008415; P:GO:0044260; P:GO:0090304; P:GO:0010467; F:GO:0003886	-	EC:2.1.1.37	SignalP (SIGNALP)
	-	0				IPR003618
	-	0				-
	-	0				-

Caenorhabditis briggsae	vacuolar protein sorting 11	10	P:GO:0040010; C:GO:0030897; P:GO:0008219; F:GO:0046872; P:GO:0000003; P:GO:0018996; P:GO:0010171; F:GO:0005515; P:GO:0009792; P:GO:0040018	-		IPR001841; IPR013083; PTHR23323 (PANTHER), PTHR23323:SF24 (PANTHER), PF12451 (PFAM), SSF57850 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	tpr domain containing protein	2	P:GO:0040010; P:GO:0040017	-		-
Perkinsus marinus ATCC 50983	d- topoisomerase 2-	10	P:GO:0000910; P:GO:0006355; P:GO:0000003; F:GO:0005524; F:GO:0003700; F:GO:0003918; C:GO:0005694; P:GO:0006265; P:GO:0009792; P:GO:0016246	-	EC:5.99.1.3	IPR002205; IPR013758; IPR013760; PTHR10169 (PANTHER), PTHR10169:SF2 (PANTHER)
	-	0				-
Ailuropoda melanoleuca	member ras oncogene family	23	C:GO:0000785; C:GO:0005654; P:GO:0007052; C:GO:0042470; F:GO:0005525; P:GO:0030521; P:GO:0006611; P:GO:0051301; P:GO:0006184; P:GO:0006259; C:GO:0005829; C:GO:0005643; P:GO:0007067; F:GO:0003713; P:GO:0007286; P:GO:0007165; P:GO:0045893; F:GO:0003682; F:GO:0003924; P:GO:0006606; F:GO:0050681; P:GO:0006405; P:GO:0044419	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001806; IPR013753; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF269 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein C50D2.9 [Caenorhabditis elegans]	2	F:GO:0016773; P:GO:0005975	-	EC:2.7.1.0	SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	3-hydroxy-3-methylglutaryl-coenzyme a reductase	6	F:GO:0016616; C:GO:0044425; F:GO:0050662; P:GO:0006694; P:GO:0044281; P:GO:0044237	-	EC:1.1.1.0	IPR002202; IPR004554; IPR009023; IPR009029; IPR023074; IPR023076; G3DSA:1.10.3270.10 (GENE3D), G3DSA:3.30.70.420 (GENE3D)
Caenorhabditis briggsae	Hypothetical protein CBG20279 [Caenorhabditis briggsae]	2	P:GO:0016311; F:GO:0004721	-	EC:3.1.3.16	IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-elo-1 protein	1	C:GO:0016021	-		-
Caenorhabditis remanei	hypothetical protein CRE_19702 [Caenorhabditis remanei]	0		P:GO:0008152; F:GO:0003824		-
Caenorhabditis briggsae	briggsae cbr-tat-3 protein	7	C:GO:0016021; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0015914; F:GO:0000287; F:GO:0004012	-	EC:3.6.3.1	IPR001757; PTHR11939:SF14 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein K06A5.8 [Caenorhabditis elegans]	1	F:GO:0005515	-		PTHR19863 (PANTHER), PTHR19863:SF2 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0006629; F:GO:0016788; F:GO:0016787		-
	-	0				-
Caenorhabditis briggsae	alkyldihydroxyacetonephosphate synthase	6	F:GO:0050660; P:GO:0009792; F:GO:0016491; P:GO:0040007; F:GO:0016740; P:GO:0002119	-		PTHR11748 (PANTHER), PTHR11748:SF3 (PANTHER)
Caenorhabditis elegans	alpha- -glucosyltransferase alg10-b	2	C:GO:0016020; P:GO:0040011	-		IPR007006; PTHR12989:SF10 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				PTHR22989 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis remanei	briggsae cbr-set-18 protein	1	F:GO:0005515	-		-
Caenorhabditis remanei	briggsae cbr-mlt-7 protein	4	F:GO:0020037; P:GO:0055114; F:GO:0004601; P:GO:0006979	-	EC:1.11.1.7	IPR002007; PTHR11475 (PANTHER), PTHR11475:SF9 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	P:GO:0009792	-		-
	-	0				-
	-	0				-

Caenorhabditis briggsae	d- replication licensing factor mcm4	17	F:GO:0003678; F:GO:0016851; P:GO:0006268; C:GO:0005730; P:GO:0040007; P:GO:0015995; C:GO:0042555; F:GO:0005524; P:GO:0002119; C:GO:0000785; F:GO:0016887; F:GO:0005515; P:GO:0030174; P:GO:0006997; F:GO:0003697; P:GO:0009792; F:GO:0003682	-	EC:6.6.1.1	IPR001208; IPR003593; IPR008047; IPR012340; IPR016027; IPR018525; G3DSA:3.30.1640.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR11630 (PANTHER), PTHR11630:SF45 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	d- replication licensing factor mcm4	20	F:GO:0003678; F:GO:0016851; P:GO:0006268; C:GO:0005730; F:GO:0046872; P:GO:0040007; P:GO:0015995; C:GO:0042555; F:GO:0009055; F:GO:0005524; P:GO:0002119; C:GO:0000785; F:GO:0016887; F:GO:0005515; P:GO:0030174; P:GO:0006997; F:GO:0003697; P:GO:0009792; P:GO:0006350; F:GO:0003682	-	EC:6.6.1.1	IPR001208; IPR003593; IPR008047; IPR012340; IPR016027; IPR018525; G3DSA:3.30.1640.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR11630 (PANTHER), PTHR11630:SF45 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	phosphatidylinositol glycan anchor class n	4	P:GO:0006506; F:GO:0016740; C:GO:0005783; C:GO:0044425	-		IPR000917; IPR007070; IPR017849; IPR017850; IPR017852
Caenorhabditis briggsae	briggsae cbr-puf-12 protein	0		P:GO:0000003; F:GO:0003723; F:GO:0005488; P:GO:0018991		-
Caenorhabditis elegans	yqjq_caeel ame: full=uncharacterized protein	0		P:GO:0044249		-
Ancylostoma caninum	transforming growth factor beta	2	P:GO:0040007; F:GO:0008083	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Schistosoma japonicum	endonuclease-reverse transcriptase	0		F:GO:0003723; P:GO:0006278; F:GO:0004519; F:GO:0003964		-
Pan troglodytes	protein rer1	2	P:GO:0006890; C:GO:0030173	-		SignalP (SIGNALP)
	-	0				-

Loa loa	kinesin family member 13a	6	P:GO:0007018; F:GO:0005515; F:GO:0005524; F:GO:0003777; P:GO:0015031; C:GO:0005874	-		IPR001752; PTHR16012 (PANTHER), PTHR16012:SF65 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	yrinic acid -diamide mitochondrial precursor	3	P:GO:0009236; F:GO:0008817; F:GO:0005524	-	EC:2.5.1.17	IPR002779; IPR016030; IPR017858
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	udp-n-acetyl-alpha-d-galactosamine:polypeptide n-acetylgalactosaminyltransferase 11 (c-t11)	1	C:GO:0044464	-		-
Caenorhabditis briggsae	Hypothetical protein CBG16766 [Caenorhabditis briggsae]	0				PTHR21579 (PANTHER), PTHR21579:SF2 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	gns1 sur4 family protein	1	C:GO:0016021	-		-
Caenorhabditis elegans	briggsae cbr-rpc-1 protein	3	P:GO:0006350; F:GO:0003899; F:GO:0003677	-	EC:2.7.7.6	IPR015700; PTHR19376 (PANTHER)
Caenorhabditis elegans	a transferase-like family member (acl-6)	0		F:GO:0008415; P:GO:0008152		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	P:GO:0007155; C:GO:0005604	-		IPR002049; IPR013032; G3DSA:2.10.25.10 (GENE3D), PTHR10574 (PANTHER), PTHR10574:SF56 (PANTHER), SSF57196 (SUPERFAMILY)
	-	0				-
Caenorhabditis remanei	transmembrane amino acid transporter protein	3	P:GO:0019915; C:GO:0016020; P:GO:0040011	-		IPR013057; PTHR22950 (PANTHER), SignalP (SIGNALP)
Caenorhabditis remanei	briggsae cbr-pif-1 protein	9	F:GO:0042162; F:GO:0033682; F:GO:0005524; F:GO:0017116; F:GO:0043141; F:GO:0000287; C:GO:0000784; P:GO:0051974; P:GO:0032204	-		IPR010285; PTHR23274 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	solute carrier family 27 (fatty acid transporter) member 4	9	P:GO:0046474; C:GO:0044464; P:GO:0050896; P:GO:0044283; P:GO:0042439; P:GO:0050789; F:GO:0016877; F:GO:0005488; P:GO:0015908	-		PTHR11968 (PANTHER), PTHR11968:SF15 (PANTHER)
	-	0				-
Loa loa	hypothetical protein LOAG_09400 [Loa loa]	0				-

	-	0				-
Caenorhabditis briggsae	tpr domain containing protein	1	F:GO:0005488	-		-
	-	0				SignalP (SIGNALP)
Macaca mulatta	PREDICTED: hypothetical protein LOC100427250 [Macaca mulatta]	0				-
	-	0				-
Loa loa	hypothetical protein LOAG_08413 [Loa loa]	0				IPR010916
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	2	P:GO:0007186; C:GO:0016021	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis remanei	hypothetical protein CRE_16805 [Caenorhabditis remanei]	0				IPR004988
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	transmembrane protein 167b	2	C:GO:0000139; C:GO:0016021	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	ser thr protein phosphatase family protein	0		F:GO:0016787; C:GO:0016021		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	thioredoxin family protein	5	P:GO:0040035; P:GO:0045454; P:GO:0040010; P:GO:0019915; P:GO:0006898	-		-
Loa loa	negative elongation factor c d	0		F:GO:0003746; P:GO:0016481; C:GO:0005634		IPR006942
Ancylostoma ceylanicum	metalloprotease 1 precursor	2	F:GO:0046872; F:GO:0008237	-		IPR001506; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
Ailuropoda melanoleuca	sodium potassium-transporting atpase subunit alpha-3-like	19	F:GO:0005515; P:GO:0045989; P:GO:0045822; F:GO:0003869; C:GO:0005792; C:GO:0016323; C:GO:0016021; F:GO:0046872; P:GO:0006754; C:GO:0042383; F:GO:0005391; P:GO:0045823; P:GO:0042493; P:GO:0031947; P:GO:0006813; P:GO:0002026; F:GO:0005524; P:GO:0008217; P:GO:0006814	-	EC:3.1.3.41; EC:3.6.3.9	IPR000695; IPR001757; IPR005834; G3DSA:1.20.1110.10 (GENE3D), PTHR11939:SF100 (PANTHER), SSF56784 (SUPERFAMILY)
Ancylostoma caninum	secreted protein 4 precursor	0		C:GO:0005576		-
	-	0				-

Homo sapiens	major histocompatibility class dm alpha	6	C:GO:0042613; P:GO:0002504; C:GO:0031902; C:GO:0005765; C:GO:0016021; P:GO:0006955	-		IPR003006; IPR013783; PTHR19944 (PANTHER), PTHR19944:SF13 (PANTHER)
	-	0				-
Loa loa	cathepsin a	2	F:GO:0004185; P:GO:0006508	-	EC:3.4.16.0	IPR001563; G3DSA:3.40.50.1820 (GENE3D), PTHR11802:SF9 (PANTHER), SSF53474 (SUPERFAMILY)
	-	0				-
Loa loa	protein-tyrosine phosphatase containing protein	0		P:GO:0016311; F:GO:0016791; P:GO:0006470; F:GO:0016787; F:GO:0004725; F:GO:0004721		G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF76 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
	-	0				-
Haemonchus contortus	nicotinic acetylcholine receptor non-alpha subunit	6	F:GO:0004872; C:GO:0045211; C:GO:0030054; P:GO:0006811; C:GO:0016021; F:GO:0004889	-		IPR002394; IPR006201; IPR006202; PTHR18945:SF72 (PANTHER)
Caenorhabditis remanei	serotonin octopamine receptor family member (ser-7)	4	P:GO:0007186; C:GO:0016021; P:GO:0007165; F:GO:0004930	-		-
	-	0				-
	-	0				-
	-	0				PTHR12064 (PANTHER), PTHR12064:SF4 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-anc-1 protein	0		F:GO:0003677		PTHR11915 (PANTHER), PTHR11915:SF54 (PANTHER)
Brugia malayi	bromodomain containing protein	2	F:GO:0005488; P:GO:0033563	-		IPR001487; IPR001965; IPR011011; IPR013083; IPR019542; IPR019786; IPR019787; PTHR13793 (PANTHER), PTHR13793:SF29 (PANTHER)
Caenorhabditis elegans	four domain-type voltage-gated ion channel alpha-1 subunit	4	C:GO:0016021; F:GO:0005216; P:GO:0006811; P:GO:0055085	-		PTHR10037 (PANTHER), PTHR10037:SF60 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021		-

Brugia malayi	riken cd- 5730509k17 gene	0		C:GO:0005932; C:GO:0005929; C:GO:0005737; C:GO:0005856; P:GO:0030030; P:GO:0008150; C:GO:0042995; C:GO:0005575		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Ailuropoda melanoleuca	ptbp1 protein	10	C:GO:0005730; P:GO:0008380; C:GO:0030530; F:GO:0004519; C:GO:0005654; F:GO:0005515; F:GO:0003697; P:GO:0006397; F:GO:0008187; F:GO:0000166	-		IPR012677; PTHR11546 (PANTHER), PTHR11546:SF4 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	hippocampus abundant transcript 1	5	P:GO:0015904; P:GO:0055085; C:GO:0016021; P:GO:0046677; F:GO:0015520	-		-
Caenorhabditis briggsae	Hypothetical protein CBG19875 [Caenorhabditis briggsae]	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	peroxisomal membrane protein related family member (pmp-5)	4	F:GO:0042626; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		-
	-	0				-
Caenorhabditis elegans	hypothetical protein C18C4.5 [Caenorhabditis elegans]	0				-
	-	0				IPR002995; PTHR23427 (PANTHER), PTHR23427:SF1 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	histone h2a	12	P:GO:0040010; C:GO:0000786; P:GO:0045132; P:GO:0040035; F:GO:0003677; P:GO:0010171; P:GO:0002119; P:GO:0040011; P:GO:0006334; P:GO:0002009; P:GO:0009792; C:GO:0005634	-		IPR002119; IPR007125; IPR009072

Caenorhabditis briggsae	sodium:neurotransmitter symporter family protein	10	P:GO:0007274; F:GO:0005277; F:GO:0005328; P:GO:0015870; P:GO:0001504; P:GO:0015871; F:GO:0030165; P:GO:0040017; C:GO:0045211; C:GO:0005887	-		IPR000175; PTHR11616:SF17 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	peptidase c13 family protein	7	P:GO:0009792; F:GO:0008233; C:GO:0005770; P:GO:0040015; C:GO:0045177; P:GO:0000003; P:GO:0006508	-		IPR001096; PTHR12000:SF4 (PANTHER)
Caenorhabditis remanei	cre-npr-19 protein	2	P:GO:0007186; C:GO:0016021	-		G3DSA:1.20.1070.10 (GENE3D), PTHR22718 (PANTHER), PTHR22718:SF8 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	dy-min 1-like	14	P:GO:0043653; C:GO:0005829; C:GO:0005777; P:GO:0007006; C:GO:0005741; C:GO:0005792; F:GO:0005515; F:GO:0003924; C:GO:0005801; P:GO:0008152; P:GO:0007275; P:GO:0007154; C:GO:0005783; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Caenorhabditis elegans	dy-min 1-like	14	P:GO:0043653; C:GO:0005829; C:GO:0005777; P:GO:0007006; C:GO:0005741; C:GO:0005792; F:GO:0005515; F:GO:0003924; C:GO:0005801; P:GO:0008152; P:GO:0007275; P:GO:0007154; C:GO:0005783; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-

Caenorhabditis elegans	vesicle-associated membrane protein 2	25	C:GO:0030054; P:GO:0009749; P:GO:0016079; F:GO:0005516; P:GO:0006892; P:GO:0017156; C:GO:0060203; F:GO:0005543; C:GO:0030672; F:GO:0008022; F:GO:0017075; F:GO:0032403; P:GO:0017157; P:GO:0006461; C:GO:0005792; P:GO:0006944; C:GO:0070044; C:GO:0019717; C:GO:0005802; C:GO:0048471; C:GO:0042589; F:GO:0017022; P:GO:0015031; C:GO:0005887; C:GO:0070032	-		IPR001388; IPR016444; G3DSA:1.20.5.110 (GENE3D), PTHR21136 (PANTHER), PTHR21136:SF28 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				IPR008160; PTHR10499 (PANTHER), PTHR10499:SF115 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Homo sapiens	fibronectin 1 protein	13	P:GO:0018149; P:GO:0016477; P:GO:0001525; P:GO:0008360; C:GO:0005793; C:GO:0031093; P:GO:0034446; F:GO:0005518; C:GO:0005577; F:GO:0008201; C:GO:0005578; F:GO:0005201; P:GO:0006953	-		SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-pqn-95 protein	0		F:GO:0005515		IPR013032; SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis remanei	elegans protein partially confirmed by transcript evidence	2	F:GO:0003676; F:GO:0000166	-		IPR019363; PTHR13390 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	epithelial fusion failure family member (eff-1)	0				-
	-	0				-

	-	0				-
Caenorhabditis briggsae	rap gtpase-activating protein	4	F:GO:0005096; C:GO:0005622; P:GO:0051056; F:GO:0005515	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Brugia malayi	gtpase_rho	4	C:GO:0016020; C:GO:0005622; F:GO:0005525; P:GO:0007264	-		-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG01587 [Caenorhabditis briggsae]	0				IPR000938
Caenorhabditis remanei	hypothetical protein CRE_30788 [Caenorhabditis remanei]	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	r- binding identical	5	F:GO:0003723; P:GO:0009792; C:GO:0005622; P:GO:0006378; F:GO:0000166	-		-
Ailuropoda melanoleuca	filamin alpha isoform 2	28	F:GO:0004871; C:GO:0005802; P:GO:0043433; P:GO:0034394; C:GO:0015629; P:GO:0050821; P:GO:0051220; C:GO:0005576; C:GO:0005829; F:GO:0001948; P:GO:0051764; P:GO:0043123; F:GO:0051015; F:GO:0048365; P:GO:0045022; P:GO:0007195; F:GO:0042803; F:GO:0034989; P:GO:0031532; F:GO:0034988; C:GO:0005886; F:GO:0008134; P:GO:0042177; C:GO:0005634; P:GO:0042993; C:GO:0005938; P:GO:0043113	-		-
	-	0				IPR017441; SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis briggsae	beta- -glucuronosyltransferase	2	C:GO:0016021; F:GO:0015018	-	EC:2.4.1.135	IPR005027; G3DSA:3.90.550.10 (GENE3D), PTHR10896:SF2 (PANTHER), SSF53448 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Loa loa	pre-mr--processing factor 19	12	P:GO:0000209; P:GO:0045665; C:GO:0016607; P:GO:0008610; F:GO:0034450; P:GO:0001833; P:GO:0000245; C:GO:0000151; C:GO:0005681; F:GO:0042802; P:GO:0048711; C:GO:0005811	-		-
Caenorhabditis elegans	sh3 and multiple ankyrin repeat domains protein 3-like	2	C:GO:0044464; F:GO:0005515	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR23031 (PANTHER), PTHR23031:SF3 (PANTHER)
	-	0				-
Caenorhabditis remanei	uncoordi-ted family member (unc-70)	0		F:GO:0005200; F:GO:0003779; C:GO:0008091		-
	-	0				SignalP (SIGNALP)
Loa loa	cardiac ankyrin repeat partial	2	F:GO:0004672; F:GO:0000166	-		-
	-	0				-
	-	0				-
Brugia malayi	elegans protein partially confirmed by transcript evidence	1	F:GO:0016787	-		IPR015868; PTHR12544:SF3 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	succinyl- ligase	7	P:GO:0006105; C:GO:0005739; P:GO:0006099; P:GO:0006781; F:GO:0004775; F:GO:0005524; F:GO:0005515	-	EC:6.2.1.5	IPR005809; IPR005811; IPR013650; IPR013815; IPR013816; IPR016102; IPR017866; SSF56059 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Loa loa	protein ki-se domain containing protein	2	F:GO:0005488; F:GO:0016301	-		-
	-	0				IPR000082
Caenorhabditis remanei	briggsae cbr-dep-1 protein	5	F:GO:0004725; P:GO:0040026; P:GO:0040027; P:GO:0006470; C:GO:0016021	-	EC:3.1.3.48	-
Caenorhabditis remanei	elegans protein confirmed by transcript evidence	2	P:GO:0045449; C:GO:0005634	-		IPR015633; PTHR12081:SF7 (PANTHER)
	-	0				-

Caenorhabditis elegans	cystathionine gamma-lyase	13	P:GO:0019346; P:GO:0018272; F:GO:0004123; P:GO:0030308; F:GO:0016769; P:GO:0006749; P:GO:0008285; F:GO:0004121; P:GO:0070814; P:GO:0051289; P:GO:0009792; F:GO:0030170; P:GO:0019344	-	EC:4.4.1.1; EC:4.4.1.8	IPR000277; IPR015421; IPR015422; IPR015424; PTHR11808:SF15 (PANTHER)
Caenorhabditis elegans	hypothetical protein C30B5.5 [Caenorhabditis elegans]	2	P:GO:0007186; C:GO:0016021	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	immunoglobulin i-set domain containing protein	0		F:GO:0005509; F:GO:0003824		-
	-	0				-
Caenorhabditis remanei	briggsae cbr-set-14 protein	0		F:GO:0046872; F:GO:0008270		PTHR12197 (PANTHER), PTHR12197:SF9 (PANTHER)
	-	0				-
	-	0				PTHR11600 (PANTHER), PTHR11600:SF98 (PANTHER)
Ixodes scapularis	mothers against decapentaplegic homolog 3	67	F:GO:0019901; C:GO:0005637; F:GO:0005160; P:GO:0032909; P:GO:0048340; P:GO:0030878; P:GO:0045216; C:GO:0043235; P:GO:0010551; P:GO:0001701; P:GO:0031053; F:GO:0008134; P:GO:0007050; F:GO:0042803; P:GO:0048701; F:GO:0031625; P:GO:0001933; F:GO:0008013; P:GO:0035413; F:GO:0030618; P:GO:0006917; P:GO:0048589; P:GO:0045944; P:GO:0006919; P:GO:0008637; P:GO:0001819; P:GO:0019049;	-		IPR001132; IPR003619; IPR008984; IPR013019; IPR013790; IPR017855; PTHR13703:SF19 (PANTHER)

Caenorhabditis briggsae	protein mto1-like mitochondrial	5	F:GO:0005488; P:GO:0045333; F:GO:0003824; P:GO:0008033; C:GO:0005739	-		IPR002218; PTHR11806 (PANTHER)
Caenorhabditis remanei	elegans protein partially confirmed by transcript evidence	0		C:GO:0034703; P:GO:0055080; F:GO:0005261		-
	-	0				-
	-	0				-
Homo sapiens	complement c1r subcomponent precursor	6	F:GO:0004252; P:GO:0045087; F:GO:0005509; P:GO:0006958; C:GO:0005576; P:GO:0006508	-	EC:3.4.21.0	-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	xanthine dehydroge-se	8	F:GO:0004855; F:GO:0009055; F:GO:0005506; F:GO:0004854; P:GO:0055114; P:GO:0008340; F:GO:0051537; F:GO:0050660	-	EC:1.17.3.2; EC:1.17.1.4	-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical kda protein in ste6-los1 intergenic	1	C:GO:0016021	-		IPR002809; IPR008568
Caenorhabditis elegans	hypothetical kda protein in ste6-los1 intergenic	0				IPR002809; IPR008568; SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical kda protein in ste6-los1 intergenic	0				IPR002809; IPR008568; SignalP (SIGNALP)
Ailuropoda melanoleuca	hla-b associated transcript 1	22	F:GO:0015184; P:GO:0015804; C:GO:0016607; P:GO:0006461; F:GO:0043008; P:GO:0000245; C:GO:0005681; P:GO:0046784; F:GO:0042802; P:GO:0006520; F:GO:0017070; F:GO:0015175; C:GO:0005688; P:GO:0055085; C:GO:0000346; F:GO:0042605; C:GO:0005687; C:GO:0005887; F:GO:0004004; F:GO:0005524; P:GO:0010501; F:GO:0030621	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis briggsae	eb module family protein	4	P:GO:0018991; P:GO:0040010; P:GO:0040035; P:GO:0040011	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	methyltransferase like 6	2	F:GO:0008168; P:GO:0032259	-	EC:2.1.1.0	-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	polymerase (d- directed) epsilon	11	P:GO:0040035; P:GO:0009792; F:GO:0003887; P:GO:0006260; F:GO:0003677; P:GO:0006997; P:GO:0040011; C:GO:0005634; F:GO:0008270; F:GO:0000166; P:GO:0002009	-	EC:2.7.7.7	PTHR10670 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	general transcription factor iih subunit 1	2	P:GO:0008152; F:GO:0016740	-		-
Caenorhabditis briggsae	deoxyribonuclease ii	2	P:GO:0006259; F:GO:0004531	-	EC:3.1.22.1	IPR004947; PTHR10858:SF10 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG08769 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	ring box protein	9	C:GO:0005737; P:GO:0042787; P:GO:0008283; F:GO:0005515; F:GO:0004842; P:GO:0019915; C:GO:0005634; F:GO:0008270; C:GO:0019005	-	EC:6.3.2.19	IPR001841; IPR013083; PTHR11210 (PANTHER), PTHR11210:SF2 (PANTHER), SSF57850 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Ailuropoda melanoleuca	pctaire protein ki-se 1	4	P:GO:0006468; F:GO:0005515; F:GO:0005524; F:GO:0004693	-	EC:2.7.11.22	-
Caenorhabditis elegans	major facilitator superfamily protein	2	P:GO:0006810; P:GO:0019915	-		IPR011701; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11662 (PANTHER), PTHR11662:SF17 (PANTHER), SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	briggsae cbr-nlr-1 protein	0				IPR001791; IPR008985; IPR012680; IPR013320; PTHR10127 (PANTHER), PTHR10127:SF2 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	cysteine synthase	6	C:GO:0005737; F:GO:0030170; F:GO:0004124; F:GO:0005515; P:GO:0006535; F:GO:0016740	-	EC:2.5.1.47	-
Caenorhabditis elegans	uncoordi-ted family member (unc-22)	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	pp-loop atpase superfamily protein	12	P:GO:0006412; C:GO:0005829; P:GO:0034227; P:GO:0048598; P:GO:0048599; P:GO:0007283; F:GO:0005524; F:GO:0016740; P:GO:0040025; P:GO:0002098; F:GO:0000049; P:GO:0006974	-	EC:3.6.5.3	PTHR11807 (PANTHER), PTHR11807:SF3 (PANTHER), SSF52402 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Loa loa	actin-related protein 10	0		C:GO:0005869; C:GO:0005737; C:GO:0005856; P:GO:0008150; P:GO:0007018; F:GO:0005515		IPR004000; G3DSA:3.30.420.40 (GENE3D), PTHR11937:SF14 (PANTHER), SSF53067 (SUPERFAMILY)
Callithrix jacchus	fumarate hydratase	7	C:GO:0045239; C:GO:0005759; P:GO:0048873; P:GO:0006106; P:GO:0006108; P:GO:0006099; F:GO:0004333	-	EC:4.2.1.2	IPR008948; IPR018951; G3DSA:1.10.40.30 (GENE3D), PTHR11444 (PANTHER), PTHR11444:SF1 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	tbc (tre-2 bub2 cdc16) domain family member (tbc-18)	3	F:GO:0005097; C:GO:0005622; P:GO:0032313	-		IPR004012; PTHR22957 (PANTHER), PTHR22957:SF53 (PANTHER)
	-	0				-
Homo sapiens	fk506 binding protein 13kda	5	C:GO:0005789; P:GO:0006457; F:GO:0005528; F:GO:0005515; F:GO:0003755	-	EC:5.2.1.8	-
	-	0				-
	-	0				-
	-	0				-

	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	tr- (adenine-n -)-methyltransferase catalytic subunit trmt61a	5	P:GO:0040010; F:GO:0016429; P:GO:0040035; P:GO:0030488; P:GO:0006898	-	EC:2.1.1.36	IPR014816; G3DSA:3.10.330.20 (GENE3D), G3DSA:3.40.50.150 (GENE3D), PIRSF017269 (PIR), PTHR12133 (PANTHER), SSF53335 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	b-box zinc finger family protein	2	F:GO:0046872; C:GO:0005622	-		PTHR12846 (PANTHER), PTHR12846:SF2 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG05657 [Caenorhabditis briggsae]	0		C:GO:0016021; P:GO:0055085; F:GO:0005215; P:GO:0006810		PTHR11600 (PANTHER), PTHR11600:SF35 (PANTHER)
Pongo abelii	leucine aminopeptidase 3	7	F:GO:0030145; F:GO:0008235; F:GO:0004177; F:GO:0000287; P:GO:0006508; F:GO:0008270; C:GO:0005739	-	EC:3.4.11.0	IPR000819; IPR011356; G3DSA:3.40.630.10 (GENE3D), PTHR11963 (PANTHER), SSF53187 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis remanei	elegans protein partially confirmed by transcript evidence	3	C:GO:0034703; F:GO:0005261; P:GO:0055080	-		-
Brugia malayi	protein-tyrosine phosphatase containing protein	2	F:GO:0004725; P:GO:0006470	-	EC:3.1.3.48	SignalP (SIGNALP)
	-	0				IPR015650; PTHR13140 (PANTHER)
Caenorhabditis elegans	briggsae cbr-cpt-6 protein	1	F:GO:0016740	-		-
Caenorhabditis elegans	alanine aminotransferase	5	F:GO:0030170; P:GO:0000003; F:GO:0016847; P:GO:0009058; F:GO:0008483	-	EC:4.4.1.14; EC:2.6.1.0	IPR001176; IPR004839; IPR015421; IPR015422; IPR015424; PTHR11751 (PANTHER), PTHR11751:SF29 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Pan troglodytes	actin related protein 2 3 subunit 41kda	6	C:GO:0005737; F:GO:0005200; C:GO:0005885; P:GO:0030833; P:GO:0006928; F:GO:0003779	-		SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis briggsae	carboxypeptidase b	1	F:GO:0004180	-		IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), SSF53187 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-nsy-1 protein	4	P:GO:0006468; F:GO:0005515; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	-
Necator americanus	c-type lectin precursor	0		F:GO:0005488; F:GO:0005529		-

Pongo abelii	glutathione s-transferase kappa 1	5	C:GO:0005777; F:GO:0004364; F:GO:0015035; F:GO:0042802; C:GO:0030288	-	EC:2.5.1.18	IPR001853; IPR012336; PTHR13887 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	activating sig-l cointegrator 1 complex subunit 3-like 1	12	P:GO:0018991; C:GO:0005681; F:GO:0008026; P:GO:0040007; F:GO:0003677; F:GO:0005524; P:GO:0007601; P:GO:0002119; F:GO:0005515; P:GO:0000354; C:GO:0005682; P:GO:0009792	-		IPR001650; IPR003593; IPR011545; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR11752 (PANTHER), PTHR11752:SF7 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	activating sig-l cointegrator 1 complex subunit 3-like 1	12	P:GO:0018991; C:GO:0005681; F:GO:0008026; P:GO:0040007; F:GO:0003677; F:GO:0005524; P:GO:0007601; P:GO:0002119; F:GO:0005515; P:GO:0000354; C:GO:0005682; P:GO:0009792	-		IPR001650; IPR003593; IPR011545; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR11752 (PANTHER), PTHR11752:SF7 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis remanei	procollagen- 2-oxoglutarate 5-dioxyge-se 3	5	F:GO:0046872; F:GO:0016705; P:GO:0032870; P:GO:0008045; C:GO:0005783	-		-
Caenorhabditis elegans	hypothetical protein F57B10.9 [Caenorhabditis elegans]	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				PTHR14167 (PANTHER), PTHR14167:SF2 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	choline ethanolamine ki-se	10	F:GO:0005080; F:GO:0004103; P:GO:0006646; C:GO:0005938; P:GO:0006612; F:GO:0004305; F:GO:0000166; F:GO:0019904; F:GO:0005069; C:GO:0005887	-	EC:2.7.1.32; EC:2.7.1.82	IPR011009; G3DSA:3.10.450.110 (GENE3D)

Caenorhabditis briggsae	briggsae cbr-pkc-2 protein	2	F:GO:0004672; F:GO:0000166	-		-
Pongo abelii	integrin beta-2 precursor	14	C:GO:0008305; P:GO:0006915; P:GO:0007267; P:GO:0006954; P:GO:0008360; P:GO:0007229; F:GO:0001948; F:GO:0004872; P:GO:0007160; P:GO:0050730; F:GO:0019901; P:GO:0007159; P:GO:0007275; P:GO:0030593	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis remanei	hypothetical protein CRE_04697 [Caenorhabditis remanei]	0				IPR000242; G3DSA:3.90.190.10 (GENE3D)
	-	0				-
	-	0				-
Caenorhabditis elegans	eating: abnormal pharyngeal pumping family member (eat-20)	4	F:GO:0005488; P:GO:0007275; P:GO:0009987; C:GO:0016020	-		IPR000742; IPR002052; IPR003645; IPR006209; IPR006210; IPR013032; IPR013111; G3DSA:2.10.25.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF8 (PANTHER), SignalP (SIGNALP), SSF57196 (SUPERFAMILY)
Caenorhabditis remanei	briggsae cbr-deg-1 protein	9	F:GO:0005272; P:GO:0015693; P:GO:0007517; P:GO:0006816; P:GO:0040018; P:GO:0040011; P:GO:0008219; C:GO:0016021; P:GO:0006814	-		IPR001873; G3DSA:2.60.470.10 (GENE3D), PTHR11690:SF17 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-
Homo sapiens	ah-k nucleoprotein	3	C:GO:0005634; F:GO:0005515; P:GO:0007399	-		-
	-	0				-
Caenorhabditis remanei	tyrosylprotein sulfotransferase 1	1	F:GO:0008476	-	EC:2.8.2.20	-
	-	0				-
	-	0				-
Caenorhabditis remanei	ryanodine receptor 1b	8	F:GO:0004872; P:GO:0006629; F:GO:0005219; P:GO:0006816; P:GO:0006874; P:GO:0055085; F:GO:0005509; C:GO:0016021	-		IPR015925; PTHR13715:SF8 (PANTHER)
	-	0				SignalP (SIGNALP)
Strongylocentrotus purpuratus	kiaa1636 protein	0				-

	-	0				-
	-	0				-
Saccoglossus kowalevskii	-d-dependent deacetylase sirtuin-6	12	F:GO:0070403; F:GO:0008270; P:GO:0006476; C:GO:0005730; C:GO:0005724; P:GO:0006342; P:GO:0006471; F:GO:0005515; F:GO:0046969; F:GO:0003956; C:GO:0005654; F:GO:0003950	-	EC:2.4.2.31; EC:2.4.2.30	IPR003000; G3DSA:3.40.50.1220 (GENE3D), SSF52467 (SUPERFAMILY)
	-	0				-
Pongo abelii	cathepsin l	5	C:GO:0005576; C:GO:0005764; P:GO:0006508; F:GO:0005515; F:GO:0004197	-	EC:3.4.22.0	IPR013128; IPR013201; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF57 (PANTHER), SSF54001 (SUPERFAMILY)
	-	0				PTHR11295 (PANTHER), PTHR11295:SF6 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Homo sapiens	isoform cra_c	8	P:GO:0045730; C:GO:0005829; F:GO:0004083; P:GO:0043456; F:GO:0004619; F:GO:0019901; P:GO:0006110; F:GO:0004082	-	EC:3.1.3.13; EC:5.4.2.1; EC:5.4.2.4	SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-lmp-1 protein	3	C:GO:0043231; C:GO:0044444; C:GO:0016020	-		IPR002000; SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	solute carrier family member 37	8	P:GO:0048250; P:GO:0040010; F:GO:0005488; F:GO:0005381; C:GO:0016021; C:GO:0005743; P:GO:0034755; P:GO:0009792	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF77 (PANTHER)
	-	0				-

Ailuropoda melanoleuca	spectrin beta 2	14	P:GO:0007182; C:GO:0008091; C:GO:0005730; C:GO:0005829; C:GO:0031430; F:GO:0003779; C:GO:0043234; C:GO:0032437; P:GO:0051693; F:GO:0032403; P:GO:0007184; C:GO:0005886; F:GO:0005516; F:GO:0005200	-		IPR001849; IPR011993; PTHR11915 (PANTHER), PTHR11915:SF48 (PANTHER), SSF50729 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	maf protein	1	F:GO:0005515	-		IPR003697; G3DSA:3.90.950.10 (GENE3D), SSF52972 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	snf2 family n-termi-l domain containing protein	3	F:GO:0005524; F:GO:0004386; F:GO:0003677	-		IPR000330; IPR001650; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10799 (PANTHER), PTHR10799:SF75 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	family with sequence similarity member a	1	F:GO:0005515	-		IPR012486; IPR021819; PTHR13239 (PANTHER)
Caenorhabditis elegans	family with sequence similarity member a	1	F:GO:0005515	-		IPR012486; IPR021819; PTHR13239 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis remanei	briggsae cbr-acy-2 protein	9	C:GO:0016021; F:GO:0004016; P:GO:0007188; P:GO:0009190; P:GO:0002119; F:GO:0000166; P:GO:0040011; P:GO:0040015; C:GO:0005886	-	EC:4.6.1.1	IPR001054; PTHR11920 (PANTHER), PTHR11920:SF12 (PANTHER)
Caenorhabditis briggsae	glycosylation related family member (gly-5)	5	C:GO:0016021; C:GO:0005794; F:GO:0005515; F:GO:0016757; F:GO:0005529	-		PTHR11675 (PANTHER)
	-	0				-
Branchiostoma floridae	atp-binding cassette superfamily	2	F:GO:0016887; F:GO:0005524	-		IPR003439; G3DSA:3.40.50.300 (GENE3D), PTHR19222 (PANTHER), PTHR19222:SF16 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis remanei	elegans protein partially confirmed by transcript evidence	3	F:GO:0015144; C:GO:0016021; P:GO:0002119	-		IPR012435; SignalP (SIGNALP)
	-	0				-
Nematostella vectensis	neurogenic locus notch	0		F:GO:0005488; F:GO:0005509; F:GO:0004867		-

Caenorhabditis briggsae	briggsae cbr-ugt-45 protein	0		P:GO:0008152; F:GO:0016758		SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	ortin family member (fpn-)	0		F:GO:0005381; C:GO:0016021; P:GO:0006826		IPR009716; SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	alpha- -mannosyltransferase alg9-like	0		P:GO:0006506; C:GO:0031227; F:GO:0000030; F:GO:0016757		-
	-	0				-
Equus caballus	n-ethylmaleimide-sensitive factor attachment alpha	14	P:GO:0045176; P:GO:0006892; P:GO:0007420; P:GO:0006891; P:GO:0006508; P:GO:0006944; C:GO:0070044; F:GO:0004190; F:GO:0019905; P:GO:0006886; C:GO:0005576; C:GO:0005783; C:GO:0005794; P:GO:0030182	-	EC:3.4.23.0	-
Caenorhabditis remanei	tubulin beta chain	6	P:GO:0007018; F:GO:0005525; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000217; IPR002453; IPR003008
Caenorhabditis briggsae	zo- pellucida-like domain containing protein	0				IPR001507; PTHR22907 (PANTHER)
Caenorhabditis elegans	briggsae cbr-npp-3 protein	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		C:GO:0016021; C:GO:0016020; F:GO:0008375		IPR003406; PTHR19297:SF4 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-asah-1 protein	0		P:GO:0006629; C:GO:0005764		-
Loa loa	fat tumor suppressor homolog 1	1	C:GO:0016020	-		IPR002126; IPR015919; PTHR10596 (PANTHER), PTHR10596:SF74 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)

Caenorhabditis briggsae	briggsae cbr-tol-1 protein	2	F:GO:0005515; C:GO:0016020	-		IPR000157; IPR001611; PR00019 (PRINTS), G3DSA:3.40.50.10140 (GENE3D), G3DSA:3.80.10.10 (GENE3D), PTHR23154 (PANTHER), PTHR23154:SF118 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)
Caenorhabditis briggsae	domain containing protein	1	F:GO:0005085	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Loa loa	protein-tyrosine phosphatase containing protein	2	P:GO:0016311; F:GO:0004721	-	EC:3.1.3.16	IPR000242; G3DSA:3.90.190.10 (GENE3D), PTHR23219 (PANTHER), PTHR23219:SF2 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis briggsae	calcium binding egf domain containing protein	0		C:GO:0016021; F:GO:0004222; C:GO:0016020; F:GO:0016787; F:GO:0003674; P:GO:0050896; F:GO:0008270; P:GO:0007275; F:GO:0008237; P:GO:0030154; P:GO:0009790; C:GO:0005576; F:GO:0008233; P:GO:0006508; F:GO:0046872; F:GO:0005509; P:GO:0007601		IPR000859; PTHR10127 (PANTHER), PTHR10127:SF72 (PANTHER)
	-	0				-
Caenorhabditis elegans	hunchback	17	P:GO:0045941; F:GO:0008270; P:GO:0007417; P:GO:0042659; P:GO:0001763; P:GO:0007402; P:GO:0007400; P:GO:0035290; F:GO:0016563; P:GO:0040034; P:GO:0007362; P:GO:0008293; C:GO:0005622; F:GO:0003677; P:GO:0007427; P:GO:0007431; P:GO:0035289	-		IPR015880; PTHR10032 (PANTHER), PTHR10032:SF69 (PANTHER)
Apis mellifera	aromatic amino acid decarboxylase	4	F:GO:0004837; P:GO:0044237; F:GO:0004058; P:GO:0044281	-	EC:4.1.1.25; EC:4.1.1.28	IPR002129; IPR010977; IPR015424; G3DSA:1.20.1340.10 (GENE3D)

Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	6	P:GO:0043652; F:GO:0042626; C:GO:0005886; F:GO:0005524; P:GO:0012501; C:GO:0016021	-		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	9	P:GO:0033700; P:GO:0012501; P:GO:0043652; C:GO:0016021; F:GO:0042626; C:GO:0005622; F:GO:0005548; F:GO:0005524; C:GO:0016324	-		-
Ailuropoda melanoleuca	type alpha 2	8	F:GO:0005201; F:GO:0030674; C:GO:0005615; P:GO:0016337; C:GO:0005578; P:GO:0009749; P:GO:0030198; C:GO:0042383	-		-
Haemonchus contortus	gaba a glycine receptor subunit	6	F:GO:0004872; C:GO:0045211; C:GO:0030054; F:GO:0005230; P:GO:0006811; C:GO:0016021	-		IPR006201; PTHR18945:SF14 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis remanei	briggsae cbr-rpy-1 protein	7	C:GO:0005856; C:GO:0045211; P:GO:0007268; C:GO:0030054; F:GO:0033130; P:GO:0019915; F:GO:0008270	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	briggsae cbr-tag-96 protein	0		F:GO:0016740; P:GO:0046835; P:GO:0016310; F:GO:0000166; C:GO:0005737; F:GO:0005524; F:GO:0016301; P:GO:0006012; P:GO:0008152; F:GO:0016773; F:GO:0004335		IPR014721; IPR019539; IPR020568
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	phenylalanyl-tr- synthetase mitochondrial	7	C:GO:0005625; P:GO:0006432; P:GO:0008033; F:GO:0004826; F:GO:0000166; C:GO:0005759; F:GO:0000049	-	EC:6.1.1.20	IPR002319; IPR004530; IPR005121; IPR006195; G3DSA:3.30.930.10 (GENE3D), SSF55681 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	P:GO:0019915	-		SignalP (SIGNALP)
Caenorhabditis remanei	briggsae cbr-sro-1 protein	2	P:GO:0007186; C:GO:0016021	-		PTHR19264 (PANTHER), PTHR19264:SF1 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis remanei	serpentine class e protein 39	0				-
	-	0				-
	-	0				-
Haemochus contortus	elegans protein confirmed by transcript evidence	1	F:GO:0016740	-		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	myosin via	5	P:GO:0009792; F:GO:0003779; C:GO:0016459; F:GO:0005524; F:GO:0003774	-		IPR001609; IPR004009; PTHR13140 (PANTHER), PTHR13140:SF26 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis remanei	aldo keto reductase family protein	4	P:GO:0055114; P:GO:0043050; F:GO:0016491; P:GO:0040011	-		IPR001395; IPR023210; PTHR11732:SF34 (PANTHER)
Caenorhabditis elegans	gex interacting protein family member (gei-3)	0		C:GO:0005634		-
	-	0				-
	-	0				-
Caenorhabditis remanei	briggsae cbr-unc-122 protein	0				-
	-	0				-
Caenorhabditis remanei	briggsae cbr-dhs-20 protein	0		P:GO:0055114; F:GO:0005488; F:GO:0016491; P:GO:0008152; F:GO:0003824		IPR002198; IPR016040; PTHR19410:SF25 (PANTHER)
	-	0				-
Caenorhabditis elegans	tpa: zinc finger protein	0		F:GO:0003676; F:GO:0008270; F:GO:0005515; C:GO:0005622		IPR007087; IPR015880
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis remanei	briggsae cbr-wht-4 protein	3	C:GO:0016020; F:GO:0016887; F:GO:0005524	-		PTHR19241 (PANTHER), PTHR19241:SF30 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	multidrug resistance protein 3	12	P:GO:0007595; C:GO:0016021; F:GO:0042626; P:GO:0006855; C:GO:0046581; F:GO:0005524; F:GO:0005515; P:GO:0014070; P:GO:0033280; P:GO:0009792; P:GO:0046686; C:GO:0005794	-		-
	-	0				-
Caenorhabditis remanei	elegans protein confirmed by transcript evidence	2	P:GO:0016311; F:GO:0004721	-	EC:3.1.3.16	G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Brugia malayi	apoptosis antagonizing transcription factor	0		C:GO:0005634		IPR012617; PTHR15565 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0004725; P:GO:0016311; F:GO:0016791; F:GO:0004721; F:GO:0008138; F:GO:0016787; P:GO:0000003; P:GO:0006470; P:GO:0009792		-
	-	0				-
Caenorhabditis elegans	tlc domain-containing protein 2	1	C:GO:0016020	-		SignalP (SIGNALP)
Caenorhabditis remanei	leucine rich repeat family protein	2	F:GO:0003676; F:GO:0000166	-		-
	-	0				-
	-	0				-
	-	0				PTHR10151 (PANTHER), PTHR10151:SF28 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				IPR001810
Oscheius sp. (strain CEW1)	vitellogenin structural genes (yolk protein genes) protein isoform a	4	P:GO:0009792; P:GO:0008340; P:GO:0040010; F:GO:0005515	-		SignalP (SIGNALP)
Oscheius sp. (strain CEW1)	vitellogenin structural genes (yolk protein genes) family member (vit-2)	4	P:GO:0009792; F:GO:0005515; P:GO:0040010; P:GO:0008340	-		SignalP (SIGNALP)

Caenorhabditis elegans	jumonji domain containing 6	13	P:GO:0048024; P:GO:0070079; F:GO:0033749; P:GO:0048513; P:GO:0018395; F:GO:0070815; P:GO:0006350; F:GO:0042802; P:GO:0030154; P:GO:0002376; P:GO:0070078; F:GO:0033746; C:GO:0005634	-		IPR003347; IPR013129; PTHR12480 (PANTHER), SSF51197 (SUPERFAMILY)
Caenorhabditis briggsae	glucosamine--fructose-6-phosphate aminotransferase	9	P:GO:0000910; F:GO:0004360; P:GO:0016051; P:GO:0009792; C:GO:0005737; P:GO:0000003; P:GO:0040007; F:GO:0005529; P:GO:0002119	-	EC:2.6.1.16	IPR000583; IPR001347; IPR005855; IPR017932; G3DSA:3.40.50.10490 (GENE3D), G3DSA:3.60.20.10 (GENE3D), PTHR10937 (PANTHER), PS51464 (PROFILE), SSF53697 (SUPERFAMILY), SSF56235 (SUPERFAMILY)
Caenorhabditis briggsae	glucosamine--fructose-6-phosphate aminotransferase	9	P:GO:0000910; F:GO:0004360; P:GO:0016051; P:GO:0009792; C:GO:0005737; P:GO:0000003; P:GO:0040007; F:GO:0005529; P:GO:0002119	-	EC:2.6.1.16	IPR000583; IPR001347; IPR005855; IPR017932; G3DSA:3.40.50.10490 (GENE3D), G3DSA:3.60.20.10 (GENE3D), PTHR10937 (PANTHER), PS51464 (PROFILE), SSF53697 (SUPERFAMILY), SSF56235 (SUPERFAMILY)
Caenorhabditis briggsae	glucosamine--fructose-6-phosphate aminotransferase	9	P:GO:0000910; F:GO:0004360; P:GO:0016051; P:GO:0009792; C:GO:0005737; P:GO:0000003; P:GO:0040007; F:GO:0005529; P:GO:0002119	-	EC:2.6.1.16	IPR000583; IPR001347; IPR005855; IPR017932; G3DSA:3.40.50.10490 (GENE3D), G3DSA:3.60.20.10 (GENE3D), PTHR10937 (PANTHER), PS51464 (PROFILE), SSF53697 (SUPERFAMILY), SSF56235 (SUPERFAMILY)
Caenorhabditis elegans	h+-atpase v-type subunit	6	F:GO:0046933; C:GO:0016021; P:GO:0015986; C:GO:0033179; C:GO:0045263; C:GO:0005774	-	EC:3.6.3.14	-
Caenorhabditis briggsae	proteasome (macropain) 26s non- 9	6	F:GO:0005515; P:GO:0051437; P:GO:0051436; C:GO:0044424; P:GO:0070682; P:GO:0031145	-		-
	-	0				-
Loa loa	uracil phosphoribosyltransferase	2	C:GO:0044424; F:GO:0016740	-		-

Homo sapiens	interleukin-32 isoform b	5	P:GO:0006955; P:GO:0006952; C:GO:0005615; P:GO:0007155; F:GO:0005125	-		-
	-	0				-
	-	0				-
Dictyocaulus viviparus	protein l3i10 isoform a	0				SignalP (SIGNALP)
Dictyocaulus viviparus	protein l3i10 isoform b	0				-
Dictyocaulus viviparus	protein l3i10 isoform a	0				SignalP (SIGNALP)
Caenorhabditis elegans	lam-2	2	P:GO:0007155; C:GO:0005578	-		IPR002049; IPR013032; PR00011 (PRINTS), G3DSA:2.10.25.10 (GENE3D), PTHR10574 (PANTHER), PTHR10574:SF48 (PANTHER), SSF57196 (SUPERFAMILY)
Caenorhabditis elegans	protein tyrosine phosphatase isoform cra_a	7	F:GO:0042802; C:GO:0005768; F:GO:0008138; P:GO:0006470; P:GO:0019915; C:GO:0016020; F:GO:0004727	-		IPR000242; IPR000387; G3DSA:3.90.190.10 (GENE3D), PTHR23339 (PANTHER), PTHR23339:SF23 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis elegans	protein tyrosine phosphatase isoform cra_a	7	F:GO:0042802; C:GO:0005768; F:GO:0008138; P:GO:0006470; P:GO:0019915; C:GO:0016020; F:GO:0004727	-		IPR000242; IPR000387; G3DSA:3.90.190.10 (GENE3D), PTHR23339 (PANTHER), PTHR23339:SF23 (PANTHER), SSF52799 (SUPERFAMILY)
Haemonchus contortus	myosin heavy chain	6	C:GO:0032982; F:GO:0003779; F:GO:0005524; F:GO:0003774; C:GO:0031672; P:GO:0007626	-		IPR002928; IPR015650; PTHR13140 (PANTHER)
Caenorhabditis elegans	a-phase-promoting complex subunit 2-like	1	F:GO:0005515	-		-
Caenorhabditis briggsae	glutathione reductase	9	C:GO:0005829; P:GO:0045454; P:GO:0055114; P:GO:0000003; F:GO:0009055; P:GO:0006749; F:GO:0004362; F:GO:0050660; F:GO:0050661	-	EC:1.8.1.7	IPR000815; IPR012999; IPR013027; PR00411 (PRINTS), G3DSA:3.50.50.60 (GENE3D), PTHR22912 (PANTHER), PTHR22912:SF27 (PANTHER), SignalP (SIGNALP), SSF51905 (SUPERFAMILY)
Micromonas pusilla CCMP1545	protein	1	C:GO:0005739	-		-
Sorghum bicolor	hypothetical protein SORBIDRAFT_0070s002020 [Sorghum bicolor]	0				-
Caenorhabditis elegans	hypothetical protein H20J04.3 [Caenorhabditis elegans]	0		F:GO:0046872; P:GO:0008150; F:GO:0008270; F:GO:0005515; C:GO:0005575; F:GO:0003677		IPR006578
	-	0				IPR006578

Caenorhabditis elegans	glutaminyl-tr- synthetase	4	C:GO:0005737; F:GO:0004819; P:GO:0006425; F:GO:0005524	-	EC:6.1.1.18	IPR000924; IPR004514; IPR011035; IPR014729; IPR020056; IPR020058; IPR020059; IPR020061; SSF52374 (SUPERFAMILY)
Caenorhabditis elegans	glutaminyl-tr- synthetase	4	C:GO:0005737; F:GO:0004819; P:GO:0006425; F:GO:0005524	-	EC:6.1.1.18	IPR000924; IPR004514; IPR011035; IPR014729; IPR020056; IPR020058; IPR020059; IPR020061; G3DSA:3.90.800.10 (GENE3D), SSF52374 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-ttr-53 protein	0		F:GO:0046872; P:GO:0006508; F:GO:0008237; F:GO:0016787; F:GO:0004222; F:GO:0008233; F:GO:0008270		-
Caenorhabditis elegans	kiaa1219 protein	0		F:GO:0005096; P:GO:0051056; P:GO:0032859; F:GO:0017123; F:GO:0046982; F:GO:0005515; C:GO:0005622		PTHR21344 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-tag-325 protein	0		P:GO:0007165; F:GO:0005515; C:GO:0005622		IPR001202; G3DSA:2.20.70.10 (GENE3D), PTHR13173 (PANTHER), PTHR13173:SF10 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	aminotransferase class-iii	4	F:GO:0008453; F:GO:0030170; C:GO:0005739; P:GO:0019544	-	EC:2.6.1.44	-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	neuralized family protein	3	F:GO:0046872; P:GO:0009792; P:GO:0000003	-		IPR006573; PTHR12429 (PANTHER)
Caenorhabditis elegans	budding uninhibited by benzimidazoles 1 homolog beta	1	F:GO:0005488	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	eukaryotic translation initiation factor 2a	4	P:GO:0006413; F:GO:0005488; P:GO:0006417; C:GO:0005737	-		PTHR13227 (PANTHER)
Caenorhabditis briggsae	eukaryotic translation initiation factor 2a	3	F:GO:0003743; P:GO:0006412; C:GO:0044424	-	EC:3.6.5.3	IPR013979; IPR015943; PTHR13227 (PANTHER), SSF50960 (SUPERFAMILY)
Brugia malayi	ubiquitin ligase	0		F:GO:0046872; F:GO:0016874; F:GO:0008270; F:GO:0005515; F:GO:0004842		-
Caenorhabditis elegans	rho gtpase activating protein 27	5	C:GO:0005622; P:GO:0043089; F:GO:0030675; P:GO:0006898; F:GO:0017124	-		IPR000198; IPR001849; IPR008936; IPR011993; IPR015767; SSF50729 (SUPERFAMILY)

Mus musculus	ribosomal protein l35	10	C:GO:0005730; P:GO:0009792; P:GO:0002119; F:GO:0003729; F:GO:0003735; F:GO:0005515; P:GO:0000003; C:GO:0022625; P:GO:0040007; P:GO:0006414	-		IPR001854; IPR018254; PTHR13872 (PANTHER)
Caenorhabditis briggsae	transmembrane and ubiquitin-like domain containing 1	1	C:GO:0044464	-		-
Caenorhabditis briggsae	transmembrane and ubiquitin-like domain containing 1	1	C:GO:0044464	-		-
	-	0				-
	-	0				-
Sus scrofa	amine oxidase (flavin containing) domain 2	21	P:GO:0033169; P:GO:0043433; P:GO:0008283; F:GO:0034648; P:GO:0021983; F:GO:0016491; P:GO:0034720; F:GO:0050660; C:GO:0005667; P:GO:0010553; P:GO:0034339; F:GO:0032454; F:GO:0003700; P:GO:0045944; P:GO:0046886; F:GO:0003682; F:GO:0010843; F:GO:0030374; F:GO:0050681; P:GO:0001701; F:GO:0016564	-		IPR002937; G3DSA:1.10.287.80 (GENE3D), G3DSA:3.50.50.60 (GENE3D), G3DSA:3.90.660.10 (GENE3D), PTHR10742 (PANTHER), PTHR10742:SF35 (PANTHER), SSF51905 (SUPERFAMILY), SSF54373 (SUPERFAMILY)
Sus scrofa	amine oxidase (flavin containing) domain 2	21	P:GO:0033169; P:GO:0043433; P:GO:0008283; F:GO:0034648; P:GO:0021983; F:GO:0016491; P:GO:0034720; F:GO:0050660; C:GO:0005667; P:GO:0010553; P:GO:0034339; F:GO:0032454; F:GO:0003700; P:GO:0045944; P:GO:0046886; F:GO:0003682; F:GO:0010843; F:GO:0030374; F:GO:0050681; P:GO:0001701; F:GO:0016564	-		IPR002937; G3DSA:1.10.287.80 (GENE3D), G3DSA:3.50.50.60 (GENE3D), G3DSA:3.90.660.10 (GENE3D), PTHR10742 (PANTHER), PTHR10742:SF35 (PANTHER), SSF51905 (SUPERFAMILY), SSF54373 (SUPERFAMILY)

Sus scrofa	amine oxidase (flavin containing) domain 2	21	P:GO:0033169; P:GO:0043433; P:GO:0008283; F:GO:0034648; P:GO:0021983; F:GO:0016491; P:GO:0034720; F:GO:0050660; C:GO:0005667; P:GO:0010553; P:GO:0034339; F:GO:0032454; F:GO:0003700; P:GO:0045944; P:GO:0046886; F:GO:0003682; F:GO:0010843; F:GO:0030374; F:GO:0050681; P:GO:0001701; F:GO:0016564	-		IPR002937; G3DSA:1.10.287.80 (GENE3D), G3DSA:3.50.50.60 (GENE3D), G3DSA:3.90.660.10 (GENE3D), PTHR10742 (PANTHER), PTHR10742:SF35 (PANTHER), SSF51905 (SUPERFAMILY), SSF54373 (SUPERFAMILY)
Sus scrofa	amine oxidase (flavin containing) domain 2	21	P:GO:0033169; P:GO:0043433; P:GO:0008283; F:GO:0034648; P:GO:0021983; F:GO:0016491; P:GO:0034720; F:GO:0050660; C:GO:0005667; P:GO:0010553; P:GO:0034339; F:GO:0032454; F:GO:0003700; P:GO:0045944; P:GO:0046886; F:GO:0003682; F:GO:0010843; F:GO:0030374; F:GO:0050681; P:GO:0001701; F:GO:0016564	-		IPR002937; G3DSA:1.10.287.80 (GENE3D), G3DSA:3.50.50.60 (GENE3D), G3DSA:3.90.660.10 (GENE3D), PTHR10742 (PANTHER), PTHR10742:SF35 (PANTHER), SSF51905 (SUPERFAMILY), SSF54373 (SUPERFAMILY)
Homo sapiens	chromosome 4 open reading frame 7	1	C:GO:0005576	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	serca (sarco-endoplasmic reticulum calcium atpase) family member (sca-1)	12	F:GO:0005515; P:GO:0006816; C:GO:0016021; C:GO:0033017; F:GO:0046872; P:GO:0006754; C:GO:0005635; P:GO:0051282; F:GO:0005388; P:GO:0007274; C:GO:0005811; F:GO:0005524	-	EC:3.6.3.8	IPR001757; IPR004014; IPR008250; IPR018303; G3DSA:1.20.1110.10 (GENE3D), G3DSA:2.70.150.10 (GENE3D), G3DSA:3.40.1110.10 (GENE3D), PTHR11939:SF94 (PANTHER), SSF81653 (SUPERFAMILY), SSF81660 (SUPERFAMILY), SSF81665 (SUPERFAMILY)

Caenorhabditis elegans	calcium-transporting atpase sarcoplasmic endoplasmic reticulum type (calcium pump)	7	F:GO:0005388; C:GO:0016021; F:GO:0046872; P:GO:0006754; F:GO:0005524; P:GO:0006816; C:GO:0033017	-	EC:3.6.3.8	IPR001757; IPR004014; IPR005782; IPR005834; IPR006068; IPR008250; IPR018303; G3DSA:1.20.1110.10 (GENE3D), G3DSA:2.70.150.10 (GENE3D), G3DSA:3.40.1110.10 (GENE3D), PTHR11939:SF94 (PANTHER), SSF56784 (SUPERFAMILY), SSF81653 (SUPERFAMILY), SSF81660 (SUPERFAMILY), SSF81665 (SUPERFAMILY)
Caenorhabditis elegans	calcium-transporting atpase sarcoplasmic endoplasmic reticulum type (calcium pump)	7	F:GO:0005388; C:GO:0016021; F:GO:0046872; P:GO:0006754; F:GO:0005524; P:GO:0006816; C:GO:0033017	-	EC:3.6.3.8	IPR001757; IPR004014; IPR005782; IPR005834; IPR006068; IPR008250; IPR018303; G3DSA:1.20.1110.10 (GENE3D), G3DSA:2.70.150.10 (GENE3D), G3DSA:3.40.1110.10 (GENE3D), PTHR11939:SF94 (PANTHER), SSF56784 (SUPERFAMILY), SSF81653 (SUPERFAMILY), SSF81660 (SUPERFAMILY), SSF81665 (SUPERFAMILY)
Caenorhabditis elegans	transmembrane protein 56	1	C:GO:0016020	-		IPR006634; SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	glycoprotein-n-acetylgalactosamine 3-beta-galactosyltransferase 1	5	P:GO:0009247; P:GO:0016267; P:GO:0021551; C:GO:0016021; F:GO:0016263	-	EC:2.4.1.122	IPR003378; PTHR23033 (PANTHER), PTHR23033:SF1 (PANTHER), SignalP (SIGNALP)
Gobiocypris rarus	low quality protein: tubulin alpha-1c chain-like	7	P:GO:0007018; F:GO:0005525; F:GO:0005515; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000217; IPR002452; IPR003008
Caenorhabditis elegans	uncoordi-ted family member (unc-83)	0				-
Caenorhabditis elegans	osta1_caeel ame: full=organic solute transporter alpha-like protein	4	C:GO:0016021; P:GO:0009792; P:GO:0006810; F:GO:0005215	-		IPR005178; PTHR23423:SF3 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	uncoordi-ted family member (unc-52)	2	P:GO:0030239; C:GO:0005578	-		IPR007110; IPR013783; PTHR10574 (PANTHER), PTHR10574:SF20 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	succi-te dehydroge-se	8	P:GO:0006810; P:GO:0022900; C:GO:0016021; C:GO:0005749; F:GO:0009055; P:GO:0006099; F:GO:0020037; F:GO:0000104	-	EC:1.3.99.1	IPR000701; IPR014314; IPR014361; IPR018495; G3DSA:1.20.1300.10 (GENE3D), PTHR10978 (PANTHER), SignalP (SIGNALP), SSF81343 (SUPERFAMILY)

Loa loa	2-aminoethanethiol dioxyge-se	0		F:GO:0046872; C:GO:0005739; P:GO:0055114; F:GO:0016491; F:GO:0016702; F:GO:0047800; C:GO:0005575		-
Drosophila ananassae	GF16318 [Drosophila a--ssae]	0				-
Caenorhabditis elegans	jnk sapk-associated protein	12	P:GO:0016192; C:GO:0016021; F:GO:0019894; P:GO:0046328; F:GO:0005078; C:GO:0005925; C:GO:0030140; F:GO:0019901; P:GO:0008045; P:GO:0050908; C:GO:0005576; F:GO:0004888	-		IPR019143; PTHR13886 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	6	C:GO:0005737; F:GO:0005078; F:GO:0019894; P:GO:0046328; P:GO:0016192; F:GO:0019901	-		IPR019143; PTHR13886 (PANTHER)
Caenorhabditis elegans	mitogen-activated protein ki-se 8 interacting protein 3	6	C:GO:0005737; F:GO:0005078; F:GO:0019894; P:GO:0046328; P:GO:0016192; F:GO:0019901	-		IPR015943; IPR019143; PTHR13886 (PANTHER), SSF101908 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	6	C:GO:0005737; F:GO:0005078; F:GO:0019894; P:GO:0046328; P:GO:0016192; F:GO:0019901	-		IPR015943; IPR019143; PTHR13886 (PANTHER), SSF101908 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	6	C:GO:0005737; F:GO:0005078; F:GO:0019894; P:GO:0046328; P:GO:0016192; F:GO:0019901	-		IPR015943; IPR019143; PTHR13886 (PANTHER), SSF101908 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	6	C:GO:0005737; F:GO:0005078; F:GO:0019894; P:GO:0046328; P:GO:0016192; F:GO:0019901	-		IPR015943; IPR019143; PTHR13886 (PANTHER), SSF101908 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	6	C:GO:0005737; F:GO:0005078; F:GO:0019894; P:GO:0046328; P:GO:0016192; F:GO:0019901	-		IPR015943; IPR019143; PTHR13886 (PANTHER), SSF101908 (SUPERFAMILY)
Caenorhabditis briggsae	f-box domain containing protein	0				-

Caenorhabditis elegans	isoform c	7	P:GO:0002119; P:GO:0006144; F:GO:0003876; P:GO:0009168; F:GO:0005515; P:GO:0040010; P:GO:0040011	-	EC:3.5.4.6	IPR001365; PTHR11359 (PANTHER), SSF51556 (SUPERFAMILY)
Trichomonas vaginalis G3	collagen-binding surface protein	0		F:GO:0008061; P:GO:0006030; F:GO:0005488; C:GO:0005576		-
Caenorhabditis elegans	anion bicarbo-te porter family member (abts-1)	13	P:GO:0006814; C:GO:0043229; F:GO:0015106; P:GO:0015701; C:GO:0016021; F:GO:0015293; P:GO:0006821; F:GO:0005515; C:GO:0016324; C:GO:0016323; F:GO:0005452; C:GO:0005737; P:GO:0015992	-		IPR003020; IPR003024; IPR011531; IPR013769; IPR016152; G3DSA:1.10.287.570 (GENE3D), PTHR11453:SF8 (PANTHER)
Caenorhabditis briggsae	anion bicarbo-te porter family member (abts-1)	13	P:GO:0006814; C:GO:0043229; F:GO:0015106; P:GO:0015701; C:GO:0016021; F:GO:0015293; P:GO:0006821; F:GO:0005515; C:GO:0016324; C:GO:0016323; F:GO:0005452; C:GO:0005737; P:GO:0015992	-		IPR003020; IPR003024; IPR011531; IPR013769; IPR016152; G3DSA:1.10.287.570 (GENE3D), PTHR11453:SF8 (PANTHER)
Loa loa	karyopherin beta 1	10	C:GO:0005829; F:GO:0008565; F:GO:0008270; P:GO:0000060; C:GO:0005643; F:GO:0008139; P:GO:0006607; F:GO:0019904; C:GO:0005654; P:GO:0006610	-		IPR001494; IPR011989; IPR016024; PTHR10527 (PANTHER), PTHR10527:SF1 (PANTHER)
Caenorhabditis brenneri	elegans protein confirmed by transcript evidence	0		P:GO:0016539		IPR001534; SignalP (SIGNALP)
Ornithorhynchus anatinus	ribosomal protein s12	4	F:GO:0003735; C:GO:0022627; C:GO:0005739; P:GO:0006414	-		IPR000530; IPR004038; G3DSA:3.30.1330.30 (GENE3D), SSF55315 (SUPERFAMILY)
Brugia malayi	es2 protein	2	F:GO:0005515; P:GO:0045132	-		IPR019148; PTHR12940 (PANTHER)
Brugia malayi	es2 protein	2	F:GO:0005515; P:GO:0045132	-		IPR019148; PTHR12940 (PANTHER)
Brugia malayi	es2 protein	2	F:GO:0005515; P:GO:0045132	-		IPR019148; PTHR12940 (PANTHER)

Brugia malayi	splicing arginine serine-rich 7	6	P:GO:0008380; F:GO:0003723; F:GO:0005515; C:GO:0005634; P:GO:0008406; F:GO:0000166	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG06078 [Caenorhabditis briggsae]	0				PTHR13923 (PANTHER), PTHR13923:SF1 (PANTHER)
Loa loa	arsenical pump-driving atpase	9	F:GO:0046872; F:GO:0016491; F:GO:0005515; P:GO:0006810; P:GO:0055114; F:GO:0016787; F:GO:0005524; C:GO:0005783; P:GO:0006875	-		-
Caenorhabditis elegans	cg9383-pa	8	P:GO:0048024; P:GO:0051726; P:GO:0007517; F:GO:0005515; P:GO:0006334; C:GO:0035059; P:GO:0048813; C:GO:0005678	-		IPR006818
Caenorhabditis elegans	protein ki-se c	5	P:GO:0006468; F:GO:0046872; F:GO:0019992; F:GO:0004698; F:GO:0005524	-		IPR002219; IPR008973; IPR015727; IPR020454; G3DSA:2.60.40.150 (GENE3D), G3DSA:3.30.60.20 (GENE3D), SSF57889 (SUPERFAMILY)
Caenorhabditis briggsae	sig-l recognition particle 9 kda protein	5	C:GO:0005786; P:GO:0045900; F:GO:0008312; F:GO:0005515; P:GO:0006614	-	EC:3.6.5.4	-
Caenorhabditis briggsae	general vesicular transport factor p115	5	F:GO:0042802; P:GO:0032940; P:GO:0019915; P:GO:0006898; P:GO:0040039	-		IPR006955
Caenorhabditis elegans	otu domain containing 7a	1	F:GO:0008233	-		PTHR13367 (PANTHER), PTHR13367:SF6 (PANTHER)
Caenorhabditis elegans	otud7b protein	4	P:GO:0016579; F:GO:0005488; F:GO:0004221; C:GO:0044424	-	EC:3.1.2.15	IPR003323; IPR009060; PTHR13367 (PANTHER), PTHR13367:SF6 (PANTHER)
Caenorhabditis elegans	otu domain containing 7a	0		P:GO:0008150; F:GO:0008270; F:GO:0008233; C:GO:0005575; F:GO:0003677		PTHR13367 (PANTHER), PTHR13367:SF6 (PANTHER)
Loa loa	dedicator of cytokinesis protein 2	0		F:GO:0005525; P:GO:0050790; F:GO:0051020; P:GO:0008150; C:GO:0005575; F:GO:0005085		PTHR23317 (PANTHER), PTHR23317:SF27 (PANTHER), SignalP (SIGNALP)

Loa loa	dedicator of cytokinesis protein 6	0		P:GO:0032259; F:GO:0051020; F:GO:0005085; F:GO:0008168; F:GO:0005525; P:GO:0050790; C:GO:0005575; P:GO:0008150; F:GO:0005488		PTHR23317 (PANTHER), PTHR23317:SF27 (PANTHER)
Caenorhabditis briggsae	g1 to s phase transition 1	7	F:GO:0003746; P:GO:0006479; F:GO:0005525; F:GO:0005515; F:GO:0003747; F:GO:0016779; F:GO:0003924	-	EC:2.7.7.0; EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000795; IPR004161; IPR009000; G3DSA:2.40.30.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF36 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	ras-related protein orab-1	18	P:GO:0008340; P:GO:0007264; P:GO:0006355; P:GO:0040007; P:GO:0006913; P:GO:0018996; F:GO:0005524; P:GO:0002119; P:GO:0040011; F:GO:0008134; P:GO:0006898; P:GO:0006886; P:GO:0048477; P:GO:0009792; C:GO:0005794; C:GO:0005783; C:GO:0005634; F:GO:0005525	-		-
Caenorhabditis briggsae	stress-induced-phosphoprotein 1	1	F:GO:0005488	-		-
Brugia malayi	elegans protein partially confirmed by transcript evidence	13	P:GO:0030900; P:GO:0048041; P:GO:0003007; P:GO:0030036; P:GO:0021575; C:GO:0044425; F:GO:0005515; C:GO:0015629; P:GO:0007165; P:GO:0050790; F:GO:0005096; C:GO:0044430; P:GO:0001843	-		IPR000198; IPR008936; PTHR12659 (PANTHER)
Caenorhabditis elegans	r- binding motif protein 5	2	F:GO:0005515; P:GO:0000003	-		IPR000504; IPR001876; IPR012677; G3DSA:4.10.1060.10 (GENE3D), PTHR13948 (PANTHER), PTHR13948:SF5 (PANTHER), SSF54928 (SUPERFAMILY), SSF90209 (SUPERFAMILY)

Caenorhabditis elegans	r- binding motif protein 5	2	F:GO:0005515; P:GO:0000003	-		IPR000504; IPR001876; IPR012677; G3DSA:4.10.1060.10 (GENE3D), PTHR13948 (PANTHER), PTHR13948:SF5 (PANTHER), SSF54928 (SUPERFAMILY), SSF90209 (SUPERFAMILY)
Caenorhabditis elegans	r- binding motif protein 5	2	F:GO:0005515; P:GO:0000003	-		IPR000504; IPR001876; IPR012677; G3DSA:4.10.1060.10 (GENE3D), PTHR13948 (PANTHER), PTHR13948:SF5 (PANTHER), SSF54928 (SUPERFAMILY), SSF90209 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	leucine rich repeat family protein	0		F:GO:0016787; F:GO:0005515; F:GO:0004721		IPR003599; IPR007110; IPR013783; G3DSA:3.80.10.10 (GENE3D), PTHR10489 (PANTHER), PTHR10489:SF25 (PANTHER), SSF48726 (SUPERFAMILY), SSF52058 (SUPERFAMILY)
Caenorhabditis elegans	leucine rich repeat family protein	0		F:GO:0016787; F:GO:0005515; F:GO:0004721		IPR003599; IPR007110; IPR013783; G3DSA:3.80.10.10 (GENE3D), PTHR10489 (PANTHER), PTHR10489:SF25 (PANTHER), SSF48726 (SUPERFAMILY), SSF52058 (SUPERFAMILY)
Caenorhabditis elegans	leucine rich repeat family protein	0		F:GO:0016787; F:GO:0005515; F:GO:0004721		-
	-	0				-
	-	0				-
Caenorhabditis elegans	solute carrier family 23 member 2-like	3	C:GO:0016021; P:GO:0055085; F:GO:0005215	-		IPR006043; PTHR11119:SF8 (PANTHER), SignalP (SIGNALP)
Brugia malayi	hypothetical protein Bm1_48395 [Brugia malayi]	0				IPR017956
Brugia malayi	hypothetical protein Bm1_48395 [Brugia malayi]	0				IPR017956
Caenorhabditis briggsae	egf-like domain containing protein	0		P:GO:0016539; F:GO:0004180; F:GO:0005509; F:GO:0030246; P:GO:0007156; C:GO:0016020		-
Caenorhabditis briggsae	lipoic acid synthetase	7	P:GO:0040010; F:GO:0051539; P:GO:0002119; P:GO:0008152; P:GO:0009792; F:GO:0016992; C:GO:0005737	-	EC:2.8.1.8	IPR013785; PTHR10949 (PANTHER), SSF102114 (SUPERFAMILY)
Caenorhabditis briggsae	arginyl-tr- synthetase	7	P:GO:0006420; C:GO:0017101; C:GO:0005739; F:GO:0005524; F:GO:0034618; F:GO:0004814; F:GO:0000049	-	EC:6.1.1.19	IPR001278; IPR001412; IPR005148; IPR008909; IPR009080; IPR014729; IPR015945; G3DSA:1.10.730.10 (GENE3D), SSF52374 (SUPERFAMILY)

Loa loa	3-phosphoinositide-dependent protein ki-se 1	10	P:GO:0046620; P:GO:0007276; P:GO:0001558; P:GO:0045793; P:GO:0006916; F:GO:0005515; F:GO:0016301; P:GO:0007166; P:GO:0006468; P:GO:0006974	-		-
Caenorhabditis briggsae	chromosome 2 open reading frame 30	3	F:GO:0001948; C:GO:0005788; P:GO:0030433	-		IPR009011; IPR012913; G3DSA:2.70.130.10 (GENE3D), PTHR15414 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	F:GO:0005488; P:GO:0009987	-		IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR15508 (PANTHER)
Caenorhabditis elegans	vacuolar atp synthase subunit ac39	6	F:GO:0008553; P:GO:0015986; P:GO:0008593; P:GO:0007035; C:GO:0000220; C:GO:0005886	-	EC:3.6.3.6	IPR002843; PTHR11028 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis briggsae	mitogen-activated protein ki-se 11	14	P:GO:0007166; P:GO:0006468; C:GO:0005654; P:GO:0007265; P:GO:0007243; F:GO:0004708; F:GO:0005515; F:GO:0008339; P:GO:0006928; C:GO:0005829; P:GO:0048856; P:GO:0006935; P:GO:0006950; F:GO:0005524	-		IPR000719; IPR003527; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF55 (PANTHER)
Caenorhabditis elegans	briggsae cbr-dys-1 protein	11	F:GO:0005277; P:GO:0015870; C:GO:0005856; P:GO:0007517; C:GO:0045202; P:GO:0007271; F:GO:0003779; P:GO:0046716; P:GO:0040017; C:GO:0016010; C:GO:0005737	-		IPR002017; IPR018159; G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF46 (PANTHER), SSF46966 (SUPERFAMILY)
Brugia malayi	elegans protein confirmed by transcript evidence	8	P:GO:0040022; P:GO:0050789; P:GO:0007126; P:GO:0018991; F:GO:0005515; C:GO:0044444; C:GO:0030529; P:GO:0051729	-		IPR009604; IPR010920; G3DSA:2.30.30.100 (GENE3D), PTHR12854 (PANTHER), PTHR12854:SF7 (PANTHER)

Caenorhabditis briggsae	k-cl cotransporter	6	C:GO:0005887; C:GO:0005624; P:GO:0055085; P:GO:0006811; F:GO:0015379; P:GO:0006884	-		IPR004841; PTHR11827 (PANTHER), PTHR11827:SF5 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	k-cl cotransporter	6	C:GO:0005887; C:GO:0005624; P:GO:0055085; P:GO:0006811; F:GO:0015379; P:GO:0006884	-		-
Loa loa	adaptin ear-binding coat-associated	4	C:GO:0005905; C:GO:0030125; F:GO:0005515; P:GO:0006897	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-nhr-48 protein	0		F:GO:0043565; F:GO:0003700; F:GO:0003677; C:GO:0005634; F:GO:0004879; F:GO:0008270; P:GO:0006355; F:GO:0046872; P:GO:0006350; F:GO:0003707; P:GO:0045449		-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-nhr-48 protein	0		F:GO:0043565; F:GO:0003700; F:GO:0003677; C:GO:0005634; F:GO:0004879; F:GO:0008270; P:GO:0006355; F:GO:0005515; F:GO:0046872; P:GO:0006350; F:GO:0003707; P:GO:0045449		-
Caenorhabditis elegans	zinc finger protein	3	F:GO:0008270; C:GO:0005622; F:GO:0005515	-		IPR015880
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	F:GO:0008270; C:GO:0005622; F:GO:0005515	-		-
Caenorhabditis elegans	zinc finger protein	3	F:GO:0008270; C:GO:0005622; F:GO:0005515	-		IPR015880
	-	0				-

Caenorhabditis elegans	tripartite motif-containing 23	0		F:GO:0019003; P:GO:0015986; C:GO:0005634; F:GO:0003924; F:GO:0005525; P:GO:0007264; F:GO:0046872; P:GO:0016567; C:GO:0016020; P:GO:0007154; F:GO:0016874; C:GO:0045263; F:GO:0004842; C:GO:0000139; P:GO:0008152; F:GO:0000166; P:GO:0006471; C:GO:0005737; C:GO:0005765; C:GO:0005764; C:GO:0005794; F:GO:0035091; F:GO:0008270; C:GO:0005622; F:GO:0005515; P:GO:0040010		IPR001841; IPR013083; IPR018957; PTHR13139 (PANTHER), PTHR13139:SF3 (PANTHER), SSF57850 (SUPERFAMILY)
Brugia malayi	lmbr1-like conserved region family protein	0		F:GO:0004872		IPR006876; IPR008075; PTHR12625 (PANTHER)
Anopheles gambiae str. PEST	lipocalin-1 interacting membrane receptor	0		F:GO:0004872		IPR006876; IPR008075; PTHR12625 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	proteasomal atpase-associated factor 1	0		P:GO:0044419; C:GO:0000502; F:GO:0005515		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR22847 (PANTHER)
Loa loa	eukaryotic-type d- large subunit family protein	0		P:GO:0006269; F:GO:0003896		IPR007238
Brugia malayi	ring finger protein 1	0		F:GO:0046872; F:GO:0008270; F:GO:0005515		-
Loa loa	domain containing protein	0		F:GO:0046872; P:GO:0007165; C:GO:0005622		IPR000198; IPR002219; IPR008936; G3DSA:3.30.60.20 (GENE3D), PTHR23174 (PANTHER), SSF57889 (SUPERFAMILY)
Caenorhabditis elegans	gl actin (drosophila neuroligin-like) homolog family member (nrx-1)	0				SignalP (SIGNALP)
Caenorhabditis briggsae	60s ribosomal protein l4	4	C:GO:0005840; F:GO:0003735; P:GO:0006412; F:GO:0005515	-	EC:3.6.5.3	IPR002136; IPR013000; G3DSA:3.40.1370.10 (GENE3D), PTHR19431 (PANTHER)
Caenorhabditis briggsae	60s ribosomal protein l4	4	C:GO:0005840; F:GO:0003735; P:GO:0006412; F:GO:0005515	-	EC:3.6.5.3	IPR002136; IPR013000; G3DSA:3.40.1370.10 (GENE3D), PTHR19431 (PANTHER)

Angiostrongylus cantonensis	60s ribosomal protein l4 l1	9	C:GO:0005730; C:GO:0005773; F:GO:0003735; C:GO:0005886; F:GO:0005515; C:GO:0005618; C:GO:0022625; C:GO:0009507; P:GO:0006412	-	EC:3.6.5.3	-
Angiostrongylus cantonensis	60s ribosomal protein l4 l1	9	C:GO:0005730; C:GO:0005773; F:GO:0003735; C:GO:0005886; F:GO:0005515; C:GO:0005618; C:GO:0022625; C:GO:0009507; P:GO:0006412	-	EC:3.6.5.3	IPR002136; G3DSA:3.40.1370.10 (GENE3D), PTHR19431 (PANTHER)
Caenorhabditis briggsae	60s ribosomal protein l4	4	C:GO:0005840; F:GO:0003735; P:GO:0006412; F:GO:0005515	-	EC:3.6.5.3	IPR002136; IPR013000; G3DSA:3.40.1370.10 (GENE3D), PTHR19431 (PANTHER)
Caenorhabditis briggsae	60s ribosomal protein l4	4	C:GO:0005840; F:GO:0003735; P:GO:0006412; F:GO:0005515	-	EC:3.6.5.3	IPR002136; IPR013000; G3DSA:3.40.1370.10 (GENE3D), PTHR19431 (PANTHER)
Caenorhabditis elegans	-dh-ubiquinone oxidoreductase 75 kda mitochondrial precursor	19	P:GO:0006810; P:GO:0040010; P:GO:0046034; P:GO:0008340; P:GO:0006800; P:GO:0006915; F:GO:0051537; F:GO:0008137; C:GO:0005747; F:GO:0046872; P:GO:0000003; F:GO:0009055; P:GO:0051881; C:GO:0005758; F:GO:0051539; P:GO:0006120; P:GO:0002119; F:GO:0005515; P:GO:0009792	-	EC:1.6.5.3	IPR000283; IPR001041; IPR006656; IPR010228; IPR012675; IPR019574; G3DSA:3.40.50.740 (GENE3D), PTHR11615 (PANTHER), PTHR11615:SF10 (PANTHER), SSF53706 (SUPERFAMILY), SSF54862 (SUPERFAMILY)
	-	0				IPR011001
Caenorhabditis elegans	hypothetical protein F41C3.8 [Caenorhabditis elegans]	1	P:GO:0006952	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-vab-2 protein	0		C:GO:0016020		IPR001799; IPR008972; PTHR11304:SF23 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	4	F:GO:0046872; F:GO:0004879; F:GO:0003677; P:GO:0045449	-		IPR000536; IPR001628; IPR001723; IPR008946; IPR013088; PR00350 (PRINTS), PTHR11865 (PANTHER), PTHR11865:SF238 (PANTHER), SSF57716 (SUPERFAMILY)

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	4	F:GO:0046872; F:GO:0004879; F:GO:0003677; P:GO:0045449	-		IPR000536; IPR001628; IPR001723; IPR008946; IPR013088; PR00350 (PRINTS), PTHR11865 (PANTHER), PTHR11865:SF238 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis briggsae	small subunit ribosomal protein 1	9	P:GO:0040035; P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; P:GO:0018996; F:GO:0005515; P:GO:0040007; P:GO:0006412	-	EC:3.6.5.3	IPR001593; IPR018281
Caenorhabditis briggsae	ribosomal protein l22	11	P:GO:0040010; F:GO:0003735; P:GO:0000003; P:GO:0006414; P:GO:0046632; P:GO:0002119; F:GO:0008201; P:GO:0009792; P:GO:0040015; P:GO:0040018; C:GO:0022625	-		SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-mrp-4 protein	12	P:GO:0007427; P:GO:0055085; P:GO:0006941; F:GO:0008307; C:GO:0005863; F:GO:0000146; C:GO:0016021; F:GO:0042626; C:GO:0031672; F:GO:0005524; F:GO:0042803; P:GO:0030241	-		IPR001140; IPR003439; IPR003593; IPR011527; IPR017871; IPR017940; G3DSA:1.20.1560.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF34 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	3	F:GO:0005089; C:GO:0005622; P:GO:0035023	-		-
Loa loa	oligonucleotide oligosaccharide-binding fold containing 2b	6	C:GO:0070876; P:GO:0000724; F:GO:0005515; F:GO:0003697; P:GO:0010212; P:GO:0031576	-		IPR012340; IPR016027; PTHR13356 (PANTHER)
Loa loa	oligonucleotide oligosaccharide-binding fold containing 2b	6	C:GO:0070876; P:GO:0000724; F:GO:0005515; F:GO:0003697; P:GO:0010212; P:GO:0031576	-		IPR012340; IPR016027; PTHR13356 (PANTHER)

Caenorhabditis briggsae	transcription initiation factor tfiid subunit 2	7	P:GO:0010552; P:GO:0006367; F:GO:0010843; P:GO:0000086; C:GO:0033276; F:GO:0005515; C:GO:0005669	-		PTHR15137 (PANTHER), PTHR15137:SF7 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		IPR004202; G3DSA:4.10.49.10 (GENE3D), SignalP (SIGNALP), SSF81427 (SUPERFAMILY)
Caenorhabditis elegans	proliferation-associated protein 2g4	8	C:GO:0005730; F:GO:0031625; F:GO:0003677; F:GO:0003700; C:GO:0030529; P:GO:0045892; C:GO:0005737; F:GO:0016787	-		IPR000994; IPR004545; IPR011991; PTHR10804:SF11 (PANTHER), SSF46785 (SUPERFAMILY)
Caenorhabditis elegans	g chain low resolution structures of bovine mitochondrial f1-atpase during controlled dehydration: hydration state	9	F:GO:0008553; F:GO:0046933; C:GO:0000275; P:GO:0015986; P:GO:0006911; F:GO:0005515; F:GO:0046961; P:GO:0009792; C:GO:0005811	-	EC:3.6.3.6; EC:3.6.3.14	IPR000131; G3DSA:1.10.287.80 (GENE3D), G3DSA:3.40.1380.10 (GENE3D), PTHR11693:SF5 (PANTHER)
	-	0				-
Brugia malayi	smc3 protein	6	P:GO:0051276; F:GO:0042802; F:GO:0005524; P:GO:0007067; C:GO:0005694; P:GO:0006974	-		IPR003395; G3DSA:3.40.50.300 (GENE3D), PTHR18937 (PANTHER), PTHR18937:SF8 (PANTHER), SSF52540 (SUPERFAMILY)
Brugia malayi	r- polymerase 2	12	F:GO:0003899; F:GO:0003968; F:GO:0004672; P:GO:0006367; C:GO:0005730; F:GO:0046872; P:GO:0006355; F:GO:0031625; P:GO:0008380; C:GO:0005665; F:GO:0003677; P:GO:0006368	-	EC:2.7.7.6; EC:2.7.7.48	IPR007073; IPR007075; IPR007081; PTHR19376 (PANTHER), PTHR19376:SF14 (PANTHER), SSF64484 (SUPERFAMILY)
Brugia malayi	r- polymerase 2	12	F:GO:0003899; F:GO:0003968; F:GO:0004672; P:GO:0006367; C:GO:0005730; F:GO:0046872; P:GO:0006355; F:GO:0031625; P:GO:0008380; C:GO:0005665; F:GO:0003677; P:GO:0006368	-	EC:2.7.7.6; EC:2.7.7.48	IPR007073; IPR007075; IPR007081; PTHR19376 (PANTHER), PTHR19376:SF14 (PANTHER), SSF64484 (SUPERFAMILY)

Brugia malayi	r- polymerase 2	12	F:GO:0003899; F:GO:0003968; F:GO:0004672; P:GO:0006367; C:GO:0005730; F:GO:0046872; P:GO:0006355; F:GO:0031625; P:GO:0008380; C:GO:0005665; F:GO:0003677; P:GO:0006368	-	EC:2.7.7.6; EC:2.7.7.48	IPR007073; IPR007075; IPR007081; PTHR19376 (PANTHER), PTHR19376:SF14 (PANTHER), SSF64484 (SUPERFAMILY)
Brugia malayi	r- polymerase 2	12	F:GO:0003899; F:GO:0003968; F:GO:0004672; P:GO:0006367; C:GO:0005730; F:GO:0046872; P:GO:0006355; F:GO:0031625; P:GO:0008380; C:GO:0005665; F:GO:0003677; P:GO:0006368	-	EC:2.7.7.6; EC:2.7.7.48	IPR007073; IPR007075; IPR007081; PTHR19376 (PANTHER), PTHR19376:SF14 (PANTHER), SSF64484 (SUPERFAMILY)
	-	0				-
Loa loa	chromodomain helicase d- binding protein	11	F:GO:0004003; P:GO:0042766; F:GO:0046872; P:GO:0006333; P:GO:0007517; F:GO:0016564; F:GO:0003677; C:GO:0005700; C:GO:0016581; F:GO:0031491; P:GO:0048813	-		SignalP (SIGNALP)
Loa loa	splicing factor 3b subunit 3	4	P:GO:0006461; F:GO:0005515; P:GO:0000375; C:GO:0030532	-		IPR004871; PTHR10644 (PANTHER), PTHR10644:SF1 (PANTHER)
Loa loa	splicing factor 3b subunit 3	4	P:GO:0006461; F:GO:0005515; P:GO:0000375; C:GO:0030532	-		IPR004871; PTHR10644 (PANTHER), PTHR10644:SF1 (PANTHER)
Loa loa	splicing factor 3b subunit 3	4	P:GO:0006461; F:GO:0005515; P:GO:0000375; C:GO:0030532	-		IPR004871; PTHR10644 (PANTHER), PTHR10644:SF1 (PANTHER)
Loa loa	splicing factor 3b subunit 3	4	P:GO:0006461; F:GO:0005515; P:GO:0000375; C:GO:0030532	-		IPR004871; PTHR10644 (PANTHER), PTHR10644:SF1 (PANTHER)
Loa loa	prion-like-(q n-rich)-domain-bearing protein protein partially confirmed by transcript evidence	0		F:GO:0016455; P:GO:0006357; C:GO:0016592		IPR001660; IPR010993; IPR013761

Caenorhabditis briggsae	1-acylglycerol-3-phosphate o-acyltransferase 6 (lysophosphatidic acid zeta)	10	P:GO:0006656; C:GO:0016021; P:GO:0006637; P:GO:0030879; C:GO:0005624; F:GO:0003841; P:GO:0019432; P:GO:0065007; F:GO:0004366; C:GO:0005783	-	EC:2.3.1.51; EC:2.3.1.15	IPR002123; PTHR23063 (PANTHER), PTHR23063:SF2 (PANTHER), SignalP (SIGNALP), SSF69593 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	phosphatidylethanolamine-binding protein	0				IPR001858; IPR008914; PTHR11362 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	phosphatidylethanolamine-binding protein	0				IPR001858; IPR008914; PTHR11362 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	tld family protein	3	C:GO:0005622; F:GO:0005515; P:GO:0016998	-		IPR006571; PTHR23354 (PANTHER), PTHR23354:SF8 (PANTHER), PF07534 (PFAM)
Caenorhabditis elegans	tld family protein	3	C:GO:0005622; F:GO:0005515; P:GO:0016998	-		IPR006571; PTHR23354 (PANTHER), PTHR23354:SF8 (PANTHER), PF07534 (PFAM)
	-	0				-
Caenorhabditis elegans	subfamily member 2	3	F:GO:0005488; P:GO:0008284; P:GO:0008340	-		IPR001305; IPR001623; IPR002939; IPR003095; IPR008971; IPR015609; IPR018253; G3DSA:2.60.260.20 (GENE3D), PTHR11821:SF72 (PANTHER)
Caenorhabditis briggsae	probable protein-tyrosine phosphatase	6	F:GO:0004725; P:GO:0009792; F:GO:0008138; P:GO:0006470; P:GO:0000003; P:GO:0002009	-	EC:3.1.3.48	IPR000340; IPR000387; IPR016130; G3DSA:3.90.190.10 (GENE3D), PTHR10367 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis briggsae	probable protein-tyrosine phosphatase	6	F:GO:0004725; P:GO:0009792; F:GO:0008138; P:GO:0006470; P:GO:0000003; P:GO:0002009	-	EC:3.1.3.48	IPR000340; IPR000387; IPR016130; G3DSA:3.90.190.10 (GENE3D), PTHR10367 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis briggsae	annexin a13	4	C:GO:0044464; F:GO:0005544; F:GO:0005509; F:GO:0005515	-		IPR001464; IPR018252; IPR018502; PTHR10502:SF30 (PANTHER)
Caenorhabditis elegans	uncoordi-ted protein isoform confirmed by transcript evidence	7	F:GO:0005089; C:GO:0005829; F:GO:0004672; F:GO:0000166; P:GO:0035023; P:GO:0008624; P:GO:0007185	-		IPR000219; IPR001452; G3DSA:2.30.30.40 (GENE3D), PTHR22826 (PANTHER), PTHR22826:SF47 (PANTHER)
Caenorhabditis elegans	uncoordi-ted protein isoform confirmed by transcript evidence	7	F:GO:0005089; C:GO:0005829; F:GO:0004672; F:GO:0000166; P:GO:0035023; P:GO:0008624; P:GO:0007185	-		IPR000219; PTHR22826 (PANTHER), PTHR22826:SF47 (PANTHER)

Loa loa	sumo-activating enzyme subunit 2	4	F:GO:0008047; P:GO:0016925; F:GO:0019948; F:GO:0046982	-		IPR000127; IPR009036; IPR016040; G3DSA:1.10.3240.10 (GENE3D), G3DSA:3.10.290.20 (GENE3D)
Loa loa	sumo-activating enzyme subunit 2	4	F:GO:0008047; P:GO:0016925; F:GO:0019948; F:GO:0046982	-		IPR000127; IPR009036; IPR016040; G3DSA:1.10.3240.10 (GENE3D), G3DSA:3.10.290.20 (GENE3D)
Caenorhabditis briggsae	mitochondrial ribosomal protein l35	4	C:GO:0005840; F:GO:0003735; P:GO:0006412; C:GO:0005739	-	EC:3.6.5.3	IPR019338; IPR021137; SignalP (SIGNALP)
Brugia malayi	r-se h family protein	1	F:GO:0005488	-		IPR002156; IPR012337; G3DSA:3.30.420.10 (GENE3D), PTHR10642 (PANTHER), SignalP (SIGNALP)
Loa loa	#NAME?	5	P:GO:0055114; F:GO:0016491; P:GO:0040010; P:GO:0002119; P:GO:0040011	-		IPR001395; IPR023210; PTHR11732:SF34 (PANTHER)
Heliconius melpomene	endonuclease-reverse transcriptase	2	F:GO:0005488; F:GO:0003824	-		IPR015706; PTHR19446:SF100 (PANTHER)
Heliconius melpomene	endonuclease-reverse transcriptase	0		F:GO:0003723; P:GO:0006508; P:GO:0006278; F:GO:0008270; F:GO:0004519; F:GO:0004197; C:GO:0005622; F:GO:0003964		IPR000477; IPR015706; PTHR19446:SF100 (PANTHER), SSF56672 (SUPERFAMILY)
Heliconius melpomene	endonuclease-reverse transcriptase	0		F:GO:0004197; F:GO:0030528; F:GO:0003964; F:GO:0008270; F:GO:0003723; P:GO:0006278; P:GO:0006508; C:GO:0005622; F:GO:0004519; P:GO:0045449		IPR000477; IPR015706; PTHR19446:SF100 (PANTHER), SSF56672 (SUPERFAMILY)
Heliconius melpomene	endonuclease-reverse transcriptase	2	F:GO:0005488; F:GO:0003824	-		IPR015706; PTHR19446:SF100 (PANTHER)
Heliconius melpomene	endonuclease-reverse transcriptase	2	F:GO:0005488; F:GO:0003824	-		IPR015706; PTHR19446:SF100 (PANTHER)
Loa loa	eukaryotic translation initiation factor 4e member 2	7	F:GO:0003743; P:GO:0006413; C:GO:0005845; P:GO:0018991; F:GO:0000339; F:GO:0005515; C:GO:0005737	-		IPR001040
Heligmosomoides polygyrus	elegans protein confirmed by transcript evidence	4	C:GO:0005576; F:GO:0005515; F:GO:0019842; F:GO:0005501	-		-

Heligmosomoides polygyrus	elegans protein confirmed by transcript evidence	4	C:GO:0005576; F:GO:0005515; F:GO:0019842; F:GO:0005501	-		-
	-	0				-
Caenorhabditis briggsae	r- binding identical	5	F:GO:0003723; P:GO:0009792; C:GO:0005622; P:GO:0006378; F:GO:0000166	-		IPR000504; IPR012677; IPR015465; PTHR10432 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	r- binding identical	4	C:GO:0005622; P:GO:0009792; F:GO:0000166; F:GO:0003723	-		-
Brugia malayi	myeloid lymphoid or mixed lineage-leukemia translocation to 3 homolog	1	P:GO:0003002	-		IPR005033; PTHR23195:SF13 (PANTHER)
Caenorhabditis elegans	50s ribosomal protein l10	6	P:GO:0040010; C:GO:0005840; P:GO:0002119; P:GO:0006898; P:GO:0009792; P:GO:0040018	-		IPR001790
Brugia malayi	50s ribosomal protein l10	0		C:GO:0005840		-
Caenorhabditis elegans	50s ribosomal protein l10	6	P:GO:0040010; C:GO:0005840; P:GO:0002119; P:GO:0006898; P:GO:0009792; P:GO:0040018	-		IPR001790
Caenorhabditis elegans	mitogen activated protein ki-se ki-se ki-se mekk5	3	F:GO:0005515; F:GO:0004672; F:GO:0000166	-		-
Caenorhabditis elegans	mtm family member (mtm-6)	0		F:GO:0046872; P:GO:0016311; F:GO:0016791; F:GO:0016787; F:GO:0004725; F:GO:0008270		IPR000306; IPR011011; IPR013083; IPR017455; PTHR10807 (PANTHER), PTHR10807:SF11 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-vit-6 protein	0		P:GO:0006869; F:GO:0005319; F:GO:0045735; P:GO:0006886; C:GO:0005576; F:GO:0008565		IPR001747; IPR015816; IPR015819
Caenorhabditis briggsae	briggsae cbr-vit-6 protein	0		P:GO:0006869; F:GO:0005319; F:GO:0045735; P:GO:0006886; C:GO:0005576; F:GO:0008565		-

Caenorhabditis briggsae	gbf1 protein	13	C:GO:0000139; F:GO:0005515; C:GO:0005829; F:GO:0016563; F:GO:0003677; F:GO:0005086; P:GO:0006892; P:GO:0045449; P:GO:0006890; C:GO:0005634; P:GO:0046903; P:GO:0048205; C:GO:0005739	-		PTHR10663 (PANTHER), PTHR10663:SF8 (PANTHER)
Caenorhabditis briggsae	gbf1 protein	13	C:GO:0000139; F:GO:0005515; C:GO:0005829; F:GO:0016563; F:GO:0003677; F:GO:0005086; P:GO:0006892; P:GO:0045449; P:GO:0006890; C:GO:0005634; P:GO:0046903; P:GO:0048205; C:GO:0005739	-		PTHR10663 (PANTHER), PTHR10663:SF8 (PANTHER)
Caenorhabditis briggsae	gbf1 protein	13	C:GO:0000139; F:GO:0005515; C:GO:0005829; F:GO:0016563; F:GO:0003677; F:GO:0005086; P:GO:0006892; P:GO:0045449; P:GO:0006890; C:GO:0005634; P:GO:0046903; P:GO:0048205; C:GO:0005739	-		PTHR10663 (PANTHER), PTHR10663:SF8 (PANTHER)
Caenorhabditis briggsae	gbf1 protein	13	C:GO:0000139; F:GO:0005515; C:GO:0005829; F:GO:0016563; F:GO:0003677; F:GO:0005086; P:GO:0006892; P:GO:0045449; P:GO:0006890; C:GO:0005634; P:GO:0046903; P:GO:0048205; C:GO:0005739	-		PTHR10663 (PANTHER), PTHR10663:SF8 (PANTHER)

Caenorhabditis briggsae	gbf1 protein	13	C:GO:0000139; F:GO:0005515; C:GO:0005829; F:GO:0016563; F:GO:0003677; F:GO:0005086; P:GO:0006892; P:GO:0045449; P:GO:0006890; C:GO:0005634; P:GO:0046903; P:GO:0048205; C:GO:0005739	-		PTHR10663 (PANTHER), PTHR10663:SF8 (PANTHER)
Caenorhabditis briggsae	gbf1 protein	13	C:GO:0000139; F:GO:0005515; C:GO:0005829; F:GO:0016563; F:GO:0003677; F:GO:0005086; P:GO:0006892; P:GO:0045449; P:GO:0006890; C:GO:0005634; P:GO:0046903; P:GO:0048205; C:GO:0005739	-		PTHR10663 (PANTHER), PTHR10663:SF8 (PANTHER)
Caenorhabditis briggsae	protein ltv1 homolog	6	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0005515; P:GO:0016246; P:GO:0040007	-		IPR007307; PTHR21531 (PANTHER)
Homo sapiens	apc11 a-phase promoting complex subunit 11 homolog isoform cra_b	12	C:GO:0005829; F:GO:0008270; P:GO:0051436; P:GO:0051437; P:GO:0070979; P:GO:0051301; P:GO:0031145; F:GO:0004842; F:GO:0005515; P:GO:0007067; C:GO:0005654; C:GO:0005680	-	EC:6.3.2.19	-
	-	0				-
	-	0				-
Caenorhabditis briggsae	d- topoisomeraseii_beta	10	C:GO:0043229; P:GO:0071103; P:GO:0000910; P:GO:0006259; P:GO:0006355; P:GO:0000003; F:GO:0000166; P:GO:0009792; F:GO:0003916; P:GO:0016246	-		IPR002205; IPR013757; IPR013760; PTHR10169 (PANTHER), PTHR10169:SF2 (PANTHER)

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0030246; F:GO:0004500; C:GO:0016021; F:GO:0003824; P:GO:0009792; C:GO:0005576; P:GO:0006548; P:GO:0016052		IPR005018; IPR015920; SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0008270; P:GO:0019915		IPR007087; SignalP (SIGNALP)
Schistosoma mansoni	b chain helical extension of the neuro-l s-re complex into the spacegroup i 21 21 21	10	F:GO:0005515; P:GO:0051046; P:GO:0023061; P:GO:0065008; P:GO:0010646; P:GO:0060341; P:GO:0006887; C:GO:0044425; C:GO:0031410; C:GO:0005886	-		IPR000727; IPR010989; G3DSA:1.20.5.110 (GENE3D)
Caenorhabditis elegans	transcription factor jmjc domain-containing protein	7	F:GO:0051864; P:GO:0034720; F:GO:0032453; P:GO:0070544; P:GO:0045892; F:GO:0005506; C:GO:0005634	-	EC:1.14.11.27	IPR003347; IPR013109; IPR022777; SSF51197 (SUPERFAMILY)
Caenorhabditis elegans	actin	18	P:GO:0007126; P:GO:0007108; P:GO:0040007; P:GO:0007517; P:GO:0000281; P:GO:0040035; P:GO:0030036; C:GO:0005865; F:GO:0005524; C:GO:0005938; P:GO:0002119; F:GO:0016887; F:GO:0005515; C:GO:0005884; F:GO:0005200; P:GO:0040039; P:GO:0006898; P:GO:0009792	-		IPR004000; IPR004001; IPR020902; G3DSA:2.30.36.70 (GENE3D), G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), SSF53067 (SUPERFAMILY)

Caenorhabditis elegans	actin	18	P:GO:0007126; P:GO:0007108; P:GO:0040007; P:GO:0007517; P:GO:0000281; P:GO:0040035; P:GO:0030036; C:GO:0005865; F:GO:0005524; C:GO:0005938; P:GO:0002119; F:GO:0016887; F:GO:0005515; C:GO:0005884; F:GO:0005200; P:GO:0040039; P:GO:0006898; P:GO:0009792	-		IPR004000; IPR004001; IPR020902; G3DSA:2.30.36.70 (GENE3D), G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), SSF53067 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	cell division cycle related family member (cdc-14)	11	P:GO:0040010; P:GO:0000910; C:GO:0030496; P:GO:0060284; F:GO:0004725; F:GO:0005515; C:GO:0005819; P:GO:0045786; P:GO:0009792; C:GO:0005737; P:GO:0006974	-	EC:3.1.3.48	-
Caenorhabditis elegans	cell division cycle related family member (cdc-14)	11	P:GO:0040010; P:GO:0000910; C:GO:0030496; P:GO:0060284; F:GO:0004725; F:GO:0005515; C:GO:0005819; P:GO:0045786; P:GO:0009792; C:GO:0005737; P:GO:0006974	-	EC:3.1.3.48	IPR000242; IPR000340; IPR000387; IPR016130; G3DSA:3.90.190.10 (GENE3D), PTHR23339 (PANTHER), PTHR23339:SF27 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis elegans	cell division cycle related family member (cdc-14)	11	P:GO:0040010; P:GO:0000910; C:GO:0030496; P:GO:0060284; F:GO:0004725; F:GO:0005515; C:GO:0005819; P:GO:0045786; P:GO:0009792; C:GO:0005737; P:GO:0006974	-	EC:3.1.3.48	IPR000242; IPR000340; IPR000387; IPR016130; G3DSA:3.90.190.10 (GENE3D), PTHR23339 (PANTHER), PTHR23339:SF27 (PANTHER), SSF52799 (SUPERFAMILY)

Caenorhabditis elegans	d--directed r- polymerase ii subunit rpb2	15	F:GO:0003899; P:GO:0040010; P:GO:0008340; F:GO:0004672; P:GO:0006367; F:GO:0046872; P:GO:0000003; P:GO:0008380; C:GO:0005665; F:GO:0003677; P:GO:0002119; F:GO:0005515; P:GO:0006368; F:GO:0032549; P:GO:0009792	-	EC:2.7.7.6	IPR013838
Caenorhabditis elegans	fts and hook-interacting protein	6	P:GO:0008333; P:GO:0045022; P:GO:0007032; F:GO:0005515; P:GO:0007040; C:GO:0070695	-		IPR019384; PTHR21705 (PANTHER)
Brugia malayi	low-density lipoprotein receptor	7	F:GO:0030229; C:GO:0005624; P:GO:0042221; P:GO:0034447; F:GO:0005515; P:GO:0050794; C:GO:0016020	-		IPR002172; IPR006210; IPR011042; G3DSA:2.10.25.10 (GENE3D), PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER), SSF63825 (SUPERFAMILY)
Brugia malayi	low-density lipoprotein receptor repeat class b containing protein	0		F:GO:0004872; C:GO:0016021; C:GO:0016020		IPR011042
Brugia malayi	low-density lipoprotein receptor	10	F:GO:0005041; P:GO:0042221; F:GO:0005515; P:GO:0007613; C:GO:0005624; P:GO:0034447; P:GO:0007165; P:GO:0007399; F:GO:0030229; C:GO:0005886	-		IPR002172; IPR006210; IPR011042; G3DSA:2.10.25.10 (GENE3D), PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER), SSF63825 (SUPERFAMILY)
Brugia malayi	low-density lipoprotein receptor	7	F:GO:0030229; C:GO:0005624; P:GO:0042221; P:GO:0034447; F:GO:0005515; P:GO:0050794; C:GO:0016020	-		IPR002172; IPR006210; IPR011042; G3DSA:2.10.25.10 (GENE3D), PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER), SSF63825 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Lepeophtheirus salmonis	ubiquitin	5	C:GO:0005737; P:GO:0000003; P:GO:0040007; C:GO:0005634; P:GO:0002119	-		IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), PTHR10666:SF9 (PANTHER), SignalP (SIGNALP), SSF54236 (SUPERFAMILY)

Caenorhabditis elegans	bess motif family protein	0		P:GO:0008355; F:GO:0003702; F:GO:0003677; C:GO:0005634; P:GO:0048813; P:GO:0045941; P:GO:0007616; F:GO:0008270; P:GO:0008345; P:GO:0007613; F:GO:0016251; P:GO:0006357; P:GO:0007611; F:GO:0005515; P:GO:0040011; F:GO:0046872; P:GO:0007416		IPR006578
Caenorhabditis briggsae	briggsae cbr-ttr-47 protein	1	P:GO:0040011	-		-
Caenorhabditis briggsae	unidentified vitellogenin-linked transcript family member (uvt-5)	0		F:GO:0016757		-
Caenorhabditis elegans	n-termi-l domain containing protein	0		C:GO:0016021		IPR013922; PTHR15615 (PANTHER)
Caenorhabditis elegans	eukaryotic translation initiation factor 3 subunit d	4	F:GO:0003743; C:GO:0005852; F:GO:0005515; P:GO:0001732	-		IPR007783
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	acyl-coa dehydroge-se	4	P:GO:0009792; P:GO:0008152; F:GO:0016627; P:GO:0040010	-		IPR006089; IPR006090; IPR009075; PTHR10909 (PANTHER), PTHR10909:SF10 (PANTHER)
Caenorhabditis sp. PS1010	er degradation-enhancing alpha-mannosidase-like 1	1	C:GO:0016020	-		SignalP (SIGNALP)
Caenorhabditis elegans	midasin homolog	0		C:GO:0005634; F:GO:0000166; F:GO:0003674; F:GO:0008134; F:GO:0017111; F:GO:0005524; F:GO:0016887; C:GO:0005575; P:GO:0006355; C:GO:0005622; P:GO:0008150; P:GO:0043254		PTHR22908 (PANTHER), PTHR22908:SF13 (PANTHER)
Caenorhabditis elegans	displaced go-d family member (dig-1)	1	F:GO:0003824	-		IPR003961; IPR007110; IPR008957; IPR013783; PR00014 (PRINTS), PTHR10489 (PANTHER), PTHR10489:SF3 (PANTHER), SSF48726 (SUPERFAMILY)
Strongylocentrotus purpuratus	atp-binding cassette superfamily	1	F:GO:0017111	-	EC:3.6.1.15	G3DSA:3.40.50.300 (GENE3D), PTHR19229 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-rgl-1 protein	1	P:GO:0040010	-		IPR000159; IPR008937; G3DSA:3.10.20.90 (GENE3D), PTHR23113:SF29 (PANTHER), SSF54236 (SUPERFAMILY)
Caenorhabditis elegans	coiled-coil domain-containing protein 141-like	0		F:GO:0005515		SSF46966 (SUPERFAMILY)
Caenorhabditis elegans	coiled-coil domain-containing protein 141-like	0		F:GO:0005515		SSF46966 (SUPERFAMILY)

Caenorhabditis briggsae	briggsae cbr-rbg-2 protein	0		F:GO:0030234; P:GO:0043087; C:GO:0005625; F:GO:0046982		-
Caenorhabditis briggsae	low quality protein: tyrosine-protein phosphatase non-receptor type 13-like	10	P:GO:0040022; C:GO:0043229; F:GO:0005488; P:GO:0045132; P:GO:0040007; P:GO:0002119; P:GO:0042127; P:GO:0008406; F:GO:0016787; P:GO:0040020	-		IPR000299; IPR011019; IPR011993; IPR014352; IPR018979; IPR018980; IPR019748; IPR019749; IPR019750; G3DSA:3.10.20.90 (GENE3D), PTHR23280 (PANTHER), SSF50729 (SUPERFAMILY), SSF54236 (SUPERFAMILY)
	-	0				-
Brugia malayi	ubiquitin specific peptidase 7 (herpes virus-associated)	12	P:GO:0006511; F:GO:0004221; F:GO:0002039; P:GO:0051090; F:GO:0008022; F:GO:0031625; F:GO:0004197; F:GO:0004843; F:GO:0008134; P:GO:0016579; C:GO:0005737; C:GO:0005634	-	EC:3.1.2.15; EC:3.4.22.0	IPR001394; IPR002083; IPR008974; IPR013322; IPR018200; PTHR10420 (PANTHER), PTHR10420:SF43 (PANTHER), PF12436 (PFAM), SSF54001 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	peptidyl-prolyl cis-trans isomerase nima-interacting 1	9	P:GO:0060393; P:GO:0030512; P:GO:0006457; P:GO:0007088; F:GO:0050816; P:GO:0051443; F:GO:0003755; F:GO:0050815; P:GO:0042127	-	EC:5.2.1.8	IPR000297; IPR001202; G3DSA:2.20.70.10 (GENE3D), G3DSA:3.10.50.40 (GENE3D), PTHR10657 (PANTHER), SSF54534 (SUPERFAMILY)
Caenorhabditis briggsae	exocyst complex component 6b	2	C:GO:0000145; P:GO:0006904	-		IPR007225
Dictyocaulus filaria	fmrfamide-related peptide flp-21 precursor	0				-
Gallus gallus	telomere-associated protein rif1	0		F:GO:0005488		-
	-	0				-
Caenorhabditis briggsae	multiple pdz domain protein family member (mpz-1)	2	F:GO:0005515; C:GO:0016021	-		G3DSA:2.30.42.10 (GENE3D), PTHR19964 (PANTHER), PTHR19964:SF5 (PANTHER)

Homo sapiens	indoleamine -dioxyge-se 1	24	F:GO:0004833; P:GO:0032496; P:GO:0032693; P:GO:0002666; P:GO:0070233; P:GO:0033555; P:GO:0002534; F:GO:0016597; F:GO:0020037; F:GO:0009055; C:GO:0005829; P:GO:0007610; P:GO:0032735; P:GO:0002830; P:GO:0007565; F:GO:0019825; P:GO:0019441; P:GO:0046007; P:GO:0034276; P:GO:0055114; F:GO:0033754; P:GO:0002678; C:GO:0005625; P:GO:0043065	-	EC:1.13.11.11; EC:1.13.11.52	IPR000898; SSF140959 (SUPERFAMILY)
Caenorhabditis briggsae	endoplasmic reticulum metallopeptidase 1	4	F:GO:0008233; P:GO:0040011; C:GO:0016021; P:GO:0006508	-		PTHR12147 (PANTHER), PS51257 (PROFILE), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	uncoordi-ted family member (unc-11)	13	C:GO:0005829; P:GO:0016183; C:GO:0008021; P:GO:0007270; P:GO:0048268; F:GO:0030276; F:GO:0005545; F:GO:0004177; C:GO:0030131; C:GO:0005905; P:GO:0007269; P:GO:0042331; P:GO:0006898	-	EC:3.4.11.0	IPR008942; IPR011417; IPR013809; IPR014712; PTHR22951 (PANTHER), PTHR22951:SF3 (PANTHER), SSF89009 (SUPERFAMILY)
Aedes aegypti	ring finger and ccch-type zinc finger domains 2	1	F:GO:0005488	-		PTHR13139 (PANTHER), PTHR13139:SF1 (PANTHER)
Aedes aegypti	ring finger and ccch-type zinc finger domains 2	1	F:GO:0005488	-		IPR000571; G3DSA:4.10.1000.10 (GENE3D), PTHR13139 (PANTHER), SSF90229 (SUPERFAMILY)
Caenorhabditis elegans	membrane calcium atpase family member (mca-3)	5	F:GO:0005388; C:GO:0016021; P:GO:0006754; F:GO:0005524; P:GO:0006816	-	EC:3.6.3.8	IPR001757; IPR005834; IPR006068; IPR006069; IPR006408; IPR008250; IPR018303; G3DSA:1.20.1110.10 (GENE3D), G3DSA:3.40.1110.10 (GENE3D), PTHR11939:SF76 (PANTHER), SSF56784 (SUPERFAMILY), SSF81660 (SUPERFAMILY), SSF81665 (SUPERFAMILY)

Caenorhabditis elegans	membrane calcium atpase family member (mca-3)	7	F:GO:0005388; C:GO:0016021; P:GO:0006754; F:GO:0005524; P:GO:0006816; C:GO:0005794; C:GO:0005886	-	EC:3.6.3.8	IPR001757; IPR005834; IPR006068; IPR006069; IPR006408; IPR008250; IPR018303; G3DSA:1.20.1110.10 (GENE3D), G3DSA:3.40.1110.10 (GENE3D), PTHR11939:SF76 (PANTHER), SSF56784 (SUPERFAMILY), SSF81660 (SUPERFAMILY), SSF81665 (SUPERFAMILY)
	-	0				-
	-	0				-
Loa loa	zinc finger protein	13	P:GO:0040010; F:GO:0003723; F:GO:0008270; C:GO:0071011; P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0040011; P:GO:0000398; P:GO:0006898; P:GO:0002121; P:GO:0002009; P:GO:0009792	-		IPR001878; IPR013084; G3DSA:3.30.1370.10 (GENE3D), PTHR11208 (PANTHER), PTHR11208:SF6 (PANTHER), SSF57756 (SUPERFAMILY)
Caenorhabditis briggsae	heterogeneous nuclear ribonucleoprotein	1	F:GO:0005515	-		-
Caenorhabditis briggsae	heterogeneous nuclear ribonucleoprotein h3	1	F:GO:0003676	-		-
Caenorhabditis elegans	heterogeneous nuclear ribonucleoprotein h3	1	F:GO:0003676	-		SignalP (SIGNALP)
Caenorhabditis elegans	heterogeneous nuclear ribonucleoprotein h3	1	F:GO:0003676	-		IPR000504; IPR012677; PTHR13976 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
Loa loa	protein ki-se domain containing protein	1	F:GO:0016301	-		PTHR13902 (PANTHER), PTHR13902:SF12 (PANTHER)
Brugia malayi	protein ki-se domain containing protein	14	F:GO:0030291; P:GO:0007243; F:GO:0004674; C:GO:0005625; F:GO:0019870; F:GO:0005524; P:GO:0042326; P:GO:0033673; F:GO:0005515; F:GO:0000287; P:GO:0003084; P:GO:0046777; C:GO:0042598; C:GO:0005737	-	EC:2.7.11.0	IPR000719; IPR002290; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR13902 (PANTHER), PTHR13902:SF12 (PANTHER), PF12202 (PFAM)

Brugia malayi	protein ki-se domain containing protein	14	F:GO:0030291; P:GO:0007243; F:GO:0004674; C:GO:0005625; F:GO:0019870; F:GO:0005524; P:GO:0042326; P:GO:0033673; F:GO:0005515; F:GO:0000287; P:GO:0003084; P:GO:0046777; C:GO:0042598; C:GO:0005737	-	EC:2.7.11.0	IPR000719; IPR002290; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR13902 (PANTHER), PTHR13902:SF12 (PANTHER), PF12202 (PFAM)
Brugia malayi	wd repeat domain 45	0		F:GO:0003674; P:GO:0008150; C:GO:0005575		-
	-	0				-
Loa loa	brca1 associated protein	10	P:GO:0007265; P:GO:0009968; P:GO:0000165; F:GO:0046872; F:GO:0042802; F:GO:0008139; F:GO:0004842; F:GO:0000166; C:GO:0000151; C:GO:0005737	-	EC:6.3.2.19	IPR001607; IPR001841; IPR011422; IPR013083; IPR018957; PTHR10420 (PANTHER), PTHR10420:SF8 (PANTHER), SignalP (SIGNALP), SSF57850 (SUPERFAMILY)
Caenorhabditis elegans	vacuolar protein sorting 13d	3	P:GO:0040010; P:GO:0002119; P:GO:0040011	-		IPR009543; PTHR16166 (PANTHER), PTHR16166:SF24 (PANTHER)
Caenorhabditis briggsae	peptidase s9 prolyl oligopeptidase active site domain protein	1	F:GO:0016787	-		IPR011042; SignalP (SIGNALP)
Caenorhabditis briggsae	d--directed r- beta subunit family protein	9	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0003899; F:GO:0003677; P:GO:0006350; F:GO:0032549; P:GO:0040007; C:GO:0005634	-	EC:2.7.7.6	IPR009674; IPR015712; PTHR20856:SF5 (PANTHER)
Loa loa	wd repeat domain 22	1	C:GO:0080008	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR15574 (PANTHER), PTHR15574:SF3 (PANTHER)
Caenorhabditis elegans	phosphoacetylglucosamine mutase	4	P:GO:0009792; F:GO:0046872; P:GO:0005975; F:GO:0016868	-	EC:5.4.2.0	IPR005843; G3DSA:3.30.310.50 (GENE3D), PTHR22573 (PANTHER), PTHR22573:SF3 (PANTHER), SSF55957 (SUPERFAMILY)
Brugia malayi	tetratricopeptide repeat protein 5	0		F:GO:0003674; F:GO:0005488; P:GO:0006281; C:GO:0005737; P:GO:0008150; C:GO:0005575; C:GO:0005634		IPR008940; IPR011990; IPR013026; IPR019734; PTHR23083 (PANTHER), PTHR23083:SF8 (PANTHER), SSF48452 (SUPERFAMILY)

Caenorhabditis briggsae	golgi phosphoprotein 3	3	P:GO:0009792; P:GO:0008340; P:GO:0010171	-		-
Brugia malayi	dep domain containing 1	0		P:GO:0023034; F:GO:0003674; P:GO:0050790; P:GO:0007165; C:GO:0005575; C:GO:0005622; F:GO:0005515; F:GO:0005096; P:GO:0008150		IPR000591; IPR011991; PTHR16206 (PANTHER), SSF46785 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0045132; P:GO:0010171; F:GO:0005515	-		-
Caenorhabditis briggsae	ribosomal protein l21	8	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; F:GO:0005515; P:GO:0000003; P:GO:0040007; P:GO:0006412	-	EC:3.6.5.3	IPR001147; IPR008991; IPR018259; G3DSA:2.30.30.70 (GENE3D)
Caenorhabditis briggsae	ribosomal protein l21	8	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; F:GO:0005515; P:GO:0000003; P:GO:0040007; P:GO:0006412	-	EC:3.6.5.3	IPR001147; IPR008991; IPR018259; G3DSA:2.30.30.70 (GENE3D)
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG22497 [Caenorhabditis briggsae]	0		P:GO:0055114; F:GO:0005488; F:GO:0016491		PTHR12596 (PANTHER), PTHR12596:SF3 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG22497 [Caenorhabditis briggsae]	0		P:GO:0055114; F:GO:0005488; F:GO:0016491		PTHR12596 (PANTHER), PTHR12596:SF3 (PANTHER)
Caenorhabditis elegans	helicase conserved c-termi-l domain containing protein	3	F:GO:0005488; P:GO:0008152; F:GO:0016787	-		-
	-	0				-
Caenorhabditis elegans	zn-finger in ran binding protein and others containing protein	5	P:GO:0021954; F:GO:0003676; C:GO:0005622; F:GO:0000166; F:GO:0008270	-		-
Caenorhabditis elegans	zn-finger in ran binding protein and others containing protein	5	P:GO:0021954; F:GO:0003676; C:GO:0005622; F:GO:0000166; F:GO:0008270	-		-

Caenorhabditis briggsae	protein ki-se domain containing protein	0		F:GO:0004674; F:GO:0004672; P:GO:0006468; F:GO:0000166; F:GO:0005524; F:GO:0016301; P:GO:0000154; F:GO:0000179; F:GO:0008649		IPR018628
Caenorhabditis briggsae	protein ki-se domain containing protein	0		F:GO:0004674; F:GO:0004672; P:GO:0006468; F:GO:0000166; F:GO:0005524; F:GO:0016301; P:GO:0000154; F:GO:0000179; F:GO:0008649		IPR018628
Caenorhabditis briggsae	protein ki-se domain containing protein	0		F:GO:0004674; F:GO:0004672; P:GO:0006468; F:GO:0000166; F:GO:0005524; F:GO:0016301; P:GO:0000154; F:GO:0000179; F:GO:0008649		IPR018628
Ixodes scapularis	ecm 18	0		F:GO:0005529; F:GO:0003674; C:GO:0016021; P:GO:0007155; C:GO:0016020; F:GO:0008233; C:GO:0005615; F:GO:0005509; F:GO:0004872; P:GO:0008150; F:GO:0005488; P:GO:0055114; F:GO:0047712; F:GO:0005515; C:GO:0005886; C:GO:0005576; F:GO:0016491; C:GO:0005575		IPR002919; G3DSA:2.10.25.10 (GENE3D), SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0016301; F:GO:0005488; F:GO:0005515		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR10316 (PANTHER), PTHR10316:SF7 (PANTHER)
Caenorhabditis briggsae	amp deami-se	6	P:GO:0002119; P:GO:0006144; F:GO:0003876; P:GO:0009168; P:GO:0040010; P:GO:0040011	-	EC:3.5.4.6	-
Angiostrongylus cantonensis	ribosomal protein l19	4	P:GO:0000022; F:GO:0003735; C:GO:0022625; P:GO:0006412	-	EC:3.6.5.3	SignalP (SIGNALP)

Caenorhabditis elegans	suppressor of lineage defect family member (sli-1)	5	P:GO:0007166; F:GO:0004871; C:GO:0005634; F:GO:0005509; F:GO:0005515	-		-
Caenorhabditis elegans	atp-dependent r- helicase ddx51	6	P:GO:0002119; F:GO:0005488; P:GO:0040010; F:GO:0016787; P:GO:0008340; P:GO:0006898	-		IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF34 (PANTHER), SSF52540 (SUPERFAMILY)
Loa loa	extra sexcombs	8	P:GO:0048666; P:GO:0016458; F:GO:0042054; P:GO:0006355; P:GO:0016571; C:GO:0044428; F:GO:0005488; P:GO:0040029	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; IPR020472; PTHR10253 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	C:GO:0016020; P:GO:0006810	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				PTHR21095 (PANTHER)
Brugia malayi	rhodanese-like domain containing protein	0		P:GO:0000087; P:GO:0006470; F:GO:0004725; C:GO:0005622		IPR000751
Brugia malayi	rhodanese-like domain containing protein	0		P:GO:0000087; P:GO:0006470; F:GO:0004725; C:GO:0005622		IPR000751; PTHR10828:SF14 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; C:GO:0016020; F:GO:0008375		IPR003406; PTHR19297:SF3 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	F:GO:0046872; F:GO:0008233; P:GO:0000003; P:GO:0007413	-		IPR001506; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF73 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	F:GO:0008233; P:GO:0007413	-		IPR001506; IPR006026; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF73 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	F:GO:0046872; F:GO:0008233; P:GO:0000003; P:GO:0007413	-		IPR001506; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF73 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	F:GO:0046872; F:GO:0008233; P:GO:0000003; P:GO:0007413	-		IPR001506; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF73 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	a chain crystal spectroscopic and catalytic properties of cobalt copper nickel and mercury derivatives of the zinc endopeptidase a correlation of structure and proteolytic activity	4	F:GO:0046872; F:GO:0008233; P:GO:0000003; P:GO:0007413	-		IPR001506; IPR006026; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF73 (PANTHER), SSF55486 (SUPERFAMILY)

Caenorhabditis elegans	a chain crystal spectroscopic and catalytic properties of cobalt copper nickel and mercury derivatives of the zinc endopeptidase a correlation of structure and proteolytic activity	4	F:GO:0046872; F:GO:0008233; P:GO:0000003; P:GO:0007413	-		IPR001506; IPR006026; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF73 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	thiosulfate sulfurtransferase	2	C:GO:0016020; C:GO:0005739	-		IPR001763; PTHR11364 (PANTHER)
Caenorhabditis elegans	phosphorylated adaptor for r-	3	P:GO:0009987; C:GO:0005654; C:GO:0005737	-		-
Caenorhabditis elegans	phosphorylated adaptor for r-	3	P:GO:0009987; C:GO:0005654; C:GO:0005737	-		-
Caenorhabditis elegans	claspin homolog (xenopus laevis)	1	P:GO:0009987	-		PTHR14396 (PANTHER)
	-	0				-
Caenorhabditis elegans	class member 1	5	F:GO:0046872; P:GO:0044262; P:GO:0032501; F:GO:0015923; C:GO:0016020	-		IPR000602; IPR011013; IPR011330; IPR011682; IPR013780; IPR015341; G3DSA:1.20.1270.50 (GENE3D), PTHR11607 (PANTHER), PTHR11607:SF4 (PANTHER), SSF88688 (SUPERFAMILY)
Caenorhabditis briggsae	elongation factor tu homologue precursor	12	F:GO:0003746; P:GO:0008340; C:GO:0005743; P:GO:0040007; P:GO:0000003; C:GO:0042645; P:GO:0006414; P:GO:0002119; F:GO:0005515; F:GO:0003924; P:GO:0009792; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000795; IPR004160; IPR004161; IPR004541; IPR005225; IPR009000; IPR009001; G3DSA:2.40.30.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23115 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Loa loa	oxysterol binding 9	1	P:GO:0006810	-		IPR001849; IPR010916; IPR011993; PTHR10219 (PANTHER), PTHR10219:SF3 (PANTHER), SSF50729 (SUPERFAMILY)
Caenorhabditis briggsae	hexosaminidase domain-containing protein	1	F:GO:0016798	-		IPR013781; IPR015883; IPR017853; PTHR21040 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	glycosyl hydrolase family catalytic domain containing protein	1	F:GO:0016787	-		IPR017853; PTHR21040 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	angio-associated migratory cell protein	5	P:GO:0009987; P:GO:0000003; P:GO:0002119; C:GO:0044464; P:GO:0040018	-		-
Caenorhabditis briggsae	calponin transgelin	2	P:GO:0002119; P:GO:0040007	-		-
Caenorhabditis elegans	ferritin	5	F:GO:0042802; P:GO:0006879; F:GO:0008199; P:GO:0040010; P:GO:0006826	-		-

Caenorhabditis elegans	ferritin	7	F:GO:0042802; P:GO:0006879; F:GO:0016491; F:GO:0008199; P:GO:0040010; P:GO:0055114; P:GO:0006826	-		-
Loa loa	heavy unconventio-l myosin family member (hum-2)	20	C:GO:0043005; P:GO:0007267; P:GO:0006582; C:GO:0016023; F:GO:0000166; P:GO:0030048; P:GO:0065008; F:GO:0000149; P:GO:0006887; F:GO:0046983; P:GO:0048513; F:GO:0003779; F:GO:0003774; P:GO:0050794; P:GO:0019226; P:GO:0032400; C:GO:0042641; P:GO:0044249; C:GO:0016459; P:GO:0048066	-		IPR002710; PTHR13140 (PANTHER), PTHR13140:SF15 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	proteasome subunit alpha type 4	9	P:GO:0051436; P:GO:0051437; F:GO:0042802; F:GO:0004298; P:GO:0031145; C:GO:0019773; P:GO:0044419; C:GO:0005737; C:GO:0005634	-	EC:3.4.25.0	-
Caenorhabditis briggsae	fructose-bisphosphate aldolase	3	P:GO:0006096; F:GO:0004332; F:GO:0042802	-	EC:4.1.2.13	IPR000741; IPR013785; SSF51569 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	protein tyrosine receptor d	8	P:GO:0008340; P:GO:0000003; P:GO:0018996; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0006898; P:GO:0009792	-		IPR003961; IPR008957; IPR013783; PR00014 (PRINTS), PTHR10489 (PANTHER)
Caenorhabditis elegans	heat shock 70 kda protein 13 precursor	1	F:GO:0005524	-		IPR001023; IPR013126; G3DSA:3.30.30.30 (GENE3D), G3DSA:3.30.420.40 (GENE3D), PTHR19375:SF1 (PANTHER), SSF53067 (SUPERFAMILY)
	-	0				-
	-	0				IPR011989
	-	0				IPR011989
	-	0				-
	-	0				IPR011989

	-	0				IPR011989
	-	0				IPR011989
	-	0				IPR011989
	-	0				IPR011989
Carassius auratus	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	12	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040002; P:GO:0040010; P:GO:0008340; P:GO:0040011; C:GO:0005576; P:GO:0019915; P:GO:0006898; F:GO:0042302; P:GO:0002009	-		IPR002486; IPR008160; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER)
Caenorhabditis briggsae	d-3-phosphoglycerate dehydroge-se	9	P:GO:0040010; P:GO:0006098; P:GO:0055114; F:GO:0004617; F:GO:0004455; F:GO:0051287; F:GO:0005515; P:GO:0009792; P:GO:0006564	-	EC:1.1.1.95; EC:1.1.1.86	-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	78 kda glucose-regulated protein precursor	25	C:GO:0005793; P:GO:0051603; P:GO:0043154; P:GO:0030512; P:GO:0021680; C:GO:0030176; P:GO:0021589; C:GO:0005788; P:GO:0031398; C:GO:0008303; C:GO:0042470; F:GO:0043027; F:GO:0043022; P:GO:0006983; C:GO:0005576; P:GO:0006916; C:GO:0009986; P:GO:0006987; P:GO:0040019; F:GO:0051082; P:GO:0042149; F:GO:0051787; C:GO:0048471; C:GO:0005634; F:GO:0005524	-		IPR001023; IPR013126; IPR018181; G3DSA:1.20.1270.10 (GENE3D), G3DSA:2.60.34.10 (GENE3D), G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), PTHR19375:SF1 (PANTHER), SSF100920 (SUPERFAMILY), SSF100934 (SUPERFAMILY), SSF53067 (SUPERFAMILY)

Caenorhabditis briggsae	78 kda glucose-regulated protein precursor	25	C:GO:0005793; P:GO:0051603; P:GO:0043154; P:GO:0030512; P:GO:0021680; C:GO:0030176; P:GO:0021589; C:GO:0005788; P:GO:0031398; C:GO:0008303; C:GO:0042470; F:GO:0043027; F:GO:0043022; P:GO:0006983; C:GO:0005576; P:GO:0006916; C:GO:0009986; P:GO:0006987; P:GO:0040019; F:GO:0051082; P:GO:0042149; F:GO:0051787; C:GO:0048471; C:GO:0005634; F:GO:0005524	-		IPR001023; IPR013126; IPR018181; G3DSA:1.20.1270.10 (GENE3D), G3DSA:2.60.34.10 (GENE3D), G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), PTHR19375:SF1 (PANTHER), SSF100920 (SUPERFAMILY), SSF100934 (SUPERFAMILY), SSF53067 (SUPERFAMILY)
	-	0				-
Homo sapiens	cytochrome c oxidase subunit vb	4	F:GO:0046872; C:GO:0005743; P:GO:0007585; F:GO:0004129	-	EC:1.9.3.1	IPR002124; IPR020893; SSF57802 (SUPERFAMILY)
	-	0				IPR000276
Caenorhabditis briggsae	peroxisomal biogenesis factor 12	5	F:GO:0046872; P:GO:0006625; C:GO:0005778; F:GO:0005515; C:GO:0016021	-		IPR001841; IPR006845; IPR013083; PTHR12888 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	5	F:GO:0004930; P:GO:0007165; P:GO:0007186; C:GO:0042995; P:GO:0032501	-		IPR000832; IPR001879; IPR017981; IPR017983; PTHR12011 (PANTHER), PTHR12011:SF13 (PANTHER), SSF111418 (SUPERFAMILY)
Brugia malayi	phd-finger family protein	8	P:GO:0043967; F:GO:0005515; P:GO:0090304; P:GO:0034645; P:GO:0006915; P:GO:0048523; C:GO:0005634; P:GO:0007049	-		IPR001965; IPR011011; IPR013083; IPR019786; IPR019787; PTHR10333 (PANTHER), PTHR10333:SF20 (PANTHER)
Caenorhabditis briggsae	small subunit ribosomal protein 14	8	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; P:GO:0018996; P:GO:0040010; P:GO:0000003; P:GO:0006412	-	EC:3.6.5.3	IPR001971; PTHR11759:SF1 (PANTHER), SSF53137 (SUPERFAMILY)

Caenorhabditis briggsae	small subunit ribosomal protein 14	8	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; P:GO:0018996; P:GO:0040010; P:GO:0000003; P:GO:0006412	-	EC:3.6.5.3	IPR001971; PTHR11759:SF1 (PANTHER), SSF53137 (SUPERFAMILY)
Caenorhabditis briggsae	glucose transporter	3	P:GO:0040007; P:GO:0006810; P:GO:0002119	-		IPR005828; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11600 (PANTHER), PTHR11600:SF12 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	dicer-1	15	P:GO:0007279; F:GO:0005515; C:GO:0016442; P:GO:0033227; P:GO:0042078; P:GO:0048813; P:GO:0035087; P:GO:0030422; C:GO:0005737; F:GO:0003676; P:GO:0007367; P:GO:0045448; F:GO:0016443; P:GO:0031054; C:GO:0005634	-		IPR003100; PTHR14950 (PANTHER), PTHR14950:SF3 (PANTHER), SSF101690 (SUPERFAMILY)
Caenorhabditis elegans	copb2_caeel ame: full=probable coatomer subunit beta ame: full=beta -coat protein short=beta -cop	6	P:GO:0009792; P:GO:0002119; P:GO:0032940; P:GO:0048599; P:GO:0006886; P:GO:0006898	-		PTHR19876 (PANTHER), PTHR19876:SF2 (PANTHER)
Caenorhabditis elegans	copb2_caeel ame: full=probable coatomer subunit beta ame: full=beta -coat protein short=beta -cop	6	P:GO:0009792; P:GO:0002119; P:GO:0032940; P:GO:0048599; P:GO:0006886; P:GO:0006898	-		PTHR19876 (PANTHER), PTHR19876:SF2 (PANTHER)
Caenorhabditis briggsae	g-protein sig-lling modulator	1	F:GO:0005515	-		IPR003109; PTHR10098 (PANTHER), PTHR10098:SF11 (PANTHER)
Caenorhabditis elegans	protein trs85 homolog	6	P:GO:0009987; P:GO:0000003; P:GO:0032501; P:GO:0045927; P:GO:0040011; P:GO:0009653	-		PTHR12975 (PANTHER)
Caenorhabditis briggsae	proteasome 26s subunit subunit 4 atpase	9	P:GO:0000022; P:GO:0006511; C:GO:0008540; F:GO:0004175; F:GO:0005524; F:GO:0016887; P:GO:0008283; C:GO:0005737; P:GO:0006974	-		-

Caenorhabditis elegans	spliceosome associated	3	F:GO:0005515; F:GO:0003676; F:GO:0000166	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF51 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	headcase protein	5	P:GO:0048519; P:GO:0048666; P:GO:0008152; P:GO:0009653; P:GO:0007424	-		PTHR13425 (PANTHER)
Caenorhabditis briggsae	headcase protein	5	P:GO:0048519; P:GO:0048666; P:GO:0008152; P:GO:0009653; P:GO:0007424	-		PTHR13425 (PANTHER)
	-	0				IPR013169
Brugia malayi	prolyl endopeptidase	8	F:GO:0046872; F:GO:0004252; F:GO:0042277; P:GO:0006508; C:GO:0005634; C:GO:0005829; F:GO:0008237; C:GO:0005739	-	EC:3.4.21.0	IPR001375; IPR002470; IPR002471; G3DSA:3.40.50.1820 (GENE3D), PTHR11757:SF2 (PANTHER), SSF53474 (SUPERFAMILY)
	-	0				IPR001357; G3DSA:3.40.50.10190 (GENE3D)
Caenorhabditis briggsae	g-patch domain containing protein	0		F:GO:0003676; C:GO:0005622		IPR000467
Caenorhabditis elegans	briggsae cbr-jph-1 protein	0				-
Caenorhabditis elegans	briggsae cbr-jph-1 protein	0				-
Caenorhabditis elegans	ubiquitin specific protease 32	5	P:GO:0009792; P:GO:0006511; F:GO:0005509; F:GO:0004221; C:GO:0044464	-	EC:3.1.2.15	IPR001394; PTHR10420 (PANTHER), PTHR10420:SF68 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis elegans	ubiquitin specific protease 32	5	P:GO:0009792; P:GO:0006511; F:GO:0005509; F:GO:0004221; C:GO:0044464	-	EC:3.1.2.15	IPR001394; PTHR10420 (PANTHER), PTHR10420:SF68 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis briggsae	transthyretin-like family protein	0				-
	-	0				-
Caenorhabditis elegans	ribosomal small subunit	9	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0003735; P:GO:0018996; C:GO:0015935; P:GO:0008340; P:GO:0040007; P:GO:0006412	-	EC:3.6.5.3	IPR005680; IPR006032; IPR012340; IPR016027
Caenorhabditis elegans	elongation factor tu (ef-tu)	8	P:GO:0009792; F:GO:0003746; F:GO:0005525; C:GO:0005622; P:GO:0040010; P:GO:0000003; P:GO:0006414; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000795; IPR004160; IPR004161; IPR004541; IPR009000; IPR009001; G3DSA:2.40.30.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23115 (PANTHER), SSF52540 (SUPERFAMILY)

Brugia malayi	serine threonine-protein ki-se 11	17	F:GO:0030275; P:GO:0060070; P:GO:0051291; P:GO:0007409; P:GO:0033762; P:GO:0016310; C:GO:0005737; P:GO:0030111; F:GO:0004674; C:GO:0043234; P:GO:0060770; P:GO:0051896; F:GO:0032403; P:GO:0033993; C:GO:0005634; P:GO:0045722; P:GO:0001894	-	EC:2.7.11.0	IPR000719; IPR002290; IPR008271; IPR011009; IPR015735; IPR017441; IPR017442; IPR020636; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
	-	0				-
Brugia malayi	serine threonine-protein ki-se 11	17	F:GO:0030275; P:GO:0060070; P:GO:0051291; P:GO:0007409; P:GO:0033762; P:GO:0016310; C:GO:0005737; P:GO:0030111; F:GO:0004674; C:GO:0043234; P:GO:0060770; P:GO:0051896; F:GO:0032403; P:GO:0033993; C:GO:0005634; P:GO:0045722; P:GO:0001894	-	EC:2.7.11.0	IPR000719; IPR002290; IPR008271; IPR011009; IPR015735; IPR017441; IPR017442; IPR020636; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
Caenorhabditis briggsae	ribosomal protein s16	10	P:GO:0000022; P:GO:0009792; P:GO:0002119; F:GO:0003735; C:GO:0005811; P:GO:0018996; P:GO:0000003; C:GO:0022627; P:GO:0040007; P:GO:0006412	-	EC:3.6.5.3	IPR000754; IPR014721; IPR020568; IPR020574
Caenorhabditis elegans	i uaiaretic acid resistant family member (ndg-4)	3	P:GO:0009792; P:GO:0010171; P:GO:0040010	-		PTHR11161 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	i uaiaretic acid resistant family member (ndg-4)	3	P:GO:0009792; P:GO:0010171; P:GO:0040010	-		PTHR11161 (PANTHER), SignalP (SIGNALP)

Caenorhabditis elegans	rab11 family interacting protein 4 (class ii)	9	P:GO:0006810; F:GO:0005515; C:GO:0016020; C:GO:0043231; P:GO:0044238; P:GO:0050794; C:GO:0044444; P:GO:0044249; P:GO:0007049	-		-
	-	0				-
Loa loa	briggsae cbr-npp-5 protein	0		P:GO:0000003; C:GO:0005643; P:GO:0040010; P:GO:0009792; P:GO:0006810		IPR007252
Caenorhabditis elegans	patched family protein	1	C:GO:0016020	-		IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER)
Caenorhabditis elegans	granulin	1	C:GO:0044424	-		IPR000118; PTHR12274 (PANTHER), SSF57277 (SUPERFAMILY)
	-	0				-
Equus caballus	ribosomal protein l10	6	P:GO:0007283; F:GO:0003735; C:GO:0022625; C:GO:0005634; C:GO:0005783; P:GO:0006414	-		IPR001197; IPR016180; IPR018255; G3DSA:3.90.1170.10 (GENE3D)
Caenorhabditis briggsae	adam 10	12	F:GO:0008270; P:GO:0008347; P:GO:0003007; P:GO:0007298; F:GO:0004222; P:GO:0006508; P:GO:0006911; P:GO:0048542; P:GO:0007519; P:GO:0007220; P:GO:0007166; P:GO:0007513	-	EC:3.4.24.0	IPR001590; IPR001762; G3DSA:3.40.390.10 (GENE3D), PTHR11905 (PANTHER), PTHR11905:SF4 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis briggsae	phosphatidylinositol transfer membrane-associated 1	11	P:GO:0006810; P:GO:0007602; F:GO:0005548; P:GO:0016056; F:GO:0046872; P:GO:0007601; C:GO:0044425; P:GO:0006629; C:GO:0044446; C:GO:0005783; C:GO:0005886	-		IPR001666; IPR004177; PTHR10658:SF6 (PANTHER)
	-	0				-
Brugia malayi	laminin subunit beta-1	5	P:GO:0000003; P:GO:0010171; P:GO:0040010; F:GO:0005515; P:GO:0040011	-		IPR002049; IPR013032; PD968187 (PRODOM), PR00011 (PRINTS), G3DSA:2.10.25.10 (GENE3D), PTHR10574 (PANTHER), PTHR10574:SF36 (PANTHER), SSF57196 (SUPERFAMILY)
Caenorhabditis elegans	transmembrane emp24 protein transport domain containing 5	1	C:GO:0044444	-		IPR000348; IPR015717; PTHR22811 (PANTHER), SignalP (SIGNALP)

Caenorhabditis elegans	transmembrane emp24 protein transport domain containing 5	1	C:GO:0044444	-		IPR000348; IPR015717; PTHR22811 (PANTHER), SignalP (SIGNALP)
Tribolium castaneum	wd40 protein	2	F:GO:0016740; P:GO:0051013	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR19861 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	sy-ptic glycoprotein sc2	4	C:GO:0005737; P:GO:0006629; F:GO:0016627; C:GO:0016021	-		IPR001104; IPR019955; G3DSA:3.10.20.90 (GENE3D), PTHR10556 (PANTHER), PTHR10556:SF16 (PANTHER)
Caenorhabditis briggsae	transducin -like 2	1	F:GO:0005515	-		PS51257 (PROFILE), SignalP (SIGNALP)
Caenorhabditis elegans	in family member (-b-1)	0		F:GO:0005515		-
Caenorhabditis elegans	protein-tyrosine phosphatase containing protein	3	F:GO:0016791; P:GO:0009792; P:GO:0000003	-	EC:3.1.3.0	IPR000242; IPR000387; IPR016130; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
Nematostella vectensis	protein	0		F:GO:0016787		-
Loa loa	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	receptor tyrosine ki-se-like orphan receptor 1	16	P:GO:0016477; P:GO:0007411; C:GO:0030424; C:GO:0032809; F:GO:0004674; C:GO:0030425; P:GO:0005975; P:GO:0040035; P:GO:0007169; F:GO:0005524; C:GO:0031594; F:GO:0005515; F:GO:0004714; C:GO:0005887; P:GO:0006468; P:GO:0045200	-	EC:2.7.11.0; EC:2.7.10.1	IPR000001; IPR003598; IPR007110; IPR013098; IPR013783; IPR013806; IPR020067; PTHR10489 (PANTHER), PTHR10489:SF20 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	nuclear pore complex protein family member (npp-21)	4	P:GO:0040015; P:GO:0000003; P:GO:0002119; P:GO:0040011	-		-
	-	0				-
Caenorhabditis elegans	death-associated protein	0				PTHR13177 (PANTHER)
Caenorhabditis briggsae	sb:cb283 protein	3	C:GO:0005622; P:GO:0006508; F:GO:0004177	-	EC:3.4.11.0	IPR000819; IPR011356; G3DSA:3.40.630.10 (GENE3D), PTHR11963 (PANTHER), PTHR11963:SF2 (PANTHER), SSF53187 (SUPERFAMILY)
Caenorhabditis briggsae	sb:cb283 protein	3	C:GO:0005622; P:GO:0006508; F:GO:0004177	-	EC:3.4.11.0	IPR000819; IPR011356; G3DSA:3.40.630.10 (GENE3D), PTHR11963 (PANTHER), PTHR11963:SF2 (PANTHER), SSF53187 (SUPERFAMILY)
Caenorhabditis elegans	coiled-coil domain-containing protein 51	1	C:GO:0044464	-		-
Caenorhabditis elegans	coiled-coil domain-containing protein 51	1	C:GO:0044464	-		-
						IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)

						IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)
Brugia malayi	uridine-cytidine ki-se 2	8	C:GO:0005792; P:GO:0007631; P:GO:0016579; P:GO:0071453; P:GO:0048678; F:GO:0016301; C:GO:0005829; F:GO:0000166	-		-
Caenorhabditis elegans	cytochrome c1	10	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0009055; P:GO:0018991; F:GO:0020037; P:GO:0040010; P:GO:0008340; P:GO:0040019; C:GO:0016021	-		IPR002326; IPR009056; IPR021157
Caenorhabditis briggsae	fructose-bisphosphate aldolase c	3	P:GO:0006096; F:GO:0004332; F:GO:0042802	-	EC:4.1.2.13	IPR000741; IPR013785; SSF51569 (SUPERFAMILY)
Brugia malayi	ubiquitin specific	2	F:GO:0016787; P:GO:0000289	-		PTHR15728 (PANTHER)
	-	0				-
Caenorhabditis elegans	mitochondrial ribosomal	4	P:GO:0009792; P:GO:0002119; F:GO:0005515; P:GO:0040010	-		PTHR12899 (PANTHER), SSF53137 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	formin-like 3 isoform 1	0		F:GO:0005488; F:GO:0003779; P:GO:0016043; C:GO:0015629; P:GO:0030036		IPR010472; IPR010473; IPR014768; IPR016024; PTHR23213 (PANTHER), PTHR23213:SF24 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-bre-3 protein	15	P:GO:0007411; P:GO:0075015; P:GO:0016325; P:GO:0033227; P:GO:0045165; P:GO:0001744; C:GO:0005737; P:GO:0046662; P:GO:0007299; P:GO:0006688; P:GO:0042248; P:GO:0030720; C:GO:0005887; P:GO:0045434; F:GO:0019187	-		PTHR16779 (PANTHER), SignalP (SIGNALP), SSF53448 (SUPERFAMILY)
Caenorhabditis elegans	sensory axon guidance family member (sax-7)	5	P:GO:0048812; P:GO:0065008; P:GO:0048513; P:GO:0048667; C:GO:0044459	-		IPR003598; IPR003599; IPR003961; IPR007110; IPR008957; IPR013098; IPR013783; PTHR10489 (PANTHER), PTHR10489:SF39 (PANTHER), SignalP (SIGNALP), SSF48726 (SUPERFAMILY)

Caenorhabditis elegans	sensory axon guidance family member (sax-7)	5	P:GO:0048812; P:GO:0065008; P:GO:0048513; P:GO:0048667; C:GO:0044459	-		IPR003598; IPR003599; IPR003961; IPR007110; IPR008957; IPR013098; IPR013783; PTHR10489 (PANTHER), PTHR10489:SF39 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	ribonuclease h2 subunit b	0		C:GO:0005634		IPR019024; PTHR13383 (PANTHER), PTHR13383:SF1 (PANTHER)
Caenorhabditis sp. PS1010	briggsae cbr-cdh-4 protein	5	P:GO:0007411; P:GO:0007163; C:GO:0044459; P:GO:0007155; P:GO:0007413	-		IPR002126; IPR015919; IPR020894; PTHR10596 (PANTHER), PTHR10596:SF74 (PANTHER)
Caenorhabditis briggsae	u3 small nucleolar homolog	11	P:GO:0040010; C:GO:0005840; C:GO:0005730; P:GO:0006364; F:GO:0019843; P:GO:0040035; P:GO:0002119; F:GO:0005515; P:GO:0006898; F:GO:0030519; P:GO:0009792	-		SignalP (SIGNALP)
Caenorhabditis briggsae	laminin a	11	P:GO:0050896; F:GO:0005488; C:GO:0005605; P:GO:0007399; P:GO:0007155; P:GO:0048513; P:GO:0006928; P:GO:0040011; P:GO:0050794; P:GO:0009653; P:GO:0009790	-		IPR001791; IPR008985; IPR012680; IPR013320; PTHR10574 (PANTHER), PTHR10574:SF17 (PANTHER)
Caenorhabditis briggsae	armadillo repeat-containing	1	F:GO:0005488	-		IPR006911; IPR011989; IPR016024
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0016491; P:GO:0009792; F:GO:0004867; F:GO:0005515		IPR002223; IPR006150; IPR020901; PTHR10083 (PANTHER), PTHR10083:SF36 (PANTHER)
Caenorhabditis briggsae	neutral sphingomyeli-se (n-smase) activation associated factor	0		F:GO:0016740; F:GO:0016905		-
Caenorhabditis elegans	transport protein sec61 subunit alpha 2	8	P:GO:0009792; C:GO:0005789; F:GO:0015450; P:GO:0055085; P:GO:0000003; C:GO:0016021; F:GO:0043022; P:GO:0015031	-		IPR002208; IPR019561; IPR023201; PTHR10906:SF1 (PANTHER), SignalP (SIGNALP)
Brugia malayi	transport protein sec61 subunit alpha 2	8	P:GO:0009792; C:GO:0005789; F:GO:0015450; P:GO:0055085; P:GO:0000003; C:GO:0016021; F:GO:0043022; P:GO:0015031	-		IPR002208; IPR023201; PTHR10906:SF1 (PANTHER), SignalP (SIGNALP)

Caenorhabditis briggsae	leukotriene a4 hydrolase	4	P:GO:0006954; F:GO:0005488; F:GO:0070011; P:GO:0044238	-		IPR001930; IPR015211; IPR016024; PTHR11533:SF4 (PANTHER)
Caenorhabditis elegans	myosin id	4	F:GO:0003779; C:GO:0016459; F:GO:0005524; F:GO:0003774	-		IPR000048; IPR001609; IPR010926; PTHR13140 (PANTHER), PTHR13140:SF31 (PANTHER), SSF52540 (SUPERFAMILY)
Brugia malayi	innexin family protein	5	P:GO:0040035; C:GO:0005921; P:GO:0040010; P:GO:0040011; P:GO:0002009	-		SignalP (SIGNALP)
Caenorhabditis elegans	coronin 7	2	C:GO:0044444; C:GO:0043229	-		IPR001680; IPR011046; IPR015505; IPR015943; IPR017986; IPR019775; IPR019781
	-	0				-
Loa loa	host cell factor 1	15	C:GO:0071339; P:GO:0045787; P:GO:0006013; P:GO:0043254; P:GO:0045449; F:GO:0042802; F:GO:0004476; F:GO:0008080; P:GO:0019046; F:GO:0003700; P:GO:0044419; C:GO:0070688; F:GO:0003713; C:GO:0005737; P:GO:0006366	-	EC:5.3.1.8	IPR006652; IPR015915; PTHR23244 (PANTHER), PTHR23244:SF36 (PANTHER), SSF117281 (SUPERFAMILY)
Caenorhabditis briggsae	cationic amino acid transporter	5	P:GO:0019915; C:GO:0016021; F:GO:0015171; C:GO:0005886; P:GO:0003333	-		IPR002293; IPR004841; PTHR11785:SF74 (PANTHER)
Caenorhabditis elegans	eukaryotic translation initiation factor 3 subunit c	6	C:GO:0005829; P:GO:0000003; C:GO:0005852; F:GO:0005515; P:GO:0006413; F:GO:0003743	-		IPR000717; IPR008905; IPR011991; PTHR13937 (PANTHER), SSF46785 (SUPERFAMILY)
Caenorhabditis briggsae	otu-like cysteine protease family protein	1	F:GO:0016787	-		-
Loa loa	importin subunit alpha-4	6	C:GO:0005737; C:GO:0005643; P:GO:0007292; F:GO:0005515; F:GO:0008565; P:GO:0006607	-		IPR000225; IPR002652; IPR011989; IPR016024; PTHR23316 (PANTHER)
	-	0				-
Caenorhabditis elegans	cyclin h	5	C:GO:0043234; F:GO:0004672; P:GO:0045449; C:GO:0005654; P:GO:0006366	-		IPR005479; IPR006670; IPR006671; IPR011028; IPR013763; IPR015429; IPR015432; PIRSF028758 (PIR)

Loa loa	histone-lysine n- h3 lysine-79 specific	1	F:GO:0008168	-	EC:2.1.1.0	IPR013110; G3DSA:3.40.50.150 (GENE3D), PTHR21451 (PANTHER), SSF53335 (SUPERFAMILY)
Loa loa	dot1- histone h3 methyltransferase (cerevisiae) isoform cra_a	1	F:GO:0042054	-		IPR013110; G3DSA:3.40.50.150 (GENE3D), PTHR21451 (PANTHER), SSF53335 (SUPERFAMILY)
Loa loa	dot1- histone h3 methyltransferase (cerevisiae) isoform cra_a	1	F:GO:0042054	-		IPR013110; G3DSA:3.40.50.150 (GENE3D), PTHR21451 (PANTHER), SSF53335 (SUPERFAMILY)
Caenorhabditis briggsae	membrane-associated protein	4	P:GO:0016477; P:GO:0018991; F:GO:0005515; P:GO:0010172	-		IPR019137; PTHR12093 (PANTHER), PTHR12093:SF4 (PANTHER)
Caenorhabditis briggsae	seryl-tr- synthetase	4	C:GO:0005737; F:GO:0005524; P:GO:0006434; F:GO:0004828	-	EC:6.1.1.11	IPR002314; IPR002317; IPR006195; IPR010978; G3DSA:3.30.930.10 (GENE3D), SignalP (SIGNALP), SSF55681 (SUPERFAMILY)
	-	0				IPR001969
Caenorhabditis elegans	dab (drosophila disabled) homolog family member (dab-1)	10	P:GO:0007411; P:GO:0007417; F:GO:0042169; C:GO:0016021; P:GO:0042051; P:GO:0045500; P:GO:0007413; C:GO:0016323; C:GO:0005737; F:GO:0017124	-		-
	-	0				-
Caenorhabditis elegans	chaperonin containing subunit 2	9	C:GO:0005737; P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0006457; F:GO:0005524; F:GO:0051082; P:GO:0040007; P:GO:0006898	-		IPR002194; IPR002423; IPR012716; IPR017998; G3DSA:1.10.560.10 (GENE3D), G3DSA:3.30.260.10 (GENE3D), G3DSA:3.50.7.10 (GENE3D), SSF52029 (SUPERFAMILY), SSF54849 (SUPERFAMILY)
Caenorhabditis elegans	ribosomal protein l12	12	P:GO:0000022; P:GO:0006412; P:GO:0040010; F:GO:0003723; F:GO:0003735; P:GO:0000003; P:GO:0032940; P:GO:0002119; P:GO:0006898; P:GO:0009792; C:GO:0005811; C:GO:0022625	-	EC:3.6.5.3	IPR000911; IPR020783; IPR020784; IPR020785; PTHR11661:SF2 (PANTHER)

Caenorhabditis elegans	capping protein (actin filament) muscle z- beta	18	C:GO:0030863; P:GO:0030032; C:GO:0030027; C:GO:0016020; P:GO:0035046; P:GO:0040010; C:GO:0071203; P:GO:0006928; P:GO:0009792; P:GO:0002119; C:GO:0008290; P:GO:0000578; P:GO:0051693; F:GO:0051015; P:GO:0010171; C:GO:0030018; P:GO:0040022; P:GO:0040035	-		IPR001698; SSF90096 (SUPERFAMILY)
Caenorhabditis elegans	lysosomal alpha-mannosidase (mannosidase alpha class 2b member 1)	2	F:GO:0004553; F:GO:0005488	-	EC:3.2.1.0	-
Caenorhabditis briggsae	proteasome subunit alpha type 7-	14	P:GO:0040010; P:GO:0051436; P:GO:0051437; P:GO:0000003; F:GO:0042802; F:GO:0004298; P:GO:0031145; P:GO:0002119; P:GO:0040011; C:GO:0019773; P:GO:0044419; P:GO:0009792; C:GO:0005737; C:GO:0005634	-	EC:3.4.25.0	-
Caenorhabditis elegans	translocase of inner mitochondrial membrane 50 homolog	6	P:GO:0009792; C:GO:0005743; P:GO:0055085; P:GO:0000003; C:GO:0016021; P:GO:0015031	-		IPR004274; G3DSA:3.40.50.1000 (GENE3D), PTHR12210 (PANTHER), PTHR12210:SF3 (PANTHER), SSF56784 (SUPERFAMILY)
	-	0				-
	-	0				-
Heliconius melpomene	endonuclease-reverse transcriptase	1	F:GO:0005488	-		IPR000477; IPR015706; G3DSA:3.30.70.270 (GENE3D), SSF56672 (SUPERFAMILY)

Heliconius melpomene	endonuclease-reverse transcriptase	0		C:GO:0005672; P:GO:0016337; F:GO:0003702; P:GO:0006367; C:GO:0030027; F:GO:0003677; C:GO:0015629; F:GO:0008270; F:GO:0003964; F:GO:0003723; C:GO:0005916; P:GO:0006278; F:GO:0005515; C:GO:0005622; F:GO:0004519; F:GO:0045296; F:GO:0005198		IPR000477; SSF56672 (SUPERFAMILY)
Plasmodium yoelii yoelii str. 17XNL	antigen 332	0		C:GO:0001533; P:GO:0030216		PR00211 (PRINTS), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-flp-9 protein	0		P:GO:0007218		-
Nasonia vitripennis	r--binding protein 35a	6	P:GO:0008380; F:GO:0003729; P:GO:0006397; P:GO:0007173; C:GO:0005634; F:GO:0000166	-		PTHR13976 (PANTHER), PTHR13976:SF2 (PANTHER)
Caenorhabditis elegans	phenylalanyl tr- synthetase family member (frs-1)	5	C:GO:0005737; F:GO:0004826; F:GO:0005524; P:GO:0006432; F:GO:0000049	-	EC:6.1.1.20	IPR002319; IPR006195; G3DSA:3.30.930.10 (GENE3D), PTHR11538:SF15 (PANTHER), SSF55681 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-ceh-60 protein	0		P:GO:0006355; F:GO:0043565; P:GO:0045449; F:GO:0030528; F:GO:0003700; C:GO:0005634; F:GO:0003677		IPR012287; PTHR11850 (PANTHER), PTHR11850:SF2 (PANTHER)
	-	0				-
Caenorhabditis briggsae	pre-b-cell leukemia transcription factor 3	17	P:GO:0008340; P:GO:0018991; F:GO:0005515; P:GO:0040027; P:GO:0040010; P:GO:0006898; P:GO:0006355; C:GO:0005737; P:GO:0009792; F:GO:0003677; P:GO:0007388; P:GO:0007501; P:GO:0042692; P:GO:0010171; C:GO:0005634; P:GO:0016477; P:GO:0007387	-		-

Caenorhabditis briggsae	pre-b-cell leukemia transcription factor 3	17	P:GO:0008340; P:GO:0018991; F:GO:0005515; P:GO:0040027; P:GO:0040010; P:GO:0006898; P:GO:0006355; C:GO:0005737; P:GO:0009792; F:GO:0003677; P:GO:0007388; P:GO:0007501; P:GO:0042692; P:GO:0010171; C:GO:0005634; P:GO:0016477; P:GO:0007387	-		IPR001356; IPR005542; IPR009057; IPR012287; IPR017970; PTHR11850 (PANTHER), PTHR11850:SF2 (PANTHER)
	-	0				G3DSA:2.40.10.10 (GENE3D)
	-	0				IPR015880
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	golgi reassembly stacking protein 2	2	C:GO:0005794; F:GO:0005515	-		-
Caenorhabditis briggsae	heterogeneous nuclear ribonucleoprotein a1	11	P:GO:0051168; C:GO:0005681; C:GO:0005730; P:GO:0050658; P:GO:0008380; F:GO:0005515; P:GO:0051170; F:GO:0003697; P:GO:0006397; C:GO:0005654; C:GO:0005737	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF13 (PANTHER), SSF54928 (SUPERFAMILY)
Loa loa	d-glucuronyl c5 epimerase	0		C:GO:0016021; F:GO:0016857; P:GO:0006024		IPR010598
	-	0				-
	-	0				-
Barentsia elongata	ribosomal protein s11	5	F:GO:0003735; F:GO:0005515; C:GO:0022627; F:GO:0019843; P:GO:0006414	-		-
Caenorhabditis elegans	briggsae cbr-tag-164 protein	0		C:GO:0016021		-
	-	0				-
Caenorhabditis briggsae	hir histone cell cycle regulation defective homolog a	3	P:GO:0009792; P:GO:0040010; P:GO:0000003	-		IPR011494; PTHR13831 (PANTHER)
Caenorhabditis briggsae	isovaleryl coenzyme a dehydroge-se	3	F:GO:0050660; P:GO:0055114; F:GO:0003995	-	EC:1.3.99.3	IPR006089; IPR006090; IPR006091; IPR009075; IPR009100; PTHR10909 (PANTHER), PTHR10909:SF10 (PANTHER)
Loa loa	mitochondrial-processing peptidase subunit alpha	4	F:GO:0046872; P:GO:0016485; C:GO:0005759; F:GO:0016787	-		IPR007863; IPR011237; IPR011249; PTHR11851 (PANTHER), PTHR11851:SF49 (PANTHER)

	-	0				-
	-	0				-
	-	0				-
Brugia malayi	nck-associated protein 1	23	P:GO:0007492; P:GO:0045176; P:GO:0030032; P:GO:0018991; C:GO:0030027; F:GO:0005515; C:GO:0016020; P:GO:0007417; P:GO:0048617; P:GO:0001756; P:GO:0048340; P:GO:0050821; P:GO:0030950; P:GO:0048570; P:GO:0035050; P:GO:0032880; P:GO:0045175; P:GO:0001843; P:GO:0006915; P:GO:0008078; P:GO:0010172; P:GO:0007354; P:GO:0001701	-		IPR019137; PTHR12093 (PANTHER), PTHR12093:SF4 (PANTHER)
Caenorhabditis elegans	rab3a interacting partial	2	F:GO:0005515; F:GO:0017112	-		PTHR14430 (PANTHER)
Caenorhabditis elegans	hla-b associated transcript 5	0				IPR000073; G3DSA:3.40.50.1820 (GENE3D), PTHR12277 (PANTHER), PTHR12277:SF3 (PANTHER), SSF53474 (SUPERFAMILY)
Angiostrongylus cantonensis	elegans protein confirmed by transcript evidence	0				IPR021010; SSF141739 (SUPERFAMILY)
Caenorhabditis briggsae	serine hydroxymethyltransferase	15	C:GO:0005829; P:GO:0006565; P:GO:0019264; C:GO:0005739; P:GO:0046655; P:GO:0032259; F:GO:0004372; F:GO:0016597; F:GO:0008732; P:GO:0051289; F:GO:0042803; F:GO:0030170; P:GO:0009113; C:GO:0005634; P:GO:0009790	-	EC:2.1.2.1	IPR001085; IPR015421; IPR015422; IPR015424; IPR019798
Caenorhabditis briggsae	mosc domain-containing protein mitochondrial	4	F:GO:0030170; F:GO:0030151; F:GO:0003824; F:GO:0005515	-		IPR005302; IPR005303; IPR011037; PTHR14237 (PANTHER), SSF141673 (SUPERFAMILY)

Caenorhabditis elegans	zinc finger protein family member (zfp-1)	6	F:GO:0003700; F:GO:0005488; P:GO:0007482; P:GO:0002168; P:GO:0007591; C:GO:0005634	-		PTHR13793 (PANTHER), PTHR13793:SF1 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-wrn-1 protein	2	P:GO:0044237; F:GO:0016787	-		-
Taeniopygia guttata	ventricular myosin heavy chain	0		C:GO:0005634; F:GO:0046982; P:GO:0030049; C:GO:0030017; F:GO:0005524; P:GO:0007512; F:GO:0042803; F:GO:0030898; P:GO:0055010; C:GO:0016459; P:GO:0035050; C:GO:0005925; F:GO:0000166; C:GO:0005737; F:GO:0016887; F:GO:0003779; F:GO:0003774; P:GO:0000302; C:GO:0005730; C:GO:0005859; F:GO:0008307; P:GO:0055005; F:GO:0005516; F:GO:0005515; P:GO:0006936; F:GO:0000146; C:GO:0032982;		-
Caenorhabditis elegans	lim domain family member (lim-8)	2	F:GO:0008270; F:GO:0005515	-		IPR001781; PTHR15551 (PANTHER)
Brugia malayi	fructose- -bisphosphatase 1	3	P:GO:0016051; C:GO:0005737; F:GO:0042132	-	EC:3.1.3.11	IPR000146; G3DSA:3.30.540.10 (GENE3D), SSF56655 (SUPERFAMILY)
Caenorhabditis elegans	spindle-pole body protein	1	F:GO:0005488	-		PD936484 (PRODOM), SignalP (SIGNALP)
Caenorhabditis elegans	n-alpha-acetyltransferase catalytic subunit	1	F:GO:0008080	-		IPR000182; IPR016181; PTHR23091 (PANTHER), PTHR23091:SF3 (PANTHER)
	-	0				-
Brugia malayi	hypothetical protein Bm1_07015 [Brugia malayi]	0				IPR019193
Caenorhabditis briggsae	cral n-terminus family protein	0		P:GO:0040010; F:GO:0005215; C:GO:0005622; P:GO:0006810		IPR001251; PTHR23324 (PANTHER), PTHR23324:SF3 (PANTHER)

Caenorhabditis elegans	superkiller viralicidic activity 2-like 2	9	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0008026; F:GO:0003676; P:GO:0040010; F:GO:0005524; P:GO:0040011; P:GO:0002009	-		IPR011545; G3DSA:3.40.50.300 (GENE3D), PTHR11752 (PANTHER), PTHR11752:SF2 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	thioesterase superfamily member 2	4	F:GO:0042802; F:GO:0016291; C:GO:0005739; P:GO:0051289	-		SignalP (SIGNALP)
Brugia malayi	wd-repeat protein	0				IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR19856 (PANTHER)
Brugia malayi	hypothetical protein Bm1_49115 [Brugia malayi]	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	F:GO:0016787; F:GO:0005515	-		PTHR15829 (PANTHER), PTHR15829:SF3 (PANTHER)
	-	0				-
Caenorhabditis elegans	tpr domain containing protein	14	C:GO:0005654; P:GO:0000003; P:GO:0070979; F:GO:0005515; P:GO:0007275; P:GO:0051437; C:GO:0005680; P:GO:0051436; P:GO:0008283; P:GO:0007091; C:GO:0005829; C:GO:0005813; C:GO:0005876; P:GO:0031145	-		IPR001440; IPR011990; IPR013026; IPR019734; PTHR12558 (PANTHER), PTHR12558:SF11 (PANTHER), SSF48452 (SUPERFAMILY)
Brugia malayi	sy-pse-associated protein 1	0		C:GO:0005634		IPR005607; PTHR16019 (PANTHER), SSF140383 (SUPERFAMILY)
Caenorhabditis elegans	urb1 ribosome biogenesis 1 homolog	0		F:GO:0003674; F:GO:0005488; P:GO:0008150; F:GO:0005515; C:GO:0005634; C:GO:0005730		-
	-	0				SignalP (SIGNALP)
Candida tropicalis MYA-3404	negative affector of salt tolerance	0		C:GO:0009986; P:GO:0006950; C:GO:0005694; P:GO:0007067; C:GO:0000775; C:GO:0005737; F:GO:0005524; P:GO:0051276; F:GO:0005515; C:GO:0005618; F:GO:0005198; F:GO:0005488		-

Candida tropicalis MYA-3404	negative affector of salt tolerance	0		C:GO:0009986; P:GO:0007067; F:GO:0003924; C:GO:0005694; F:GO:0005525; F:GO:0005524; C:GO:0000775; F:GO:0005198; C:GO:0005618; P:GO:0006413; C:GO:0019861; P:GO:0006412; F:GO:0000166; C:GO:0005737; F:GO:0005488; P:GO:0006950; P:GO:0051276; F:GO:0003743; C:GO:0005622; F:GO:0005515		-
Candida tropicalis MYA-3404	negative affector of salt tolerance	0		C:GO:0009986; P:GO:0006950; C:GO:0005694; P:GO:0007067; C:GO:0000775; C:GO:0005737; F:GO:0005524; P:GO:0051276; F:GO:0005515; C:GO:0005618; F:GO:0005198; F:GO:0005488		-
Caenorhabditis elegans	mtap_caeel ame: full= s-methyl-5 -thioadenosine phosphorylase ame: full=5 -methylthioadenosine phosphorylase short=mta phosphorylase short=mtapase	2	P:GO:0044237; F:GO:0016763	-	EC:2.4.2.0	IPR000845; IPR001369; IPR010044; G3DSA:3.40.50.1580 (GENE3D), PTHR11904:SF1 (PANTHER), SSF53167 (SUPERFAMILY)
Loa loa	calmodulin	2	P:GO:0009792; F:GO:0005509	-		IPR011992; IPR018247; IPR018248; IPR018249; PTHR23050 (PANTHER), PTHR23050:SF20 (PANTHER), SSF47473 (SUPERFAMILY)
Caenorhabditis briggsae	ribonucleotide reductase m2 polypeptide	9	C:GO:0005737; P:GO:0009263; P:GO:0006260; F:GO:0046914; F:GO:0005515; P:GO:0055114; P:GO:0051290; P:GO:0009186; F:GO:0004748	-	EC:1.17.4.1	IPR000358; IPR009078; IPR012348

Caenorhabditis briggsae	proteasome subunit alpha type-2	11	P:GO:0009615; P:GO:0051436; P:GO:0051437; F:GO:0004298; P:GO:0031145; P:GO:0002119; F:GO:0005515; C:GO:0019773; P:GO:0009792; C:GO:0005737; C:GO:0005634	-	EC:3.4.25.0	IPR000426; IPR001353; G3DSA:3.60.20.10 (GENE3D), PTHR11599 (PANTHER), PTHR11599:SF16 (PANTHER), PS51475 (PROFILE), SSF56235 (SUPERFAMILY)
Loa loa	ectonucleoside triphosphate diphosphohydrolase 7	5	P:GO:0032502; C:GO:0043231; F:GO:0016787; C:GO:0044444; C:GO:0016020	-		IPR000407; PTHR11782:SF5 (PANTHER)
Caenorhabditis brenneri	polymerase iii (d- directed) polypeptide b	11	F:GO:0003899; P:GO:0009615; P:GO:0048565; P:GO:0032728; P:GO:0045089; F:GO:0046872; P:GO:0031017; P:GO:0009304; F:GO:0003677; F:GO:0032549; C:GO:0005634	-	EC:2.7.7.6	-
Caenorhabditis brenneri	polymerase iii (d- directed) polypeptide b	11	F:GO:0003899; P:GO:0009615; P:GO:0048565; P:GO:0032728; P:GO:0045089; F:GO:0046872; P:GO:0031017; P:GO:0009304; F:GO:0003677; F:GO:0032549; C:GO:0005634	-	EC:2.7.7.6	-
Caenorhabditis elegans	transcription elongation factor spt6	5	P:GO:0040010; P:GO:0048856; P:GO:0002119; P:GO:0009792; P:GO:0006350	-		IPR006641; G3DSA:1.10.3500.10 (GENE3D), PTHR10145 (PANTHER), PTHR10145:SF1 (PANTHER)
Caenorhabditis elegans	dep domain containing protein	1	P:GO:0040010	-		PTHR13179 (PANTHER)
Caenorhabditis elegans	transmembrane protein 32	0		P:GO:0009058; F:GO:0016740; C:GO:0016021		IPR002060; IPR008949; PTHR21181 (PANTHER), PTHR21181:SF5 (PANTHER)
Caenorhabditis elegans	bifunctio-l aminoacyl-tr- synthetase	4	F:GO:0000166; F:GO:0004812; P:GO:0006418; C:GO:0005737	-		IPR000924; IPR011035; IPR020056; IPR020059; PTHR10119:SF11 (PANTHER)
Caenorhabditis elegans	lycan beta homolog family member (sgcb-1)	0				IPR006875; PTHR21142 (PANTHER)
Homo sapiens	mucin cell surface associated	5	C:GO:0005576; C:GO:0016324; C:GO:0005737; C:GO:0005887; C:GO:0005634	-		SignalP (SIGNALP)

Caenorhabditis elegans	briggsae cbr-cogc-8 protein	0				-
Caenorhabditis briggsae	briggsae cbr-unc-5 protein	0		F:GO:0004872; P:GO:0007165; F:GO:0005515		IPR000884; IPR003598; IPR007110; IPR013098; IPR013783; PR01705 (PRINTS), G3DSA:2.20.100.10 (GENE3D), PTHR12582 (PANTHER), PTHR12582:SF2 (PANTHER), SSF48726 (SUPERFAMILY)
Brugia malayi	tata box binding protein -associated factor	6	P:GO:0002119; F:GO:0004017; F:GO:0003676; F:GO:0004765; P:GO:0040010; F:GO:0005524	-	EC:2.7.4.3; EC:2.7.1.71	IPR003959; G3DSA:3.40.50.300 (GENE3D), PTHR12595 (PANTHER), SSF52540 (SUPERFAMILY)
Danio rerio	serine threonine-protein phosphatase 2a regulatory subunit b subunit gamma	0		F:GO:0005509; C:GO:0005737; C:GO:0005634		IPR011992; IPR018249; PTHR12085 (PANTHER), SSF47473 (SUPERFAMILY)
Brugia malayi	nipped-b-like protein	0		F:GO:0005488; P:GO:0034088; C:GO:0032116; F:GO:0005515		PTHR21704 (PANTHER), PTHR21704:SF5 (PANTHER)
Caenorhabditis briggsae	cop9 sig-losome complex subunit 4	7	P:GO:0040035; P:GO:0002119; F:GO:0005515; P:GO:0000910; P:GO:0040011; P:GO:0040007; C:GO:0008180	-		SignalP (SIGNALP)
Caenorhabditis briggsae	cop9 sig-losome complex subunit 4	7	P:GO:0040035; P:GO:0002119; F:GO:0005515; P:GO:0000910; P:GO:0040011; P:GO:0040007; C:GO:0008180	-		IPR000717; IPR011990; IPR011991; IPR013026; IPR019734; PTHR10855 (PANTHER), PTHR10855:SF2 (PANTHER), SSF46785 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein H24G06.1 [Caenorhabditis elegans]	3	P:GO:0009792; P:GO:0040035; F:GO:0005515	-		-
Caenorhabditis briggsae	renin receptor isoform 2	6	P:GO:0050789; P:GO:0040007; P:GO:0002119; P:GO:0040011; P:GO:0009792; C:GO:0016020	-		IPR012493; SignalP (SIGNALP)
Caenorhabditis elegans	suppressor of activated let-60 ras family member (sur-2)	3	P:GO:0044260; P:GO:0090304; P:GO:0010467	-		IPR021629; PTHR12691 (PANTHER), PTHR12691:SF3 (PANTHER)
Caenorhabditis sp. PS1010	hypothetical protein Csp3_JD07.006 [Caenorhabditis sp. PS1010]	0				-
Caenorhabditis briggsae	briggsae cbr-pink-1 protein	1	F:GO:0005488	-		-
	-	0				-
Brugia malayi	elegans protein confirmed by transcript evidence	0		F:GO:0003676; F:GO:0005524; F:GO:0008026		-
Caenorhabditis elegans	mif4g domain containing	1	F:GO:0005515	-		IPR003890; IPR016021; PTHR23254 (PANTHER), PTHR23254:SF10 (PANTHER)
Brugia malayi	breast cancer anti-estrogen resistance	1	P:GO:0007414	-		IPR021901; PTHR10654 (PANTHER)

Caenorhabditis elegans	5 -3 exoribonuclease 2	9	F:GO:0008270; F:GO:0003676; F:GO:0004534; C:GO:0005730; P:GO:0045449; F:GO:0005515; P:GO:0006353; P:GO:0000738; P:GO:0006397	-		IPR001878; IPR004859
Caenorhabditis elegans	5 -3 exoribonuclease 2	9	F:GO:0008270; F:GO:0003676; F:GO:0004534; C:GO:0005730; P:GO:0045449; F:GO:0005515; P:GO:0006353; P:GO:0000738; P:GO:0006397	-		IPR001878; IPR004859
Caenorhabditis elegans	briggsae cbr-ugt-62 protein	1	P:GO:0040010	-		-
Tetrahymena thermophila	viral a-type inclusion	0		C:GO:0005882; F:GO:0042802; C:GO:0005923; C:GO:0030054; F:GO:0003779; C:GO:0016459; F:GO:0003774; F:GO:0005515; P:GO:0008150; F:GO:0005198		PD936484 (PRODOM)
Caenorhabditis elegans	nuclear hormone receptor family member (nhr-49)	5	F:GO:0046872; F:GO:0004879; F:GO:0003677; P:GO:0045449; F:GO:0005515	-		IPR000536; IPR001628; IPR001723; IPR008946; IPR013088; PR00350 (PRINTS), PTHR11865 (PANTHER), PTHR11865:SF195 (PANTHER), SSF57716 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Oscheius tipulae	briggsae cbr-vit-6 protein	3	P:GO:0006810; F:GO:0022892; P:GO:0033036	-		-
Oscheius sp. (strain CEW1)	briggsae cbr-vit-6 protein	6	P:GO:0009792; F:GO:0022892; P:GO:0006810; P:GO:0040010; P:GO:0033036; P:GO:0008340	-		SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-lin-66 protein	4	P:GO:0040017; P:GO:0040035; F:GO:0005515; P:GO:0002119	-		IPR020845
Tribolium castaneum	wd repeat protein 26	0		C:GO:0005737		-
Caenorhabditis briggsae	patched family protein	4	P:GO:0040025; P:GO:0040018; P:GO:0040011; C:GO:0016020	-		IPR000731; IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER), SignalP (SIGNALP), SSF82866 (SUPERFAMILY)

Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	4	P:GO:0023034; F:GO:0046872; C:GO:0016021; F:GO:0005515	-		IPR001478; G3DSA:2.30.42.10 (GENE3D)
Mus musculus	PREDICTED: hypothetical protein [Mus musculus]	0				-
Caenorhabditis elegans	sensory axon guidance family member (sax-2)	1	F:GO:0005515	-		PTHR12295 (PANTHER), PTHR12295:SF6 (PANTHER)
	-	0				-
Caenorhabditis elegans	coiled-coil domain containing 97	0		F:GO:0003674; P:GO:0008150		-
	-	0				PR01217 (PRINTS)
Loa loa	fms interacting protein	1	P:GO:0009987	-		IPR019163; PTHR13375 (PANTHER)
Ostertagia ostertagi	cysteine protei-se	1	F:GO:0008234	-		IPR000169; IPR000668; IPR013128; IPR015643; G3DSA:3.90.70.10 (GENE3D), SSF54001 (SUPERFAMILY)
Caenorhabditis briggsae	tetratricopeptide repeat protein 38	0		F:GO:0005488		-
Caenorhabditis elegans	snf2 family n-termi-l domain containing protein	3	F:GO:0003676; C:GO:0005634; F:GO:0000166	-		-
Caenorhabditis elegans	gex interacting protein family member (gei-4)	1	F:GO:0005515	-		PTHR22084 (PANTHER)
	-	0				-
	-	0				-
Brugia malayi	valyl-tr- synthetase	4	C:GO:0043229; F:GO:0000166; F:GO:0004812; P:GO:0006418	-		IPR002300; IPR002303; IPR009080; IPR013155; IPR014729; G3DSA:1.10.730.10 (GENE3D), PTHR11946 (PANTHER), SSF52374 (SUPERFAMILY)
Caenorhabditis elegans	protein phosphatase 2c containing protein	15	P:GO:0006470; C:GO:0005739; F:GO:0046872; P:GO:0040007; P:GO:0007584; C:GO:0008287; P:GO:0007623; F:GO:0003677; F:GO:0004722; F:GO:0046983; P:GO:0007067; F:GO:0003700; P:GO:0042023; P:GO:0006350; C:GO:0005634	-		IPR001932; IPR014045; IPR015655; PTHR13832:SF98 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-smp-1 protein	3	C:GO:0016021; P:GO:0007275; F:GO:0004872	-		IPR001627; IPR002165; IPR003659; IPR015943; IPR016201; G3DSA:3.30.1680.10 (GENE3D), PTHR11036 (PANTHER), PTHR11036:SF29 (PANTHER)
Caenorhabditis elegans	hypothetical protein F57A8.1 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	udp-n-acetylglucosamine:a-3-d-mannoside b- -n-acetylglucosaminyltransferase i	2	F:GO:0016757; C:GO:0016020	-		-
Caenorhabditis elegans	xenotropic and polytropic retrovirus receptor 1	6	P:GO:0010171; F:GO:0004872; P:GO:0018991; P:GO:0040010; C:GO:0016021; P:GO:0009615	-		IPR004331; PTHR10783 (PANTHER), PTHR10783:SF4 (PANTHER)

Caenorhabditis elegans	26s proteasome subunit s9	5	C:GO:0005875; C:GO:0008541; P:GO:0006508; F:GO:0005488; F:GO:0004175	-		PTHR10678 (PANTHER), PTHR10678:SF2 (PANTHER)
Caenorhabditis briggsae	carboxypeptidase regulatory region-containing	1	P:GO:0000003	-		IPR008969; IPR013784; IPR014766; PTHR23303 (PANTHER), PTHR23303:SF1 (PANTHER)
Brugia malayi	negative elongation factor a	0		C:GO:0016021; P:GO:0006813; F:GO:0030955; F:GO:0003674; F:GO:0003746; C:GO:0005575; P:GO:0006350; F:GO:0005249; P:GO:0008150; P:GO:0045449		PTHR13328 (PANTHER)
Caenorhabditis elegans	gtp binding protein 2	2	F:GO:0042802; F:GO:0000166	-		-
Caenorhabditis briggsae	d ki-se family family member (dkf-2)	8	C:GO:0005737; P:GO:0006468; F:GO:0046872; P:GO:0045087; P:GO:0023034; F:GO:0004697; F:GO:0005524; C:GO:0016020	-	EC:2.7.11.13	IPR015727; G3DSA:1.10.510.10 (GENE3D)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR022559; PD030565 (PRODOM), SignalP (SIGNALP)
Caenorhabditis elegans	uncharacterized fam18-like protein cg5021	0		C:GO:0016021; P:GO:0008150		IPR008564
Caenorhabditis elegans	uncharacterized fam18-like protein cg5021	0		C:GO:0016021; P:GO:0008150		IPR008564
Caenorhabditis elegans	vacuolar protein sorting 8 homolog	0		F:GO:0046872; F:GO:0005488; F:GO:0003674; F:GO:0008270; F:GO:0005515; C:GO:0005575		IPR011046; IPR015943
Caenorhabditis elegans	tubulin tyrosine ligase like family member (ttll-4)	4	F:GO:0004835; P:GO:0006464; C:GO:0044464; F:GO:0005524	-	EC:6.3.2.25	IPR004344; PTHR12241:SF9 (PANTHER), SSF56059 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	ceramide ki-se	3	F:GO:0004143; C:GO:0044464; P:GO:0007205	-	EC:2.7.1.107	-
Ancylostoma caninum	venom-allergen-like protein family member (vap-1)	1	P:GO:0040011	-		SignalP (SIGNALP)
Caenorhabditis elegans	isoform a	4	P:GO:0006470; F:GO:0046872; F:GO:0004722; C:GO:0008287	-		-
Caenorhabditis elegans	isoform a	4	P:GO:0006470; F:GO:0046872; F:GO:0004722; C:GO:0008287	-		-

Caenorhabditis briggsae	domain containing protein	2	F:GO:0005515; P:GO:0009792	-		IPR000198; IPR008936; PTHR23178 (PANTHER)
Caenorhabditis elegans	u3 small nucleolar r- interacting protein 2	1	F:GO:0034511	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR19865 (PANTHER)
Caenorhabditis briggsae	pterin-4-alpha-carbinolamine dehydratase	2	F:GO:0008124; P:GO:0006729	-	EC:4.2.1.96	IPR001533
Ailuropoda melanoleuca	serologically defined colon cancer antigen 1	0		F:GO:0003676; F:GO:0003674; C:GO:0005737; F:GO:0008270; P:GO:0008150; C:GO:0005575; C:GO:0005634		-
	-	0				-
Caenorhabditis elegans	cation efflux system protein	1	P:GO:0006810	-		IPR002524; G3DSA:1.20.1510.10 (GENE3D), SignalP (SIGNALP)
Caenorhabditis elegans	organic cation transporter	4	P:GO:0019915; C:GO:0016021; P:GO:0055085; F:GO:0005215	-		IPR005828; IPR005829; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11600 (PANTHER), PTHR11600:SF44 (PANTHER), SignalP (SIGNALP)
Trichomonas vaginalis G3	pre-rr- processing and ribosome nuclear localization sequence nucleolar	0		P:GO:0060271; F:GO:0003676; P:GO:0060041; P:GO:0010842; F:GO:0000166; P:GO:0007018		-
Aedes aegypti	nucleolar and coiled-body phosphoprotein 1	3	P:GO:0048731; P:GO:0016043; P:GO:0009987	-		-
Loa loa	pdz domain containing protein	5	P:GO:0009792; P:GO:0040007; P:GO:0040035; F:GO:0005515; P:GO:0002119	-		IPR001478; G3DSA:2.30.42.10 (GENE3D)
Caenorhabditis elegans	briggsae cbr-sel-2 protein	4	C:GO:0005737; P:GO:0008104; F:GO:0051018; P:GO:0042675	-		-
Caenorhabditis elegans	briggsae cbr-sel-2 protein	4	C:GO:0005737; P:GO:0008104; F:GO:0051018; P:GO:0042675	-		-
Caenorhabditis elegans	briggsae cbr-sel-2 protein	4	C:GO:0005737; P:GO:0008104; F:GO:0051018; P:GO:0042675	-		-
Caenorhabditis elegans	briggsae cbr-gck-2 protein	5	F:GO:0004672; P:GO:0042059; P:GO:0048149; P:GO:0032008; P:GO:0006468	-		IPR001180; PTHR22986 (PANTHER), PTHR22986:SF76 (PANTHER), PS50219 (PROFILE)
Caenorhabditis elegans	briggsae cbr-gck-2 protein	5	F:GO:0004672; P:GO:0042059; P:GO:0048149; P:GO:0032008; P:GO:0006468	-		IPR001180; PTHR22986 (PANTHER), PTHR22986:SF76 (PANTHER), PS50219 (PROFILE)

Caenorhabditis elegans	zinc nfx1-type containing 1	0		F:GO:0046872; P:GO:0006508; F:GO:0008168; F:GO:0003674; P:GO:0008150; C:GO:0005575		G3DSA:3.40.50.300 (GENE3D), PTHR10887 (PANTHER), PTHR10887:SF10 (PANTHER), SSF52540 (SUPERFAMILY)
Strongylocentrotus purpuratus	nfx1-type zinc finger-containing protein 1	0		F:GO:0005524; P:GO:0006508; F:GO:0008168; F:GO:0000166; F:GO:0017111		PTHR10887 (PANTHER), PTHR10887:SF10 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	kiaa1404 protein	0		P:GO:0006508; F:GO:0008168		G3DSA:3.40.50.300 (GENE3D), PTHR10887 (PANTHER), PTHR10887:SF10 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	zinc nfx1-type containing 1	0		F:GO:0046872; P:GO:0006508; F:GO:0008168; F:GO:0003674; P:GO:0008150; C:GO:0005575		G3DSA:3.40.50.300 (GENE3D), PTHR10887 (PANTHER), PTHR10887:SF10 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				IPR018378; SignalP (SIGNALP)
	-	0				-
	-	0				IPR018378; SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				IPR018378; SignalP (SIGNALP)
Caenorhabditis elegans	kinesin-like protein family member (klp-12)	4	P:GO:0009792; F:GO:0005515; P:GO:0007067; F:GO:0003824	-		IPR001752; IPR019821; PTHR16012 (PANTHER), PTHR16012:SF173 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	kinesin-like protein family member (klp-12)	4	P:GO:0009792; F:GO:0005515; P:GO:0007067; F:GO:0003824	-		IPR001752; IPR019821; PTHR16012 (PANTHER), PTHR16012:SF173 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG16936 [Caenorhabditis briggsae]	0				IPR000436; IPR016060; SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG16936 [Caenorhabditis briggsae]	0				IPR000436; IPR016060; PTHR19325 (PANTHER), PTHR19325:SF25 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG16936 [Caenorhabditis briggsae]	0				IPR000436; IPR016060; SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein F13H6.1 [Caenorhabditis elegans]	4	F:GO:0005488; P:GO:0040010; P:GO:0040011; P:GO:0001703	-		PTHR23233 (PANTHER), PTHR23233:SF1 (PANTHER)
Caenorhabditis briggsae	3-ketodihydrosphingosine reductase	6	C:GO:0005789; C:GO:0005615; F:GO:0047560; F:GO:0005488; P:GO:0030148; P:GO:0006666	-	EC:1.1.1.102	IPR002198; IPR002347; IPR016040; PTHR19410:SF40 (PANTHER), SignalP (SIGNALP), SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	glycosyltransferase aer61 precursor	0		F:GO:0003674; F:GO:0016740; P:GO:0008152; C:GO:0005783; C:GO:0005576; C:GO:0005575; F:GO:0016757		IPR007657; PTHR20961 (PANTHER), SignalP (SIGNALP)

Caenorhabditis elegans	receptor expression-enhancing protein 5	1	F:GO:0005515	-		-
Caenorhabditis elegans	receptor expression-enhancing protein 5	1	F:GO:0005515	-		-
Caenorhabditis elegans	myc binding protein 2	1	F:GO:0005488	-		IPR004939; PTHR12846 (PANTHER), PTHR12846:SF2 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; P:GO:0006898; P:GO:0019915; P:GO:0009792; P:GO:0002119; P:GO:0040017; P:GO:0016246; P:GO:0040011; P:GO:0040010		-
Caenorhabditis briggsae	briggsae cbr-oma-2 protein	3	P:GO:0048599; F:GO:0008270; F:GO:0005515	-		IPR000571; G3DSA:4.10.1000.10 (GENE3D), PTHR12547 (PANTHER), PTHR12547:SF17 (PANTHER), SSF90229 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	teneurin family member (ten-1)	0		F:GO:0016740; P:GO:0007366; F:GO:0030246; C:GO:0016021; C:GO:0016020; F:GO:0004714; C:GO:0005578; C:GO:0005576; P:GO:0007160; C:GO:0005886; P:GO:0007155		PTHR11219 (PANTHER), PTHR11219:SF4 (PANTHER)
Caenorhabditis elegans	g-protein coupled receptor	4	F:GO:0004983; F:GO:0005515; P:GO:0007186; C:GO:0016021	-		IPR000276; IPR000611; IPR017452; G3DSA:1.20.1070.10 (GENE3D), PTHR19264 (PANTHER), PTHR19264:SF92 (PANTHER), SSF81321 (SUPERFAMILY)
Caenorhabditis elegans	-d synthetase 1	6	F:GO:0016810; F:GO:0005515; F:GO:0005524; F:GO:0003952; C:GO:0005829; P:GO:0009435	-	EC:6.3.5.1	IPR003010; PTHR23090 (PANTHER), PTHR23090:SF1 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-hum-5 protein	0		F:GO:0005524; F:GO:0003779; F:GO:0000166; F:GO:0003774; C:GO:0016459		-
Angiostrongylus cantonensis	heat shock protein family member (hsp-)	1	P:GO:0009408	-		-
Angiostrongylus cantonensis	heat shock protein family member (hsp-)	1	P:GO:0009408	-		-

Caenorhabditis briggsae	nuclear receptor nhr-1	5	F:GO:0046872; P:GO:0045449; F:GO:0003677; F:GO:0004879; F:GO:0005515	-		IPR000536; IPR001628; IPR001723; IPR008946; IPR013088; IPR018247; PR00350 (PRINTS), PTHR11865 (PANTHER), PTHR11865:SF218 (PANTHER), SSF57716 (SUPERFAMILY)
	-	0				IPR001810; IPR022364; G3DSA:1.20.1280.50 (GENE3D)
Caenorhabditis elegans	itbl_caeel ame: full=uncharacterized integrin beta-like protein flags: precursor	2	C:GO:0016021; P:GO:0007155	-		IPR001169; IPR002165; IPR003659; IPR016201; PTHR10082:SF5 (PANTHER), SignalP (SIGNALP)
Loa loa	zinc c2h2 type family protein	0		F:GO:0008270; C:GO:0005622		IPR001781; IPR015880; SSF57667 (SUPERFAMILY)
synthetic construct	cystatin b	7	P:GO:0042981; C:GO:0005737; C:GO:0005730; F:GO:0002020; F:GO:0004869; P:GO:0010466; P:GO:0008344	-		IPR000010; IPR001713; IPR018073; G3DSA:3.10.450.10 (GENE3D), PTHR11414 (PANTHER), PTHR11414:SF1 (PANTHER), SSF54403 (SUPERFAMILY)
Caenorhabditis briggsae	hydroxysteroid (17-beta) dehydroge-se 4	14	P:GO:0000038; P:GO:0060009; F:GO:0032934; C:GO:0005739; F:GO:0033989; P:GO:0033540; P:GO:0055114; F:GO:0015248; F:GO:0030283; F:GO:0003857; F:GO:0005515; F:GO:0004303; P:GO:0008203; C:GO:0005782	-	EC:4.2.1.107 ; EC:1.1.1.51; EC:1.1.1.35; EC:1.1.1.62	IPR002198; IPR002347; IPR003033; IPR016040; IPR020904; G3DSA:3.30.1050.10 (GENE3D), PTHR19410:SF50 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	component of oligomeric golgi complex 5	5	P:GO:0009792; C:GO:0043231; P:GO:0040010; C:GO:0044444; P:GO:0040039	-		PTHR13228 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0016539		IPR001534; SignalP (SIGNALP)
	-	0				IPR001534; SignalP (SIGNALP)
Caenorhabditis elegans	in family member (-b-1)	7	C:GO:0043197; P:GO:0007015; P:GO:0031175; C:GO:0030426; F:GO:0005515; C:GO:0030175; C:GO:0030864	-		IPR001660; IPR010993; IPR013761; IPR021129; PTHR16154 (PANTHER), PTHR16154:SF3 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	beta (bile acid) 2	7	P:GO:0006629; P:GO:0009056; P:GO:0018991; F:GO:0004553; P:GO:0040011; P:GO:0044237; C:GO:0016020	-	EC:3.2.1.0	IPR006775; IPR008928; IPR014551; PTHR12654 (PANTHER), PF12215 (PFAM), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)

Haemonchus contortus	acetylcholine regulator unc-	1	P:GO:0006904	-		IPR001619; G3DSA:3.40.50.1910 (GENE3D), PTHR11679:SF7 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	phytochelatin synthase	15	C:GO:0005829; F:GO:0005507; P:GO:0008219; P:GO:0042742; F:GO:0045551; P:GO:0046938; P:GO:0006955; P:GO:0052544; P:GO:0046685; F:GO:0016756; F:GO:0005515; P:GO:0009809; P:GO:0042344; F:GO:0046870; P:GO:0046686	-	EC:1.1.1.195; EC:2.3.2.15	IPR007719; SSF54001 (SUPERFAMILY)
Caenorhabditis elegans	acyl- synthetase long-chain family member 4	2	F:GO:0003824; P:GO:0008152	-		IPR000873; G3DSA:2.30.38.10 (GENE3D), G3DSA:3.40.50.980 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF8 (PANTHER), SignalP (SIGNALP), SSF56801 (SUPERFAMILY)
Caenorhabditis briggsae	nfx1-type zinc finger-containing protein 1	0		P:GO:0006355; P:GO:0006508; F:GO:0008168; F:GO:0003674; F:GO:0008270; P:GO:0008150; C:GO:0005634; C:GO:0005575		PTHR10887 (PANTHER), PTHR10887:SF2 (PANTHER)
Caenorhabditis briggsae	nfx1-type zinc finger-containing protein 1	0		P:GO:0006355; P:GO:0006508; F:GO:0008168; F:GO:0003674; P:GO:0008150; F:GO:0008270; C:GO:0005575; C:GO:0005634		PTHR10887 (PANTHER), PTHR10887:SF2 (PANTHER)
Caenorhabditis briggsae	nfx1-type zinc finger-containing protein 1	0		P:GO:0006355; P:GO:0006508; F:GO:0008168; F:GO:0003674; F:GO:0008270; P:GO:0008150; C:GO:0005634; C:GO:0005575		PTHR10887 (PANTHER), PTHR10887:SF2 (PANTHER)
	-	0				-
Caenorhabditis elegans	ras association (af-6) domain family 1	4	F:GO:0005515; P:GO:0009987; P:GO:0023052; C:GO:0044424	-		SignalP (SIGNALP)
Caenorhabditis elegans	mgc79752 protein	2	P:GO:0008152; F:GO:0016491	-		IPR002198; IPR002347; IPR016040; PTHR19410:SF76 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				-

Caenorhabditis elegans	isoform b	1	F:GO:0005515	-		IPR019149; G3DSA:3.40.50.1820 (GENE3D), PTHR13617 (PANTHER), PTHR13617:SF2 (PANTHER), SSF53474 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	r--binding protein with serine-rich domain 1	7	P:GO:0008380; F:GO:0003676; F:GO:0005515; P:GO:0006350; P:GO:0016071; C:GO:0005634; F:GO:0000166	-		IPR000504; IPR012677; PTHR15481 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	r--binding protein with serine-rich domain 1	7	P:GO:0008380; F:GO:0003676; F:GO:0005515; P:GO:0006350; P:GO:0016071; C:GO:0005634; F:GO:0000166	-		IPR000504; IPR012677; PTHR15481 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
	-	0				-
Macaca mulatta	heat shock 70kda protein 1a	18	F:GO:0047485; P:GO:0042026; P:GO:0090084; C:GO:0005739; P:GO:0030308; F:GO:0031625; C:GO:0016607; F:GO:0044183; P:GO:0006916; P:GO:0008285; C:GO:0016234; F:GO:0005524; P:GO:0006402; C:GO:0048471; C:GO:0030529; F:GO:0051082; P:GO:0006986; C:GO:0005783	-		-
Brugia malayi	hypothetical protein Bm1_12105 [Brugia malayi]	0				-
Caenorhabditis elegans	ferm domain (-ezrin-radixin-moesin) family member (frm-1)	1	F:GO:0005488	-		-
	-	0				
Caenorhabditis elegans	ferm domain (-ezrin-radixin-moesin) family member (frm-1)	0		F:GO:0005488; C:GO:0019898; F:GO:0008092; F:GO:0005515		
Caenorhabditis elegans	ferm domain (-ezrin-radixin-moesin) family member (frm-1)	1	F:GO:0005488	-		-
Caenorhabditis elegans	ferm domain (-ezrin-radixin-moesin) family member (frm-1)	1	F:GO:0005488	-		-
Caenorhabditis elegans	wd repeat domain-containing protein 83	3	C:GO:0005737; C:GO:0005681; P:GO:0000398	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR22842 (PANTHER)

Caenorhabditis elegans	vacuolar protein sorting 36	4	C:GO:0005770; C:GO:0005764; P:GO:0016197; F:GO:0043130	-		IPR007286; IPR021648; PTHR13128 (PANTHER), PTHR13128:SF6 (PANTHER), SSF46785 (SUPERFAMILY), SSF50729 (SUPERFAMILY)
Caenorhabditis elegans	tmco4_caeel ame: full=uncharacterized membrane protein	0				IPR007941
	-	0				-
Caenorhabditis sp. PS1010	yl58_caeel ame: full=uncharacterized protein	3	P:GO:0040010; P:GO:0040035; F:GO:0005515	-		IPR012816; SSF143990 (SUPERFAMILY)
	-	0				-
Loa loa	ubiquitin	5	C:GO:0005737; P:GO:0000003; P:GO:0040007; C:GO:0005634; P:GO:0002119	-		-
Caenorhabditis briggsae	barrier-to-autointegration factor	16	P:GO:0009615; C:GO:0005829; F:GO:0003690; P:GO:0051276; P:GO:0007059; F:GO:0042802; P:GO:0040035; P:GO:0010171; P:GO:0019059; P:GO:0019047; P:GO:0040011; P:GO:0006997; C:GO:0005635; C:GO:0000779; C:GO:0005654; P:GO:0009792	-		IPR004122; PD019964 (PRODOM), PTHR12912:SF2 (PANTHER)
						PS51257 (PROFILE)
						PS51257 (PROFILE)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	sex-determining protein fem-1	3	F:GO:0005515; P:GO:0008152; F:GO:0003824	-		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF131 (PANTHER)
Loa loa	u1 zinc finger	9	P:GO:0009792; F:GO:0003723; P:GO:0040010; P:GO:0000003; P:GO:0008340; P:GO:0006898; C:GO:0030529; C:GO:0005634; F:GO:0008270	-		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	2	P:GO:0006541; F:GO:0004359	-	EC:3.5.1.2	IPR002110; IPR012338; IPR015868; IPR020683; G3DSA:1.10.1500.10 (GENE3D), PTHR12544:SF3 (PANTHER)
Caenorhabditis elegans	acetolactate synthase-like protein	5	F:GO:0030976; C:GO:0016021; P:GO:0009792; F:GO:0000287; F:GO:0016740	-		IPR000399; IPR011766; IPR012000; IPR012001; G3DSA:3.40.50.1220 (GENE3D), G3DSA:3.40.50.970 (GENE3D), PTHR18968 (PANTHER), PTHR18968:SF7 (PANTHER), SSF52467 (SUPERFAMILY), SSF52518 (SUPERFAMILY)

Pongo abelii	tissue factor pathway inhibitor	0		F:GO:0030414; P:GO:0007598; C:GO:0005615; P:GO:0007596; F:GO:0004867; F:GO:0004866; C:GO:0005576; C:GO:0005886		-
Caenorhabditis elegans	cation efflux family protein	0		F:GO:0008324; C:GO:0016021; C:GO:0016020; P:GO:0055085; P:GO:0006812		IPR002524; G3DSA:1.20.1510.10 (GENE3D), G3DSA:3.30.70.1350 (GENE3D)
Caenorhabditis briggsae	nucleotide binding protein 1 (coli)	7	F:GO:0046872; P:GO:0065008; P:GO:0016226; F:GO:0005524; F:GO:0051539; F:GO:0017111; C:GO:0005829	-	EC:3.6.1.15	IPR000808; IPR003593; IPR019591; G3DSA:3.40.50.300 (GENE3D), PTHR23264 (PANTHER), PTHR23264:SF8 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	hect domain containing 1	3	F:GO:0016874; F:GO:0005515; P:GO:0000003	-		-
Caenorhabditis elegans	hect domain containing 1	3	F:GO:0016874; F:GO:0005515; P:GO:0000003	-		-
Caenorhabditis elegans	hect domain containing 1	3	F:GO:0016874; F:GO:0005515; P:GO:0000003	-		-
Caenorhabditis elegans	hect domain containing 1	3	F:GO:0016874; F:GO:0005515; P:GO:0000003	-		-
Loa loa	f-box domain containing protein	6	C:GO:0031981; P:GO:0044267; P:GO:0022402; P:GO:0050794; F:GO:0003824; F:GO:0005488	-		-
Loa loa	f-box domain containing protein	6	C:GO:0031981; P:GO:0044267; P:GO:0022402; P:GO:0050794; F:GO:0003824; F:GO:0005488	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005488	-		IPR013781; IPR017853; PTHR23208 (PANTHER), PTHR23208:SF13 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	ribosomal protein s6 polypeptide 2	8	C:GO:0005829; P:GO:0007243; F:GO:0004674; F:GO:0005524; F:GO:0005515; F:GO:0000287; C:GO:0005654; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017441; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR22985 (PANTHER), PTHR22985:SF67 (PANTHER)

Brugia malayi	gtp-binding protein sar1b	23	P:GO:0000003; P:GO:0035293; P:GO:0040007; P:GO:0006898; F:GO:0005525; C:GO:0005789; P:GO:0048081; P:GO:0035050; P:GO:0007029; P:GO:0018996; P:GO:0006886; P:GO:0050774; F:GO:0046872; C:GO:0030134; P:GO:0007264; P:GO:0009792; P:GO:0002119; P:GO:0007186; C:GO:0032580; C:GO:0005811; F:GO:0003924; C:GO:0005634; P:GO:0032940	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001412; IPR005225; IPR006687; IPR006689; G3DSA:3.40.50.300 (GENE3D), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	dep domain-containing	1	P:GO:0040010	-		IPR022046; PTHR13179 (PANTHER)
Caenorhabditis elegans	fibrinogen-binding protein a	0		C:GO:0005618; P:GO:0007155; C:GO:0009986; C:GO:0016020; C:GO:0005576; F:GO:0005515; P:GO:0009405		-
Caenorhabditis elegans	fibrinogen-binding protein a	0		C:GO:0005618; P:GO:0007155; C:GO:0009986; C:GO:0016020; C:GO:0005576; F:GO:0005515; P:GO:0009405		-
Caenorhabditis elegans	wd-repeat protein 37	0				PTHR19855 (PANTHER), PTHR19855:SF12 (PANTHER)

Haemonchus contortus	adp atp translocase	18	F:GO:0008233; P:GO:0055085; P:GO:0040010; P:GO:0008340; C:GO:0016021; C:GO:0005743; P:GO:0040002; P:GO:0040035; F:GO:0005471; P:GO:0015867; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0015866; P:GO:0006898; P:GO:0002009; P:GO:0009792; C:GO:0005811	-		-
	-	0				-
Loa loa	h aca ribonucleoprotein complex non-core subunit -f1	7	P:GO:0040010; F:GO:0005488; C:GO:0005732; P:GO:0040035; P:GO:0019915; P:GO:0042254; P:GO:0006898	-		IPR007504; IPR009000
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	P:GO:0009792; P:GO:0000003	-		-
Caenorhabditis remanei	zag-1	5	F:GO:0003700; F:GO:0043565; C:GO:0005634; F:GO:0008270; P:GO:0006355	-		IPR001356; IPR007087; IPR009057; IPR012287; IPR013087; IPR015880; IPR017970; PTHR13919 (PANTHER), PTHR13919:SF1 (PANTHER), SSF57667 (SUPERFAMILY)
Angiostrongylus cantonensis	briggsae cbr-pod-1 protein	0				IPR015049; IPR015505
	-	0				-
Nippostrongylus brasiliensis	globin	6	F:GO:0020037; C:GO:0005615; C:GO:0005737; F:GO:0005344; P:GO:0015671; F:GO:0019825	-		IPR000971; IPR009050; IPR012085; IPR012292
Nippostrongylus brasiliensis	globin	6	F:GO:0020037; C:GO:0005615; C:GO:0005737; F:GO:0005344; P:GO:0015671; F:GO:0019825	-		-
	-	0				-
Brugia malayi	ccr4-not transcription subunit 3	7	C:GO:0005737; P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0005515; P:GO:0008340; P:GO:0040007	-		IPR007282; PTHR23326 (PANTHER)

Caenorhabditis elegans	ccr4-not transcription subunit 3	5	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0008340; P:GO:0040007	-		IPR007207; IPR007282; PTHR23326 (PANTHER)
Caenorhabditis elegans	not-like (yeast ccr4 not complex component) family member (ntl-3)	5	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0008340; P:GO:0040007	-		IPR007207; IPR007282; IPR012270; PTHR23326 (PANTHER)
Caenorhabditis elegans	ccr4-not transcription subunit 3	6	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0008340; P:GO:0040007; C:GO:0044424	-		IPR007207; IPR007282; IPR012270; PTHR23326 (PANTHER)
Caenorhabditis elegans	hypothetical protein Y4C6B.7 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	Hypothetical protein CBG13961 [Caenorhabditis briggsae]	0		P:GO:0000003		-
Debaryomyces hansenii CBS767	bifunctio-l r-se h acid phosphatase	0		F:GO:0003674; C:GO:0016021; C:GO:0012511; C:GO:0005575		-
Brugia malayi	pab-dependent poly -specific ribonuclease subunit 2	7	P:GO:0006355; P:GO:0044267; F:GO:0016787; F:GO:0046983; P:GO:0050896; F:GO:0003677; C:GO:0005634	-		PTHR15728 (PANTHER)
Brugia malayi	pab-dependent poly -specific ribonuclease subunit 2	7	P:GO:0006355; P:GO:0044267; F:GO:0016787; F:GO:0046983; P:GO:0050896; F:GO:0003677; C:GO:0005634	-		PTHR15728 (PANTHER)
Brugia malayi	pab-dependent poly -specific ribonuclease subunit 2	7	P:GO:0006355; P:GO:0044267; F:GO:0016787; F:GO:0046983; P:GO:0050896; F:GO:0003677; C:GO:0005634	-		PTHR15728 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	kiaa1259 protein	0		F:GO:0003676; F:GO:0004386; F:GO:0005524; C:GO:0031011; C:GO:0005634; F:GO:0003677		-
	-	0				-
	-	0				-

Brugia malayi	negative elongation factor e	0		C:GO:0005634; C:GO:0005739; F:GO:0003676; F:GO:0000166; F:GO:0003723; F:GO:0003746; C:GO:0005654; C:GO:0005730; F:GO:0005515; P:GO:0006350		SignalP (SIGNALP)
Caenorhabditis elegans	receptor family ligand binding region containing protein	5	P:GO:0007186; C:GO:0016021; P:GO:0007165; F:GO:0004965; F:GO:0004930	-		IPR001828; IPR002455; IPR002456; IPR017978; G3DSA:3.40.50.2300 (GENE3D), PTHR10519 (PANTHER), PTHR10519:SF3 (PANTHER), SignalP (SIGNALP), SSF53822 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	leucine-rich repeat flightless-interacting protein 2	2	F:GO:0005515; P:GO:0009792	-		IPR019139; PD936484 (PRODOM)
Brugia malayi	chromodomain helicase d- binding protein 1-like	1	F:GO:0005488	-		IPR001357; IPR001650; G3DSA:3.40.50.10190 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR10799 (PANTHER), PTHR10799:SF74 (PANTHER), SSF52540 (SUPERFAMILY), SSF52949 (SUPERFAMILY)
Caenorhabditis elegans	btb poz domain-containing protein kctd3	1	P:GO:0009792	-		IPR000210; IPR001680; IPR003131; IPR007087; IPR011046; IPR011333; IPR015943; PTHR15859 (PANTHER)
Caenorhabditis elegans	btb poz domain-containing protein kctd3	1	P:GO:0009792	-		IPR000210; IPR001680; IPR003131; IPR007087; IPR011046; IPR011333; IPR015943; PTHR15859 (PANTHER)
Caenorhabditis elegans	btb poz domain-containing protein kctd3	2	P:GO:0009792; C:GO:0016020	-		-
Caenorhabditis elegans	btb poz domain-containing protein kctd3	1	P:GO:0009792	-		-
Caenorhabditis elegans	btb poz domain-containing protein kctd3	1	P:GO:0009792	-		-
Caenorhabditis elegans	btb poz domain-containing protein kctd3	1	P:GO:0009792	-		-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	-dh:ubiquinone ndufb6 b17	5	P:GO:0009792; P:GO:0002119; P:GO:0008340; P:GO:0040007; P:GO:0006898	-		-
Caenorhabditis elegans	-dh:ubiquinone ndufb6 b17	5	P:GO:0009792; P:GO:0002119; P:GO:0008340; P:GO:0040007; P:GO:0006898	-		-
Loa loa	splicing factor u2af large subunit	6	P:GO:0008380; F:GO:0003723; F:GO:0005515; P:GO:0006397; C:GO:0005634; F:GO:0000166	-		IPR000504; IPR012677; SSF54928 (SUPERFAMILY)

Loa loa	splicing factor u2af large subunit	6	P:GO:0008380; F:GO:0003723; F:GO:0005515; P:GO:0006397; C:GO:0005634; F:GO:0000166	-		-
Brugia malayi	protein ki-se domain containing protein	11	P:GO:0006468; C:GO:0005929; C:GO:0030425; F:GO:0005515; P:GO:0034606; F:GO:0004713; C:GO:0030424; P:GO:0034608; F:GO:0005524; C:GO:0043025; F:GO:0004674	-	EC:2.7.10.0; EC:2.7.11.0	IPR000719; IPR001245; IPR008266; IPR011009; IPR020685; IPR020764; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
Caenorhabditis briggsae	f-box domain-containing protein	0		F:GO:0003676; F:GO:0000166; F:GO:0005515		SignalP (SIGNALP)
Caenorhabditis elegans	f-box domain-containing protein	0		F:GO:0003676; F:GO:0000166; F:GO:0005515		-
Caenorhabditis briggsae	f-box domain-containing protein	0		F:GO:0003676; F:GO:0000166; F:GO:0005515		SignalP (SIGNALP)
Caenorhabditis briggsae	f-box domain-containing protein	0		F:GO:0003676; F:GO:0000166; F:GO:0005515		SignalP (SIGNALP)
Brugia malayi	mediator protein 4	0				PTHR13208 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0004222; F:GO:0016787; F:GO:0008270; F:GO:0008237; C:GO:0031012; F:GO:0008233; P:GO:0006508; F:GO:0046872; P:GO:0008152; F:GO:0005509		IPR000585; PTHR10201 (PANTHER), PTHR10201:SF6 (PANTHER), SignalP (SIGNALP)
	-	0				-
Loa loa	hypothetical protein LOAG_06796 [Loa loa]	0				SignalP (SIGNALP)
Caenorhabditis elegans	vh1 dual-specificity phosphatase family member (vhp-1)	5	C:GO:0005737; F:GO:0008138; P:GO:0016311; F:GO:0005515; C:GO:0005634	-		IPR000340; IPR000387; IPR016130; IPR020422; G3DSA:3.90.190.10 (GENE3D), PTHR10159 (PANTHER), PTHR10159:SF35 (PANTHER), SSF52799 (SUPERFAMILY)

Brugia malayi	katanin p60 (atpase-containing) subunit a 1	13	C:GO:0043005; P:GO:0048699; P:GO:0007017; C:GO:0005815; F:GO:0008568; P:GO:0051329; F:GO:0046982; P:GO:0051179; P:GO:0006996; F:GO:0008017; F:GO:0005524; P:GO:0008152; C:GO:0000922	-	EC:3.6.4.3	IPR003959; G3DSA:3.40.50.300 (GENE3D), PTHR23074 (PANTHER), PTHR23074:SF19 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-rad-26 protein	0		F:GO:0004386; F:GO:0003676; F:GO:0005524; C:GO:0016021; F:GO:0005515; F:GO:0003677		-
	-	0				-
Brugia malayi	activating sig-l cointegrator 1 complex subunit 3-like 1 isoform 1	12	P:GO:0018991; C:GO:0005681; F:GO:0008026; P:GO:0040007; F:GO:0003677; F:GO:0005524; P:GO:0007601; P:GO:0002119; F:GO:0005515; P:GO:0000354; C:GO:0005682; P:GO:0009792	-		IPR004179; G3DSA:1.10.150.20 (GENE3D), G3DSA:1.10.3380.10 (GENE3D), G3DSA:2.60.40.150 (GENE3D), PTHR11752 (PANTHER), PTHR11752:SF7 (PANTHER)
Brugia malayi	u5 small nuclear ribonucleoprotein 200 kda helicase	11	P:GO:0018991; F:GO:0004004; C:GO:0071011; P:GO:0000381; P:GO:0040007; F:GO:0003677; F:GO:0005524; P:GO:0002119; C:GO:0005682; C:GO:0071013; P:GO:0009792	-		IPR004179; G3DSA:2.60.40.150 (GENE3D), PTHR11752 (PANTHER), PTHR11752:SF7 (PANTHER)
Brugia malayi	activating sig-l cointegrator 1 complex subunit 3-like 1 isoform 1	12	P:GO:0018991; C:GO:0005681; F:GO:0008026; P:GO:0040007; F:GO:0003677; F:GO:0005524; P:GO:0007601; P:GO:0002119; F:GO:0005515; P:GO:0000354; C:GO:0005682; P:GO:0009792	-		IPR004179; G3DSA:1.10.150.20 (GENE3D), G3DSA:1.10.3380.10 (GENE3D), G3DSA:2.60.40.150 (GENE3D), PTHR11752 (PANTHER), PTHR11752:SF7 (PANTHER)

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis briggsae	cytosolic non-specific dipeptidase	4	F:GO:0008237; F:GO:0016805; P:GO:0006508; F:GO:0005515	-	EC:3.4.13.0	IPR001261; IPR002933; IPR011650; G3DSA:3.30.70.360 (GENE3D), G3DSA:3.40.630.10 (GENE3D), PTHR11014 (PANTHER), PTHR11014:SF15 (PANTHER), SSF53187 (SUPERFAMILY)
Caenorhabditis briggsae	wd repeat domain 46	3	P:GO:0002119; P:GO:0009792; P:GO:0040007	-		IPR001680; IPR011046; IPR012952; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PD023243 (PRODOM), PTHR14085 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-atp-4 protein	8	P:GO:0040010; F:GO:0015078; P:GO:0008340; C:GO:0000276; P:GO:0015986; P:GO:0000003; P:GO:0002119; P:GO:0009792	-		-
Brugia malayi	amino acid permease family protein	2	P:GO:0055085; C:GO:0016020	-		IPR000076; IPR004841; PTHR11827 (PANTHER), PTHR11827:SF2 (PANTHER)
Caenorhabditis briggsae	alkylation repair homolog 4 (coli)	1	P:GO:0009792	-		IPR005123; G3DSA:2.60.120.590 (GENE3D), PTHR12463 (PANTHER), SSF51197 (SUPERFAMILY)
Trichomonas vaginalis G3	ankyrin repeat protein	0		F:GO:0003674; P:GO:0008150		IPR002110; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER), PTHR18958:SF306 (PANTHER)
Loa loa	-dh-dependent fumarate reductase	2	F:GO:0016627; P:GO:0008152	-		IPR003953; G3DSA:3.50.50.60 (GENE3D), G3DSA:3.90.700.10 (GENE3D), PTHR11632 (PANTHER), PTHR11632:SF3 (PANTHER), SSF51905 (SUPERFAMILY), SSF56425 (SUPERFAMILY)
Caenorhabditis elegans	rho guanine nucleotide exchange factor 9-like	1	P:GO:0040011	-		IPR000108; IPR000219; IPR001452; IPR011511; G3DSA:2.30.30.40 (GENE3D), PTHR22834 (PANTHER), PTHR22834:SF2 (PANTHER), SSF103657 (SUPERFAMILY)
Caenorhabditis elegans	ribonucleases p mrp protein subunit pop1	6	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040010; P:GO:0000003; P:GO:0006898	-		-
Caenorhabditis briggsae	d- replication complex gins protein psf1	0		P:GO:0006260; C:GO:0005634		IPR005339; IPR021151; PTHR12914:SF2 (PANTHER)
	-	0				-
Loa loa	microtubule associated-protein orbit	6	P:GO:0009987; F:GO:0005488; C:GO:0043234; C:GO:0005856; C:GO:0044446; C:GO:0005737	-		IPR011989; PTHR21567 (PANTHER), PTHR21567:SF12 (PANTHER), PF12348 (PFAM)

Caenorhabditis briggsae	fha domain containing protein	6	P:GO:0040035; C:GO:0005622; F:GO:0005515; P:GO:0040011; P:GO:0006898; P:GO:0002009	-		IPR000253; IPR001159; IPR008984; PTHR23308 (PANTHER), PTHR23308:SF2 (PANTHER), SSF54768 (SUPERFAMILY)
	-	0				-
						IPR003961; IPR008957; IPR013098; IPR013783; PR00014 (PRINTS), PTHR19900 (PANTHER), PTHR19900:SF7 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0008150; C:GO:0005575		IPR003169; G3DSA:3.30.1490.40 (GENE3D), PTHR14445 (PANTHER), PTHR14445:SF5 (PANTHER)
Brugia malayi	chromosome 1 open reading frame 9	1	C:GO:0044464	-		IPR012919; PTHR12953 (PANTHER), PS51469 (PROFILE)
Brugia malayi	ligase atp-dependent	7	P:GO:0006281; F:GO:0003909; F:GO:0046872; F:GO:0005515; F:GO:0000166; P:GO:0033151; C:GO:0005654	-		IPR000977; IPR012309; IPR012310; IPR012340; IPR016027; IPR016059; G3DSA:3.30.470.30 (GENE3D), PTHR10459 (PANTHER), PTHR10459:SF11 (PANTHER), SSF56091 (SUPERFAMILY)
Loa loa	wd and tetratricopeptide repeats 1	1	P:GO:0019915	-		IPR001680; IPR011046; IPR011990; IPR013026; IPR015943; IPR017986; IPR019734; IPR019775; IPR019781; IPR019782; PTHR15574 (PANTHER), PTHR15574:SF6 (PANTHER), SSF48452 (SUPERFAMILY)
Loa loa	wd and tetratricopeptide repeats 1	1	P:GO:0019915	-		IPR001680; IPR011046; IPR011990; IPR013026; IPR015943; IPR017986; IPR019734; IPR019775; IPR019781; IPR019782; PTHR15574 (PANTHER), PTHR15574:SF6 (PANTHER), SSF48452 (SUPERFAMILY)
Loa loa	wd and tetratricopeptide repeats 1	1	P:GO:0019915	-		IPR001680; IPR011046; IPR011990; IPR013026; IPR015943; IPR017986; IPR019734; IPR019775; IPR019781; IPR019782; PTHR15574 (PANTHER), PTHR15574:SF6 (PANTHER), SSF48452 (SUPERFAMILY)
Loa loa	wd and tetratricopeptide repeats 1	1	P:GO:0019915	-		IPR001680; IPR011046; IPR011990; IPR013026; IPR015943; IPR017986; IPR019734; IPR019775; IPR019781; IPR019782; PTHR15574 (PANTHER), PTHR15574:SF6 (PANTHER), SSF48452 (SUPERFAMILY)
	-	0				-
Loa loa	proprotein convertase subtilisin kexin type furin	3	F:GO:0004252; P:GO:0000003; P:GO:0006508	-	EC:3.4.21.0	IPR000209; IPR002884; IPR008979; IPR015500; IPR022398; G3DSA:2.60.120.260 (GENE3D), PTHR10795:SF14 (PANTHER), SignalP (SIGNALP)

Brugia malayi	cleavage and polyadenylation specificity factor subunit 4	6	P:GO:0009792; P:GO:0002119; F:GO:0003676; F:GO:0005515; P:GO:0000910; F:GO:0008270	-		IPR000571; IPR001878; G3DSA:4.10.1000.10 (GENE3D), PTHR23102 (PANTHER), PTHR23102:SF14 (PANTHER), SSF90229 (SUPERFAMILY)
Brugia malayi	cleavage and polyadenylation specificity factor subunit 4	6	P:GO:0009792; P:GO:0002119; F:GO:0003676; F:GO:0005515; P:GO:0000910; F:GO:0008270	-		IPR000571; IPR001878; G3DSA:4.10.1000.10 (GENE3D), PTHR23102 (PANTHER), PTHR23102:SF14 (PANTHER), SSF90229 (SUPERFAMILY)
Brugia malayi	cleavage and polyadenylation specificity factor subunit 4	6	P:GO:0009792; P:GO:0002119; F:GO:0003676; F:GO:0005515; P:GO:0000910; F:GO:0008270	-		IPR000571; IPR001878; G3DSA:4.10.1000.10 (GENE3D), PTHR23102 (PANTHER), PTHR23102:SF14 (PANTHER), SSF90229 (SUPERFAMILY)
Caenorhabditis elegans	pleckstrin homology domain family f (with fyve domain) member 2	3	F:GO:0008270; F:GO:0005515; C:GO:0030133	-		IPR000306; IPR001849; IPR011011; IPR011993; IPR013083; IPR017455; PTHR22835 (PANTHER), PTHR22835:SF40 (PANTHER), SSF50729 (SUPERFAMILY)
Caenorhabditis elegans	non-claret disjunctio-l	3	F:GO:0005488; P:GO:0032502; P:GO:0007126	-		IPR001752; PTHR16012 (PANTHER), PTHR16012:SF170 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	F:GO:0005488; P:GO:0032502; P:GO:0007126	-		IPR001752; PTHR16012 (PANTHER), PTHR16012:SF170 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-ile-2 protein	4	P:GO:0018991; C:GO:0016021; P:GO:0009792; F:GO:0005529	-		IPR005052; IPR008985; IPR013320; PTHR12223:SF6 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	cation transporting atpase protein isoform partially confirmed by transcript evidence	5	F:GO:0016820; F:GO:0016887; F:GO:0000166; P:GO:0008152; C:GO:0016020	-	EC:3.6.3.0	IPR001757; IPR005834; IPR018303; G3DSA:3.40.1110.10 (GENE3D), G3DSA:3.40.50.1000 (GENE3D), PTHR11939:SF54 (PANTHER), SSF56784 (SUPERFAMILY), SSF81660 (SUPERFAMILY)
Caenorhabditis elegans	cation transporting atpase protein isoform partially confirmed by transcript evidence	5	F:GO:0016820; F:GO:0016887; F:GO:0000166; P:GO:0008152; C:GO:0016020	-	EC:3.6.3.0	IPR001757; IPR005834; IPR018303; G3DSA:3.40.1110.10 (GENE3D), G3DSA:3.40.50.1000 (GENE3D), PTHR11939:SF54 (PANTHER), SSF56784 (SUPERFAMILY), SSF81660 (SUPERFAMILY)
Caenorhabditis elegans	fumarylacetoacetate hydrolase	6	F:GO:0004334; F:GO:0046872; P:GO:0006572; P:GO:0006527; C:GO:0005829; P:GO:0006559	-	EC:3.7.1.2	IPR002529; IPR005959; IPR011234; IPR015377; PTHR11820 (PANTHER)
	-	0				-

Caenorhabditis briggsae	riken cd- 2310046k01	7	P:GO:0009792; C:GO:0005887; F:GO:0005515; P:GO:0034605; P:GO:0032218; F:GO:0032217; P:GO:0006898	-		IPR009357
Caenorhabditis briggsae	riken cd- 2310046k01	3	P:GO:0009792; P:GO:0006898; C:GO:0016020	-		IPR009357
Caenorhabditis briggsae	riken cd- 2310046k01	7	P:GO:0009792; C:GO:0005887; F:GO:0005515; P:GO:0034605; P:GO:0032218; F:GO:0032217; P:GO:0006898	-		IPR009357
Drosophila melanogaster	catsup protein	0		C:GO:0016020; P:GO:0055085; P:GO:0030001; F:GO:0046873		SignalP (SIGNALP)
Caenorhabditis briggsae	zinc dhhc-type containing 20	1	F:GO:0046872	-		PTHR22883 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	zinc dhhc-type containing 20	1	F:GO:0046872	-		PTHR22883 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	metallophosphoesterase 1	6	P:GO:0016192; F:GO:0046872; C:GO:0005793; C:GO:0044446; F:GO:0016787; C:GO:0005794	-		IPR004843; G3DSA:3.60.21.10 (GENE3D), PTHR13315 (PANTHER), SignalP (SIGNALP), SSF56300 (SUPERFAMILY)
Caenorhabditis elegans	cg17180 cg17180-pa	0				IPR019314; PTHR13440 (PANTHER)
	-	0				-
Caenorhabditis briggsae	cat eye syndrome chromosome candidate 5	1	C:GO:0005739	-		G3DSA:3.40.50.1000 (GENE3D), PTHR14269 (PANTHER), PTHR14269:SF2 (PANTHER)
Brugia malayi	helicase conserved c-termi-l domain containing protein	0		F:GO:0003676; F:GO:0004386; F:GO:0005524; F:GO:0016787; F:GO:0008026		-
Loa loa	small nuclear ribonucleoprotein sm d1	5	F:GO:0003676; C:GO:0030532; C:GO:0071011; P:GO:0000398; C:GO:0071013	-		-
Loa loa	small nuclear ribonucleoprotein sm d1	5	F:GO:0003676; C:GO:0030532; C:GO:0071011; P:GO:0000398; C:GO:0071013	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	solute carrier family 25 member 39	1	C:GO:0016020	-		IPR001993; IPR002067; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF43 (PANTHER), SignalP (SIGNALP)

Caenorhabditis elegans	solute carrier family 25 member 40	3	C:GO:0016020; C:GO:0005739; P:GO:0006810	-		IPR001993; IPR002067; IPR002113; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF43 (PANTHER)
Caenorhabditis elegans	e3 ubiquitin-protein ligase ubr2	0		P:GO:0030163; F:GO:0008270; F:GO:0004842; F:GO:0005515		PTHR21497 (PANTHER), PTHR21497:SF6 (PANTHER)
Brugia malayi	calcium homeostasis endoplasmic reticulum protein	0		F:GO:0003723; F:GO:0003676; C:GO:0000786; P:GO:0006396; P:GO:0007283; F:GO:0003677; C:GO:0005634; C:GO:0005622		PTHR12323 (PANTHER)
Brugia malayi	btb poz domain containing protein	0		F:GO:0046872; F:GO:0008270; F:GO:0005515; C:GO:0005622		IPR007087; IPR015880; SSF57667 (SUPERFAMILY)
Brugia malayi	zinc c2h2 type family protein	0		F:GO:0008270; C:GO:0005622		IPR007087; IPR015880; SSF57667 (SUPERFAMILY)
Caenorhabditis elegans	yqw3_caeel ame: full=uncharacterized protein	7	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040002; P:GO:0040010; P:GO:0000003; P:GO:0045132	-		PTHR13361 (PANTHER), PTHR13361:SF2 (PANTHER)
Caenorhabditis elegans	armadillo beta-catenin-like repeat family protein	0		C:GO:0005643; F:GO:0005488; C:GO:0005737; P:GO:0006886; F:GO:0005515; C:GO:0005634; P:GO:0006606; F:GO:0008565		IPR011989; IPR016024; PTHR23316 (PANTHER)
Caenorhabditis elegans	acyl- :lysophosphatidylglycerol acyltransferase 1	5	C:GO:0005737; P:GO:0009792; F:GO:0008415; C:GO:0016021; P:GO:0008152	-		IPR002123; PTHR10983 (PANTHER), PTHR10983:SF2 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	small subunit ribosomal protein 21	9	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; P:GO:0018996; F:GO:0005515; P:GO:0040010; P:GO:0000003; P:GO:0006412	-	EC:3.6.5.3	IPR001931
Caenorhabditis elegans	notchless homolog 1	7	C:GO:0005730; P:GO:0002119; P:GO:0007219; P:GO:0001826; P:GO:0000003; P:GO:0040007; P:GO:0006898	-		IPR001632; IPR001680; IPR011046; IPR012972; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR19848 (PANTHER)

Caenorhabditis briggsae	notchless homolog 1	7	C:GO:0005730; P:GO:0002119; P:GO:0007219; P:GO:0001826; P:GO:0000003; P:GO:0006898; P:GO:0040007	-		IPR001632; IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR19848 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	3	P:GO:0050789; P:GO:0009987; C:GO:0005622	-		IPR002913; G3DSA:3.30.530.20 (GENE3D), PTHR12659 (PANTHER), SSF55961 (SUPERFAMILY)
Loa loa	d- damage-binding protein 1	10	P:GO:0043161; P:GO:0000718; P:GO:0000075; F:GO:0003684; C:GO:0031464; C:GO:0031465; P:GO:0042787; F:GO:0005515; C:GO:0005654; C:GO:0005737	-		PTHR10644 (PANTHER), PTHR10644:SF3 (PANTHER)
Caenorhabditis briggsae	phospholipase a-2-activating protein	6	P:GO:0006954; F:GO:0005515; P:GO:0040010; F:GO:0016005; P:GO:0009987; P:GO:0008152	-		IPR015155; PTHR19849 (PANTHER)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0000003; P:GO:0040011; P:GO:0010171; P:GO:0040010; P:GO:0006898; P:GO:0002119		-
Caenorhabditis elegans	nucleoside diphosphate ki-se	4	P:GO:0009209; F:GO:0000166; F:GO:0016301; P:GO:0046131	-		-
Caenorhabditis briggsae	mitochondrial ribosomal protein l39	1	C:GO:0005739	-		IPR015552; IPR018163; PTHR11451 (PANTHER)
	-	0				-
Loa loa	polymerase (d- directed) epsilon 3 (p17 subunit)	5	P:GO:0006260; F:GO:0003677; C:GO:0005622; F:GO:0005515; F:GO:0016779	-	EC:2.7.7.0	IPR003958; IPR009072; PTHR11064 (PANTHER)
Caenorhabditis briggsae	nucleolar protein 6	0		C:GO:0005694; C:GO:0000794; F:GO:0003723; P:GO:0006364; C:GO:0005634; C:GO:0005730		IPR005554
Caenorhabditis elegans	pin2-interacting protein x1	5	F:GO:0003676; P:GO:0051276; C:GO:0000776; P:GO:0065007; C:GO:0044428	-		IPR000467; PTHR23149 (PANTHER), PTHR23149:SF1 (PANTHER)

Caenorhabditis elegans	jumonji domain containing 2a	5	P:GO:0016568; F:GO:0005488; P:GO:0044238; P:GO:0044260; F:GO:0016491	-		-
Caenorhabditis elegans	hypothetical protein C24G6.3 [Caenorhabditis elegans]	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	dual specificity mitogen-activated protein ki-se ki-se 6	7	P:GO:0043065; F:GO:0004674; F:GO:0005524; F:GO:0005515; P:GO:0042493; P:GO:0000187; P:GO:0060048	-	EC:2.7.11.0	IPR000719; IPR002290; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF36 (PANTHER)
Caenorhabditis briggsae	proteasome (macropain) activator subunit 4	0		F:GO:0005488		IPR011989
Caenorhabditis elegans	prion-like-(q n-rich)-domain-bearing protein family member (pqn-35)	0				-
Caenorhabditis elegans	prion-like-(q n-rich)-domain-bearing protein family member (pqn-35)	0				-
Loa loa	bromodomain containing 9	5	P:GO:0002119; F:GO:0005515; P:GO:0009792; P:GO:0000003; P:GO:0010171	-		IPR021900; PTHR22881 (PANTHER), PTHR22881:SF3 (PANTHER)
Caenorhabditis elegans	bromodomain containing 9	5	P:GO:0002119; F:GO:0005515; P:GO:0009792; P:GO:0000003; P:GO:0010171	-		IPR001487; IPR021900; PTHR22881 (PANTHER), PTHR22881:SF3 (PANTHER)
Caenorhabditis elegans	bromodomain containing 9	5	P:GO:0002119; F:GO:0005515; P:GO:0009792; P:GO:0000003; P:GO:0010171	-		IPR001487; IPR021900; PTHR22881 (PANTHER), PTHR22881:SF3 (PANTHER)
Caenorhabditis elegans	bromodomain containing 9	5	P:GO:0002119; F:GO:0005515; P:GO:0009792; P:GO:0000003; P:GO:0010171	-		IPR001487; IPR021900; PTHR22881 (PANTHER), PTHR22881:SF3 (PANTHER)
Caenorhabditis elegans	est2_caeel ame: full=esterase cm06b1	1	F:GO:0005515	-		IPR002018; IPR019826; G3DSA:3.40.50.1820 (GENE3D), PTHR11559:SF21 (PANTHER), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	est2_caeel ame: full=esterase cm06b1	1	F:GO:0005515	-		IPR002018; IPR019826; G3DSA:3.40.50.1820 (GENE3D), PTHR11559:SF21 (PANTHER), SSF53474 (SUPERFAMILY)
Tribolium castaneum	amsh	0		F:GO:0003674; C:GO:0005575		SignalP (SIGNALP)
Caenorhabditis elegans	n-acetylglucosamine-6-phosphate deacetylase	3	P:GO:0005975; F:GO:0016810; F:GO:0005515	-		IPR006680; G3DSA:3.20.20.140 (GENE3D), PTHR11113 (PANTHER), SSF51556 (SUPERFAMILY)

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	10	P:GO:0009056; P:GO:0048856; P:GO:0016486; F:GO:0004222; P:GO:0006508; C:GO:0044444; P:GO:0007275; F:GO:0042803; P:GO:0044237; C:GO:0016020	-	EC:3.4.24.0	IPR000718; IPR008753; IPR018497; G3DSA:3.40.390.10 (GENE3D), PTHR11733:SF15 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	d--directed r- polymerase ii subunit rpb2	15	F:GO:0003899; P:GO:0040010; P:GO:0008340; F:GO:0004672; P:GO:0006367; F:GO:0046872; P:GO:0000003; P:GO:0008380; C:GO:0005665; F:GO:0003677; P:GO:0002119; F:GO:0005515; P:GO:0006368; F:GO:0032549; P:GO:0009792	-	EC:2.7.7.6	IPR007120; IPR007644; IPR007645; IPR007646; IPR007647; IPR015712; G3DSA:3.90.1100.10 (GENE3D), PTHR20856:SF7 (PANTHER), SSF64484 (SUPERFAMILY)
Caenorhabditis briggsae	d- polymerase delta catalytic subunit	14	C:GO:0005875; P:GO:0000910; F:GO:0003887; F:GO:0008310; C:GO:0043625; F:GO:0003677; P:GO:0006272; P:GO:0035188; P:GO:0002119; F:GO:0000166; P:GO:0006898; P:GO:0006273; P:GO:0009792; P:GO:0006974	-	EC:2.7.7.7	IPR006133; IPR006134; IPR006172; IPR012337; IPR017964; G3DSA:3.30.420.10 (GENE3D), G3DSA:3.90.1600.10 (GENE3D), PTHR10322 (PANTHER), PTHR10322:SF4 (PANTHER), SSF56672 (SUPERFAMILY)
Caenorhabditis briggsae	dead eye	2	P:GO:0006810; C:GO:0005634	-		IPR007231
Loa loa	hypothetical protein LOAG_00531 [Loa loa]	0				-

Caenorhabditis elegans	mr- capping enzyme	17	P:GO:0040010; P:GO:0008340; P:GO:0006259; C:GO:0005622; P:GO:0000003; F:GO:0008186; P:GO:0018996; F:GO:0016791; P:GO:0010171; F:GO:0016740; P:GO:0019915; P:GO:0002119; P:GO:0006370; P:GO:0040017; P:GO:0006898; P:GO:0002009; P:GO:0009792	-	EC:3.1.3.0	IPR000340; IPR000387; IPR001339; IPR016130; G3DSA:3.30.470.30 (GENE3D), G3DSA:3.90.190.10 (GENE3D), PTHR10367 (PANTHER), SSF52799 (SUPERFAMILY), SSF56091 (SUPERFAMILY)
Brugia malayi	cleavage stimulation factor subunit 2	7	C:GO:0005730; P:GO:0006378; P:GO:0008380; F:GO:0003676; F:GO:0005515; P:GO:0006379; F:GO:0000166	-		IPR000504; IPR012677; PTHR23139 (PANTHER), PTHR23139:SF8 (PANTHER), SignalP (SIGNALP), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein T23B3.2 [Caenorhabditis elegans]	1	C:GO:0016021	-		IPR000612; SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein W02D7.3 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	psp family protein	0		P:GO:0006397; P:GO:0008380; F:GO:0003676; F:GO:0008270; F:GO:0003674; C:GO:0005575; C:GO:0005681; F:GO:0046872; P:GO:0008150		IPR006568; PTHR13316 (PANTHER)
Haemonchus contortus	zinc metallopeptidase	2	P:GO:0008152; F:GO:0008237	-		IPR000718; IPR008753; G3DSA:1.10.1380.10 (GENE3D), PTHR11733:SF15 (PANTHER), SignalP (SIGNALP), SSF55486 (SUPERFAMILY)
Caenorhabditis briggsae	mesoderm induction early response 1	1	P:GO:0000003	-		IPR000949; IPR001005; IPR009057; IPR017884; PTHR10865 (PANTHER), PTHR10865:SF1 (PANTHER)
Caenorhabditis briggsae	myb-like d--binding domain containing protein	3	P:GO:0009987; P:GO:0000003; C:GO:0044424	-		IPR000949; IPR001005; IPR009057; IPR017884; PTHR10865 (PANTHER), PTHR10865:SF1 (PANTHER)
Caenorhabditis elegans	membrane-bound transcription factor site 2	0		P:GO:0001501; P:GO:0006508; F:GO:0003674; C:GO:0016020; F:GO:0008233; P:GO:0008150; F:GO:0004222		IPR008915; PTHR13325 (PANTHER)
Caenorhabditis elegans	ypc1_caeel ame: full=uncharacterized protein	0				-
Loa loa	abnormal cell lineage protein 37	4	F:GO:0003723; C:GO:0005634; F:GO:0000166; P:GO:0008380	-		-
	-	0				SignalP (SIGNALP)

Heligmosomoides polygyrus	cytosolic glutathione s-transferase 1	4	P:GO:0008340; P:GO:0040010; F:GO:0005515; F:GO:0016740	-		IPR004045; IPR004046; IPR010987; IPR012335; IPR012336; IPR017933; PTHR11571 (PANTHER), PTHR11571:SF6 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	a chain crystal spectroscopic and catalytic properties of cobalt copper nickel and mercury derivatives of the zinc endopeptidase a correlation of structure and proteolytic activity	2	F:GO:0016787; P:GO:0007413	-		IPR001506; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF73 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	high choriolytic enzyme 1 precursor	2	F:GO:0016787; P:GO:0007413	-		IPR001506; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF73 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	high choriolytic enzyme 1 precursor	2	F:GO:0016787; P:GO:0007413	-		IPR001506; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF73 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	hatching enzyme	2	F:GO:0016787; P:GO:0007413	-		IPR001506; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF73 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	novel protein hatching enzymes	2	F:GO:0016787; P:GO:0007413	-		IPR001506; IPR006026; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF73 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein F56E10.1 [Caenorhabditis elegans]	0				IPR011990; PTHR23405 (PANTHER), PTHR23405:SF2 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0051301; P:GO:0009792; P:GO:0007126		IPR008574
Caenorhabditis briggsae	briggsae cbr-lin-36 protein	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		IPR006612; IPR015880
Caenorhabditis elegans	g e synthetase (glutamate-ammonia ligase) family member (gln-3)	7	P:GO:0045213; P:GO:0007416; P:GO:0006542; F:GO:0005524; F:GO:0004356; P:GO:0006538; C:GO:0005737	-	EC:6.3.1.2	SignalP (SIGNALP)
Loa loa	chitin binding peritrophin-a domain containing protein	0		P:GO:0000281; F:GO:0008061; P:GO:0051301; P:GO:0007275; P:GO:0009790; C:GO:0005576; F:GO:0005515; P:GO:0007049; P:GO:0006030		IPR002557; G3DSA:2.170.140.10 (GENE3D), PTHR23301 (PANTHER)

Caenorhabditis briggsae	briggsae cbr-cpg-2 protein	0		P:GO:0000281; F:GO:0008061; P:GO:0051301; P:GO:0009792; P:GO:0007275; P:GO:0009790; C:GO:0005576; P:GO:0030703; F:GO:0005515; P:GO:0007049; P:GO:0006030		IPR002557; G3DSA:2.170.140.10 (GENE3D), PTHR23301 (PANTHER)
Loa loa	chitin binding peritrophin-a domain containing protein	0		P:GO:0000281; F:GO:0008061; P:GO:0051301; P:GO:0007275; P:GO:0009790; C:GO:0005576; F:GO:0005515; P:GO:0007049; P:GO:0006030		IPR002557; G3DSA:2.170.140.10 (GENE3D), PTHR23301 (PANTHER)
Loa loa	chitin binding peritrophin-a domain containing protein	0		P:GO:0000281; F:GO:0008061; P:GO:0051301; P:GO:0007275; P:GO:0009790; C:GO:0005576; F:GO:0005515; P:GO:0007049; P:GO:0006030		IPR002557; G3DSA:2.170.140.10 (GENE3D), PTHR23301 (PANTHER)
Caenorhabditis elegans	g e synthetase (glutamate-ammonia ligase) family member (gln-3)	7	P:GO:0045213; P:GO:0007416; P:GO:0006542; F:GO:0005524; F:GO:0004356; P:GO:0006538; C:GO:0005737	-	EC:6.3.1.2	IPR008146; IPR008147; IPR014746; PTHR20852 (PANTHER), PTHR20852:SF14 (PANTHER), SSF55931 (SUPERFAMILY)
Loa loa	chitin binding peritrophin-a domain containing protein	0		P:GO:0000281; F:GO:0008061; P:GO:0051301; P:GO:0007275; P:GO:0009790; C:GO:0005576; F:GO:0005515; P:GO:0007049; P:GO:0006030		IPR002557; G3DSA:2.170.140.10 (GENE3D), PTHR23301 (PANTHER)
Caenorhabditis elegans	pecanex-like protein 1	1	P:GO:0040011	-		-
Caenorhabditis elegans	pecanex-like protein 1	1	P:GO:0040011	-		-
Caenorhabditis elegans	pecanex-like protein 1	0		C:GO:0016021; P:GO:0040011		-
Caenorhabditis elegans	pecanex-like protein 1	0		C:GO:0016021; P:GO:0040011		-
Caenorhabditis briggsae	skeletal muscle cells re-entry induced	3	P:GO:0018991; F:GO:0005488; P:GO:0040011	-		-

Caenorhabditis elegans	boc homolog	2	P:GO:0009987; C:GO:0044464	-		IPR003598; IPR003599; IPR007110; IPR013783; PTHR10489 (PANTHER), SignalP (SIGNALP), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	abnormal chemotaxis family member (tax-6)	4	P:GO:0006470; P:GO:0051533; F:GO:0004722; F:GO:0005515	-		IPR004843; IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF15 (PANTHER), SSF56300 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	cg13189-pa	4	P:GO:0030001; C:GO:0016020; F:GO:0046873; P:GO:0055085	-		SignalP (SIGNALP)
Caenorhabditis elegans	zinc zip family	4	C:GO:0016021; F:GO:0046873; P:GO:0034220; P:GO:0006829	-		-
Caenorhabditis briggsae	kinesin-like protein family member (klp-4)	5	P:GO:0007018; F:GO:0005515; F:GO:0005524; F:GO:0003777; C:GO:0005874	-		IPR000253; IPR008984; PTHR16012 (PANTHER), PTHR16012:SF67 (PANTHER)
Taeniopygia guttata	splicing arginine serine-rich 4	2	F:GO:0005488; P:GO:0008380	-		IPR000504; IPR012677; PTHR10548 (PANTHER), SSF54928 (SUPERFAMILY)
Salmo salar	splicing arginine serine-rich 5	7	P:GO:0040009; P:GO:0007283; P:GO:0008380; F:GO:0003723; P:GO:0007275; C:GO:0005882; C:GO:0005634	-		IPR000504; IPR012677; PTHR10548 (PANTHER), SSF54928 (SUPERFAMILY)
Loa loa	splicing arginine serine-rich 5	3	C:GO:0005882; F:GO:0003676; F:GO:0000166	-		-
Taeniopygia guttata	splicing arginine serine-rich 4	4	P:GO:0008380; F:GO:0005488; P:GO:0016311; F:GO:0004721	-	EC:3.1.3.16	IPR000504; IPR012677; PTHR10548 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	ccr4-not transcription complex subunit 1	2	P:GO:0048731; P:GO:0009987	-		PTHR13162 (PANTHER)
Ancylostoma ceylanicum	secreted protein 5 precursor	0		C:GO:0005576		IPR014044
Ancylostoma caninum	secreted protein asp-2	0		F:GO:0009055; P:GO:0019646; P:GO:0040011; P:GO:0006898; C:GO:0005576		IPR001283; IPR014044; PTHR10334:SF11 (PANTHER)
Caenorhabditis elegans	ethylmalonic encephalopathy 1	2	F:GO:0016787; C:GO:0005739	-		IPR001279; G3DSA:3.60.15.10 (GENE3D), PTHR11935 (PANTHER), PTHR11935:SF10 (PANTHER), SSF56281 (SUPERFAMILY)
Caenorhabditis briggsae	large subunit ribosomal protein 32	7	P:GO:0002119; C:GO:0005840; F:GO:0003735; P:GO:0018996; P:GO:0000003; P:GO:0040007; P:GO:0006412	-	EC:3.6.5.3	IPR001515; IPR018263; PTHR23413 (PANTHER)

Caenorhabditis elegans	merlin moesin ezrin radixin	5	C:GO:0005856; P:GO:0009792; C:GO:0005737; F:GO:0008092; C:GO:0019898	-		IPR000299; IPR000798; IPR014352; IPR018979; IPR019748; IPR019749; IPR019750; G3DSA:3.10.20.90 (GENE3D), PTHR23281 (PANTHER), PTHR23281:SF1 (PANTHER), SSF54236 (SUPERFAMILY)
Caenorhabditis elegans	fas associated factor 1	7	F:GO:0005515; P:GO:0048518; P:GO:0008219; P:GO:0030163; P:GO:0050794; C:GO:0044444; C:GO:0005634	-		IPR001012; IPR006577; G3DSA:3.10.20.90 (GENE3D), PTHR23322 (PANTHER), PTHR23322:SF5 (PANTHER), SSF54236 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-rnf-121 protein	2	F:GO:0008270; F:GO:0005515	-		IPR001841; IPR013083; IPR018957; PTHR13407 (PANTHER), SSF57850 (SUPERFAMILY)
	-	0				-
Plasmodium vivax Sal-1	hypothetical protein [Plasmodium vivax Sal-1]	0				-
Plasmodium vivax Sal-1	hypothetical protein [Plasmodium vivax Sal-1]	0				-
	-	0				-
Plasmodium vivax Sal-1	hypothetical protein [Plasmodium vivax Sal-1]	0				-
Caenorhabditis briggsae	zinc finger protein 622	6	P:GO:0009792; F:GO:0046872; C:GO:0005622; P:GO:0016246; P:GO:0040010; P:GO:0000003	-		IPR003604; IPR007087; IPR015880; IPR022755; PTHR13182 (PANTHER), SSF57667 (SUPERFAMILY)
Brugia malayi	disco-interacting protein 2 homolog c	2	P:GO:0008152; F:GO:0016874	-		IPR000873; G3DSA:2.30.38.10 (GENE3D), G3DSA:3.40.50.980 (GENE3D), PTHR22754 (PANTHER), PTHR22754:SF8 (PANTHER), SSF56801 (SUPERFAMILY)
Caenorhabditis elegans	family with sequence similarity member isoform cra_a	1	F:GO:0005515	-		-
Caenorhabditis elegans	family with sequence similarity member isoform cra_a	1	F:GO:0005515	-		-
Angiostrongylus cantonensis	grp1 protein	2	P:GO:0040018; F:GO:0005515	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Heligmosomoides polygyrus	tropomyosin	6	C:GO:0005737; P:GO:0009790; P:GO:0007015; P:GO:0034609; P:GO:0040011; F:GO:0051015	-		IPR000533; G3DSA:1.20.5.340 (GENE3D), PTHR19269 (PANTHER), PTHR19269:SF11 (PANTHER)
Heligmosomoides polygyrus	tropomyosin	6	C:GO:0005737; P:GO:0009790; P:GO:0007015; P:GO:0034609; P:GO:0040011; F:GO:0051015	-		IPR000533; PD936484 (PRODOM), G3DSA:1.20.5.340 (GENE3D), PTHR19269 (PANTHER), PTHR19269:SF11 (PANTHER)
Heligmosomoides polygyrus	tropomyosin	6	C:GO:0005737; P:GO:0009790; P:GO:0007015; P:GO:0034609; P:GO:0040011; F:GO:0051015	-		IPR000533; G3DSA:1.20.5.340 (GENE3D), PTHR19269 (PANTHER), PTHR19269:SF11 (PANTHER)

Brugia malayi	d- replication licensing factor mcm3	16	F:GO:0016851; P:GO:0006268; P:GO:0000910; P:GO:0007049; P:GO:0045449; P:GO:0015995; C:GO:0042555; P:GO:0040035; F:GO:0003677; F:GO:0005524; C:GO:0000785; F:GO:0016887; F:GO:0005515; P:GO:0030174; P:GO:0009792; F:GO:0003682	-	EC:6.6.1.1	IPR001208; IPR008046; IPR012340; IPR016027; PTHR11630 (PANTHER), PTHR11630:SF46 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	4	P:GO:0006284; F:GO:0005488; F:GO:0019104; C:GO:0042644	-		-
Caenorhabditis elegans	sy-ptic vesicle-associated integral membrane	5	C:GO:0008021; F:GO:0005484; P:GO:0035149; P:GO:0016081; C:GO:0005886	-		IPR001388; G3DSA:1.20.5.110 (GENE3D), PTHR21136 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical kda protein in chromosome iii	11	P:GO:0006412; P:GO:0051078; P:GO:0001745; P:GO:0048132; P:GO:0048137; P:GO:0007067; P:GO:0007054; P:GO:0008315; C:GO:0005737; C:GO:0005634; P:GO:0030718	-	EC:3.6.5.3	IPR004405; IPR005140; IPR005141
Caenorhabditis briggsae	cancer susceptibility candidate 3	6	P:GO:0044238; P:GO:0044260; F:GO:0042802; P:GO:0008298; C:GO:0030529; C:GO:0005634	-		IPR018545
Caenorhabditis briggsae	cancer susceptibility candidate 3	6	P:GO:0044238; P:GO:0044260; F:GO:0042802; P:GO:0008298; C:GO:0030529; C:GO:0005634	-		IPR018545

Caenorhabditis briggsae	briggsae cbr-ceh-20 protein	20	P:GO:0008340; F:GO:0030528; P:GO:0018991; F:GO:0005515; P:GO:0040027; P:GO:0040010; P:GO:0006898; P:GO:0009952; P:GO:0030326; C:GO:0005667; P:GO:0009792; F:GO:0043565; P:GO:0007501; P:GO:0042692; F:GO:0003700; P:GO:0010171; P:GO:0045944; P:GO:0009954; F:GO:0003682; P:GO:0016477	-		IPR001356; IPR005542; IPR009057; IPR012287; IPR017970; PTHR11850 (PANTHER), PTHR11850:SF2 (PANTHER)
Caenorhabditis briggsae	hepatocyte growth factor-regulated tyrosine ki-se substrate	4	C:GO:0005829; C:GO:0005769; P:GO:0046426; F:GO:0019904	-		IPR000306; IPR002014; IPR003903; IPR008942; IPR011011; IPR013083; IPR017455; IPR018205; PTHR13856 (PANTHER), PTHR13856:SF9 (PANTHER), PF12210 (PFAM)
Caenorhabditis briggsae	hepatocyte growth factor-regulated tyrosine ki-se substrate	4	C:GO:0005829; C:GO:0005769; P:GO:0046426; F:GO:0019904	-		IPR000306; IPR002014; IPR003903; IPR008942; IPR011011; IPR013083; IPR017455; IPR018205; PTHR13856 (PANTHER), PTHR13856:SF9 (PANTHER), PF12210 (PFAM)
Caenorhabditis briggsae	exocyst complex component 3	0		F:GO:0003674; P:GO:0006887; P:GO:0008150; P:GO:0015031; P:GO:0006810; C:GO:0005575		IPR010326; PTHR21292:SF5 (PANTHER)
Caenorhabditis briggsae	exocyst complex component 3	0		F:GO:0003674; P:GO:0006887; P:GO:0008150; P:GO:0015031; P:GO:0006810; C:GO:0005575		IPR010326; PTHR21292:SF5 (PANTHER)
Caenorhabditis elegans	briggsae cbr-ehbp-1 protein	0		F:GO:0005509		IPR022735
Caenorhabditis briggsae	ys96_caeel ame: full= g-protein coupled receptor-like protein	1	P:GO:0040010	-		IPR000276; IPR017452; G3DSA:1.20.1070.10 (GENE3D), PTHR19264 (PANTHER), SSF81321 (SUPERFAMILY)
Caenorhabditis briggsae	nucleoporin 50kda	1	P:GO:0000003	-		IPR011993; PTHR13118 (PANTHER), SSF50729 (SUPERFAMILY)

Caenorhabditis briggsae	peptidylglycine alpha-hydroxylating monooxyge-se	20	P:GO:0008340; F:GO:0051087; C:GO:0016020; P:GO:0016458; P:GO:0007613; P:GO:0035186; P:GO:0021954; P:GO:0030708; P:GO:0006697; P:GO:0030713; F:GO:0035302; P:GO:0006518; C:GO:0005730; P:GO:0001700; P:GO:0035075; F:GO:0004504; P:GO:0055114; F:GO:0003682; C:GO:0005783; F:GO:0005507	-	EC:1.14.17.3	IPR000323; IPR000720; IPR000945; IPR008977; IPR014784; PTHR10157:SF3 (PANTHER), PF03712 (PFAM), SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG08512 [Caenorhabditis briggsae]	0				IPR007087; IPR015880
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	acetyl- hydrolase transferase family protein	6	F:GO:0008775; F:GO:0019239; C:GO:0005811; P:GO:0009168; P:GO:0006084; F:GO:0016787	-	EC:2.8.3.8	IPR003702; G3DSA:3.40.810.20 (GENE3D), PTHR21432:SF11 (PANTHER), SSF100950 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	prion-like-(q n-rich)-domain-bearing protein family member (pqn-83)	3	P:GO:0002119; P:GO:0000003; P:GO:0040011	-		SignalP (SIGNALP)
Caenorhabditis elegans	prion-like-(q n-rich)-domain-bearing protein family member (pqn-83)	3	P:GO:0002119; P:GO:0000003; P:GO:0040011	-		IPR001464; IPR002619; PTHR10502:SF11 (PANTHER)
Brugia malayi	hypothetical protein [Brugia malayi]	0		F:GO:0003676; F:GO:0046872; F:GO:0008270		IPR000571; G3DSA:4.10.1000.10 (GENE3D), PTHR12547 (PANTHER), PTHR12547:SF17 (PANTHER), SSF90229 (SUPERFAMILY)
Brugia malayi	hypothetical protein [Brugia malayi]	1	F:GO:0046872	-		SignalP (SIGNALP)
Caenorhabditis briggsae	fox-1 homolog c-like	1	F:GO:0003676	-		IPR000504; IPR012677; PTHR15597 (PANTHER), PTHR15597:SF2 (PANTHER), SignalP (SIGNALP), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	hexoki-se family protein	4	P:GO:0060361; F:GO:0005524; P:GO:0006096; F:GO:0004396	-	EC:2.7.1.1	IPR001312; IPR022673; G3DSA:3.40.367.20 (GENE3D), SSF53067 (SUPERFAMILY)
Caenorhabditis elegans	hexoki-se family protein	4	P:GO:0060361; F:GO:0005524; P:GO:0006096; F:GO:0004396	-	EC:2.7.1.1	IPR001312; IPR022673; G3DSA:3.40.367.20 (GENE3D), SSF53067 (SUPERFAMILY)

Caenorhabditis briggsae	dihydrolipoamide dehydroge-se	21	C:GO:0043159; P:GO:0048240; F:GO:0004148; P:GO:0007369; P:GO:0010510; C:GO:0005759; C:GO:0019861; P:GO:0006120; P:GO:0007568; F:GO:0009055; C:GO:0045252; P:GO:0009106; P:GO:0051068; F:GO:0050660; P:GO:0045454; F:GO:0051287; C:GO:0045254; P:GO:0006103; P:GO:0006508; F:GO:0043544; P:GO:0042391	-	EC:1.8.1.4	IPR000815; IPR001327; IPR006258; IPR012999; IPR013027; PR00411 (PRINTS), G3DSA:3.50.50.60 (GENE3D), PTHR22912 (PANTHER), SignalP (SIGNALP), SSF51905 (SUPERFAMILY)
Loa loa	r--binding protein	4	P:GO:0006397; F:GO:0017091; F:GO:0000166; F:GO:0003730	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF55 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Ailuropoda melanoleuca	alpha-actinin-4-like isoform 3	21	P:GO:0001666; F:GO:0047485; C:GO:0030863; C:GO:0043234; F:GO:0005509; P:GO:0051271; C:GO:0005730; P:GO:0042981; P:GO:0051017; F:GO:0051015; F:GO:0001882; P:GO:0051272; C:GO:0001725; P:GO:0048549; C:GO:0031143; F:GO:0005178; C:GO:0048471; C:GO:0030529; F:GO:0042803; P:GO:0015031; P:GO:0032417	-		-
	-	0				-
Steinernema carpocapsae	aspartic protease	5	C:GO:0005623; P:GO:0008219; F:GO:0005515; P:GO:0040011; F:GO:0008233	-		IPR001461; IPR001969; IPR009007; IPR012848; IPR021109; PTHR13683:SF53 (PANTHER), SignalP (SIGNALP)
Steinernema carpocapsae	aspartic protease	5	C:GO:0005623; P:GO:0008219; F:GO:0005515; P:GO:0040011; F:GO:0008233	-		IPR001461; IPR001969; IPR009007; IPR012848; IPR021109; PTHR13683:SF53 (PANTHER), SignalP (SIGNALP)

Steinernema carpocapsae	aspartic protease	5	C:GO:0005623; P:GO:0008219; F:GO:0005515; P:GO:0040011; F:GO:0008233	-		IPR001461; IPR001969; IPR009007; IPR012848; IPR021109; PTHR13683:SF53 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	exocyst complex component 8	6	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040018; P:GO:0000003; P:GO:0040011	-		IPR001849; IPR016159; PTHR21426 (PANTHER), PTHR21426:SF9 (PANTHER), SSF50729 (SUPERFAMILY)
Caenorhabditis elegans	ylb8_caeel ame: full=uncharacterized protein	0				IPR017871
Caenorhabditis elegans	ylb8_caeel ame: full=uncharacterized protein	0				IPR017871
Caenorhabditis elegans	ylb8_caeel ame: full=uncharacterized protein	0				IPR017871
Caenorhabditis briggsae	neuroendocrine convertase	5	F:GO:0004252; P:GO:0002165; C:GO:0005576; P:GO:0006508; P:GO:0035187	-	EC:3.4.21.0	IPR002884; IPR008979; IPR015500; G3DSA:2.60.120.260 (GENE3D), PTHR10795:SF11 (PANTHER)
Caenorhabditis elegans	briggsae cbr-cpg-3 protein	0				-
Caenorhabditis elegans	briggsae cbr-cpg-3 protein	0				-
Brugia malayi	o-linked n-acetylglucosamine transferase (udp-n-acetylglucosamine:polypeptide-n-acetylglucosaminyl transferase)	10	C:GO:0005829; F:GO:0042277; P:GO:0070207; P:GO:0006493; F:GO:0048029; P:GO:0007584; F:GO:0016262; F:GO:0005515; P:GO:0007165; C:GO:0070688	-	EC:2.4.1.94	IPR001440; IPR011717; IPR011990; IPR013026; IPR019734; PTHR23083 (PANTHER), PTHR23083:SF21 (PANTHER), SSF48452 (SUPERFAMILY)
Loa loa	pellino family protein	2	F:GO:0005515; P:GO:0048522	-		-
Caenorhabditis briggsae	briggsae cbr-tag-53 protein	5	F:GO:0005488; P:GO:0018991; P:GO:0040010; P:GO:0040011; C:GO:0016020	-		IPR000742; IPR000859; IPR002165; IPR003659; IPR006210; IPR006652; IPR013032; IPR015915; IPR016201; IPR017937; G3DSA:2.10.25.10 (GENE3D), PTHR10574 (PANTHER), PTHR10574:SF3 (PANTHER), SSF117281 (SUPERFAMILY), SSF57196 (SUPERFAMILY)
Caenorhabditis briggsae	39s ribosomal protein mitochondrial	4	P:GO:0009792; C:GO:0005840; F:GO:0003735; P:GO:0006412	-	EC:3.6.5.3	SignalP (SIGNALP)
Brugia malayi	innexin family protein	4	P:GO:0040035; P:GO:0040010; P:GO:0040011; P:GO:0002009	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0000003		SignalP (SIGNALP)
Angiostrongylus cantonensis	galactoside- 12-like	3	P:GO:0009792; F:GO:0005529; F:GO:0005515	-		-

Angiostrongylus cantonensis	galactoside- 12-like	3	P:GO:0009792; F:GO:0005529; F:GO:0005515	-		IPR001079; IPR008985; IPR013320; PTHR11346:SF4 (PANTHER)
Caenorhabditis briggsae	ctp synthase ii	6	F:GO:0016874; C:GO:0016323; C:GO:0016324; P:GO:0006220; F:GO:0005488; C:GO:0005739	-		IPR000630; IPR000991; IPR004468; IPR017456; IPR017926; G3DSA:3.40.50.300 (GENE3D), G3DSA:3.40.50.880 (GENE3D), PTHR11550 (PANTHER), SSF52317 (SUPERFAMILY), SSF52540 (SUPERFAMILY)
Loa loa	spectrin beta	12	P:GO:0007184; F:GO:0005516; C:GO:0043234; F:GO:0032403; C:GO:0008091; F:GO:0004725; F:GO:0003779; P:GO:0007182; C:GO:0032437; F:GO:0005200; C:GO:0005634; C:GO:0005886	-	EC:3.1.3.48	IPR001715; G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF48 (PANTHER), SSF46966 (SUPERFAMILY)
Loa loa	mh2 domain containing protein	15	P:GO:0009653; P:GO:0006915; P:GO:0048522; P:GO:0048513; P:GO:0031324; P:GO:0050896; C:GO:0044424; P:GO:0009888; P:GO:0006355; P:GO:0051239; P:GO:0016043; P:GO:0010629; P:GO:0030154; P:GO:0009790; F:GO:0005515	-		IPR001132; IPR008984; IPR013790; IPR017855
Loa loa	mothers against dpp protein	15	P:GO:0009653; P:GO:0010605; P:GO:0006915; P:GO:0048522; P:GO:0048513; P:GO:0050896; C:GO:0044424; P:GO:0048523; P:GO:0009888; P:GO:0006355; P:GO:0051239; P:GO:0016043; P:GO:0030154; P:GO:0009790; F:GO:0005515	-		IPR001132; IPR008984; IPR013790; IPR017855
	-	0				-

Caenorhabditis elegans	ubx domain containing 2	0		C:GO:0016020; C:GO:0005635; C:GO:0005634; F:GO:0003674; C:GO:0005789; C:GO:0005575; F:GO:0005515; C:GO:0005783; P:GO:0006986; P:GO:0008150		IPR001012; G3DSA:3.10.20.90 (GENE3D), PTHR13020 (PANTHER), PTHR13020:SF5 (PANTHER), SSF54236 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein C34D10.1 [Caenorhabditis elegans]	0		F:GO:0005198; C:GO:0016021; F:GO:0005515		-
	-	0				IPR000477
Podospora anserina S mat+	plasma membrane proteolipid 3	3	C:GO:0016020; P:GO:0043581; P:GO:0006810	-		-
	-	0				-
	-	0				-
Loa loa	lactoylglutathione lyase	2	F:GO:0046872; F:GO:0004462	-	EC:4.4.1.5	IPR004360; IPR004361; IPR018146; G3DSA:3.10.180.10 (GENE3D), PTHR10374 (PANTHER), SSF54593 (SUPERFAMILY)
Caenorhabditis elegans	integrin alpha-ps2	11	P:GO:0009792; F:GO:0004872; P:GO:0002119; P:GO:0007229; P:GO:0018991; P:GO:0032940; P:GO:0007155; P:GO:0040007; P:GO:0006898; P:GO:0040039; C:GO:0008305	-		IPR013649; G3DSA:2.60.40.1510 (GENE3D), G3DSA:2.60.40.1530 (GENE3D), PTHR23220 (PANTHER), PTHR23220:SF11 (PANTHER), SSF69179 (SUPERFAMILY)
Caenorhabditis elegans	tlc domain containing 1	1	C:GO:0016021	-		IPR006634; SignalP (SIGNALP)
Caenorhabditis elegans	tlc domain containing 1	1	C:GO:0016021	-		IPR006634; SignalP (SIGNALP)
Caenorhabditis elegans	ribosomal protein s8	12	P:GO:0008340; P:GO:0051726; P:GO:0040007; F:GO:0003735; P:GO:0000003; P:GO:0006414; C:GO:0022627; P:GO:0019915; P:GO:0002119; F:GO:0005515; P:GO:0006898; P:GO:0009790	-		IPR001047; IPR018283; IPR022309; PTHR10394 (PANTHER), PTHR10394:SF1 (PANTHER)

Brugia malayi	aurin family member (cnt-2)	9	P:GO:0006810; F:GO:0008060; P:GO:0032312; F:GO:0008270; P:GO:0000003; F:GO:0005515; F:GO:0000166; P:GO:0009792; C:GO:0044424	-		IPR001164; IPR011993; PTHR23180 (PANTHER), PTHR23180:SF21 (PANTHER)
Caenorhabditis elegans	atp-dependent helicase brm	8	P:GO:0040010; P:GO:0045449; P:GO:0040035; F:GO:0003677; F:GO:0005524; F:GO:0004386; P:GO:0009792; C:GO:0005634	-		SignalP (SIGNALP)
	-	0				-
						IPR001442; IPR008160; IPR016187; PTHR10499 (PANTHER), PTHR10499:SF78 (PANTHER)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	6	F:GO:0043492; F:GO:0022892; F:GO:0016820; F:GO:0000166; P:GO:0008152; C:GO:0016020	-	EC:3.6.3.0	SignalP (SIGNALP), SSF81665 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	6	F:GO:0042625; F:GO:0005548; P:GO:0006869; F:GO:0000166; P:GO:0008152; C:GO:0016020	-		SignalP (SIGNALP), SSF81665 (SUPERFAMILY)
Polysphondylium pallidum PN500	epithelial cell transforming sequence 2 oncogene protein	2	P:GO:0023034; P:GO:0050794	-		IPR000219; PTHR12673 (PANTHER), PTHR12673:SF6 (PANTHER)
Caenorhabditis briggsae	ynv9_caeel ame: full=uncharacterized protein flags: precursor	1	F:GO:0005488	-		SSF57501 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis briggsae	aconitase mitochondrial	18	P:GO:0008340; F:GO:0016747; C:GO:0005739; P:GO:0040007; P:GO:0040035; P:GO:0006099; F:GO:0051539; F:GO:0051538; P:GO:0002119; F:GO:0005515; F:GO:0003994; P:GO:0040011; P:GO:0006102; P:GO:0009792; F:GO:0005506; P:GO:0006101; C:GO:0005634; P:GO:0016246	-	EC:2.3.1.0; EC:4.2.1.3	IPR000573; IPR001030; IPR006248; IPR015928; IPR015931; IPR015932; IPR015937; IPR018136; IPR020610; SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG18891 [Caenorhabditis briggsae]	0				-

	-	0				-
Loa loa	cullin 4b	0		F:GO:0003674; C:GO:0031461; F:GO:0031625; C:GO:0005575; P:GO:0006511		IPR001373; IPR011991; IPR016158; IPR019559; G3DSA:4.10.1030.10 (GENE3D), PTHR11932 (PANTHER), PTHR11932:SF22 (PANTHER), SSF46785 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	serine threonine-protein phosphatase 4 catalytic subunit	16	P:GO:0001525; P:GO:0007126; P:GO:0018991; C:GO:0030289; F:GO:0004704; P:GO:0016311; F:GO:0046872; P:GO:0040007; P:GO:0007052; C:GO:0005813; F:GO:0004722; P:GO:0002119; F:GO:0005515; P:GO:0009792; C:GO:0005634; P:GO:0006468	-		IPR004843; IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF22 (PANTHER), SignalP (SIGNALP), SSF56300 (SUPERFAMILY)
Caenorhabditis elegans	inositol-requiring 1 alpha-like	14	P:GO:0000003; F:GO:0005515; C:GO:0030176; P:GO:0010467; P:GO:0046777; P:GO:0090304; F:GO:0004521; P:GO:0040017; P:GO:0007050; F:GO:0004674; P:GO:0006987; P:GO:0006917; F:GO:0000287; F:GO:0005524	-	EC:2.7.11.0	SignalP (SIGNALP)
Caenorhabditis elegans	wapl (drosophila wings apart-like cohesin interactor) family member (wapl-1)	3	P:GO:0018991; P:GO:0040010; P:GO:0040011	-		IPR012502; IPR022771; PTHR22100 (PANTHER), PTHR22100:SF7 (PANTHER)
Caenorhabditis elegans	diacylglycerol ki-se eta2	1	F:GO:0005515	-		-
Caenorhabditis elegans	phosphatidylcholine:ceramide cholinephosphotransferase	3	F:GO:0047493; C:GO:0016021; P:GO:0006686	-	EC:2.7.8.3	PTHR21290 (PANTHER), PTHR21290:SF3 (PANTHER)
Brugia malayi	stip1-like proteiny and u box-containing protein 1	11	P:GO:0007411; P:GO:0045941; P:GO:0070983; P:GO:0008407; P:GO:0006911; F:GO:0004842; P:GO:0007350; C:GO:0030018; F:GO:0005488; C:GO:0005634; P:GO:0007476	-	EC:6.3.2.19	SignalP (SIGNALP)

Caenorhabditis elegans	briggsae cbr-ubh-1 protein	1	P:GO:0040010	-		IPR001965; IPR011011; IPR013083; IPR019786; IPR019787; PTHR10615 (PANTHER), PTHR10615:SF11 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	chitin synthase	5	P:GO:0009792; P:GO:0000003; C:GO:0005887; F:GO:0016758; P:GO:0040010	-	EC:2.4.1.0	IPR004835; G3DSA:3.90.550.10 (GENE3D), PTHR22914 (PANTHER), SignalP (SIGNALP), SSF53448 (SUPERFAMILY)
Caenorhabditis briggsae	protein ki-se c substrate 80k-h	2	F:GO:0005515; C:GO:0005783	-		SignalP (SIGNALP)
Caenorhabditis briggsae	protein ki-se c substrate 80k-h	2	F:GO:0005515; C:GO:0005783	-		IPR009011; IPR011992; IPR012913; IPR018247; IPR018249; G3DSA:2.70.130.10 (GENE3D), PTHR12630 (PANTHER), PTHR12630:SF1 (PANTHER), SSF47473 (SUPERFAMILY)
Caenorhabditis elegans	proline synthetase co-transcribed protein	0		P:GO:0008150; C:GO:0005575		IPR001608; IPR011078; G3DSA:3.20.20.10 (GENE3D), SignalP (SIGNALP), SSF51419 (SUPERFAMILY)
Loa loa	homeobox protein pknox1	0		C:GO:0005667; F:GO:0003677; C:GO:0005634; F:GO:0046982; P:GO:0010551; P:GO:0006357; F:GO:0030528; P:GO:0030218; P:GO:0006355; P:GO:0030217; F:GO:0003705; F:GO:0016563; P:GO:0043010; F:GO:0003700; P:GO:0045944; P:GO:0001525; C:GO:0005737; P:GO:0045449; F:GO:0043565; F:GO:0005515; P:GO:0030097		IPR001356; IPR009057; IPR012287; PTHR11211 (PANTHER), PTHR11211:SF3 (PANTHER)
Caenorhabditis elegans	cytidine deami-se	9	P:GO:0009790; F:GO:0046872; C:GO:0005622; F:GO:0047844; F:GO:0003723; F:GO:0005515; P:GO:0006217; F:GO:0004126; P:GO:0009451	-	EC:3.5.4.14; EC:3.5.4.5	-
Caenorhabditis elegans	ubiquitin carboxyl-termi-l hydrolase family protein	0		F:GO:0016787; F:GO:0004221; P:GO:0006511		-
Caenorhabditis elegans	ubiquitin carboxyl-termi-l hydrolase family protein	0		F:GO:0016787; F:GO:0004221; P:GO:0006511		-

Caenorhabditis elegans	type alpha isoform cra_b	8	P:GO:0018996; P:GO:0009792; P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		IPR003961; IPR008957; IPR013783; PTHR19143 (PANTHER), PTHR19143:SF3 (PANTHER)
	-	0				-
Caenorhabditis elegans	ymq4_caeel ame: full=uncharacterized protein	0				-
Caenorhabditis briggsae	cysteine protease atg4d	1	F:GO:0016787	-		-
Caenorhabditis briggsae	ophagy (yeast atg homolog) family member (atg-)	0		P:GO:0006914; C:GO:0005737; F:GO:0016787; F:GO:0008234; F:GO:0008233; P:GO:0006810; P:GO:0015031		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	C:GO:0016020; P:GO:0006821	-		IPR000615; IPR021134
Haemochus contortus	isoform a	9	C:GO:0005945; F:GO:0003872; F:GO:0003677; F:GO:0005524; C:GO:0005700; F:GO:0005515; P:GO:0006096; P:GO:0006338; C:GO:0005634	-	EC:2.7.1.11	IPR000023; IPR009161; IPR015912; IPR022953; G3DSA:3.40.50.450 (GENE3D), PTHR13697 (PANTHER)
Harpegnathos saltator	serine peptidase kunitz 2	2	F:GO:0008233; C:GO:0005576	-		IPR002223; IPR020901; PTHR10083 (PANTHER), PTHR10083:SF39 (PANTHER)
Harpegnathos saltator	serine protei-se	2	F:GO:0008233; C:GO:0005576	-		IPR002223; IPR020901; PTHR10083 (PANTHER), PTHR10083:SF39 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0008104		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0008104		PTHR16166 (PANTHER), PTHR16166:SF25 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0008104		PTHR16166 (PANTHER), PTHR16166:SF25 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0008104		PTHR16166 (PANTHER), PTHR16166:SF25 (PANTHER)
Caenorhabditis briggsae	atp-binding sub-family a member 1	5	P:GO:0033036; P:GO:0006810; C:GO:0044464; P:GO:0009987; F:GO:0005488	-		IPR006162; PTHR19229 (PANTHER), PTHR19229:SF25 (PANTHER)
Caenorhabditis briggsae	atp-binding sub-family a member 1	5	P:GO:0033036; P:GO:0006810; C:GO:0044464; P:GO:0009987; F:GO:0005488	-		IPR006162; PTHR19229 (PANTHER), PTHR19229:SF25 (PANTHER)

Caenorhabditis briggsae	serine threonine-protein ki-se vrk	6	P:GO:0016572; P:GO:0018107; P:GO:0030717; P:GO:0007143; F:GO:0035184; F:GO:0000166	-		IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF17 (PANTHER)
Caenorhabditis elegans	serine threonine-protein ki-se vrk	2	F:GO:0004672; F:GO:0000166	-		IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF17 (PANTHER)
Caenorhabditis elegans	subfamily member 1	3	F:GO:0003676; F:GO:0005515; P:GO:0044267	-		IPR001623; IPR003095; IPR015609; PTHR11821:SF30 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	-like protein subfamily c member 1	1	F:GO:0005488	-		IPR001005; IPR001623; IPR003095; IPR009057; IPR012287; IPR014778; IPR015609; IPR017877; IPR017884; PTHR11821:SF30 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG22485 [Caenorhabditis briggsae]	0		F:GO:0003676		-
Caenorhabditis elegans	integral membrane	1	F:GO:0005515	-		IPR008547; G3DSA:3.40.50.1820 (GENE3D), SSF53474 (SUPERFAMILY)
Camponotus floridanus	poly(adp-ribose) polymerase	5	F:GO:0003676; F:GO:0003950; P:GO:0006471; C:GO:0005634; C:GO:0005739	-	EC:2.4.2.30	IPR006061; IPR008893; IPR012317; G3DSA:3.90.228.10 (GENE3D), PTHR15447 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	ras suppressor protein 1	3	C:GO:0005829; F:GO:0005515; P:GO:0007265	-		IPR001611; IPR003591; PR00019 (PRINTS), G3DSA:3.80.10.10 (GENE3D), PTHR23155 (PANTHER), PTHR23155:SF21 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)
Brugia malayi	transmembrane protein 38a	3	C:GO:0016020; F:GO:0005261; P:GO:0015672	-		IPR007866; PTHR12454:SF2 (PANTHER)
Caenorhabditis briggsae	trimeric intracellular cation channel type b	3	C:GO:0016021; F:GO:0005261; P:GO:0015672	-		IPR007866; PTHR12454:SF2 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-sel-2 protein	6	C:GO:0005737; P:GO:0008104; F:GO:0051018; P:GO:0042675; C:GO:0016020; C:GO:0005634	-		-
Plasmodium chabaudi chabaudi	hypothetical protein PC101070.00.0 [Plasmodium chabaudi chabaudi]	0				-
Caenorhabditis briggsae	briggsae cbr-mel-28 protein	0		P:GO:0006355; F:GO:0003677		-
Caenorhabditis elegans	deoxyhypusine synthase	3	P:GO:0009792; F:GO:0005515; P:GO:0008612	-		IPR002773; SSF52467 (SUPERFAMILY)
	-	0				IPR007527; IPR013032

Caenorhabditis briggsae	glycine cleavage system h protein	4	P:GO:0009792; C:GO:0005960; C:GO:0005739; P:GO:0019464	-		-
	-	0				-
Loa loa	gpi transamidase component pig-t	0		C:GO:0042765; P:GO:0051402; F:GO:0003923; C:GO:0005737; C:GO:0016023; C:GO:0016021; F:GO:0005515; P:GO:0030182		-
	-	0				-
	-	0				-
Ostertagia ostertagi	sxc2 protein	0				IPR003582
Loa loa	timeless protein	0		P:GO:0042127; P:GO:0051301; C:GO:0000790; P:GO:0007067; P:GO:0007623; P:GO:0001658; C:GO:0005634; F:GO:0003677; F:GO:0046982; P:GO:0010553; P:GO:0002009; P:GO:0030324; F:GO:0042803; P:GO:0048754; P:GO:0006974; P:GO:0007049; P:GO:0001822; P:GO:0006350; P:GO:0042753; P:GO:0009790; P:GO:0007275; P:GO:0033261; P:GO:0016481; P:GO:0045449; P:GO:0048511; F:GO:0005515		IPR006906
	-	0				-
Caenorhabditis elegans	transmembrane protein 185b	0		C:GO:0016021; C:GO:0016020		IPR019396; PTHR13568 (PANTHER), SignalP (SIGNALP)

Caenorhabditis briggsae	pabpn1 protein	17	P:GO:0040010; C:GO:0005730; P:GO:0006378; P:GO:0000003; P:GO:0008380; F:GO:0008143; P:GO:0002119; F:GO:0005515; F:GO:0000166; P:GO:0040011; C:GO:0030529; P:GO:0006898; C:GO:0005654; P:GO:0009792; C:GO:0005737; P:GO:0016973; P:GO:0040019	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF61 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	pabpn1 protein	17	P:GO:0040010; C:GO:0005730; P:GO:0006378; P:GO:0000003; P:GO:0008380; F:GO:0008143; P:GO:0002119; F:GO:0005515; F:GO:0000166; P:GO:0040011; C:GO:0030529; P:GO:0006898; C:GO:0005654; P:GO:0009792; C:GO:0005737; P:GO:0016973; P:GO:0040019	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF61 (PANTHER), SSF54928 (SUPERFAMILY)
Leishmania major strain Friedlin	chromosome segregation protein smc	0		C:GO:0005694; C:GO:0005737; P:GO:0051301; F:GO:0005524; P:GO:0051276; C:GO:0005575; F:GO:0005515; P:GO:0000917; P:GO:0008150; P:GO:0007049		-

Brugia malayi	paired amphipathic helix protein sin3a isoform 1	17	C:GO:0000785; P:GO:0000122; F:GO:0003714; P:GO:0034613; P:GO:0010243; P:GO:0051329; P:GO:0007568; P:GO:0043619; C:GO:0000776; F:GO:0003677; F:GO:0003700; F:GO:0032403; F:GO:0003682; C:GO:0005634; P:GO:0043066; P:GO:0001701; P:GO:0006260	-		PTHR12346 (PANTHER)
Brugia malayi	paired amphipathic helix repeat family protein	4	F:GO:0030528; P:GO:0045449; P:GO:0007399; C:GO:0000785	-		PTHR12346 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG13624 [Caenorhabditis briggsae]	0		F:GO:0046872; F:GO:0008270; F:GO:0005515		-
Caenorhabditis elegans	lipid phosphate phosphohydrolase 1	6	P:GO:0009987; P:GO:0006629; P:GO:0040010; P:GO:0023033; F:GO:0016791; C:GO:0005886	-	EC:3.1.3.0	IPR000326; IPR016118; PTHR10165 (PANTHER), PTHR10165:SF22 (PANTHER), SignalP (SIGNALP)
Loa loa	s1 r--binding domain-containing protein 1	1	P:GO:0006139	-		IPR005227; IPR006641; IPR023097; G3DSA:1.10.3500.10 (GENE3D), PTHR10724 (PANTHER)
Homo sapiens	alpha (gene sequence 28)	0		P:GO:0043154		IPR004931
Caenorhabditis briggsae	deah (asp-glu-ala-his) box polypeptide 15	18	P:GO:0016246; C:GO:0005689; P:GO:0040010; P:GO:0006898; P:GO:0006397; P:GO:0040011; F:GO:0003676; P:GO:0009792; P:GO:0002009; P:GO:0008380; P:GO:0002119; C:GO:0030686; P:GO:0006200; F:GO:0004004; F:GO:0005524; P:GO:0006364; P:GO:0040035; C:GO:0005739	-		IPR001650; IPR002464; IPR007502; IPR011545; IPR011709; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR18934 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	5 -3 exoribonuclease 2	6	P:GO:0044260; C:GO:0005622; P:GO:0090304; F:GO:0005515; F:GO:0004527; P:GO:0010467	-		-

Caenorhabditis briggsae	camp-dependent protein ki-se catalytic	6	P:GO:0009792; P:GO:0002119; P:GO:0000003; P:GO:0040007; F:GO:0004674; F:GO:0000166	-	EC:2.7.11.0	IPR000719; IPR011009; IPR015746; IPR017441; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR22985 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR022559; PD030565 (PRODOM), SignalP (SIGNALP)
Caenorhabditis elegans	isoform b	4	P:GO:0008340; P:GO:0040035; P:GO:0040039; P:GO:0002119	-		IPR018619
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR020376; SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	2	F:GO:0050662; F:GO:0000166	-		G3DSA:2.10.60.10 (GENE3D), SignalP (SIGNALP), SSF57302 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	cgmp-dependent protein ki-se egl-4	6	P:GO:0006468; F:GO:0046872; F:GO:0030553; P:GO:0007275; F:GO:0005524; F:GO:0004692	-	EC:2.7.11.12	IPR000595; IPR000719; IPR002374; IPR008271; IPR011009; IPR014710; IPR017441; IPR017442; IPR018488; IPR018490; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22985 (PANTHER), PTHR22985:SF90 (PANTHER)
Caenorhabditis elegans	p21 -activated ki-se 7	5	P:GO:0006468; F:GO:0005524; P:GO:0006916; F:GO:0004674; C:GO:0005739	-	EC:2.7.11.0	IPR000095; G3DSA:3.90.810.10 (GENE3D), PTHR12779 (PANTHER)
Brugia malayi	protein ki-se domain containing protein	39	P:GO:0010907; C:GO:0043005; C:GO:0005901; P:GO:0010557; P:GO:0030010; P:GO:0051054; P:GO:0007420; F:GO:0005102; P:GO:0009790; P:GO:0043467; N:GO:2000112; P:GO:0043409; F:GO:0005010; P:GO:0031328; P:GO:0050793; P:GO:0007409; P:GO:0051262; F:GO:0043560; C:GO:0016021; F:GO:0019904; P:GO:0006468; F:GO:0005524; P:GO:0048009; P:GO:0045768; F:GO:0005520; P:GO:0030238; P:GO:0065008;	-		IPR000719; IPR001245; IPR008266; IPR011009; IPR020635; IPR020685; IPR020772; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
Caenorhabditis elegans	aspergillus nuclear division related family member (nud-2)	0				-

Caenorhabditis briggsae	polymerase (d--directed) delta interacting protein 2	1	C:GO:0005739	-		-
	-	0				-
Caenorhabditis briggsae	vacuolar protein sorting-associated protein 33a	7	P:GO:0016192; P:GO:0043473; C:GO:0005768; C:GO:0044446; F:GO:0005515; C:GO:0031090; P:GO:0051641	-		IPR001619; G3DSA:3.40.50.1910 (GENE3D), PTHR11679:SF1 (PANTHER)
Loa loa	hypothetical protein LOAG_11160 [Loa loa]	0				IPR011990; SSF48452 (SUPERFAMILY)
Loa loa	proteasome (macropain) 26s non- 2	4	P:GO:0042176; C:GO:0000502; F:GO:0030234; F:GO:0005515	-		-
Loa loa	proteasome (macropain) 26s non- 2	4	P:GO:0042176; C:GO:0000502; F:GO:0030234; F:GO:0005515	-		-
Loa loa	proteasome (macropain) 26s non- 2	4	P:GO:0042176; C:GO:0000502; F:GO:0030234; F:GO:0005515	-		-
Loa loa	proteasome (macropain) 26s non- 2	4	P:GO:0042176; C:GO:0000502; F:GO:0030234; F:GO:0005515	-		-
Loa loa	proteasome (macropain) 26s non- 2	4	P:GO:0042176; C:GO:0000502; F:GO:0030234; F:GO:0005515	-		-
Loa loa	member ras oncogene family	19	P:GO:0000910; C:GO:0045171; C:GO:0005739; P:GO:0007264; P:GO:0006355; P:GO:0006913; F:GO:0004767; C:GO:0005905; F:GO:0005546; C:GO:0042470; F:GO:0005524; C:GO:0031253; F:GO:0003924; F:GO:0008134; P:GO:0006886; P:GO:0016197; C:GO:0045334; C:GO:0005634; F:GO:0005525	-	EC:3.1.4.12; EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001806; IPR002078; IPR003579; IPR005225; IPR013753; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF228 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein H20J04.3 [Caenorhabditis elegans]	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein H20J04.3 [Caenorhabditis elegans]	0				-
Ostertagia ostertagi	depsiphilin	6	P:GO:0007218; C:GO:0016021; P:GO:0007165; C:GO:0005886; F:GO:0005529; F:GO:0004930	-		-

	-	0				SignalP (SIGNALP)
	-	0				-
Loa loa	tetratricopeptide repeat domain 7b	0		F:GO:0005488		IPR011990; PTHR23083 (PANTHER), PTHR23083:SF7 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	mitochondrial ribosomal protein l21	3	P:GO:0040010; C:GO:0044444; C:GO:0043229	-		IPR001787; SSF141091 (SUPERFAMILY)
Caenorhabditis elegans	methyltransferase type 11	2	P:GO:0008152; F:GO:0008168	-	EC:2.1.1.0	IPR013216; G3DSA:3.40.50.150 (GENE3D), PTHR10108 (PANTHER), PTHR10108:SF17 (PANTHER), SSF53335 (SUPERFAMILY)
Caenorhabditis briggsae	protein cwc15 homolog	6	P:GO:0009792; C:GO:0005681; F:GO:0003723; F:GO:0005515; P:GO:0006898; P:GO:0000398	-		IPR006973
Caenorhabditis elegans	hypothetical protein ZK418.2 [Caenorhabditis elegans]	0				-
Pongo abelii	myeloid leukemia factor 2	5	P:GO:0006952; C:GO:0005737; C:GO:0005634; F:GO:0005515; C:GO:0005925	-		IPR019376; PTHR13105 (PANTHER), PTHR13105:SF4 (PANTHER)
Caenorhabditis briggsae	general transcription factor polypeptide alpha 56kda	11	P:GO:0040010; P:GO:0006367; F:GO:0046872; P:GO:0010171; F:GO:0005515; P:GO:0006368; P:GO:0040011; P:GO:0006898; C:GO:0005654; P:GO:0002009; P:GO:0009792	-		IPR013083; PTHR13097 (PANTHER), SSF57783 (SUPERFAMILY)
Caenorhabditis elegans	ester hydrolase c11orf54 homolog	3	F:GO:0016788; C:GO:0005634; F:GO:0008270	-		IPR015021; SSF117856 (SUPERFAMILY)
Caenorhabditis elegans	ester hydrolase c11orf54 homolog	4	F:GO:0016788; C:GO:0005634; F:GO:0008270; F:GO:0005515	-		-
Caenorhabditis briggsae	Hypothetical protein CBG18736 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	activator 1 36	2	F:GO:0005515; F:GO:0016787	-		IPR008921; IPR013748; G3DSA:1.20.272.10 (GENE3D)
	-	0				-
Caenorhabditis brenneri	protein fam32a	2	P:GO:0040010; P:GO:0009792	-		-
Caenorhabditis brenneri	protein fam32a	2	P:GO:0040010; P:GO:0009792	-		-
Caenorhabditis briggsae	methyltransferase like 2 isoform 1	2	P:GO:0008152; F:GO:0008168	-	EC:2.1.1.0	IPR013217; G3DSA:3.40.50.150 (GENE3D), PTHR22809 (PANTHER), SSF53335 (SUPERFAMILY)

Pan troglodytes	ribosomal protein s27a	9	F:GO:0030528; F:GO:0046872; F:GO:0003735; P:GO:0006414; C:GO:0022627; P:GO:0016567; F:GO:0005515; C:GO:0005634; P:GO:0045941	-		IPR000626; IPR002906; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), PTHR10666:SF2 (PANTHER), SSF54236 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	i lweq domain containing protein	4	C:GO:0005856; F:GO:0005515; P:GO:0009987; F:GO:0005198	-		IPR006077; IPR015009; IPR015710; IPR015711; G3DSA:1.20.1410.10 (GENE3D)
Harpegnathos saltator	histone-lysine n-methyltransferase setmar	0		F:GO:0016740; F:GO:0004803; P:GO:0006313; F:GO:0008168; C:GO:0005634; F:GO:0003677; F:GO:0016787; F:GO:0008270; F:GO:0018024; P:GO:0016568; P:GO:0015074; P:GO:0006281; C:GO:0005575; F:GO:0046872; F:GO:0004519		-
Caenorhabditis elegans	hypothetical protein Y55F3BL.1 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	hypothetical protein Y55F3BL.1 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0051028; F:GO:0000166; C:GO:0005634		G3DSA:3.10.450.50 (GENE3D), PTHR10662 (PANTHER), PTHR10662:SF21 (PANTHER), SSF54427 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	F:GO:0005488	-		IPR001304; IPR002035; IPR013032; IPR016186; IPR016187; G3DSA:3.40.50.410 (GENE3D), PTHR22802 (PANTHER), PTHR22802:SF6 (PANTHER), SSF53300 (SUPERFAMILY), SSF57196 (SUPERFAMILY)
Caenorhabditis elegans	cell death abnormality family member (ced-4)	13	C:GO:0005829; P:GO:0043281; P:GO:0043065; C:GO:0005625; C:GO:0005739; F:GO:0051434; C:GO:0005624; P:GO:0008361; F:GO:0005524; F:GO:0051432; C:GO:0048471; P:GO:0043066; C:GO:0005634	-		IPR002182
	-	0				-

Bombyx mori	isoform b	0		F:GO:0003842; P:GO:0055114; C:GO:0005759; P:GO:0006562		-
	-	0				-
Caenorhabditis briggsae	ubiquitin carboxyl-termi-l hydrolase 5	1	F:GO:0016787	-		IPR001394; IPR009060; IPR018200; G3DSA:1.10.8.10 (GENE3D), SSF54001 (SUPERFAMILY)
Caenorhabditis briggsae	ubiquitin carboxyl-termi-l hydrolase 5	1	F:GO:0016787	-		IPR001394; IPR009060; IPR018200; G3DSA:1.10.8.10 (GENE3D), SSF54001 (SUPERFAMILY)
Caenorhabditis briggsae	ubiquitin carboxyl-termi-l hydrolase 5	1	F:GO:0016787	-		IPR001394; IPR009060; IPR018200; G3DSA:1.10.8.10 (GENE3D), SSF54001 (SUPERFAMILY)
	-	0				IPR003677; PTHR21593 (PANTHER)
Caenorhabditis briggsae	udp-n-acetyl-alpha-d-galactosamine:polypeptide n-acetylgalactosaminyltransferase 11 (c-t11)	2	C:GO:0016020; F:GO:0016757	-		IPR001173; G3DSA:3.90.550.10 (GENE3D), PTHR11675 (PANTHER), SSF53448 (SUPERFAMILY)
Caenorhabditis elegans	isoform a	0		F:GO:0046872; F:GO:0008270		IPR000260; IPR001452; PTHR22883 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	cytochrome c oxidase subunit vib isoform 1	7	P:GO:0009792; P:GO:0002119; P:GO:0040010; P:GO:0000003; P:GO:0008340; C:GO:0005739; F:GO:0004129	-	EC:1.9.3.1	IPR003213; PD015172 (PRODOM), PTHR11387 (PANTHER)
Caenorhabditis elegans	briggsae cbr-hum-5 protein	4	F:GO:0003779; C:GO:0016459; F:GO:0005524; F:GO:0003774	-		IPR001609; PTHR13140 (PANTHER), PTHR13140:SF31 (PANTHER), SSF52540 (SUPERFAMILY)
Loa loa	transcription initiation factor tfiid subunit 6	2	P:GO:0006350; C:GO:0005634	-		PTHR10221 (PANTHER), PTHR10221:SF7 (PANTHER)
Caenorhabditis briggsae	atp-dependent r- helicase dhx8	4	F:GO:0003723; F:GO:0005524; F:GO:0005515; F:GO:0008026	-		IPR007502; PTHR18934 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	glucosyl glucuronosyl transferases	2	P:GO:0044238; F:GO:0016757	-		IPR002213; G3DSA:3.40.50.2000 (GENE3D), PTHR11926:SF3 (PANTHER), SSF53756 (SUPERFAMILY)
Caenorhabditis elegans	loss of estine family member (lit-1)	10	F:GO:0004707; F:GO:0047485; P:GO:0008586; P:GO:0030178; P:GO:0007492; F:GO:0005524; P:GO:0016318; P:GO:0007474; P:GO:0042332; P:GO:0006468	-	EC:2.7.11.24	IPR000719; IPR002290; IPR003527; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF65 (PANTHER)

Caenorhabditis elegans	loss of estine family member (lit-1)	10	F:GO:0004707; F:GO:0047485; P:GO:0008586; P:GO:0030178; P:GO:0007492; F:GO:0005524; P:GO:0016318; P:GO:0007474; P:GO:0042332; P:GO:0006468	-	EC:2.7.11.24	IPR000719; IPR002290; IPR003527; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF65 (PANTHER)
	-	0				-
Loa loa	hypothetical protein LOAG_07027 [Loa loa]	0				-
Caenorhabditis elegans	ctcl tumor antigen l14-2	1	F:GO:0005515	-		PD936484 (PRODOM), PTHR18911 (PANTHER)
Brugia malayi	cell cycle regulator mat89bb homolog	0		P:GO:0007049; P:GO:0007346; P:GO:0051301; P:GO:0007067; F:GO:0005515		IPR019355; PTHR12955 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR001534
Caenorhabditis elegans	let-23 fertility effector regulator family member (lfe-2)	0		F:GO:0008440		-
Caenorhabditis elegans	cation transporting atpase protein isoform partially confirmed by transcript evidence	5	F:GO:0016820; F:GO:0016887; F:GO:0000166; P:GO:0008152; C:GO:0016020	-	EC:3.6.3.0	IPR000150; IPR001757; IPR004014; IPR005834; IPR006544; IPR008250; IPR018303; G3DSA:2.70.150.10 (GENE3D), G3DSA:3.40.1110.10 (GENE3D), G3DSA:3.40.50.1000 (GENE3D), PTHR11939:SF54 (PANTHER), PF12409 (PFAM), SSF56784 (SUPERFAMILY), SSF81653 (SUPERFAMILY), SSF81660 (SUPERFAMILY), SSF81665 (SUPERFAMILY)
Caenorhabditis briggsae	cation transporting atpase protein isoform partially confirmed by transcript evidence	5	F:GO:0016820; F:GO:0016887; F:GO:0000166; P:GO:0008152; C:GO:0016020	-	EC:3.6.3.0	IPR000150; IPR001757; G3DSA:3.40.50.1000 (GENE3D), PTHR11939:SF54 (PANTHER), SSF56784 (SUPERFAMILY), SSF81665 (SUPERFAMILY)
Caenorhabditis briggsae	set (trithorax polycomb) domain containing family member (set-33)	4	P:GO:0009792; P:GO:0016246; P:GO:0040007; P:GO:0002119	-		-
Caenorhabditis elegans	clathrin light chain	5	P:GO:0009987; P:GO:0006810; C:GO:0030118; C:GO:0012505; P:GO:0009792	-		-
	-	0				SignalP (SIGNALP)
Brugia malayi	ubiquitin-like modifier activating enzyme 1	4	F:GO:0005524; F:GO:0008641; P:GO:0006464; F:GO:0016874	-		IPR020003
Brugia malayi	ubiquitin-like modifier activating enzyme 1	4	F:GO:0005524; F:GO:0008641; P:GO:0006464; F:GO:0016874	-		IPR000011; IPR000127; IPR000594; IPR009036; IPR016040; IPR018074; IPR018075; IPR018965; IPR019572; G3DSA:1.10.3240.10 (GENE3D), PTHR10953 (PANTHER), PTHR10953:SF4 (PANTHER)

Dracunculus medinensis	heat shock protein 70	2	F:GO:0005524; P:GO:0006950	-		-
Caenorhabditis elegans	solute carrier family 17 (sodium phosphate) member 2	4	P:GO:0055085; F:GO:0015114; P:GO:0006811; C:GO:0044425	-		-
Caenorhabditis elegans	variable abnormal morphology family member (vab-10)	0		P:GO:0007423; P:GO:0016199; P:GO:0030716; P:GO:0007517; C:GO:0005912; C:GO:0000235; P:GO:0007409; F:GO:0008092; P:GO:0007017; F:GO:0005509; P:GO:0016319; P:GO:0035149; P:GO:0035147; P:GO:0048813; F:GO:0008017; C:GO:0005874; F:GO:0003779; P:GO:0016204; P:GO:0007475; P:GO:0016203; P:GO:0007026; C:GO:0045169; C:GO:0030426; P:GO:0000226; C:GO:0005856; P:GO:0030036; F:GO:0005515;		-
Caenorhabditis elegans	etoposide-induced protein homolog isoform 2	3	P:GO:0006917; P:GO:0042493; P:GO:0030308	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	cullin family member (cul-2)	3	C:GO:0031461; P:GO:0006511; F:GO:0031625	-		IPR001373; IPR011991; IPR016157; IPR016158; IPR016159; IPR019559; G3DSA:1.20.1310.10 (GENE3D), G3DSA:4.10.1030.10 (GENE3D), PTHR11932 (PANTHER), PTHR11932:SF18 (PANTHER), SSF46785 (SUPERFAMILY)
Caenorhabditis elegans	splicing factor 3b subunit 3	5	P:GO:0008380; F:GO:0003676; C:GO:0005681; F:GO:0005515; P:GO:0006397	-		IPR004871; PTHR10644 (PANTHER), PTHR10644:SF1 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0005524; F:GO:0016887; C:GO:0016021; F:GO:0003993		PTHR11567 (PANTHER), PTHR11567:SF6 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0005524; F:GO:0016887; C:GO:0016021; F:GO:0003993		PTHR11567 (PANTHER), PTHR11567:SF6 (PANTHER), SignalP (SIGNALP)

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0005524; F:GO:0016887; C:GO:0016021; F:GO:0003993		PTHR11567 (PANTHER), PTHR11567:SF6 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0040015; P:GO:0018996; P:GO:0040035; P:GO:0040011; P:GO:0002119; P:GO:0009792; P:GO:0040007; P:GO:0040018		PTHR11909 (PANTHER), PTHR11909:SF11 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	pms2 postmeiotic segregation increased 2 (cerevisiae)	6	F:GO:0032138; F:GO:0032407; P:GO:0006298; F:GO:0003697; P:GO:0009792; C:GO:0005634	-		-
Caenorhabditis elegans	d-3-phosphoglycerate dehydroge-se	9	P:GO:0040010; P:GO:0006098; P:GO:0055114; F:GO:0004617; F:GO:0004455; F:GO:0051287; F:GO:0005515; P:GO:0009792; P:GO:0006564	-	EC:1.1.1.95; EC:1.1.1.86	IPR006139; IPR006140; IPR015508; IPR016040; PTHR10996 (PANTHER), SSF51735 (SUPERFAMILY), SSF52283 (SUPERFAMILY)
Caenorhabditis elegans	d-3-phosphoglycerate dehydroge-se	9	P:GO:0040010; P:GO:0006098; P:GO:0055114; F:GO:0004617; F:GO:0004455; F:GO:0051287; F:GO:0005515; P:GO:0009792; P:GO:0006564	-	EC:1.1.1.95; EC:1.1.1.86	IPR006139; IPR006140; IPR015508; IPR016040; PTHR10996 (PANTHER), SSF51735 (SUPERFAMILY), SSF52283 (SUPERFAMILY)
Loa loa	homology domain containing protein	0				IPR022158
	-	0				-
Caenorhabditis briggsae	cytochrome c oxidase assembly	10	C:GO:0016020; P:GO:0040007; P:GO:0006898; P:GO:0006461; P:GO:0009792; P:GO:0002119; P:GO:0065007; F:GO:0005507; P:GO:0040035; C:GO:0005739	-		IPR003782; IPR012335; IPR012336; IPR022272
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	ash1 (or homeotic)-like	1	P:GO:0044237	-		IPR001025; IPR001214; IPR001965; IPR003616; IPR006560; IPR011011; IPR013083; IPR019787; G3DSA:2.170.270.10 (GENE3D), PTHR22884 (PANTHER), PTHR22884:SF27 (PANTHER), SSF82199 (SUPERFAMILY)

	-	0				-
Caenorhabditis briggsae	methylcrotonoyl-coenzyme a carboxylase 2	10	P:GO:0015936; P:GO:0040010; F:GO:0004525; F:GO:0003723; P:GO:0006396; F:GO:0005524; P:GO:0002119; C:GO:0005759; F:GO:0004485; P:GO:0009792	-	EC:3.1.26.3; EC:6.4.1.4	IPR000022; IPR011762; IPR011763; G3DSA:3.90.226.10 (GENE3D), PTHR22855 (PANTHER), PTHR22855:SF13 (PANTHER), SSF52096 (SUPERFAMILY)
Caenorhabditis briggsae	cg16916 protein	17	C:GO:0001673; P:GO:0006310; P:GO:0008340; P:GO:0006281; C:GO:0008540; F:GO:0004175; P:GO:0006457; P:GO:0000003; P:GO:0006508; F:GO:0005524; P:GO:0002119; F:GO:0016887; F:GO:0005515; F:GO:0009378; P:GO:0030163; P:GO:0009792; C:GO:0005737	-		IPR003593; IPR003959; IPR003960; IPR005937; G3DSA:3.40.50.300 (GENE3D), PTHR23073 (PANTHER), PTHR23073:SF8 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	cg16916 protein	17	C:GO:0001673; P:GO:0006310; P:GO:0008340; P:GO:0006281; C:GO:0008540; F:GO:0004175; P:GO:0006457; P:GO:0000003; P:GO:0006508; F:GO:0005524; P:GO:0002119; F:GO:0016887; F:GO:0005515; F:GO:0009378; P:GO:0030163; P:GO:0009792; C:GO:0005737	-		IPR003593; IPR003959; IPR003960; IPR005937; G3DSA:3.40.50.300 (GENE3D), PTHR23073 (PANTHER), PTHR23073:SF8 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis brenneri	microtubule-associated proteins 1a 1b light chain 3a precursor	1	F:GO:0005515	-		IPR004241; G3DSA:3.10.20.90 (GENE3D), PTHR10969:SF1 (PANTHER), SSF54236 (SUPERFAMILY)
Candida albicans SC5314	sjchgc01393 protein	0				-
Candida albicans SC5314	sjchgc01393 protein	0				-
Trichostrongylus colubriformis	globin	6	F:GO:0020037; C:GO:0005615; C:GO:0005737; F:GO:0005344; P:GO:0015671; F:GO:0019825	-		-
Caenorhabditis elegans	cysteine-rich hydrophobic domain 1	1	C:GO:0044464	-		IPR019383; PTHR13005 (PANTHER)

Trichostrongylus colubriformis	globin	6	F:GO:0020037; C:GO:0005615; C:GO:0005737; F:GO:0005344; P:GO:0015671; F:GO:0019825	-		IPR000971; IPR009050; IPR012085; IPR012292; SignalP (SIGNALP)
Ancylostoma ceylanicum	tissue factor pathway inhibitor a	3	F:GO:0008233; F:GO:0004867; C:GO:0005576	-		IPR002223; IPR020901; PTHR10083 (PANTHER), PTHR10083:SF39 (PANTHER)
Caenorhabditis elegans	protein-tyrosine phosphatase containing protein	2	F:GO:0016791; F:GO:0005515	-	EC:3.1.3.0	-
Trichostrongylus colubriformis	globin	6	F:GO:0020037; C:GO:0005615; C:GO:0005737; F:GO:0005344; P:GO:0015671; F:GO:0019825	-		IPR000971; IPR009050; IPR012085; IPR012292; SignalP (SIGNALP)
Candida albicans SC5314	sjchgc01393 protein	0				-
Caenorhabditis elegans	polymerase iii (d- directed) polypeptide c	7	P:GO:0040010; P:GO:0000003; P:GO:0045087; P:GO:0010171; F:GO:0016740; P:GO:0002119; P:GO:0006350	-		IPR008806; PTHR12949 (PANTHER), PF02002 (PFAM), SSF46785 (SUPERFAMILY)
Caenorhabditis elegans	fyve zinc finger family protein	0		F:GO:0046872; F:GO:0005524; P:GO:0044267; P:GO:0046488; F:GO:0016307; F:GO:0008270; F:GO:0005515		-
Caenorhabditis elegans	btb poz domain containing protein	1	F:GO:0005515	-		IPR000210; IPR002083; IPR008974; IPR011333; IPR013069; IPR013089; IPR013322; PTHR23230:SF169 (PANTHER), SignalP (SIGNALP)
	-	0				-
Loa loa	elegans protein partially confirmed by transcript evidence	0				PTHR19327 (PANTHER)
Pongo abelii	histone-lysine n-methyltransferase setmar	4	F:GO:0005488; P:GO:0006313; F:GO:0016740; F:GO:0004803	-		PTHR23016 (PANTHER)
Caenorhabditis elegans	sulfite oxidase	5	F:GO:0046914; F:GO:0016491; P:GO:0040017; P:GO:0040010; P:GO:0000003	-		-
Caenorhabditis elegans	exocyst complex component 2	1	P:GO:0000003	-		PTHR13043 (PANTHER)

Caenorhabditis elegans	sorting nexin 14	0		P:GO:0007154; P:GO:0015031; C:GO:0016021; C:GO:0016020; P:GO:0006810; F:GO:0003674; P:GO:0007165; C:GO:0005575; F:GO:0005515; F:GO:0004871; F:GO:0035091; P:GO:0008150		IPR000342; IPR001683; IPR003114; IPR013937; IPR016137; PTHR22775 (PANTHER), PTHR22775:SF5 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	ccaat enhancer-binding protein zeta	7	F:GO:0005488; P:GO:0040007; P:GO:0000003; P:GO:0002119; P:GO:0006898; P:GO:0009792; P:GO:0006350	-		IPR005612; PTHR12048 (PANTHER)
	-	0				-
Brugia malayi	kh domain r- sig-l transduction associated 1	10	P:GO:0040035; P:GO:0002119; P:GO:0006468; F:GO:0003723; P:GO:0018996; P:GO:0040010; F:GO:0005524; P:GO:0040011; C:GO:0016021; F:GO:0004674	-	EC:2.7.11.0	IPR004087; G3DSA:3.30.1370.10 (GENE3D), PTHR11208 (PANTHER), PTHR11208:SF22 (PANTHER), SSF54791 (SUPERFAMILY)
Brugia malayi	kh domain containing protein	11	P:GO:0040010; F:GO:0003723; F:GO:0004674; C:GO:0016021; P:GO:0040035; P:GO:0018996; F:GO:0005524; P:GO:0002119; P:GO:0040011; C:GO:0005737; P:GO:0006468	-	EC:2.7.11.0	SignalP (SIGNALP)
Caenorhabditis elegans	aldo-keto reductase	8	P:GO:0042840; P:GO:0046185; C:GO:0016324; P:GO:0055114; P:GO:0019853; F:GO:0047939; F:GO:0004032; C:GO:0005829	-	EC:1.1.1.19; EC:1.1.1.21	IPR001395; IPR018170; IPR020471; IPR023210; PTHR11732:SF34 (PANTHER)
Caenorhabditis elegans	abnormal embryonic partitioning of cytoplasm family member (par-3)	4	P:GO:0048856; P:GO:0007275; C:GO:0044464; P:GO:0009987	-		IPR010916; PTHR16484 (PANTHER), PTHR16484:SF2 (PANTHER)
	-	0				-
Loa loa	programmed cell death 6 interacting protein	0		F:GO:0003674; P:GO:0015031; P:GO:0006810		IPR004328; G3DSA:1.25.40.280 (GENE3D), PTHR23030 (PANTHER), PTHR23030:SF11 (PANTHER)

Loa loa	npl (yeast nuclear protein localization) homolog family member (npl-)	6	P:GO:0007030; P:GO:0006944; F:GO:0005515; C:GO:0043231; C:GO:0044444; F:GO:0008270	-		IPR007716; IPR007717; PTHR12710 (PANTHER)
Caenorhabditis briggsae	npl (yeast nuclear protein localization) homolog family member (npl-)	6	P:GO:0007030; P:GO:0006944; F:GO:0046872; F:GO:0005515; C:GO:0043231; C:GO:0044444	-		IPR001876; IPR007716; IPR007717; PTHR12710 (PANTHER), SSF90209 (SUPERFAMILY)
Caenorhabditis elegans	ophagy (yeast atg homolog) family member (atg-)	1	C:GO:0044464	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR19878 (PANTHER)
Drosophila virilis	serine protease	0		P:GO:0006508; F:GO:0004252; F:GO:0008236; P:GO:0006911; F:GO:0016787; F:GO:0003824; F:GO:0008233		-
Haemaphysalis longicornis	tick serine protei-se	0		P:GO:0006508; F:GO:0004252; F:GO:0008236; P:GO:0006911; F:GO:0016787; F:GO:0003824; F:GO:0008233		IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR19355 (PANTHER), PTHR19355:SF174 (PANTHER), SignalP (SIGNALP)
Drosophila virilis	serine protease	0		P:GO:0006508; F:GO:0004252; F:GO:0008236; P:GO:0006911; F:GO:0016787; F:GO:0003824; F:GO:0008233		IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR19355 (PANTHER), PTHR19355:SF174 (PANTHER), SignalP (SIGNALP)
Drosophila mojavensis	proclotting enzyme	0		P:GO:0006508; F:GO:0004252; F:GO:0008236; F:GO:0016787; F:GO:0003824; F:GO:0008233		IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR19355 (PANTHER), PTHR19355:SF174 (PANTHER)
Haemaphysalis longicornis	serine protease	0		P:GO:0006508; F:GO:0004252; F:GO:0008236; P:GO:0006911; F:GO:0016787; F:GO:0003824; F:GO:0008233		IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR19355 (PANTHER), PTHR19355:SF174 (PANTHER), SignalP (SIGNALP)
Ciona intestinalis	novel protein	0		F:GO:0046872; P:GO:0055114; F:GO:0009055; F:GO:0016491; F:GO:0020037; F:GO:0005506; F:GO:0004497		-

Caenorhabditis elegans	cln3 protein	29	P:GO:0008340; P:GO:0043086; C:GO:0044433; C:GO:0005776; P:GO:0001508; P:GO:0006672; C:GO:0044431; P:GO:0007040; F:GO:0048306; C:GO:0005764; C:GO:0016021; P:GO:0016242; P:GO:0008306; C:GO:0005770; P:GO:0043524; P:GO:0051480; P:GO:0046662; P:GO:0045861; P:GO:0016485; P:GO:0009792; P:GO:0006687; P:GO:0042133; C:GO:0031090; P:GO:0006520; C:GO:0005769; P:GO:0050885; P:GO:0035235;	-		IPR003492; IPR016196; IPR018460
Caenorhabditis elegans	udp-glucose:glycoprotein glucosyltransferase containing protein	5	F:GO:0003980; P:GO:0006457; C:GO:0005788; C:GO:0005793; F:GO:0051082	-		IPR009448
Loa loa	btb and math domain containing protein partially confirmed by transcript evidence	2	P:GO:0009792; F:GO:0005515	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	sy-ptophysin sy-ptoporin family protein	0		C:GO:0016020		-
Loa loa	regulation of nuclear pre-mr- domain containing 1b	0		F:GO:0003674; C:GO:0005575		IPR006569; IPR006903; IPR008942; PTHR12460 (PANTHER)
Caenorhabditis elegans	neighbor of cox4	7	P:GO:0009792; P:GO:0000003; P:GO:0040007; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		IPR005366; PTHR12941:SF2 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-ubxn-1 protein	1	F:GO:0005515	-		IPR001012; G3DSA:3.10.20.90 (GENE3D), PTHR13020 (PANTHER), PTHR13020:SF4 (PANTHER), SSF54236 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	6	F:GO:0046933; C:GO:0016021; P:GO:0015986; C:GO:0033179; C:GO:0045263; C:GO:0005773	-	EC:3.6.3.14	IPR000245; IPR002379; IPR011555; PTHR10263 (PANTHER), SignalP (SIGNALP)
	-	0				-

Culex quinquefasciatus	40s ribosomal protein s9	4	F:GO:0003735; C:GO:0015935; P:GO:0006412; F:GO:0019843	-	EC:3.6.5.3	SignalP (SIGNALP)
Culex quinquefasciatus	40s ribosomal protein s9	4	F:GO:0003735; C:GO:0015935; P:GO:0006412; F:GO:0019843	-	EC:3.6.5.3	SignalP (SIGNALP)
Brugia malayi	40s ribosomal protein	10	P:GO:0009792; P:GO:0010171; P:GO:0002119; F:GO:0003735; P:GO:0040010; C:GO:0015935; P:GO:0000003; P:GO:0008340; P:GO:0006412; F:GO:0019843	-	EC:3.6.5.3	SignalP (SIGNALP)
Brugia malayi	40s ribosomal protein	10	P:GO:0009792; P:GO:0010171; P:GO:0002119; F:GO:0003735; P:GO:0040010; C:GO:0015935; P:GO:0000003; P:GO:0008340; P:GO:0006412; F:GO:0019843	-	EC:3.6.5.3	SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0055114; F:GO:0016491		-
Brugia malayi	zinc c2h2 type family protein	1	F:GO:0005515	-		IPR015880
Caenorhabditis briggsae	Hypothetical protein CBG22132 [Caenorhabditis briggsae]	0				IPR006210; IPR013032
Caenorhabditis briggsae	temporarily assigned gene -me family member (tag-60)	0		P:GO:0008340; F:GO:0005515		-
Caenorhabditis elegans	temporarily assigned gene -me family member (tag-60)	0		P:GO:0008340; F:GO:0005515		-
Caenorhabditis briggsae	pdz domain-containing	2	F:GO:0005515; P:GO:0008340	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR14191 (PANTHER)
Caenorhabditis elegans	pdz domain-containing	2	F:GO:0005515; P:GO:0008340	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR14191 (PANTHER)
Caenorhabditis elegans	pdz domain-containing	2	F:GO:0005515; P:GO:0008340	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR14191 (PANTHER)
Caenorhabditis elegans	pdz domain-containing	2	F:GO:0005515; P:GO:0008340	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR14191 (PANTHER)
Caenorhabditis elegans	pdz domain-containing	2	F:GO:0005515; P:GO:0008340	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR14191 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0008150; C:GO:0005575		-
Caenorhabditis briggsae	briggsae cbr-sys-1 protein	0		F:GO:0005488		IPR011989; IPR016024
Nematostella vectensis	predicted protein [Nematostella vectensis]	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0005515		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0005515		-

Brugia malayi	mediator complex subunit rgr-1	6	F:GO:0030528; P:GO:0040007; P:GO:0002119; F:GO:0008134; P:GO:0009792; P:GO:0006350	-		-
Caenorhabditis briggsae	26s proteasome regulatory subunit s3	9	P:GO:0009792; P:GO:0042176; P:GO:0002119; F:GO:0005515; P:GO:0000003; P:GO:0008340; F:GO:0030234; C:GO:0000502; P:GO:0040007	-		IPR000717; IPR011990; IPR011991; IPR013143; IPR013586; PTHR10758 (PANTHER), SSF46785 (SUPERFAMILY)
Caenorhabditis briggsae	26s proteasome regulatory subunit s3	9	P:GO:0009792; P:GO:0042176; P:GO:0002119; F:GO:0005515; P:GO:0000003; P:GO:0008340; F:GO:0030234; C:GO:0000502; P:GO:0040007	-		IPR000717; IPR011990; IPR011991; IPR013143; IPR013586; PTHR10758 (PANTHER), SSF46785 (SUPERFAMILY)
Caenorhabditis briggsae	26s proteasome regulatory subunit s3	9	P:GO:0009792; P:GO:0042176; P:GO:0002119; F:GO:0005515; P:GO:0000003; P:GO:0008340; F:GO:0030234; C:GO:0000502; P:GO:0040007	-		IPR000717; IPR011990; IPR011991; IPR013143; IPR013586; PTHR10758 (PANTHER), SSF46785 (SUPERFAMILY)
Loa loa	zinc finger protein 37 homolog	0		F:GO:0003676; F:GO:0016455; P:GO:0008150; F:GO:0008270; P:GO:0006357; C:GO:0016592; C:GO:0005622		IPR007087; IPR013087; IPR015880; PTHR14596 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				PTHR19303 (PANTHER), PTHR19303:SF2 (PANTHER)
Loa loa	regulator of nonsense transcripts 1	16	P:GO:0000184; C:GO:0000785; F:GO:0005515; F:GO:0008270; P:GO:0006406; P:GO:0006449; F:GO:0003677; F:GO:0003723; C:GO:0000932; F:GO:0003682; F:GO:0004004; P:GO:0071044; F:GO:0005524; P:GO:0006260; P:GO:0007049; P:GO:0006281	-		G3DSA:3.40.50.300 (GENE3D), PTHR10887 (PANTHER), PTHR10887:SF26 (PANTHER), SSF52540 (SUPERFAMILY)

	-	0				-
	-	0				-
Caenorhabditis briggsae	myosin-2 essential light chain	3	P:GO:0009792; F:GO:0016491; F:GO:0005509	-		IPR002048; IPR011992; IPR018249; PTHR23048 (PANTHER), SSF47473 (SUPERFAMILY)
Loa loa	temporarily assigned gene -me family member (tag-76)	15	P:GO:0030423; C:GO:0016442; F:GO:0003743; P:GO:0030422; P:GO:0006342; P:GO:0006402; F:GO:0035198; P:GO:0035279; P:GO:0007367; C:GO:0005850; P:GO:0035196; C:GO:0048471; F:GO:0019899; C:GO:0005634; P:GO:0007416	-		-
	-	0				-
	-	0				-
Loa loa	eph receptor a4	10	P:GO:0007411; P:GO:0030900; P:GO:0007391; F:GO:0004872; F:GO:0004713; P:GO:0009988; F:GO:0005515; F:GO:0000166; P:GO:0007628; P:GO:0009952	-	EC:2.7.10.0	IPR000719; IPR001245; IPR001660; IPR011009; IPR011510; IPR020685; G3DSA:1.10.510.10 (GENE3D), PTHR23256:SF59 (PANTHER)
Loa loa	chitin binding peritrophin-a domain containing protein	1	F:GO:0005488	-		-
Caenorhabditis briggsae	chitin binding peritrophin-a domain containing protein	1	F:GO:0005515	-		-
Brugia malayi	chitin binding peritrophin-a domain containing protein	1	F:GO:0005515	-		-
Caenorhabditis elegans	phosphatidylserine synthase 1	3	P:GO:0006659; P:GO:0040018; C:GO:0016021	-		IPR004277; SignalP (SIGNALP)
Caenorhabditis elegans	fidgetin-like 1	6	F:GO:0017111; P:GO:0046034; P:GO:0000003; F:GO:0042802; F:GO:0005524; F:GO:0000287	-	EC:3.6.1.15	IPR003593; IPR003959; IPR003960; IPR015415; G3DSA:1.10.8.60 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23074 (PANTHER), PTHR23074:SF17 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	ef hand family protein	11	P:GO:0047497; P:GO:0006915; F:GO:0005509; P:GO:0007264; P:GO:0019725; P:GO:0002119; F:GO:0005515; C:GO:0031307; F:GO:0016787; P:GO:0015031; F:GO:0005525	-		IPR011992; IPR013566; IPR013567; IPR013684; IPR018247; IPR018249; IPR020860; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF13 (PANTHER), SSF47473 (SUPERFAMILY), SSF52540 (SUPERFAMILY)

Caenorhabditis elegans	nuclear hormone receptor e75	0		F:GO:0004887; F:GO:0043565; F:GO:0003700; F:GO:0003677; C:GO:0005634; F:GO:0004879; F:GO:0008270; P:GO:0043053; P:GO:0006355; F:GO:0004872; F:GO:0046872; P:GO:0006350; P:GO:0045449; F:GO:0003707		-
	-	0				-
Caenorhabditis elegans	pdz domain-containing	2	F:GO:0005515; P:GO:0008340	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR14191 (PANTHER)
Loa loa	splicing factor 14 kda subunit	6	F:GO:0003723; P:GO:0006397; C:GO:0005634; F:GO:0000166; P:GO:0008380; F:GO:0005515	-		IPR000504; IPR012677; PTHR22630 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	phosphorylase b ki-se	10	F:GO:0004339; F:GO:0005516; C:GO:0016021; F:GO:0008607; F:GO:0005524; F:GO:0004812; F:GO:0016301; P:GO:0006418; P:GO:0005977; C:GO:0005737	-	EC:3.2.1.3	IPR008734; IPR011613
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	yow5_caeel ame: full=uncharacterized protein	0		F:GO:0005515		-
Caenorhabditis briggsae	yow5_caeel ame: full=uncharacterized protein	1	F:GO:0005515	-		-
	-	0				-
Caenorhabditis elegans	hypothetical protein F59G1.4 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				IPR001810; IPR022364; G3DSA:1.20.1280.50 (GENE3D)

Homo sapiens	immunoglobulin m heavy chain	18	P:GO:0050853; P:GO:0043410; P:GO:0019882; F:GO:0005515; F:GO:0003823; C:GO:0005624; P:GO:0002455; C:GO:0016021; C:GO:0009897; P:GO:0050731; P:GO:0045022; P:GO:0045807; C:GO:0019815; C:GO:0048471; C:GO:0042571; P:GO:0000187; F:GO:0004888; P:GO:0030890	-		IPR003006; IPR003596; IPR003597; IPR007110; IPR013106; IPR013783; PTHR23266 (PANTHER), PTHR23266:SF3 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	monofunctio-l c1-tetrahydrofolate mitochondrial precursor	7	P:GO:0009257; F:GO:0004488; F:GO:0004329; F:GO:0004477; P:GO:0006730; F:GO:0005524; C:GO:0005739	-	EC:1.5.1.5; EC:6.3.4.3; EC:3.5.4.9	IPR000559; G3DSA:3.40.50.300 (GENE3D), PTHR10025 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein K04C2.2 [Caenorhabditis elegans]	5	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0040010; P:GO:0006898	-		IPR007015; PTHR13213:SF5 (PANTHER)
Caenorhabditis elegans	u2 small nuclear ribonucleoprotein	8	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0005488; P:GO:0040010; P:GO:0008340; P:GO:0040011; P:GO:0006898	-		IPR015016; PTHR12097 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Brugia malayi	zgc:162613 protein	0		F:GO:0003674; P:GO:0008150		IPR006968; IPR018202; PTHR12770:SF10 (PANTHER)
Brugia malayi	cd- sequence bc017158	0		F:GO:0003674; C:GO:0016020; P:GO:0008150; C:GO:0005575		IPR006968; PTHR12770:SF11 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	choline ethanolaminephosphotransferase 1	4	C:GO:0043231; P:GO:0008654; F:GO:0016780; C:GO:0016020	-	EC:2.7.8.0	IPR000462; IPR014472; PTHR10414 (PANTHER), PTHR10414:SF4 (PANTHER)
Caenorhabditis briggsae	large subunit ribosomal protein 6	3	C:GO:0005840; F:GO:0003735; P:GO:0006412	-	EC:3.6.5.3	IPR001747; IPR011030; PTHR23345 (PANTHER), SSF48431 (SUPERFAMILY)

Caenorhabditis elegans	briggsae cbr-vit-2 protein	6	P:GO:0009792; F:GO:0005319; F:GO:0005515; P:GO:0040010; P:GO:0006869; P:GO:0008340	-		IPR001747; IPR011030; PTHR23345 (PANTHER), SSF48431 (SUPERFAMILY)
Brugia malayi	math (meprin-associated traf homology) domain containing family member (math-33)	3	P:GO:0032501; P:GO:0045927; F:GO:0016787	-		-
Brugia malayi	metallopeptidase family m24 containing protein	10	P:GO:0006281; P:GO:0045449; P:GO:0006260; P:GO:0018996; F:GO:0003677; C:GO:0035101; C:GO:0005694; P:GO:0009792; P:GO:0001703; P:GO:0001672	-		IPR000994; IPR013719; IPR013953; PTHR13980 (PANTHER), PTHR13980:SF6 (PANTHER)
Brugia malayi	fact complex subunit	10	P:GO:0006281; P:GO:0045449; P:GO:0006260; P:GO:0018996; F:GO:0003677; C:GO:0035101; C:GO:0005694; P:GO:0009792; P:GO:0001703; P:GO:0001672	-		IPR000994; IPR013719; IPR013953; PTHR13980 (PANTHER), PTHR13980:SF6 (PANTHER)
Loa loa	chitin binding peritrophin-a domain containing protein	0		F:GO:0008061; P:GO:0006030; C:GO:0005576		IPR002557; G3DSA:2.170.140.10 (GENE3D), PTHR23301 (PANTHER)
Loa loa	chitin binding peritrophin-a domain containing protein	0		F:GO:0008061; P:GO:0006030; C:GO:0005576		IPR002557; G3DSA:2.170.140.10 (GENE3D), PTHR23301 (PANTHER)
Loa loa	chitin binding peritrophin-a domain containing protein	0		F:GO:0008061; P:GO:0006030; C:GO:0005576		IPR002557; G3DSA:2.170.140.10 (GENE3D), PTHR23301 (PANTHER)
Drosophila ananassae	chitin binding peritrophin-a domain containing protein	0		F:GO:0008061; P:GO:0006030; C:GO:0005576		IPR002557; G3DSA:2.170.140.10 (GENE3D), PTHR23301 (PANTHER)
Loa loa	chitin binding peritrophin-a domain containing protein	0		F:GO:0008061; P:GO:0006030; C:GO:0005576		IPR002557; G3DSA:2.170.140.10 (GENE3D), PTHR23301 (PANTHER)
Loa loa	mast c-terminus family protein	10	P:GO:0007026; F:GO:0051010; P:GO:0021987; P:GO:0021769; C:GO:0005881; C:GO:0005938; P:GO:0000279; C:GO:0005819; C:GO:0005694; C:GO:0005794	-		IPR011989; IPR016024; PTHR21567 (PANTHER), PTHR21567:SF10 (PANTHER)

Loa loa	mast c-terminus family protein	10	P:GO:0007026; F:GO:0051010; P:GO:0021987; P:GO:0021769; C:GO:0005881; C:GO:0005938; P:GO:0000279; C:GO:0005819; C:GO:0005694; C:GO:0005794	-		IPR011989; IPR016024; PTHR21567 (PANTHER), PTHR21567:SF10 (PANTHER)
Loa loa	briggsae cbr-ttr-16 protein	0		P:GO:0016539		IPR001534; SignalP (SIGNALP)
Caenorhabditis briggsae	mannose- 1	15	F:GO:0042802; C:GO:0005792; C:GO:0012505; C:GO:0005793; C:GO:0005794; F:GO:0003677; C:GO:0030017; C:GO:0031090; F:GO:0005509; C:GO:0016021; P:GO:0006888; C:GO:0005634; C:GO:0005783; F:GO:0005537; C:GO:0044446	-		-
	-	0				-
Caenorhabditis elegans	tudor domain-containing protein 3	0		P:GO:0006397; C:GO:0005634; P:GO:0016226; F:GO:0003676; C:GO:0005737; F:GO:0003723; F:GO:0003674; F:GO:0051536; C:GO:0005575; P:GO:0008150; F:GO:0005198		PTHR13681 (PANTHER), PTHR13681:SF4 (PANTHER)
Caenorhabditis elegans	splicing factor (suppressor of white apricot) related family member (swp-1)	1	F:GO:0005488	-		IPR000061; IPR019147; PTHR13161 (PANTHER), PTHR13161:SF2 (PANTHER), SSF109905 (SUPERFAMILY)
Loa loa	testis-specific serine ki-se 6	5	P:GO:0006468; P:GO:0035092; F:GO:0005524; F:GO:0000287; F:GO:0004674	-	EC:2.7.11.0	-
Caenorhabditis elegans	nuclear transcription x-box binding 1	3	F:GO:0005488; P:GO:0000122; P:GO:0045347	-		IPR000967; IPR001374; PTHR12360 (PANTHER), SSF82708 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	mtm family member (mtm-6)	4	P:GO:0016311; F:GO:0004721; F:GO:0046872; P:GO:0000278	-	EC:3.1.3.16	IPR010569; IPR016130; IPR017906; PTHR10807 (PANTHER), PTHR10807:SF11 (PANTHER), SSF50729 (SUPERFAMILY), SSF52799 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-swm-1 protein	0				-
Caenorhabditis briggsae	briggsae cbr-vang-1 protein	1	P:GO:0009792	-		IPR009539; PTHR20886:SF1 (PANTHER)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0005515		-
Ostertagia ostertagi	metalloprotease 1 precursor	1	F:GO:0008233	-		IPR000859; PTHR10127 (PANTHER), PTHR10127:SF60 (PANTHER)
Ostertagia ostertagi	metalloprotease 1 precursor	1	F:GO:0008233	-		IPR000859; PTHR10127 (PANTHER), PTHR10127:SF60 (PANTHER)
Brugia malayi	transmembrane emp24 domain-containing protein 9 precursor	6	C:GO:0005789; P:GO:0009953; P:GO:0006810; P:GO:0000003; P:GO:0040011; C:GO:0016021	-		-
Syngamus trachea	globin	6	F:GO:0020037; C:GO:0005576; C:GO:0005737; F:GO:0005344; P:GO:0015671; F:GO:0019825	-		-
Drosophila simulans	arsenite inducible r- associated protein aip-1	1	F:GO:0046872	-		IPR000058; PTHR14677 (PANTHER), PTHR14677:SF2 (PANTHER), SSF118310 (SUPERFAMILY)
Drosophila mojavensis	conserved domain protein	0		F:GO:0030414; F:GO:0005509; F:GO:0004867; C:GO:0005576		SignalP (SIGNALP)
	-	0				-
Homo sapiens	adp-ribosylation factor 3	16	F:GO:0005057; C:GO:0000139; F:GO:0005515; F:GO:0008270; F:GO:0005525; P:GO:0015031; C:GO:0005829; P:GO:0032312; P:GO:0006892; P:GO:0006890; C:GO:0048471; F:GO:0003924; C:GO:0005886; P:GO:0048205; F:GO:0008060; C:GO:0030017	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR006689; G3DSA:3.40.50.300 (GENE3D), PTHR11711:SF30 (PANTHER), PS51417 (PROFILE), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	rwd domain containing 1	0		F:GO:0003674; C:GO:0005575		IPR006575; IPR016135; PTHR12292 (PANTHER)
Caenorhabditis elegans	atad3a protein	4	C:GO:0005743; F:GO:0005515; F:GO:0005524; F:GO:0017111	-	EC:3.6.1.15	IPR003959; G3DSA:3.40.50.300 (GENE3D), PTHR23075 (PANTHER), SSF52540 (SUPERFAMILY)

Caenorhabditis briggsae	arginyl-tr- synthetase mitochondrial	4	P:GO:0006412; F:GO:0005488; F:GO:0016874; C:GO:0005737	-	EC:3.6.5.3	IPR001278; IPR008909; IPR009080; G3DSA:1.10.730.10 (GENE3D)
Caenorhabditis elegans	guanine nucleotide-binding protein beta 5 (g protein beta5)	2	P:GO:0007186; C:GO:0005834	-	EC:3.6.5.1	IPR001632; IPR001680; IPR011046; IPR015943; IPR016346; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR19850 (PANTHER), PTHR19850:SF12 (PANTHER)
	-	0				-
Brugia malayi	briggsae cbr-dpy-22 protein	3	P:GO:0050789; P:GO:0032501; P:GO:0032502	-		-
Tribolium castaneum	cg14607 cg14607-pa	0				-
Caenorhabditis elegans	prion-like-(q n-rich)-domain-bearing protein family member (pqn-87)	0				-
Caenorhabditis elegans	protein ndrg3	0		F:GO:0003674; C:GO:0005575		IPR004142; G3DSA:3.40.50.1820 (GENE3D), PTHR11034:SF7 (PANTHER), SSF53474 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	inositol -trisphosphate receptor	4	F:GO:0004872; F:GO:0005262; P:GO:0006811; C:GO:0016020	-		-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-rig-4 protein	0		P:GO:0007155; C:GO:0016021; C:GO:0016020		-
Caenorhabditis briggsae	briggsae cbr-fum-1 protein	9	P:GO:0009792; C:GO:0045239; F:GO:0005515; P:GO:0006106; P:GO:0040010; P:GO:0000003; P:GO:0006099; P:GO:0006898; F:GO:0004333	-	EC:4.2.1.2	IPR000362; IPR008948; IPR018951; IPR020557; IPR022761; G3DSA:1.10.40.30 (GENE3D), G3DSA:1.20.200.10 (GENE3D), PTHR11444 (PANTHER), PTHR11444:SF1 (PANTHER)
	-	0				-
Caenorhabditis elegans	splicing factor subunit 1	11	P:GO:0000389; F:GO:0003723; C:GO:0005730; P:GO:0040002; P:GO:0040035; C:GO:0005684; F:GO:0005515; P:GO:0006898; P:GO:0002009; P:GO:0009792; P:GO:0016246	-		IPR000061; IPR000626; IPR019954; IPR019955; IPR019956; IPR022030; G3DSA:3.10.20.90 (GENE3D), PTHR15316 (PANTHER), SSF109905 (SUPERFAMILY), SSF54236 (SUPERFAMILY)
Caenorhabditis elegans	sh3-binding domain protein 5-like	0		F:GO:0003674; C:GO:0005575		IPR007940

Caenorhabditis elegans	26s protease regulatory subunit s10b	7	C:GO:0005737; F:GO:0008233; F:GO:0005515; P:GO:0030163; F:GO:0005524; C:GO:0000502; F:GO:0017111	-	EC:3.6.1.15	-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	P:GO:0006810	-		IPR011701; IPR016196; G3DSA:1.20.1250.20 (GENE3D), PTHR10924 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG15940 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	hat family dimerisation domain containing protein	2	F:GO:0003676; F:GO:0046983	-		-
Dirofilaria immitis	ecdysone inducible protein 75	2	F:GO:0004872; F:GO:0005488	-		IPR000536; IPR001628; IPR001723; IPR008946; IPR013088; PR00350 (PRINTS), PTHR11865 (PANTHER), PTHR11865:SF120 (PANTHER), SSF57716 (SUPERFAMILY)
	-	0				-
Homo sapiens	ap-2 complex subunit mu-1	14	P:GO:0016192; C:GO:0005829; C:GO:0030125; C:GO:0030132; C:GO:0005739; C:GO:0030133; F:GO:0008289; C:GO:0030131; C:GO:0005778; C:GO:0030666; P:GO:0050690; F:GO:0005515; F:GO:0005215; P:GO:0006886	-		IPR001392; IPR008968; IPR015629; G3DSA:2.60.40.1170 (GENE3D), PTHR11998 (PANTHER)
Caenorhabditis briggsae	tubulin-specific chaperone c	0		F:GO:0003674; F:GO:0005488; C:GO:0005856; P:GO:0007023; P:GO:0006457; F:GO:0051087; C:GO:0005575; C:GO:0005874		IPR006599; IPR012945; IPR017901; PTHR15139 (PANTHER)
Caenorhabditis briggsae	tubulin-specific chaperone c	0		F:GO:0003674; F:GO:0005488; C:GO:0005856; P:GO:0007023; P:GO:0006457; F:GO:0051087; C:GO:0005575; C:GO:0005874		IPR006599; IPR012945; IPR017901; PTHR15139 (PANTHER)
Caenorhabditis briggsae	tubulin-specific chaperone c	1	C:GO:0043229	-		IPR006599; IPR012945; IPR017901; PTHR15139 (PANTHER)

Caenorhabditis briggsae	tubulin-specific chaperone c	0		F:GO:0003674; F:GO:0005488; C:GO:0005856; P:GO:0007023; P:GO:0006457; F:GO:0051087; C:GO:0005575; C:GO:0005874		IPR006599; IPR012945; IPR017901; PTHR15139 (PANTHER)
Brugia malayi	bat2 n-terminus family protein	0		F:GO:0008022		IPR004827
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				PTHR23076 (PANTHER), PTHR23076:SF7 (PANTHER), SignalP (SIGNALP)
Pediculus humanus corporis	chromosome 14 open reading frame 10	0		C:GO:0005737; F:GO:0005509; C:GO:0005634		PTHR12085 (PANTHER)
Brugia malayi	cd- sequence bc056474	1	C:GO:0016021	-		-
Mus musculus	component of oligomeric golgi complex 6	1	C:GO:0017119	-		IPR010490
Caenorhabditis elegans	spectrin alpha chain	28	P:GO:0007026; P:GO:0008360; C:GO:0031594; P:GO:0030721; P:GO:0007417; P:GO:0007009; P:GO:0016337; C:GO:0016323; F:GO:0005509; P:GO:0008302; C:GO:0008091; C:GO:0005794; C:GO:0045170; P:GO:0002168; F:GO:0003779; F:GO:0008017; P:GO:0030707; C:GO:0045169; P:GO:0007308; P:GO:0045478; P:GO:0042062; P:GO:0007274; C:GO:0005811; P:GO:0030727; P:GO:0048790; F:GO:0005516; P:GO:0007294	-		IPR002017; IPR018159; G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF48 (PANTHER), SSF46966 (SUPERFAMILY)
Caenorhabditis elegans	unidentified vitellogenin-linked transcript family member (uvt-5)	1	F:GO:0016757	-		IPR002495; G3DSA:3.90.550.10 (GENE3D), PTHR11183 (PANTHER), PTHR11183:SF6 (PANTHER), SSF53448 (SUPERFAMILY)
Caenorhabditis elegans	unidentified vitellogenin-linked transcript family member (uvt-5)	1	F:GO:0016757	-		IPR002495; G3DSA:3.90.550.10 (GENE3D), PTHR11183 (PANTHER), PTHR11183:SF6 (PANTHER), SSF53448 (SUPERFAMILY)
Caenorhabditis elegans	unidentified vitellogenin-linked transcript family member (uvt-5)	0		F:GO:0005515; F:GO:0016757		IPR002495; G3DSA:3.90.550.10 (GENE3D), PTHR11183 (PANTHER), PTHR11183:SF6 (PANTHER), SSF53448 (SUPERFAMILY)

Caenorhabditis briggsae	btb poz domain containing protein	0		P:GO:0006397; F:GO:0005515; C:GO:0005634		IPR000210; IPR011333; IPR013069; IPR013089; PTHR23230:SF176 (PANTHER)
Caenorhabditis elegans	serine threonine-protein phosphatase 5	5	C:GO:0005737; F:GO:0046872; F:GO:0004722; P:GO:0006470; C:GO:0005634	-		IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF12 (PANTHER), SSF56300 (SUPERFAMILY)
Caenorhabditis elegans	citrate synthase	31	P:GO:0006101; P:GO:0006107; C:GO:0031594; F:GO:0004108; F:GO:0019901; P:GO:0071374; P:GO:0040010; C:GO:0005759; P:GO:0046777; C:GO:0005624; P:GO:0044262; C:GO:0005794; P:GO:0046827; C:GO:0005829; P:GO:0051447; P:GO:0006099; P:GO:0018105; P:GO:0009792; P:GO:0043457; C:GO:0005952; P:GO:0002119; P:GO:0006950; C:GO:0048471; F:GO:0032403; P:GO:0001707; P:GO:0051966; C:GO:0005886;	-	EC:2.3.3.1; EC:2.7.11.11	IPR002020; IPR010109; IPR016141; IPR016142; IPR019810
Caenorhabditis elegans	neuro-l symmetry protein partially confirmed by transcript evidence	1	F:GO:0005515	-		-
	-	0				-
Brugia malayi	an1-like zinc finger family protein	0		C:GO:0005737; F:GO:0008270; C:GO:0005840		IPR000058; IPR000626; IPR019955; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF118310 (SUPERFAMILY), SSF54236 (SUPERFAMILY)
Brugia malayi	an1-like zinc finger family protein	0		C:GO:0005737; F:GO:0008270; C:GO:0005840		IPR000058; IPR000626; IPR019955; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), SSF118310 (SUPERFAMILY), SSF54236 (SUPERFAMILY)

Caenorhabditis elegans	dihydrolipoyl mitochondrial	21	C:GO:0043159; P:GO:0048240; F:GO:0004148; P:GO:0007369; P:GO:0010510; C:GO:0005759; C:GO:0019861; P:GO:0006120; P:GO:0007568; F:GO:0009055; C:GO:0045252; P:GO:0009106; P:GO:0051068; F:GO:0050660; P:GO:0045454; F:GO:0051287; C:GO:0045254; P:GO:0006103; P:GO:0006508; F:GO:0043544; P:GO:0042391	-	EC:1.8.1.4	IPR004099; IPR006258; IPR013027; IPR016156; PR00411 (PRINTS), G3DSA:3.50.50.60 (GENE3D), PTHR22912 (PANTHER), SSF51905 (SUPERFAMILY)
Brugia malayi	sr protein	9	F:GO:0003729; C:GO:0005681; P:GO:0000381; P:GO:0006376; C:GO:0000785; F:GO:0005515; F:GO:0000166; C:GO:0035062; F:GO:0016787	-		IPR000504; IPR012677; PTHR23147 (PANTHER), SSF54928 (SUPERFAMILY)
Brugia malayi	sr protein	9	F:GO:0003729; C:GO:0005681; P:GO:0000381; P:GO:0006376; C:GO:0000785; F:GO:0005515; F:GO:0000166; C:GO:0035062; F:GO:0016787	-		-
Ancylostoma ceylanicum	macrophage migration inhibitory factor	16	P:GO:0035468; P:GO:0042325; P:GO:0006955; P:GO:0009966; P:GO:0002684; P:GO:0042127; P:GO:0051047; P:GO:0032268; F:GO:0004167; P:GO:0048523; P:GO:0048583; N:GO:0035556; P:GO:0006950; P:GO:0033036; F:GO:0005488; P:GO:0048598	-	EC:5.3.3.12	IPR001398; IPR014347; PTHR11954:SF4 (PANTHER), SSF55331 (SUPERFAMILY)
Loa loa	ubiquitin carboxyl-termi-l	1	F:GO:0016787	-		IPR002083; IPR008974; IPR013322; PTHR10420 (PANTHER), PTHR10420:SF10 (PANTHER)

Caenorhabditis briggsae	acetyl- hydrolase transferase family protein	6	F:GO:0019239; C:GO:0005811; P:GO:0009168; P:GO:0006084; F:GO:0016787; F:GO:0016740	-		IPR003702; G3DSA:3.40.1080.10 (GENE3D), G3DSA:3.40.810.20 (GENE3D), PTHR21432:SF11 (PANTHER), SSF100950 (SUPERFAMILY)
Caenorhabditis briggsae	acetyl- hydrolase transferase family protein	6	F:GO:0019239; C:GO:0005811; P:GO:0009168; P:GO:0006084; F:GO:0016787; F:GO:0016740	-		IPR003702; G3DSA:3.40.1080.10 (GENE3D), G3DSA:3.40.810.20 (GENE3D), PTHR21432:SF11 (PANTHER), SSF100950 (SUPERFAMILY)
Caenorhabditis briggsae	acetyl- hydrolase transferase family protein	6	F:GO:0019239; C:GO:0005811; P:GO:0009168; P:GO:0006084; F:GO:0016787; F:GO:0016740	-		IPR003702; G3DSA:3.40.1080.10 (GENE3D), G3DSA:3.40.810.20 (GENE3D), PTHR21432:SF11 (PANTHER), SSF100950 (SUPERFAMILY)
Caenorhabditis briggsae	acetyl- hydrolase transferase family protein	6	F:GO:0019239; C:GO:0005811; P:GO:0009168; P:GO:0006084; F:GO:0016787; F:GO:0016740	-		IPR003702; G3DSA:3.40.1080.10 (GENE3D), G3DSA:3.40.810.20 (GENE3D), PTHR21432:SF11 (PANTHER), SSF100950 (SUPERFAMILY)
	-	0				-
Loa loa	mps one binder ki-se activator-like 1a	6	C:GO:0005737; F:GO:0019209; P:GO:0035329; C:GO:0005634; P:GO:0046777; F:GO:0019900	-		IPR005301; PTHR22599:SF8 (PANTHER)
Caenorhabditis elegans	alanine-glyoxylate aminotransferase (oxalosis i hyperoxaluria i glycolicaciduria serine-pyruvate aminotransferase)	5	C:GO:0005777; C:GO:0005739; F:GO:0008483; P:GO:0009058; F:GO:0030170	-	EC:2.6.1.0	IPR000192; IPR015421; IPR015422; IPR015424; PTHR21152 (PANTHER), PTHR21152:SF5 (PANTHER)
Caenorhabditis elegans	alanine-glyoxylate aminotransferase (oxalosis i hyperoxaluria i glycolicaciduria serine-pyruvate aminotransferase)	5	C:GO:0005777; C:GO:0005739; F:GO:0008483; P:GO:0009058; F:GO:0030170	-	EC:2.6.1.0	IPR000192; IPR015421; IPR015422; IPR015424; PTHR21152 (PANTHER), PTHR21152:SF5 (PANTHER)
Caenorhabditis elegans	adapter molecule crk	9	P:GO:0016477; P:GO:0043652; P:GO:0006915; F:GO:0005070; P:GO:0031532; F:GO:0032403; P:GO:0007165; P:GO:0009653; C:GO:0005886	-		IPR000980; IPR001452; IPR011511; G3DSA:2.30.30.40 (GENE3D), PTHR19969 (PANTHER), PTHR19969:SF2 (PANTHER), SSF55550 (SUPERFAMILY)
Loa loa	briggsae cbr-oig-4 protein	0				-
Caenorhabditis briggsae	inositol polyphosphate-5- 40kda	1	F:GO:0004437	-		PTHR12997 (PANTHER), PTHR12997:SF2 (PANTHER)
Caenorhabditis elegans	hypothetical protein C09E8.1 [Caenorhabditis elegans]	0		F:GO:0005328; C:GO:0016020; P:GO:0006836; C:GO:0005887		-

	-	0				-
Caenorhabditis elegans	prolactin regulatory element-binding protein	1	P:GO:0006350	-		-
Caenorhabditis elegans	mgc68553 protein	0		F:GO:0003674; P:GO:0008150; C:GO:0005575		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-let-2 protein	5	C:GO:0005587; F:GO:0016787; F:GO:0005488; F:GO:0030020; P:GO:0016043	-		IPR001442; IPR016187; PTHR10499 (PANTHER), PTHR10499:SF78 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	bt (bacillus thuringiensis) toxin resistant family member (bre-1)	11	P:GO:0042350; F:GO:0008831; P:GO:0045226; F:GO:0008446; P:GO:0019673; P:GO:0075015; P:GO:0006664; F:GO:0005515; P:GO:0017085; F:GO:0050662; C:GO:0005634	-	EC:1.1.1.133; EC:4.2.1.47	IPR001509; IPR006368; IPR016040; IPR020904; G3DSA:3.90.25.10 (GENE3D), PTHR10366 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	bt (bacillus thuringiensis) toxin resistant family member (bre-1)	11	P:GO:0042350; F:GO:0008831; P:GO:0045226; F:GO:0008446; P:GO:0019673; P:GO:0075015; P:GO:0006664; F:GO:0005515; P:GO:0017085; F:GO:0050662; C:GO:0005634	-	EC:1.1.1.133; EC:4.2.1.47	IPR001509; IPR006368; IPR016040; IPR020904; G3DSA:3.90.25.10 (GENE3D), PTHR10366 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	-dh dehydroge-se 1 beta subcomplex subunit 7	8	P:GO:0040010; P:GO:0008340; F:GO:0008137; C:GO:0005739; P:GO:0040035; P:GO:0002119; P:GO:0009792; C:GO:0016020	-	EC:1.6.5.3	IPR008698
Caenorhabditis elegans	hypothetical protein M01H9.3 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	glutamate semialdehyde dehydroge-se	9	P:GO:0040010; C:GO:0005743; P:GO:0055114; F:GO:0004350; P:GO:0006898; P:GO:0006561; F:GO:0004349; C:GO:0005811; F:GO:0017084	-	EC:1.2.1.41; EC:2.7.2.11	IPR016161; IPR016162; PTHR11063 (PANTHER), PTHR11063:SF2 (PANTHER)
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	40s ribosomal protein s12	9	P:GO:0009792; P:GO:0010171; P:GO:0002119; F:GO:0003735; P:GO:0040017; P:GO:0040010; P:GO:0000003; C:GO:0022627; P:GO:0006412	-	EC:3.6.5.3	IPR000530; IPR001313; IPR004038; G3DSA:3.30.1330.30 (GENE3D), SSF55315 (SUPERFAMILY)
Caenorhabditis briggsae	lipoate-protein ligase	4	C:GO:0005737; P:GO:0006464; F:GO:0016415; P:GO:0009107	-		IPR000544; IPR004143; IPR020605; PD006086 (PRODOM), G3DSA:3.90.1550.10 (GENE3D), PTHR10993 (PANTHER), SSF55681 (SUPERFAMILY)
Caenorhabditis briggsae	nnmt pnmt temt family protein	2	F:GO:0005515; F:GO:0008168	-	EC:2.1.1.0	IPR000940; G3DSA:3.40.50.150 (GENE3D), PTHR10867:SF3 (PANTHER), SSF53335 (SUPERFAMILY)
Caenorhabditis briggsae	collagen type xviii alpha 1	6	C:GO:0005604; P:GO:0007155; C:GO:0030054; F:GO:0005198; F:GO:0005488; P:GO:0040035	-		IPR010515; IPR016186; IPR016187; PTHR10499 (PANTHER), PTHR10499:SF7 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein B0041.8 [Caenorhabditis elegans]	0				-
Loa loa	kelch-like protein	3	P:GO:0050807; F:GO:0003779; P:GO:0016049	-		IPR000210; IPR006652; IPR011333; IPR011705; IPR013069; IPR013089; IPR015915; PTHR23230:SF157 (PANTHER), SSF117281 (SUPERFAMILY)
Loa loa	kelch-like protein	3	P:GO:0050807; F:GO:0003779; P:GO:0016049	-		IPR000210; IPR006652; IPR011333; IPR011705; IPR013069; IPR013089; IPR015915; PTHR23230:SF157 (PANTHER), SSF117281 (SUPERFAMILY)
Loa loa	ring ca-l kelch protein	3	P:GO:0050807; F:GO:0003779; P:GO:0016049	-		IPR000210; IPR006652; IPR011333; IPR011705; IPR013069; IPR013089; IPR015915; PTHR23230:SF157 (PANTHER), SSF117281 (SUPERFAMILY)
Loa loa	kelch-like protein	3	P:GO:0050807; F:GO:0003779; P:GO:0016049	-		IPR000210; IPR006652; IPR011333; IPR011705; IPR013069; IPR013089; IPR015915; PTHR23230:SF157 (PANTHER), SSF117281 (SUPERFAMILY)
Caenorhabditis elegans	nuclear pore complex protein family member (npp-6)	6	P:GO:0006997; P:GO:0000003; P:GO:0040007; P:GO:0006898; P:GO:0040039; P:GO:0002119	-		IPR021717
Caenorhabditis briggsae	briggsae cbr-npp-6 protein	6	P:GO:0006997; P:GO:0000003; P:GO:0040007; P:GO:0006898; P:GO:0040039; P:GO:0002119	-		IPR021717

Enterobacteria phage S13	protein a	6	F:GO:0004519; F:GO:0003910; F:GO:0005524; F:GO:0003677; F:GO:0004857; F:GO:0008270	-	EC:6.5.1.1	IPR008683; IPR008684
Caenorhabditis elegans	briggsae cbr-dlg-1 protein	57	P:GO:0030838; P:GO:0048608; C:GO:0019717; P:GO:0031579; F:GO:0032947; P:GO:0008284; P:GO:0002369; F:GO:0008022; P:GO:0050680; C:GO:0009925; C:GO:0014069; C:GO:0001772; P:GO:0043297; P:GO:0032880; P:GO:0042982; P:GO:0007268; C:GO:0016327; P:GO:0032147; P:GO:0048745; P:GO:0043268; P:GO:0046956; C:GO:0031594; P:GO:0042391; P:GO:0051726; C:GO:0030315; P:GO:0001771; P:GO:0008049;	-		IPR001452; IPR001478; IPR004172; IPR008144; IPR008145; IPR015143; IPR020590; G3DSA:2.30.30.40 (GENE3D), G3DSA:2.30.42.10 (GENE3D), G3DSA:3.30.63.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23119 (PANTHER), PTHR23119:SF2 (PANTHER), SSF101288 (SUPERFAMILY), SSF52540 (SUPERFAMILY)

Caenorhabditis elegans	briggsae cbr-dlg-1 protein	57	P:GO:0030838; P:GO:0048608; C:GO:0019717; P:GO:0031579; F:GO:0032947; P:GO:0008284; P:GO:0002369; F:GO:0008022; P:GO:0050680; C:GO:0009925; C:GO:0014069; C:GO:0001772; P:GO:0043297; P:GO:0032880; P:GO:0042982; P:GO:0007268; C:GO:0016327; P:GO:0032147; P:GO:0048745; P:GO:0043268; P:GO:0046956; C:GO:0031594; P:GO:0042391; P:GO:0051726; C:GO:0030315; P:GO:0001771; P:GO:0008049;	-		IPR001452; IPR001478; IPR004172; IPR008144; IPR008145; IPR015143; IPR020590; G3DSA:2.30.30.40 (GENE3D), G3DSA:2.30.42.10 (GENE3D), G3DSA:3.30.63.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23119 (PANTHER), PTHR23119:SF2 (PANTHER), SSF101288 (SUPERFAMILY), SSF52540 (SUPERFAMILY)
Brugia malayi	ribosomal protein l23a-like	12	P:GO:0040010; P:GO:0051726; F:GO:0019843; F:GO:0003735; P:GO:0040035; P:GO:0006414; P:GO:0002119; F:GO:0005515; F:GO:0000166; P:GO:0009792; P:GO:0040018; C:GO:0022625	-		IPR012677; PTHR11620 (PANTHER)
Caenorhabditis elegans	tgf-beta resistance-associated protein trag isoform 2	0				-
Brugia malayi	fimbrin plastin	3	P:GO:0016321; F:GO:0003779; F:GO:0005509	-		IPR001589; IPR001715; IPR011992; IPR018249; PTHR19961 (PANTHER), PTHR19961:SF8 (PANTHER), SSF47473 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG05152 [Caenorhabditis briggsae]	0		F:GO:0005096; P:GO:0051056; C:GO:0005622		-
Caenorhabditis elegans	coatomer subunit beta	8	F:GO:0005515; P:GO:0032940; P:GO:0016192; P:GO:0000003; P:GO:0008340; P:GO:0006886; C:GO:0030126; F:GO:0005198	-		IPR011710; PTHR10635 (PANTHER)

Caenorhabditis elegans	coatomer subunit beta	8	F:GO:0005515; P:GO:0032940; P:GO:0016192; P:GO:0000003; P:GO:0008340; P:GO:0006886; C:GO:0030126; F:GO:0005198	-		IPR011710; PTHR10635 (PANTHER)
	-	0				-
Loa loa	cytoplasmic intermediate filament protein	1	P:GO:0007275	-		IPR001322; IPR001664; G3DSA:2.60.40.1260 (GENE3D), PTHR23239:SF13 (PANTHER), SSF74853 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	bifunctio-l atp-dependent dihydroxyacetone ki-se fad-amp lyase	2	F:GO:0005488; F:GO:0003824	-		IPR000923; IPR004006; IPR004007; IPR012734; G3DSA:3.30.1180.20 (GENE3D), G3DSA:3.40.50.10440 (GENE3D), PS51480 (PROFILE), PS51481 (PROFILE), SignalP (SIGNALP), SSF82549 (SUPERFAMILY)
Caenorhabditis briggsae	pyruvate ki-se	8	P:GO:0009792; F:GO:0004743; F:GO:0016830; P:GO:0006725; F:GO:0005515; F:GO:0030955; F:GO:0000287; P:GO:0006096	-	EC:2.7.1.40	IPR001697; IPR015793; IPR015794; IPR015813
Brugia malayi	calcium homeostasis endoplasmic reticulum protein	4	C:GO:0005737; P:GO:0008285; P:GO:0006874; P:GO:0007399	-		-
Loa loa	hypothetical protein LOAG_09335 [Loa loa]	0				-
Homo sapiens	ribosomal protein l13a	4	F:GO:0003735; C:GO:0015934; C:GO:0005829; P:GO:0006414	-		IPR005755; IPR005822
Caenorhabditis elegans	briggsae cbr-hex-3 protein	3	P:GO:0005975; F:GO:0004553; F:GO:0043169	-	EC:3.2.1.0	IPR017853; PTHR21040 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	4	F:GO:0005089; C:GO:0005622; P:GO:0000003; P:GO:0035023	-		-
Loa loa	n-acetyltransferase 13	5	C:GO:0005737; F:GO:0008415; P:GO:0006474; F:GO:0005515; P:GO:0001756	-		IPR000182; IPR016181; PTHR23091 (PANTHER), PTHR23091:SF2 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	ki-se-like protein splice variant 2	4	P:GO:0006468; F:GO:0005524; F:GO:0004672; F:GO:0005515	-		IPR000719; IPR011009; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR12984 (PANTHER), PTHR12984:SF3 (PANTHER)
	-	0				IPR000519; SignalP (SIGNALP)

Caenorhabditis briggsae	deleted in colorectal carcinoma	7	P:GO:0007411; C:GO:0043005; F:GO:0005515; C:GO:0044425; P:GO:0007165; P:GO:0048522; F:GO:0004888	-		IPR003598; IPR003599; IPR003961; IPR007110; IPR008957; IPR009138; IPR013098; IPR013783; PR00014 (PRINTS), PTHR10489 (PANTHER), PTHR10489:SF55 (PANTHER), SignalP (SIGNALP), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	pip ki-se protein 1	2	P:GO:0046488; F:GO:0016307	-		IPR002498; G3DSA:3.30.800.10 (GENE3D), PTHR23086:SF5 (PANTHER), SSF56104 (SUPERFAMILY)
Caenorhabditis briggsae	cell death abnormality family member (ced-7)	5	P:GO:0043652; F:GO:0016887; C:GO:0005886; P:GO:0012501; F:GO:0000166	-		PTHR19229 (PANTHER), PTHR19229:SF18 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	cell death abnormality family member (ced-7)	4	P:GO:0043652; C:GO:0005886; P:GO:0012501; F:GO:0017111	-	EC:3.6.1.15	IPR003439; G3DSA:3.40.50.300 (GENE3D), PTHR19229 (PANTHER), PTHR19229:SF18 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	cell death abnormality family member (ced-7)	5	P:GO:0043652; F:GO:0016887; C:GO:0005886; P:GO:0012501; F:GO:0000166	-		PTHR19229 (PANTHER), PTHR19229:SF18 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	cell death abnormality family member (ced-7)	4	P:GO:0043652; C:GO:0005886; P:GO:0012501; F:GO:0017111	-	EC:3.6.1.15	IPR003439; IPR003593; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR19229 (PANTHER), PTHR19229:SF18 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	phenylalanyl-tr- beta subunit	7	C:GO:0005625; F:GO:0004826; F:GO:0003723; F:GO:0005524; F:GO:0000287; P:GO:0006432; C:GO:0005829	-	EC:6.1.1.20	IPR005146; IPR005147; IPR009061; IPR020825; PTHR10947 (PANTHER), PS51483 (PROFILE)
Caenorhabditis elegans	cutaneous t cell lymphoma tumor antigen rrm rnp	0		F:GO:0003676; F:GO:0003723; F:GO:0046872; F:GO:0000166; P:GO:0006397; F:GO:0008270; P:GO:0040010; P:GO:0010171		IPR000504; IPR012677; PTHR14398 (PANTHER), SSF54928 (SUPERFAMILY)
Streptococcus pyogenes	collagen-like surface protein	0		F:GO:0003676; F:GO:0004386; F:GO:0005524; C:GO:0005618; C:GO:0009986; F:GO:0003677		-
	-	0				-
Brugia malayi	guanine nucleotide-binding protein gamma-1 subunit	4	P:GO:0007186; F:GO:0004871; P:GO:0007165; C:GO:0005834	-	EC:3.6.5.1	SignalP (SIGNALP)

Caenorhabditis elegans	hypoxanthine-guanine phosphoribosyltransferase	18	P:GO:0006168; P:GO:0045964; P:GO:0006178; F:GO:0004422; P:GO:0032263; F:GO:0002060; C:GO:0005829; P:GO:0019915; P:GO:0007610; P:GO:0032264; C:GO:0005694; F:GO:0042802; P:GO:0046100; F:GO:0000287; P:GO:0016043; P:GO:0006166; P:GO:0007399; P:GO:0032940	-	EC:2.4.2.8	IPR000836; IPR005904; G3DSA:3.40.50.2020 (GENE3D), PTHR22573 (PANTHER), PTHR22573:SF8 (PANTHER), SSF53271 (SUPERFAMILY)
Caenorhabditis briggsae	dual oxidase	18	P:GO:0018149; P:GO:0006979; P:GO:0006952; F:GO:0016174; P:GO:0040032; F:GO:0005509; C:GO:0016021; P:GO:0042338; P:GO:0055114; P:GO:0040007; F:GO:0004601; F:GO:0009055; P:GO:0002119; P:GO:0040011; F:GO:0020037; F:GO:0050660; P:GO:0009792; C:GO:0005882	-	EC:1.6.3.1; EC:1.11.1.7	IPR001221; IPR013112; IPR013121; IPR013130; IPR017927; IPR017938; G3DSA:2.40.30.10 (GENE3D), G3DSA:3.40.50.80 (GENE3D), PTHR11972 (PANTHER), PTHR11972:SF6 (PANTHER), SignalP (SIGNALP), SSF52343 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	protein sidekick	4	C:GO:0005887; P:GO:0042675; P:GO:0046533; P:GO:0007155	-		IPR003961; IPR008957; IPR013783; PTHR10489 (PANTHER), PTHR10489:SF57 (PANTHER)
Caenorhabditis elegans	briggsae cbr-tdc-1 protein	4	F:GO:0030170; P:GO:0019752; P:GO:0006519; F:GO:0016831	-	EC:4.1.1.0	-
Caenorhabditis briggsae	aromatic amino acid decarboxylase	8	F:GO:0030170; P:GO:0006519; F:GO:0004837; P:GO:0018991; P:GO:0048148; P:GO:0019752; F:GO:0004058; P:GO:0007626	-	EC:4.1.1.25; EC:4.1.1.28	IPR002129; IPR010977; IPR015421; IPR015422; IPR015424; IPR021115; G3DSA:1.20.1340.10 (GENE3D), PTHR11999:SF11 (PANTHER)

Caenorhabditis briggsae	aromatic amino acid decarboxylase	8	F:GO:0030170; P:GO:0006519; F:GO:0004837; P:GO:0018991; P:GO:0048148; P:GO:0019752; F:GO:0004058; P:GO:0007626	-	EC:4.1.1.25; EC:4.1.1.28	IPR002129; IPR010977; IPR015421; IPR015422; IPR015424; IPR021115; G3DSA:1.20.1340.10 (GENE3D), PTHR11999:SF11 (PANTHER)
Caenorhabditis briggsae	aromatic amino acid decarboxylase	8	F:GO:0030170; P:GO:0006519; F:GO:0004837; P:GO:0018991; P:GO:0048148; P:GO:0019752; F:GO:0004058; P:GO:0007626	-	EC:4.1.1.25; EC:4.1.1.28	IPR002129; IPR010977; IPR015421; IPR015422; IPR015424; IPR021115; G3DSA:1.20.1340.10 (GENE3D), PTHR11999:SF11 (PANTHER)
Caenorhabditis briggsae	aromatic amino acid decarboxylase	8	F:GO:0030170; P:GO:0006519; F:GO:0004837; P:GO:0018991; P:GO:0048148; P:GO:0019752; F:GO:0004058; P:GO:0007626	-	EC:4.1.1.25; EC:4.1.1.28	IPR002129; IPR010977; IPR015421; IPR015422; IPR015424; IPR021115; G3DSA:1.20.1340.10 (GENE3D), PTHR11999:SF11 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-ten-1 protein	2	C:GO:0016021; P:GO:0042051	-		IPR000742; IPR006210; IPR013032; IPR013111; G3DSA:2.10.25.10 (GENE3D), PTHR11219 (PANTHER), PTHR11219:SF4 (PANTHER), SSF57196 (SUPERFAMILY)
Brugia malayi	anion exchange protein	3	P:GO:0006811; F:GO:0015291; C:GO:0016020	-		IPR003020; IPR011531; IPR013769; IPR016152; G3DSA:1.10.287.570 (GENE3D), PTHR11453:SF9 (PANTHER)
	-	0				IPR002919; IPR013032; G3DSA:2.10.25.10 (GENE3D)
Caenorhabditis elegans	wd repeat domain 23	0		F:GO:0003674; P:GO:0008150; F:GO:0005515; C:GO:0080008; C:GO:0005575		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR19847 (PANTHER), PTHR19847:SF4 (PANTHER)
Caenorhabditis elegans	wd repeat domain 23	0		F:GO:0003674; P:GO:0008150; F:GO:0005515; C:GO:0080008; C:GO:0005575		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR19847 (PANTHER), PTHR19847:SF4 (PANTHER)
Caenorhabditis elegans	wd repeat domain 23	0		F:GO:0003674; P:GO:0008150; F:GO:0005515; C:GO:0080008; C:GO:0005575		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR19847 (PANTHER), PTHR19847:SF4 (PANTHER)
Caenorhabditis elegans	ran gtpase activating protein 1	2	C:GO:0043229; C:GO:0048471	-		G3DSA:3.80.10.10 (GENE3D), PTHR13824 (PANTHER), PTHR13824:SF8 (PANTHER), SSF52047 (SUPERFAMILY)
Brugia malayi	briggsae cbr-zyx-1 protein	1	F:GO:0005515	-		-

Caenorhabditis elegans	2-acylglycerol o-acyltransferase 1	4	P:GO:0006629; F:GO:0008415; C:GO:0016021; C:GO:0005783	-		IPR007130
Haemonchus contortus	heat shock protein family member (hsp-)	0		P:GO:0006950; P:GO:0009408		-
	-	0				-
Caenorhabditis elegans	abnormal cell migration family member (mig-10)	2	F:GO:0005515; P:GO:0007165	-		-
Caenorhabditis elegans	abnormal cell migration family member (mig-10)	2	F:GO:0005515; P:GO:0007165	-		-
Caenorhabditis briggsae	wd repeat-containing protein 3	2	F:GO:0003824; P:GO:0006898	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR22847 (PANTHER), PTHR22847:SF48 (PANTHER)
Caenorhabditis briggsae	wd repeat-containing protein 3	2	P:GO:0006898; F:GO:0003824	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR22847 (PANTHER)
Caenorhabditis briggsae	wd repeat-containing protein 3	2	P:GO:0006898; F:GO:0003824	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR22847 (PANTHER)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	7	P:GO:0009056; P:GO:0005975; F:GO:0043169; F:GO:0005515; P:GO:0008340; F:GO:0003796; P:GO:0043170	-	EC:3.2.1.17	IPR013781; IPR017853; PTHR23208 (PANTHER), PTHR23208:SF13 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	7	P:GO:0009056; P:GO:0005975; F:GO:0043169; F:GO:0005515; P:GO:0008340; F:GO:0003796; P:GO:0043170	-	EC:3.2.1.17	IPR013781; IPR017853; PTHR23208 (PANTHER), PTHR23208:SF13 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-lys-8 protein	3	P:GO:0008152; P:GO:0008340; F:GO:0005515	-		PTHR23208 (PANTHER), PTHR23208:SF13 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-lys-8 protein	3	P:GO:0008152; P:GO:0008340; F:GO:0005515	-		PTHR23208 (PANTHER), PTHR23208:SF13 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	7	P:GO:0009056; P:GO:0005975; F:GO:0043169; F:GO:0005515; P:GO:0008340; F:GO:0003796; P:GO:0043170	-	EC:3.2.1.17	IPR013781; IPR017853; PTHR23208 (PANTHER), PTHR23208:SF13 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	7	P:GO:0009056; P:GO:0005975; F:GO:0043169; F:GO:0005515; P:GO:0008340; F:GO:0003796; P:GO:0043170	-	EC:3.2.1.17	IPR013781; IPR017853; PTHR23208 (PANTHER), PTHR23208:SF13 (PANTHER)
	-	0				SignalP (SIGNALP)

Loa loa	presenilin spe-4	4	C:GO:0016020; P:GO:0016048; F:GO:0005515; P:GO:0007399	-		IPR001108; PTHR10202:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG21915 [Caenorhabditis briggsae]	0				-
Loa loa	viral a-type inclusion protein repeat containing protein	0				IPR019139
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	ain family member (clp-1)	5	C:GO:0016021; P:GO:0008219; C:GO:0005622; P:GO:0006508; F:GO:0004198	-		IPR000169; IPR001300; IPR022682; IPR022683; IPR022684; G3DSA:2.60.120.380 (GENE3D), G3DSA:3.90.70.10 (GENE3D), PTHR10183 (PANTHER), PTHR10183:SF45 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis elegans	ain family member (clp-1)	5	C:GO:0016021; P:GO:0008219; C:GO:0005622; P:GO:0006508; F:GO:0004198	-		IPR000169; IPR001300; IPR022682; IPR022683; IPR022684; G3DSA:2.60.120.380 (GENE3D), G3DSA:3.90.70.10 (GENE3D), PTHR10183 (PANTHER), PTHR10183:SF45 (PANTHER), SSF54001 (SUPERFAMILY)
Loa loa	cleavage and polyadenylation specificity factor subunit 2	0		F:GO:0003723; C:GO:0005737; P:GO:0006398; P:GO:0008380; F:GO:0016787; P:GO:0006397; F:GO:0005515; C:GO:0005634		IPR011108; PTHR11203 (PANTHER), PTHR11203:SF5 (PANTHER)
Caenorhabditis briggsae	heat shock 70kda protein 9	9	P:GO:0006457; P:GO:0006611; C:GO:0042645; C:GO:0009986; F:GO:0019899; P:GO:0006916; F:GO:0005524; F:GO:0051082; P:GO:0006950	-		IPR019651; SignalP (SIGNALP)
Caenorhabditis elegans	yo30_caeel ame: full=gilt-like protein flags: precursor	0		C:GO:0005576		IPR004911; PTHR13234:SF2 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-unc-68 protein	8	F:GO:0004872; P:GO:0006629; F:GO:0005219; P:GO:0006816; P:GO:0006874; P:GO:0055085; F:GO:0005509; C:GO:0016021	-		IPR003608; IPR013333; IPR014821; IPR015925; IPR016093; G3DSA:2.80.10.50 (GENE3D), PTHR13715:SF11 (PANTHER)

Caenorhabditis elegans	6-phosphofructo-2-ki-se fructose- -biphosphatase 1	19	P:GO:0006094; P:GO:0007243; F:GO:0004331; P:GO:0032868; P:GO:0046835; P:GO:0031100; P:GO:0033762; C:GO:0043540; P:GO:0051384; P:GO:0033133; P:GO:0006003; F:GO:0070095; P:GO:0006096; F:GO:0042802; F:GO:0003873; P:GO:0042594; P:GO:0051591; F:GO:0005524; F:GO:0019900	-	EC:3.1.3.46; EC:2.7.1.105	IPR003094; IPR013078; G3DSA:3.40.50.1240 (GENE3D), PTHR10606:SF11 (PANTHER), SSF53254 (SUPERFAMILY)
Caenorhabditis elegans	hydroxypyruvate isomerase	0		F:GO:0008903; F:GO:0016853		IPR012307; IPR013022; PTHR12110 (PANTHER)
	-	0				IPR000436
Caenorhabditis briggsae	briggsae cbr-ckr-1 protein	1	F:GO:0004871	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	transportin 1	12	P:GO:0040010; P:GO:0000060; P:GO:0000003; F:GO:0008139; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0006898; P:GO:0009792; C:GO:0044424; P:GO:0016246	-		IPR000357; IPR001494; IPR011989; IPR016024; IPR021133; PTHR10527 (PANTHER), PTHR10527:SF3 (PANTHER)
Caenorhabditis elegans	transportin 1	12	P:GO:0040010; P:GO:0000060; P:GO:0000003; F:GO:0008139; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0006898; P:GO:0009792; C:GO:0044424; P:GO:0016246	-		IPR000357; IPR001494; IPR011989; IPR016024; IPR021133; PTHR10527 (PANTHER), PTHR10527:SF3 (PANTHER)
Caenorhabditis elegans	deoxyribonuclease ii	3	P:GO:0006259; P:GO:0007275; F:GO:0004520	-		IPR004947; PTHR10858:SF1 (PANTHER), SignalP (SIGNALP)
Tribolium castaneum	anopheles stephensi	0				IPR000626; IPR019955; G3DSA:3.10.20.90 (GENE3D), SSF54236 (SUPERFAMILY)

Caenorhabditis briggsae	briggsae cbr-dcp-66 protein	7	P:GO:0040010; P:GO:0040027; P:GO:0040035; P:GO:0040026; P:GO:0040011; P:GO:0006898; P:GO:0002009	-		PTHR13455 (PANTHER), PTHR13455:SF1 (PANTHER)
Caenorhabditis elegans	briggsae cbr-imb-6 protein	0				-
Caenorhabditis elegans	briggsae cbr-imb-6 protein	0				-
Loa loa	ring finger ubc associated family member (rfp-1)	3	F:GO:0005515; P:GO:0006664; C:GO:0005634	-		PD936484 (PRODOM), PTHR23163 (PANTHER)
Loa loa	ring finger protein 20	1	F:GO:0046872	-		IPR001841; IPR013083; IPR017907; IPR018957; PTHR23163 (PANTHER), SSF57850 (SUPERFAMILY)
Loa loa	ring finger ubc associated family member (rfp-1)	3	F:GO:0005515; P:GO:0006664; C:GO:0005634	-		PD936484 (PRODOM), PTHR23163 (PANTHER)
Loa loa	ring finger protein 20	1	F:GO:0046872	-		-
	-	0				-
Caenorhabditis elegans	malate synthase a	2	P:GO:0006099; F:GO:0004474	-	EC:2.3.3.9	IPR001465; IPR006252; IPR011076; G3DSA:1.20.1220.12 (GENE3D), G3DSA:3.20.20.360 (GENE3D), PTHR21631 (PANTHER)
Caenorhabditis elegans	isocitrate lyase	4	F:GO:0004451; P:GO:0019752; P:GO:0055114; F:GO:0051864	-	EC:4.1.3.1; EC:1.14.11.27	IPR000918; IPR001465; IPR006252; IPR006254; IPR011076; IPR015813; IPR018523; G3DSA:1.20.1220.12 (GENE3D), G3DSA:3.20.20.360 (GENE3D), PTHR21631 (PANTHER)
Caenorhabditis elegans	camp-regulated phosphoprotein 19	0		C:GO:0005737		IPR006760
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-itsn-1 protein	10	P:GO:0045746; F:GO:0005515; P:GO:0051124; C:GO:0042734; C:GO:0045179; P:GO:0008104; P:GO:0045860; P:GO:0002052; C:GO:0005886; P:GO:0048488	-		IPR000108; IPR001452; G3DSA:2.30.30.40 (GENE3D), PTHR11216 (PANTHER), PTHR11216:SF24 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-itsn-1 protein	10	P:GO:0045746; F:GO:0005515; P:GO:0051124; C:GO:0042734; C:GO:0045179; P:GO:0008104; P:GO:0045860; P:GO:0002052; C:GO:0005886; P:GO:0048488	-		IPR000108; IPR001452; G3DSA:2.30.30.40 (GENE3D), PTHR11216 (PANTHER), PTHR11216:SF24 (PANTHER)

Caenorhabditis elegans	intersectin 1 (sh3 domain protein)	13	C:GO:0005829; F:GO:0005509; P:GO:0007264; F:GO:0005085; C:GO:0030139; P:GO:0051897; F:GO:0005515; P:GO:0008624; C:GO:0030027; P:GO:0048488; P:GO:0043524; C:GO:0005886; F:GO:0019209	-		IPR001452; G3DSA:2.30.30.40 (GENE3D), PTHR11216 (PANTHER), PTHR11216:SF24 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-itsn-1 protein	10	P:GO:0045746; F:GO:0005515; P:GO:0051124; C:GO:0042734; C:GO:0045179; P:GO:0008104; P:GO:0045860; P:GO:0002052; C:GO:0005886; P:GO:0048488	-		IPR000108; IPR001452; G3DSA:2.30.30.40 (GENE3D), PTHR11216 (PANTHER), PTHR11216:SF24 (PANTHER)
Caenorhabditis elegans	membrane palmitoylated 5 (maguk p55 subfamily member 5)	18	C:GO:0043296; P:GO:0008078; P:GO:0045176; P:GO:0040010; P:GO:0016337; P:GO:0007420; P:GO:0001841; P:GO:0002011; P:GO:0060059; P:GO:0045199; P:GO:0016332; P:GO:0035050; F:GO:0005515; C:GO:0001917; C:GO:0031226; P:GO:0055008; C:GO:0005737; C:GO:0005634	-		IPR008144; IPR008145; IPR020590; G3DSA:3.30.63.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23122 (PANTHER), PTHR23122:SF5 (PANTHER), SSF52540 (SUPERFAMILY)
Homo sapiens	wd repeat-containing protein 5	5	C:GO:0071339; F:GO:0042800; F:GO:0035064; P:GO:0045449; P:GO:0051568	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR22847 (PANTHER), PTHR22847:SF48 (PANTHER)
Caenorhabditis elegans	rr--processing protein fcf1 homolog	3	P:GO:0040010; P:GO:0006898; P:GO:0002119	-		IPR006596; IPR006984; G3DSA:3.40.50.1010 (GENE3D), SSF88723 (SUPERFAMILY)
Caenorhabditis elegans	ectonucleotide pyrophosphatase phosphodiesterase 4 (function)	1	F:GO:0003824	-		IPR002591; IPR017849; IPR017850; PTHR10151 (PANTHER), PTHR10151:SF11 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	ectonucleotide pyrophosphatase phosphodiesterase 4	1	F:GO:0003824	-		IPR002591; IPR017849; IPR017850; PTHR10151 (PANTHER), PTHR10151:SF11 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	ectonucleotide pyrophosphatase phosphodiesterase 4	1	F:GO:0003824	-		-

Loa loa	kh domain containing protein	1	P:GO:0009987	-		IPR004087; IPR004088; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR11208 (PANTHER), PTHR11208:SF8 (PANTHER), SSF54791 (SUPERFAMILY)
Loa loa	kh domain containing protein	1	P:GO:0009987	-		IPR004087; IPR004088; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR11208 (PANTHER), PTHR11208:SF8 (PANTHER), SSF54791 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	cleavage and polyadenylation specificity factor subunit 6	3	F:GO:0003676; F:GO:0000166; F:GO:0005515	-		-
Caenorhabditis elegans	cleavage and polyadenylation specificity factor subunit 6	3	F:GO:0003676; F:GO:0000166; F:GO:0005515	-		-
Oscheius sp. (strain CEW1)	vitellogenin structural genes (yolk protein genes) family member (vit-6)	6	P:GO:0009792; F:GO:0005515; P:GO:0006810; P:GO:0040010; P:GO:0033036; P:GO:0008340	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	complement component 6	0		P:GO:0045766; P:GO:0043065; P:GO:0045917; P:GO:0006919; P:GO:0006917; F:GO:0003674; C:GO:0005579; P:GO:0019835; C:GO:0005576; F:GO:0005515; P:GO:0001701; P:GO:0001970; P:GO:0045087; P:GO:0006958; P:GO:0006956; C:GO:0005615		IPR000436; IPR016060; SignalP (SIGNALP)
Homo sapiens	complement component 6	0		P:GO:0045766; P:GO:0043065; P:GO:0045917; P:GO:0006919; P:GO:0006917; F:GO:0003674; C:GO:0005579; P:GO:0019835; C:GO:0005576; F:GO:0005515; P:GO:0001701; P:GO:0001970; P:GO:0045087; P:GO:0006958; P:GO:0006956; C:GO:0005615		IPR000436; IPR016060; SignalP (SIGNALP)

Caenorhabditis briggsae	r--specific adenosine deami-se b1	5	F:GO:0005515; F:GO:0004000; P:GO:0000003; P:GO:0016071; C:GO:0031981	-	EC:3.5.4.4	IPR002466; PTHR10910 (PANTHER), PTHR10910:SF15 (PANTHER)
Brugia malayi	40s ribosomal protein s19s	8	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; P:GO:0018996; P:GO:0000003; P:GO:0040007; P:GO:0006412	-	EC:3.6.5.3	IPR001266; IPR018277; SSF46785 (SUPERFAMILY)
Caenorhabditis briggsae	proteasome subunit alpha type 6	13	P:GO:0006511; P:GO:0008340; P:GO:0000003; F:GO:0004298; P:GO:0018996; P:GO:0002119; F:GO:0005515; P:GO:0040011; C:GO:0019773; P:GO:0009792; C:GO:0005737; P:GO:0040015; C:GO:0005634	-	EC:3.4.25.0	IPR001353; G3DSA:3.60.20.10 (GENE3D), PTHR11599 (PANTHER), PTHR11599:SF11 (PANTHER), PS51475 (PROFILE), SSF56235 (SUPERFAMILY)
Caenorhabditis briggsae	proteasome subunit alpha type 6	13	P:GO:0006511; P:GO:0008340; P:GO:0000003; F:GO:0004298; P:GO:0018996; P:GO:0002119; F:GO:0005515; P:GO:0040011; C:GO:0019773; P:GO:0009792; C:GO:0005737; P:GO:0040015; C:GO:0005634	-	EC:3.4.25.0	IPR001353; G3DSA:3.60.20.10 (GENE3D), PTHR11599 (PANTHER), PTHR11599:SF11 (PANTHER), PS51475 (PROFILE), SSF56235 (SUPERFAMILY)
Caenorhabditis briggsae	proteasome subunit alpha type 6	13	P:GO:0006511; P:GO:0008340; P:GO:0000003; F:GO:0004298; P:GO:0018996; P:GO:0002119; F:GO:0005515; P:GO:0040011; C:GO:0019773; P:GO:0009792; C:GO:0005737; P:GO:0040015; C:GO:0005634	-	EC:3.4.25.0	IPR001353; G3DSA:3.60.20.10 (GENE3D), PTHR11599 (PANTHER), PTHR11599:SF11 (PANTHER), PS51475 (PROFILE), SSF56235 (SUPERFAMILY)
Brugia malayi	brain tumor protein	3	F:GO:0008270; C:GO:0005622; F:GO:0005515	-		IPR000315; IPR001841; IPR013083; IPR017907; IPR018957; PTHR13712 (PANTHER), PTHR13712:SF6 (PANTHER), SSF57850 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)

Brugia malayi	zinc c2h2 type family protein	0		F:GO:0003676; P:GO:0030536; P:GO:0046580; P:GO:0006099; F:GO:0008270; P:GO:0046672; C:GO:0005634; C:GO:0005622		IPR007087
	-	0				-
	-	0				-
Caenorhabditis briggsae	methionine aminopeptidase	5	P:GO:0009987; P:GO:0006508; F:GO:0008270; F:GO:0008235; F:GO:0004177	-	EC:3.4.11.0	IPR000994; IPR001714; IPR002467
	-	0				-
Caenorhabditis briggsae	briggsae cbr-asp-2 protein	0		P:GO:0006508; F:GO:0004190; F:GO:0016787; F:GO:0008233		IPR001461; IPR009007; IPR021109; PTHR13683:SF53 (PANTHER)
	-	0				
Caenorhabditis briggsae	aspartic protease 2b	0		P:GO:0006508; F:GO:0004190; F:GO:0016787; F:GO:0008233		IPR001461; IPR009007; IPR021109; PTHR13683:SF53 (PANTHER)
Caenorhabditis elegans	aspartyl protease family member (asp-2)	5	P:GO:0008219; P:GO:0006508; F:GO:0004190; F:GO:0005515; P:GO:0040011	-	EC:3.4.23.0	IPR001461; IPR001969; IPR009007; IPR021109; PTHR13683:SF53 (PANTHER)
Loa loa	hypothetical protein LOAG_07630 [Loa loa]	0				
Caenorhabditis elegans	aspartyl protease family member (asp-2)	5	P:GO:0008219; P:GO:0006508; F:GO:0004190; F:GO:0005515; P:GO:0040011	-	EC:3.4.23.0	IPR001461; IPR001969; IPR009007; IPR021109; PTHR13683:SF53 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	8	C:GO:0005737; C:GO:0005730; C:GO:0008287; F:GO:0004722; F:GO:0005515; P:GO:0006470; P:GO:0040011; P:GO:0019915	-		IPR004843; IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF19 (PANTHER), SSF56300 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	8	C:GO:0005737; C:GO:0005730; C:GO:0008287; F:GO:0004722; F:GO:0005515; P:GO:0006470; P:GO:0040011; P:GO:0019915	-		IPR004843; IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF19 (PANTHER), SSF56300 (SUPERFAMILY)

Caenorhabditis briggsae	cdc5 cell division cycle 5-like	13	P:GO:0016070; P:GO:0000910; F:GO:0003676; C:GO:0031981; P:GO:0040007; P:GO:0045449; P:GO:0000003; P:GO:0018996; P:GO:0002119; F:GO:0005515; P:GO:0009792; P:GO:0001703; P:GO:0006974	-		IPR015495; IPR021786; PTHR10641:SF17 (PANTHER)
Homo sapiens	ubiquitin d	16	F:GO:0070628; P:GO:0010243; F:GO:0004930; C:GO:0016021; C:GO:0016235; C:GO:0005737; P:GO:0006511; P:GO:0043123; P:GO:0035417; P:GO:0034612; P:GO:0016567; P:GO:0034341; P:GO:0070842; C:GO:0005634; P:GO:0043011; P:GO:0043065	-		IPR000626; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), PTHR10666:SF5 (PANTHER), SSF54236 (SUPERFAMILY)
Caenorhabditis briggsae	transmembrane amino acid transporter protein	5	P:GO:0019915; C:GO:0016021; P:GO:0040010; F:GO:0008270; P:GO:0040011	-		IPR013057; PTHR22950 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	protein sidekick	3	P:GO:0030154; P:GO:0048731; C:GO:0016021	-		IPR003961; IPR008957; IPR013783; PR00014 (PRINTS), PTHR10489 (PANTHER)
Caenorhabditis elegans	phospholipase beta 4	10	C:GO:0005829; F:GO:0004629; C:GO:0030425; C:GO:0005792; P:GO:0043267; P:GO:0007165; F:GO:0051019; C:GO:0014069; C:GO:0005634; C:GO:0005790	-		IPR000008; IPR000909; IPR001192; IPR001711; IPR008973; IPR009535; IPR014815; IPR017946; IPR018029; G3DSA:1.20.1230.10 (GENE3D), G3DSA:2.60.40.150 (GENE3D), PTHR10336 (PANTHER), PTHR10336:SF8 (PANTHER)
Caenorhabditis elegans	phospholipase beta 4	10	C:GO:0005829; F:GO:0004629; C:GO:0030425; C:GO:0005792; P:GO:0043267; P:GO:0007165; F:GO:0051019; C:GO:0014069; C:GO:0005634; C:GO:0005790	-		IPR000008; IPR000909; IPR001192; IPR001711; IPR008973; IPR009535; IPR014815; IPR017946; IPR018029; G3DSA:1.20.1230.10 (GENE3D), G3DSA:2.60.40.150 (GENE3D), PTHR10336 (PANTHER), PTHR10336:SF8 (PANTHER)

Caenorhabditis elegans	phospholipase beta 4	10	C:GO:0005829; F:GO:0004629; C:GO:0030425; C:GO:0005792; P:GO:0043267; P:GO:0007165; F:GO:0051019; C:GO:0014069; C:GO:0005634; C:GO:0005790	-		IPR000008; IPR000909; IPR001192; IPR001711; IPR008973; IPR009535; IPR014815; IPR017946; IPR018029; G3DSA:1.20.1230.10 (GENE3D), G3DSA:2.60.40.150 (GENE3D), PTHR10336 (PANTHER), PTHR10336:SF8 (PANTHER)
Loa loa	r- polymerase ii subunit a c-termi-l domain phosphatase ssu72	3	F:GO:0004721; P:GO:0006397; C:GO:0005634	-	EC:3.1.3.16	IPR006811; PTHR20383:SF3 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-pad-1 protein	1	P:GO:0006810	-		-
Caenorhabditis elegans	pyrroline-5-carboxylate reductase 1	6	F:GO:0005488; F:GO:0004735; P:GO:0034599; P:GO:0055114; P:GO:0006561; C:GO:0005739	-	EC:1.5.1.2	IPR000304; IPR004455; IPR008927; IPR016040; SSF51735 (SUPERFAMILY)
	succi-te dehydroge-se	13	P:GO:0006810; C:GO:0005875; F:GO:0048039; F:GO:0051537; C:GO:0005749; F:GO:0046872; F:GO:0009055; P:GO:0006099; F:GO:0051539; F:GO:0051538; F:GO:0005515; P:GO:0006121; F:GO:0008177	-	EC:1.3.5.1	-
Caenorhabditis briggsae	mitotic spindle assembly checkpoint protein mad2a	9	P:GO:0007094; P:GO:0051436; C:GO:0005829; C:GO:0005643; C:GO:0000776; C:GO:0005816; C:GO:0048471; P:GO:0031145; F:GO:0042803	-		-
Caenorhabditis briggsae	n-acetylated alpha-linked acidic dipeptidase 2-like	3	C:GO:0016020; P:GO:0006508; F:GO:0004181	-	EC:3.4.17.0	IPR007484; G3DSA:3.40.630.10 (GENE3D), G3DSA:3.50.30.30 (GENE3D), PTHR10404 (PANTHER), PTHR10404:SF15 (PANTHER), SSF53187 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Loa loa	briggsae cbr-acy-4 protein	3	P:GO:0009190; F:GO:0000166; F:GO:0016849	-		PTHR11920 (PANTHER), PTHR11920:SF14 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-abf-2 protein	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-abf-2 protein	0				-
Caenorhabditis briggsae	briggsae cbr-abf-2 protein	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-abf-2 protein	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-abf-2 protein	0				SignalP (SIGNALP)

Caenorhabditis elegans	ank repeat and lem domain-containing protein kiaa0692	0		F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150; C:GO:0005635; C:GO:0005575		IPR002110; IPR020683; PTHR20976 (PANTHER)
Caenorhabditis briggsae	prion-like-(q n-rich)-domain-bearing protein family member (pqn-44)	0				IPR012937; PTHR12974 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG09307 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	malic enzyme -dp(+)- mitochondrial	6	F:GO:0046872; F:GO:0051287; C:GO:0005759; F:GO:0016619; P:GO:0006108; P:GO:0055114	-	EC:1.1.1.38	IPR001891; IPR012301; IPR012302; IPR015884; IPR016040; G3DSA:3.40.50.10380 (GENE3D), PTHR23406 (PANTHER), PTHR23406:SF2 (PANTHER), SSF51735 (SUPERFAMILY), SSF53223 (SUPERFAMILY)
Caenorhabditis briggsae	elongator complex protein 3	8	F:GO:0051536; P:GO:0006357; F:GO:0046872; F:GO:0008607; C:GO:0008023; P:GO:0007409; F:GO:0004402; C:GO:0005737	-	EC:2.3.1.48	IPR000182; IPR006638; IPR007197; IPR016181; G3DSA:3.80.30.20 (GENE3D), PTHR11135 (PANTHER), SSF102114 (SUPERFAMILY)
Caenorhabditis briggsae	coatomer protein subunit beta 2 (beta prime)	13	F:GO:0005080; C:GO:0030126; C:GO:0005829; P:GO:0006890; P:GO:0048599; P:GO:0032940; P:GO:0006891; P:GO:0002119; P:GO:0048205; P:GO:0006898; P:GO:0006886; F:GO:0005198; P:GO:0009792	-		IPR006692; PTHR19876 (PANTHER), PTHR19876:SF2 (PANTHER)
Caenorhabditis briggsae	coatomer protein subunit beta 2 (beta prime)	13	F:GO:0005080; C:GO:0030126; C:GO:0005829; P:GO:0006890; P:GO:0048599; P:GO:0032940; P:GO:0006891; P:GO:0002119; P:GO:0048205; P:GO:0006898; P:GO:0006886; F:GO:0005198; P:GO:0009792	-		IPR006692; PTHR19876 (PANTHER), PTHR19876:SF2 (PANTHER)
Caenorhabditis elegans	briggsae cbr-wrm-1 protein	5	P:GO:0050789; F:GO:0005515; P:GO:0007275; C:GO:0044424; P:GO:0006350	-		IPR011989; IPR016024; PTHR23315 (PANTHER), PTHR23315:SF2 (PANTHER)
	-	0				-

Caenorhabditis elegans	cyclin dependent ki-se 4	14	P:GO:0006468; P:GO:0000080; P:GO:0040011; C:GO:0044464; P:GO:0002009; P:GO:0007067; F:GO:0004674; P:GO:0007126; P:GO:0002119; P:GO:0048869; P:GO:0050794; P:GO:0010171; F:GO:0005524; P:GO:0040035	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF82 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein C49H3.4 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	sm protein	0				IPR001163; IPR006649; IPR010920; G3DSA:2.30.30.100 (GENE3D)
	-	0				-
Caenorhabditis briggsae	mitochondrial dicarboxylate carrier	16	P:GO:0055085; P:GO:0015743; F:GO:0015141; P:GO:0015709; F:GO:0015116; F:GO:0015140; P:GO:0015744; C:GO:0016021; C:GO:0005743; P:GO:0008272; F:GO:0015117; F:GO:0005515; P:GO:0006094; F:GO:0015297; P:GO:0006817; F:GO:0015114	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF29 (PANTHER)
Brugia malayi	kh domain containing protein	3	P:GO:0009987; P:GO:0007275; P:GO:0061061	-		PTHR10603 (PANTHER)
Loa loa	amop domain containing protein	0		P:GO:0007160; C:GO:0016021		IPR000436; PTHR13802 (PANTHER), PTHR13802:SF2 (PANTHER)
Loa loa	amop domain containing protein	0		P:GO:0007160; C:GO:0016021		IPR000436; PTHR13802 (PANTHER), PTHR13802:SF2 (PANTHER)
Caenorhabditis elegans	peptidylglycine alpha-amidating monooxyge-se	4	F:GO:0046914; F:GO:0004497; P:GO:0044237; C:GO:0016020	-		IPR001258; IPR011042; IPR013017; PTHR10680 (PANTHER), SSF63829 (SUPERFAMILY)
Caenorhabditis elegans	peptidylglycine alpha-amidating monooxyge-se	4	F:GO:0046914; F:GO:0004497; P:GO:0044237; C:GO:0016020	-		IPR001258; IPR011042; IPR013017; PTHR10680 (PANTHER), SSF63829 (SUPERFAMILY)
Caenorhabditis elegans	peptidylglycine alpha-amidating monooxyge-se	4	F:GO:0046914; F:GO:0004497; P:GO:0044237; C:GO:0016020	-		IPR001258; IPR011042; IPR013017; PTHR10680 (PANTHER), SSF63829 (SUPERFAMILY)
Caenorhabditis elegans	gtpase activating protein family member (gap-3)	0		P:GO:0007165; F:GO:0005515; C:GO:0005622		IPR008936; G3DSA:1.10.494.10 (GENE3D)

Caenorhabditis briggsae	gtpase activating protein family member (gap-3)	0		P:GO:0007165; F:GO:0005515; C:GO:0005622		-
Caenorhabditis briggsae	speckle-type poz	1	F:GO:0005515	-		-
Loa loa	calcyclin binding protein	11	C:GO:0005641; C:GO:0043005; C:GO:0005625; P:GO:0045740; C:GO:0044297; P:GO:0055007; P:GO:0060416; P:GO:0007568; P:GO:0071277; C:GO:0005737; P:GO:0060548	-		SignalP (SIGNALP)
Caenorhabditis elegans	isoform a	0		F:GO:0003674; P:GO:0008150; C:GO:0005575		IPR018908; SignalP (SIGNALP)
Loa loa	otu domain containing 5	1	F:GO:0016787	-		IPR003323; IPR003903; PTHR12419 (PANTHER), SSF54001 (SUPERFAMILY)
Loa loa	otu domain containing 5	1	F:GO:0016787	-		IPR003323; PTHR12419 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis briggsae	coatomer protein subunit beta 2 (beta prime)	13	F:GO:0005080; C:GO:0030126; P:GO:0006890; P:GO:0048599; P:GO:0032940; P:GO:0006891; F:GO:0016905; P:GO:0002119; P:GO:0006898; P:GO:0030903; P:GO:0006886; F:GO:0005198; P:GO:0009792	-	EC:2.7.11.7	IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; IPR020472; PTHR19876 (PANTHER), PTHR19876:SF2 (PANTHER)
Caenorhabditis briggsae	coatomer protein subunit beta 2 (beta prime)	13	F:GO:0005080; C:GO:0030126; P:GO:0006890; P:GO:0048599; P:GO:0032940; P:GO:0006891; F:GO:0016905; P:GO:0002119; P:GO:0006898; P:GO:0030903; P:GO:0006886; F:GO:0005198; P:GO:0009792	-	EC:2.7.11.7	IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; IPR020472; PTHR19876 (PANTHER), PTHR19876:SF2 (PANTHER)

Caenorhabditis briggsae	coatomer protein subunit beta 2 (beta prime)	13	F:GO:0005080; C:GO:0030126; P:GO:0006890; P:GO:0048599; P:GO:0032940; P:GO:0006891; F:GO:0016905; P:GO:0002119; P:GO:0006898; P:GO:0030903; P:GO:0006886; F:GO:0005198; P:GO:0009792	-	EC:2.7.11.7	IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; IPR020472; PTHR19876 (PANTHER), PTHR19876:SF2 (PANTHER)
Caenorhabditis elegans	chromosome segregation protein smc	0		C:GO:0005694; F:GO:0005524; P:GO:0051276; F:GO:0005515		-
Angiostrongylus cantonensis	nematode cuticle collagen n-termi-l domain containing protein	1	F:GO:0042302	-		IPR002486; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	C:GO:0043231; C:GO:0044444	-		-
	-	0				-
Sus scrofa	60s acidic ribosomal protein p1	5	F:GO:0003735; F:GO:0003723; F:GO:0005515; C:GO:0022625; P:GO:0006414	-		IPR001813; IPR001859; PTHR21141 (PANTHER), PTHR21141:SF6 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Haemonchus contortus	peroxiredoxin 1 variant 2	13	P:GO:0032872; P:GO:0042744; F:GO:0005515; P:GO:0034101; P:GO:0042267; P:GO:0008283; P:GO:0019430; F:GO:0008379; P:GO:0045454; P:GO:0042345; P:GO:0055114; C:GO:0005634; C:GO:0005739	-		IPR000866; IPR012335; IPR012336; IPR017936; IPR019479; G3DSA:3.30.1020.10 (GENE3D), PTHR10681 (PANTHER), PTHR10681:SF8 (PANTHER)

Haemonchus contortus	peroxiredoxin 1 variant 2	13	P:GO:0032872; P:GO:0042744; F:GO:0005515; P:GO:0034101; P:GO:0042267; P:GO:0008283; P:GO:0019430; F:GO:0008379; P:GO:0045454; P:GO:0042345; P:GO:0055114; C:GO:0005634; C:GO:0005739	-		IPR000866; IPR012335; IPR012336; IPR017936; IPR019479; G3DSA:3.30.1020.10 (GENE3D), PTHR10681 (PANTHER), PTHR10681:SF8 (PANTHER)
Haemonchus contortus	peroxiredoxin 1 variant 2	13	P:GO:0032872; P:GO:0042744; F:GO:0005515; P:GO:0034101; P:GO:0042267; P:GO:0008283; P:GO:0019430; F:GO:0008379; P:GO:0045454; P:GO:0042345; P:GO:0055114; C:GO:0005634; C:GO:0005739	-		IPR000866; IPR012335; IPR012336; IPR017936; IPR019479; PTHR10681 (PANTHER), PTHR10681:SF8 (PANTHER)
Haemonchus contortus	peroxiredoxin 1 variant 2	13	P:GO:0032872; P:GO:0042744; F:GO:0005515; P:GO:0034101; P:GO:0042267; P:GO:0008283; P:GO:0019430; F:GO:0008379; P:GO:0045454; P:GO:0042345; P:GO:0055114; C:GO:0005634; C:GO:0005739	-		IPR000866; IPR012335; IPR012336; IPR017936; IPR019479; PTHR10681 (PANTHER), PTHR10681:SF8 (PANTHER)
Haemonchus contortus	peroxiredoxin 1 variant 2	13	P:GO:0032872; P:GO:0042744; F:GO:0005515; P:GO:0034101; P:GO:0042267; P:GO:0008283; P:GO:0019430; F:GO:0008379; P:GO:0045454; P:GO:0042345; P:GO:0055114; C:GO:0005634; C:GO:0005739	-		IPR000866; IPR012335; IPR012336; IPR017936; IPR019479; G3DSA:3.30.1020.10 (GENE3D), PTHR10681 (PANTHER), PTHR10681:SF8 (PANTHER)

Haemonchus contortus	peroxiredoxin 1 variant 2	13	P:GO:0032872; P:GO:0042744; F:GO:0005515; P:GO:0034101; P:GO:0042267; P:GO:0008283; P:GO:0019430; F:GO:0008379; P:GO:0045454; P:GO:0042345; P:GO:0055114; C:GO:0005634; C:GO:0005739	-		IPR000866; IPR012335; IPR012336; IPR017936; IPR019479; G3DSA:3.30.1020.10 (GENE3D), PTHR10681 (PANTHER), PTHR10681:SF8 (PANTHER)
Strongylocentrotus purpuratus	mucin 68d	0		F:GO:0008061; P:GO:0006030; C:GO:0005576		-
Caenorhabditis briggsae	fatty acid synthase-like	15	F:GO:0008144; F:GO:0004312; P:GO:0006633; C:GO:0043231; F:GO:0016788; F:GO:0008270; F:GO:0016829; C:GO:0005625; P:GO:0055114; P:GO:0006084; F:GO:0000036; F:GO:0016491; C:GO:0044444; F:GO:0070402; F:GO:0042803	-	EC:2.3.1.85	IPR000794; IPR011032; IPR013149; IPR016040; IPR020843; PTHR11712:SF5 (PANTHER), SSF51735 (SUPERFAMILY), SSF53335 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	8	P:GO:0018996; P:GO:0009792; P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		PTHR19143 (PANTHER), PTHR19143:SF3 (PANTHER)
Haemonchus contortus	aspartyl protease family member (asp-2)	2	P:GO:0008219; F:GO:0005515	-		IPR001461; IPR001969; IPR009007; IPR012848; IPR021109; PTHR13683:SF53 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	cog2 protein	9	P:GO:0040010; P:GO:0040035; P:GO:0030334; P:GO:0002119; F:GO:0005515; P:GO:0040039; P:GO:0048477; P:GO:0009792; P:GO:0035262	-		IPR009316; PF12022 (PFAM), SignalP (SIGNALP)

Caenorhabditis elegans	cog2 protein	9	P:GO:0040035; P:GO:0009792; P:GO:0030334; P:GO:0002119; F:GO:0005515; P:GO:0040010; P:GO:0035262; P:GO:0040039; P:GO:0048477	-		IPR009316; PF12022 (PFAM)
Caenorhabditis elegans	component of oligomeric golgi complex 2	10	P:GO:0040010; P:GO:0040035; P:GO:0030334; P:GO:0002119; F:GO:0005515; P:GO:0040039; P:GO:0048477; C:GO:0044464; P:GO:0009792; P:GO:0035262	-		IPR009316; PF12022 (PFAM), SignalP (SIGNALP)
Caenorhabditis elegans	component of oligomeric golgi complex 2	10	P:GO:0040010; P:GO:0040035; P:GO:0030334; P:GO:0002119; F:GO:0005515; P:GO:0040039; P:GO:0048477; C:GO:0044464; P:GO:0009792; P:GO:0035262	-		IPR009316; PF12022 (PFAM), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0016539		IPR001534
Caenorhabditis elegans	translation elongation factor g	10	F:GO:0003746; P:GO:0040010; P:GO:0070125; C:GO:0005739; P:GO:0000003; P:GO:0002119; F:GO:0003924; P:GO:0006898; P:GO:0009792; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000640; IPR005517; IPR009022; IPR014721; IPR020568; PTHR23115 (PANTHER), PTHR23115:SF4 (PANTHER)
Caenorhabditis elegans	translation elongation factor g	10	F:GO:0003746; P:GO:0040010; P:GO:0070125; C:GO:0005739; P:GO:0000003; P:GO:0002119; F:GO:0003924; P:GO:0006898; P:GO:0009792; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000640; IPR005517; IPR009022; IPR014721; IPR020568; PTHR23115 (PANTHER), PTHR23115:SF4 (PANTHER)

Caenorhabditis elegans	uncoordi-ted family member (unc-89)	0		F:GO:0005200; P:GO:0006468; P:GO:0001701; C:GO:0030018; C:GO:0030017; C:GO:0030016; F:GO:0005524; P:GO:0007512; F:GO:0004674; C:GO:0031430; F:GO:0004672; P:GO:0003007; F:GO:0000166; P:GO:0043056; P:GO:0045214; C:GO:0031674; C:GO:0031672; F:GO:0008307; F:GO:0005515; P:GO:0055003; P:GO:0006936; P:GO:0055002		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Brugia malayi	tia-1 homologue	9	P:GO:0002009; F:GO:0003676; P:GO:0009792; P:GO:0000003; P:GO:0040007; P:GO:0010171; F:GO:0000166; P:GO:0002119; P:GO:0040011	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF66 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	tia-1 homologue	9	P:GO:0002009; F:GO:0003676; P:GO:0009792; P:GO:0000003; P:GO:0040007; P:GO:0010171; F:GO:0000166; P:GO:0002119; P:GO:0040011	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF66 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	-dh oxidase	4	P:GO:0008152; F:GO:0016491; P:GO:0043581; F:GO:0010181	-		IPR001155; IPR013785; PTHR22893 (PANTHER), PTHR22893:SF6 (PANTHER), SSF51395 (SUPERFAMILY)

Angiostrongylus cantonensis	polymerase ii (d- directed) polypeptide h	16	F:GO:0003899; P:GO:0040010; F:GO:0008270; F:GO:0004672; P:GO:0006367; C:GO:0005730; P:GO:0040035; P:GO:0008380; C:GO:0005665; P:GO:0002119; F:GO:0005515; P:GO:0006368; P:GO:0040039; P:GO:0006898; P:GO:0009792; P:GO:0040018	-	EC:2.7.7.6	-
Caenorhabditis elegans	ras-related protein rab-2a	14	C:GO:0005625; P:GO:0007264; C:GO:0000139; F:GO:0004767; C:GO:0005624; F:GO:0019003; C:GO:0042470; C:GO:0033116; P:GO:0006888; C:GO:0043025; F:GO:0003924; P:GO:0006886; C:GO:0005789; F:GO:0005525	-	EC:3.1.4.12; EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001806; IPR002078; IPR003579; IPR005225; IPR013753; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF246 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	6	P:GO:0040035; P:GO:0002119; F:GO:0005515; P:GO:0040002; P:GO:0040010; P:GO:0006898	-		-
Loa loa	hypothetical protein LOAG_03184 [Loa loa]	0				-
Brugia malayi	hypothetical protein Bm1_17075 [Brugia malayi]	0				-
Loa loa	hypothetical protein LOAG_03184 [Loa loa]	0				-
Loa loa	hypothetical protein LOAG_03184 [Loa loa]	0				-
Loa loa	hypothetical protein LOAG_03184 [Loa loa]	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0016311; F:GO:0016791; F:GO:0008138; F:GO:0004725; P:GO:0008340		-
Loa loa	kiaa1370 protein	0				PTHR13199 (PANTHER)
Culex quinquefasciatus	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		IPR002919; IPR013032; G3DSA:2.10.25.10 (GENE3D), PTHR23259 (PANTHER), SignalP (SIGNALP)
Culex quinquefasciatus	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		IPR002919; IPR013032; G3DSA:2.10.25.10 (GENE3D), PTHR23259 (PANTHER), SignalP (SIGNALP)

Caenorhabditis elegans	germi-l center ki-se family member (gck-1)	5	F:GO:0042802; P:GO:0006468; P:GO:0007015; F:GO:0004702; F:GO:0005524	-		IPR000719; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF95 (PANTHER)
Caenorhabditis briggsae	cell cycle control protein cwf19	0		F:GO:0003824		-
	-	0				-
	-	0				-
Brugia malayi	arid bright d- binding domain-containing protein	0		C:GO:0005622		IPR016197; G3DSA:2.30.30.270 (GENE3D), PF11717 (PFAM)
Brugia malayi	arid bright d- binding domain-containing protein	0				-
Caenorhabditis elegans	calmodulin regulated spectrin-associated protein 1	0		F:GO:0003674; P:GO:0008150; F:GO:0005515; C:GO:0005874; C:GO:0005575		IPR001715; IPR022613; PTHR21595 (PANTHER)
Ancylostoma caninum	activation-associated secreted protein-1	1	P:GO:0051179	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0016740; P:GO:0008152; C:GO:0005615; F:GO:0005515; C:GO:0005576		-
Caenorhabditis briggsae	glycogen debranching enzyme	6	P:GO:0009792; F:GO:0004135; P:GO:0005978; F:GO:0043169; F:GO:0004134; P:GO:0006508	-	EC:3.2.1.33; EC:2.4.1.25	IPR008928; IPR010401
Hydra magnipapillata	pygopus homolog 1	0		F:GO:0046872; P:GO:0001822; P:GO:0016055; F:GO:0008270; P:GO:0009791; F:GO:0005515; C:GO:0005634		IPR001965; IPR011011; IPR013083; IPR019786; IPR019787; PTHR23194 (PANTHER), PTHR23194:SF6 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-lin-13 protein	0		P:GO:0001702; C:GO:0005634; F:GO:0003677; P:GO:0040027; F:GO:0003676; F:GO:0003674; F:GO:0046872; P:GO:0006355; F:GO:0003700; P:GO:0007275; P:GO:0008150; P:GO:0045449; P:GO:0007398; P:GO:0045893; F:GO:0008270; P:GO:0045786; C:GO:0005622; F:GO:0005515		IPR007087; IPR015880; PTHR23224 (PANTHER), PTHR23224:SF459 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis briggsae	pyruvate dehydroge-se component x	1	F:GO:0016747	-	EC:2.3.1.0	IPR001078; G3DSA:3.30.559.10 (GENE3D), PTHR23151 (PANTHER), PTHR23151:SF9 (PANTHER), SSF52777 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)

	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	nuclear receptor nhr-86	4	F:GO:0046872; F:GO:0004879; F:GO:0003677; P:GO:0045449	-		IPR001628; IPR008946; IPR013088; PTHR11865 (PANTHER), PTHR11865:SF235 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis elegans	serine threonine protein ki-se	23	F:GO:0035091; P:GO:0030307; P:GO:0008340; P:GO:0006468; P:GO:0008360; P:GO:0008286; P:GO:0023034; P:GO:0008362; P:GO:0040010; P:GO:0007424; P:GO:0040018; P:GO:0043053; C:GO:0005737; P:GO:0006916; P:GO:0019915; C:GO:0009986; P:GO:0046622; F:GO:0004674; P:GO:0042306; C:GO:0005886; F:GO:0005516; F:GO:0005524; P:GO:0050773	-	EC:2.7.11.0	IPR000719; IPR000961; IPR008271; IPR011009; IPR015744; IPR017442; IPR017892; G3DSA:1.10.510.10 (GENE3D), PTHR22985 (PANTHER), SignalP (SIGNALP)
Brugia malayi	mi-2	14	C:GO:0005700; F:GO:0031491; P:GO:0040027; P:GO:0048813; P:GO:0006333; C:GO:0016581; P:GO:0007517; P:GO:0046580; F:GO:0046872; F:GO:0003677; P:GO:0001709; P:GO:0042766; F:GO:0004003; F:GO:0016564	-		IPR009462; IPR012957; PTHR10799 (PANTHER), PTHR10799:SF64 (PANTHER)
Brugia malayi	chromodomain helicase d- binding protein 3	15	C:GO:0000785; F:GO:0030528; F:GO:0005515; F:GO:0008270; P:GO:0006357; P:GO:0040027; P:GO:0006333; C:GO:0016581; P:GO:0046580; F:GO:0003677; P:GO:0001709; P:GO:0006338; F:GO:0004003; F:GO:0003682; F:GO:0005524	-		IPR000330; IPR000953; IPR001650; IPR001965; IPR009462; IPR009463; IPR012957; IPR013083; IPR014001; IPR014021; IPR016197; IPR019787; G3DSA:2.40.50.40 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR10799 (PANTHER), PTHR10799:SF64 (PANTHER), SSF52540 (SUPERFAMILY)

Brugia malayi	chromodomain helicase d- binding protein 3	15	C:GO:0000785; F:GO:0030528; F:GO:0005515; F:GO:0008270; P:GO:0006357; P:GO:0040027; P:GO:0006333; C:GO:0016581; P:GO:0046580; F:GO:0003677; P:GO:0001709; P:GO:0006338; F:GO:0004003; F:GO:0003682; F:GO:0005524	-		IPR000330; IPR000953; IPR001650; IPR001965; IPR009462; IPR009463; IPR012957; IPR013083; IPR014001; IPR014021; IPR016197; IPR019787; G3DSA:2.40.50.40 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR10799 (PANTHER), PTHR10799:SF64 (PANTHER), SSF52540 (SUPERFAMILY)
Brugia malayi	chromodomain helicase d- binding protein 3	15	C:GO:0000785; F:GO:0030528; F:GO:0005515; F:GO:0008270; P:GO:0006357; P:GO:0040027; P:GO:0006333; C:GO:0016581; P:GO:0046580; F:GO:0003677; P:GO:0001709; P:GO:0006338; F:GO:0004003; F:GO:0003682; F:GO:0005524	-		IPR000330; IPR000953; IPR001650; IPR001965; IPR009462; IPR009463; IPR012957; IPR013083; IPR014001; IPR014021; IPR016197; IPR019787; G3DSA:2.40.50.40 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR10799 (PANTHER), PTHR10799:SF64 (PANTHER), SSF52540 (SUPERFAMILY)
Brugia malayi	chromodomain helicase d- binding protein 3	15	C:GO:0000785; F:GO:0030528; F:GO:0005515; F:GO:0008270; P:GO:0006357; P:GO:0040027; P:GO:0006333; C:GO:0016581; P:GO:0046580; F:GO:0003677; P:GO:0001709; P:GO:0006338; F:GO:0004003; F:GO:0003682; F:GO:0005524	-		IPR000330; IPR000953; IPR001650; IPR001965; IPR009462; IPR009463; IPR012957; IPR013083; IPR014001; IPR014021; IPR016197; IPR019787; G3DSA:2.40.50.40 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR10799 (PANTHER), PTHR10799:SF64 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	tbc1 domain member 22b	4	F:GO:0005097; C:GO:0005622; F:GO:0032555; P:GO:0032313	-		IPR000195; G3DSA:1.10.8.270 (GENE3D), PTHR22957 (PANTHER), PTHR22957:SF26 (PANTHER)
	-	0				-
Caenorhabditis elegans	cg3004-pa	3	P:GO:0019915; P:GO:0040018; P:GO:0002119	-		IPR001680; IPR011047; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR19842 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	cation efflux family protein	4	C:GO:0016021; P:GO:0000003; F:GO:0008324; P:GO:0055085	-		IPR002524; G3DSA:1.20.1510.10 (GENE3D), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-shw-3 protein	8	C:GO:0008076; C:GO:0005622; F:GO:0005249; F:GO:0005515; P:GO:0055085; P:GO:0046959; P:GO:0006813; F:GO:0008270	-		IPR013099; IPR015572; G3DSA:1.10.287.70 (GENE3D), PTHR11537 (PANTHER), SignalP (SIGNALP), SSF81324 (SUPERFAMILY)
Nippostrongylus brasiliensis	globin	6	F:GO:0020037; C:GO:0005576; C:GO:0005737; F:GO:0005344; P:GO:0015671; F:GO:0019825	-		-
Loa loa	sig-l peptidase complex catalytic subunit sec11a	7	P:GO:0002119; P:GO:0018996; P:GO:0006465; P:GO:0000003; C:GO:0016021; F:GO:0008236; P:GO:0006508	-		IPR001733; IPR011056; IPR015927; IPR019756; IPR019758; IPR019759
Mus musculus	melanoma inhibitory activity protein 3 precursor	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	s-adenosyl-l-methionine-dependent methyltransferase ftsjd2	4	F:GO:0004483; P:GO:0080009; P:GO:0006370; P:GO:0000003	-	EC:2.1.1.57	-
Caenorhabditis elegans	briggsae cbr-puf-12 protein	0		F:GO:0003723; P:GO:0000003; F:GO:0005488; P:GO:0018991		-
Caenorhabditis briggsae	phosphofurin acidic cluster sorting protein 2	0		C:GO:0005739; C:GO:0005783		IPR019381; PTHR13280 (PANTHER), PTHR13280:SF4 (PANTHER)
Caenorhabditis briggsae	phosphofurin acidic cluster sorting protein 2	0		C:GO:0005739; C:GO:0005783		IPR019381; PTHR13280 (PANTHER), PTHR13280:SF4 (PANTHER)
Caenorhabditis elegans	peptidase (mitochondrial processing) beta	4	C:GO:0005743; F:GO:0046872; P:GO:0019538; F:GO:0008237	-		-
Caenorhabditis elegans	peptidase (mitochondrial processing) beta	4	C:GO:0005743; F:GO:0046872; P:GO:0019538; F:GO:0008237	-		IPR007863; IPR011237; IPR011249; PTHR11851 (PANTHER), PTHR11851:SF58 (PANTHER)
Brugia malayi	small glutamine-rich tetratricopeptide repeat - isoform cra_a	5	P:GO:0009792; P:GO:0000003; P:GO:0040007; F:GO:0005515; P:GO:0002119	-		IPR001440; IPR011990; IPR013026; IPR019734; IPR023114; PTHR22904 (PANTHER), PTHR22904:SF11 (PANTHER), SSF48452 (SUPERFAMILY)

Ixodes scapularis	platelet-activating factor isoform beta1 subunit	55	C:GO:0031512; P:GO:0021766; F:GO:0042803; P:GO:0008090; P:GO:0050885; C:GO:0033267; P:GO:0000132; C:GO:0030426; C:GO:0031252; F:GO:0008201; P:GO:0045494; C:GO:0005625; P:GO:0007268; P:GO:0007405; P:GO:0010977; C:GO:0005829; C:GO:0000776; P:GO:0051081; P:GO:0045176; F:GO:0047179; C:GO:0042598; P:GO:0007611; P:GO:0021540; C:GO:0031513; F:GO:0034452; F:GO:0045505; C:GO:0048471;	-	EC:2.3.1.149	-
Caenorhabditis briggsae	arginyl-tr- synthetase	4	C:GO:0005739; F:GO:0000166; F:GO:0004812; P:GO:0006418	-		IPR001278; IPR014729; IPR015945; SSF52374 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR001534; SignalP (SIGNALP)
Ancylostoma caninum	abnormal dauer formation family member (daf-16)	4	F:GO:0003700; F:GO:0043565; C:GO:0005634; P:GO:0006355	-		-
Caenorhabditis briggsae	pyruvate dehydroge-se	19	P:GO:0030307; P:GO:0007548; P:GO:0008286; P:GO:0006974; C:GO:0005759; P:GO:0018106; P:GO:0006090; P:GO:0007283; F:GO:0004740; P:GO:0006916; P:GO:0030036; F:GO:0004674; P:GO:0006006; P:GO:0007165; F:GO:0000155; P:GO:0048477; C:GO:0005886; P:GO:0046620; F:GO:0005524	-	EC:2.7.11.2; EC:2.7.11.0	-

Caenorhabditis briggsae	pyruvate dehydroge-se	19	P:GO:0030307; P:GO:0007548; P:GO:0008286; P:GO:0006974; C:GO:0005759; P:GO:0018106; P:GO:0006090; P:GO:0007283; F:GO:0004740; P:GO:0006916; P:GO:0030036; F:GO:0004674; P:GO:0006006; P:GO:0007165; F:GO:0000155; P:GO:0048477; C:GO:0005886; P:GO:0046620; F:GO:0005524	-	EC:2.7.11.2; EC:2.7.11.0	-
	-	0				-
Caenorhabditis briggsae	protein phosphatase	7	P:GO:0040010; P:GO:0044238; P:GO:0044260; P:GO:0000003; F:GO:0005515; P:GO:0035303; P:GO:0009792	-		IPR007062; PTHR12398 (PANTHER), PTHR12398:SF7 (PANTHER)
Loa loa	smc proteins flexible hinge domain containing protein	6	C:GO:0005737; P:GO:0044403; C:GO:0000228; C:GO:0000796; P:GO:0007076; F:GO:0046982	-		PTHR18937 (PANTHER), PTHR18937:SF9 (PANTHER)
Caenorhabditis elegans	briggsae cbr-adm-2 protein	0		P:GO:0006508; C:GO:0016021; F:GO:0004222; F:GO:0008270; C:GO:0031012		IPR001590; IPR001762; G3DSA:3.40.390.10 (GENE3D), PTHR11905 (PANTHER), PTHR11905:SF15 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-adm-2 protein	0		P:GO:0006508; C:GO:0016021; F:GO:0004222; F:GO:0008270; C:GO:0031012		IPR001590; IPR001762; G3DSA:3.40.390.10 (GENE3D), PTHR11905 (PANTHER), PTHR11905:SF15 (PANTHER), SSF55486 (SUPERFAMILY)
Brugia malayi	large subunit ribosomal protein 28	5	P:GO:0009792; P:GO:0002119; C:GO:0005622; F:GO:0005515; P:GO:0040007	-		IPR002672

Caenorhabditis briggsae	heat shock 70kda protein 5 (glucose-regulated 78kda)	30	C:GO:0005793; P:GO:0030433; P:GO:0043154; F:GO:0051087; P:GO:0030512; P:GO:0021680; C:GO:0030176; P:GO:0021589; C:GO:0005788; P:GO:0031398; C:GO:0008303; P:GO:0060904; C:GO:0042470; F:GO:0043027; F:GO:0005509; F:GO:0043022; P:GO:0006983; C:GO:0005576; F:GO:0030674; P:GO:0006916; C:GO:0009986; F:GO:0031625; P:GO:0006987; P:GO:0040019; F:GO:0051082; P:GO:0042149; F:GO:0051787; C:GO:0048471;	-		IPR001023; IPR013126; IPR018181; G3DSA:1.20.1270.10 (GENE3D), G3DSA:2.60.34.10 (GENE3D), G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), PTHR19375:SF1 (PANTHER), SSF100920 (SUPERFAMILY), SSF100934 (SUPERFAMILY), SSF53067 (SUPERFAMILY)
Caenorhabditis briggsae	heat shock 70kda protein 5 (glucose-regulated 78kda)	28	P:GO:0030433; F:GO:0051087; P:GO:0043154; P:GO:0030512; P:GO:0021680; C:GO:0030176; P:GO:0021589; C:GO:0005788; P:GO:0031398; C:GO:0008303; P:GO:0060904; C:GO:0042470; F:GO:0043027; F:GO:0005509; F:GO:0043022; P:GO:0006983; F:GO:0030674; P:GO:0006916; C:GO:0009986; F:GO:0031625; P:GO:0006987; F:GO:0051082; P:GO:0042149; F:GO:0051787; C:GO:0048471; C:GO:0005634; F:GO:0005524	-		IPR001023; IPR013126; IPR018181; G3DSA:1.20.1270.10 (GENE3D), G3DSA:2.60.34.10 (GENE3D), G3DSA:3.30.30.30 (GENE3D), G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), PTHR19375:SF1 (PANTHER), SignalP (SIGNALP), SSF100920 (SUPERFAMILY), SSF100934 (SUPERFAMILY), SSF53067 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	nucleoporin seh1	6	P:GO:0006999; P:GO:0006810; P:GO:0051315; P:GO:0007080; C:GO:0000776; C:GO:0031080	-		SignalP (SIGNALP)
Caenorhabditis briggsae	nfi (nuclear factor i) family member (nfi-1)	0		P:GO:0006260; P:GO:0006355; P:GO:0006350; P:GO:0045449; F:GO:0003700; C:GO:0005622; C:GO:0005634		-
Caenorhabditis briggsae	7sk snr- methylphosphate capping enzyme	6	P:GO:0009792; P:GO:0002119; P:GO:0040010; P:GO:0000003; P:GO:0040011; F:GO:0016740	-		IPR010675; G3DSA:3.40.50.150 (GENE3D), PTHR12315 (PANTHER), SSF53335 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Loa loa	homocysteine s-methyltransferase	0		F:GO:0008168; F:GO:0008898; F:GO:0016740; P:GO:0008150; C:GO:0005575		IPR003726; PTHR21091 (PANTHER), PTHR21091:SF4 (PANTHER)
Caenorhabditis elegans	thioredoxin domain-containing protein 9	9	P:GO:0040035; P:GO:0009792; P:GO:0046785; P:GO:0035046; P:GO:0018991; P:GO:0045454; P:GO:0000910; P:GO:0040002; P:GO:0040011	-		IPR012335; IPR012336; IPR013766; PTHR21148 (PANTHER), PTHR21148:SF11 (PANTHER)
Caenorhabditis elegans	phosphorylase ki-se	4	F:GO:0016301; F:GO:0004339; P:GO:0005977; F:GO:0005516	-	EC:3.2.1.3	IPR008734; IPR008928; IPR011613; PTHR10749:SF1 (PANTHER)
Caenorhabditis briggsae	flap endonuclease-1	3	F:GO:0004519; P:GO:0006281; F:GO:0003677	-		-
Angiostrongylus cantonensis	x-box binding protein 1	2	F:GO:0003677; F:GO:0005515	-		IPR004827; IPR011616; G3DSA:1.20.5.170 (GENE3D), PTHR13301 (PANTHER), PTHR13301:SF13 (PANTHER)
Angiostrongylus cantonensis	x-box binding protein 1	5	F:GO:0003700; F:GO:0043565; F:GO:0046983; C:GO:0005634; P:GO:0006355	-		SignalP (SIGNALP)
Candida glabrata CBS 138	choline-phosphate cytidylyltransferase	1	F:GO:0003824	-		IPR004820; IPR004821; IPR014729; PTHR10739 (PANTHER), PTHR10739:SF13 (PANTHER), SSF52374 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)

	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG14241 [Caenorhabditis briggsae]	0				-
Haemonchus contortus	glutamate dehydroge-se	17	P:GO:0000003; F:GO:0070403; F:GO:0070728; F:GO:0004353; P:GO:0040010; C:GO:0005759; F:GO:0043531; F:GO:0005525; C:GO:0005743; P:GO:0006537; P:GO:0007616; F:GO:0004352; P:GO:0019459; P:GO:0055114; F:GO:0019899; F:GO:0005524; P:GO:0032024	-	EC:1.4.1.3; EC:1.4.1.2	IPR006095; IPR006096; IPR006097; IPR014362; IPR016040; G3DSA:1.10.287.140 (GENE3D), G3DSA:3.40.192.10 (GENE3D), PTHR11606 (PANTHER), SSF51735 (SUPERFAMILY), SSF53223 (SUPERFAMILY)
Caenorhabditis briggsae	isoform cra_a	1	F:GO:0005488	-		IPR011989; IPR016024
Caenorhabditis elegans	hypothetical protein F26F12.3 [Caenorhabditis elegans]	0		F:GO:0003676; F:GO:0046872; F:GO:0008270; F:GO:0005515		SignalP (SIGNALP)
Caenorhabditis briggsae	rab3 gtpase-activating protein non-catalytic subunit	2	F:GO:0030234; F:GO:0005515	-		IPR000923; PTHR12472 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	r--binding protein 10-like	3	F:GO:0005515; P:GO:0000003; C:GO:0005634	-		IPR000467; IPR015880; PTHR13948 (PANTHER), PTHR13948:SF5 (PANTHER)
Caenorhabditis elegans	r--binding protein 10-like	3	F:GO:0005515; P:GO:0000003; C:GO:0005634	-		IPR000467; IPR015880; PTHR13948 (PANTHER), PTHR13948:SF5 (PANTHER)
Caenorhabditis elegans	isoform d	0		F:GO:0005096; P:GO:0051056; C:GO:0005622		PTHR21344 (PANTHER), SSF111347 (SUPERFAMILY)
Caenorhabditis elegans	isoform d	0		F:GO:0005096; P:GO:0051056; C:GO:0005622		PTHR21344 (PANTHER), SSF111347 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0008270; C:GO:0005622		-
Ancylostoma caninum	venom-allergen-like protein family member (vap-1)	0		P:GO:0040011; P:GO:0006898; C:GO:0005576		IPR001283; IPR013032; IPR014044; IPR018244; PTHR10334:SF11 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	iq calmodulin-binding motif domain protein	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	mitochondrial ribosomal protein s14	5	C:GO:0005840; F:GO:0003735; F:GO:0005515; P:GO:0006412; C:GO:0005739	-	EC:3.6.5.3	IPR001209; G3DSA:4.10.830.10 (GENE3D), PTHR19836:SF4 (PANTHER), SSF57716 (SUPERFAMILY)

Caenorhabditis briggsae	caax alpha	19	P:GO:0042221; P:GO:0018991; P:GO:0040007; F:GO:0004660; P:GO:0040011; C:GO:0005829; P:GO:0023052; F:GO:0008017; F:GO:0043014; P:GO:0009792; P:GO:0002009; P:GO:0018347; P:GO:0002119; C:GO:0005875; P:GO:0090045; P:GO:0010171; F:GO:0004661; P:GO:0040035; P:GO:0090044	-	EC:2.5.1.58	IPR002088; IPR008940; PTHR11129 (PANTHER), PTHR11129:SF1 (PANTHER), SSF48439 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	subfamily member 13	1	F:GO:0005515	-		IPR011989; IPR016024
Caenorhabditis elegans	subfamily member 13	1	F:GO:0005515	-		IPR011989; IPR016024
Caenorhabditis elegans	subfamily member 13	1	F:GO:0005515	-		IPR011989; IPR016024
Ancylostoma caninum	secreted protein 4 precursor	0		P:GO:0006898; C:GO:0005576		IPR014044; SignalP (SIGNALP)
Ancylostoma caninum	secreted protein 4 precursor	0		P:GO:0006898; C:GO:0005576		IPR014044; SignalP (SIGNALP)
Ancylostoma caninum	secreted protein 5 precursor	0		C:GO:0005576		IPR014044; SignalP (SIGNALP)
Ancylostoma caninum	secreted protein 5 precursor	0		P:GO:0006898; C:GO:0005576		IPR001283; IPR014044; PTHR10334:SF11 (PANTHER)
Ancylostoma caninum	secreted protein 5 precursor	0		P:GO:0006898; C:GO:0005576		IPR001283; IPR014044; PTHR10334:SF11 (PANTHER)
Ancylostoma caninum	secreted protein 5 precursor	0		C:GO:0005576		IPR014044; SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	receptor-type tyrosine-protein phosphatase n2	7	P:GO:0006470; C:GO:0043195; C:GO:0005624; P:GO:0034260; F:GO:0004725; F:GO:0005515; C:GO:0030141	-	EC:3.1.3.48	IPR000242; IPR000387; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF36 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Vitis vinifera	hypothetical protein [Vitis vinifera]	0				-

Loa loa	cytoplasmic polyadenylation element-binding protein 1	13	C:GO:0030054; F:GO:0003729; P:GO:0006417; C:GO:0030425; C:GO:0000932; P:GO:0007130; C:GO:0005624; P:GO:0048168; F:GO:0005515; F:GO:0000166; C:GO:0045211; P:GO:0006397; C:GO:0014069	-		IPR000504; IPR012677; PTHR12566 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	peptide chain release factor 1	4	C:GO:0005737; P:GO:0006415; F:GO:0016149; F:GO:0016787	-		IPR000352; G3DSA:3.30.160.200 (GENE3D), PTHR11075 (PANTHER), PTHR11075:SF11 (PANTHER), SSF75620 (SUPERFAMILY)
Gallus gallus	ftsj methyltransferase domain-containing protein 1	0		F:GO:0016740; P:GO:0032259; C:GO:0016021; C:GO:0016020; F:GO:0008168; F:GO:0003676; F:GO:0003674; C:GO:0005575; P:GO:0008150		PTHR16121 (PANTHER)
Callithrix jacchus	ribosomal protein l39-like	4	F:GO:0003735; F:GO:0003723; C:GO:0022625; P:GO:0006414	-		IPR000077; IPR020083; PD007914 (PRODOM)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	exonuclease nef-	1	F:GO:0004527	-		IPR006055; IPR012337; IPR013520; G3DSA:3.30.420.10 (GENE3D), PTHR12801 (PANTHER), PTHR12801:SF11 (PANTHER)
	-	0				PR01217 (PRINTS), SignalP (SIGNALP)
Caenorhabditis briggsae	lipoma preferred partner lpp	4	F:GO:0046872; F:GO:0005515; P:GO:0060030; C:GO:0044464	-		SignalP (SIGNALP)
Caenorhabditis elegans	lipoma preferred partner lpp	4	C:GO:0005886; F:GO:0005515; P:GO:0060030; F:GO:0008270	-		-
Caenorhabditis briggsae	Hypothetical protein CBG07025 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)

Caenorhabditis elegans	arp3 actin-related protein 3 homolog	21	P:GO:0050775; C:GO:0030056; C:GO:0030027; C:GO:0000139; P:GO:0043519; C:GO:0005884; P:GO:0010631; P:GO:0046677; P:GO:0034314; F:GO:0003779; P:GO:0009792; C:GO:0060076; P:GO:0051789; C:GO:0005885; P:GO:0045666; P:GO:0016331; P:GO:0010592; P:GO:0009743; F:GO:0005524; C:GO:0002102; P:GO:0051491	-		SignalP (SIGNALP)
Loa loa	hypothetical protein LOAG_04573 [Loa loa]	0				IPR005579; PTHR13557 (PANTHER)
Brugia malayi	nuclear pore complex protein family member (npp-21)	4	P:GO:0040015; P:GO:0000003; P:GO:0002119; P:GO:0040011	-		-
Caenorhabditis elegans	protein o-linked mannose -n-acetylglucosaminyltransferase	2	F:GO:0016757; C:GO:0044464	-		G3DSA:3.90.550.10 (GENE3D), PTHR14592 (PANTHER), PTHR14592:SF1 (PANTHER), SSF53448 (SUPERFAMILY)
Caenorhabditis elegans	nicalin	8	F:GO:0022834; P:GO:0000003; P:GO:0007271; C:GO:0044446; P:GO:0040011; C:GO:0016020; C:GO:0005783; C:GO:0005634	-		IPR007484; G3DSA:3.40.630.10 (GENE3D), SignalP (SIGNALP), SSF53187 (SUPERFAMILY)
	-	0				-
Brugia malayi	chromosome 6 open reading frame 106	0		F:GO:0003674; C:GO:0005575		IPR009060; G3DSA:1.10.8.10 (GENE3D), PTHR20930 (PANTHER)
Caenorhabditis briggsae	dynein heavy chain	5	P:GO:0007018; C:GO:0030286; F:GO:0016887; F:GO:0005524; F:GO:0003777	-		IPR013594
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	6	P:GO:0002119; P:GO:0046686; C:GO:0005764; P:GO:0040002; P:GO:0040010; P:GO:0008340	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	6	P:GO:0002119; P:GO:0046686; C:GO:0005764; P:GO:0040002; P:GO:0040010; P:GO:0008340	-		-

Caenorhabditis elegans	phosphoglucose isomerase	19	C:GO:0005829; P:GO:0008340; F:GO:0048029; C:GO:0005625; P:GO:0046185; P:GO:0007611; P:GO:0043154; F:GO:0016866; F:GO:0005125; C:GO:0005615; P:GO:0019242; F:GO:0004347; C:GO:0019717; P:GO:0006096; P:GO:0006094; P:GO:0051156; P:GO:0009792; F:GO:0008083; P:GO:0043524	-	EC:5.3.1.9	IPR001672; IPR018189; IPR023096; G3DSA:3.40.50.10490 (GENE3D), PS51463 (PROFILE), SSF53697 (SUPERFAMILY)
	-	0				-
	-	0				IPR014044
	-	0				-
Schistosoma mansoni	elongator complex protein 1	1	P:GO:0043581	-		IPR006849
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0005488; P:GO:0042331; P:GO:0006886; P:GO:0050804; F:GO:0008565		IPR016024; PTHR12363 (PANTHER), PTHR12363:SF3 (PANTHER)
Caenorhabditis briggsae	importin isoform cra_b	1	P:GO:0006810	-		IPR011989; IPR013598; IPR016024; PTHR12363 (PANTHER), PTHR12363:SF3 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0005488; P:GO:0042331; P:GO:0006886; P:GO:0050804; F:GO:0008565		IPR011989; IPR016024; PTHR12363 (PANTHER), PTHR12363:SF3 (PANTHER)
Caenorhabditis elegans	dy-ctin subunit 1	1	C:GO:0044424	-		IPR022157; PD936484 (PRODOM), PTHR18916 (PANTHER), PTHR18916:SF2 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-tag-18 protein	0				-
Caenorhabditis briggsae	-dph dependent diflavin oxidoreductase 1	8	F:GO:0016491; F:GO:0050661; F:GO:0005515; F:GO:0010181; P:GO:0055114; P:GO:0008219; F:GO:0050660; C:GO:0005829	-		IPR001094; IPR001433; IPR001709; IPR003097; IPR008254; IPR017927; IPR017938; IPR023173; G3DSA:2.40.30.10 (GENE3D), G3DSA:3.40.50.360 (GENE3D), G3DSA:3.40.50.80 (GENE3D), PTHR19384 (PANTHER), PTHR19384:SF10 (PANTHER), SignalP (SIGNALP), SSF52218 (SUPERFAMILY), SSF52343 (SUPERFAMILY)
Caenorhabditis elegans	upf2 regulator of nonsense transcripts homolog	3	C:GO:0005737; F:GO:0005515; P:GO:0016070	-		IPR003890; IPR016021; IPR016024; PTHR12839 (PANTHER)

Caenorhabditis elegans	sorting and assembly machinery component 50 homolog (cerevisiae)	7	P:GO:0040010; C:GO:0031966; P:GO:0000003; C:GO:0019867; P:GO:0002119; P:GO:0006898; P:GO:0009792	-		IPR000184
	-	0				-
Apis mellifera	peroxiredoxin 6	2	F:GO:0016491; F:GO:0016209	-		IPR000866; IPR012335; IPR012336; IPR017936; G3DSA:3.30.1020.10 (GENE3D), PTHR10681 (PANTHER), PTHR10681:SF17 (PANTHER)
	-	0				-
	-	0				-
Strongylocentrotus purpuratus	polymerase (d- directed) epsilon 3 (p17 subunit)	1	F:GO:0005488	-		IPR003958; IPR009072; PTHR11064 (PANTHER), SignalP (SIGNALP)
	-	0				IPR007087
Caenorhabditis elegans	- h exchanger family member (nhx-9)	6	P:GO:0009792; F:GO:0015385; P:GO:0055085; P:GO:0006885; C:GO:0016021; P:GO:0006814	-		IPR018416; IPR018422
Caenorhabditis elegans	dual oxidase 1	12	P:GO:0018149; P:GO:0006979; P:GO:0006952; P:GO:0040032; P:GO:0042338; F:GO:0046872; P:GO:0040007; F:GO:0016491; P:GO:0002119; P:GO:0040011; P:GO:0009792; C:GO:0005882	-		PTHR11972 (PANTHER), PTHR11972:SF1 (PANTHER)
	-	0				-
Caenorhabditis elegans	isoform g	2	C:GO:0031012; F:GO:0016787	-		IPR002223; IPR003599; IPR007110; IPR010909; IPR013783; IPR020901; PTHR10083 (PANTHER), PTHR10083:SF39 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	mitogen-activated protein ki-se ki-se ki-se 7 interacting protein 1	1	F:GO:0005515	-		IPR001932; IPR014045; IPR015655; PTHR13832:SF100 (PANTHER)
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	rain ki-se homolog family member (mbk-2)	13	F:GO:0030145; P:GO:0006468; P:GO:0045725; F:GO:0005515; P:GO:0007275; F:GO:0004713; P:GO:0042771; F:GO:0004674; F:GO:0000287; C:GO:0005634; F:GO:0005524; P:GO:0007608; C:GO:0005938	-	EC:2.7.10.0; EC:2.7.11.0	IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF30 (PANTHER)
Caenorhabditis briggsae	clc-type chloride channel family member (clh-2)	11	P:GO:0009792; F:GO:0005247; C:GO:0005902; C:GO:0005886; F:GO:0005515; P:GO:0055085; P:GO:0000003; C:GO:0016021; C:GO:0005626; C:GO:0015629; P:GO:0006821	-		IPR001807; IPR014743; PTHR11689:SF5 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	adhesion regulating molecule 1	3	F:GO:0005515; P:GO:0009987; C:GO:0044424	-		IPR006773
Caenorhabditis briggsae	sorting nexin isoform cra_c	5	F:GO:0035091; F:GO:0004871; F:GO:0005515; C:GO:0016021; P:GO:0007154	-		IPR003114; PTHR22775 (PANTHER), PTHR22775:SF4 (PANTHER)
Caenorhabditis briggsae	methylcrotonoyl-coenzyme a carboxylase 1	7	P:GO:0019752; C:GO:0005743; F:GO:0016874; P:GO:0034641; F:GO:0009374; F:GO:0005524; C:GO:0005794	-		IPR000089; IPR001882; IPR005479; IPR005481; IPR005482; IPR011053; IPR011054; IPR011761; IPR011764; IPR013815; IPR013816; IPR013817; IPR016185; G3DSA:2.40.50.100 (GENE3D), PTHR18866 (PANTHER), PTHR18866:SF19 (PANTHER), SSF56059 (SUPERFAMILY)
Caenorhabditis elegans	yot0_caeel ame: full=upf0057 membrane protein	0		C:GO:0016021		IPR000612; SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	zinc transporter zip3	2	P:GO:0006829; F:GO:0005385	-		IPR003689; PTHR11040 (PANTHER), PTHR11040:SF5 (PANTHER)
Caenorhabditis elegans	calcium-binding protein p22	3	F:GO:0016491; F:GO:0005509; P:GO:0040011	-		IPR002048; IPR008080; IPR011992; IPR018247; IPR018248; IPR018249; PTHR23056 (PANTHER), PTHR23056:SF4 (PANTHER), SSF47473 (SUPERFAMILY)
Strongylocentrotus purpuratus	nuclease harbi1-like	0		C:GO:0005737; F:GO:0016787; F:GO:0004518; C:GO:0005634		PTHR22930 (PANTHER), SignalP (SIGNALP)

Caenorhabditis elegans	heavy chain non-muscle	14	P:GO:0051234; P:GO:0007010; P:GO:0007275; F:GO:0003779; F:GO:0032559; F:GO:0003774; P:GO:0030154; P:GO:0002376; C:GO:0042995; P:GO:0048646; C:GO:0044459; P:GO:0008152; C:GO:0016459; C:GO:0005938	-		PD968187 (PRODOM), PTHR13140 (PANTHER), PTHR13140:SF23 (PANTHER)
	-	0				-
	-	0				IPR007087
	-	0				IPR007087
Caenorhabditis elegans	tbc domain containing protein	1	F:GO:0005515	-		IPR001849; IPR011993; SSF50729 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Homo sapiens	testis enhanced gene transcript (bax inhibitor 1) isoform cra_a	7	P:GO:0007283; C:GO:0005887; P:GO:0030324; C:GO:0005626; C:GO:0005634; P:GO:0043066; C:GO:0005783	-		IPR006213; IPR006214; PTHR23291:SF4 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	vasa- and belle-like helicase family member (vbh-1)	8	P:GO:0009792; P:GO:0002119; F:GO:0008026; F:GO:0003676; C:GO:0043186; P:GO:0042006; F:GO:0005524; P:GO:0040007	-		IPR000629; IPR001650; IPR011545; IPR014001; IPR014014; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF59 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	novel protein human and mouse neuroblastoma-amplified protein	0				SignalP (SIGNALP)

synthetic construct	cd74 major histocompatibility class ii invariant chain	35	P:GO:0048146; C:GO:0005771; C:GO:0005764; F:GO:0005215; P:GO:0006814; P:GO:0070374; F:GO:0042289; P:GO:0045060; P:GO:0043030; P:GO:0006952; P:GO:0019883; P:GO:0051085; F:GO:0001540; P:GO:0019886; P:GO:0016064; P:GO:0043518; P:GO:0050731; P:GO:0030890; P:GO:0045582; P:GO:0001516; F:GO:0004896; C:GO:0005887; P:GO:0045581; P:GO:0043066; P:GO:0006886; F:GO:0042802; C:GO:0005794;	-		IPR011988; IPR015386; IPR022339; PTHR14093 (PANTHER), PTHR14093:SF5 (PANTHER)
Pan troglodytes	cd74 antigen (invariant polypeptide of major histocompatibility class ii antigen-associated) isoform cra_d	35	P:GO:0048146; C:GO:0005771; C:GO:0005764; F:GO:0005215; P:GO:0006814; P:GO:0070374; F:GO:0042289; P:GO:0045060; P:GO:0043030; P:GO:0006952; P:GO:0019883; P:GO:0051085; F:GO:0001540; P:GO:0019886; P:GO:0016064; P:GO:0043518; P:GO:0050731; P:GO:0030890; P:GO:0045582; P:GO:0001516; F:GO:0004896; C:GO:0005887; P:GO:0045581; P:GO:0043066; P:GO:0006886; F:GO:0042802; C:GO:0005794:	-		-
Brugia malayi	melanoma antigen family 4	0				IPR002190; IPR003006

Homo sapiens	thymosin beta-10	5	F:GO:0003785; C:GO:0005856; P:GO:0042989; P:GO:0007286; C:GO:0005737	-		-
	-	0				-
Caenorhabditis briggsae	importin subunit alpha-1	4	C:GO:0005737; C:GO:0005643; P:GO:0006606; F:GO:0008565	-		-
Pediculus humanus corporis	cop9 constitutive photomorphogenic homolog subunit 2	10	F:GO:0004871; C:GO:0005730; C:GO:0008180; F:GO:0003714; P:GO:0007165; P:GO:0016481; P:GO:0008283; C:GO:0005737; P:GO:0030182; P:GO:0006366	-		IPR000717; IPR011991; IPR013143; PTHR10678 (PANTHER), PTHR10678:SF3 (PANTHER), SSF46785 (SUPERFAMILY)
Pediculus humanus corporis	cop9 constitutive photomorphogenic homolog subunit 2	10	F:GO:0004871; C:GO:0005730; C:GO:0008180; F:GO:0003714; P:GO:0007165; P:GO:0016481; P:GO:0008283; C:GO:0005737; P:GO:0030182; P:GO:0006366	-		IPR000717; IPR011991; IPR013143; PTHR10678 (PANTHER), PTHR10678:SF3 (PANTHER), SSF46785 (SUPERFAMILY)
Pediculus humanus corporis	cop9 constitutive photomorphogenic homolog subunit 2	10	F:GO:0004871; C:GO:0005730; C:GO:0008180; F:GO:0003714; P:GO:0007165; P:GO:0016481; P:GO:0008283; C:GO:0005737; P:GO:0030182; P:GO:0006366	-		IPR000717; IPR011991; IPR013143; PTHR10678 (PANTHER), PTHR10678:SF3 (PANTHER), SSF46785 (SUPERFAMILY)
Loa loa	scavenger receptor class a- c-type lectin (agap009143-pa)	1	F:GO:0004872	-		-
Brugia malayi	nfkb activating protein	12	F:GO:0005515; P:GO:0040027; P:GO:0040010; P:GO:0006898; P:GO:0040011; C:GO:0005737; C:GO:0005730; P:GO:0010171; F:GO:0003682; P:GO:0001703; P:GO:0046638; F:GO:0016564	-		IPR009269

Brugia malayi	nfkb activating protein	12	F:GO:0005515; P:GO:0040027; P:GO:0040010; P:GO:0006898; P:GO:0040011; C:GO:0005737; C:GO:0005730; P:GO:0010171; F:GO:0003682; P:GO:0001703; P:GO:0046638; F:GO:0016564	-		IPR009269
	-	0				-
Loa loa	elegans protein partially confirmed by transcript evidence	0		P:GO:0000003; P:GO:0005975; P:GO:0009792; P:GO:0019915		-
Caenorhabditis briggsae	briggsae cbr-vig-1 protein	1	P:GO:0009792	-		IPR006861; PTHR12299 (PANTHER), PTHR12299:SF5 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-vig-1 protein	1	P:GO:0009792	-		IPR006861; PTHR12299 (PANTHER), PTHR12299:SF5 (PANTHER)
Loa loa	elegans protein partially confirmed by transcript evidence	0		P:GO:0000003; P:GO:0005975; P:GO:0009792; P:GO:0019915		-
Caenorhabditis briggsae	briggsae cbr-vig-1 protein	1	P:GO:0009792	-		IPR006861; PTHR12299 (PANTHER), PTHR12299:SF5 (PANTHER)
Caenorhabditis briggsae	beta-lactamase family protein	0				-
Caenorhabditis elegans	viral a-type inclusion protein	0		F:GO:0051082; F:GO:0016787; P:GO:0007269; C:GO:0019717; C:GO:0005783; C:GO:0045202; P:GO:0050808; F:GO:0030165; P:GO:0007416; C:GO:0030054; C:GO:0005737; C:GO:0042734; C:GO:0030426; P:GO:0055114; P:GO:0006457; F:GO:0032440; C:GO:0005856; F:GO:0005515; F:GO:0016491		-
Caenorhabditis elegans	viral a-type inclusion protein	1	C:GO:0044464	-		-

Angiostrongylus cantonensis	isoamylase n-termi-l domain protein	0		F:GO:0019901; P:GO:0006633; F:GO:0016787; C:GO:0005952; F:GO:0016301; P:GO:0005975; P:GO:0046320; F:GO:0003824; C:GO:0005654; F:GO:0004553; F:GO:0005515; C:GO:0005829; C:GO:0031588		PTHR10343 (PANTHER), PTHR10343:SF3 (PANTHER)
Angiostrongylus cantonensis	isoamylase n-termi-l domain protein	0		F:GO:0019901; P:GO:0006633; F:GO:0016787; C:GO:0005952; F:GO:0016301; P:GO:0005975; P:GO:0046320; F:GO:0003824; C:GO:0005654; F:GO:0004553; F:GO:0005515; C:GO:0005829; C:GO:0031588		PTHR10343 (PANTHER), PTHR10343:SF3 (PANTHER)
Angiostrongylus cantonensis	n-ethylmaleimide-sensitive factor attachment beta	5	F:GO:0019905; C:GO:0005794; P:GO:0006886; F:GO:0008270; C:GO:0005783	-		-
	-	0				-

Strongylocentrotus purpuratus	tyramine receptor	36	P:GO:0001963; P:GO:0044092; P:GO:0051051; P:GO:0009628; P:GO:0043085; P:GO:0051480; P:GO:0060255; C:GO:0044425; P:GO:0048522; P:GO:0051046; P:GO:0007212; P:GO:0030814; P:GO:0044260; P:GO:0008277; P:GO:0030900; P:GO:0051050; P:GO:0031326; P:GO:0023061; C:GO:0005886; P:GO:0010627; P:GO:0035467; P:GO:0007611; C:GO:0043005; P:GO:0009605; P:GO:0010959; F:GO:0004952; P:GO:0016043;	-		-
Brugia malayi	nf-kappa-b inhibitor-like protein 2	0		F:GO:0005488		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF58 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	6	F:GO:0046872; F:GO:0004879; F:GO:0003677; P:GO:0045449; F:GO:0005515; P:GO:0000003	-		IPR001628; IPR013088; PR00350 (PRINTS), PTHR11865 (PANTHER), PTHR11865:SF236 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis elegans	ferm domain (-ezrin-radixin-moesin) family member (frm-1)	9	F:GO:0008092; P:GO:0009888; P:GO:0048598; C:GO:0043232; C:GO:0016327; P:GO:0030154; C:GO:0044444; P:GO:0048513; P:GO:0016043	-		IPR008379; PTHR23280 (PANTHER)
Caenorhabditis briggsae	ferm domain (-ezrin-radixin-moesin) family member (frm-1)	10	F:GO:0008092; P:GO:0035151; C:GO:0045169; C:GO:0005918; P:GO:0048598; P:GO:0045216; C:GO:0045170; P:GO:0035321; P:GO:0060857; N:GO:0071842	-		IPR008379; PTHR23280 (PANTHER)
Caenorhabditis elegans	ferm domain (-ezrin-radixin-moesin) family member (frm-1)	1	F:GO:0005515	-		-

Caenorhabditis briggsae	ferm domain (-ezrin-radixin-moesin) family member (frm-1)	10	F:GO:0008092; P:GO:0035151; C:GO:0045169; C:GO:0005918; P:GO:0048598; P:GO:0045216; C:GO:0045170; P:GO:0035321; P:GO:0060857; N:GO:0071842	-		IPR008379; PTHR23280 (PANTHER)
Caenorhabditis elegans	pa2l_caeel ame: full=phospholipase a2-like protein flags: precursor	0		C:GO:0016021; P:GO:0016042; P:GO:0006644		SignalP (SIGNALP)
Caenorhabditis elegans	dihydrolipoamide s-succinyltransferase (e2 component of 2-oxo-glutarate complex) isoform cra_a	10	F:GO:0031072; P:GO:0006103; C:GO:0005739; P:GO:0006734; F:GO:0051087; P:GO:0006099; C:GO:0005792; F:GO:0004149; C:GO:0045252; C:GO:0005886	-	EC:2.3.1.61	IPR001078; G3DSA:3.30.559.10 (GENE3D), PTHR23151 (PANTHER), PTHR23151:SF8 (PANTHER), SSF52777 (SUPERFAMILY)
Bursaphelenchus xylophilus	60s ribosomal protein l5	9	P:GO:0040035; P:GO:0009792; P:GO:0010171; P:GO:0002119; C:GO:0005840; F:GO:0008097; F:GO:0003735; P:GO:0040010; P:GO:0006412	-	EC:3.6.5.3	IPR005484; IPR005485; G3DSA:3.30.420.100 (GENE3D), PTHR23410:SF1 (PANTHER), SSF53137 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-bag-1 protein	0		P:GO:0006915; P:GO:0016049; P:GO:0006950; P:GO:0006457; F:GO:0051087; F:GO:0005515		-
Caenorhabditis elegans	pyruvate dehydroge-se component x	2	F:GO:0016747; C:GO:0044444	-	EC:2.3.1.0	IPR001078; IPR004167; G3DSA:3.30.559.10 (GENE3D), PTHR23151 (PANTHER), PTHR23151:SF9 (PANTHER), SSF52777 (SUPERFAMILY)
	-	0				PTHR14429 (PANTHER), PTHR14429:SF3 (PANTHER)
	-	0				PTHR14429 (PANTHER), PTHR14429:SF3 (PANTHER)
	-	0				-
	-	0				-

Caenorhabditis elegans	translation initiation factor 2 gamma subunit	20	P:GO:0016568; F:GO:0003743; P:GO:0006413; P:GO:0040010; F:GO:0008270; F:GO:0004781; P:GO:0006333; P:GO:0000003; F:GO:0018024; P:GO:0010171; P:GO:0002119; C:GO:0000785; F:GO:0005515; P:GO:0040011; F:GO:0003924; P:GO:0009792; P:GO:0040018; F:GO:0003682; C:GO:0005634; F:GO:0005525	-	EC:2.7.7.4; EC:2.1.1.43; EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000795; G3DSA:3.40.50.300 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF9 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	b-cell cll lymphoma 7b	0		F:GO:0003674; F:GO:0003779; P:GO:0008150; C:GO:0005575		IPR006804; PTHR12767:SF1 (PANTHER)
	-	0				-
Caenorhabditis elegans	cytochrome p450 family protein	6	P:GO:0016539; F:GO:0009055; F:GO:0004497; F:GO:0020037; P:GO:0055114; C:GO:0044464	-		IPR001128; PTHR19383:SF165 (PANTHER)
Caenorhabditis elegans	family with sequence similarity member a	1	C:GO:0005783	-		IPR019154; PTHR21357 (PANTHER)
Caenorhabditis elegans	1110033m05rik protein	0		C:GO:0005576		IPR019154; PTHR21357 (PANTHER)
Caenorhabditis elegans	u528_caeel ame: full=upf0528 protein	0				-
Caenorhabditis elegans	1110033m05rik protein	0				IPR019154; PTHR21357 (PANTHER)
Caenorhabditis elegans	1110033m05rik protein	0				IPR019154; PTHR21357 (PANTHER)
Caenorhabditis briggsae	carboxyl transferase domain containing protein	3	F:GO:0016874; P:GO:0008152; F:GO:0000166	-		IPR000022; IPR011762; IPR011763; G3DSA:3.90.226.10 (GENE3D), PTHR18866 (PANTHER), PTHR18866:SF6 (PANTHER), SSF52096 (SUPERFAMILY)
Caenorhabditis elegans	telomerase-binding protein est1a	2	F:GO:0005488; C:GO:0044424	-		IPR019458; PTHR15696 (PANTHER), SSF48452 (SUPERFAMILY)
Caenorhabditis elegans	telomerase-binding protein est1a	2	F:GO:0005488; C:GO:0044424	-		IPR019458; PTHR15696 (PANTHER), SSF48452 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	F:GO:0004067; P:GO:0006528	-	EC:3.5.1.1	IPR002110; IPR006033; IPR006034; IPR020683; IPR020827; G3DSA:3.40.50.1170 (GENE3D), G3DSA:3.40.50.40 (GENE3D), PTHR11707:SF3 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	F:GO:0004067; P:GO:0006528	-	EC:3.5.1.1	IPR002110; IPR006033; IPR006034; IPR020683; IPR020827; G3DSA:3.40.50.1170 (GENE3D), G3DSA:3.40.50.40 (GENE3D), PTHR11707:SF3 (PANTHER)

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	F:GO:0004067; P:GO:0006528	-	EC:3.5.1.1	IPR002110; IPR006033; IPR006034; IPR020683; IPR020827; G3DSA:3.40.50.1170 (GENE3D), G3DSA:3.40.50.40 (GENE3D), PTHR11707:SF3 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	F:GO:0004067; P:GO:0006528	-	EC:3.5.1.1	IPR002110; IPR006033; IPR006034; IPR020683; IPR020827; G3DSA:3.40.50.1170 (GENE3D), G3DSA:3.40.50.40 (GENE3D), PTHR11707:SF3 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	F:GO:0004067; P:GO:0006528	-	EC:3.5.1.1	IPR002110; IPR006033; IPR006034; IPR020683; IPR020827; G3DSA:3.40.50.1170 (GENE3D), G3DSA:3.40.50.40 (GENE3D), PTHR11707:SF3 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	F:GO:0004067; P:GO:0006528	-	EC:3.5.1.1	IPR002110; IPR006033; IPR006034; IPR020683; IPR020827; G3DSA:3.40.50.1170 (GENE3D), G3DSA:3.40.50.40 (GENE3D), PTHR11707:SF3 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	F:GO:0004067; P:GO:0006528	-	EC:3.5.1.1	IPR002110; IPR006033; IPR006034; IPR020683; IPR020827; G3DSA:3.40.50.1170 (GENE3D), G3DSA:3.40.50.40 (GENE3D), PTHR11707:SF3 (PANTHER)
Caenorhabditis elegans	aldehyde dehydroge-se 7 member a1	9	F:GO:0004029; C:GO:0005829; P:GO:0055114; F:GO:0008802; F:GO:0004043; P:GO:0006081; C:GO:0005739; C:GO:0005634; P:GO:0007605	-	EC:1.2.1.3; EC:1.2.1.8; EC:1.2.1.31	IPR015590; IPR016160; IPR016161; IPR016162; IPR016163; PTHR11699:SF26 (PANTHER)
Caenorhabditis briggsae	cytochrome c oxidase subunit via polypeptide 1	5	C:GO:0005743; P:GO:0040010; P:GO:0000003; P:GO:0008340; C:GO:0044425	-		IPR001349; IPR018507
Ancylostoma caninum	secreted protein 5 precursor	0		C:GO:0005576		IPR001283; IPR014044; SignalP (SIGNALP)
Caenorhabditis briggsae	elegans lipl-3 partially confirmed by transcript evidence	5	P:GO:0006629; F:GO:0005488; P:GO:0044281; P:GO:0044237; F:GO:0004806	-	EC:3.1.1.3	IPR000073; IPR006693; G3DSA:3.40.50.1820 (GENE3D), PTHR11005 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0006508; F:GO:0004222; F:GO:0008270; C:GO:0031012		IPR011705; IPR013089
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG21271 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	dopey family member 1	0		P:GO:0007275; P:GO:0006810; P:GO:0015031		-
	-	0				PR00021 (PRINTS), PR01217 (PRINTS)
	-	0				PR00021 (PRINTS), PR01217 (PRINTS)

Lodderomyces elongisporus NRRL YB-4239	alanyl-tr- synthetase	4	F:GO:0004812; P:GO:0006412; P:GO:0043039; F:GO:0000166	-	EC:3.6.5.3	IPR002318; IPR018162; IPR018164; IPR018165; G3DSA:3.30.930.10 (GENE3D), PTHR11777 (PANTHER), SignalP (SIGNALP), SSF55681 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	variant sh3 domain containing protein	0		P:GO:0008150; C:GO:0005575		IPR001452; IPR011511; G3DSA:2.30.30.40 (GENE3D), PTHR14167 (PANTHER), PTHR14167:SF4 (PANTHER)
Brugia malayi	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Brugia malayi	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis elegans	transbilayer amphipath transporters (subfamily iv p-type atpase) family member (tat-5)	7	C:GO:0016021; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0015914; F:GO:0000287; F:GO:0004012	-	EC:3.6.3.1	IPR001757; IPR008250; IPR018303; G3DSA:2.70.150.10 (GENE3D), G3DSA:3.40.1110.10 (GENE3D), PTHR11939:SF9 (PANTHER), SSF81653 (SUPERFAMILY), SSF81660 (SUPERFAMILY), SSF81665 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-mab-20 protein	3	P:GO:0030534; P:GO:0007626; P:GO:0048666	-		-
Caenorhabditis briggsae	semaphorin 2a	3	P:GO:0030534; P:GO:0007626; P:GO:0048666	-		SignalP (SIGNALP)
Caenorhabditis briggsae	semaphorin 2a	3	P:GO:0030534; P:GO:0007626; P:GO:0048666	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	eps (human endocytosis) related family member (eps-8)	1	F:GO:0005515	-		IPR013625; PTHR12287 (PANTHER), PTHR12287:SF1 (PANTHER), SSF50729 (SUPERFAMILY)
Caenorhabditis briggsae	c10orf28 protein	0		F:GO:0000166		IPR012677; PTHR21678 (PANTHER)
Homo sapiens	barrier-to-autointegration factor	9	P:GO:0050792; F:GO:0003677; P:GO:0019047; C:GO:0005694; C:GO:0005634; C:GO:0005829; P:GO:0009615; P:GO:0044419; P:GO:0019059	-		-
Caenorhabditis briggsae	chaperonin containing subunit 7	12	C:GO:0005739; P:GO:0006457; P:GO:0040007; C:GO:0005832; F:GO:0042802; P:GO:0040035; F:GO:0005524; P:GO:0002119; P:GO:0040011; P:GO:0006898; F:GO:0051082; P:GO:0009792	-		IPR002423; IPR012720; IPR017998; G3DSA:1.10.560.10 (GENE3D), G3DSA:3.30.260.10 (GENE3D), G3DSA:3.50.7.10 (GENE3D), SSF52029 (SUPERFAMILY)
Brugia malayi	ring finger protein 5	1	F:GO:0005488	-		PTHR12313 (PANTHER)

Caenorhabditis briggsae	briggsae cbr-ubh-3 protein	18	F:GO:0004197; P:GO:0007412; P:GO:0016579; P:GO:0040010; P:GO:0042755; P:GO:0043407; P:GO:0008283; F:GO:0043130; C:GO:0005829; P:GO:0007628; C:GO:0043025; F:GO:0004221; C:GO:0030424; F:GO:0008242; F:GO:0031694; P:GO:0006950; C:GO:0005886; P:GO:0050905	-	EC:3.4.22.0; EC:3.1.2.15; EC:3.4.19.0	-
Ancylostoma caninum	scp-like extracellular protein	2	P:GO:0006898; P:GO:0040011	-		IPR001283; IPR014044; PTHR10334:SF11 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-hsp-43 protein	0		P:GO:0009408; F:GO:0005515		-
Homo sapiens	selenoprotein 1	3	P:GO:0045454; F:GO:0008430; C:GO:0005737	-		-
	-	0				-
Macaca mulatta	ubiquitin	2	C:GO:0005634; C:GO:0005737	-		IPR000626; IPR019955; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), PTHR10666:SF9 (PANTHER), SSF54236 (SUPERFAMILY)
Caenorhabditis briggsae	#NAME?	7	P:GO:0040010; P:GO:0002119; P:GO:0008152; C:GO:0005759; P:GO:0006898; F:GO:0051082; P:GO:0009792	-		IPR000740; IPR009012; PTHR21237:SF8 (PANTHER)
Loa loa	integrator complex	2	P:GO:0009790; P:GO:0009653	-		IPR022145
	-	0				-
Caenorhabditis briggsae	ham-2	2	P:GO:0010171; F:GO:0005488	-		IPR007087; IPR015880; PTHR23228 (PANTHER), PTHR23228:SF45 (PANTHER)
Caenorhabditis elegans	pot family protein	3	C:GO:0016020; P:GO:0006810; F:GO:0005215	-		PTHR11654 (PANTHER), PTHR11654:SF12 (PANTHER)
	-	0				-
Caenorhabditis elegans	mitochondrial ribosomal	0		F:GO:0003735; P:GO:0006412; C:GO:0005840; F:GO:0019843		-
	-	0				-

Haemonchus contortus	hexoki-se type ii	8	F:GO:0004396; P:GO:0007595; C:GO:0005741; F:GO:0005536; P:GO:0046835; F:GO:0005524; F:GO:0005515; P:GO:0006096	-	EC:2.7.1.1	IPR001312; IPR022672; G3DSA:3.30.420.40 (GENE3D), SSF53067 (SUPERFAMILY)
Saccoglossus kowalevskii	mannose c type 1	0		C:GO:0009986; F:GO:0004888; C:GO:0016021; F:GO:0005529; P:GO:0006897; C:GO:0005576; P:GO:0007165; F:GO:0004872; P:GO:0009405; P:GO:0008150; P:GO:0007155; F:GO:0005537; F:GO:0005488		IPR001304; IPR016186; IPR016187; PTHR22802 (PANTHER), PTHR22802:SF5 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	hed family member (ptc-3)	6	P:GO:0009792; P:GO:0002119; P:GO:0040018; P:GO:0018996; P:GO:0000003; P:GO:0040011	-		PTHR10796 (PANTHER), PTHR10796:SF34 (PANTHER)
Caenorhabditis briggsae	hed family member (ptc-3)	17	P:GO:0009653; P:GO:0000003; F:GO:0005515; C:GO:0016020; P:GO:0009612; P:GO:0040018; P:GO:0032526; P:GO:0040011; P:GO:0008283; P:GO:0014070; P:GO:0018996; P:GO:0048513; P:GO:0009792; P:GO:0002119; P:GO:0042493; P:GO:0032355; P:GO:0060429	-		PTHR10796 (PANTHER), PTHR10796:SF34 (PANTHER)
Caenorhabditis briggsae	patched homolog 2	10	P:GO:0009792; F:GO:0004872; P:GO:0002119; P:GO:0040018; P:GO:0018996; P:GO:0043588; P:GO:0000003; P:GO:0040011; P:GO:0042633; C:GO:0016020	-		IPR000731; IPR003392; PD019290 (PRODOM), PTHR10796 (PANTHER), PTHR10796:SF34 (PANTHER)

Caenorhabditis briggsae	hed family member (ptc-3)	6	P:GO:0009792; P:GO:0002119; P:GO:0040018; P:GO:0018996; P:GO:0000003; P:GO:0040011	-		PTHR10796 (PANTHER), PTHR10796:SF34 (PANTHER)
Loa loa	ferm domain (-ezrin-radixin-moesin) family member (frm-1)	2	C:GO:0044424; F:GO:0008092	-		IPR000299; IPR011993; IPR014847; IPR018980; PTHR23280 (PANTHER), SSF50729 (SUPERFAMILY)
Loa loa	ferm domain (-ezrin-radixin-moesin) family member (frm-1)	2	C:GO:0044424; F:GO:0008092	-		IPR000299; IPR011993; IPR014847; IPR018980; PTHR23280 (PANTHER), SSF50729 (SUPERFAMILY)
Loa loa	beta-catenin armadillo related family member (bar-1)	0		P:GO:0001708; P:GO:0040028; C:GO:0005913; C:GO:0005634; P:GO:0040026; P:GO:0007265; P:GO:0016055; P:GO:0002009; P:GO:0007155; P:GO:0006898; P:GO:0040035; P:GO:0030334; P:GO:0043058; C:GO:0030054; P:GO:0045944; C:GO:0005737; P:GO:0007617; P:GO:0042659; F:GO:0003713; C:GO:0005625; C:GO:0005624; F:GO:0008134; F:GO:0005515; P:GO:0040011; P:GO:0040010; P:GO:0018991		PTHR23315 (PANTHER), PTHR23315:SF3 (PANTHER)
	-	0				-
Haemonchus contortus	thioredoxin reductase 1	13	C:GO:0005829; P:GO:0042744; C:GO:0005739; P:GO:0045454; P:GO:0055114; F:GO:0009055; F:GO:0050660; F:GO:0050661; P:GO:0008283; P:GO:0001707; F:GO:0004791; C:GO:0005634; F:GO:0015035	-	EC:1.8.1.9	IPR001327; IPR004099; IPR006338; IPR013027; IPR016156; PR00411 (PRINTS), G3DSA:3.50.50.60 (GENE3D), PTHR22912 (PANTHER), SSF51905 (SUPERFAMILY)

Haemonchus contortus	thioredoxin reductase 1	13	C:GO:0005829; P:GO:0042744; C:GO:0005739; P:GO:0045454; P:GO:0055114; F:GO:0009055; F:GO:0050660; F:GO:0050661; P:GO:0008283; P:GO:0001707; F:GO:0004791; C:GO:0005634; F:GO:0015035	-	EC:1.8.1.9	IPR001327; IPR004099; IPR006338; IPR013027; IPR016156; PR00411 (PRINTS), G3DSA:3.50.50.60 (GENE3D), PTHR22912 (PANTHER), SSF51905 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	probable ribonuclease zc3h12d	3	F:GO:0016787; F:GO:0008270; F:GO:0003676	-		IPR000571; IPR021869; PTHR12876 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				IPR000210; IPR011333; IPR013089; PTHR23230:SF181 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-psr-1 protein	8	P:GO:0035212; P:GO:0046329; P:GO:0018395; F:GO:0005515; F:GO:0070815; P:GO:0043066; P:GO:0006350; C:GO:0005634	-		-
Caenorhabditis elegans	briggsae cbr-psr-1 protein	8	P:GO:0035212; P:GO:0046329; P:GO:0018395; F:GO:0005515; F:GO:0070815; P:GO:0043066; P:GO:0006350; C:GO:0005634	-		SSF51197 (SUPERFAMILY)

Caenorhabditis elegans	bifunctio-l arginine demethylase and lysyl-hydroxylase jmjd6	26	P:GO:0007166; P:GO:0030324; P:GO:0048024; P:GO:0001822; P:GO:0042116; P:GO:0070079; P:GO:0007507; P:GO:0001568; P:GO:0048821; F:GO:0033749; F:GO:0016702; P:GO:0018395; F:GO:0046872; F:GO:0070815; P:GO:0060041; F:GO:0042802; P:GO:0006915; P:GO:0033077; P:GO:0070078; P:GO:0045449; P:GO:0055114; F:GO:0004872; P:GO:0043654; F:GO:0033746; C:GO:0005886; C:GO:0005634	-	EC:1.13.11.0	IPR003347; IPR013129; PTHR12480 (PANTHER), SSF51197 (SUPERFAMILY)
Caenorhabditis elegans	bifunctio-l arginine demethylase and lysyl-hydroxylase jmjd6	26	P:GO:0007166; P:GO:0030324; P:GO:0048024; P:GO:0001822; P:GO:0042116; P:GO:0070079; P:GO:0007507; P:GO:0001568; P:GO:0048821; F:GO:0033749; F:GO:0016702; P:GO:0018395; F:GO:0046872; F:GO:0070815; P:GO:0060041; F:GO:0042802; P:GO:0006915; P:GO:0033077; P:GO:0070078; P:GO:0045449; P:GO:0055114; F:GO:0004872; P:GO:0043654; F:GO:0033746; C:GO:0005886; C:GO:0005634	-	EC:1.13.11.0	IPR003347; IPR013129; PTHR12480 (PANTHER), SSF51197 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein F55A12.2 [Caenorhabditis elegans]	1	P:GO:0040010	-		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				IPR003124
Caenorhabditis elegans	mon2 homolog isoform 1	2	P:GO:0015031; F:GO:0005488	-		-

Caenorhabditis elegans	zinc zz type family protein	7	P:GO:0007271; F:GO:0005515; P:GO:0040017; C:GO:0016010; F:GO:0005277; P:GO:0015870; P:GO:0046716	-		-
Caenorhabditis elegans	golgi golgin subfamily 5	4	C:GO:0031985; F:GO:0005515; P:GO:0048193; C:GO:0016020	-		PD936484 (PRODOM)
Caenorhabditis briggsae	component of oligomeric golgi complex 4	2	P:GO:0006810; C:GO:0044464	-		IPR013167
Caenorhabditis briggsae	major facilitator superfamily protein	1	P:GO:0006810	-		IPR011701; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11662 (PANTHER), PTHR11662:SF21 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	aspartyl aminopeptidase	3	F:GO:0046872; C:GO:0005737; F:GO:0070011	-		IPR001948; G3DSA:2.30.250.10 (GENE3D), G3DSA:3.40.630.10 (GENE3D), SignalP (SIGNALP), SSF101821 (SUPERFAMILY), SSF53187 (SUPERFAMILY)
Caenorhabditis briggsae	aspartyl aminopeptidase	3	F:GO:0046872; C:GO:0005737; F:GO:0070011	-		IPR001948; G3DSA:3.40.630.10 (GENE3D), SSF53187 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Loa loa	seven in absentia homolog 1	13	P:GO:0043161; P:GO:0007411; F:GO:0008270; P:GO:0006915; P:GO:0007049; C:GO:0008021; F:GO:0008022; P:GO:0007283; C:GO:0005769; F:GO:0004842; P:GO:0042787; C:GO:0030877; C:GO:0005634	-	EC:6.3.2.19	-
Caenorhabditis briggsae	leucine zipper and ctnnbip1 domain containing	0		F:GO:0008013; P:GO:0010212; F:GO:0003674; P:GO:0008150; C:GO:0005575		IPR009428
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0009793; C:GO:0005575		IPR011989; IPR019156; PTHR13255 (PANTHER)
Caenorhabditis briggsae	riken cd- 1300012g16 gene	1	C:GO:0005764	-		IPR007000
Caenorhabditis briggsae	Hypothetical protein CBG01673 [Caenorhabditis briggsae]	4	F:GO:0017111; P:GO:0050789; C:GO:0005622; F:GO:0000166	-	EC:3.6.1.15	PTHR22908 (PANTHER), PTHR22908:SF13 (PANTHER)
Brugia malayi	tb2 hva22 family protein	1	F:GO:0005515	-		IPR004345; PTHR12300:SF13 (PANTHER), SignalP (SIGNALP)

Caenorhabditis elegans	yo93_caeel ame: full=uncharacterized protein	0		P:GO:0000003; P:GO:0040011; P:GO:0040010; P:GO:0006898; P:GO:0002119; P:GO:0009792; P:GO:0040018		-
Caenorhabditis elegans	isoform a	0		P:GO:0055114; C:GO:0005739; F:GO:0016491; F:GO:0004129		-
Caenorhabditis elegans	iron-sulfur cluster assembly 1 mitochondrial precursor	9	P:GO:0040010; P:GO:0006783; F:GO:0051536; F:GO:0003676; P:GO:0016226; P:GO:0002119; P:GO:0006898; F:GO:0005198; P:GO:0009792	-		IPR000361; PTHR10072:SF27 (PANTHER)
Brugia malayi	hypothetical protein Bm1_23545 [Brugia malayi]	0				-
Loa loa	kinesin family protein	0		F:GO:0005524; F:GO:0000166; F:GO:0003777; F:GO:0003774; P:GO:0007018; F:GO:0005515; C:GO:0005874; C:GO:0000795		-
Caenorhabditis briggsae	udp-gal:beta c beta - polypeptide 2	1	F:GO:0016757	-		IPR002659; PTHR11214:SF13 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-ncbp-1 protein	0		F:GO:0005488; P:GO:0008380; P:GO:0016070; P:GO:0006397; P:GO:0031047; F:GO:0005515; P:GO:0006370; C:GO:0005634		IPR016021; IPR016024
Loa loa	protein ki-se domain containing protein	6	F:GO:0004674; F:GO:0005524; P:GO:0000082; P:GO:0006350; C:GO:0005634; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR002290; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF83 (PANTHER)
Loa loa	protein ki-se domain containing protein	6	F:GO:0004674; F:GO:0005524; P:GO:0000082; P:GO:0006350; C:GO:0005634; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR002290; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF83 (PANTHER)
Loa loa	protein ki-se domain containing protein	6	F:GO:0004674; F:GO:0005524; P:GO:0000082; P:GO:0006350; C:GO:0005634; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR002290; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF83 (PANTHER)

	-	0				-
Brugia malayi	briggsae cbr-clu-1 protein	0		F:GO:0003674; F:GO:0005488; P:GO:0008150; C:GO:0005575		IPR007967; IPR011990; PTHR12601 (PANTHER), SSF103107 (SUPERFAMILY), SSF48452 (SUPERFAMILY)
Caenorhabditis elegans	-	0				-
	-	0				-
Caenorhabditis elegans	ribonucleoside-diphosphate reductase large subunit	13	P:GO:0009263; F:GO:0004748; P:GO:0055114; P:GO:0040007; P:GO:0006260; P:GO:0040035; P:GO:0051290; F:GO:0005524; P:GO:0002119; F:GO:0005515; P:GO:0040017; C:GO:0005971; P:GO:0009792	-	EC:1.17.4.1	IPR000276; IPR000788; IPR005144; IPR008926; IPR013346; IPR013509; G3DSA:3.20.70.20 (GENE3D), PTHR11573:SF6 (PANTHER), SSF51998 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	mitochondrial carrier homolog 2	1	C:GO:0016020	-		PTHR10780 (PANTHER), PTHR10780:SF1 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-elt-3 protein	1	F:GO:0005488	-		IPR000679; IPR013088; PTHR10071 (PANTHER), PTHR10071:SF15 (PANTHER), SSF57716 (SUPERFAMILY)
Brugia malayi	hbs1-like protein	2	F:GO:0016740; F:GO:0000166	-		IPR000795; IPR004160; IPR009000; IPR009001; IPR015033; G3DSA:2.40.30.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF38 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	e1a binding protein p400	5	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0040010; P:GO:0040011	-		IPR017877; PTHR10799 (PANTHER), PTHR10799:SF45 (PANTHER)
Caenorhabditis briggsae	mitochondrial ribosomal	3	C:GO:0005840; F:GO:0003735; P:GO:0006412	-	EC:3.6.5.3	IPR000244; IPR009027; IPR020070; PTHR21368:SF16 (PANTHER)
Brugia malayi	threonyl-tr- synthetase	4	F:GO:0004829; F:GO:0005515; P:GO:0006418; C:GO:0005829	-	EC:6.1.1.3	IPR002320; IPR004154; G3DSA:3.30.930.10 (GENE3D), PTHR11451 (PANTHER), PTHR11451:SF5 (PANTHER), SSF55681 (SUPERFAMILY)
Loa loa	structure-specific recognition protein	11	P:GO:0040010; P:GO:0000910; P:GO:0040035; F:GO:0003677; P:GO:0010171; P:GO:0007413; P:GO:0002119; P:GO:0040011; P:GO:0009792; P:GO:0040018; C:GO:0005634	-		SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR001534; SignalP (SIGNALP)

Brugia malayi	mitochondrial ribosomal protein s21	7	P:GO:0006412; P:GO:0040010; F:GO:0003735; C:GO:0005763; P:GO:0002119; P:GO:0006898; P:GO:0009792	-	EC:3.6.5.3	IPR001911; PTHR21109 (PANTHER)
Caenorhabditis elegans	hydroxyacyl-coenzyme a dehydroge-se 3-ketoacyl-coenzyme a thiolase enoyl-coenzyme a hydratase (trifunctio-l protein) beta subunit	11	F:GO:0016508; F:GO:0000062; F:GO:0003988; C:GO:0005743; C:GO:0016507; C:GO:0042645; F:GO:0003857; P:GO:0006635; F:GO:0016509; P:GO:0009792; F:GO:0004300	-	EC:4.2.1.74; EC:2.3.1.16; EC:1.1.1.35; EC:1.1.1.211 ; EC:4.2.1.17	IPR002155; IPR016038; IPR016039; IPR020610; IPR020613; IPR020615; IPR020616; IPR020617; PTHR18919:SF5 (PANTHER)
	-	0				-
Caenorhabditis elegans	biotin protein ligase family member (bpl-1)	6	F:GO:0005488; C:GO:0043231; F:GO:0018271; P:GO:0043687; C:GO:0044446; C:GO:0005737	-		IPR004143; IPR004408; G3DSA:3.30.930.10 (GENE3D), SSF55681 (SUPERFAMILY)
	-	0				-
Ancylostoma caninum	mater-l embryonic leucine zipper ki-se	7	P:GO:0008016; F:GO:0004674; P:GO:0048821; F:GO:0005524; F:GO:0005515; C:GO:0005737; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR015739; IPR017442; IPR020636; G3DSA:1.10.510.10 (GENE3D)
Ancylostoma caninum	mater-l embryonic leucine zipper ki-se	7	P:GO:0008016; F:GO:0004674; P:GO:0048821; F:GO:0005524; F:GO:0005515; C:GO:0005737; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR015739; IPR017442; IPR020636; G3DSA:1.10.510.10 (GENE3D)
Ancylostoma caninum	protein ki-se domain containing protein	3	P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	-
Ancylostoma caninum	mater-l embryonic leucine zipper ki-se	5	P:GO:0008016; F:GO:0004674; P:GO:0048821; F:GO:0005524; P:GO:0006468	-	EC:2.7.11.0	-
Ancylostoma caninum	mater-l embryonic leucine zipper ki-se	5	F:GO:0004674; F:GO:0005524; P:GO:0032501; P:GO:0065007; P:GO:0006468	-	EC:2.7.11.0	-
Caenorhabditis briggsae	viral a-type inclusion protein repeat containing protein	4	P:GO:0000003; P:GO:0002119; P:GO:0040011; P:GO:0040015	-		PD936484 (PRODOM)

Caenorhabditis elegans	cg32645 cg32645-pb	4	P:GO:0009792; P:GO:0010171; P:GO:0040017; P:GO:0006898	-		PTHR11161 (PANTHER), SignalP (SIGNALP)
Brugia malayi	nipped-b homolog	31	P:GO:0007605; F:GO:0042826; P:GO:0034613; P:GO:0003151; P:GO:0006974; F:GO:0008022; C:GO:0032116; P:GO:0040018; F:GO:0070087; P:GO:0060325; F:GO:0047485; P:GO:0071481; P:GO:0061010; P:GO:0034088; P:GO:0045444; P:GO:0050890; P:GO:0031065; P:GO:0007420; P:GO:0010553; P:GO:0048703; P:GO:0048592; P:GO:0035261; P:GO:0045995; P:GO:0045778; P:GO:0042471; P:GO:0042634; P:GO:0061038;	-		PTHR21704 (PANTHER), PTHR21704:SF5 (PANTHER)
Caenorhabditis elegans	-like 2	13	F:GO:0003678; P:GO:0040010; C:GO:0071339; P:GO:0006310; P:GO:0000910; P:GO:0040035; F:GO:0005524; P:GO:0002119; F:GO:0016887; P:GO:0006898; P:GO:0016481; P:GO:0009792; P:GO:0016246	-		-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	talin 1	6	F:GO:0005158; C:GO:0001726; P:GO:0007016; C:GO:0005856; C:GO:0005925; F:GO:0005200	-		IPR000299; IPR011993; IPR014352; IPR015710; IPR018979; IPR019747; IPR019748; IPR019749; SSF54236 (SUPERFAMILY)
Caenorhabditis briggsae	talin 1	6	F:GO:0005158; C:GO:0001726; P:GO:0007016; C:GO:0005856; C:GO:0005925; F:GO:0005200	-		IPR000299; IPR011993; IPR014352; IPR015710; IPR018979; IPR019747; IPR019748; IPR019749; SSF54236 (SUPERFAMILY)

Caenorhabditis briggsae	deah (asp-glu-ala-his) box polypeptide 38	6	F:GO:0008026; F:GO:0003676; C:GO:0005681; F:GO:0005515; F:GO:0005524; P:GO:0000398	-		IPR007502; IPR011709; PTHR18934 (PANTHER), SSF52540 (SUPERFAMILY)
Strongylocentrotus purpuratus	ankyrin unc44	0		C:GO:0016021; C:GO:0016020; C:GO:0005576; P:GO:0006887; P:GO:0007268; C:GO:0044279; P:GO:0009405; C:GO:0044218; C:GO:0042734		IPR002110; IPR018170; IPR020683; PTHR18958 (PANTHER)
Strongylocentrotus purpuratus	ankyrin unc44	0		C:GO:0016021; C:GO:0016020; C:GO:0005576; P:GO:0006887; P:GO:0007268; C:GO:0044279; P:GO:0009405; C:GO:0044218; C:GO:0042734		IPR002110; IPR018170; IPR020683; PTHR18958 (PANTHER)
Caenorhabditis elegans	myotubularin	1	P:GO:0046716	-		IPR000387; IPR010569; IPR016130; IPR017906; PTHR10807 (PANTHER), PTHR10807:SF6 (PANTHER), SSF50729 (SUPERFAMILY), SSF52799 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	eukaryotic initiation factor family member (eif-)	1	P:GO:0009792	-		IPR013906; IPR023194
Caenorhabditis elegans	large subunit ribosomal protein 23	10	P:GO:0006412; C:GO:0005840; P:GO:0006355; P:GO:0040007; F:GO:0003735; P:GO:0000003; P:GO:0018996; P:GO:0002119; P:GO:0007165; P:GO:0009792	-	EC:3.6.5.3	IPR000218; IPR001610; IPR019972; PTHR11761:SF4 (PANTHER)
Loa loa	topoisomerase iii alpha	10	P:GO:0007276; P:GO:0006268; P:GO:0007126; F:GO:0008270; F:GO:0003917; F:GO:0005524; C:GO:0016605; F:GO:0005515; C:GO:0005694; P:GO:0006265	-	EC:5.99.1.2	IPR000380; IPR013497; IPR013824
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0008150; C:GO:0005575		IPR018785
Caenorhabditis elegans	hypothetical protein Y49G5B.1 [Caenorhabditis elegans]	0				SignalP (SIGNALP)

Caenorhabditis briggsae	gpi-anchor transamidase	2	F:GO:0004197; P:GO:0006508	-	EC:3.4.22.0	IPR001096; PTHR12000:SF1 (PANTHER)
Loa loa	cuticlin 1	0				-
Caenorhabditis briggsae	protein	5	C:GO:0016020; F:GO:0015250; C:GO:0043025; C:GO:0005929; P:GO:0006833	-		IPR000425; IPR022357; PTHR19139:SF25 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-eat-3 protein	9	C:GO:0030061; P:GO:0045768; C:GO:0030425; C:GO:0005741; C:GO:0005758; P:GO:0007601; P:GO:0007007; F:GO:0003924; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	PTHR11566 (PANTHER), PTHR11566:SF8 (PANTHER)
	-	0				-
Loa loa	myotubularin-related family protein	0		P:GO:0016311; F:GO:0016791		IPR017906; IPR022587; PTHR10807 (PANTHER), PTHR10807:SF3 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-ttm-2 protein	0				-
Caenorhabditis briggsae	galactosyltransferase family protein	3	F:GO:0016757; P:GO:0005975; C:GO:0016021	-		IPR003859; G3DSA:3.90.550.10 (GENE3D), PTHR19300:SF2 (PANTHER), SSF53448 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Loa loa	dual oxidase maturation factor 1	0		C:GO:0005789; C:GO:0016021; C:GO:0016020; P:GO:0015031		IPR018469
Caenorhabditis elegans	general transcription factor 3c polypeptide 3	3	P:GO:0040010; F:GO:0005488; P:GO:0006898	-		IPR011990; IPR013026; IPR019734; PTHR23082 (PANTHER), SSF48452 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG07002 [Caenorhabditis briggsae]	4	P:GO:0040035; P:GO:0002119; P:GO:0040007; P:GO:0006898	-		IPR009668
Caenorhabditis elegans	inhibitor of kappa light polypeptide gene enhancer in b- ki- se complex-associated protein	0		F:GO:0016301; C:GO:0008023; C:GO:0005737; F:GO:0008607; P:GO:0006350; P:GO:0045449; P:GO:0006357; C:GO:0005634		IPR006849
Branchiostoma floridae	multidrug resistance protein family member (mrp-5)	8	P:GO:0002119; F:GO:0042626; P:GO:0040002; P:GO:0040017; P:GO:0055085; P:GO:0040010; F:GO:0005524; C:GO:0016021	-		IPR003439; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF17 (PANTHER), SSF52540 (SUPERFAMILY)

Caenorhabditis briggsae	briggsae cbr-ppn-1 protein	3	F:GO:0004185; F:GO:0004867; P:GO:0006508	-	EC:3.4.16.0	IPR002223; IPR020901; PTHR10083 (PANTHER), PTHR10083:SF32 (PANTHER)
	-	0				-
	-	0				-
Brugia malayi	transmembrane protein 98	1	C:GO:0044464	-		SignalP (SIGNALP)
Brugia malayi	transmembrane protein 98	1	C:GO:0044464	-		SignalP (SIGNALP)
Caenorhabditis elegans	zinc metallopeptidase	6	C:GO:0016021; F:GO:0004222; F:GO:0003676; P:GO:0032259; P:GO:0006508; F:GO:0008168	-	EC:3.4.24.0; EC:2.1.1.0	IPR000718; IPR002052; IPR018497; G3DSA:3.40.390.10 (GENE3D), PTHR11733:SF15 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	heavy unconventio-l myosin family member (hum-2)	2	F:GO:0005515; F:GO:0000166	-		PTHR13140 (PANTHER), PTHR13140:SF15 (PANTHER)
Caenorhabditis elegans	heavy unconventio-l myosin family member (hum-2)	2	F:GO:0005515; F:GO:0000166	-		PTHR13140 (PANTHER), PTHR13140:SF15 (PANTHER)
Dictyocaulus viviparus	briggsae cbr-unc-15 protein	4	C:GO:0030016; C:GO:0032982; F:GO:0003774; F:GO:0005515	-		-
Caenorhabditis briggsae	-dh dehydroge-se	0		C:GO:0016020; C:GO:0005743; C:GO:0070469; C:GO:0005739; P:GO:0006810; P:GO:0006120; F:GO:0003954; P:GO:0022900; P:GO:0032981		IPR019342; PTHR21268 (PANTHER)
Caenorhabditis briggsae	lin-5 interacting protein family member (lfi-1)	4	P:GO:0009987; C:GO:0043232; C:GO:0044446; F:GO:0005515	-		-
	-	0				-
	-	0				-
Loa loa	topoisomerase ii beta	20	P:GO:0001764; C:GO:0005654; F:GO:0008094; F:GO:0008144; P:GO:0006974; P:GO:0007409; P:GO:0006355; P:GO:0030900; P:GO:0006265; F:GO:0003918; C:GO:0009330; P:GO:0009792; C:GO:0005694; P:GO:0006266; P:GO:0007059; P:GO:0030263; F:GO:0003700; F:GO:0005524; P:GO:0043065; P:GO:0000910	-	EC:5.99.1.3	IPR001154; IPR001241; IPR002205; IPR003594; IPR013506; IPR013758; IPR013759; IPR013760; IPR014721; IPR018522; IPR020568; IPR020899; G3DSA:3.30.1490.30 (GENE3D), PTHR10169 (PANTHER), PTHR10169:SF2 (PANTHER)

Loa loa	topoisomerase ii beta	20	P:GO:0001764; C:GO:0005654; F:GO:0008094; F:GO:0008144; P:GO:0006974; P:GO:0007409; P:GO:0006355; P:GO:0030900; P:GO:0006265; F:GO:0003918; C:GO:0009330; P:GO:0009792; C:GO:0005694; P:GO:0006266; P:GO:0007059; P:GO:0030263; F:GO:0003700; F:GO:0005524; P:GO:0043065; P:GO:0000910	-	EC:5.99.1.3	IPR001154; IPR001241; IPR002205; IPR003594; IPR013506; IPR013758; IPR013759; IPR013760; IPR014721; IPR018522; IPR020568; IPR020899; G3DSA:3.30.1490.30 (GENE3D), PTHR10169 (PANTHER), PTHR10169:SF2 (PANTHER)
Loa loa	topoisomerase ii beta	20	P:GO:0001764; C:GO:0005654; F:GO:0008094; F:GO:0008144; P:GO:0006974; P:GO:0007409; P:GO:0006355; P:GO:0030900; P:GO:0006265; F:GO:0003918; C:GO:0009330; P:GO:0009792; C:GO:0005694; P:GO:0006266; P:GO:0007059; P:GO:0030263; F:GO:0003700; F:GO:0005524; P:GO:0043065; P:GO:0000910	-	EC:5.99.1.3	IPR001154; IPR001241; IPR002205; IPR003594; IPR013506; IPR013758; IPR013759; IPR013760; IPR014721; IPR018522; IPR020568; IPR020899; G3DSA:3.30.1490.30 (GENE3D), PTHR10169 (PANTHER), PTHR10169:SF2 (PANTHER)
Caenorhabditis briggsae	mmp37-like mitochondrial precursor	2	P:GO:0030150; C:GO:0031314	-		IPR015222
Loa loa	cleft lip and palate transmembrane protein 1-like protein	0		P:GO:0006915; C:GO:0016021; C:GO:0016020		IPR008429
Caenorhabditis elegans	monocarboxylate transporter	0		P:GO:0055085		IPR011701; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11360 (PANTHER), PTHR11360:SF10 (PANTHER)
	-	0				-
Brugia malayi	c-myc promoter-binding protein irlb	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr--s-7 protein	1	F:GO:0008233	-		IPR001506; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF80 (PANTHER), SignalP (SIGNALP), SSF55486 (SUPERFAMILY)

Caenorhabditis briggsae	phosphatidylinositol-5-phosphate 4- type alpha	3	P:GO:0046488; P:GO:0016310; F:GO:0016308	-	EC:2.7.1.68	IPR002498; G3DSA:3.30.800.10 (GENE3D), G3DSA:3.30.810.10 (GENE3D), PTHR23086:SF3 (PANTHER), SSF56104 (SUPERFAMILY)
Caenorhabditis briggsae	phosphatidylinositol-5-phosphate 4- type alpha	3	P:GO:0046488; P:GO:0016310; F:GO:0016308	-	EC:2.7.1.68	IPR002498; G3DSA:3.30.800.10 (GENE3D), G3DSA:3.30.810.10 (GENE3D), PTHR23086:SF3 (PANTHER), SSF56104 (SUPERFAMILY)
Caenorhabditis briggsae	phosphatidylinositol-5-phosphate 4-ki-se type-2 alpha	3	P:GO:0046488; P:GO:0016310; F:GO:0016308	-	EC:2.7.1.68	-
Caenorhabditis briggsae	phosphatidylinositol-5-phosphate 4-ki-se type-2 alpha	3	P:GO:0046488; P:GO:0016310; F:GO:0016308	-	EC:2.7.1.68	-
Ancylostoma caninum	secreted protein asp-2	0		P:GO:0040011; C:GO:0005576		IPR001283; IPR014044; IPR018244; PTHR10334:SF11 (PANTHER)
Ixodes scapularis	spermatogenesis-associated protein 20	0		F:GO:0003674; F:GO:0003824; C:GO:0005575		PTHR12145 (PANTHER)
Caenorhabditis briggsae	formin homology 2 domain containing protein	1	F:GO:0005515	-		IPR010472; IPR016024; PTHR23213 (PANTHER), PTHR23213:SF12 (PANTHER)
Caenorhabditis briggsae	formin homology 2 domain containing protein	1	F:GO:0005515	-		IPR010472; IPR016024; PTHR23213 (PANTHER), PTHR23213:SF12 (PANTHER)
	-	0				-
Drosophila ananassae	elegans protein confirmed by transcript evidence	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	scavenger receptor class member 2	1	C:GO:0044464	-		IPR002159
Loa loa	c2 domain containing protein	0				-
Dictyocaulus viviparus	putative protein [Dictyocaulus viviparus]	0				-
Caenorhabditis briggsae	leucine rich repeat family protein	4	P:GO:0051438; F:GO:0005515; C:GO:0031462; F:GO:0004842	-	EC:6.3.2.19	IPR011989; IPR016024; G3DSA:3.80.10.10 (GENE3D), PTHR12904 (PANTHER), PTHR12904:SF6 (PANTHER), SSF52047 (SUPERFAMILY)
Caenorhabditis briggsae	leucine rich repeat family protein	1	F:GO:0005515	-		G3DSA:3.80.10.10 (GENE3D)
Caenorhabditis briggsae	leucine rich repeat family protein	4	P:GO:0051438; F:GO:0005515; C:GO:0031462; F:GO:0004842	-	EC:6.3.2.19	IPR011989; IPR016024; G3DSA:3.80.10.10 (GENE3D), PTHR12904 (PANTHER), PTHR12904:SF6 (PANTHER), SSF52047 (SUPERFAMILY)
Caenorhabditis briggsae	leucine rich repeat family protein	4	P:GO:0051438; F:GO:0005515; C:GO:0031462; F:GO:0004842	-	EC:6.3.2.19	IPR011989; IPR016024; G3DSA:3.80.10.10 (GENE3D), PTHR12904 (PANTHER), PTHR12904:SF6 (PANTHER), SSF52047 (SUPERFAMILY)
Caenorhabditis briggsae	leucine rich repeat family protein	4	P:GO:0051438; F:GO:0005515; C:GO:0031462; F:GO:0004842	-	EC:6.3.2.19	IPR011989; IPR016024; G3DSA:3.80.10.10 (GENE3D), PTHR12904 (PANTHER), PTHR12904:SF6 (PANTHER), SSF52047 (SUPERFAMILY)
Brugia malayi	cleavage and polyadenylation specific factor 3-like	2	P:GO:0006396; C:GO:0044424	-		PTHR11203 (PANTHER), PTHR11203:SF8 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)

Caenorhabditis elegans	growth arrest and d--damage-inducible proteins-interacting protein 1	2	C:GO:0005634; P:GO:0007049	-		IPR018472
	-	0				-
Caenorhabditis elegans	c-type lectin family member (clec-152)	0				IPR002035; G3DSA:3.40.50.410 (GENE3D), SignalP (SIGNALP), SSF53300 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	integrator complex subunit 2	2	P:GO:0032501; P:GO:0040007	-		-
Loa loa	integrator complex subunit 2	2	P:GO:0032501; P:GO:0040007	-		-
Caenorhabditis elegans	charged multivesicular body protein 3	13	P:GO:0009792; P:GO:0002119; C:GO:0005768; P:GO:0040018; F:GO:0005515; P:GO:0018996; P:GO:0040010; P:GO:0008340; P:GO:0040011; P:GO:0009987; P:GO:0019915; C:GO:0016020; P:GO:0015031	-		IPR005024; PTHR10476 (PANTHER), PTHR10476:SF1 (PANTHER)
Caenorhabditis elegans	charged multivesicular body protein 3	13	P:GO:0009792; P:GO:0002119; C:GO:0005768; P:GO:0040018; F:GO:0005515; P:GO:0018996; P:GO:0040010; P:GO:0008340; P:GO:0040011; P:GO:0009987; P:GO:0019915; C:GO:0016020; P:GO:0015031	-		SignalP (SIGNALP)
Caenorhabditis elegans	tim44-like domain containing protein	10	P:GO:0040010; F:GO:0008270; F:GO:0015450; C:GO:0005744; P:GO:0000003; P:GO:0006626; P:GO:0002119; F:GO:0005515; P:GO:0006898; P:GO:0009792	-		IPR007379; PTHR10721 (PANTHER), PTHR10721:SF1 (PANTHER), SSF54427 (SUPERFAMILY)
Caenorhabditis elegans	abnormal dye filling protein isoform partially confirmed by transcript evidence	4	F:GO:0005515; C:GO:0005694; P:GO:0009987; C:GO:0044446	-		SignalP (SIGNALP)
Caenorhabditis elegans	abnormal dye filling protein isoform partially confirmed by transcript evidence	4	F:GO:0005515; C:GO:0005694; P:GO:0009987; C:GO:0044446	-		PD968187 (PRODOM), PTHR23159 (PANTHER), PTHR23159:SF6 (PANTHER)

Caenorhabditis elegans	abnormal dye filling protein isoform partially confirmed by transcript evidence	4	F:GO:0005515; C:GO:0005694; P:GO:0009987; C:GO:0044446	-		PD936484 (PRODOM), PTHR23159 (PANTHER), PTHR23159:SF6 (PANTHER)
Caenorhabditis elegans	hypothetical protein C26B9.1 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	briggsae cbr-igcm-1 protein	0		C:GO:0016020		IPR003599; IPR003961; IPR007110; IPR008957; IPR013098; IPR013783; PTHR11640 (PANTHER), PTHR11640:SF2 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	regulator of g protein sig-ling family member (rgs-7)	0		F:GO:0004871		IPR000008; IPR008973; IPR018029; G3DSA:2.60.40.150 (GENE3D)
Caenorhabditis briggsae	d- replication complex gins protein psf2	9	P:GO:0040007; P:GO:0040035; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0006898; P:GO:0009792; P:GO:0001703	-		-
Caenorhabditis briggsae	protoheme ix farnesyltransferase family protein	5	P:GO:0048034; C:GO:0005886; F:GO:0008495; C:GO:0016021; C:GO:0031966	-		IPR006369; PTHR11048 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	yfe5_caeel ame: full=uncharacterized protein flags: precursor	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical kda protein in chromosome	4	P:GO:0009792; P:GO:0002119; P:GO:0040010; P:GO:0040011	-		IPR011989; IPR012954; IPR016024; PTHR13457 (PANTHER)
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
Loa loa	speckle-type poz protein	9	P:GO:0007367; P:GO:0043065; P:GO:0042067; P:GO:0007349; P:GO:0016567; P:GO:0046330; F:GO:0005515; P:GO:0030162; C:GO:0005634	-		-
Caenorhabditis briggsae	rho gtpase-activating protein 26	5	F:GO:0005096; C:GO:0005622; F:GO:0005515; P:GO:0009987; P:GO:0019915	-		IPR000198; IPR001849; IPR008936; IPR011993; PTHR12552 (PANTHER), PTHR12552:SF1 (PANTHER), SSF50729 (SUPERFAMILY)
Caenorhabditis briggsae	ap1 gamma subunit binding protein 1	3	P:GO:0006810; F:GO:0005509; C:GO:0005737	-		-
Pan troglodytes	PREDICTED: hypothetical protein [Pan troglodytes]	0				-
Caenorhabditis briggsae	bromodomain and wd repeat domain containing 2	1	P:GO:0050794	-		IPR011046; IPR015943

Caenorhabditis briggsae	zinc finger protein 7-like	0		P:GO:0006355; F:GO:0046872; F:GO:0003676; F:GO:0003674; P:GO:0040027; F:GO:0008270; C:GO:0005634; C:GO:0005622		IPR007087; IPR015880; PTHR23224 (PANTHER), PTHR23224:SF465 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis briggsae	zinc finger protein 555	0		P:GO:0040027; F:GO:0003677; C:GO:0005634; F:GO:0003676; F:GO:0008270; F:GO:0003674; P:GO:0006355; C:GO:0005622; F:GO:0046872		IPR007087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis briggsae	zinc finger protein 555	0		P:GO:0040027; F:GO:0003677; C:GO:0005634; F:GO:0003676; F:GO:0008270; F:GO:0003674; P:GO:0006355; C:GO:0005622; F:GO:0046872		IPR007087; IPR015880; PTHR23224 (PANTHER), PTHR23224:SF461 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis briggsae	zinc finger protein 555	0		P:GO:0040027; F:GO:0003677; C:GO:0005634; F:GO:0003676; F:GO:0008270; F:GO:0003674; P:GO:0006355; C:GO:0005622; F:GO:0046872		IPR007087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	transformation transcription domain-associated protein	1	P:GO:0009987	-		-
Caenorhabditis briggsae	transformation transcription domain-associated protein	1	P:GO:0009987	-		-
	-	0				IPR007726
Brugia malayi	r- polymerase ii associated protein 2	5	P:GO:0040035; P:GO:0009792; P:GO:0006898; P:GO:0040039; P:GO:0002009	-		IPR007308; IPR010916; PTHR14732 (PANTHER), PS51479 (PROFILE)
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
Caenorhabditis briggsae	heat shock protein family member (hsp-)	0		P:GO:0009408		IPR002068; PTHR11527 (PANTHER), PTHR11527:SF28 (PANTHER)
Caenorhabditis elegans	receptor type guanylyl cyclase	7	F:GO:0004383; F:GO:0004672; F:GO:0008528; F:GO:0005524; C:GO:0016020; P:GO:0006468; P:GO:0006182	-	EC:4.6.1.2	IPR001170; IPR001828; G3DSA:3.40.50.2300 (GENE3D), PTHR11920 (PANTHER), PTHR11920:SF2 (PANTHER), SSF53822 (SUPERFAMILY)

Caenorhabditis elegans	receptor type guanylyl cyclase	7	F:GO:0004383; F:GO:0004672; F:GO:0008528; F:GO:0005524; C:GO:0016020; P:GO:0006468; P:GO:0006182	-	EC:4.6.1.2	IPR001170; IPR001828; G3DSA:3.40.50.2300 (GENE3D), PTHR11920 (PANTHER), PTHR11920:SF2 (PANTHER), SSF53822 (SUPERFAMILY)
Loa loa	entric chromosome binding protein family member (hcp-6)	4	C:GO:0043234; F:GO:0005515; P:GO:0007067; C:GO:0005634	-		-
Brugia malayi	cleavage and polyadenylation factor i homolog (cerevisiae)	28	[illegible]; P:GO:0000122; P:GO:0030423; F:GO:0030169; F:GO:0005515; P:GO:0006388; P:GO:0040010; P:GO:0040015; P:GO:0007507; F:GO:0008329; F:GO:0017069; C:GO:0016021; P:GO:0035087; P:GO:0045736; C:GO:0005737; F:GO:0005044; P:GO:0031124; P:GO:0009792; F:GO:0004861; F:GO:0005529; F:GO:0051733; P:GO:0002119; P:GO:0006910; C:GO:0000214; F:GO:0051736; P:GO:0045087; F:GO:0005524; P:GO:0040035	-		IPR010655; G3DSA:3.40.50.300 (GENE3D), PTHR12755 (PANTHER), PF03205 (PFAM), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	zinc finger protein	0		F:GO:0003676; F:GO:0046872; F:GO:0016874; F:GO:0008270; F:GO:0004842; F:GO:0005515		IPR001841; PTHR11685 (PANTHER), PTHR11685:SF17 (PANTHER), SignalP (SIGNALP), SSF57850 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	nucleoporin 155kda	2	F:GO:0005515; C:GO:0005635	-		-
Caenorhabditis elegans	nucleoporin 155kda	2	F:GO:0005515; C:GO:0005635	-		-
Caenorhabditis elegans	nucleoporin 155kda	2	F:GO:0005515; C:GO:0005635	-		-
Caenorhabditis elegans	nucleoporin 155kda	2	F:GO:0005515; C:GO:0005635	-		-
Caenorhabditis elegans	nucleoporin 155kda	2	F:GO:0005515; C:GO:0005635	-		-

Caenorhabditis elegans	nuclear pore complex protein family member (npp-8)	9	P:GO:0006810; P:GO:0040007; P:GO:0040035; P:GO:0002119; F:GO:0005515; P:GO:0006997; C:GO:0005635; P:GO:0009792; C:GO:0016020	-		IPR004870; IPR014908; PTHR10350:SF3 (PANTHER)
Caenorhabditis elegans	nucleoporin 155kda	2	F:GO:0005515; C:GO:0005635	-		-
	-	0				IPR000436
	-	0				IPR000436; SignalP (SIGNALP)
Caenorhabditis elegans	isoform cra_b	8	P:GO:0000278; P:GO:0048699; P:GO:0006996; P:GO:0009792; P:GO:0050794; C:GO:0043229; P:GO:0022403; F:GO:0005488	-		IPR001849; IPR002219; IPR011993; G3DSA:3.30.60.20 (GENE3D), PTHR22988 (PANTHER), PTHR22988:SF1 (PANTHER), SSF50729 (SUPERFAMILY), SSF57889 (SUPERFAMILY)
Ailuropoda melanoleuca	40s ribosomal protein s5	9	P:GO:0006413; F:GO:0003729; F:GO:0008270; P:GO:0006355; F:GO:0003735; P:GO:0006450; C:GO:0022627; F:GO:0005515; C:GO:0005634	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Pan troglodytes	proteasome (macropain) beta 4	11	P:GO:0051436; P:GO:0051437; F:GO:0004298; C:GO:0045111; C:GO:0005813; P:GO:0031145; F:GO:0001530; P:GO:0002862; P:GO:0044419; C:GO:0005839; C:GO:0005634	-	EC:3.4.25.0	IPR001353; G3DSA:3.60.20.10 (GENE3D), PTHR11599 (PANTHER), PTHR11599:SF5 (PANTHER), PS51476 (PROFILE), SSF56235 (SUPERFAMILY)
Ancylostoma caninum	metalloprotease 1 precursor	2	F:GO:0046872; F:GO:0008237	-		IPR001506; IPR006026; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	P:GO:0055085; C:GO:0016021	-		IPR011701; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11662 (PANTHER), PTHR11662:SF11 (PANTHER), SignalP (SIGNALP)

Caenorhabditis briggsae	ribosomal r-	10	P:GO:0040010; P:GO:0031167; F:GO:0003676; P:GO:0000003; P:GO:0002119; P:GO:0040039; P:GO:0006898; P:GO:0009792; F:GO:0008168; C:GO:0005634	-	EC:2.1.1.0	IPR008162; IPR012920; IPR015507
	-	0				-
Ostertagia ostertagi	heat shock protein family member (hsp-)	1	P:GO:0006950	-		IPR001436; IPR002068; IPR008978; G3DSA:2.60.40.790 (GENE3D), PTHR11527 (PANTHER), PTHR11527:SF28 (PANTHER)
	-	0				-
Caenorhabditis elegans	tbc1 domain member 5	2	P:GO:0019915; F:GO:0005515	-		SignalP (SIGNALP)
Caenorhabditis elegans	tbc1 domain member 5	2	P:GO:0019915; F:GO:0005515	-		SignalP (SIGNALP)
Caenorhabditis elegans	tbc1 domain member 5	2	P:GO:0019915; F:GO:0005515	-		IPR000195; G3DSA:1.10.8.270 (GENE3D), PTHR22957 (PANTHER), PTHR22957:SF25 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	tbc1 domain member 5	2	P:GO:0019915; F:GO:0005515	-		IPR000195; G3DSA:1.10.8.270 (GENE3D), PTHR22957 (PANTHER), PTHR22957:SF25 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	carbonic ydrase family member (cah-4)	0		P:GO:0000003; P:GO:0040011		-
	-	0				-
Caenorhabditis elegans	hypothetical protein Y34B4A.4 [Caenorhabditis elegans]	3	F:GO:0005085; C:GO:0005622; P:GO:0051056	-		IPR008937; PTHR23113:SF40 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG18218 [Caenorhabditis briggsae]	3	P:GO:0007275; P:GO:0000003; P:GO:0009987	-		-
Caenorhabditis briggsae	translocon-associated protein gamma	3	C:GO:0030176; C:GO:0005784; P:GO:0006613	-		IPR009779; SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR013883
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR013883
Physcomitrella patens	d1 chromosomal isoform a	0		C:GO:0000785; F:GO:0004540; P:GO:0006396; F:GO:0003680; F:GO:0003677; C:GO:0005634; C:GO:0005737; F:GO:0003723; F:GO:0008270; F:GO:0003696; P:GO:0006355; F:GO:0003690		IPR017956; IPR020478

Caenorhabditis briggsae	innexin family protein	4	P:GO:0019915; C:GO:0016021; C:GO:0005921; F:GO:0008233	-		PS51257 (PROFILE), SignalP (SIGNALP)
	-	0				-
						-
Ornithorhynchus anatinus	pot1 protection of telomeres 1 homolog	0		P:GO:0040010; P:GO:0000723; C:GO:0000784; F:GO:0003677		IPR012340; IPR016027; G3DSA:2.40.50.210 (GENE3D)
Caenorhabditis briggsae	rho guanyl-nucleotide exchange factor	1	P:GO:0000003	-		IPR000219
Brugia malayi	myosin xviiia	4	C:GO:0005856; C:GO:0005730; F:GO:0042802; C:GO:0005794	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR13140 (PANTHER), PTHR13140:SF14 (PANTHER), SSF52540 (SUPERFAMILY)
Taeniopygia guttata	sequestosome 1	6	F:GO:0005515; C:GO:0043231; P:GO:0044237; P:GO:0006915; P:GO:0048522; C:GO:0044444	-		IPR000270; IPR000433; G3DSA:3.10.20.240 (GENE3D), PTHR15090 (PANTHER), SSF54277 (SUPERFAMILY)
Taeniopygia guttata	sequestosome 1	6	F:GO:0005515; C:GO:0043231; P:GO:0044237; P:GO:0006915; P:GO:0048522; C:GO:0044444	-		IPR000270; IPR000433; G3DSA:3.10.20.240 (GENE3D), PTHR15090 (PANTHER), SSF54277 (SUPERFAMILY)
Taeniopygia guttata	sequestosome 1	6	F:GO:0005515; C:GO:0043231; P:GO:0044237; P:GO:0006915; P:GO:0048522; C:GO:0044444	-		IPR000433; G3DSA:3.10.20.240 (GENE3D), PTHR15090 (PANTHER), SSF54277 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	cwf19-like protein 1	1	F:GO:0003824	-		-
Caenorhabditis elegans	cwf19-like protein 1	1	F:GO:0003824	-		-
Caenorhabditis elegans	citin family member (cex-1)	0				-
	-	0				-
Caenorhabditis briggsae	nuclear vcp-like	4	F:GO:0004176; F:GO:0005524; P:GO:0006508; F:GO:0004252	-	EC:3.4.21.0	IPR003959; G3DSA:3.40.50.300 (GENE3D), PTHR23077 (PANTHER), PTHR23077:SF16 (PANTHER), SSF52540 (SUPERFAMILY)
Loa loa	frizzled smoothened family membrane region containing protein	7	P:GO:0007186; F:GO:0004926; C:GO:0016021; P:GO:0007165; P:GO:0007275; P:GO:0016055; F:GO:0004930	-		-
Caenorhabditis briggsae	briggsae cbr-nmy-2 protein	9	F:GO:0008307; C:GO:0044449; P:GO:0048739; C:GO:0016459; P:GO:0048251; P:GO:0006939; F:GO:0005515; F:GO:0000166; P:GO:0030241	-		IPR000048; IPR001609; G3DSA:4.10.270.10 (GENE3D), PTHR13140 (PANTHER), PTHR13140:SF23 (PANTHER), SSF52540 (SUPERFAMILY)

Caenorhabditis elegans	temporarily assigned gene -me family member (tag-333)	0		F:GO:0005515		-
	-	0				-
	-	0				-
	-	0				IPR000436; IPR016060; SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	1-acylglycerol-3-phosphate o-acyltransferase 2 (lysophosphatidic acid beta)	5	F:GO:0008415; P:GO:0008544; C:GO:0044444; P:GO:0008654; C:GO:0016020	-		IPR002123; G3DSA:3.40.1130.10 (GENE3D), PTHR10434 (PANTHER), SignalP (SIGNALP), SSF69593 (SUPERFAMILY)
Caenorhabditis elegans	1-acylglycerol-3-phosphate o-acyltransferase 2 (lysophosphatidic acid beta)	5	F:GO:0008415; P:GO:0008544; C:GO:0044444; P:GO:0008654; C:GO:0016020	-		IPR002123; G3DSA:3.40.1130.10 (GENE3D), PTHR10434 (PANTHER), SignalP (SIGNALP), SSF69593 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-ain-1 protein	0		F:GO:0005515		-
Caenorhabditis elegans	briggsae cbr-ain-1 protein	1	F:GO:0005515	-		SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-ain-1 protein	0		F:GO:0005515		-
Caenorhabditis briggsae	ubiquitin-like modifier-activating enzyme 5	8	C:GO:0005737; F:GO:0046872; F:GO:0005515; F:GO:0071566; F:GO:0005524; F:GO:0016616; F:GO:0048037; P:GO:0071569	-	EC:1.1.1.0	IPR000594; IPR006140; IPR009036; IPR016040; PTHR10953 (PANTHER), PTHR10953:SF9 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				PTHR13167 (PANTHER), PTHR13167:SF7 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	dipeptidyl peptidase 9	1	F:GO:0016787	-		IPR001375; IPR002469; G3DSA:2.140.10.30 (GENE3D), G3DSA:3.40.50.1820 (GENE3D), PTHR11731 (PANTHER), PTHR11731:SF8 (PANTHER), SSF53474 (SUPERFAMILY), SSF82171 (SUPERFAMILY)
Caenorhabditis elegans	tbc1 domain member 16	0		F:GO:0005096; P:GO:0032313; C:GO:0005622; F:GO:0005097		IPR000195; G3DSA:1.10.8.270 (GENE3D), PTHR22957 (PANTHER), PTHR22957:SF33 (PANTHER)
Loa loa	hypothetical protein LOAG_14117 [Loa loa]	0				-
	-	0				SignalP (SIGNALP)
Callithrix jacchus	programmed cell death 5	2	F:GO:0003677; P:GO:0006917	-		SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; C:GO:0016020; F:GO:0005215; P:GO:0006810; F:GO:0008158		IPR003392; PTHR10796 (PANTHER), PTHR10796:SF12 (PANTHER), SSF82866 (SUPERFAMILY)
Caenorhabditis elegans	Hypothetical protein Y45G12C.13 [Caenorhabditis elegans]	0				PTHR23016 (PANTHER)

Loa loa	rbm25 protein	5	F:GO:0003729; P:GO:0006915; P:GO:0000381; F:GO:0005515; C:GO:0016607	-		IPR002483; G3DSA:1.20.1390.10 (GENE3D), PTHR18806 (PANTHER), SSF101233 (SUPERFAMILY)
Loa loa	aldo-keto reductase	4	P:GO:0009792; P:GO:0040010; P:GO:0002119; P:GO:0040011	-		IPR001395; IPR018170; IPR020471; IPR023210; PTHR11732:SF34 (PANTHER)
Loa loa	hypothetical upf0049 protein in chromosome	0		F:GO:0016740; P:GO:0006479; F:GO:0008276; P:GO:0007098; F:GO:0008168; P:GO:0040025; C:GO:0005634; P:GO:0000003; C:GO:0005737; P:GO:0040020; P:GO:0009790; F:GO:0005515; P:GO:0040010; P:GO:0042127; P:GO:0040035		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	kinesin-associated protein 3	5	P:GO:0051179; C:GO:0043229; F:GO:0032266; F:GO:0005515; P:GO:0050794	-		IPR008658; PTHR15605:SF1 (PANTHER), PF05804 (PFAM)
	-	0				-
Caenorhabditis elegans	sig-l recognition particle 54 kda protein	17	F:GO:0008144; C:GO:0005829; C:GO:0005786; F:GO:0030942; F:GO:0043021; C:GO:0005730; F:GO:0008312; C:GO:0016607; P:GO:0000003; P:GO:0006617; F:GO:0019003; P:GO:0002119; F:GO:0005515; F:GO:0003924; P:GO:0042493; P:GO:0006616; F:GO:0005525	-	EC:3.6.5.4; EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3	IPR000897; IPR003593; IPR013822; G3DSA:3.40.50.300 (GENE3D), PTHR11564 (PANTHER), PTHR11564:SF5 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis brenneri	isoleucyl-tr- synthetase	1	F:GO:0003824	-		IPR002301; IPR009080; IPR013155; G3DSA:1.10.730.10 (GENE3D), PTHR11946 (PANTHER)

Caenorhabditis elegans	hypothetical protein F25G6.9 [Caenorhabditis elegans]	0		F:GO:0008312; F:GO:0030942; C:GO:0005786; P:GO:0006614; C:GO:0048500; F:GO:0005515; P:GO:0045900		IPR022542
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				G3DSA:2.10.90.10 (GENE3D), SignalP (SIGNALP), SSF57501 (SUPERFAMILY)
Brugia malayi	high mobility group protein	11	P:GO:0008348; P:GO:0043388; P:GO:0035218; F:GO:0016564; F:GO:0008301; P:GO:0000122; F:GO:0008134; P:GO:0007379; P:GO:0006338; C:GO:0005634; F:GO:0003702	-		IPR000135; IPR000910; IPR009071; PTHR13711 (PANTHER)
Caenorhabditis elegans	tm2d4_caeel ame: full=tm2 domain-containing protein	0				SignalP (SIGNALP)
Caenorhabditis briggsae	vacuolar protein sorting-associated protein 54	1	P:GO:0006810	-		IPR019515; PTHR12965 (PANTHER)
Caenorhabditis elegans	r- binding identical	0		F:GO:0003676; F:GO:0000166; P:GO:0009792		-
Caenorhabditis briggsae	bestrophin family protein	2	P:GO:0040011; P:GO:0040018	-		IPR000615; IPR021134; SignalP (SIGNALP)
Caenorhabditis elegans	pleckstrin homology domain family member 3	1	F:GO:0005488	-		IPR002219; PTHR12326 (PANTHER)
Ailuropoda melanoleuca	heterogeneous nuclear ribonucleoprotein u-like protein 1-like	6	P:GO:0008380; C:GO:0030530; P:GO:0045449; F:GO:0003723; F:GO:0005515; P:GO:0009615	-		PTHR12381 (PANTHER), PTHR12381:SF10 (PANTHER)
	-	0				-
Caenorhabditis elegans	thioredoxin peroxidase 1	21	C:GO:0008385; P:GO:0032496; P:GO:0042744; F:GO:0008022; F:GO:0051920; F:GO:0019901; P:GO:0033673; F:GO:0043027; F:GO:0004601; P:GO:0045454; P:GO:0008284; P:GO:0001893; F:GO:0042802; P:GO:0051881; P:GO:0030099; C:GO:0005769; P:GO:0007005; P:GO:0055114; P:GO:0051092; P:GO:0043066; C:GO:0005739	-	EC:1.11.1.15; EC:1.11.1.7	-

Caenorhabditis elegans	motile sperm domain-containing protein 2	0		C:GO:0005856; C:GO:0016021; F:GO:0005198		IPR001251; PTHR19993 (PANTHER)
Loa loa	novel protein (zgc:55794)	0		F:GO:0003674; C:GO:0005575		PTHR13532 (PANTHER)
Caenorhabditis elegans	3-hydroxyacyl- dehydroge-se -d-binding	3	P:GO:0008152; F:GO:0016491; F:GO:0005488	-		IPR006108; IPR006176; IPR008927; IPR013328; IPR016040; PTHR23309 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	protein jagu-l	6	P:GO:0009792; C:GO:0005789; P:GO:0040010; P:GO:0000003; P:GO:0040011; C:GO:0016021	-		IPR009787; SignalP (SIGNALP)
Caenorhabditis briggsae	endoplasmic reticulum metallopeptidase 1	4	F:GO:0008233; P:GO:0040011; C:GO:0016021; P:GO:0006508	-		IPR007484; G3DSA:3.40.630.10 (GENE3D), PTHR12147 (PANTHER), SSF53187 (SUPERFAMILY)
Caenorhabditis briggsae	structural mainte-nce of chromosomes protein 5	2	P:GO:0009792; P:GO:0045132	-		-
Caenorhabditis briggsae	structural mainte-nce of chromosomes protein 5	2	P:GO:0009792; P:GO:0045132	-		-
	-	0				-
Caenorhabditis briggsae	cg12024- isoform b	0				IPR003892; IPR009060; G3DSA:1.10.8.10 (GENE3D), PTHR13467 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0008152; F:GO:0005515; F:GO:0016790	-	EC:3.1.2.0	IPR014940
Caenorhabditis briggsae	delta-6 fatty acid desaturase	5	P:GO:0006633; F:GO:0016717; F:GO:0005515; F:GO:0020037; P:GO:0055114	-	EC:1.14.19.0	IPR001199; IPR005804; IPR012171; IPR022272; PTHR19353 (PANTHER)
	-	0				-
	-	0				IPR000436; IPR016060; SignalP (SIGNALP)
Brugia malayi	ef hand family protein	0		F:GO:0005509; F:GO:0004871		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	probable sulfotransferase	1	F:GO:0008146	-	EC:2.8.2.0	-
Caenorhabditis briggsae	briggsae cbr-cdc- protein	2	F:GO:0017111; F:GO:0005524	-	EC:3.6.1.15	IPR003593; IPR003959; IPR003960; G3DSA:3.40.50.300 (GENE3D), PTHR23077 (PANTHER), PTHR23077:SF7 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	briggsae cbr-teg-1 protein	0		F:GO:0005515		-
Caenorhabditis elegans	gon4l protein	0		P:GO:0006355; F:GO:0003677; C:GO:0005634		-

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	8	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0040015; P:GO:0040010; P:GO:0008340; P:GO:0040011; F:GO:0004129	-	EC:1.9.3.1	IPR004204; SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	translation initiation factor eif-2b subunit gamma	0		F:GO:0016740; P:GO:0009058; C:GO:0005851; F:GO:0005085; P:GO:0014003; P:GO:0006413; C:GO:0005737; F:GO:0008135; F:GO:0016779; C:GO:0005575; P:GO:0051716; F:GO:0003743		-
Caenorhabditis elegans	translation initiation factor eif-2b subunit gamma	0		F:GO:0016740; P:GO:0009058; C:GO:0005851; F:GO:0005085; P:GO:0014003; P:GO:0006413; C:GO:0005737; F:GO:0008135; F:GO:0016779; C:GO:0005575; P:GO:0051716; F:GO:0003743		-
	-	0				SignalP (SIGNALP)
Dictyocaulus viviparus	calcium-independent phospholipase a2-gamma	5	P:GO:0016042; C:GO:0043231; F:GO:0016787; C:GO:0044444; C:GO:0016020	-		IPR002641; IPR016035; G3DSA:3.40.1090.10 (GENE3D), PTHR18958 (PANTHER), PTHR18958:SF28 (PANTHER)
Caenorhabditis briggsae	copine family protein	2	F:GO:0005515; P:GO:0008340	-		IPR000008; IPR002035; IPR008973; IPR010734; G3DSA:2.60.40.150 (GENE3D), PTHR10857 (PANTHER), SSF53300 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0008340; F:GO:0005515		G3DSA:2.60.40.150 (GENE3D)

Pan troglodytes	phosphatidylethanolamine-binding protein 1	40	C:GO:0019717; C:GO:0005791; P:GO:0001933; P:GO:0060409; C:GO:0005625; P:GO:0007420; P:GO:0051602; F:GO:0004867; F:GO:0005102; P:GO:0010243; C:GO:0043679; C:GO:0005615; P:GO:0045471; P:GO:0043409; F:GO:0008429; P:GO:0002026; P:GO:0051592; P:GO:0006979; P:GO:0007568; P:GO:0048240; P:GO:0009408; C:GO:0005794; P:GO:0051412; P:GO:0014823; P:GO:0042755; F:GO:0005524; P:GO:0010951;	-		-
	-	0				-
Brugia malayi	elegans protein partially confirmed by transcript evidence	1	P:GO:0006810	-		IPR003280; IPR013099; G3DSA:1.10.287.70 (GENE3D), PTHR11003 (PANTHER), PTHR11003:SF7 (PANTHER), SignalP (SIGNALP), SSF81324 (SUPERFAMILY)
Loa loa	cell cycle-regulated factor p78	0		P:GO:0007099; C:GO:0005634		PTHR13233 (PANTHER)
Loa loa	transcription initiation factor tfiid subunit 1	22	F:GO:0002039; P:GO:0006367; P:GO:0000080; F:GO:0004402; P:GO:0018107; P:GO:0006974; F:GO:0017025; P:GO:0046777; P:GO:0010552; C:GO:0005730; P:GO:0032436; P:GO:0018105; F:GO:0004674; F:GO:0003713; F:GO:0043565; P:GO:0006368; C:GO:0045120; P:GO:0042493; C:GO:0005669; F:GO:0070577; P:GO:0016573; C:GO:0071339	-	EC:2.3.1.48; EC:2.7.11.0	IPR001487; IPR018359; PTHR13900 (PANTHER)
	-	0				-

Brugia malayi	polyphosphoinositide phosphatase	13	P:GO:0008219; P:GO:0043473; P:GO:0016311; P:GO:0030384; P:GO:0007626; F:GO:0017120; C:GO:0055037; F:GO:0005515; P:GO:0010976; P:GO:0007033; C:GO:0010008; C:GO:0005794; C:GO:0005783	-		IPR002013; PTHR11200 (PANTHER), PTHR11200:SF9 (PANTHER)
Brugia malayi	polyphosphoinositide phosphatase	7	F:GO:0017120; C:GO:0055037; F:GO:0005515; P:GO:0010976; C:GO:0010008; C:GO:0005783; C:GO:0005794	-		IPR002013; PTHR11200 (PANTHER), PTHR11200:SF9 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR001534; SignalP (SIGNALP)
Caenorhabditis elegans	copper-transporting atpase 1	50	P:GO:0010468; P:GO:0015677; P:GO:0031069; P:GO:0048813; C:GO:0043005; C:GO:0005802; F:GO:0004008; C:GO:0030140; P:GO:0043588; P:GO:0010273; P:GO:0051542; C:GO:0005783; P:GO:0042417; P:GO:0051353; C:GO:0005829; P:GO:0030199; C:GO:0016323; P:GO:0002082; F:GO:0032767; P:GO:0006754; P:GO:0042093; P:GO:0018205; P:GO:0006570; P:GO:0019430; P:GO:0001974; P:GO:0042414; P:GO:0007626;	-	EC:3.6.3.4	IPR001757; PTHR11939:SF38 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	nitric oxide synthase 1 adaptor protein	5	P:GO:0046662; F:GO:0005515; P:GO:0040017; C:GO:0016010; P:GO:0046716	-		PTHR11232 (PANTHER), PTHR11232:SF17 (PANTHER)
Caenorhabditis elegans	dmx-like 1	0		F:GO:0003674; P:GO:0008150		IPR022033; PTHR13950 (PANTHER), PTHR13950:SF1 (PANTHER), SignalP (SIGNALP)
	-	0				-

	-	0				-
Ancylostoma ceylanicum	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) isoform 2	4	F:GO:0030414; F:GO:0008200; C:GO:0031012; F:GO:0008237	-		IPR002223; IPR020901; PTHR10083 (PANTHER), PTHR10083:SF39 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	yoy6_caeel ame: full=uncharacterized protein	1	F:GO:0005488	-		PTHR12268 (PANTHER), PTHR12268:SF3 (PANTHER)
Caenorhabditis briggsae	yoy6_caeel ame: full=uncharacterized protein	1	F:GO:0005488	-		PTHR12268 (PANTHER), PTHR12268:SF3 (PANTHER)
Caenorhabditis briggsae	yoy6_caeel ame: full=uncharacterized protein	1	F:GO:0005488	-		PTHR12268 (PANTHER), PTHR12268:SF3 (PANTHER)
Caenorhabditis elegans	ribosomal protein l14p l23e containing protein	3	F:GO:0003735; C:GO:0015934; P:GO:0006412	-	EC:3.6.5.3	-
Brugia malayi	nuclear distribution gene c homolog	8	P:GO:0007097; C:GO:0005794; P:GO:0043434; F:GO:0005515; P:GO:0007067; C:GO:0005634; P:GO:0051301; C:GO:0005874	-		IPR007052; IPR008978; IPR017447; G3DSA:2.60.40.790 (GENE3D), PTHR12356 (PANTHER), PTHR12356:SF3 (PANTHER)
Loa loa	inositol -pentakisphosphate 2-ki-se	3	F:GO:0000166; F:GO:0016301; C:GO:0044424	-		IPR009286
Caenorhabditis briggsae	hit zinc finger family protein	0				IPR007529; PTHR13483 (PANTHER), SSF144232 (SUPERFAMILY)
Caenorhabditis elegans	mitochondrial ribosomal	7	P:GO:0009792; P:GO:0002119; F:GO:0003735; P:GO:0000003; C:GO:0015934; P:GO:0040007; P:GO:0006412	-	EC:3.6.5.3	IPR001063; IPR005727; SignalP (SIGNALP)
	-	0				-
	-	0				-
Oryctolagus cuniculus	protein	0				-
Caenorhabditis briggsae	carboxypeptidase d	9	C:GO:0005737; F:GO:0030160; F:GO:0046872; C:GO:0005624; F:GO:0004180; F:GO:0003779; C:GO:0043231; F:GO:0008237; P:GO:0007216	-		IPR000834; IPR008969; IPR014766; G3DSA:3.40.630.10 (GENE3D), PTHR11532 (PANTHER), PTHR11532:SF2 (PANTHER), SignalP (SIGNALP), SSF53187 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	transmembrane protein	7	C:GO:0000139; C:GO:0005764; P:GO:0055085; P:GO:0040010; F:GO:0005351; P:GO:0008643; C:GO:0016021	-		IPR004853; IPR012404; PTHR13146 (PANTHER), SignalP (SIGNALP), SSF103481 (SUPERFAMILY)

Mus musculus	ribosomal protein s16	7	F:GO:0003735; F:GO:0003723; F:GO:0005515; P:GO:0006364; C:GO:0022627; P:GO:0042274; P:GO:0006414	-		IPR000754; IPR014721; IPR020568; IPR020574
	-	0				-
Loa loa	regulator of nonsense transcripts 1	17	P:GO:0000184; C:GO:0000785; F:GO:0005515; F:GO:0008270; P:GO:0006406; P:GO:0006449; F:GO:0003677; P:GO:0009790; F:GO:0003723; C:GO:0000932; F:GO:0003682; F:GO:0004004; P:GO:0071044; F:GO:0005524; P:GO:0006260; P:GO:0007049; P:GO:0006281	-		IPR006935; G3DSA:3.40.50.300 (GENE3D), PTHR10887 (PANTHER), PTHR10887:SF26 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	protein timeless homolog	0				PTHR22940 (PANTHER), PTHR22940:SF6 (PANTHER)
Caenorhabditis briggsae	mater-l effect lethal family member (mel-11)	3	P:GO:0051017; F:GO:0005515; P:GO:0001889	-		IPR002110; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER), PTHR18958:SF166 (PANTHER)
Caenorhabditis elegans	mater-l effect lethal family member (mel-11)	1	F:GO:0005515	-		IPR020683; PTHR18958 (PANTHER), PTHR18958:SF166 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	peroxidasin homolog	11	P:GO:0042744; P:GO:0055114; P:GO:0000003; C:GO:0005615; F:GO:0004601; F:GO:0005515; F:GO:0020037; C:GO:0031012; F:GO:0005201; P:GO:0030198; C:GO:0005783	-	EC:1.11.1.7	IPR002007; IPR003598; IPR007110; IPR010255; IPR013098; IPR013783; IPR019791; PTHR11475 (PANTHER), PTHR11475:SF10 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis briggsae	deah (asp-glu-ala-his) box polypeptide 35	4	F:GO:0008026; F:GO:0003676; F:GO:0005524; P:GO:0006396	-		-
Loa loa	protein cereblon	4	P:GO:0044248; P:GO:0044267; P:GO:0006508; C:GO:0044424	-		IPR003111; IPR015947; PTHR14255 (PANTHER)
Loa loa	protein cereblon	4	P:GO:0044248; P:GO:0044267; P:GO:0006508; C:GO:0044424	-		IPR003111; IPR015947; PTHR14255 (PANTHER)

Caenorhabditis briggsae	isopentenyl-diphosphate delta-isomerase	1	F:GO:0003824	-		IPR000086; IPR011876; IPR015797; PS51462 (PROFILE)
Ostertagia ostertagi	venom-allergen-like protein family member (vap-1)	0		P:GO:0040011; C:GO:0005576		IPR001283; IPR014044; PTHR10334:SF9 (PANTHER), SignalP (SIGNALP)
	-	0				-
Brugia malayi	mgc80099 protein	1	P:GO:0009792	-		SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; C:GO:0016020; P:GO:0055085; F:GO:0005215; P:GO:0006810		IPR005828; PTHR11600 (PANTHER)
Caenorhabditis elegans	actin-like protein 6b	7	C:GO:0071565; P:GO:0006333; F:GO:0005524; P:GO:0007399; F:GO:0005515; F:GO:0005200; C:GO:0016514	-		IPR004000; IPR004001; G3DSA:3.30.420.40 (GENE3D), PTHR11937:SF32 (PANTHER), SSF53067 (SUPERFAMILY)
Caenorhabditis elegans	r3h domain-containing protein c19orf22 homolog	0		F:GO:0003676; F:GO:0003674; P:GO:0008150; C:GO:0005575; C:GO:0005634		SSF82708 (SUPERFAMILY)
Caenorhabditis elegans	phosphatidylserine decarboxylase	3	P:GO:0040010; F:GO:0004609; P:GO:0008654	-	EC:4.1.1.65	IPR003817; IPR005221; SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-rga-2 protein	0		P:GO:0000003; F:GO:0005096; P:GO:0040010; P:GO:0007165; P:GO:0009792; C:GO:0005622		-
Caenorhabditis briggsae	rho gtpase-activating protein 20	1	P:GO:0050789	-		IPR000198; IPR008936; PTHR23179 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	rho gtpase-activating protein 20	1	P:GO:0050789	-		IPR000198; IPR008936; PTHR23179 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	rnp-1 like r--binding protein	2	P:GO:0009792; F:GO:0000166	-		IPR000504; IPR012677; IPR015465; PTHR10432 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis brenneri	protein phosphatase 1f	2	F:GO:0005515; F:GO:0003824	-		SignalP (SIGNALP)
Caenorhabditis elegans	heterogeneous nuclear ribonucleoprotein l	8	P:GO:0008380; C:GO:0045120; F:GO:0003723; F:GO:0005515; C:GO:0044428; P:GO:0006397; C:GO:0030529; F:GO:0000166	-		IPR000504; IPR006536; IPR012677; PTHR11546 (PANTHER), PTHR11546:SF5 (PANTHER), SSF54928 (SUPERFAMILY)

Loa loa	d- topoisomerase 2-binding protein 1	7	P:GO:0080090; P:GO:0006270; P:GO:0031323; C:GO:0043229; P:GO:0034622; F:GO:0005488; P:GO:0060255	-		-
Brugia malayi	msp domain protein	0		C:GO:0005856; F:GO:0005198		-
Caenorhabditis elegans	p21-activated ki-se family member (pak-1)	15	C:GO:0005925; P:GO:0007411; P:GO:0006468; P:GO:0008360; F:GO:0005515; P:GO:0050803; P:GO:0007155; F:GO:0005525; C:GO:0016021; P:GO:0007391; F:GO:0004674; C:GO:0005856; F:GO:0005524; P:GO:0050770; N:GO:0035556	-	EC:2.7.11.0	IPR000095; IPR000719; IPR011009; IPR015750; IPR017441; IPR017442; G3DSA:3.30.200.20 (GENE3D), G3DSA:3.90.810.10 (GENE3D), PTHR22986 (PANTHER)
Caenorhabditis elegans	heat shock protein	2	P:GO:0009408; F:GO:0005515	-		IPR001436; IPR002068; IPR008978; G3DSA:2.60.40.790 (GENE3D), PTHR11527 (PANTHER), PTHR11527:SF31 (PANTHER)
Caenorhabditis elegans	sodium potassium-dependent atpase beta-2 subunit	13	P:GO:0006814; P:GO:0040010; F:GO:0005391; C:GO:0016021; P:GO:0006813; P:GO:0000003; P:GO:0006754; P:GO:0010171; P:GO:0002119; P:GO:0040011; P:GO:0006898; P:GO:0009792; P:GO:0040018	-	EC:3.6.3.9	IPR000402; G3DSA:1.20.5.170 (GENE3D), PTHR11523:SF7 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	sodium potassium-dependent atpase beta-2 subunit	13	P:GO:0006814; P:GO:0040010; F:GO:0005391; C:GO:0016021; P:GO:0006813; P:GO:0000003; P:GO:0006754; P:GO:0010171; P:GO:0002119; P:GO:0040011; P:GO:0006898; P:GO:0009792; P:GO:0040018	-	EC:3.6.3.9	-

Caenorhabditis elegans	sodium potassium-dependent atpase beta-2 subunit	13	P:GO:0006814; P:GO:0040010; F:GO:0005391; C:GO:0016021; P:GO:0006813; P:GO:0000003; P:GO:0006754; P:GO:0010171; P:GO:0002119; P:GO:0040011; P:GO:0006898; P:GO:0009792; P:GO:0040018	-	EC:3.6.3.9	IPR000402; G3DSA:1.20.5.170 (GENE3D), PTHR11523:SF7 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	sodium potassium-dependent atpase beta-2 subunit	13	P:GO:0006814; P:GO:0040010; F:GO:0005391; C:GO:0016021; P:GO:0006813; P:GO:0000003; P:GO:0006754; P:GO:0010171; P:GO:0002119; P:GO:0040011; P:GO:0006898; P:GO:0009792; P:GO:0040018	-	EC:3.6.3.9	IPR000402; G3DSA:1.20.5.170 (GENE3D), PTHR11523:SF7 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	chromodomain-helicase-d--binding protein 1	12	C:GO:0005703; C:GO:0005705; F:GO:0008026; P:GO:0006333; P:GO:0035042; P:GO:0007476; F:GO:0003677; F:GO:0005524; C:GO:0000785; P:GO:0048477; F:GO:0003682; C:GO:0005634	-		IPR000330; IPR000953; IPR001650; IPR014001; IPR014021; IPR016197; G3DSA:2.40.50.40 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR10799 (PANTHER), PTHR10799:SF70 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				IPR000210; IPR011333
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	swi snf matrix actin dependent regulator of subfamily member isoform cra_a	12	C:GO:0071564; C:GO:0071565; P:GO:0006357; C:GO:0017053; C:GO:0005730; F:GO:0042802; F:GO:0003677; C:GO:0016514; F:GO:0003713; P:GO:0045892; P:GO:0045893; P:GO:0006338	-		IPR001005; IPR007526; IPR009057; IPR011991; IPR012287; IPR014778; IPR017884; PTHR12802 (PANTHER), PTHR12802:SF7 (PANTHER)

Caenorhabditis elegans	glyci-mide ribonucleotide synthetase-aminoimidazole ribonucleotide synthetase-glyci-mide ribonucleotide transformylase	7	P:GO:0010035; F:GO:0005488; F:GO:0016874; P:GO:0009168; P:GO:0048513; F:GO:0004644; P:GO:0010033	-	EC:2.1.2.2	IPR000115; IPR000728; IPR010918; IPR011054; IPR011761; IPR013815; IPR013816; IPR013817; IPR016185; IPR016188; IPR020559; IPR020560; IPR020561; IPR020562; G3DSA:3.30.1330.10 (GENE3D), G3DSA:3.90.650.10 (GENE3D), PTHR10520 (PANTHER), PTHR10520:SF2 (PANTHER), SSF56059 (SUPERFAMILY)
Caenorhabditis elegans	cgmp-dependent protein ki-se foraging	2	F:GO:0004672; P:GO:0000003	-		IPR000595; IPR002373; IPR014710; IPR018488; IPR018490; PTHR11635 (PANTHER)
Brugia malayi	riken cd- 2610019a05 gene	4	F:GO:0005488; F:GO:0004672; P:GO:0031323; P:GO:0016310	-		-
Brugia malayi	riken cd- 2610019a05 gene	4	F:GO:0005488; F:GO:0004672; P:GO:0031323; P:GO:0016310	-		IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF22 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	small optic lobes protein	0		F:GO:0004198; F:GO:0004197; F:GO:0016787; C:GO:0005737; F:GO:0008270; F:GO:0008234; F:GO:0008233; P:GO:0006508; C:GO:0005622; P:GO:0007399; P:GO:0007632; F:GO:0005488		IPR001876
Caenorhabditis elegans	small optic lobes protein	0		F:GO:0004198; F:GO:0004197; F:GO:0016787; C:GO:0005737; F:GO:0008270; F:GO:0008234; F:GO:0008233; P:GO:0006508; C:GO:0005622; P:GO:0007399; P:GO:0007632; F:GO:0005488		IPR001876
Caenorhabditis briggsae	multiple coagulation factor deficiency isoform cra_b	6	P:GO:0009792; P:GO:0006810; F:GO:0005509; C:GO:0044444; P:GO:0019752; C:GO:0005576	-		IPR002048; IPR011992; IPR018247; IPR018249; PTHR23104 (PANTHER), SSF47473 (SUPERFAMILY)

Caenorhabditis briggsae	multiple coagulation factor deficiency isoform cra_b	6	P:GO:0009792; P:GO:0006810; F:GO:0005509; C:GO:0044444; P:GO:0019752; C:GO:0005576	-		IPR002048; IPR011992; IPR018247; IPR018249; PTHR23104 (PANTHER), SSF47473 (SUPERFAMILY)
Caenorhabditis elegans	multiple coagulation factor deficiency isoform cra_b	5	P:GO:0009792; P:GO:0006810; C:GO:0044444; P:GO:0019752; C:GO:0005576	-		IPR002048; IPR011992; IPR018247; IPR018249; PTHR23104 (PANTHER), SignalP (SIGNALP), SSF47473 (SUPERFAMILY)
Brugia malayi	ankrd13d protein	0				IPR002110; IPR003903; IPR020683; IPR021832; PTHR12447 (PANTHER)
Ancylostoma caninum	ribosomal protein s4	7	P:GO:0009792; C:GO:0005840; F:GO:0003735; F:GO:0005515; P:GO:0007420; P:GO:0006412; F:GO:0019843	-	EC:3.6.5.3	-
Caenorhabditis briggsae	briggsae cbr-ten-1 protein	0		C:GO:0016021; C:GO:0016020; P:GO:0007165		IPR011042; IPR013090; PTHR11219 (PANTHER), PTHR11219:SF4 (PANTHER), SSF63829 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-ten-1 protein	2	P:GO:0007366; C:GO:0016020	-		IPR011042; PTHR11219 (PANTHER), PTHR11219:SF4 (PANTHER), SSF63829 (SUPERFAMILY)
Caenorhabditis briggsae	odd oz ten-m homolog 4	0		F:GO:0003674; P:GO:0001702; C:GO:0016020; P:GO:0007165; C:GO:0005575		IPR011042; PTHR11219 (PANTHER), PTHR11219:SF4 (PANTHER), SSF63829 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	uncharacterized protein c18orf8	1	F:GO:0005515	-		IPR009755; PTHR12897 (PANTHER)
Caenorhabditis elegans	kinesin family member 23	5	P:GO:0007049; C:GO:0030496; F:GO:0005515; C:GO:0005819; C:GO:0005654	-		IPR001752; IPR019821; PTHR16012 (PANTHER), PTHR16012:SF60 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
Schistosoma mansoni	rabkinesin-6-related [Schistosoma mansoni]	0		F:GO:0005524; F:GO:0000166; F:GO:0003777; F:GO:0003774; P:GO:0007018; C:GO:0005874		-
Caenorhabditis briggsae	uncoordi-ted family member (unc-60)	14	P:GO:0042067; P:GO:0016319; P:GO:0007409; P:GO:0035286; P:GO:0008585; P:GO:0030041; P:GO:0001737; C:GO:0005737; F:GO:0003727; F:GO:0003779; P:GO:0010591; C:GO:0005875; P:GO:0007298; P:GO:0000910	-		IPR002108; G3DSA:3.40.20.10 (GENE3D), PTHR11913 (PANTHER), PTHR11913:SF12 (PANTHER), SSF55753 (SUPERFAMILY)

Haemonchus contortus	pra1 family protein 3	2	F:GO:0005515; P:GO:0000003	-		IPR004895; PTHR12859 (PANTHER)
Caenorhabditis briggsae	cdgsh iron sulfur domain 1	5	P:GO:0043457; F:GO:0005506; F:GO:0051537; C:GO:0016021; C:GO:0005741	-		IPR006622; IPR018967; PTHR13680 (PANTHER), PTHR13680:SF2 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-grh-1 protein	3	P:GO:0002119; P:GO:0000003; P:GO:0040007	-		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical upf0028 protein in chromosome	5	C:GO:0016021; P:GO:0046470; P:GO:0009653; F:GO:0004622; C:GO:0005789	-	EC:3.1.1.5	-
	-	0				-
						IPR003599; IPR007110; IPR010939; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF9 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis briggsae	sh2 domain-containing adapter protein b	0		C:GO:0016020; P:GO:0006915; C:GO:0005737; P:GO:0001525; F:GO:0001948; P:GO:0007275; P:GO:0030154; P:GO:0007165; C:GO:0005575; F:GO:0005515; F:GO:0005070; P:GO:0042100; C:GO:0005886		IPR000980; PTHR15127 (PANTHER), PTHR15127:SF7 (PANTHER), SSF55550 (SUPERFAMILY)
Caenorhabditis briggsae	accessory gland protein	1	P:GO:0000003	-		-
Loa loa	infection response gene protein partially confirmed by transcript evidence	1	P:GO:0045087	-		IPR012816; SSF143990 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	protein downstream neighbor of son-like protein	1	P:GO:0048856	-		-
Caenorhabditis elegans	protein downstream neighbor of son-like protein	1	P:GO:0048856	-		-
Caenorhabditis elegans	protein downstream neighbor of son-like protein	1	P:GO:0048856	-		-
	-	0				-
Loa loa	briggsae cbr-cdh-4 protein	0		P:GO:0007413; C:GO:0016021; C:GO:0016020; P:GO:0007411; P:GO:0007163; F:GO:0005509; C:GO:0005886; P:GO:0007156; P:GO:0007155		-
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	cullin 1	12	P:GO:0007050; C:GO:0005829; P:GO:0051437; C:GO:0019005; P:GO:0009887; P:GO:0008285; F:GO:0004842; P:GO:0008629; F:GO:0005515; P:GO:0000082; P:GO:0031146; C:GO:0005654	-	EC:6.3.2.19	IPR001373; IPR011991; IPR016157; IPR016158; IPR016159; IPR019559; G3DSA:1.20.1310.10 (GENE3D), G3DSA:4.10.1030.10 (GENE3D), PTHR11932 (PANTHER), PTHR11932:SF17 (PANTHER), SSF46785 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	5	P:GO:0002119; P:GO:0040002; P:GO:0040010; C:GO:0044464; P:GO:0008340	-		IPR010987; IPR012336; PTHR12289 (PANTHER), PTHR12289:SF17 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein C48E7.1 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
Caenorhabditis elegans	glycolipid transfer protein	6	P:GO:0055114; F:GO:0017089; C:GO:0005737; P:GO:0008340; F:GO:0051861; P:GO:0046836	-		IPR014830; PTHR10219 (PANTHER)
Caenorhabditis briggsae	chromobox protein homolog 1 (heterochromatin protein 1 homolog beta)	0		F:GO:0003682; P:GO:0009792; C:GO:0000785; P:GO:0006333; C:GO:0005634		IPR000953; IPR001525; IPR016197; G3DSA:2.40.50.40 (GENE3D), PTHR10629:SF1 (PANTHER)
Caenorhabditis elegans	protein phosphatase 2c containing protein	5	C:GO:0008287; F:GO:0004722; P:GO:0006470; F:GO:0005509; C:GO:0005739	-		IPR001932; IPR014045; IPR015655; PTHR13832:SF98 (PANTHER)
Nippostrongylus brasiliensis	elegans protein partially confirmed by transcript evidence	1	P:GO:0009792	-		SignalP (SIGNALP)
Nippostrongylus brasiliensis	elegans protein partially confirmed by transcript evidence	1	P:GO:0009792	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	diaphanous homolog 2	1	F:GO:0005515	-		IPR015425; PTHR23213 (PANTHER), PTHR23213:SF12 (PANTHER)
Caenorhabditis elegans	tbc1 domain family member 23-like	0		P:GO:0032313; F:GO:0005097; C:GO:0005622		IPR001763; PTHR13297 (PANTHER)
Caenorhabditis briggsae	abnormal cell lineage family member (lin-10)	4	C:GO:0005737; P:GO:0007163; C:GO:0005886; P:GO:0016081	-		IPR006020; IPR011993; PTHR12345 (PANTHER), PTHR12345:SF1 (PANTHER), SSF50729 (SUPERFAMILY)
Caenorhabditis briggsae	abnormal cell lineage family member (lin-10)	4	C:GO:0005737; P:GO:0007163; C:GO:0005886; P:GO:0016081	-		IPR006020; IPR011993; PTHR12345 (PANTHER), PTHR12345:SF1 (PANTHER), SignalP (SIGNALP), SSF50729 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				PTHR23241 (PANTHER), PTHR23241:SF5 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	spectrin beta chain	4	F:GO:0005200; C:GO:0008091; F:GO:0003779; F:GO:0016787	-		IPR002017; IPR018159; PD936484 (PRODOM), G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF48 (PANTHER), SSF46966 (SUPERFAMILY)

Caenorhabditis briggsae	heterogeneous nuclear ribonucleoprotein a b	2	F:GO:0003676; F:GO:0000166	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF15 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	arginine ki-se	4	C:GO:0016021; F:GO:0005524; F:GO:0005515; F:GO:0004054	-	EC:2.7.3.3	-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR001534; SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	mitochondrial -dh:ubiquinone oxidoreductase esss	3	P:GO:0002119; P:GO:0009792; P:GO:0040007	-		-
	-	0				-
Brugia malayi	2700029m09rik protein	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	huntingtin interacting protein	18	P:GO:0030324; P:GO:0048268; P:GO:0007405; F:GO:0005543; C:GO:0009986; F:GO:0003779; F:GO:0030276; P:GO:0048260; P:GO:0006915; P:GO:0007165; P:GO:0040036; P:GO:0009887; C:GO:0043229; P:GO:0009953; C:GO:0005887; C:GO:0044444; P:GO:0008152; P:GO:0045879	-		IPR011417; PTHR10407 (PANTHER), PTHR10407:SF4 (PANTHER)
Caenorhabditis elegans	briggsae cbr-npp-3 protein	0				-
Caenorhabditis briggsae	interferon-related developmental regulator 2	0		F:GO:0003674; F:GO:0005488; C:GO:0005575		IPR006921; IPR007701; PTHR12354 (PANTHER), PTHR12354:SF4 (PANTHER)
Caenorhabditis briggsae	interferon-related developmental regulator 2	0		F:GO:0003674; F:GO:0005488; C:GO:0005575		IPR006921; IPR007701; PTHR12354 (PANTHER), PTHR12354:SF4 (PANTHER)
Ancylostoma ceylanicum	briggsae cbr-vap-1 protein	0		C:GO:0005576		IPR014044

Caenorhabditis briggsae	aldehyde dehydroge-se 9 member a1	15	C:GO:0005829; F:GO:0043176; C:GO:0015630; P:GO:0042445; P:GO:0001889; P:GO:0055114; P:GO:0045329; F:GO:0051287; F:GO:0019145; P:GO:0006081; P:GO:0042136; F:GO:0042803; F:GO:0047105; F:GO:0004029; C:GO:0005634	-	EC:1.2.1.19; EC:1.2.1.47; EC:1.2.1.3	SignalP (SIGNALP)
Caenorhabditis elegans	target of erk ki-se mpk-1 protein isoform confirmed by transcript evidence	0		P:GO:0007165; P:GO:0023034; F:GO:0005515; C:GO:0005622		-
Caenorhabditis elegans	target of erk ki-se mpk-1 protein isoform confirmed by transcript evidence	0		P:GO:0007165; P:GO:0023034; F:GO:0005515; C:GO:0005622		-
Caenorhabditis briggsae	Hypothetical protein CBG09291 [Caenorhabditis briggsae]	0				-
Loa loa	double-strand-break repair protein rad21 homolog	6	P:GO:0006996; P:GO:0045132; F:GO:0005515; P:GO:0040011; P:GO:0009792; C:GO:0005634	-		IPR006909; IPR023093; PTHR12585 (PANTHER), PTHR12585:SF6 (PANTHER), SSF46785 (SUPERFAMILY)
Homo sapiens	immunoglobulin light chain variable region	0				IPR003596; IPR007110; IPR013106; IPR013783; PTHR23267 (PANTHER), PTHR23267:SF14 (PANTHER), SignalP (SIGNALP), SSF48726 (SUPERFAMILY)
Loa loa	protein-tyrosine phosphatase containing protein	1	F:GO:0004721	-	EC:3.1.3.16	IPR000242; IPR000387; IPR016130; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis briggsae	o-sialoglycoprotein endopeptidase-like 1	1	F:GO:0070011	-		SignalP (SIGNALP)
Loa loa	hypothetical protein LOAG_06829 [Loa loa]	0				G3DSA:3.80.10.10 (GENE3D), SSF52058 (SUPERFAMILY)
Caenorhabditis briggsae	syntaxin 5	9	P:GO:0042147; F:GO:0047485; P:GO:0006903; C:GO:0005730; F:GO:0005484; P:GO:0016081; P:GO:0006886; C:GO:0031201; C:GO:0005794	-		-
Haemonchus contortus	hexoki-se	5	P:GO:0060361; P:GO:0005975; F:GO:0005515; F:GO:0004396; F:GO:0000166	-	EC:2.7.1.1	IPR001312; IPR019807; IPR022672; IPR022673; G3DSA:3.40.367.20 (GENE3D), SSF53067 (SUPERFAMILY)
	-	0				-
	-	0				-

	-	0				-
Caenorhabditis elegans	n-myc downstream regulated	0				IPR004142; G3DSA:3.40.50.1820 (GENE3D), PTHR11034:SF2 (PANTHER), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical kda protein in chromosome	0				IPR004142; G3DSA:3.40.50.1820 (GENE3D), PTHR11034:SF2 (PANTHER), SSF53474 (SUPERFAMILY)
Brugia malayi	hypothetical protein Bm1_55095 [Brugia malayi]	0				-
	-	0				-
Caenorhabditis elegans	26s proteasome non-atpase regulatory subunit 8	1	C:GO:0044424	-		IPR006746; IPR019280
Caenorhabditis elegans	translocon-associated protein subunit delta precursor	3	C:GO:0044464; F:GO:0005515; P:GO:0040011	-		IPR002114; IPR008855; SignalP (SIGNALP)
Caenorhabditis elegans	translocon-associated protein subunit delta precursor	3	C:GO:0044464; F:GO:0005515; P:GO:0040011	-		IPR002114; IPR008855; SignalP (SIGNALP)
Caenorhabditis elegans	herpud family member 2	0		F:GO:0003674; P:GO:0006986; C:GO:0016021; C:GO:0016020; P:GO:0008150; P:GO:0007283; C:GO:0005575		PTHR12943 (PANTHER), PTHR12943:SF2 (PANTHER)
Caenorhabditis elegans	homocysteine-responsive endoplasmic reticulum-resident ubiquitin-like domain member 2 protein	0		P:GO:0006986; C:GO:0016021; P:GO:0006983; C:GO:0016020; C:GO:0005875		IPR019955; G3DSA:3.10.20.90 (GENE3D), PTHR12943 (PANTHER), PTHR12943:SF2 (PANTHER), SSF54236 (SUPERFAMILY)
Caenorhabditis elegans	homocysteine-responsive endoplasmic reticulum-resident ubiquitin-like domain member 2 protein	0		P:GO:0006986; C:GO:0016021; P:GO:0006983; C:GO:0016020; C:GO:0005875		IPR019955; G3DSA:3.10.20.90 (GENE3D), PTHR12943 (PANTHER), PTHR12943:SF2 (PANTHER), SSF54236 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	brefeldin a-inhibited guanine nucleotide-exchange protein 1-like	12	P:GO:0040010; F:GO:0008060; C:GO:0005622; F:GO:0005086; P:GO:0006887; P:GO:0000003; P:GO:0032012; P:GO:0002119; P:GO:0040011; P:GO:0006898; F:GO:0017022; P:GO:0009792	-		IPR011989; IPR015403; IPR016024; PTHR10663 (PANTHER), PTHR10663:SF16 (PANTHER)

Caenorhabditis briggsae	brefeldin a-inhibited guanine nucleotide-exchange protein 1-like	12	P:GO:0040010; F:GO:0008060; C:GO:0005622; F:GO:0005086; P:GO:0006887; P:GO:0000003; P:GO:0032012; P:GO:0002119; P:GO:0040011; P:GO:0006898; F:GO:0017022; P:GO:0009792	-		IPR011989; IPR015403; IPR016024; PTHR10663 (PANTHER), PTHR10663:SF16 (PANTHER)
Caenorhabditis briggsae	brefeldin a-inhibited guanine nucleotide-exchange protein 1-like	12	P:GO:0040010; F:GO:0008060; C:GO:0005622; F:GO:0005086; P:GO:0006887; P:GO:0000003; P:GO:0032012; P:GO:0002119; P:GO:0040011; P:GO:0006898; F:GO:0017022; P:GO:0009792	-		IPR011989; IPR015403; IPR016024; PTHR10663 (PANTHER), PTHR10663:SF16 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR009673; SignalP (SIGNALP)
Caenorhabditis elegans	msp-domain protein 1 variant	6	C:GO:0044297; P:GO:0019915; P:GO:0040018; P:GO:0000003; F:GO:0005198; C:GO:0031143	-		IPR000535; IPR008962; PTHR22947 (PANTHER)
Brugia malayi	histone h2a	14	P:GO:0006952; P:GO:0040010; C:GO:0000786; P:GO:0006281; P:GO:0018991; P:GO:0045449; P:GO:0040035; F:GO:0043565; P:GO:0002119; P:GO:0040011; P:GO:0006334; P:GO:0006997; P:GO:0009792; C:GO:0005634	-		-
	-	0				-
Loa loa	palmitoyltransferase zdhhc17	8	F:GO:0019706; F:GO:0004871; P:GO:0042953; F:GO:0015095; F:GO:0046872; C:GO:0030660; P:GO:0043123; F:GO:0005515	-		IPR002110; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER), PTHR18958:SF137 (PANTHER)

Caenorhabditis elegans	kiaa0966 protein	4	P:GO:0006629; C:GO:0005795; C:GO:0005798; F:GO:0016787	-		IPR002013; PTHR11200 (PANTHER), PTHR11200:SF11 (PANTHER)
Caenorhabditis elegans	fibulin-1 isoform c precursor	1	F:GO:0005515	-		IPR000152; IPR001881; IPR013032; IPR013091; IPR018097; G3DSA:2.10.25.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF89 (PANTHER), SSF57196 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	chromosome transmission fidelity	3	F:GO:0005488; F:GO:0016787; P:GO:0006974	-		G3DSA:1.10.8.60 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23389 (PANTHER), SSF52540 (SUPERFAMILY)
Loa loa	lin-9 homolog (elegans)	1	C:GO:0070176	-		IPR010561; PTHR21689 (PANTHER), PTHR21689:SF3 (PANTHER)
	-	0				-
	-	0				-
synthetic construct	ribosomal protein s11	5	F:GO:0003735; F:GO:0005515; C:GO:0022627; F:GO:0019843; P:GO:0006414	-		IPR000266; IPR012340; IPR016027; IPR019978; IPR019979; PTHR10744:SF2 (PANTHER)
Ancylostoma caninum	histone h3	4	C:GO:0000786; F:GO:0003677; P:GO:0006334; C:GO:0005634	-		IPR000164; IPR007125; IPR009072
Caenorhabditis briggsae	tubulin alpha 1	12	P:GO:0040010; C:GO:0043234; P:GO:0035046; P:GO:0002119; F:GO:0005515; P:GO:0007017; P:GO:0040017; F:GO:0000166; P:GO:0040039; P:GO:0006898; P:GO:0002009; P:GO:0009792	-		IPR000217; IPR002452; IPR003008; PTHR11588:SF11 (PANTHER)
	-	0				-
Ailuropoda melanoleuca	tumor translatio-lly-controlled 1	9	P:GO:0009615; F:GO:0005509; C:GO:0005771; C:GO:0045298; P:GO:0006874; C:GO:0005615; P:GO:0006916; F:GO:0005515; P:GO:0006816	-		IPR011057; IPR011323; IPR018103; IPR018105

Ailuropoda melanoleuca	tumor translatio-lly-controlled 1	9	P:GO:0009615; F:GO:0005509; C:GO:0005771; C:GO:0045298; P:GO:0006874; C:GO:0005615; P:GO:0006916; F:GO:0005515; P:GO:0006816	-		IPR011057; IPR011323; IPR018103; IPR018105
Pongo abelii	tumor translatio-lly-controlled 1	9	P:GO:0009615; F:GO:0005509; C:GO:0005771; C:GO:0045298; P:GO:0006874; C:GO:0005615; P:GO:0006916; F:GO:0005515; P:GO:0006816	-		IPR011057; IPR011323; IPR018103; IPR018105
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	actin-depolymerizing factor	2	F:GO:0003779; C:GO:0005622	-		IPR002108; G3DSA:3.40.20.10 (GENE3D), PTHR11913 (PANTHER), PTHR11913:SF12 (PANTHER), SSF55753 (SUPERFAMILY)
Caenorhabditis elegans	fusion (involved in t(12 16) in malig-nt liposarcoma)	7	P:GO:0021954; F:GO:0008270; F:GO:0003676; C:GO:0005730; P:GO:0008380; F:GO:0005515; F:GO:0000166	-		IPR000504; IPR001876; IPR012677; PR01228 (PRINTS), G3DSA:4.10.1060.10 (GENE3D), PTHR23238 (PANTHER), PTHR23238:SF2 (PANTHER), SSF54928 (SUPERFAMILY), SSF90209 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Rattus norvegicus	type alpha 2	0		P:GO:0001501; F:GO:0046332; P:GO:0007266; C:GO:0005584; F:GO:0042802; C:GO:0005581; P:GO:0043589; P:GO:0070208; P:GO:0030199; C:GO:0005615; C:GO:0031012; F:GO:0030674; P:GO:0008217; F:GO:0048407; F:GO:0005515; C:GO:0005886; C:GO:0005576; P:GO:0007179; P:GO:0001568; F:GO:0005201		-
	-	0				SignalP (SIGNALP)
	-	0				-

synthetic construct	lipolysis stimulated lipoprotein receptor	11	P:GO:0009790; C:GO:0005730; F:GO:0004872; C:GO:0034362; C:GO:0005794; C:GO:0005886; C:GO:0042627; P:GO:0001889; C:GO:0016021; P:GO:0019216; C:GO:0034361	-		-
Caenorhabditis briggsae	briggsae cbr-abt-2 protein	2	F:GO:0017111; F:GO:0000166	-	EC:3.6.1.15	IPR003439; IPR003593; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR19229 (PANTHER), PTHR19229:SF25 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
Loa loa	briggsae cbr-tag-340 protein	0		F:GO:0015485; F:GO:0017127; P:GO:0008150; P:GO:0006694; C:GO:0005575		IPR019498; PTHR12136 (PANTHER), PTHR12136:SF2 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	zinc finger and btb domain containing 1	0		F:GO:0003677; C:GO:0005634; F:GO:0003676; F:GO:0008270; C:GO:0005575; C:GO:0005622; F:GO:0005515; F:GO:0046872; P:GO:0006350; P:GO:0008150; P:GO:0045449		IPR007087; IPR015880; PTHR14596 (PANTHER), SSF57667 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	lipophorin receptor	1	P:GO:0009792	-		SignalP (SIGNALP)
Caenorhabditis elegans	lipophorin receptor	1	P:GO:0009792	-		SignalP (SIGNALP)
Caenorhabditis briggsae	zinc finger and btb domain containing 40	0		F:GO:0003677; C:GO:0005634; F:GO:0003676; P:GO:0000003; F:GO:0003674; F:GO:0008270; C:GO:0005813; C:GO:0005575; P:GO:0006355; C:GO:0005730; C:GO:0005622; F:GO:0046872; P:GO:0008150		IPR007087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)
Branchiostoma floridae	small subunit processome component 20 homolog	3	F:GO:0005488; C:GO:0031981; P:GO:0006364	-		IPR011430
Caenorhabditis elegans	major facilitator superfamily protein	0		C:GO:0016021; C:GO:0016020; P:GO:0055085; F:GO:0005215; P:GO:0006810		IPR005829; IPR011701; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11600 (PANTHER), PTHR11600:SF28 (PANTHER)
Caenorhabditis elegans	transmembrane protein 188	0		C:GO:0016021; C:GO:0016020		IPR019168

Caenorhabditis elegans	transmembrane protein 188	0		C:GO:0016021; C:GO:0016020		IPR019168
Caenorhabditis elegans	transmembrane protein 188	0		C:GO:0016021; C:GO:0016020		IPR019168
Caenorhabditis elegans	transmembrane protein 188	0		C:GO:0016021; C:GO:0016020		IPR019168
Caenorhabditis elegans	px domain containing protein	3	F:GO:0035091; F:GO:0005515; P:GO:0007154	-		IPR001683; PTHR15454 (PANTHER), PTHR15454:SF6 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	px domain containing protein	3	F:GO:0035091; F:GO:0005515; P:GO:0007154	-		IPR001683; PTHR15454 (PANTHER), PTHR15454:SF6 (PANTHER), SignalP (SIGNALP)
Yarrowia lipolytica	YALI0F12793p [Yarrowia lipolytica]	0				-
Macaca mulatta	ribosomal protein s29	10	P:GO:0001525; P:GO:0001570; F:GO:0008270; P:GO:0051726; F:GO:0003735; P:GO:0006414; C:GO:0022627; F:GO:0005515; P:GO:0060218; P:GO:0009790	-		-
Loa loa	sumo-1 activating enzyme subunit 1	5	F:GO:0043008; P:GO:0016925; F:GO:0008022; F:GO:0019948; F:GO:0046982	-		IPR000011; IPR000594; IPR009036; IPR016040; PTHR10953 (PANTHER), PTHR10953:SF30 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-let-19 protein	9	P:GO:0006367; P:GO:0045944; F:GO:0004872; F:GO:0016455; F:GO:0046966; C:GO:0016592; F:GO:0003713; P:GO:0009792; P:GO:0030521	-		IPR009401; PTHR12950 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-lrs-1 protein	5	F:GO:0004823; P:GO:0006429; F:GO:0005515; F:GO:0005524; C:GO:0005829	-	EC:6.1.1.4	IPR009080; IPR013155; IPR014729; IPR015413; G3DSA:1.10.730.10 (GENE3D), PTHR11946 (PANTHER), PTHR11946:SF10 (PANTHER), SSF52374 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-rbc-2 protein	0				-

Caenorhabditis elegans	sh3-domain grb2-like endophilin b2	8	F:GO:0005515; C:GO:0016020; C:GO:0043231; P:GO:0044237; P:GO:0009792; P:GO:0007126; P:GO:0044238; C:GO:0044444	-		IPR004148; IPR013606; PTHR10661 (PANTHER), PTHR10661:SF12 (PANTHER), SSF103657 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-dnj-11 protein	8	P:GO:0040010; F:GO:0005488; P:GO:0034645; P:GO:0090304; P:GO:0000003; P:GO:0008356; P:GO:0010467; P:GO:0009792	-		IPR001623; IPR015609; PTHR11821:SF29 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	innexin family protein	4	P:GO:0019915; P:GO:0009792; P:GO:0008340; P:GO:0000003	-		IPR000990
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	3	P:GO:0019915; P:GO:0009792; P:GO:0040010	-		-
Caenorhabditis briggsae	supervillin	1	P:GO:0045132	-		IPR007122; IPR015628; G3DSA:3.40.20.10 (GENE3D), SSF55753 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG08094 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)
Caenorhabditis elegans	l80003_1guanylyl cyclase	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	ki-se suppressor of ras	1	F:GO:0004672	-		IPR000719; IPR002219; IPR017441; G3DSA:3.30.200.20 (GENE3D), G3DSA:3.30.60.20 (GENE3D), PTHR23257 (PANTHER), PTHR23257:SF90 (PANTHER), SSF57889 (SUPERFAMILY)
Gallus gallus	PREDICTED: similar to Ac1147 [Gallus gallus]	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	zinc nfx1-type containing 1	1	F:GO:0005488	-		PTHR10887 (PANTHER), PTHR10887:SF10 (PANTHER)

Caenorhabditis briggsae	abnormal dauer formation family member (daf-16)	18	P:GO:0009411; P:GO:0002821; P:GO:0008286; P:GO:0008340; P:GO:0043065; F:GO:0033613; P:GO:0010564; P:GO:0006355; F:GO:0031625; F:GO:0043565; P:GO:0046890; P:GO:0002119; F:GO:0003700; P:GO:0060537; P:GO:0043620; P:GO:0034605; C:GO:0005737; C:GO:0005634	-		IPR001766; IPR011991; IPR018122; SSF46785 (SUPERFAMILY)
Ancylostoma ceylanicum	abnormal dauer formation family member (daf-16)	22	P:GO:0002821; P:GO:0008340; F:GO:0008270; P:GO:0008286; P:GO:0046890; P:GO:0065008; P:GO:0006355; P:GO:0060537; P:GO:0009411; C:GO:0005737; P:GO:0010564; P:GO:0040008; P:GO:0043620; F:GO:0031625; F:GO:0043565; P:GO:0002119; F:GO:0033613; F:GO:0003700; P:GO:0034605; P:GO:0048523; C:GO:0005634; P:GO:0043065	-		IPR001766; IPR011991; IPR018122; SSF46785 (SUPERFAMILY)
Caenorhabditis briggsae	abnormal dauer formation family member (daf-16)	18	P:GO:0009411; P:GO:0002821; P:GO:0008286; P:GO:0008340; P:GO:0043065; F:GO:0033613; P:GO:0010564; P:GO:0006355; F:GO:0031625; F:GO:0043565; P:GO:0046890; P:GO:0002119; F:GO:0003700; P:GO:0060537; P:GO:0043620; P:GO:0034605; C:GO:0005737; C:GO:0005634	-		PTHR16166 (PANTHER), PTHR16166:SF25 (PANTHER)

Caenorhabditis elegans	liprin alpha (lar-interacting protein alpha) (sy-pse defective protein 2)	11	P:GO:0045467; P:GO:0048490; P:GO:0007416; P:GO:0008594; P:GO:0048676; C:GO:0045202; F:GO:0016491; P:GO:0007412; F:GO:0005515; P:GO:0031290; P:GO:0048841	-		PTHR12587 (PANTHER), PTHR12587:SF2 (PANTHER)
Caenorhabditis elegans	glutamate-rich wd repeat containing 1	0		F:GO:0003674; P:GO:0008150; C:GO:0005730; C:GO:0005634; C:GO:0005575		IPR022052; PTHR22850 (PANTHER), PTHR22850:SF6 (PANTHER)
Caenorhabditis elegans	transcriptio-l adaptor 2 (ada2 yeast)-like	3	P:GO:0048856; P:GO:0007275; P:GO:0050789	-		IPR001005; IPR009057; IPR017884; PTHR12374 (PANTHER)
Loa loa	histone deacetylase	14	F:GO:0016566; P:GO:0000122; F:GO:0004407; F:GO:0003714; P:GO:0007043; P:GO:0030183; C:GO:0005737; P:GO:0006954; C:GO:0000118; P:GO:0007399; F:GO:0003682; P:GO:0016568; P:GO:0045843; P:GO:0001570	-		IPR000286; PTHR10625:SF21 (PANTHER), SSF52768 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein Y48G9A.3 [Caenorhabditis elegans]	1	P:GO:0000003	-		SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-cogc-3 protein	6	P:GO:0043170; P:GO:0034613; P:GO:0048193; C:GO:0044431; P:GO:0015031; C:GO:0016020	-		-
Caenorhabditis elegans	ubl3 protein	1	C:GO:0005622	-		IPR000626; IPR019955; G3DSA:3.10.20.90 (GENE3D), PTHR13169 (PANTHER), SSF54236 (SUPERFAMILY)
Loa loa	laterally symmetric (defective in lateral asymmetry) family member (lsy-2)	3	F:GO:0008270; F:GO:0003676; C:GO:0005622	-		IPR007087; IPR013087; IPR015880; PTHR23224 (PANTHER), PTHR23224:SF422 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	translocase of outer mitochondrial membrane 20 homolog	9	P:GO:0040010; F:GO:0015450; C:GO:0016021; C:GO:0005742; P:GO:0000003; P:GO:0006626; P:GO:0002119; F:GO:0051082; P:GO:0009792	-		IPR002056; IPR022422; G3DSA:1.20.960.10 (GENE3D)

	-	0				-
Leishmania major strain Friedlin	myosin heavy chain	2	C:GO:0043232; F:GO:0005515	-		SignalP (SIGNALP)
Caenorhabditis elegans	loc446287 protein	2	P:GO:0055114; F:GO:0003995	-	EC:1.3.99.3	-
	-	0				-
	-	0				-
Caenorhabditis elegans	cy romatosis (human disease gene) homolog family member (cyld-1)	0		F:GO:0003735; P:GO:0006412; F:GO:0004221; C:GO:0005840; P:GO:0006511; C:GO:0005622		-
Caenorhabditis briggsae	blastula protease-10	1	F:GO:0008233	-		IPR001506; IPR006026; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	8	F:GO:0046872; F:GO:0016491; P:GO:0040018; P:GO:0040010; P:GO:0000003; P:GO:0008340; P:GO:0040011; P:GO:0008152	-		IPR001128; IPR002401; IPR017972; PTHR19383:SF176 (PANTHER)
Caenorhabditis briggsae	calreticulin family protein	11	P:GO:0040010; P:GO:0009306; C:GO:0043005; F:GO:0005509; P:GO:0006457; P:GO:0002119; C:GO:0044425; P:GO:0007281; F:GO:0051082; P:GO:0009792; C:GO:0005783	-		IPR001580; IPR008985; IPR009033; IPR013320; IPR018124; PTHR11073:SF1 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	l-lactate dehydroge-se	5	C:GO:0005737; F:GO:0005488; F:GO:0004459; P:GO:0055114; P:GO:0006096	-	EC:1.1.1.27	IPR015955; IPR018177; IPR022383; PTHR11540 (PANTHER), PTHR11540:SF3 (PANTHER)
Caenorhabditis briggsae	l-lactate dehydroge-se	5	C:GO:0005737; F:GO:0005488; F:GO:0004459; P:GO:0055114; P:GO:0006096	-	EC:1.1.1.27	IPR001236; IPR001557; IPR011304; IPR015955; IPR016040; IPR018177; IPR022383; PTHR11540 (PANTHER), PTHR11540:SF3 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-gei-15 protein	0				-
Caenorhabditis briggsae	dihydrolipoamide acetyltransferase component of pyruvate dehydroge-se	9	P:GO:0009792; C:GO:0045254; C:GO:0005811; F:GO:0004742; F:GO:0005515; P:GO:0040010; P:GO:0000003; P:GO:0006898; P:GO:0006086	-	EC:2.3.1.12	IPR000089; IPR003016; IPR011053; G3DSA:2.40.50.100 (GENE3D), PTHR23151 (PANTHER), PTHR23151:SF9 (PANTHER)

	-	0				-
Loa loa	rnft1 protein	2	F:GO:0046872; C:GO:0016020	-		IPR001841; IPR013083; IPR017907; IPR018957; PTHR15860 (PANTHER), SSF57850 (SUPERFAMILY)
Loa loa	protein disulfide	6	P:GO:0045454; C:GO:0044444; C:GO:0043229; F:GO:0016853; P:GO:0008152; C:GO:0030529	-		IPR012335; IPR012336; IPR013766; IPR017937; PTHR18929 (PANTHER), PS51257 (PROFILE), SignalP (SIGNALP)
Caenorhabditis elegans	rest corepressor	3	F:GO:0046872; F:GO:0003676; C:GO:0005622	-		IPR000949; IPR001005; IPR007087; IPR009057; IPR014778; IPR015880; IPR017884; PTHR16089 (PANTHER)
Caenorhabditis briggsae	swi snf matrix actin dependent regulator of subfamily member 1	22	F:GO:0002039; C:GO:0005654; P:GO:0051091; P:GO:0018991; C:GO:0071565; P:GO:0040010; C:GO:0016514; P:GO:0006898; C:GO:0001741; P:GO:0015074; C:GO:0071564; P:GO:0040017; P:GO:0010552; P:GO:0045090; C:GO:0005730; P:GO:0008285; F:GO:0003676; P:GO:0002119; P:GO:0006338; P:GO:0030154; P:GO:0001835; P:GO:0040035	-		IPR006939
Harpegnathos saltator	hypothetical protein EAI_03706 [Harpeg-thos saltator]	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		IPR006578
	-	0				-
Caenorhabditis elegans	phosphatidylinositol n-acetylglucosaminyltransferase subunit c	4	F:GO:0017176; C:GO:0016021; P:GO:0016254; C:GO:0005783	-	EC:2.4.1.198	-
Caenorhabditis briggsae	briggsae cbr-sel-2 protein	7	C:GO:0005737; P:GO:0008104; F:GO:0051018; P:GO:0042675; F:GO:0016740; C:GO:0016020; C:GO:0005634	-		-
Caenorhabditis briggsae	aurin family member (cnt-2)	8	F:GO:0008060; P:GO:0032312; F:GO:0008270; P:GO:0000003; F:GO:0005515; F:GO:0000166; C:GO:0044464; P:GO:0009792	-		IPR011993; SSF50729 (SUPERFAMILY)

Caenorhabditis briggsae	calmodulin	1	F:GO:0005509	-		IPR011992; IPR018249; PTHR10891 (PANTHER), PTHR10891:SF3 (PANTHER), SSF47473 (SUPERFAMILY)
Caenorhabditis briggsae	nuclear cap-binding protein subunit 2	12	F:GO:0003723; P:GO:0046833; P:GO:0006417; P:GO:0008380; P:GO:0031047; P:GO:0006370; P:GO:0006408; F:GO:0000166; C:GO:0005737; P:GO:0000184; C:GO:0005634; P:GO:0051028	-		-
Caenorhabditis elegans	zinc finger in n-recognin family protein	0		P:GO:0030163; F:GO:0008270; F:GO:0004842; F:GO:0005515		-
Brugia malayi	laminin b2	1	C:GO:0005578	-		PD936484 (PRODOM), PTHR10574 (PANTHER), PTHR10574:SF14 (PANTHER)
Brugia malayi	hypothetical protein Bm1_25410 [Brugia malayi]	0				-
	-	0				-
Caenorhabditis elegans	major facilitator superfamily protein	3	P:GO:0019915; C:GO:0016020; P:GO:0006810	-		IPR011701; IPR016196; G3DSA:1.20.1250.20 (GENE3D), PTHR11662 (PANTHER), PTHR11662:SF21 (PANTHER)
Loa loa	probable 26s proteasome non-atpase regulatory subunit	6	P:GO:0009792; P:GO:0002119; F:GO:0005515; P:GO:0000003; P:GO:0008340; P:GO:0040007	-		-
Caenorhabditis elegans	ras association	0		P:GO:0007165		IPR000159; PTHR21298 (PANTHER), SSF54236 (SUPERFAMILY)
Caenorhabditis elegans	cgmp-dependent protein ki-se egl-4	6	P:GO:0006468; F:GO:0046872; F:GO:0030553; P:GO:0007275; F:GO:0005524; F:GO:0004692	-	EC:2.7.11.12	-
Caenorhabditis briggsae	translation initiation factor if-2	11	F:GO:0003743; P:GO:0006413; P:GO:0040010; C:GO:0016021; P:GO:0007264; P:GO:0015684; F:GO:0015093; F:GO:0003924; P:GO:0006898; C:GO:0005737; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000795; IPR015760; G3DSA:3.40.50.300 (GENE3D), PTHR23115 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	let-23 fertility effector regulator family member (lfe-2)	1	F:GO:0008440	-	EC:2.7.1.127	IPR005522; PTHR12400:SF5 (PANTHER), SSF56104 (SUPERFAMILY)
	-	0				-
Brugia malayi	th1-like homolog	1	P:GO:0006350	-		-
	-	0				-

	-	0				-
Caenorhabditis elegans	nitrilase	12	P:GO:0009684; P:GO:0051410; F:GO:0047558; F:GO:0080061; P:GO:0000003; P:GO:0019499; F:GO:0016740; C:GO:0009507; F:GO:0047427; F:GO:0080109; C:GO:0005886; C:GO:0048046	-	EC:4.2.1.65; EC:3.5.5.4	IPR000132; IPR003010; PTHR23088 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-wip-1 protein	0		P:GO:0016477; P:GO:0040010; P:GO:0008340		IPR003124; PTHR23202 (PANTHER), PTHR23202:SF3 (PANTHER)
Caenorhabditis elegans	uncoordi-ted family member (unc-84)	1	F:GO:0005515	-		-
Caenorhabditis briggsae	adp-ribosylation factor-like protein 8b	19	P:GO:0008340; C:GO:0005765; P:GO:0007264; C:GO:0030496; P:GO:0007186; P:GO:0007059; P:GO:0000003; C:GO:0031902; P:GO:0051301; F:GO:0019003; F:GO:0043014; P:GO:0007067; F:GO:0003924; F:GO:0048487; P:GO:0006886; P:GO:0009792; C:GO:0051233; F:GO:0005525; C:GO:0005634	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	SignalP (SIGNALP)
Brugia malayi	mif4g domain containing protein	2	F:GO:0005488; P:GO:0006396	-		IPR015172; IPR016021; IPR016024; PTHR12412 (PANTHER), PTHR12412:SF2 (PANTHER)
	-	0				-
Caenorhabditis elegans	alanyl-tr- synthetase	17	P:GO:0006457; P:GO:0021680; F:GO:0004813; P:GO:0006400; P:GO:0006450; F:GO:0016597; P:GO:0001942; C:GO:0005737; P:GO:0043524; P:GO:0043200; P:GO:0043588; P:GO:0050885; F:GO:0002161; F:GO:0003723; P:GO:0006419; P:GO:0030968; F:GO:0005524	-	EC:6.1.1.7	IPR003156; IPR012947; IPR018163; IPR018165; PTHR11777 (PANTHER)

Caenorhabditis elegans	alanyl-tr- synthetase	7	F:GO:0003723; C:GO:0005625; F:GO:0004813; P:GO:0006419; P:GO:0008033; F:GO:0005524; C:GO:0005737	-	EC:6.1.1.7	IPR002318; IPR003156; IPR012947; IPR018162; IPR018163; IPR018164; IPR018165; G3DSA:3.30.930.10 (GENE3D), PTHR11777 (PANTHER), SSF55681 (SUPERFAMILY)
Acyrthosiphon pisum	nuclease harbi1-like	0				-
Caenorhabditis elegans	AC103567_7Hypothetical protein Y51F10.6 [Caenorhabditis elegans]	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F55A4.8 [Caenorhabditis elegans]	0		C:GO:0016021		-
Caenorhabditis briggsae	isochorismatase domain-containing protein mitochondrial precursor	5	P:GO:0008152; C:GO:0005737; F:GO:0016787; F:GO:0042802; C:GO:0043231	-		IPR000868; PTHR14119 (PANTHER)
Loa loa	mh2 domain containing protein	5	F:GO:0003700; F:GO:0005515; C:GO:0005667; P:GO:0006355; P:GO:0007179	-		IPR003619; IPR013019; IPR013790; PTHR13703:SF13 (PANTHER)
Caenorhabditis elegans	branched chain keto acid dehydroge-se alpha polypeptide	8	F:GO:0046872; F:GO:0003826; F:GO:0003863; F:GO:0005515; F:GO:0016831; P:GO:0055114; C:GO:0005947; P:GO:0009083	-	EC:1.2.4.4; EC:4.1.1.0	-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		C:GO:0016021; P:GO:0055085		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		C:GO:0016021; P:GO:0055085		-
	-	0				-
Caenorhabditis elegans	zinc finger in n-recognin family protein	2	P:GO:0032501; P:GO:0048468	-		PTHR21725 (PANTHER)
Caenorhabditis elegans	ubiquitin protein ligase e3 component n-recognin 4	0		F:GO:0016874; C:GO:0016021; C:GO:0016020; C:GO:0005634; P:GO:0006260; F:GO:0008270; P:GO:0016567; F:GO:0005516; C:GO:0005622; F:GO:0004842; F:GO:0046872; P:GO:0008152; F:GO:0005488; C:GO:0005856		PTHR21725 (PANTHER)

Caenorhabditis elegans	mitochondrial cytochrome c oxidase subunit 4	7	P:GO:0040010; F:GO:0004129; P:GO:0008340; P:GO:0000003; P:GO:0002119; P:GO:0009792; C:GO:0005811	-	EC:1.9.3.1	-
Brugia malayi	receptor accessory protein 4	1	C:GO:0044464	-		IPR004345; PTHR12300:SF19 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	sig-l recognition particle 72 kda protein	2	F:GO:0005488; C:GO:0048500	-		IPR011990; IPR013699; IPR019734; PTHR14094 (PANTHER), PTHR14094:SF9 (PANTHER), SSF48452 (SUPERFAMILY)
	-	0				-
	-	0				-
Loa loa	phosphoglycerate ki-se	5	C:GO:0005737; F:GO:0004618; P:GO:0016310; F:GO:0005524; P:GO:0006096	-	EC:2.7.2.3	IPR001576; IPR015824; IPR015901; IPR015911
Caenorhabditis elegans	low quality protein: uncharacterized protein kiaa0467-like	0				-
Brugia malayi	dynein light chain cytoplasmic	14	F:GO:0003777; F:GO:0008092; C:GO:0005829; C:GO:0030286; C:GO:0005874; C:GO:0016459; P:GO:0007017; C:GO:0043186; P:GO:0008039; P:GO:0046907; C:GO:0019861; P:GO:0008152; C:GO:0005634; C:GO:0005886	-		-
Caenorhabditis elegans	oaz_caeel ame: full=ornithine decarboxylase antizyme short=odc-az	1	P:GO:0000003	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	pol ii c-termi-l interaction domain suppressor family member (cids-2)	1	F:GO:0005515	-		IPR006569
Caenorhabditis elegans	bifunctio-l aminoacyl-tr- synthetase	7	C:GO:0005737; F:GO:0004827; P:GO:0006433; C:GO:0017101; F:GO:0004818; P:GO:0006424; F:GO:0005524	-	EC:6.1.1.15; EC:6.1.1.17	IPR000738; IPR002314; IPR002316; IPR004154; IPR004499; IPR006195; IPR009068; IPR016061; IPR017449; G3DSA:3.30.930.10 (GENE3D), PTHR11451 (PANTHER), SSF55681 (SUPERFAMILY)
Caenorhabditis elegans	bifunctio-l aminoacyl-tr- synthetase	7	C:GO:0005737; F:GO:0004827; P:GO:0006433; C:GO:0017101; F:GO:0004818; P:GO:0006424; F:GO:0005524	-	EC:6.1.1.15; EC:6.1.1.17	IPR000738; IPR002314; IPR002316; IPR004154; IPR004499; IPR006195; IPR009068; IPR016061; IPR017449; G3DSA:3.30.930.10 (GENE3D), PTHR11451 (PANTHER), SSF55681 (SUPERFAMILY)

Caenorhabditis elegans	bifunctio-l aminoacyl-tr- synthetase	7	C:GO:0005737; F:GO:0004827; P:GO:0006433; C:GO:0017101; F:GO:0004818; P:GO:0006424; F:GO:0005524	-	EC:6.1.1.15; EC:6.1.1.17	IPR000738; IPR002314; IPR002316; IPR004154; IPR004499; IPR006195; IPR009068; IPR016061; IPR017449; G3DSA:3.30.930.10 (GENE3D), PTHR11451 (PANTHER), SSF55681 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR022559; PD030565 (PRODOM), SignalP (SIGNALP)
Pongo abelii	40s ribosomal protein sa-like	13	P:GO:0016337; F:GO:0003735; C:GO:0005604; F:GO:0004872; P:GO:0006414; C:GO:0022627; F:GO:0043022; C:GO:0005624; F:GO:0043236; C:GO:0043025; P:GO:0007165; C:GO:0005634; C:GO:0005886	-		IPR001865; IPR005707; IPR018130
Caenorhabditis elegans	sig-l transducer and activator of transcription	10	C:GO:0005737; F:GO:0042802; F:GO:0003700; F:GO:0004871; F:GO:0003677; P:GO:0007275; F:GO:0005509; P:GO:0007165; C:GO:0005634; P:GO:0006355	-		IPR000980; IPR001217; IPR008967; IPR011992; IPR013801; PTHR11801:SF3 (PANTHER), SSF55550 (SUPERFAMILY)
Caenorhabditis elegans	sig-l transducer and activator of transcription	10	C:GO:0005737; F:GO:0042802; F:GO:0003700; F:GO:0004871; F:GO:0003677; P:GO:0007275; F:GO:0005509; P:GO:0007165; C:GO:0005634; P:GO:0006355	-		IPR000980; IPR001217; IPR008967; IPR011992; IPR013801; PTHR11801:SF3 (PANTHER), SSF55550 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	hypothetical kda protein in chromosome	0		C:GO:0005739; F:GO:0003674; P:GO:0008150		IPR010625; PTHR13523 (PANTHER)
Caenorhabditis briggsae	hypothetical kda protein in chromosome	0		C:GO:0005739; F:GO:0003674; P:GO:0008150		IPR010625; PTHR13523 (PANTHER)

Brugia malayi	calcium-binding protein 39	11	P:GO:0051291; C:GO:0043234; F:GO:0004674; F:GO:0005509; P:GO:0046320; P:GO:0000003; F:GO:0005515; P:GO:0040017; P:GO:0009792; C:GO:0005737; P:GO:0040018	-	EC:2.7.11.0	IPR011989; IPR013878; IPR016024; PTHR10182 (PANTHER), PTHR10182:SF3 (PANTHER)
Caenorhabditis elegans	adipocyte plasma membrane-associated protein	1	F:GO:0003824	-		IPR004141; IPR011042; PTHR10426:SF2 (PANTHER), SSF63829 (SUPERFAMILY)
Caenorhabditis elegans	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit stt3b	10	C:GO:0008250; P:GO:0018279; C:GO:0016021; P:GO:0000003; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0009792; F:GO:0004579; P:GO:0040015	-	EC:2.4.1.119	IPR003674; PTHR13872 (PANTHER), PTHR13872:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit stt3b	10	C:GO:0008250; P:GO:0018279; C:GO:0016021; P:GO:0000003; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0009792; F:GO:0004579; P:GO:0040015	-	EC:2.4.1.119	IPR003674; PTHR13872 (PANTHER), PTHR13872:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical upf0131 protein cg2811	0		F:GO:0003674; F:GO:0016740; F:GO:0008415; P:GO:0008150; C:GO:0005575		IPR009288; IPR013024; PTHR12510 (PANTHER), SSF110857 (SUPERFAMILY)

Caenorhabditis elegans	vinculin isoform 1	20	C:GO:0005829; P:GO:0007016; P:GO:0030032; C:GO:0043034; P:GO:0090136; P:GO:0034333; F:GO:0002166; P:GO:0043297; P:GO:0030334; C:GO:0001725; C:GO:0005925; P:GO:0034394; F:GO:0003779; C:GO:0005884; F:GO:0005200; F:GO:0045294; C:GO:0005576; F:GO:0017048; C:GO:0005916; P:GO:0006936	-		SignalP (SIGNALP)
Caenorhabditis elegans	vinculin isoform 1	20	C:GO:0005829; P:GO:0007016; P:GO:0030032; C:GO:0043034; P:GO:0090136; P:GO:0034333; F:GO:0002166; P:GO:0043297; P:GO:0030334; C:GO:0001725; C:GO:0005925; P:GO:0034394; F:GO:0003779; C:GO:0005884; F:GO:0005200; F:GO:0045294; C:GO:0005576; F:GO:0017048; C:GO:0005916; P:GO:0006936	-		-
Caenorhabditis briggsae	hydroxyacyl-coenzyme a dehydroge-se	11	P:GO:0055114; P:GO:0040007; C:GO:0016507; P:GO:0019915; F:GO:0003857; P:GO:0002119; P:GO:0006635; F:GO:0050662; P:GO:0006898; P:GO:0009792; F:GO:0004300	-	EC:1.1.1.35; EC:4.2.1.17	IPR006176; IPR016040; SSF51735 (SUPERFAMILY)
Caenorhabditis briggsae	valyl-tr- synthetase	4	P:GO:0006438; F:GO:0005524; F:GO:0004832; C:GO:0005739	-	EC:6.1.1.9	IPR001412; IPR002300; IPR002303; IPR014729; PTHR11946 (PANTHER), SSF52374 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)

	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	isoform d	0		P:GO:0009116; F:GO:0003824		G3DSA:3.40.50.1580 (GENE3D)
	-	0				PTHR16950 (PANTHER), PTHR16950:SF6 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0051301; P:GO:0009792; P:GO:0007126		-
	-	0				-
Caenorhabditis elegans	nol1 nop2 sun domain member 5	0		F:GO:0003674; F:GO:0016740; P:GO:0008152; P:GO:0008150; P:GO:0032259; C:GO:0005575		IPR001678; G3DSA:3.40.50.150 (GENE3D), PTHR22807 (PANTHER), PTHR22807:SF4 (PANTHER), SSF53335 (SUPERFAMILY)
Caenorhabditis briggsae	d- ligase 1	4	P:GO:0006259; F:GO:0016874; P:GO:0006974; F:GO:0000166	-		IPR012308; IPR012310; IPR016059; G3DSA:1.10.3260.10 (GENE3D), G3DSA:3.30.470.30 (GENE3D), PTHR10459 (PANTHER), PTHR10459:SF10 (PANTHER), SSF117018 (SUPERFAMILY), SSF56091 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Angiostrongylus cantonensis	eukaryotic translation initiation factor 5	11	P:GO:0009792; C:GO:0005851; P:GO:0002119; P:GO:0006413; P:GO:0018996; F:GO:0005515; P:GO:0040010; P:GO:0000003; F:GO:0003743; P:GO:0016070; P:GO:0006898	-		IPR002735; IPR003307; IPR016021; IPR016024; IPR016189; IPR016190; G3DSA:3.30.30.50 (GENE3D), PTHR23001 (PANTHER), PTHR23001:SF1 (PANTHER)
Caenorhabditis elegans	nuclear mitogen- and stress-activated protein ki-se-1	16	P:GO:0007243; F:GO:0004674; P:GO:0016572; P:GO:0006355; P:GO:0040007; P:GO:0000003; P:GO:0042221; F:GO:0005524; P:GO:0002119; F:GO:0005515; F:GO:0000287; C:GO:0005654; P:GO:0009792; P:GO:0006950; P:GO:0007173; P:GO:0009605	-	EC:2.7.11.0	IPR000719; IPR002290; IPR008271; IPR011009; IPR017441; IPR017442; IPR020636; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)

Caenorhabditis elegans	nuclear mitogen- and stress-activated protein ki-se-1	16	P:GO:0007243; F:GO:0004674; P:GO:0016572; P:GO:0006355; P:GO:0040007; P:GO:0000003; P:GO:0042221; F:GO:0005524; P:GO:0002119; F:GO:0005515; F:GO:0000287; C:GO:0005654; P:GO:0009792; P:GO:0006950; P:GO:0007173; P:GO:0009605	-	EC:2.7.11.0	IPR000719; IPR002290; IPR008271; IPR011009; IPR017441; IPR017442; IPR020636; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
Caenorhabditis briggsae	type iii restriction res subunit family protein	0		C:GO:0000785; F:GO:0004386; F:GO:0003682; F:GO:0003677; C:GO:0005634; F:GO:0003676; P:GO:0006333; F:GO:0005524; F:GO:0008026		-
Caenorhabditis briggsae	mitochondrial import receptor subunit tom40	10	P:GO:0040010; F:GO:0015288; P:GO:0006820; P:GO:0000003; P:GO:0006626; C:GO:0005741; F:GO:0008308; C:GO:0046930; P:GO:0009792; P:GO:0040018	-		IPR001925; PTHR10802 (PANTHER)
Caenorhabditis elegans	upf0558 protein	0				G3DSA:3.40.50.150 (GENE3D), PTHR21095 (PANTHER), SSF53335 (SUPERFAMILY)
Caenorhabditis elegans	upf0558 protein	0				G3DSA:3.40.50.150 (GENE3D), PTHR21095 (PANTHER), SSF53335 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-gpa-17 protein	0		F:GO:0005525; F:GO:0019001; F:GO:0004871; F:GO:0000166; P:GO:0007165; P:GO:0007186		IPR001019; IPR011025; PTHR10218:SF16 (PANTHER)
Caenorhabditis elegans	atp-binding sub-family d member 4	8	P:GO:0055085; C:GO:0016021; F:GO:0042626; C:GO:0005622; P:GO:0006355; C:GO:0043190; F:GO:0005524; F:GO:0008134	-		IPR002078; IPR003439; IPR003593; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR11384 (PANTHER), PTHR11384:SF3 (PANTHER), SSF52540 (SUPERFAMILY)

Homo sapiens	collagen alpha-2 chain precursor	17	P:GO:0042476; F:GO:0030674; P:GO:0070208; P:GO:0043589; P:GO:0008217; F:GO:0042802; C:GO:0005615; F:GO:0046332; P:GO:0001501; F:GO:0048407; C:GO:0005584; P:GO:0030199; P:GO:0007179; F:GO:0005201; P:GO:0001568; P:GO:0007266; C:GO:0005886	-		-
Caenorhabditis briggsae	Hypothetical protein CBG21101 [Caenorhabditis briggsae]	1	F:GO:0005515	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR001534
Caenorhabditis briggsae	Hypothetical protein CBG21101 [Caenorhabditis briggsae]	1	F:GO:0005515	-		-
Caenorhabditis elegans	zinc finger protein	4	F:GO:0008270; F:GO:0003676; F:GO:0005515; F:GO:0004842	-	EC:6.3.2.19	IPR002867; PTHR11685 (PANTHER), PTHR11685:SF17 (PANTHER), SSF57850 (SUPERFAMILY)
	-	0				PTHR15111 (PANTHER)
Caenorhabditis elegans	serf-like protein	0				SignalP (SIGNALP)
Caenorhabditis elegans	mitogen-activated protein ki-se 11	14	C:GO:0005829; P:GO:0007265; P:GO:0007243; C:GO:0005625; P:GO:0040007; P:GO:0040035; F:GO:0005524; P:GO:0002119; F:GO:0005515; F:GO:0008339; C:GO:0005654; P:GO:0009792; P:GO:0006950; P:GO:0006468	-		IPR000719; IPR002290; IPR008351; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF61 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	protein xap-	2	C:GO:0005739; F:GO:0008137	-	EC:1.6.5.3	PF07225 (PFAM)
Loa loa	briggsae cbr-spr-4 protein	0		F:GO:0003676; F:GO:0005488; F:GO:0005529; F:GO:0008270; C:GO:0005622		IPR007087; IPR015880; PTHR11389 (PANTHER), SignalP (SIGNALP), SSF57667 (SUPERFAMILY)
Caenorhabditis elegans	huntingtin interacting protein 1	7	F:GO:0005515; F:GO:0005543; P:GO:0006897; P:GO:0048522; P:GO:0019222; C:GO:0030136; P:GO:0042981	-		IPR002558; G3DSA:1.20.1410.10 (GENE3D), PTHR10407 (PANTHER), PTHR10407:SF4 (PANTHER), SSF109885 (SUPERFAMILY)

Caenorhabditis elegans	huntingtin interacting protein 1	7	F:GO:0005515; F:GO:0005543; P:GO:0006897; P:GO:0048522; P:GO:0019222; C:GO:0030136; P:GO:0042981	-		IPR002558; G3DSA:1.20.1410.10 (GENE3D), PTHR10407 (PANTHER), PTHR10407:SF4 (PANTHER), SSF109885 (SUPERFAMILY)
Caenorhabditis elegans	loner iso1	5	P:GO:0007520; F:GO:0005086; P:GO:0032012; C:GO:0005622; P:GO:0002121	-		IPR000904; IPR011993; G3DSA:1.10.1000.11 (GENE3D), PTHR10663 (PANTHER), PTHR10663:SF12 (PANTHER), SSF50729 (SUPERFAMILY)
Caenorhabditis elegans	loner iso1	5	P:GO:0007520; F:GO:0005086; P:GO:0032012; C:GO:0005622; P:GO:0002121	-		IPR000904; IPR011993; G3DSA:1.10.1000.11 (GENE3D), PTHR10663 (PANTHER), PTHR10663:SF12 (PANTHER), SSF50729 (SUPERFAMILY)
Caenorhabditis elegans	heavy unconventio-l myosin family member (hum-2)	3	F:GO:0005515; F:GO:0003824; F:GO:0000166	-		IPR001609; PTHR13140 (PANTHER), PTHR13140:SF15 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	transmembrane protein	5	P:GO:0006810; C:GO:0043231; P:GO:0040010; C:GO:0044444; C:GO:0016020	-		IPR004853; PTHR13146 (PANTHER), SignalP (SIGNALP), SSF103481 (SUPERFAMILY)
Loa loa	d domain (prokaryotic heat shock protein) family member (dnj-8)	3	P:GO:0018991; P:GO:0040011; P:GO:0006898	-		IPR001623; IPR003095; IPR012335; IPR012336; IPR015609; IPR018253; PTHR11821:SF14 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	novel protein	2	P:GO:0005975; F:GO:0008081	-	EC:3.1.4.0	IPR002044; IPR013783; IPR013784
Loa loa	transformation transcription domain-associated protein isoform 1	1	P:GO:0009987	-		PTHR11139 (PANTHER), PTHR11139:SF2 (PANTHER)
Caenorhabditis briggsae	ankyrin repeat protein	1	F:GO:0003824	-		IPR002110; IPR015882; IPR020683; G3DSA:3.30.379.10 (GENE3D), PTHR18958 (PANTHER), PTHR18958:SF102 (PANTHER), SSF55545 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0004563; P:GO:0005975		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF102 (PANTHER)
	-	0				-
Caenorhabditis sp. PS1010	glucan (-alpha-) branching enzyme 1	10	C:GO:0005829; F:GO:0043169; P:GO:0040010; F:GO:0031072; F:GO:0003844; F:GO:0004553; P:GO:0000003; P:GO:0010171; P:GO:0005977; P:GO:0009792	-	EC:2.4.1.18; EC:3.2.1.0	IPR004193; IPR006047; IPR013781; IPR013783; IPR014756; IPR017853; PTHR10357 (PANTHER), PTHR10357:SF27 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-sop-3 protein	1	P:GO:0050789	-		IPR019680
Caenorhabditis briggsae	briggsae cbr-sop-3 protein	1	P:GO:0050789	-		IPR019680

Caenorhabditis elegans	myosin light polypeptide 5 regulatory	5	C:GO:0016021; P:GO:0000003; P:GO:0040010; P:GO:0006898; P:GO:0055085	-		IPR011701; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR10924 (PANTHER)
Caenorhabditis elegans	myosin light polypeptide 5 regulatory	5	C:GO:0016021; P:GO:0000003; P:GO:0040010; P:GO:0006898; P:GO:0055085	-		IPR011701; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR10924 (PANTHER)
Acyrthosiphon pisum	histone h2b	3	C:GO:0005811; C:GO:0035267; C:GO:0005694	-		IPR000558; IPR007125; IPR009072; PTHR23428:SF1 (PANTHER)
Caenorhabditis elegans	nuclear export factor crm1	11	F:GO:0008565; P:GO:0040010; P:GO:0006611; C:GO:0005643; P:GO:0051301; P:GO:0010171; P:GO:0002119; F:GO:0005049; P:GO:0040011; P:GO:0007099; P:GO:0009792	-		IPR001494; IPR011989; IPR013598; IPR016024; PTHR11223 (PANTHER), PTHR11223:SF2 (PANTHER)
Caenorhabditis briggsae	in family member (ttn-1)	6	P:GO:0009987; C:GO:0005856; F:GO:0004672; F:GO:0005515; F:GO:0000166; P:GO:0009792	-		IPR003598; IPR003599; IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	briggsae cbr-gsa-1 protein	6	P:GO:0007186; F:GO:0004871; P:GO:0050896; P:GO:0007165; F:GO:0005525; P:GO:0007608	-		IPR000367; IPR001019; IPR011025; G3DSA:3.40.50.300 (GENE3D), PTHR10218:SF33 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	uncoordi-ted family member (unc-52)	2	P:GO:0030239; C:GO:0005578	-		IPR007110; IPR013783; PTHR10574 (PANTHER), PTHR10574:SF20 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-ttr-48 protein	1	P:GO:0040011	-		IPR001534; SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	solute carrier family 30 (zinc transporter) member 2	10	F:GO:0005385; P:GO:0055085; P:GO:0040010; P:GO:0006829; C:GO:0016021; C:GO:0016023; C:GO:0005770; P:GO:0061090; F:GO:0005515; C:GO:0010008	-		IPR002524; G3DSA:1.20.1510.10 (GENE3D), SignalP (SIGNALP)
Loa loa	hypothetical protein LOAG_00085 [Loa loa]	0				-
	-	0				-

Haemonchus contortus	cytochrome c	11	P:GO:0009792; P:GO:0002119; P:GO:0040018; C:GO:0070469; F:GO:0009055; C:GO:0005759; F:GO:0020037; P:GO:0006810; P:GO:0040010; P:GO:0008340; P:GO:0022900	-		IPR002327; IPR009056
Caenorhabditis elegans	tgf-beta induced apoptosis protein 12	1	P:GO:0006350	-		PTHR13580 (PANTHER), PTHR13580:SF11 (PANTHER)
Caenorhabditis briggsae	chromosome 20 open reading frame 116	2	P:GO:0000003; C:GO:0005783	-		IPR019153; PTHR13270 (PANTHER), SSF46785 (SUPERFAMILY)
Caenorhabditis briggsae	chromosome 20 open reading frame 116	2	P:GO:0000003; C:GO:0005783	-		IPR019153; PTHR13270 (PANTHER), SignalP (SIGNALP), SSF46785 (SUPERFAMILY)
Caenorhabditis elegans	d- methyltransferase 1 associated protein 1	10	F:GO:0003714; P:GO:0040010; P:GO:0006898; P:GO:0040011; P:GO:0045892; P:GO:0009792; P:GO:0001703; P:GO:0016568; P:GO:0040035; C:GO:0005657	-		IPR001005; IPR008468; PTHR12855 (PANTHER), PTHR12855:SF7 (PANTHER)
	-	0				-
Caenorhabditis briggsae	oxysterol binding protein	2	P:GO:0008202; P:GO:0006869	-		IPR000648; PTHR10972:SF21 (PANTHER), SSF144000 (SUPERFAMILY)
Heligmosomoides polygyrus	c-type lectin-1	1	F:GO:0005488	-		IPR001304; IPR016186; IPR016187; IPR022272; PTHR22803 (PANTHER), PTHR22803:SF16 (PANTHER), SignalP (SIGNALP)
Brugia malayi	phosphatidylinositol ki-se tor2	2	F:GO:0000166; F:GO:0016772	-		IPR000403; IPR003152; IPR011009; PTHR11139 (PANTHER), PTHR11139:SF9 (PANTHER)
Caenorhabditis briggsae	serine protease inhibitor 1	0		F:GO:0030414; F:GO:0008233; F:GO:0004867; C:GO:0005576		-
Loa loa	dead (asp-glu-ala-asp) box polypeptide 46	5	P:GO:0006396; F:GO:0003676; C:GO:0016604; F:GO:0008026; F:GO:0005524	-		IPR000629; IPR001650; IPR011545; IPR014001; IPR014014; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF45 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0016539		IPR001534; SignalP (SIGNALP)
Caenorhabditis elegans	dgn-1	0		F:GO:0005509; C:GO:0016020; F:GO:0005515		IPR006644; IPR013783; IPR015919; PTHR21559 (PANTHER), PTHR21559:SF10 (PANTHER)

Caenorhabditis briggsae	proteasome (macropain) beta 1	14	P:GO:0008340; P:GO:0018991; P:GO:0051439; P:GO:0040007; F:GO:0004298; P:GO:0051603; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0009792; C:GO:0005737; C:GO:0005839; C:GO:0005634	-	EC:3.4.25.0	IPR001353; IPR016050; G3DSA:3.60.20.10 (GENE3D), PTHR11599 (PANTHER), PTHR11599:SF8 (PANTHER), PS51476 (PROFILE), SSF56235 (SUPERFAMILY)
Angiostrongylus cantonensis	abc transporter family protein	5	F:GO:0016887; P:GO:0006200; F:GO:0005524; C:GO:0043190; F:GO:0005215	-		IPR003439; IPR003593; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR19211 (PANTHER), PTHR19211:SF17 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	amidinotransferase	2	C:GO:0005737; F:GO:0016813	-	EC:3.5.3.0	G3DSA:3.75.10.10 (GENE3D), PTHR12737 (PANTHER), PTHR12737:SF1 (PANTHER), SSF55909 (SUPERFAMILY)
Pan troglodytes	glutathione peroxidase 4 (phospholipid hydroperoxidase)	18	C:GO:0005829; P:GO:0006644; P:GO:0042744; C:GO:0005625; C:GO:0005743; F:GO:0004602; P:GO:0055114; P:GO:0007283; P:GO:0006749; P:GO:0007568; F:GO:0043295; P:GO:0032355; P:GO:0006325; P:GO:0007275; C:GO:0005635; F:GO:0008430; P:GO:0050727; F:GO:0047066	-	EC:1.11.1.9; EC:1.11.1.12	-
Loa loa	elegans protein confirmed by transcript evidence	1	P:GO:0006898	-		-
	-	0				-
	-	0				-
Brugia malayi	histone h1	5	P:GO:0009792; P:GO:0002119; C:GO:0005694; P:GO:0000003; P:GO:0040007	-		IPR005818; IPR005819; IPR011991; PTHR11467 (PANTHER), SSF46785 (SUPERFAMILY)
Caenorhabditis briggsae	aspartate aminotransferase	2	P:GO:0008152; F:GO:0008483	-	EC:2.6.1.0	-

Caenorhabditis elegans	thioredoxin 2	15	F:GO:0033743; P:GO:0009725; P:GO:0006979; P:GO:0014070; P:GO:0048678; P:GO:0007584; P:GO:0042493; F:GO:0032403; P:GO:0045454; P:GO:0031669; P:GO:0009749; P:GO:0008152; F:GO:0015035; F:GO:0008113; C:GO:0005739	-	EC:1.8.4.12; EC:1.8.4.11	IPR005746; IPR012335; IPR012336; IPR013766; IPR017936; IPR017937; PTHR10438:SF13 (PANTHER)
Caenorhabditis briggsae	enhancer trap locus 4	2	F:GO:0005515; P:GO:0008340	-		PTHR22741 (PANTHER), PTHR22741:SF2 (PANTHER)
Loa loa	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis briggsae	zip zinc transporter family protein	3	P:GO:0009792; F:GO:0046873; P:GO:0006829	-		IPR003689; PTHR11040 (PANTHER), PTHR11040:SF8 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	zip zinc transporter family protein	5	P:GO:0009792; F:GO:0046873; C:GO:0005886; P:GO:0006829; F:GO:0008270	-		IPR003689; PTHR11040 (PANTHER), PTHR11040:SF8 (PANTHER), SignalP (SIGNALP)
Camponotus floridanus	integrator complex subunit 1	0		F:GO:0005488		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis briggsae	sfrs12-interacting protein 1	1	F:GO:0005515	-		IPR001878
Haemonchus contortus	phosphoenolpyruvate carboxyki-se	8	C:GO:0005625; P:GO:0006094; F:GO:0046872; F:GO:0005525; P:GO:0006107; F:GO:0016301; F:GO:0004613; C:GO:0005739	-	EC:4.1.1.32	IPR008209; IPR008210; IPR013035; IPR018091; IPR019825; G3DSA:2.170.8.10 (GENE3D), SignalP (SIGNALP), SSF53795 (SUPERFAMILY)
Loa loa	translocation protein 1	7	F:GO:0004872; C:GO:0071212; C:GO:0045111; C:GO:0016235; P:GO:0006613; C:GO:0005783; C:GO:0044425	-		IPR004728; PTHR12443:SF6 (PANTHER)
Pan troglodytes schweinfurthii	-dh dehydroge-se subunit 2	6	P:GO:0006120; C:GO:0005743; C:GO:0070469; F:GO:0008137; P:GO:0006810; C:GO:0016021	-	EC:1.6.5.3	-
Drosophila persimilis	zinc finger protein 330	4	C:GO:0000775; C:GO:0005730; C:GO:0030496; F:GO:0008270	-		IPR010531

Caenorhabditis briggsae	tyrosine aminotransferase	11	P:GO:0006103; C:GO:0005739; P:GO:0009058; P:GO:0000003; F:GO:0016847; P:GO:0006572; F:GO:0005515; P:GO:0006536; F:GO:0004838; F:GO:0030170; P:GO:0010033	-	EC:4.4.1.14; EC:2.6.1.5	-
Caenorhabditis briggsae	deoxyribose-phosphate aldolase	5	C:GO:0005737; F:GO:0004139; P:GO:0046121; P:GO:0009264; F:GO:0005515	-	EC:4.1.2.4	IPR002915; IPR011343; IPR013785; SSF51569 (SUPERFAMILY)
Caenorhabditis elegans	villin headpiece domain containing protein	1	P:GO:0045132	-		-
Caenorhabditis elegans	villin headpiece domain containing protein	1	P:GO:0045132	-		-
	-	0				-
Brugia malayi	gtpase activating protein and vps9 domains 1	3	C:GO:0005622; P:GO:0009987; P:GO:0050789	-		-
Caenorhabditis elegans	evelled related family member (dsh-1)	21	P:GO:0007166; F:GO:0004871; C:GO:0005929; P:GO:0007369; F:GO:0005515; C:GO:0016020; P:GO:0060026; C:GO:0043231; P:GO:0040007; P:GO:0007052; P:GO:0022607; P:GO:0003002; P:GO:0030030; P:GO:0009792; C:GO:0031410; P:GO:0009798; P:GO:0002119; P:GO:0048869; P:GO:0019222; P:GO:0010171; P:GO:0007399	-		IPR000591; IPR001158; IPR001478; IPR008339; IPR011991; IPR015506; G3DSA:2.30.42.10 (GENE3D), PTHR10878:SF2 (PANTHER), SSF46785 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	uncoordi-ted family member (unc-44)	2	F:GO:0005515; P:GO:0007165	-		IPR002110; IPR018120; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER), PTHR18958:SF296 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG15717 [Caenorhabditis briggsae]	0				-
	-	0				-
Hydra magnipapillata	nuclease harbi1-like	0		C:GO:0009507		-
Caenorhabditis briggsae	deah (asp-glu-ala-his) box polypeptide partial	5	F:GO:0003723; F:GO:0005524; C:GO:0005622; F:GO:0008270; F:GO:0008026	-		IPR011545; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR18934 (PANTHER), SSF52540 (SUPERFAMILY)

Brugia malayi	btb domain containing 9	2	F:GO:0005515; P:GO:0007155	-		IPR008979; IPR013089; G3DSA:2.60.120.260 (GENE3D), PTHR23230:SF181 (PANTHER)
Caenorhabditis briggsae	dihydropyridine-sensitive l-type calcium channel	7	P:GO:0065008; C:GO:0016021; N:GO:0071842; F:GO:0005216; P:GO:0007268; P:GO:0050794; P:GO:0006811	-		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				PS51257 (PROFILE)
Camponotus floridanus	uncharacterized transposase-like protein	0		F:GO:0046872; P:GO:0055114; F:GO:0009055; F:GO:0016491; F:GO:0020037; F:GO:0005506; F:GO:0004497		-
Caenorhabditis elegans	vacuolar proton atpase	7	F:GO:0005516; F:GO:0008553; C:GO:0016021; P:GO:0015986; C:GO:0045202; P:GO:0040013; C:GO:0000220	-	EC:3.6.3.6	IPR002490; PTHR11629:SF23 (PANTHER)
Caenorhabditis elegans	uncoordi-ted family member (unc-32)	5	F:GO:0015078; C:GO:0033177; C:GO:0016021; P:GO:0015986; P:GO:0040013	-		IPR002490; PTHR11629:SF1 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0004500; P:GO:0006548		-
	-	0				
Caenorhabditis briggsae	protein lsm14 homolog a	6	F:GO:0003723; P:GO:0017148; C:GO:0043234; P:GO:0033962; C:GO:0010494; F:GO:0017151	-		IPR010920; IPR019053; PTHR13586 (PANTHER)
Caenorhabditis briggsae	phosphoglucomutase 2	8	P:GO:0009792; P:GO:0002119; P:GO:0005975; F:GO:0005515; P:GO:0040010; F:GO:0000287; F:GO:0016868; C:GO:0005829	-	EC:5.4.2.0	-
	-	0				IPR003645; PR01217 (PRINTS)
Caenorhabditis elegans	briggsae cbr-swm-1 protein	1	F:GO:0005488	-		IPR002919; IPR013032; G3DSA:2.10.25.10 (GENE3D), PTHR23259 (PANTHER)
	-	0				IPR003645; PR01217 (PRINTS)
Caenorhabditis elegans	briggsae cbr-swm-1 protein	1	F:GO:0005515	-		-

Caenorhabditis briggsae	phosphoglucomutase 2	8	P:GO:0009792; P:GO:0002119; P:GO:0005975; F:GO:0005515; P:GO:0040010; F:GO:0000287; F:GO:0016868; C:GO:0005829	-	EC:5.4.2.0	-
	-	0				IPR003645; PR01217 (PRINTS)
Caenorhabditis elegans	briggsae cbr-swm-1 protein	1	F:GO:0005515	-		IPR002919; IPR013032; G3DSA:2.10.25.10 (GENE3D), PTHR23259 (PANTHER)
Caenorhabditis elegans	protein tyrosine non-receptor type 22	6	P:GO:0006470; P:GO:0050860; P:GO:0030217; F:GO:0004725; C:GO:0005737; F:GO:0017124	-	EC:3.1.3.48	SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein C44C1.1 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	chromosome 16 open reading frame 61	0		F:GO:0003674; P:GO:0008150		SignalP (SIGNALP)
Caenorhabditis briggsae	rw1 protein	1	F:GO:0005515	-		PTHR22050 (PANTHER)
	-	0				SignalP (SIGNALP)
Polysphondylium pallidum PN500	hypothetical protein PPL_02455 [Polysphondylium pallidum PN500]	0		F:GO:0030246; C:GO:0005576		-
Caenorhabditis briggsae	proteasome 26s non-atpase subunit 4	1	C:GO:0000502	-		IPR002035; IPR003903; IPR007198; G3DSA:3.40.50.410 (GENE3D), PTHR10223 (PANTHER), SSF53300 (SUPERFAMILY)
Caenorhabditis briggsae	cytochrome p450 family protein	3	F:GO:0016491; F:GO:0005506; F:GO:0005515	-		IPR001128; IPR002401; PTHR19383:SF66 (PANTHER)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	F:GO:0009055; F:GO:0008137; C:GO:0016020	-	EC:1.6.5.3	SignalP (SIGNALP)
Homo sapiens	eukaryotic translation elongation factor 1 gamma	6	F:GO:0003746; C:GO:0005853; F:GO:0005515; C:GO:0005829; P:GO:0009615; P:GO:0006414	-		-
Caenorhabditis elegans	r- polymerase rpc34 subunit family protein	5	F:GO:0003899; F:GO:0003677; P:GO:0006350; P:GO:0000003; C:GO:0005634	-	EC:2.7.7.6	IPR007832; IPR016049
	-	0				-

Caenorhabditis elegans	myosin va	15	P:GO:0048731; P:GO:0051648; C:GO:0016023; P:GO:0043473; C:GO:0044430; C:GO:0015629; F:GO:0008092; P:GO:0007154; P:GO:0023060; C:GO:0043234; P:GO:0050877; C:GO:0042995; P:GO:0065007; P:GO:0008152; P:GO:0032940	-		IPR000048; IPR001609; PTHR13140 (PANTHER), PTHR13140:SF15 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	myosin va	15	P:GO:0048731; P:GO:0051648; C:GO:0016023; P:GO:0043473; C:GO:0044430; C:GO:0015629; F:GO:0008092; P:GO:0007154; P:GO:0023060; C:GO:0043234; P:GO:0050877; C:GO:0042995; P:GO:0065007; P:GO:0008152; P:GO:0032940	-		IPR000048; IPR001609; PTHR13140 (PANTHER), PTHR13140:SF15 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	heat shock 70kd protein binding protein	3	P:GO:0042026; F:GO:0005515; C:GO:0005737	-		IPR001440; IPR006636; IPR011990; IPR013026; IPR019734; PTHR22904 (PANTHER), PTHR22904:SF34 (PANTHER), SSF48452 (SUPERFAMILY)
Caenorhabditis elegans	heat shock 70kd protein binding protein	2	P:GO:0006457; F:GO:0030674	-		IPR001440; IPR006636; IPR011990; IPR013026; IPR019734; PTHR22904 (PANTHER), PTHR22904:SF34 (PANTHER), SSF48452 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0051301; P:GO:0009792; P:GO:0007126		IPR008574
Caenorhabditis elegans	hypothetical protein ZK470.2 [Caenorhabditis elegans]	0				IPR010916
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR006696; SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	upf0451 protein c17orf61-like protein	0		C:GO:0016021; C:GO:0016020; C:GO:0005886		IPR006696; PTHR10584 (PANTHER), PTHR10584:SF8 (PANTHER), SignalP (SIGNALP)
	-	0				-

Ailuropoda melanoleuca	thioredoxin interacting protein	19	P:GO:0009749; P:GO:0000122; P:GO:0042127; P:GO:0042542; C:GO:0005758; P:GO:0009612; P:GO:0051592; P:GO:0032570; F:GO:0031625; P:GO:0050790; P:GO:0042493; P:GO:0048008; P:GO:0030216; F:GO:0004857; P:GO:0006606; C:GO:0005634; P:GO:0032355; P:GO:0043065; P:GO:0007049	-		PTHR11188 (PANTHER), PTHR11188:SF14 (PANTHER)
Caenorhabditis elegans	elav-type r- binding protein family member (etr-1)	10	P:GO:0043484; F:GO:0003729; P:GO:0008016; P:GO:0007286; P:GO:0006376; F:GO:0042835; C:GO:0005737; P:GO:0040018; C:GO:0005634; F:GO:0031369	-		IPR000504; IPR012677; IPR015903; PTHR10432 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	elav-type r- binding protein family member (etr-1)	10	P:GO:0043484; F:GO:0003729; P:GO:0008016; P:GO:0007286; P:GO:0006376; F:GO:0042835; C:GO:0005737; P:GO:0040018; C:GO:0005634; F:GO:0031369	-		IPR000504; IPR012677; IPR015903; PTHR10432 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	protein ki-se domain containing protein	5	P:GO:0006468; F:GO:0004672; F:GO:0005524; P:GO:0000003; P:GO:0040011	-		IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
Caenorhabditis elegans	novel protein vertebrate myeloid lymphoid or mixed-lineage leukemia (trithorax drosophila) translocated 4	11	P:GO:0040022; P:GO:0045132; P:GO:0040007; P:GO:0002119; F:GO:0005515; P:GO:0042127; P:GO:0008406; C:GO:0005737; F:GO:0016787; P:GO:0040020; C:GO:0005886	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR19964 (PANTHER)
	-	0				-

Caenorhabditis elegans	transformation transcription domain-associated protein	2	F:GO:0016773; F:GO:0005488	-	EC:2.7.1.0	IPR011989; PTHR11139 (PANTHER), PTHR11139:SF2 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	mps one binder ki-se activator-like 2b	4	F:GO:0016301; F:GO:0046872; P:GO:0016310; F:GO:0005515	-		-
Brugia malayi	-dh-dependent fumarate reductase	3	C:GO:0020015; F:GO:0016156; P:GO:0008152	-	EC:1.3.1.6	IPR003953; G3DSA:3.50.50.60 (GENE3D), PTHR11632 (PANTHER), PTHR11632:SF3 (PANTHER), SSF51905 (SUPERFAMILY)
Caenorhabditis briggsae	enoyl- hydratase isomerase family protein	3	P:GO:0002119; P:GO:0008152; P:GO:0040007	-		IPR001753; G3DSA:3.90.226.10 (GENE3D), PTHR11941 (PANTHER), SignalP (SIGNALP), SSF52096 (SUPERFAMILY)
Caenorhabditis elegans	nucleoporin nup43	0		C:GO:0005643; P:GO:0015031; C:GO:0005694; C:GO:0005634; P:GO:0007067; P:GO:0006810; C:GO:0000776; F:GO:0003674; P:GO:0051301; P:GO:0007059; C:GO:0005575; P:GO:0055085; P:GO:0051028; P:GO:0008150		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR22652 (PANTHER)
Caenorhabditis elegans	nucleoporin nup43	0		C:GO:0005643; P:GO:0015031; C:GO:0005694; C:GO:0005634; P:GO:0007067; P:GO:0006810; C:GO:0000776; F:GO:0003674; P:GO:0051301; P:GO:0007059; C:GO:0005575; P:GO:0055085; P:GO:0051028; P:GO:0008150		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR22652 (PANTHER)
	-	0				-
Homo sapiens	peptidylprolyl isomerase b (cyclophilin b)	7	P:GO:0006457; C:GO:0005788; C:GO:0042470; P:GO:0051169; F:GO:0042277; F:GO:0051082; F:GO:0003755	-	EC:5.2.1.8	IPR002130; IPR015891; PTHR11071 (PANTHER), PTHR11071:SF63 (PANTHER)
Caenorhabditis elegans	mgc80520 protein	0		F:GO:0003674; P:GO:0008150		-
Loa loa	autosomal zinc finger protein	1	F:GO:0005488	-		IPR007087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)

Loa loa	autosomal zinc finger protein	1	F:GO:0005488	-		IPR007087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	#NAME?	20	F:GO:0005515; P:GO:0045989; P:GO:0045822; F:GO:0003869; C:GO:0005792; C:GO:0016323; C:GO:0042470; F:GO:0046872; P:GO:0006754; C:GO:0042383; F:GO:0005391; P:GO:0045823; P:GO:0042493; P:GO:0031947; C:GO:0005890; P:GO:0006813; P:GO:0002026; F:GO:0005524; P:GO:0008217; P:GO:0006814	-	EC:3.1.3.41; EC:3.6.3.9	IPR001757; IPR004014; IPR006069; PTHR11939:SF100 (PANTHER), SSF81665 (SUPERFAMILY)
Caenorhabditis elegans	golgi vesicular membrane trafficking protein p18	2	C:GO:0016021; P:GO:0000003	-		IPR000727; G3DSA:1.20.5.110 (GENE3D), PTHR12791 (PANTHER), PTHR12791:SF10 (PANTHER)
Caenorhabditis briggsae	sn1-specific diacylglycerol lipase beta	1	F:GO:0005515	-		IPR002921; G3DSA:3.40.50.1820 (GENE3D), PTHR21493 (PANTHER), PTHR21493:SF6 (PANTHER), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-pro-2 protein	8	P:GO:0040007; P:GO:0000003; P:GO:0019915; P:GO:0002119; P:GO:0006898; P:GO:0009792; P:GO:0051729; P:GO:0016246	-		IPR005343; PTHR12687:SF4 (PANTHER)
Loa loa	nonmuscle myosin heavy chain	13	C:GO:0043005; P:GO:0048699; P:GO:0007507; P:GO:0006928; P:GO:0048468; P:GO:0051179; F:GO:0003779; N:GO:0071842; P:GO:0021591; P:GO:0030030; F:GO:0003774; F:GO:0005524; C:GO:0016459	-		IPR002928; PD936484 (PRODOM), PTHR13140 (PANTHER), PTHR13140:SF23 (PANTHER)
Caenorhabditis briggsae	inositol polyphosphate multiki-se	2	F:GO:0004428; F:GO:0016773	-	EC:2.7.1.0	IPR005522; PTHR12400:SF7 (PANTHER), SSF56104 (SUPERFAMILY)

Ciona intestinalis	multidrug resistance-associated	0		F:GO:0005524; F:GO:0016887; F:GO:0000166; C:GO:0016021; F:GO:0042626; F:GO:0017111; P:GO:0055085; P:GO:0006810		IPR001140; IPR003439; IPR003593; IPR011527; IPR017871; IPR017940; G3DSA:1.20.1560.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF22 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	lin-48 expression abnormal family member (lex-1)	7	F:GO:0017111; P:GO:0045132; P:GO:0031445; F:GO:0005524; P:GO:0009792; P:GO:0008406; P:GO:0006350	-	EC:3.6.1.15	IPR001487; IPR003593; IPR003959; IPR003960; IPR018359; G3DSA:3.40.50.300 (GENE3D), PTHR23069 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis brenneri	brain protein 44	0				IPR005336; PTHR14154 (PANTHER), PTHR14154:SF2 (PANTHER)
Caenorhabditis elegans	hypothetical protein F56A6.4 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	in family member (ttn-1)	1	P:GO:0009792	-		IPR003599; IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)
synthetic construct	cd81 antigen	11	P:GO:0030307; P:GO:0043128; F:GO:0005515; P:GO:0046813; P:GO:0008104; P:GO:0050731; P:GO:0006661; C:GO:0005887; P:GO:0000187; C:GO:0016324; P:GO:0030890	-		IPR008952; IPR018499; G3DSA:1.10.1450.10 (GENE3D), PTHR19282 (PANTHER), PTHR19282:SF19 (PANTHER)
Brugia malayi	elegans protein partially confirmed by transcript evidence	8	P:GO:0040010; F:GO:0005488; P:GO:0000070; P:GO:0040002; P:GO:0040035; P:GO:0040011; P:GO:0006898; P:GO:0009792	-		IPR011989; IPR016024; PF12422 (PFAM)
Caenorhabditis briggsae	kh domain containing protein	3	F:GO:0003676; F:GO:0005515; P:GO:0016246	-		IPR004087; IPR004088; IPR015096; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR10288 (PANTHER), PTHR10288:SF57 (PANTHER), SSF54791 (SUPERFAMILY)
Brugia malayi	kh domain containing protein	2	F:GO:0005515; P:GO:0016246	-		IPR004087; IPR004088; IPR015096; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR10288 (PANTHER), PTHR10288:SF57 (PANTHER), SSF54791 (SUPERFAMILY)
Brugia malayi	kh domain containing protein	4	F:GO:0003676; F:GO:0005515; C:GO:0005634; P:GO:0016246	-		IPR004087; IPR004088; IPR015096; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR10288 (PANTHER), PTHR10288:SF57 (PANTHER), SignalP (SIGNALP), SSF54791 (SUPERFAMILY)

Brugia malayi	kh domain containing protein	4	F:GO:0003676; F:GO:0005515; C:GO:0005634; P:GO:0016246	-		IPR004087; IPR004088; IPR015096; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR10288 (PANTHER), PTHR10288:SF57 (PANTHER), SSF54791 (SUPERFAMILY)
Brugia malayi	kh domain containing protein	3	F:GO:0003676; F:GO:0005515; P:GO:0016246	-		IPR004087; IPR004088; IPR015096; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR10288 (PANTHER), PTHR10288:SF57 (PANTHER), SSF54791 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-frm-7 protein	0		F:GO:0005488; C:GO:0005856		IPR000299; IPR011993; IPR018980; SSF50729 (SUPERFAMILY)
Brugia malayi	related to oncogene abl family member (abl-1)	7	F:GO:0004715; F:GO:0030145; F:GO:0005515; P:GO:0018108; F:GO:0005524; F:GO:0000287; P:GO:0007165	-	EC:2.7.10.2	IPR000719; IPR001245; IPR008266; IPR011009; IPR020635; IPR020685; IPR020700; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
Caenorhabditis elegans	sphingolipid delta 4 desaturase c-4 hydroxylase protein des2	6	C:GO:0005789; P:GO:0006633; F:GO:0005515; P:GO:0055114; F:GO:0016705; C:GO:0016021	-		IPR005804; PTHR12879 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Rhabditoides inermis	small subunit ribosomal protein 7	10	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; P:GO:0055085; P:GO:0000003; P:GO:0040007; C:GO:0016020; P:GO:0006412; F:GO:0005215	-	EC:3.6.5.3	IPR000554
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	briggsae cbr-pqn-34 protein	3	P:GO:0000022; P:GO:0051013; C:GO:0005819	-		IPR011033; IPR014797; PTHR21595 (PANTHER)
Caenorhabditis elegans	briggsae cbr-pqn-34 protein	3	P:GO:0000022; P:GO:0051013; C:GO:0005819	-		IPR011033; IPR014797; PTHR21595 (PANTHER)
Caenorhabditis briggsae	atp-binding sub-family b (mdr tap) member 9	6	P:GO:0006810; F:GO:0005515; C:GO:0030176; F:GO:0015197; C:GO:0043234; F:GO:0042626	-		IPR001140; IPR011527; IPR017940; G3DSA:1.20.1560.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF82 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	heterotrimeric g protein alpha subunit	4	P:GO:0007186; F:GO:0004871; P:GO:0007165; F:GO:0005525	-		IPR001019; IPR011025; G3DSA:3.40.50.300 (GENE3D), PTHR10218:SF63 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-

Haemonchus contortus	syntaxin binding protein 1	28	P:GO:0032229; P:GO:0007412; F:GO:0030347; P:GO:0006944; C:GO:0042581; P:GO:0070527; P:GO:0006904; F:GO:0047485; P:GO:0050821; F:GO:0030348; P:GO:0015031; C:GO:0042582; P:GO:0060292; C:GO:0070820; C:GO:0005829; P:GO:0043524; C:GO:0031091; F:GO:0019904; P:GO:0016188; F:GO:0042802; C:GO:0043234; P:GO:0010807; P:GO:0043312; P:GO:0002576; F:GO:0017075; P:GO:0007274; C:GO:0005886; C:GO:0005739	-		IPR001619; G3DSA:3.40.50.2060 (GENE3D), PTHR11679:SF7 (PANTHER)
	-	0				-
Caenorhabditis elegans	denn madd domain containing 5b	1	C:GO:0016021	-		IPR004012; SSF140741 (SUPERFAMILY)
Caenorhabditis elegans	denn domain-containing protein 5b	0		C:GO:0016021; C:GO:0016020		IPR004012; IPR005112; SSF140741 (SUPERFAMILY)
Caenorhabditis elegans	denn domain-containing protein 5b	0		C:GO:0016021; C:GO:0016020		IPR004012; IPR005112; SSF140741 (SUPERFAMILY)
Caenorhabditis briggsae	immunoglobulin i-set domain containing protein	1	F:GO:0005515	-		IPR003599; IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF7 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis briggsae	5-azacytidine resistance protein	2	P:GO:0000003; F:GO:0004721	-	EC:3.1.3.16	IPR001932; IPR010822; IPR022398; PTHR12320 (PANTHER), SignalP (SIGNALP)
	-	0				-
Ailuropoda melanoleuca	ribosomal protein l7a	11	F:GO:0030528; F:GO:0003729; F:GO:0003735; P:GO:0045449; P:GO:0006414; C:GO:0005624; F:GO:0003677; P:GO:0042254; C:GO:0042788; F:GO:0042803; C:GO:0022625	-		-
Caenorhabditis elegans	trab domain-containing protein	0		P:GO:0008150; C:GO:0005575		IPR002816; PTHR21530 (PANTHER)
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	serine threonine protein	1	F:GO:0004722	-		IPR004843; IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF10 (PANTHER), SSF56300 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	F:GO:0005488; P:GO:0000003; P:GO:0007186; C:GO:0016021	-		IPR000276; IPR017452; G3DSA:1.20.1070.10 (GENE3D), PTHR19264 (PANTHER), PTHR19264:SF93 (PANTHER), SignalP (SIGNALP), SSF81321 (SUPERFAMILY)
Caenorhabditis briggsae	testis expressed sequence 264	0		F:GO:0003674; P:GO:0008150		G3DSA:3.20.80.10 (GENE3D), SignalP (SIGNALP)
Caenorhabditis elegans	importin subunit beta-1	0		F:GO:0005488; P:GO:0006886; F:GO:0008565		IPR011989; IPR016024; PTHR10527 (PANTHER), PTHR10527:SF1 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	rrp15-like protein	1	F:GO:0005515	-		IPR012459; PTHR13245:SF3 (PANTHER)
	-	0				-
Caenorhabditis elegans	transformation transcription domain-associated protein	0		F:GO:0005488; F:GO:0016773		-
Caenorhabditis briggsae	annexin a13	4	F:GO:0005515; F:GO:0005509; C:GO:0044464; F:GO:0005544	-		IPR001464; IPR018252; IPR018502; PTHR10502:SF30 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	mitochondrial 39s ribosomal protein l4	10	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; F:GO:0005515; P:GO:0040010; P:GO:0000003; P:GO:0040011; P:GO:0006898; P:GO:0006412	-	EC:3.6.5.3	IPR002136; IPR013005; IPR015498; G3DSA:3.40.1370.10 (GENE3D)
Caenorhabditis briggsae	2-oxoglutarate dehydroge-se	10	P:GO:0040010; P:GO:0008340; C:GO:0031966; P:GO:0055114; P:GO:0002119; P:GO:0006096; C:GO:0005759; P:GO:0009792; F:GO:0004591; F:GO:0030976	-	EC:1.2.4.2	IPR001017; IPR005475; IPR011603; G3DSA:3.40.50.970 (GENE3D), SSF52518 (SUPERFAMILY)
Caenorhabditis briggsae	2-oxoglutarate dehydroge-se	10	P:GO:0040010; P:GO:0008340; C:GO:0031966; P:GO:0055114; P:GO:0002119; P:GO:0006096; C:GO:0005759; P:GO:0009792; F:GO:0004591; F:GO:0030976	-	EC:1.2.4.2	IPR001017; IPR005475; IPR011603; G3DSA:3.40.50.970 (GENE3D), SSF52518 (SUPERFAMILY)

Caenorhabditis briggsae	2-oxoglutarate dehydroge-se	10	P:GO:0040010; P:GO:0008340; C:GO:0031966; P:GO:0055114; P:GO:0002119; P:GO:0006096; C:GO:0005759; P:GO:0009792; F:GO:0004591; F:GO:0030976	-	EC:1.2.4.2	IPR001017; IPR005475; IPR011603; G3DSA:3.40.50.970 (GENE3D), SSF52518 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR021010; SSF141739 (SUPERFAMILY)
Caenorhabditis briggsae	protein unc-79 homolog	0		F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150; C:GO:0005575		PTHR21696 (PANTHER)
Brugia malayi	gem (nuclear organelle) associated protein 8	1	C:GO:0044424	-		-
Ancylostoma caninum	14-3-3 protein	7	C:GO:0005737; F:GO:0019904; P:GO:0018991; P:GO:0040010; P:GO:0008340; P:GO:0006898; P:GO:0043053	-		IPR000308
Ancylostoma caninum	14-3-3 protein	7	C:GO:0005737; F:GO:0019904; P:GO:0018991; P:GO:0040010; P:GO:0008340; P:GO:0006898; P:GO:0043053	-		IPR000308
Haemonchus contortus	hexoki-se family protein	17	P:GO:0018105; C:GO:0005829; P:GO:0018108; F:GO:0004672; C:GO:0005739; C:GO:0005901; P:GO:0010359; P:GO:0018107; F:GO:0005536; P:GO:0046835; F:GO:0005524; F:GO:0016887; P:GO:0006096; F:GO:0042803; P:GO:0046777; P:GO:0043066; F:GO:0004340	-	EC:2.7.1.2	IPR001312; IPR019807; IPR022672; IPR022673; G3DSA:3.40.367.20 (GENE3D), SSF53067 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	wd repeat-containing protein 3	1	P:GO:0006898	-		IPR001680; IPR011046; IPR015943; PTHR19853 (PANTHER)
Caenorhabditis elegans	wd repeat-containing protein 3	1	P:GO:0006898	-		IPR001680; IPR011046; IPR015943; PTHR19853 (PANTHER)

Physcomitrella patens subsp. patens	atp-dependent r- helicase	1	F:GO:0005488	-		IPR000629; IPR011545; IPR014001; IPR014014; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	wrapper rega-1 klingon homolog family member (wrk-1)	2	P:GO:0007611; P:GO:0009987	-		-
Caenorhabditis briggsae	wrapper rega-1 klingon homolog family member (wrk-1)	2	P:GO:0007611; P:GO:0009987	-		SignalP (SIGNALP)
synthetic construct	cystatin c	44	P:GO:0010711; P:GO:0060548; P:GO:0010951; C:GO:0031982; C:GO:0031965; P:GO:0070301; C:GO:0005615; P:GO:0043067; C:GO:0005764; P:GO:0042747; P:GO:0014070; F:GO:0001540; P:GO:0010716; P:GO:0008284; P:GO:0007420; C:GO:0043025; P:GO:0001654; P:GO:0001666; P:GO:0048678; C:GO:0005771; P:GO:0006915; P:GO:0007566; P:GO:0051789; P:GO:0042493; P:GO:0060009; F:GO:0002020; C:GO:0048471;	-		-
Caenorhabditis briggsae	amylo- 6- 4-alpha-glucanotransferase isoform 1	8	F:GO:0016798; F:GO:0004133; F:GO:0005515; C:GO:0043033; P:GO:0005977; P:GO:0009792; C:GO:0005737; F:GO:0016757	-		IPR010401; IPR013781; IPR017853
Caenorhabditis briggsae	amylo- 6- 4-alpha-glucanotransferase isoform 1	8	F:GO:0016798; F:GO:0004133; F:GO:0005515; C:GO:0043033; P:GO:0005977; P:GO:0009792; C:GO:0005737; F:GO:0016757	-		IPR010401; IPR013781; IPR017853

Caenorhabditis elegans	immunoglobulin binding protein 1	9	P:GO:0040035; P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0018991; F:GO:0005515; P:GO:0040017; P:GO:0040007; P:GO:0002009	-		IPR007304; PTHR10933:SF8 (PANTHER)
Caenorhabditis elegans	arrestin domain containing 2	0		P:GO:0007600; P:GO:0007165; F:GO:0005515		IPR011021; IPR014756; PTHR11188 (PANTHER)
Loa loa	protein phosphatase 2 (formerly 2a) catalytic beta isoform	35	[illegible] P:GO:0042542; P:GO:0043161; F:GO:0008022; P:GO:0046677; P:GO:0006672; C:GO:0000159; P:GO:0010033; P:GO:0042518; P:GO:0030155; P:GO:0007498; P:GO:0046580; C:GO:0005829; F:GO:0046982; F:GO:0046872; P:GO:0030111; F:GO:0019904; C:GO:0000775; P:GO:0008380; P:GO:0051726; P:GO:0006917; P:GO:0030308; P:GO:0007126; P:GO:0000188; P:GO:0045595; P:GO:0006470; P:GO:0045449; P:GO:0019932;	-		IPR004843; IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF21 (PANTHER), SSF56300 (SUPERFAMILY)

Brugia malayi	hdac7 protein	25	F:GO:0016566; F:GO:0005080; F:GO:0004407; F:GO:0003714; P:GO:0070932; F:GO:0042826; P:GO:0032869; P:GO:0007043; P:GO:0007507; P:GO:0030183; P:GO:0032703; F:GO:0070491; P:GO:0070933; C:GO:0005737; C:GO:0005667; C:GO:0035097; P:GO:0048742; P:GO:0090050; P:GO:0034983; P:GO:0010553; P:GO:0045668; P:GO:0006954; C:GO:0000118; F:GO:0003682; P:GO:0001570	-		IPR000286; PTHR10625:SF21 (PANTHER), SSF52768 (SUPERFAMILY)
Caenorhabditis briggsae	calcium atpase	5	F:GO:0005388; C:GO:0016021; P:GO:0006754; F:GO:0005524; P:GO:0006816	-	EC:3.6.3.8	IPR001757; IPR006068; G3DSA:1.20.1110.10 (GENE3D), PTHR11939:SF76 (PANTHER), SSF56784 (SUPERFAMILY), SSF81665 (SUPERFAMILY)
Caenorhabditis briggsae	calcium atpase	5	F:GO:0005388; C:GO:0016021; P:GO:0006754; F:GO:0005524; P:GO:0006816	-	EC:3.6.3.8	IPR001757; IPR006068; G3DSA:1.20.1110.10 (GENE3D), PTHR11939:SF76 (PANTHER), SSF56784 (SUPERFAMILY), SSF81665 (SUPERFAMILY)
Caenorhabditis briggsae	calcium atpase	5	F:GO:0005388; C:GO:0016021; P:GO:0006754; F:GO:0005524; P:GO:0006816	-	EC:3.6.3.8	IPR001757; IPR006068; G3DSA:1.20.1110.10 (GENE3D), PTHR11939:SF76 (PANTHER), SSF56784 (SUPERFAMILY), SSF81665 (SUPERFAMILY)
Caenorhabditis briggsae	calcium atpase	5	F:GO:0005388; C:GO:0016021; P:GO:0006754; F:GO:0005524; P:GO:0006816	-	EC:3.6.3.8	IPR001757; IPR006068; G3DSA:1.20.1110.10 (GENE3D), PTHR11939:SF76 (PANTHER), SSF56784 (SUPERFAMILY), SSF81665 (SUPERFAMILY)
						IPR003599; IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF9 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	mtk1 mekk4 homolog family member (mtk-1)	2	P:GO:0009987; P:GO:0043170	-		-
Loa loa	inositol -trisphosphate receptor	4	P:GO:0006810; C:GO:0043231; C:GO:0044444; C:GO:0016020	-		IPR001917; IPR015925; PTHR13715:SF2 (PANTHER)

Caenorhabditis briggsae	cysteine-rich with egf-like domains 1	1	C:GO:0016020	-		IPR000152; IPR000742; IPR002049; IPR006210; IPR006212; IPR013032; IPR013091; IPR018097; IPR021852; G3DSA:2.10.25.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF61 (PANTHER), SSF57196 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	cysteine-rich with egf-like domains 1	1	C:GO:0016020	-		-
	-	0				-
Caenorhabditis briggsae	sy-ptosomal-associated 29kda	5	P:GO:0009792; P:GO:0000003; P:GO:0040007; P:GO:0006898; P:GO:0002119	-		SignalP (SIGNALP)
Ascaris suum	briggsae cbr-flp-12 protein	0				-
Oscheius sp. (strain CEW1)	vit6_oscbr ame: full=vitellogenin-6 flags: precursor	0		P:GO:0006869; F:GO:0005319; F:GO:0045735; C:GO:0005576		-
Caenorhabditis briggsae	vitellogenin structural genes (yolk protein genes) family member (vit-2)	0		P:GO:0006869; F:GO:0005319; P:GO:0040010; F:GO:0045735; P:GO:0009792; P:GO:0008340; F:GO:0005515; C:GO:0005576		-
Caenorhabditis elegans	ccr4-not transcription subunit 1	1	F:GO:0005515	-		IPR007196; IPR018087; IPR019825; PTHR13162 (PANTHER)
Homo sapiens	thymosin beta 4	6	C:GO:0005829; C:GO:0005856; P:GO:0042989; P:GO:0030334; F:GO:0003779; C:GO:0005634	-		SignalP (SIGNALP)
Caenorhabditis elegans	filamin abp280 repeat family protein	8	P:GO:0009792; P:GO:0010171; C:GO:0005840; F:GO:0003735; F:GO:0003779; P:GO:0007126; P:GO:0000003; P:GO:0006412	-	EC:3.6.5.3	IPR001298; IPR013783; IPR014756; IPR017868; PTHR11915 (PANTHER), PTHR11915:SF24 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis elegans	ga17538	3	P:GO:0008593; P:GO:0007035; P:GO:0007424	-		-
Caenorhabditis elegans	variable abnormal morphology family member (vab-10)	1	F:GO:0003779	-		IPR001452; IPR018159; PD968187 (PRODOM), G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF49 (PANTHER), SignalP (SIGNALP), SSF46966 (SUPERFAMILY)

Caenorhabditis elegans	variable abnormal morphology family member (vab-10)	1	F:GO:0003779	-		IPR001452; IPR018159; G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF49 (PANTHER), SignalP (SIGNALP), SSF46966 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Bos taurus	heavy polypeptide 15	0		F:GO:0005524; C:GO:0016459; F:GO:0003774		-
	-	0				-
Brugia malayi	phd finger protein	0		F:GO:0046872; P:GO:0055085; F:GO:0008270; F:GO:0005515; C:GO:0005634		PTHR13793 (PANTHER), PTHR13793:SF9 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-far-7 protein	1	F:GO:0008289	-		IPR008632
Caenorhabditis briggsae	briggsae cbr-far-7 protein	1	F:GO:0008289	-		IPR008632
	-	0				IPR001205; SSF56672 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	temporarily assigned gene -me family member (tag-333)	0		P:GO:0007165; F:GO:0005515		-
Caenorhabditis elegans	briggsae cbr-rbr-2 protein	6	F:GO:0005488; C:GO:0005730; F:GO:0016563; C:GO:0019907; C:GO:0005737; P:GO:0045941	-		IPR001606; IPR001965; IPR003347; IPR004198; IPR011011; IPR013083; IPR013129; IPR013637; IPR019787; PTHR10694 (PANTHER), PTHR10694:SF1 (PANTHER), SSF51197 (SUPERFAMILY)
	-	0				-
Brugia malayi	general transcription factor polypeptide beta	11	P:GO:0000003; P:GO:0040010; P:GO:0006898; P:GO:0040011; F:GO:0016787; F:GO:0003676; P:GO:0006350; P:GO:0009792; P:GO:0002119; P:GO:0010171; C:GO:0005634	-		IPR003166; IPR011991; PTHR12716 (PANTHER), PTHR12716:SF8 (PANTHER), SSF46785 (SUPERFAMILY)
Danio rerio	nuclear receptor coactivator 4	1	F:GO:0005515	-		-
Danio rerio	nuclear receptor coactivator 4	1	F:GO:0005515	-		-
Loa loa	dead h	0				-
Caenorhabditis briggsae	briggsae cbr-dsc-4 protein	1	P:GO:0040011	-		-
Caenorhabditis briggsae	nucleoredoxin-like protein 2	4	P:GO:0009792; P:GO:0040007; F:GO:0005515; P:GO:0002119	-		SignalP (SIGNALP)
Caenorhabditis elegans	pppde peptidase domain-containing protein 1	1	P:GO:0060027	-		IPR008580; PTHR12378 (PANTHER)
Angiostrongylus cantonensis	nucleolar gtp-binding protein 2	6	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0005525; C:GO:0005622; P:GO:0040010	-		IPR023179; PTHR11089 (PANTHER), PTHR11089:SF9 (PANTHER)
	-	0				-

Caenorhabditis briggsae	protein phosphatase 1h (pp2c domain containing)	4	C:GO:0008287; F:GO:0046872; F:GO:0004722; P:GO:0006470	-		IPR001932; IPR014045; IPR015655; PTHR13832:SF96 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	smad nuclear interacting protein 1	12	P:GO:0035196; P:GO:0006355; P:GO:0040007; P:GO:0000003; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0007249; P:GO:0006898; P:GO:0009792; C:GO:0005634	-		IPR000253; IPR008984; PTHR23308 (PANTHER)
Caenorhabditis elegans	smad nuclear interacting protein 1	12	P:GO:0035196; P:GO:0006355; P:GO:0040007; P:GO:0000003; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0007249; P:GO:0006898; P:GO:0009792; C:GO:0005634	-		IPR000253; IPR008984; PTHR23308 (PANTHER)
Caenorhabditis briggsae	tumor suppressor candidate 2	0		P:GO:0007267; F:GO:0003674; P:GO:0007049; P:GO:0008283; F:GO:0005515; C:GO:0005575		PTHR15453 (PANTHER)
Caenorhabditis elegans	succinyl- synthetase small	5	F:GO:0005488; C:GO:0005743; F:GO:0003878; P:GO:0006099; F:GO:0004775	-	EC:2.3.3.8; EC:6.2.1.5	IPR003781; IPR005810; IPR005811; IPR016040; IPR016102; IPR017440; PTHR11117 (PANTHER), SignalP (SIGNALP), SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	ras family protein	6	C:GO:0005622; F:GO:0005524; F:GO:0008134; P:GO:0007264; P:GO:0006355; P:GO:0015031	-		-
Brugia malayi	general transcription factor polypeptide alpha	0				PTHR15180 (PANTHER)
Brugia malayi	abnormal go-d development family member (gon-4)	0				-
Caenorhabditis briggsae	briggsae cbr-xpg-1 protein	4	P:GO:0009792; F:GO:0003677; F:GO:0004518; P:GO:0006281	-		IPR001044; IPR006084; IPR006086; IPR008918; G3DSA:1.10.150.20 (GENE3D), G3DSA:3.40.50.1010 (GENE3D), SSF88723 (SUPERFAMILY)
	-	0				-

Caenorhabditis elegans	heavy chain non-muscle	26	P:GO:0001525; P:GO:0008360; P:GO:0030048; F:GO:0030898; F:GO:0043531; P:GO:0015031; C:GO:0001772; C:GO:0005829; F:GO:0000146; P:GO:0006509; P:GO:0043534; C:GO:0008305; C:GO:0001726; C:GO:0032154; F:GO:0043495; F:GO:0051015; C:GO:0001725; C:GO:0001931; F:GO:0042803; P:GO:0031532; P:GO:0030220; P:GO:0030224; C:GO:0005634; F:GO:0005524; P:GO:0000910; C:GO:0005826	-		IPR002928; PD936484 (PRODOM), PTHR13140 (PANTHER), PTHR13140:SF23 (PANTHER)
Loa loa	loc398088 protein	6	P:GO:0040008; P:GO:0009987; P:GO:0048856; P:GO:0048518; P:GO:0007275; P:GO:0016043	-		IPR016024
Loa loa	trak1 protein	0		F:GO:0016740; C:GO:0005769; C:GO:0005634; C:GO:0005768; C:GO:0005739; F:GO:0050811; C:GO:0005575; F:GO:0005515; P:GO:0008150; P:GO:0008333		IPR006933; PTHR15751 (PANTHER), PTHR15751:SF2 (PANTHER)
Loa loa	trak1 protein	0		F:GO:0016740; C:GO:0005769; C:GO:0005634; C:GO:0005768; C:GO:0005739; F:GO:0050811; C:GO:0005575; F:GO:0005515; P:GO:0008150; P:GO:0008333		IPR006933; PTHR15751 (PANTHER), PTHR15751:SF2 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		C:GO:0043234; F:GO:0017124; F:GO:0003824; P:GO:0008150		-
	-	0				-

Loa loa	btb domain containing 12	4	P:GO:0006281; C:GO:0043234; C:GO:0044454; F:GO:0004520	-		-
Caenorhabditis elegans	protein ki-se domain containing protein	7	P:GO:0006468; P:GO:0008360; P:GO:0051726; P:GO:0007155; F:GO:0005524; C:GO:0005634; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF86 (PANTHER)
Caenorhabditis elegans	protein ki-se domain containing protein	7	P:GO:0006468; P:GO:0008360; P:GO:0051726; P:GO:0007155; F:GO:0005524; C:GO:0005634; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF86 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis briggsae	splicing factor proline glutamine rich (polypyrimidine tract binding protein associated)	8	P:GO:0002009; P:GO:0007420; C:GO:0016021; F:GO:0003676; P:GO:0000003; P:GO:0040007; F:GO:0000166; P:GO:0002119	-		IPR000504; IPR012677; IPR012975; PTHR23189 (PANTHER), PTHR23189:SF12 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	splicing factor proline glutamine rich (polypyrimidine tract binding protein associated)	8	P:GO:0002009; P:GO:0007420; C:GO:0016021; F:GO:0003676; P:GO:0000003; P:GO:0040007; F:GO:0000166; P:GO:0002119	-		IPR000504; IPR012677; IPR012975; PTHR23189 (PANTHER), PTHR23189:SF12 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	splicing factor proline glutamine rich (polypyrimidine tract binding protein associated)	8	P:GO:0002009; P:GO:0007420; C:GO:0016021; F:GO:0003676; P:GO:0000003; P:GO:0040007; F:GO:0000166; P:GO:0002119	-		IPR000504; IPR012677; IPR012975; PTHR23189 (PANTHER), PTHR23189:SF12 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein Y69A2AR.3 [Caenorhabditis elegans]	0				-
Homo sapiens	keratin 19	11	P:GO:0060706; C:GO:0030018; F:GO:0008307; P:GO:0045214; C:GO:0043034; P:GO:0043627; F:GO:0005515; F:GO:0005200; P:GO:0044419; C:GO:0042383; C:GO:0005882	-		IPR001664; IPR002957; IPR009053; IPR016044; IPR018039; G3DSA:1.20.5.170 (GENE3D), PTHR23239:SF14 (PANTHER)
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	cytoplasmic aconitate hydratase	19	C:GO:0005829; P:GO:0006417; C:GO:0005625; C:GO:0005739; F:GO:0030350; F:GO:0046872; P:GO:0010040; P:GO:0006879; P:GO:0006099; F:GO:0051539; F:GO:0048027; C:GO:0005792; F:GO:0005515; P:GO:0009791; F:GO:0003994; P:GO:0050892; C:GO:0005794; P:GO:0006101; C:GO:0005783	-	EC:4.2.1.3	IPR001030; IPR015931; IPR015934; IPR015937
Brugia malayi	briggsae cbr-cku-70 protein	8	P:GO:0050769; P:GO:0006303; P:GO:0033151; C:GO:0044428; C:GO:0043234; F:GO:0003677; P:GO:0010212; F:GO:0003824	-		IPR005160; IPR006164; IPR016194; G3DSA:2.40.290.10 (GENE3D), PTHR12604 (PANTHER), PTHR12604:SF2 (PANTHER)
Brugia malayi	zinc c2h2 type family protein	1	F:GO:0005488	-		-
Caenorhabditis elegans	differentially expressed in fdcp 8 homolog	1	F:GO:0005488	-		-
Caenorhabditis elegans	transmembrane protein 41a	1	P:GO:0010171	-		-
Caenorhabditis elegans	mitogen-activated protein ki-se ki-se ki-se 4	6	F:GO:0004672; P:GO:0043507; F:GO:0005515; P:GO:0009792; C:GO:0005737; P:GO:0016246	-		-
Loa loa	hypothetical protein LOAG_01987 [Loa loa]	0				-
Caenorhabditis briggsae	phosphoethanolamine n-	1	F:GO:0003824	-		IPR000169; IPR002591; IPR017849; IPR017850; PTHR23071 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	atp synthase g chain	10	P:GO:0008340; C:GO:0005929; P:GO:0040010; F:GO:0015078; P:GO:0034606; P:GO:0009792; P:GO:0015986; P:GO:0010171; C:GO:0005811; C:GO:0000276	-		IPR006808; PTHR12386 (PANTHER), PTHR12386:SF1 (PANTHER)
	-	0				SignalP (SIGNALP)
Brugia malayi	sart3 protein	5	F:GO:0005488; P:GO:0030098; P:GO:0048538; P:GO:0031017; P:GO:0000245	-		PTHR23269 (PANTHER)

Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0008270; C:GO:0005622		-
Caenorhabditis elegans	neuroendocrine protein 7b2	2	C:GO:0030141; P:GO:0007218	-		IPR007945
Loa loa	hras-like suppressor 2	0		F:GO:0003674; P:GO:0008150; F:GO:0005515		IPR007053; PTHR13943 (PANTHER), PTHR13943:SF9 (PANTHER)
Loa loa	hras-like suppressor 2	0		F:GO:0003674; P:GO:0008150; F:GO:0005515		IPR007053; PTHR13943 (PANTHER), PTHR13943:SF9 (PANTHER)
Brugia malayi	dopey family member 1	1	P:GO:0006810	-		-
Caenorhabditis elegans	r- binding motif protein 12	1	F:GO:0005515	-		IPR000504; IPR012677; PTHR13976 (PANTHER), PTHR13976:SF1 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	tryptophan-rich antigen (pv-fam-a)	3	F:GO:0005515; C:GO:0044444; F:GO:0000166	-		IPR000504; IPR012677; PTHR13976 (PANTHER), PTHR13976:SF1 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	heat shock protein family member (hsp-)	4	C:GO:0005737; P:GO:0006950; C:GO:0005634; F:GO:0005515	-		IPR001436; IPR002068; IPR008978; G3DSA:2.60.40.790 (GENE3D), PTHR11527 (PANTHER), PTHR11527:SF34 (PANTHER)
Angiostrongylus cantonensis	coatomer subunit epsilon	4	P:GO:0006890; F:GO:0005515; C:GO:0030126; F:GO:0005198	-		IPR006822; IPR011990; SSF48452 (SUPERFAMILY)
Angiostrongylus cantonensis	coatomer subunit epsilon	4	P:GO:0006890; F:GO:0005515; C:GO:0030126; F:GO:0005198	-		IPR006822; IPR011990; SSF48452 (SUPERFAMILY)
Caenorhabditis elegans	mitotic control protein dis3	2	F:GO:0004540; F:GO:0003723	-		IPR001900; IPR022966; PTHR23355 (PANTHER), PTHR23355:SF13 (PANTHER)
Caenorhabditis elegans	aliphatic nitrilase	4	F:GO:0003837; P:GO:0000003; P:GO:0006208; P:GO:0006207	-	EC:3.5.1.6	IPR003010; PTHR23088 (PANTHER)
Caenorhabditis briggsae	pre-rr--processing protein tsr1 homolog	6	P:GO:0009792; F:GO:0005515; P:GO:0042254; P:GO:0040010; P:GO:0040011; C:GO:0005634	-		IPR007034; PTHR12858 (PANTHER), PTHR12858:SF1 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	alpha beta	1	F:GO:0016787	-		SignalP (SIGNALP)
Caenorhabditis briggsae	ser thr protein phosphatase	0		F:GO:0016787; F:GO:0004721		IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF16 (PANTHER), SignalP (SIGNALP), SSF56300 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	btb poz domain containing protein	1	P:GO:0000003	-		IPR000210; IPR011333; IPR013069; PTHR22743 (PANTHER), PTHR22743:SF10 (PANTHER)

Caenorhabditis elegans	aldehyde dehydroge-se 1 member l2 isoform 2	9	C:GO:0005737; F:GO:0000036; P:GO:0009058; F:GO:0016742; P:GO:0055114; P:GO:0006730; F:GO:0016155; F:GO:0048037; P:GO:0009258	-	EC:2.1.2.0; EC:1.5.1.6	IPR001555; IPR002376; IPR005793; IPR011034; IPR015518
Caenorhabditis briggsae	briggsae cbr-obr-4 protein	2	P:GO:0008202; P:GO:0006869	-		IPR000648; IPR018494; PTHR10972:SF21 (PANTHER), SSF144000 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-obr-4 protein	2	P:GO:0008202; P:GO:0006869	-		IPR000648; IPR018494; PTHR10972:SF21 (PANTHER), SSF144000 (SUPERFAMILY)
Caenorhabditis elegans	mov34 mpn pad-1 family protein	11	F:GO:0003743; C:GO:0005829; F:GO:0032403; C:GO:0005852; C:GO:0005792; P:GO:0007413; P:GO:0002119; P:GO:0040011; P:GO:0006446; P:GO:0006898; P:GO:0009792	-		IPR000555; PTHR10410 (PANTHER), PTHR10410:SF3 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	nucleolin	4	P:GO:0040010; F:GO:0003676; P:GO:0009792; C:GO:0044424	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF37 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	nucleolin	4	P:GO:0040010; F:GO:0003676; P:GO:0009792; C:GO:0044424	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF37 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	loc495387 protein	0		P:GO:0008152; F:GO:0016787; C:GO:0016021; F:GO:0004091		IPR013094; G3DSA:3.40.50.1820 (GENE3D), PTHR23024 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
Brugia malayi	wd repeat domain 57 (u5 snrnp specific)	13	P:GO:0040010; C:GO:0005681; F:GO:0003676; P:GO:0000375; C:GO:0005732; P:GO:0040035; P:GO:0002119; F:GO:0005515; P:GO:0040011; C:GO:0005682; P:GO:0006397; P:GO:0009792; F:GO:0003824	-		IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR10799 (PANTHER), PTHR10799:SF75 (PANTHER), SSF52540 (SUPERFAMILY)

Caenorhabditis elegans	nuclear receptor nhr-1	10	F:GO:0008270; P:GO:0006355; F:GO:0043565; P:GO:0002119; P:GO:0040017; F:GO:0003700; F:GO:0003707; P:GO:0040018; P:GO:0032094; C:GO:0005634	-		IPR000536; IPR001628; IPR008946; IPR013088; PR00350 (PRINTS), PTHR11865 (PANTHER), PTHR11865:SF218 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis elegans	defective spermatogenesis family member (spe-15)-like	25	P:GO:0051046; C:GO:0031941; P:GO:0030048; C:GO:0031965; F:GO:0043531; C:GO:0005794; P:GO:0006886; C:GO:0005905; C:GO:0001726; P:GO:0009792; P:GO:0048839; F:GO:0003774; P:GO:0006897; P:GO:0007268; F:GO:0051015; P:GO:0030330; C:GO:0016591; P:GO:0045944; C:GO:0048471; F:GO:0005516; F:GO:0005524; C:GO:0016459; C:GO:0005938; P:GO:0030182; C:GO:0045334	-		IPR000048; IPR001609; PTHR13140 (PANTHER), PTHR13140:SF26 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	rab beta subunit	7	F:GO:0004663; P:GO:0009792; F:GO:0005515; P:GO:0000003; P:GO:0008219; P:GO:0007601; P:GO:0018348	-	EC:2.5.1.60	IPR001330; IPR008930; G3DSA:1.50.10.20 (GENE3D), PTHR11774 (PANTHER), PTHR11774:SF5 (PANTHER)
	-	0				-
Caenorhabditis elegans	protein arginine n-methyltransferase 10	1	F:GO:0016740	-		IPR010456; G3DSA:2.70.160.11 (GENE3D), G3DSA:3.40.50.150 (GENE3D), PTHR11006 (PANTHER), PTHR11006:SF3 (PANTHER), SSF53335 (SUPERFAMILY)
Caenorhabditis elegans	protein arginine n-methyltransferase 10	1	F:GO:0016740	-		IPR010456; G3DSA:2.70.160.11 (GENE3D), G3DSA:3.40.50.150 (GENE3D), PTHR11006 (PANTHER), PTHR11006:SF3 (PANTHER), SSF53335 (SUPERFAMILY)
Caenorhabditis elegans	igf2 mr- binding	5	P:GO:0009987; C:GO:0005681; F:GO:0003676; P:GO:0000003; P:GO:0007399	-		IPR004087; IPR004088; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR10288 (PANTHER), PTHR10288:SF58 (PANTHER), SSF54791 (SUPERFAMILY)

	-	0				-
Caenorhabditis elegans	integrator complex subunit 4	9	P:GO:0040010; P:GO:0040035; P:GO:0010171; P:GO:0019915; P:GO:0002119; P:GO:0040011; P:GO:0009792; P:GO:0001703; P:GO:0016246	-		PTHR20938 (PANTHER)
	-	0				-
Caenorhabditis elegans	f-box only protein 32	4	F:GO:0005515; P:GO:0006508; C:GO:0016020; P:GO:0043053	-		PTHR13123 (PANTHER), PTHR13123:SF1 (PANTHER)
Caenorhabditis elegans	neuralized	1	F:GO:0005488	-		IPR001841; IPR006573; IPR013083; PTHR12183 (PANTHER), SSF57850 (SUPERFAMILY)
Brugia malayi	cdc23 (cell division cycle homolog)	8	P:GO:0007126; P:GO:0040035; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0006898; P:GO:0002009; P:GO:0009792	-		IPR011990; IPR013026; PTHR12558 (PANTHER), PTHR12558:SF10 (PANTHER), SSF48452 (SUPERFAMILY)
	-	0				-
Nematostella vectensis	r- (guanine-9-) methyltransferase domain containing 2	2	F:GO:0008168; P:GO:0032259	-	EC:2.1.1.0	-
	-	0				-
Caenorhabditis elegans	hypothetical protein B0336.7 [Caenorhabditis elegans]	1	F:GO:0005488	-		IPR006612
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	amop domain containing protein	2	C:GO:0016021; P:GO:0007160	-		PTHR13802 (PANTHER), PTHR13802:SF2 (PANTHER)
Caenorhabditis elegans	mitochondrial carrier protein	6	P:GO:0009792; F:GO:0005488; C:GO:0005743; P:GO:0055085; P:GO:0040010; C:GO:0016021	-		IPR001993; IPR002067; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF34 (PANTHER)
Caenorhabditis elegans	mitochondrial carrier protein	7	P:GO:0009792; F:GO:0005488; C:GO:0005743; F:GO:0022857; P:GO:0055085; P:GO:0040010; C:GO:0016021	-		IPR001993; IPR002067; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF34 (PANTHER)
Caenorhabditis briggsae	translation initiation factor if- mitochondrial	11	P:GO:0006413; P:GO:0040010; C:GO:0016021; P:GO:0007264; C:GO:0005622; P:GO:0015684; F:GO:0015093; F:GO:0008135; F:GO:0003924; P:GO:0006898; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-

Caenorhabditis briggsae	briggsae cbr-mdt-29 protein	0		P:GO:0006350; P:GO:0045449; F:GO:0005515; C:GO:0005634		-
Loa loa	disco-interacting protein 2	0		P:GO:0008152; F:GO:0003824; C:GO:0005634; F:GO:0008134		IPR010506; PTHR22754 (PANTHER), PTHR22754:SF8 (PANTHER)
Caenorhabditis briggsae	ywie_caeel ame: full=uncharacterized protein	3	P:GO:0040007; P:GO:0006898; P:GO:0002119	-		-
Caenorhabditis briggsae	vacuolar atp synthase subunit e	5	F:GO:0008553; C:GO:0000221; P:GO:0015986; F:GO:0046961; C:GO:0005886	-	EC:3.6.3.6; EC:3.6.3.14	-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	dnz1	1	F:GO:0008270	-		IPR001594; PTHR22883 (PANTHER), PS51257 (PROFILE), SignalP (SIGNALP)
Caenorhabditis elegans	dnz1	1	F:GO:0008270	-		IPR001594; PTHR22883 (PANTHER), PS51257 (PROFILE), SignalP (SIGNALP)
Caenorhabditis elegans	dnz1	1	F:GO:0008270	-		IPR001594; PTHR22883 (PANTHER), PS51257 (PROFILE), SignalP (SIGNALP)
	-	0				IPR005514; IPR009003; G3DSA:2.40.10.10 (GENE3D)
Caenorhabditis briggsae	briggsae cbr-vit-6 protein	0		F:GO:0045735; F:GO:0005319; F:GO:0008565; P:GO:0006869; P:GO:0009792; C:GO:0005576; P:GO:0006886; P:GO:0008340; P:GO:0040010		-
Caenorhabditis briggsae	phosphoinositide-3- class beta polypeptide	8	P:GO:0009987; F:GO:0001727; F:GO:0016773; P:GO:0019915; P:GO:0002119; F:GO:0005515; C:GO:0044444; F:GO:0004428	-	EC:2.7.1.0	-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Brugia malayi	lethal giant	0		F:GO:0019901; C:GO:0005737; P:GO:0006887; P:GO:0030866; P:GO:0006461; F:GO:0005515; C:GO:0030864; P:GO:0035090; C:GO:0005856		PTHR10241 (PANTHER), PTHR10241:SF10 (PANTHER)
Caenorhabditis elegans	hypothetical upf0041 protein in chromosome	0				IPR005336; PTHR14154 (PANTHER), PTHR14154:SF3 (PANTHER)

Caenorhabditis briggsae	small subunit processome component 20 homolog	3	F:GO:0005488; C:GO:0031981; P:GO:0006364	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0006508; F:GO:0004181; F:GO:0008270	-	EC:3.4.17.0	-
Loa loa	in family member (ttn-1)	0		F:GO:0004672; F:GO:0005524; F:GO:0000166; P:GO:0006468; P:GO:0009792; F:GO:0004674		IPR013783; PTHR19897 (PANTHER), PTHR19897:SF17 (PANTHER)
	-	0				-
Pongo abelii	type alpha 1	31	P:GO:0060351; P:GO:0001957; P:GO:0071363; P:GO:0007605; P:GO:0034505; P:GO:0042542; P:GO:0001649; P:GO:0009612; P:GO:0001568; P:GO:0060325; F:GO:0005201; C:GO:0005615; P:GO:0048706; P:GO:0015031; F:GO:0048407; C:GO:0005737; P:GO:0043434; P:GO:0071300; P:GO:0007601; P:GO:0010812; C:GO:0005584; F:GO:0042802; P:GO:0060346; P:GO:0032964; P:GO:0030199; P:GO:0051591;	-		IPR008160; PTHR10499 (PANTHER), PTHR10499:SF127 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG07008 [Caenorhabditis briggsae]	0		F:GO:0005509		-
Caenorhabditis elegans	novel protein containing 10 heat domains	10	C:GO:0000502; P:GO:0030433; C:GO:0030134; C:GO:0005813; C:GO:0005770; C:GO:0005769; P:GO:0007067; C:GO:0005802; C:GO:0005783; C:GO:0005634	-		IPR000357; IPR011989; IPR016024; PTHR23346 (PANTHER), PTHR23346:SF2 (PANTHER)

Caenorhabditis elegans	pla2g15 protein	12	C:GO:0005764; F:GO:0004607; F:GO:0047499; C:GO:0005625; C:GO:0005739; F:GO:0005543; P:GO:0046470; P:GO:0009062; P:GO:0019915; P:GO:0006672; C:GO:0005576; F:GO:0004622	-	EC:2.3.1.43; EC:3.1.1.5	IPR003386; SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	pp2c-like domain-containing protein cg9801	1	F:GO:0004721	-	EC:3.1.3.16	PTHR21586 (PANTHER)
Paramecium tetraurelia strain d4-2	hypothetical protein [Paramecium tetraurelia strain d4-2]	0				-
	-	0				-
Caenorhabditis elegans	dead deah box helicase family protein	7	P:GO:0040010; F:GO:0003676; P:GO:0000003; F:GO:0000166; F:GO:0004386; P:GO:0006898; C:GO:0044424	-		IPR000629; IPR011545; IPR014001; IPR014014; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF13 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	isocitrate dehydroge-se	9	C:GO:0005875; F:GO:0051287; C:GO:0005811; F:GO:0005515; P:GO:0055114; F:GO:0000287; P:GO:0006099; F:GO:0004449; C:GO:0005739	-	EC:1.1.1.41	IPR001804; IPR004434; IPR019818; PTHR11835:SF5 (PANTHER), SSF53659 (SUPERFAMILY)
Caenorhabditis elegans	related to yeast vacuolar protein sorting factor family member (vps-39)	6	P:GO:0009792; P:GO:0010171; F:GO:0005515; P:GO:0000003; P:GO:0008219; P:GO:0002009	-		IPR001180; PTHR12894 (PANTHER), PTHR12894:SF10 (PANTHER)
Caenorhabditis briggsae	rgs-gaip interacting protein gipc	1	F:GO:0005515	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR12259 (PANTHER)
Caenorhabditis briggsae	rgs-gaip interacting protein gipc	1	F:GO:0005515	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR12259 (PANTHER)
Caenorhabditis briggsae	rgs-gaip interacting protein gipc	1	F:GO:0005515	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR12259 (PANTHER)
Caenorhabditis briggsae	rgs-gaip interacting protein gipc	1	F:GO:0005515	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR12259 (PANTHER)
Caenorhabditis briggsae	rgs-gaip interacting protein gipc	1	F:GO:0005515	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR12259 (PANTHER)
	-	0				-

Epulopiscium sp. 'N.t. morphotype B'	clostripain family protein	0		C:GO:0009986; F:GO:0003677; F:GO:0046872; C:GO:0016020; C:GO:0005618; F:GO:0003735; F:GO:0004872; P:GO:0015031; P:GO:0008152; P:GO:0006412; F:GO:0003824; C:GO:0000786; P:GO:0006334; C:GO:0005840; C:GO:0020011; P:GO:0006457; F:GO:0008270; C:GO:0005622; F:GO:0005515		-
Caenorhabditis briggsae	isoform cra_a	0		P:GO:0006468; F:GO:0003677; F:GO:0003674; P:GO:0045110; F:GO:0005524; F:GO:0004674; F:GO:0004672; P:GO:0060052; C:GO:0005739; P:GO:0008219; C:GO:0000786; P:GO:0006334; P:GO:0007399; P:GO:0008380; C:GO:0030424; P:GO:0000226; P:GO:0042790; F:GO:0005515; C:GO:0005883		-
Caenorhabditis elegans	briggsae cbr-vrk-1 protein	0		F:GO:0004672; F:GO:0005524; P:GO:0006468; F:GO:0004674		-
						-
Caenorhabditis briggsae	membrane bound o-acyltransferase domain containing 1	1	C:GO:0016020	-		PTHR13906 (PANTHER), PTHR13906:SF4 (PANTHER)
	-	0				-
Caenorhabditis briggsae	kinesin-associated protein 3	5	P:GO:0051179; F:GO:0032266; F:GO:0005515; C:GO:0005871; P:GO:0050794	-		IPR000225; IPR008658; IPR011989; IPR016024; PTHR15605:SF1 (PANTHER), PF05804 (PFAM)
Loa loa	ubiquitin carboxyl-termi-l	1	F:GO:0008233	-		-
Caenorhabditis briggsae	beige beach domain containing protein	1	F:GO:0008270	-		IPR000409; IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; G3DSA:2.30.29.40 (GENE3D), PTHR13743 (PANTHER), SSF50729 (SUPERFAMILY)

Caenorhabditis elegans	t-complex protein 1 subunit eta	12	P:GO:0051086; C:GO:0005739; P:GO:0040007; C:GO:0005832; F:GO:0042802; P:GO:0040035; F:GO:0005524; P:GO:0002119; P:GO:0040011; P:GO:0006898; F:GO:0051082; P:GO:0009792	-		IPR002194; IPR002423; IPR012720; IPR017998; G3DSA:1.10.560.10 (GENE3D), G3DSA:3.30.260.10 (GENE3D), SignalP (SIGNALP), SSF54849 (SUPERFAMILY)
Caenorhabditis elegans	myosin ie	13	P:GO:0001570; P:GO:0048008; C:GO:0043234; F:GO:0000146; F:GO:0042623; P:GO:0035166; F:GO:0005515; C:GO:0015629; F:GO:0000166; P:GO:0006807; P:GO:0001822; P:GO:0030048; P:GO:0001701	-		IPR010926; PTHR13140 (PANTHER), PTHR13140:SF31 (PANTHER)
Caenorhabditis elegans	hedgehog acyltransferase	2	P:GO:0006810; C:GO:0016020	-		IPR004299; PTHR13285 (PANTHER), PTHR13285:SF8 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	uncoordi-ted family member (unc-104)	10	F:GO:0003777; P:GO:0007411; P:GO:0048490; C:GO:0005875; P:GO:0007528; C:GO:0005874; P:GO:0008345; P:GO:0047496; F:GO:0005524; P:GO:0016188	-		IPR022140; IPR022164; PTHR16012 (PANTHER), PTHR16012:SF104 (PANTHER)
Caenorhabditis elegans	uncoordi-ted family member (unc-104)	10	F:GO:0003777; P:GO:0007411; P:GO:0048490; C:GO:0005875; P:GO:0007528; C:GO:0005874; P:GO:0008345; P:GO:0047496; F:GO:0005524; P:GO:0016188	-		IPR022140; IPR022164; PTHR16012 (PANTHER), PTHR16012:SF104 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-dad-1 protein	6	C:GO:0005886; F:GO:0005515; P:GO:0007040; P:GO:0006916; C:GO:0016021; F:GO:0004579	-	EC:2.4.1.119	IPR003038
	-	0				SignalP (SIGNALP)

Loa loa	steroidogenic acute regulatory protein	7	P:GO:0042221; P:GO:0006694; P:GO:0023052; P:GO:0050789; P:GO:0009987; F:GO:0005488; C:GO:0005739	-		IPR002913; G3DSA:3.30.530.20 (GENE3D), PTHR12136 (PANTHER), SSF55961 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	cdp-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	5	F:GO:0008444; P:GO:0008654; P:GO:0000003; C:GO:0016021; P:GO:0019915	-	EC:2.7.8.5	IPR000462; PTHR14269 (PANTHER), PTHR14269:SF3 (PANTHER)
Brugia malayi	retinoblastoma-associated protein a domain containing protein	0		F:GO:0005515		PTHR13742 (PANTHER), PTHR13742:SF6 (PANTHER)
Caenorhabditis briggsae	isocitrate dehydroge-se	6	F:GO:0004450; P:GO:0055114; P:GO:0008340; P:GO:0006102; F:GO:0051287; F:GO:0000287	-	EC:1.1.1.42	IPR001804; IPR004790; IPR019818; SSF53659 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-rsp-7 protein	11	P:GO:0040010; F:GO:0003676; P:GO:0000003; P:GO:0019915; P:GO:0002119; F:GO:0005515; P:GO:0040017; F:GO:0000166; P:GO:0006898; P:GO:0009792; P:GO:0016246	-		IPR000504; IPR012677; PTHR23365 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	tho complex 4	7	P:GO:0009987; F:GO:0003723; F:GO:0005515; P:GO:0040011; F:GO:0003697; C:GO:0044428; P:GO:0051028	-		-
Caenorhabditis elegans	ankyrin repeat protein	1	P:GO:0007413	-		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF203 (PANTHER)
Brugia malayi	polyribonucleotide nucleotidyltransferase 1	3	F:GO:0016779; P:GO:0016070; C:GO:0005739	-	EC:2.7.7.0	IPR001247; IPR012162; IPR015847; IPR020568
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	transmembrane protein 144	2	C:GO:0016020; P:GO:0002119	-		IPR012435; SignalP (SIGNALP)
Caenorhabditis briggsae	- ca exchangers family member (ncx-2)	7	F:GO:0005432; P:GO:0006816; P:GO:0055085; P:GO:0040010; P:GO:0000003; C:GO:0016021; P:GO:0007154	-		IPR003644; PTHR11878 (PANTHER), PTHR11878:SF4 (PANTHER), SSF141072 (SUPERFAMILY)

Caenorhabditis briggsae	zinc dhhc-type containing 3	6	C:GO:0042765; F:GO:0008270; F:GO:0016409; P:GO:0018345; P:GO:0006605; C:GO:0005794	-		IPR001594; PTHR22883 (PANTHER), SignalP (SIGNALP)
Brugia malayi	ring ca-l kelch protein	1	P:GO:0019915	-		IPR006652; IPR013089; IPR015916; PR00501 (PRINTS), PTHR23230:SF147 (PANTHER), SSF117281 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis briggsae	briggsae cbr-cdc- protein	10	P:GO:0040010; P:GO:0007126; P:GO:0000212; P:GO:0000003; P:GO:0051301; P:GO:0008283; P:GO:0009792; F:GO:0004721; P:GO:0051729; C:GO:0005634	-	EC:3.1.3.16	IPR000751; IPR001763; PTHR10828:SF7 (PANTHER)
Brugia malayi	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F48C1.6 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	hypothetical protein F48C1.6 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	flj12716-like protein	1	P:GO:0006974	-		PTHR14374 (PANTHER)
Caenorhabditis elegans	mitochondrial chaperone bcs1	12	P:GO:0034551; P:GO:0033617; F:GO:0017111; P:GO:0040010; C:GO:0005750; P:GO:0000003; F:GO:0005524; P:GO:0002119; F:GO:0005515; P:GO:0006898; P:GO:0032981; P:GO:0009792	-	EC:3.6.1.15	IPR003959; IPR014851; IPR019742; G3DSA:3.40.50.300 (GENE3D), PTHR23070 (PANTHER), PTHR23070:SF2 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	adam 10	2	F:GO:0046872; F:GO:0008237	-		IPR002870; PTHR11905 (PANTHER), PTHR11905:SF4 (PANTHER), SignalP (SIGNALP)
	-	0				-

Caenorhabditis briggsae	cg11981-pa	14	P:GO:0008340; P:GO:0051436; P:GO:0051437; P:GO:0000003; F:GO:0004298; P:GO:0031145; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0009792; C:GO:0005737; C:GO:0005839; C:GO:0005634; P:GO:0006974	-	EC:3.4.25.0	IPR001353; IPR016050; G3DSA:3.60.20.10 (GENE3D), PTHR11599 (PANTHER), PTHR11599:SF7 (PANTHER), PS51476 (PROFILE), SSF56235 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG06707 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)
Caenorhabditis elegans	isoform c	3	P:GO:0007186; C:GO:0016021; F:GO:0004930	-		IPR017978; SignalP (SIGNALP)
Caenorhabditis elegans	amp-binding enzyme family protein	3	F:GO:0016874; P:GO:0008152; C:GO:0016021	-		IPR000873; G3DSA:3.40.50.980 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF15 (PANTHER), SSF56801 (SUPERFAMILY)
Caenorhabditis briggsae	solute carrier family 27 (fatty acid transporter) member 4	21	P:GO:0006659; F:GO:0005515; C:GO:0031526; P:GO:0015909; P:GO:0001676; C:GO:0005792; C:GO:0005902; P:GO:0001579; C:GO:0005743; P:GO:0032049; F:GO:0004467; P:GO:0006646; P:GO:0071072; P:GO:0043588; P:GO:0042760; P:GO:0006661; P:GO:0006654; C:GO:0005783; C:GO:0005901; P:GO:0006656; F:GO:0031957	-	EC:6.2.1.3	IPR000873; IPR020845; G3DSA:3.40.50.980 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF15 (PANTHER), SignalP (SIGNALP), SSF56801 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-asp-6 protein	0		P:GO:0006508; C:GO:0016021; F:GO:0004190; F:GO:0016787; P:GO:0040011; F:GO:0008233; P:GO:0008219; F:GO:0005515		IPR001461; IPR009007; IPR021109; PTHR13683:SF53 (PANTHER), SignalP (SIGNALP)

Drosophila virilis	g patch domain containing 1	7	P:GO:0010171; P:GO:0002119; F:GO:0003676; C:GO:0071011; P:GO:0019915; P:GO:0000398; C:GO:0071013	-		IPR011666; PTHR13384 (PANTHER), PTHR13384:SF8 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-smg-3 protein	0		F:GO:0005488; P:GO:0016070; F:GO:0005515		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	programmed cell death 6-interacting protein	4	P:GO:0006915; F:GO:0046983; C:GO:0005829; F:GO:0017124	-		G3DSA:1.20.120.560 (GENE3D), G3DSA:1.20.140.50 (GENE3D), PTHR23030 (PANTHER), PTHR23030:SF11 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	P:GO:0008340	-		IPR012816; SSF143990 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; P:GO:0023034		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0016887; P:GO:0008340		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; P:GO:0023034		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	P:GO:0008340	-		-
Caenorhabditis briggsae	mgc83793 protein	0				PTHR12786 (PANTHER), PTHR12786:SF1 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Ancylostoma caninum	secreted protein asp-2	2	P:GO:0040011; C:GO:0005576	-		IPR001283; IPR014044; PTHR10334:SF11 (PANTHER)
Haemonchus contortus	elegans protein confirmed by transcript evidence	3	F:GO:0015078; C:GO:0033177; P:GO:0015986	-		IPR002490; PTHR11629:SF23 (PANTHER)
Brugia malayi	lim domain binding protein	0		P:GO:0007275; F:GO:0003677; F:GO:0003712; C:GO:0005634		-
Brugia malayi	lim domain binding protein family member (ldb-1)	6	F:GO:0030528; F:GO:0005515; P:GO:0048513; P:GO:0030154; P:GO:0045449; P:GO:0007399	-		-
Brugia malayi	lim domain binding protein	0		P:GO:0007275; F:GO:0003677; F:GO:0003712; C:GO:0005634		-
	-	0				-
	-	0				-
Brugia malayi	macrophage erythroblast attacher	7	P:GO:0048821; C:GO:0015629; P:GO:0050794; C:GO:0005737; C:GO:0044430; C:GO:0005634; C:GO:0005886	-		IPR006594; IPR006595; PTHR12170 (PANTHER), PTHR12170:SF2 (PANTHER), SSF57850 (SUPERFAMILY)

Loa loa	variant sh3 domain containing protein	7	P:GO:0023033; F:GO:0005515; C:GO:0005829; P:GO:0042110; P:GO:0006915; P:GO:0048522; F:GO:0005089	-		IPR002219; G3DSA:3.30.60.20 (GENE3D), PTHR22826 (PANTHER), PTHR22826:SF53 (PANTHER), SSF57889 (SUPERFAMILY)
Caenorhabditis briggsae	ribosomal protein s15	11	F:GO:0003723; P:GO:0006364; F:GO:0003735; P:GO:0006414; C:GO:0022627; P:GO:0000056; F:GO:0003677; F:GO:0005515; P:GO:0000028; C:GO:0005654; P:GO:0009790	-		IPR002222; IPR005713; IPR020934
Caenorhabditis briggsae	ribosomal protein s15	11	F:GO:0003723; P:GO:0006364; F:GO:0003735; P:GO:0006414; C:GO:0022627; P:GO:0000056; F:GO:0003677; F:GO:0005515; P:GO:0000028; C:GO:0005654; P:GO:0009790	-		IPR002222; IPR005713
Caenorhabditis elegans	dihydroorotate dehydroge-se	8	P:GO:0043065; F:GO:0004158; C:GO:0016021; C:GO:0005743; P:GO:0055114; P:GO:0006222; P:GO:0090140; P:GO:0006207	-	EC:1.3.3.1	IPR001295; IPR012135; IPR013785; PTHR11938 (PANTHER), PTHR11938:SF7 (PANTHER), SSF51395 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	5 -amp-activated protein beta complex-interacting region containing protein	5	F:GO:0016301; P:GO:0035090; P:GO:0070050; F:GO:0030246; P:GO:0006974	-		IPR006828; PTHR10343 (PANTHER), PTHR10343:SF10 (PANTHER)
Caenorhabditis elegans	actin family protein	5	P:GO:0000003; P:GO:0040007; F:GO:0005515; P:GO:0006898; P:GO:0002119	-		IPR001849; IPR004000; PTHR11937:SF19 (PANTHER)
Caenorhabditis elegans	mitochondrial ribosomal protein l2	3	C:GO:0005840; F:GO:0003735; P:GO:0006412	-	EC:3.6.5.3	IPR002171; IPR008991; IPR012340; IPR014722; IPR016027; IPR018130; IPR022666; IPR022669; PTHR13691:SF6 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	g-t family protein	1	P:GO:0006911	-		-

Caenorhabditis briggsae	mitogen-activated protein ki-se ki-se 2	12	C:GO:0005625; F:GO:0004708; P:GO:0006468; P:GO:0000165; F:GO:0005515; F:GO:0004713; C:GO:0005938; F:GO:0005524; C:GO:0005576; C:GO:0005829; F:GO:0004674; P:GO:0007265	-	EC:2.7.10.0; EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF46 (PANTHER)
	-	0				-
	-	0				PD936484 (PRODOM)
Caenorhabditis elegans	ef hand family protein	5	P:GO:0065008; P:GO:0007268; P:GO:0006897; P:GO:0050794; C:GO:0044464	-		IPR000261; IPR002048; IPR011992; IPR018247; IPR018249; PD936484 (PRODOM), PTHR11216 (PANTHER), PTHR11216:SF34 (PANTHER), SSF47473 (SUPERFAMILY)
	-	0				-
	-	0				-
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
Loa loa	d- mismatch repair protein msh2	14	F:GO:0032139; F:GO:0032138; F:GO:0003684; P:GO:0006310; P:GO:0019724; P:GO:0002520; C:GO:0044428; F:GO:0042802; F:GO:0032559; P:GO:0019222; C:GO:0032300; P:GO:0048523; F:GO:0019899; P:GO:0006281	-		IPR000432; IPR007695; IPR007696; IPR007860; IPR007861; G3DSA:1.10.1420.10 (GENE3D), PTHR11361:SF4 (PANTHER)
	-	0				-
Caenorhabditis elegans	dead (asp-glu-ala-asp) box polypeptide 23	8	F:GO:0004004; C:GO:0005681; F:GO:0003676; F:GO:0005524; F:GO:0005515; P:GO:0000354; C:GO:0005682; C:GO:0046540	-		IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF47 (PANTHER), SSF52540 (SUPERFAMILY)
Caulobacter segnis ATCC 21756	alkaline phosphatase	0		F:GO:0016791; F:GO:0004035; F:GO:0016787; P:GO:0008152; F:GO:0003824		IPR001952; IPR017849; IPR017850; PTHR11596 (PANTHER), PTHR11596:SF11 (PANTHER)
Caenorhabditis briggsae	tensin 3	4	P:GO:0009987; F:GO:0005515; C:GO:0044464; F:GO:0016787	-		IPR014019; G3DSA:3.90.190.10 (GENE3D), PTHR12305 (PANTHER), PTHR12305:SF12 (PANTHER), SSF52799 (SUPERFAMILY)
Loa loa	trm112-like protein	0		F:GO:0003674; C:GO:0005575		-
Loa loa	trm112-like protein	0		F:GO:0003674; C:GO:0005575		IPR005651; G3DSA:2.20.25.10 (GENE3D)

Caenorhabditis elegans	rn207_caeel ame: full=probable ring finger protein 207 homolog	1	F:GO:0005488	-		-
Caenorhabditis elegans	rn207_caeel ame: full=probable ring finger protein 207 homolog	1	F:GO:0005488	-		-
	-	0				-
Caenorhabditis elegans	foie gras	1	P:GO:0006974	-		IPR021773; PTHR14374 (PANTHER)
Saccharomyces cerevisiae EC1118	branched-chain amino acid transami-se	3	P:GO:0008652; P:GO:0009081; F:GO:0008483	-	EC:2.6.1.0	IPR001544; IPR005786; G3DSA:3.30.470.10 (GENE3D)
Caenorhabditis briggsae	serine beta-lactamase-like protein mitochondrial	4	P:GO:0009792; P:GO:0040007; C:GO:0005739; P:GO:0002119	-		IPR001466; IPR012338; G3DSA:3.40.710.10 (GENE3D), PTHR22935 (PANTHER), PTHR22935:SF13 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	transmembrane protein 65	1	C:GO:0016020	-		IPR019537; PTHR21706 (PANTHER), PTHR21706:SF7 (PANTHER)
Caenorhabditis elegans	viral a-type inclusion protein	2	F:GO:0005488; C:GO:0044464	-		PD936484 (PRODOM)
Hydra magnipapillata	chromobox protein homolog 5	0				IPR008251; IPR016197; G3DSA:2.40.50.40 (GENE3D)
	-	0				-
Loa loa	mannose-6-phosphate isomerase	2	P:GO:0005975; F:GO:0004476	-	EC:5.3.1.8	IPR001250; IPR011051; IPR014710; IPR016305; IPR018050; G3DSA:1.10.441.10 (GENE3D), PTHR10309 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	nudix (nucleoside diphosphate linked moiety x)-type motif 18	2	F:GO:0016787; F:GO:0005515	-		IPR000086; IPR015797; IPR020084; IPR020476; PTHR22769 (PANTHER), PS51462 (PROFILE)
Caenorhabditis elegans	nudix (nucleoside diphosphate linked moiety x)-type motif 18	2	F:GO:0016787; F:GO:0005515	-		IPR000086; IPR015797; IPR020084; IPR020476; PTHR22769 (PANTHER), PS51462 (PROFILE)
Loa loa	hypothetical protein LOAG_06999 [Loa loa]	0		F:GO:0004864; P:GO:0043666; P:GO:0009966		IPR007062; PTHR12398 (PANTHER), PTHR12398:SF7 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-alh-7 protein	3	P:GO:0055114; F:GO:0016491; C:GO:0016021	-		IPR015590; IPR016161; IPR016162; IPR016163; PTHR11699:SF49 (PANTHER)
Caenorhabditis elegans	endonuclease-reverse transcriptase	0		F:GO:0003723; P:GO:0006278; F:GO:0004519; F:GO:0003964		-
Caenorhabditis elegans	talin 2	5	F:GO:0008092; C:GO:0030054; C:GO:0005856; C:GO:0044444; N:GO:0071842	-		IPR006077; IPR015710; IPR015711; G3DSA:1.20.1490.10 (GENE3D), SSF109885 (SUPERFAMILY)
Loa loa	r- guanine-9- methyltransferase domain containing	2	P:GO:0000003; P:GO:0006898	-		-
Caenorhabditis briggsae	helicase arip4	4	F:GO:0003676; F:GO:0005515; F:GO:0016787; F:GO:0000166	-		IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR10799 (PANTHER), PTHR10799:SF51 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				IPR011992; IPR018247; SignalP (SIGNALP), SSF47473 (SUPERFAMILY)

Caenorhabditis elegans	speckle-type poz protein	9	P:GO:0007367; P:GO:0043065; P:GO:0042067; P:GO:0007349; P:GO:0016567; P:GO:0046330; F:GO:0005515; P:GO:0030162; C:GO:0005634	-		IPR000210; IPR002083; IPR008974; IPR011333; IPR013069; IPR013089; IPR013322; PTHR23230:SF176 (PANTHER)
	-	0				-
Caenorhabditis briggsae	small nuclear ribonucleoprotein-associated protein b	13	C:GO:0005829; F:GO:0071208; C:GO:0005681; P:GO:0040007; C:GO:0005683; P:GO:0000003; P:GO:0040027; F:GO:0042802; P:GO:0000387; C:GO:0071204; P:GO:0006898; C:GO:0005654; P:GO:0009792	-		IPR001163; IPR006649; IPR010920; G3DSA:2.30.30.100 (GENE3D), PTHR10701 (PANTHER)
Callithrix jacchus	ribosomal protein l3	6	C:GO:0005730; F:GO:0003735; F:GO:0003723; F:GO:0005515; C:GO:0022625; P:GO:0006414	-		SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	7	P:GO:0009792; F:GO:0046872; P:GO:0040018; P:GO:0040017; P:GO:0040010; P:GO:0000003; P:GO:0008340	-		IPR001128; PTHR19383:SF176 (PANTHER)
Caenorhabditis elegans	briggsae cbr-cdc-6 protein	8	C:GO:0005730; C:GO:0000794; P:GO:0040007; P:GO:0040035; P:GO:0002119; P:GO:0006898; P:GO:0009792; C:GO:0005737	-		IPR003593; IPR003959; G3DSA:1.10.8.60 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR10763 (PANTHER), PTHR10763:SF5 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	h aca ribonucleoprotein complex subunit 2-like protein	8	P:GO:0040010; C:GO:0005840; C:GO:0005730; C:GO:0005732; F:GO:0030515; P:GO:0006898; P:GO:0031118; F:GO:0030559	-		IPR002415; IPR004038; IPR018492; G3DSA:3.30.1330.30 (GENE3D), PTHR23105 (PANTHER), PTHR23105:SF12 (PANTHER), SSF55315 (SUPERFAMILY)
	-	0				-

Caenorhabditis briggsae	nuclear pore complex protein nup85	13	P:GO:0051179; P:GO:0008340; C:GO:0043234; P:GO:0018991; P:GO:0040007; P:GO:0040035; C:GO:0043232; P:GO:0002119; P:GO:0040017; P:GO:0006997; C:GO:0005635; P:GO:0009792; C:GO:0016020	-			IPR011502; PTHR13373 (PANTHER), PTHR13373:SF2 (PANTHER)
Caenorhabditis briggsae	nuclear pore complex protein nup85	13	P:GO:0051179; P:GO:0008340; C:GO:0043234; P:GO:0018991; P:GO:0040007; P:GO:0040035; C:GO:0043232; P:GO:0002119; P:GO:0040017; P:GO:0006997; C:GO:0005635; P:GO:0009792; C:GO:0016020	-			IPR011502; PTHR13373 (PANTHER), PTHR13373:SF2 (PANTHER)
Caenorhabditis elegans	abc transporter	7	P:GO:0009792; F:GO:0042626; C:GO:0005743; P:GO:0055085; F:GO:0005524; P:GO:0000003; C:GO:0016021	-			IPR001140; IPR003439; IPR003593; IPR011527; IPR017871; IPR017940; G3DSA:1.20.1560.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF68 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0					SignalP (SIGNALP)
	-	0					SignalP (SIGNALP)
Caenorhabditis elegans	abc transporter	7	P:GO:0009792; F:GO:0042626; C:GO:0005743; P:GO:0055085; F:GO:0005524; P:GO:0000003; C:GO:0016021	-			IPR001140; IPR003439; IPR003593; IPR011527; IPR017871; IPR017940; G3DSA:1.20.1560.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF68 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	abc transporter	7	P:GO:0009792; F:GO:0042626; C:GO:0005743; P:GO:0055085; F:GO:0005524; P:GO:0000003; C:GO:0016021	-			IPR001140; IPR003439; IPR003593; IPR011527; IPR017871; IPR017940; G3DSA:1.20.1560.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF68 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	abc transporter	7	P:GO:0009792; F:GO:0042626; C:GO:0005743; P:GO:0055085; F:GO:0005524; P:GO:0000003; C:GO:0016021	-			IPR001140; IPR003439; IPR003593; IPR011527; IPR017871; IPR017940; G3DSA:1.20.1560.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF68 (PANTHER), SSF52540 (SUPERFAMILY)

Caenorhabditis elegans	inosine monophosphate dehydroge-se 1	6	F:GO:0003938; P:GO:0006177; F:GO:0046872; P:GO:0055114; F:GO:0018580; P:GO:0009451	-	EC:1.1.1.205; EC:1.13.11.32	IPR000644; IPR001093; IPR013785; IPR015875; PTHR11911 (PANTHER), PTHR11911:SF6 (PANTHER), SSF51412 (SUPERFAMILY), SSF54631 (SUPERFAMILY)
Caenorhabditis briggsae	inosine monophosphate dehydroge-se 1	6	F:GO:0003938; P:GO:0006177; F:GO:0046872; P:GO:0055114; F:GO:0018580; P:GO:0009451	-	EC:1.1.1.205; EC:1.13.11.32	IPR000644; IPR001093; IPR005990; IPR013785; IPR015875; IPR018529; PTHR11911 (PANTHER), PTHR11911:SF6 (PANTHER), SSF51412 (SUPERFAMILY), SSF54631 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr--s-7 protein	2	F:GO:0046872; F:GO:0008237	-		IPR001506; IPR003582; IPR006026; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF80 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	prp4 pre-mr- processing factor 4 homolog	14	P:GO:0040010; C:GO:0015030; C:GO:0005681; F:GO:0003676; C:GO:0016607; P:GO:0040035; P:GO:0008380; P:GO:0002119; C:GO:0071001; F:GO:0005515; P:GO:0040011; P:GO:0006397; P:GO:0009792; P:GO:0001703	-		IPR001680; IPR011047; IPR015943; IPR017986; IPR019781; IPR019782; PTHR19846 (PANTHER)
Caenorhabditis elegans	peptidylprolyl isomerase -like 4	8	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0006457; F:GO:0003676; P:GO:0040007; F:GO:0003755; F:GO:0000166	-	EC:5.2.1.8	IPR000504; IPR002130; IPR012677; IPR015891; PTHR11071 (PANTHER), PTHR11071:SF27 (PANTHER), SSF54928 (SUPERFAMILY)
Brugia malayi	regulator of nonsense transcripts 1	6	C:GO:0005737; P:GO:0009790; F:GO:0046872; P:GO:0000184; F:GO:0017111; F:GO:0000166	-	EC:3.6.1.15	IPR018999; PTHR10887 (PANTHER), PTHR10887:SF26 (PANTHER)
Caenorhabditis briggsae	uncoordi-ted family member (unc-89)	0				-
Caenorhabditis briggsae	yqvw_caeel ame: full=uncharacterized protein	1	P:GO:0040011	-		IPR009622
Caenorhabditis briggsae	spermatogenesis-associated serine-rich protein 2	0		F:GO:0003674; C:GO:0005737		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)

Loa loa	fk506 binding protein 12-rapamycin associated protein 1	20	F:GO:0004674; P:GO:0030838; P:GO:0032868; P:GO:0032314; C:GO:0043234; P:GO:0048565; P:GO:0043200; P:GO:0018107; P:GO:0031529; P:GO:0050731; P:GO:0045859; P:GO:0051496; F:GO:0000166; F:GO:0005515; P:GO:0007281; P:GO:0010592; P:GO:0045792; C:GO:0044444; C:GO:0005634; P:GO:0016242	-	EC:2.7.11.0	IPR011989; IPR016024
Caenorhabditis elegans	small nuclear r- activating polypeptide 50kda	6	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0006898; P:GO:0040007; P:GO:0002009	-		IPR022042; PTHR13421 (PANTHER), PTHR13421:SF6 (PANTHER)
Caenorhabditis elegans	briggsae cbr-pyc-1 protein	9	C:GO:0005875; F:GO:0004736; F:GO:0009374; P:GO:0009252; F:GO:0005524; P:GO:0006094; C:GO:0005759; C:GO:0005811; F:GO:0008716	-	EC:6.4.1.1; EC:6.3.2.4	IPR005479; IPR005481; IPR005482; IPR005483; IPR011054; IPR011761; IPR011764; IPR013785; IPR013815; IPR013816; IPR013817; IPR016185; PTHR18866 (PANTHER), PTHR18866:SF10 (PANTHER), SSF51569 (SUPERFAMILY), SSF56059 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-pyc-1 protein	9	C:GO:0005875; F:GO:0004736; F:GO:0009374; P:GO:0009252; F:GO:0005524; P:GO:0006094; C:GO:0005759; C:GO:0005811; F:GO:0008716	-	EC:6.4.1.1; EC:6.3.2.4	IPR005479; IPR005481; IPR005482; IPR005483; IPR011054; IPR011761; IPR011764; IPR013785; IPR013815; IPR013816; IPR013817; IPR016185; PTHR18866 (PANTHER), PTHR18866:SF10 (PANTHER), SSF51569 (SUPERFAMILY), SSF56059 (SUPERFAMILY)
Canis familiaris	ribosomal protein s25	7	F:GO:0003723; C:GO:0005730; F:GO:0003735; P:GO:0006414; C:GO:0022627; F:GO:0005515; P:GO:0000028	-		IPR004977; PTHR12850:SF4 (PANTHER)

Macaca mulatta	y box binding protein 1	22	F:GO:0002039; P:GO:0000122; P:GO:0070934; C:GO:0010494; P:GO:0006397; F:GO:0003697; C:GO:0071204; C:GO:0030425; P:GO:0008284; P:GO:0008380; F:GO:0043565; F:GO:0003700; P:GO:0046627; P:GO:0045944; F:GO:0003690; C:GO:0048471; F:GO:0004872; C:GO:0070937; P:GO:0043066; P:GO:0001701; F:GO:0016564; F:GO:0003729	-		SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-pqn-96 protein	0				-
	-	0				-
Caenorhabditis briggsae	endonuclease exonuclease phosphatase family protein	5	P:GO:0000003; F:GO:0004437; C:GO:0042995; P:GO:0048523; P:GO:0008152	-		IPR005135; G3DSA:3.60.10.10 (GENE3D), PTHR11200 (PANTHER), PTHR11200:SF15 (PANTHER)
Caenorhabditis elegans	ring finger protein 11	2	F:GO:0008270; F:GO:0005515	-		IPR001841; IPR013083; IPR018957; PTHR22764 (PANTHER), PTHR22764:SF3 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis elegans	ring finger protein 11	2	F:GO:0008270; F:GO:0005515	-		IPR001841; IPR013083; IPR018957; PTHR22764 (PANTHER), PTHR22764:SF3 (PANTHER), SSF57850 (SUPERFAMILY)
Brugia malayi	dedicator of cytokinesis 8	1	F:GO:0005488	-		PTHR23317 (PANTHER), PTHR23317:SF27 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-rbr-2 protein	0		F:GO:0003677; C:GO:0005634; F:GO:0016702; F:GO:0008270; P:GO:0055114; P:GO:0016568; F:GO:0016491; F:GO:0005515; C:GO:0005622; F:GO:0046872; P:GO:0006350; P:GO:0045449		IPR001965; IPR011011; IPR013083; IPR019786; PTHR10694 (PANTHER), PTHR10694:SF1 (PANTHER)

Caenorhabditis elegans	glutamate synthase	10	P:GO:0006537; P:GO:0009792; F:GO:0045181; P:GO:0002119; F:GO:0051536; F:GO:0005506; F:GO:0010181; P:GO:0040010; P:GO:0055114; F:GO:0050660	-		IPR009051; IPR012285; IPR013027; IPR016040; PR00419 (PRINTS), PTHR11938 (PANTHER), PTHR11938:SF9 (PANTHER), SSF51971 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	4	C:GO:0016021; P:GO:0008340; F:GO:0005488; P:GO:0055085	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF23 (PANTHER)
Caenorhabditis elegans	wapl (drosophila wings apart-like cohesin interactor) family member (wapl-1)	0		P:GO:0000003; F:GO:0005488; P:GO:0040011; P:GO:0040010; P:GO:0018991		IPR012502; IPR022771; PTHR22100 (PANTHER), PTHR22100:SF7 (PANTHER)
Caenorhabditis elegans	wapl (drosophila wings apart-like cohesin interactor) family member (wapl-1)	0		P:GO:0000003; F:GO:0005524; F:GO:0005488; P:GO:0040011; P:GO:0040010; P:GO:0006298; F:GO:0030983; P:GO:0018991		IPR012502; IPR022771; PTHR22100 (PANTHER), PTHR22100:SF7 (PANTHER)
Caenorhabditis briggsae	heterogeneous nuclear ribonucleoprotein f	6	C:GO:0005737; C:GO:0005730; C:GO:0030530; P:GO:0043484; F:GO:0017025; F:GO:0003727	-		IPR000504; IPR012677; PTHR13976 (PANTHER), PTHR13976:SF3 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	heterogeneous nuclear ribonucleoprotein f	6	C:GO:0005737; C:GO:0005730; C:GO:0030530; P:GO:0043484; F:GO:0017025; F:GO:0003727	-		IPR000504; IPR012677; PTHR13976 (PANTHER), PTHR13976:SF3 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	heterogeneous nuclear ribonucleoprotein f	7	C:GO:0005737; C:GO:0005730; C:GO:0030530; C:GO:0005654; P:GO:0043484; F:GO:0017025; F:GO:0003727	-		IPR000504; IPR012677; PTHR13976 (PANTHER), PTHR13976:SF3 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	aarf domain containing ki-se 1	0		C:GO:0005739; F:GO:0004672; F:GO:0005524; P:GO:0006468		IPR000719; IPR004147; IPR011009; G3DSA:3.30.200.20 (GENE3D), PTHR10566 (PANTHER), PTHR10566:SF7 (PANTHER)

Caenorhabditis elegans	snurportin 1	13	P:GO:0000003; F:GO:0005515; P:GO:0040007; P:GO:0006898; P:GO:0040011; P:GO:0006259; C:GO:0005829; P:GO:0009792; C:GO:0043234; P:GO:0002119; F:GO:0003723; C:GO:0005634; P:GO:0000387	-		IPR002652; PTHR13403 (PANTHER), PTHR13403:SF6 (PANTHER), PF11538 (PFAM), SSF56091 (SUPERFAMILY)
Caenorhabditis elegans	phosphatidylinositol glycan anchor class s	1	P:GO:0006898	-		IPR019540; PTHR21072 (PANTHER), PTHR21072:SF1 (PANTHER)
Caenorhabditis elegans	phosphatidylinositol glycan anchor class s	1	P:GO:0006898	-		IPR019540; PTHR21072 (PANTHER), PTHR21072:SF1 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-sdc-3 protein	0		F:GO:0008270; C:GO:0005622		IPR007087
Caenorhabditis elegans	polymerase (d--directed) epsilon 4 (p12 subunit)	2	F:GO:0005515; F:GO:0016740	-		IPR003958; IPR009072; PTHR10252 (PANTHER), PTHR10252:SF7 (PANTHER)
Caenorhabditis briggsae	kh domain containing protein	14	P:GO:0007424; P:GO:0044238; P:GO:0016337; P:GO:0044260; P:GO:0016043; P:GO:0009653; P:GO:0016477; P:GO:0048513; C:GO:0043231; C:GO:0044459; P:GO:0023033; F:GO:0005515; P:GO:0048523; C:GO:0044444	-		IPR004087; IPR004088; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR10288 (PANTHER), PTHR10288:SF34 (PANTHER), SSF54791 (SUPERFAMILY)
Caenorhabditis briggsae	kh domain containing protein	22	P:GO:0048468; C:GO:0044422; P:GO:0007424; P:GO:0016337; P:GO:0009790; P:GO:0009653; P:GO:0016477; P:GO:0007517; C:GO:0043231; C:GO:0042995; P:GO:0007399; C:GO:0005887; P:GO:0043066; F:GO:0005515; P:GO:0065008; P:GO:0007166; P:GO:0044267; P:GO:0023034; N:GO:0071842; C:GO:0044444; P:GO:0030030; P:GO:0035220	-		IPR004087; IPR004088; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR10288 (PANTHER), PTHR10288:SF34 (PANTHER), SSF54791 (SUPERFAMILY)

Caenorhabditis briggsae	kh domain containing protein	14	P:GO:0007424; P:GO:0044238; P:GO:0016337; P:GO:0044260; P:GO:0016043; P:GO:0009653; P:GO:0016477; P:GO:0048513; C:GO:0043231; C:GO:0044459; P:GO:0023033; F:GO:0005515; P:GO:0048523; C:GO:0044444	-		IPR004087; IPR004088; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR10288 (PANTHER), PTHR10288:SF34 (PANTHER), SSF54791 (SUPERFAMILY)
Caenorhabditis briggsae	hig1 domain family member 2a	1	P:GO:0040011	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	tpr domain containing protein	0		F:GO:0005488; P:GO:0000956		IPR011990; IPR013026; IPR019734; PTHR23083 (PANTHER), SSF48452 (SUPERFAMILY)
Caenorhabditis elegans	tpr domain containing protein	0		F:GO:0005488; P:GO:0000956		IPR011990; IPR013026; IPR019734; PTHR23083 (PANTHER), SignalP (SIGNALP), SSF48452 (SUPERFAMILY)
Caenorhabditis elegans	tpr domain containing protein	0		F:GO:0005488; P:GO:0000956		IPR011990; IPR013026; IPR019734; PTHR23083 (PANTHER), SignalP (SIGNALP), SSF48452 (SUPERFAMILY)
Caenorhabditis elegans	tpr domain containing protein	0		F:GO:0005488; P:GO:0000956		IPR011990; IPR013026; IPR019734; PTHR23083 (PANTHER), SignalP (SIGNALP), SSF48452 (SUPERFAMILY)
Laccaria bicolor S238N-H82	d- polymerase epsilon	0		F:GO:0016740; F:GO:0003677; C:GO:0005634; P:GO:0006260; F:GO:0003676; F:GO:0000166; F:GO:0003887; F:GO:0008270; F:GO:0016779; P:GO:0006139		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	subfamily member 11	6	P:GO:0006457; F:GO:0031072; F:GO:0051082; P:GO:0016556; C:GO:0005634; C:GO:0005783	-		IPR001623; IPR002939; IPR003095; IPR008971; IPR015609; IPR018253; G3DSA:2.60.260.20 (GENE3D), PTHR11821:SF69 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-cid-1 protein	0		F:GO:0003676; F:GO:0008270; F:GO:0005515		IPR007087; IPR015880
	-	0				-
Caenorhabditis elegans	hypothetical kda protein in chromosome	4	P:GO:0006071; F:GO:0008889; F:GO:0030246; P:GO:0006629	-	EC:3.1.4.46	IPR004129; IPR017946; IPR018247; PTHR22958 (PANTHER)
Brugia malayi	kiaa0467 protein	0				-

Loa loa	isoform a	8	C:GO:0070864; P:GO:0007291; F:GO:0008270; P:GO:0007279; C:GO:0005925; F:GO:0003779; C:GO:0015629; P:GO:0045856	-		SignalP (SIGNALP)
Caenorhabditis elegans	isoform a	8	C:GO:0070864; P:GO:0007291; F:GO:0008270; P:GO:0007279; C:GO:0005925; F:GO:0003779; C:GO:0015629; P:GO:0045856	-		IPR000900; IPR001781; IPR013998; PTHR11039:SF3 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis elegans	lim and sh3 domain protein lasp-	7	C:GO:0070864; P:GO:0007291; F:GO:0008270; P:GO:0007279; C:GO:0005925; F:GO:0003779; P:GO:0045856	-		IPR000900; IPR001781; IPR013998; PTHR11039:SF3 (PANTHER), SSF57716 (SUPERFAMILY)
Brugia malayi	lim domains containing 1	8	C:GO:0005737; F:GO:0046872; F:GO:0005515; P:GO:0007275; P:GO:0007165; C:GO:0005634; P:GO:0006355; F:GO:0016564	-		IPR001781; PTHR18973 (PANTHER), PTHR18973:SF60 (PANTHER), SSF57716 (SUPERFAMILY)
Brugia malayi	lim domains containing 1	8	C:GO:0005737; F:GO:0046872; F:GO:0005515; P:GO:0007275; P:GO:0007165; C:GO:0005634; P:GO:0006355; F:GO:0016564	-		IPR001781; PTHR18973 (PANTHER), PTHR18973:SF60 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis briggsae	atp synthase subunit mitochondrial	4	P:GO:0040007; P:GO:0010171; P:GO:0040035; P:GO:0002119	-		-
Caenorhabditis briggsae	briggsae cbr-eat-3 protein	10	C:GO:0030061; P:GO:0045768; C:GO:0016021; C:GO:0030425; C:GO:0005741; C:GO:0005758; P:GO:0007601; P:GO:0007007; F:GO:0003924; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001401; IPR022812; G3DSA:3.40.50.300 (GENE3D), PTHR11566 (PANTHER), PTHR11566:SF8 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	helix loop helix family member (hlh-30)	2	P:GO:0000003; P:GO:0019915	-		PTHR10014 (PANTHER), PTHR10014:SF7 (PANTHER)
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis briggsae	cleft lip and palate associated transmembrane protein 1	4	C:GO:0005887; F:GO:0005515; C:GO:0009897; P:GO:0033081	-		IPR008429; SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0000003; P:GO:0006915		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	4	P:GO:0006915; P:GO:0000003; F:GO:0030296; C:GO:0005912	-		IPR001452; IPR002110; IPR020683; G3DSA:2.30.30.40 (GENE3D), PTHR18958 (PANTHER), PTHR18958:SF32 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	4	P:GO:0006915; P:GO:0000003; F:GO:0030296; C:GO:0005912	-		IPR001452; IPR002110; IPR020683; G3DSA:2.30.30.40 (GENE3D), PTHR18958 (PANTHER), PTHR18958:SF32 (PANTHER)
Caenorhabditis briggsae	inner centromere protein	4	C:GO:0032133; C:GO:0005694; P:GO:0051225; F:GO:0019901	-		IPR005635; PTHR13142 (PANTHER)
Caenorhabditis briggsae	acid phosphatase-1	1	F:GO:0016787	-		IPR000560; G3DSA:3.40.50.1240 (GENE3D), PTHR11567 (PANTHER), PTHR11567:SF20 (PANTHER), SignalP (SIGNALP), SSF53254 (SUPERFAMILY)
Caenorhabditis briggsae	efr3 homolog a (cerevisiae)	7	P:GO:0009792; F:GO:0005488; C:GO:0005622; C:GO:0005886; P:GO:0040010; C:GO:0016021; P:GO:0006898	-		PTHR12444 (PANTHER)
Caenorhabditis elegans	riken cd- 2610003j06	0		F:GO:0003674; P:GO:0008150		-
	-	0				-
Caenorhabditis briggsae	guanylyl cyclase family member (gcy-28)	7	F:GO:0004383; F:GO:0004672; F:GO:0008528; F:GO:0005524; C:GO:0016020; P:GO:0006468; P:GO:0006182	-	EC:4.6.1.2	IPR000719; IPR001054; IPR001245; IPR011009; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11920 (PANTHER), PTHR11920:SF50 (PANTHER)
Loa loa	hypothetical protein LOAG_10146 [Loa loa]	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		-
Brugia malayi	2 -phosphodiesterase	0		C:GO:0005739; F:GO:0004527; F:GO:0016787; P:GO:0008150; F:GO:0004519; C:GO:0005575		IPR005135; G3DSA:3.60.10.10 (GENE3D), PTHR12121 (PANTHER), PTHR12121:SF12 (PANTHER)
Loa loa	zinc c2h2 type family protein	7	P:GO:0040035; P:GO:0002119; F:GO:0046872; F:GO:0017151; F:GO:0008134; C:GO:0005634; F:GO:0042826	-		-
Caenorhabditis elegans	embrane protease family member (imp-1)	1	F:GO:0005515	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	isoform b	1	F:GO:0005488	-		SignalP (SIGNALP)

Caenorhabditis elegans	zinc finger protein	2	F:GO:0008270; F:GO:0003677	-		SignalP (SIGNALP)
Camponotus floridanus	ubiquitin associated and sh3 domain-containing protein b	0				G3DSA:3.40.50.1240 (GENE3D)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	furry homolog	1	F:GO:0005515	-		PTHR12295 (PANTHER), PTHR12295:SF6 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-apb-3 protein	7	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0006810; P:GO:0007040; P:GO:0019915; P:GO:0040007	-		-
Caenorhabditis briggsae	briggsae cbr-apb-3 protein	7	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0006810; P:GO:0007040; P:GO:0019915; P:GO:0040007	-		PS51257 (PROFILE)
Caenorhabditis briggsae	briggsae cbr-apb-3 protein	7	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0006810; P:GO:0007040; P:GO:0019915; P:GO:0040007	-		-
Caenorhabditis elegans	ain family member (clp-1)	9	P:GO:0042335; P:GO:0008219; P:GO:0016540; P:GO:0006508; P:GO:0030036; P:GO:0006911; F:GO:0004198; C:GO:0005737; P:GO:0021919	-		IPR001300; G3DSA:3.90.70.10 (GENE3D), PTHR10183 (PANTHER), PTHR10183:SF45 (PANTHER), SSF54001 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	afg3-like protein 2	16	F:GO:0008270; F:GO:0017111; P:GO:0060013; P:GO:0007409; C:GO:0005743; C:GO:0016021; P:GO:0007528; F:GO:0004222; F:GO:0051082; P:GO:0021675; P:GO:0008219; P:GO:0030163; P:GO:0006508; P:GO:0042552; P:GO:0040014; F:GO:0005524	-	EC:3.6.1.15; EC:3.4.24.0	IPR000642; PTHR23076 (PANTHER), PTHR23076:SF11 (PANTHER), SSF140990 (SUPERFAMILY)

Caenorhabditis briggsae	afg3-like protein 2	7	F:GO:0004222; P:GO:0030163; F:GO:0005524; F:GO:0008568; C:GO:0016021; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0; EC:3.6.4.3	IPR000642; PTHR23076 (PANTHER), PTHR23076:SF11 (PANTHER), SSF140990 (SUPERFAMILY)
Caenorhabditis briggsae	anis1_anisi ame: full=major allergen ani s 1 ame: full=21 kda allergen ame: full=excretory gland allergen ans1 ame: allergen=ani s 1 flags: precursor	0		P:GO:0006915; F:GO:0030414; F:GO:0004867; C:GO:0005576		IPR002223; IPR020901; PTHR10083 (PANTHER), PTHR10083:SF39 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	anis1_anisi ame: full=major allergen ani s 1 ame: full=21 kda allergen ame: full=excretory gland allergen ans1 ame: allergen=ani s 1 flags: precursor	0		P:GO:0006915; F:GO:0030414; F:GO:0004867; C:GO:0005576		IPR002223; IPR020901; PTHR10083 (PANTHER), PTHR10083:SF39 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	anis1_anisi ame: full=major allergen ani s 1 ame: full=21 kda allergen ame: full=excretory gland allergen ans1 ame: allergen=ani s 1 flags: precursor	0		P:GO:0006915; F:GO:0030414; F:GO:0004867; C:GO:0005576		IPR002223; IPR020901; PTHR10083 (PANTHER), PTHR10083:SF39 (PANTHER), SignalP (SIGNALP)
Loa loa	dynein light chain	11	C:GO:0030286; P:GO:0018991; P:GO:0016319; F:GO:0042623; P:GO:0040035; P:GO:0035046; P:GO:0007052; P:GO:0007018; P:GO:0010171; F:GO:0005515; P:GO:0048813	-		IPR004942; G3DSA:3.30.450.30 (GENE3D), PTHR10779 (PANTHER), SSF103196 (SUPERFAMILY)
Caenorhabditis elegans	innexin family protein	3	P:GO:0019915; F:GO:0016787; C:GO:0044425	-		IPR000990; SignalP (SIGNALP)
Caenorhabditis briggsae	innexin family protein	4	P:GO:0019915; C:GO:0016021; C:GO:0005921; F:GO:0008234	-		IPR000990; SignalP (SIGNALP)
Loa loa	atg9	1	P:GO:0009792	-		IPR007241; PTHR13038:SF1 (PANTHER)
Caenorhabditis elegans	zinc finger protein 667	3	F:GO:0003676; C:GO:0005622; F:GO:0008270	-		IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)
Haemonchus contortus	glutathione peroxidase	4	F:GO:0004602; C:GO:0005615; P:GO:0055114; P:GO:0006979	-	EC:1.11.1.9	IPR000889; IPR012335; IPR012336; SignalP (SIGNALP)
Caenorhabditis elegans	r- binding motif protein 4	3	F:GO:0005515; P:GO:0000003; P:GO:0006396	-		IPR000504; IPR001878; IPR012677; IPR015466; PTHR10432 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				IPR000276
	-	0				-
	-	0				-
Loa loa	cuticlin 1	0		P:GO:0010171		IPR001507; PTHR22907 (PANTHER), SignalP (SIGNALP)
Heligmosomoides polygyrus	c-type lectin-1	1	F:GO:0005529	-		IPR001304; IPR016186; IPR016187; PTHR22801 (PANTHER), PTHR22801:SF9 (PANTHER)

Loa loa	moz sas family protein	5	F:GO:0016747; P:GO:0006350; C:GO:0043229; F:GO:0005488; P:GO:0006325	-	EC:2.3.1.0	IPR002717; IPR016181; PTHR10615 (PANTHER), PTHR10615:SF28 (PANTHER)
Loa loa	integrin-linked ki-se-associated serine threonine phosphatase 2c	6	P:GO:0007090; F:GO:0004722; F:GO:0005515; P:GO:0006470; C:GO:0044464; P:GO:0045786	-		IPR000222; IPR001932; IPR014045; IPR015655; PTHR13832:SF89 (PANTHER)
Caenorhabditis elegans	ribosomal protein s26	6	F:GO:0003729; F:GO:0003735; P:GO:0006414; C:GO:0022627; P:GO:0033119; F:GO:0005515	-		IPR000892
Caenorhabditis briggsae	ras-related protein rab-33b	5	C:GO:0000139; F:GO:0005525; C:GO:0005886; P:GO:0007264; P:GO:0015031	-		IPR001806; IPR003579; IPR005225; IPR013753; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF203 (PANTHER), SSF52540 (SUPERFAMILY)
Loa loa	a-macroglobulin complement component family protein	3	C:GO:0005615; F:GO:0005515; F:GO:0004866	-		IPR008930; IPR019565; IPR019742; G3DSA:1.50.10.20 (GENE3D), PTHR11412 (PANTHER), PTHR11412:SF30 (PANTHER)
Caenorhabditis elegans	glycosylation related family member (gly-12)	2	P:GO:0009792; C:GO:0016020	-		IPR004139; G3DSA:3.10.180.20 (GENE3D), G3DSA:3.90.550.10 (GENE3D), SSF53448 (SUPERFAMILY)
Nematostella vectensis	transmembrane protein 229b	0		F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150; C:GO:0005575		SignalP (SIGNALP)
Caenorhabditis elegans	foie gras	1	P:GO:0006974	-		IPR012880; PTHR14374 (PANTHER)
	-	0				-
Caenorhabditis elegans	mitochondrial precursor	4	C:GO:0005737; P:GO:0006546; F:GO:0004047; F:GO:0008483	-	EC:2.1.2.10; EC:2.6.1.0	IPR006222; PTHR13847 (PANTHER), PTHR13847:SF5 (PANTHER), SignalP (SIGNALP), SSF103025 (SUPERFAMILY)
	-	0				-
Loa loa	transmembrane cell surface protein homolog family member (ttyh-1)	0				IPR006990; PTHR12424:SF2 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	4	P:GO:0009792; P:GO:0040010; P:GO:0006898; P:GO:0002119	-		SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	4	P:GO:0009792; P:GO:0040010; P:GO:0006898; P:GO:0002119	-		SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0004672; F:GO:0005524; P:GO:0006468		IPR012877
	-	0				-

Caenorhabditis elegans	helicase conserved c-termi-l domain containing protein	6	P:GO:0002119; F:GO:0004004; F:GO:0003676; P:GO:0042254; P:GO:0040010; F:GO:0005524	-		IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF19 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	helicase conserved c-termi-l domain containing protein	6	P:GO:0002119; F:GO:0004004; F:GO:0003676; P:GO:0042254; P:GO:0040010; F:GO:0005524	-		IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF19 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	helicase conserved c-termi-l domain containing protein	6	P:GO:0002119; F:GO:0004004; F:GO:0003676; P:GO:0042254; P:GO:0040010; F:GO:0005524	-		IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF19 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	in family member (ttn-1)	4	P:GO:0009792; P:GO:0006468; F:GO:0004672; F:GO:0005524	-		-
Caenorhabditis briggsae	hect domain containing 1	7	F:GO:0003676; C:GO:0005622; P:GO:0016567; P:GO:0001843; P:GO:0000003; F:GO:0004842; F:GO:0008270	-	EC:6.3.2.19	IPR011989; IPR016024
Caenorhabditis elegans	fk506 binding protein 12-rapamycin associated protein 1	3	F:GO:0016772; P:GO:0048565; F:GO:0000166	-		IPR003151; IPR014009; PTHR11139 (PANTHER), PTHR11139:SF9 (PANTHER)
Caenorhabditis elegans	probable atp-dependent r- helicase ddx60-like	2	F:GO:0005488; F:GO:0016462	-		-
	-	0				-
Caenorhabditis briggsae	c2 domain containing protein	0				-
Caenorhabditis elegans	kex-2 proprotein convertase family member (kpc-1)	6	F:GO:0004252; C:GO:0005795; C:GO:0005886; P:GO:0000003; P:GO:0006508; C:GO:0030173	-	EC:3.4.21.0	IPR002884; IPR008979; G3DSA:2.60.120.260 (GENE3D)
Caenorhabditis elegans	kinesin light chain 1 and	5	C:GO:0005829; F:GO:0003777; C:GO:0005874; F:GO:0005515; C:GO:0005871	-		IPR001440; IPR002151; IPR002885; IPR011990; IPR013026; IPR015390; IPR015792; IPR019734; PTHR19959 (PANTHER), PTHR19959:SF20 (PANTHER), SSF48452 (SUPERFAMILY)
Brugia malayi	hypothetical protein Bm1_30495 [Brugia malayi]	0				-
Loa loa	multidrug resistance protein family member (mrp-5)	8	P:GO:0002119; F:GO:0016887; P:GO:0040002; P:GO:0040017; P:GO:0006810; P:GO:0040010; F:GO:0000166; F:GO:0005215	-		IPR003439; IPR011527; IPR017871; IPR017940; G3DSA:1.20.1560.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF14 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein B0432.13 [Caenorhabditis elegans]	0				-

Caenorhabditis elegans	10-formyltetrahydrofolate dehydroge-se	9	F:GO:0000036; P:GO:0009058; F:GO:0016742; P:GO:0006730; P:GO:0055114; F:GO:0016155; F:GO:0048037; P:GO:0009258; C:GO:0005739	-	EC:2.1.2.0; EC:1.5.1.6	IPR006163; IPR009081; IPR015590; IPR016160; IPR016161; IPR016162; IPR016163; IPR020785; PTHR11699:SF46 (PANTHER)
Caenorhabditis elegans	yip1 domain containing protein	1	C:GO:0016020	-		IPR006977; PTHR12822 (PANTHER)
Caenorhabditis elegans	abnormal embryonic partitioning of cytoplasm family member (par-3)	8	C:GO:0005737; P:GO:0007163; P:GO:0040001; F:GO:0005515; P:GO:0007155; P:GO:0007369; C:GO:0016021; P:GO:0008406	-		IPR021922; PTHR16484 (PANTHER), PTHR16484:SF2 (PANTHER)
	-	0				-
Caenorhabditis elegans	ferm domain (-ezrin-radixin-moesin) family member (frm-1)	1	F:GO:0005488	-		-
Caenorhabditis elegans	ferm domain (-ezrin-radixin-moesin) family member (frm-1)	1	F:GO:0005488	-		-
Caenorhabditis elegans	ferm domain (-ezrin-radixin-moesin) family member (frm-1)	1	F:GO:0005488	-		-
Caenorhabditis elegans	ferm domain (-ezrin-radixin-moesin) family member (frm-1)	1	F:GO:0005488	-		-
Caenorhabditis elegans	viral a-type inclusion protein repeat containing protein	0				IPR007648; G3DSA:1.20.5.500 (GENE3D), PTHR23407 (PANTHER), PTHR23407:SF2 (PANTHER)
Asterina pectinifera	h4 histone protein	19	C:GO:0005654; F:GO:0005515; P:GO:0040010; P:GO:0006898; P:GO:0040011; C:GO:0000786; P:GO:0019915; P:GO:0009792; P:GO:0045653; F:GO:0043565; P:GO:0002119; P:GO:0010171; P:GO:0006352; F:GO:0016986; P:GO:0006334; P:GO:0006952; P:GO:0048015; P:GO:0040035; P:GO:0032940	-		-

Asterina pectinifera	h4 histone protein	19	C:GO:0005654; F:GO:0005515; P:GO:0040010; P:GO:0006898; P:GO:0040011; C:GO:0000786; P:GO:0019915; P:GO:0009792; P:GO:0045653; F:GO:0043565; P:GO:0002119; P:GO:0010171; P:GO:0006352; F:GO:0016986; P:GO:0006334; P:GO:0006952; P:GO:0048015; P:GO:0040035; P:GO:0032940	-		-
Caenorhabditis elegans	briggsae cbr-plc-4 protein	17	F:GO:0004871; P:GO:0000003; F:GO:0005515; C:GO:0016020; F:GO:0004435; P:GO:0023034; C:GO:0043231; F:GO:0005509; F:GO:0005543; P:GO:0006629; P:GO:0010038; P:GO:0007165; P:GO:0048522; P:GO:0007186; P:GO:0019222; P:GO:0009725; C:GO:0044444	-	EC:3.1.4.11	IPR000008; IPR000909; IPR001192; IPR001711; IPR001849; IPR002048; IPR008973; IPR011992; IPR011993; IPR015359; IPR017946; IPR018029; IPR018247; IPR018249; G3DSA:2.60.40.150 (GENE3D), PTHR10336 (PANTHER), PTHR10336:SF27 (PANTHER), SSF47473 (SUPERFAMILY), SSF50729 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	protein ki-se family member (kin-2)	18	F:GO:0008603; F:GO:0016301; P:GO:0019933; P:GO:0008103; F:GO:0005515; P:GO:0040007; P:GO:0008355; P:GO:0040011; P:GO:0018996; P:GO:0007591; P:GO:0001932; P:GO:0007015; F:GO:0030551; C:GO:0005952; P:GO:0002119; P:GO:0010171; P:GO:0007274; P:GO:0032940	-		IPR000595; IPR002373; IPR003117; IPR012198; IPR014710; IPR018488; IPR018490; PTHR11635 (PANTHER), PTHR11635:SF17 (PANTHER)
Brugia malayi	ensangp00000014982 isoform 2	1	C:GO:0016020	-		IPR017970; SignalP (SIGNALP)

Caenorhabditis elegans	abnormal cell migration family member (mig-15)	8	F:GO:0005083; P:GO:0006468; F:GO:0000155; F:GO:0005515; F:GO:0005524; P:GO:0007165; C:GO:0016020; F:GO:0004674	-	EC:2.7.11.0	IPR001180; PTHR22986 (PANTHER), PTHR22986:SF5 (PANTHER), PS50219 (PROFILE)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		-
Caenorhabditis elegans	calcium calmodulin-dependent serine protein ki-se (maguk family)	24	P:GO:0006468; F:GO:0042043; F:GO:0004683; F:GO:0008022; P:GO:0007155; F:GO:0030165; P:GO:0006461; C:GO:0015629; C:GO:0019717; F:GO:0004713; C:GO:0016323; P:GO:0006886; C:GO:0005829; C:GO:0030425; F:GO:0004385; F:GO:0003713; C:GO:0043234; P:GO:0045944; F:GO:0032403; F:GO:0004872; F:GO:0005516; C:GO:0005625; F:GO:0005524; C:GO:0045202	-	EC:2.7.11.17; EC:2.7.10.0; EC:2.7.4.8	IPR001452; IPR001478; IPR004172; IPR008144; IPR011511; IPR014775; IPR020590; G3DSA:2.30.30.40 (GENE3D), G3DSA:2.30.42.10 (GENE3D), G3DSA:3.30.63.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23122 (PANTHER), PTHR23122:SF7 (PANTHER), SSF101288 (SUPERFAMILY), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	transducin -like 3	6	P:GO:0040010; P:GO:0045132; P:GO:0000003; P:GO:0006898; P:GO:0009792; C:GO:0044424	-		IPR001680; IPR011046; IPR013934; IPR015943; IPR017986; IPR018983; IPR019782; PTHR19854 (PANTHER), PTHR19854:SF2 (PANTHER)
Haemonchus contortus	neurotransmitter-gated ion-channel ligand binding domain containing protein	4	C:GO:0016021; C:GO:0045211; F:GO:0005230; P:GO:0006810	-		IPR006201; PTHR18945:SF13 (PANTHER)
Caenorhabditis elegans	hypothetical protein H24G06.1 [Caenorhabditis elegans]	3	P:GO:0009792; P:GO:0040035; F:GO:0005515	-		-
Caenorhabditis elegans	hypothetical protein H24G06.1 [Caenorhabditis elegans]	3	P:GO:0009792; P:GO:0040035; F:GO:0005515	-		-
Caenorhabditis briggsae	briggsae cbr-eat-18 protein	0		C:GO:0005615; F:GO:0016787		IPR000859; PTHR10127 (PANTHER), PTHR10127:SF33 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	ectonucleoside triphosphate diphosphohydrolase 5	3	C:GO:0005737; F:GO:0004382; F:GO:0045134	-	EC:3.6.1.42	IPR000407; PTHR11782:SF7 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	ectonucleoside triphosphate diphosphohydrolase 5	2	P:GO:0008152; F:GO:0016787	-		IPR000407; PTHR11782:SF7 (PANTHER), SignalP (SIGNALP)

Caenorhabditis elegans	r- helicase	1	F:GO:0042802	-		IPR001878; IPR013084; PTHR23002 (PANTHER), PTHR23002:SF11 (PANTHER), SSF57756 (SUPERFAMILY)
Caenorhabditis elegans	r- helicase	1	F:GO:0042802	-		IPR001878; IPR013084; IPR022631; PTHR23002 (PANTHER), PTHR23002:SF11 (PANTHER), SSF57756 (SUPERFAMILY)
Caenorhabditis elegans	r- helicase	1	F:GO:0042802	-		IPR001878; IPR013084; PTHR23002 (PANTHER), PTHR23002:SF11 (PANTHER), SSF57756 (SUPERFAMILY)
	-	0				-
Brugia malayi	elegans protein confirmed by transcript evidence	0		P:GO:0000003; F:GO:0005488		-
						-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	importin subunit beta-1	4	C:GO:0005829; P:GO:0006606; F:GO:0019904; C:GO:0005654	-		SignalP (SIGNALP)
Caenorhabditis elegans	importin subunit beta-1	4	C:GO:0005829; P:GO:0006606; F:GO:0019904; C:GO:0005654	-		SignalP (SIGNALP)
Caenorhabditis briggsae	phosphatidylinositol-4-phosphate 5-ki-se type i	2	P:GO:0030384; F:GO:0016307	-		-
Caenorhabditis briggsae	phosphatidylinositol-4-phosphate 5-ki-se type i	2	P:GO:0030384; F:GO:0016307	-		IPR002498; G3DSA:3.30.810.10 (GENE3D), PTHR23086:SF5 (PANTHER), SSF56104 (SUPERFAMILY)
Caenorhabditis briggsae	phosphatidylinositol-4-phosphate 5-ki-se type i	2	P:GO:0030384; F:GO:0016307	-		IPR002498; G3DSA:3.30.810.10 (GENE3D), PTHR23086:SF5 (PANTHER), SSF56104 (SUPERFAMILY)
Caenorhabditis elegans	g protein-coupled receptor 177	8	C:GO:0043229; P:GO:0043010; P:GO:0030177; P:GO:0023061; P:GO:0050708; C:GO:0044444; P:GO:0048793; C:GO:0016020	-		IPR009551; PF06664 (PFAM), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	hypothetical protein W02B8.1 [Caenorhabditis elegans]	0				IPR007087
	-	0				-
Caenorhabditis briggsae	v-raf murine sarcoma viral oncogene homolog b1	8	F:GO:0005057; P:GO:0006468; F:GO:0046872; F:GO:0005515; P:GO:0007275; F:GO:0005524; P:GO:0007165; F:GO:0004674	-	EC:2.7.11.0	-
Saccoglossus kowalevskii	chromosome 9 open reading frame 4	0		F:GO:0003674; F:GO:0004500; C:GO:0016021; C:GO:0016020; P:GO:0008150; P:GO:0006548; C:GO:0005575		IPR005018; PTHR23130 (PANTHER), PTHR23130:SF3 (PANTHER), SignalP (SIGNALP)

Nippostrongylus brasiliensis	elegans protein partially confirmed by transcript evidence	0		C:GO:0005882; P:GO:0009792; F:GO:0005515		IPR003677; PTHR21593 (PANTHER), SignalP (SIGNALP)
Nippostrongylus brasiliensis	elegans protein partially confirmed by transcript evidence	0		C:GO:0005882; P:GO:0009792; F:GO:0005515		IPR003677; PTHR21593 (PANTHER), SignalP (SIGNALP)
Nippostrongylus brasiliensis	keratin-like protein	0		C:GO:0005882		IPR003677; PTHR21593 (PANTHER)
Caenorhabditis elegans	serotonin octopamine receptor family member (ser-2)	5	C:GO:0016021; P:GO:0007165; P:GO:0007211; F:GO:0008226; F:GO:0004989	-		-
Caenorhabditis briggsae	cytoskeleton associated protein 1	4	F:GO:0005515; P:GO:0007023; C:GO:0005829; C:GO:0015630	-		IPR000938; G3DSA:3.10.20.90 (GENE3D), PTHR18916 (PANTHER), PTHR18916:SF6 (PANTHER), SSF54236 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0018991; C:GO:0016021; P:GO:0010171; F:GO:0042302; P:GO:0000003; P:GO:0009792; P:GO:0002119; P:GO:0040011; P:GO:0040007		IPR002486; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	dehydroge-se e1 and transketolase domain containing 1	3	F:GO:0004591; P:GO:0006096; F:GO:0030976	-	EC:1.2.4.2	IPR001017; IPR011603; G3DSA:3.40.50.970 (GENE3D), SSF52518 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	F:GO:0005488; C:GO:0071011	-		IPR000467; PTHR23106 (PANTHER), PTHR23106:SF1 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	zinc finger protein 37 homolog	2	F:GO:0005488; P:GO:0007275	-		-
Loa loa	d- helicase hel308	3	F:GO:0004386; F:GO:0003676; F:GO:0000166	-		G3DSA:1.10.150.20 (GENE3D)
Caenorhabditis elegans	protein phosphatase 1h (pp2c domain containing)	1	F:GO:0016787	-		IPR000222; IPR001932; IPR014045; IPR015655; PTHR13832:SF96 (PANTHER)
Ciona intestinalis	uncharacterized transposase-like protein	0		F:GO:0046872; P:GO:0055114; F:GO:0009055; F:GO:0016491; F:GO:0020037; F:GO:0005506; F:GO:0004497		IPR007087; IPR015880
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	5	F:GO:0003700; F:GO:0043565; F:GO:0046983; C:GO:0005634; P:GO:0006355	-		IPR002112; IPR004827; IPR011616; G3DSA:1.20.5.170 (GENE3D), PTHR11462 (PANTHER), PTHR11462:SF3 (PANTHER)
	-	0				-
	-	0				-

	-	0				-
Ciona intestinalis	PREDICTED: hypothetical protein [Cio- intesti-lis]	0				-
Canis familiaris	ribosomal protein l32	4	F:GO:0003735; F:GO:0005515; C:GO:0022625; P:GO:0006414	-		IPR001515; IPR018263; PTHR23413 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	mitochondrial carnitine acylcarnitine carrier protein	3	P:GO:0055085; C:GO:0016020; F:GO:0005215	-		SignalP (SIGNALP)
Caenorhabditis elegans	mitochondrial carnitine acylcarnitine carrier protein	3	P:GO:0006810; C:GO:0016020; F:GO:0005215	-		-
Caenorhabditis elegans	mitochondrial carnitine acylcarnitine carrier protein	3	P:GO:0055085; C:GO:0016020; F:GO:0005215	-		SignalP (SIGNALP)
Caenorhabditis elegans	variable abnormal morphology family member (vab-10)	0		F:GO:0005509; P:GO:0007050; F:GO:0003779		IPR002017; IPR003108; IPR011992; IPR018159; G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF49 (PANTHER), PS51460 (PROFILE), SSF46966 (SUPERFAMILY), SSF47473 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	copine v	3	P:GO:0000003; C:GO:0043025; C:GO:0043005	-		IPR002035; IPR010734; PTHR10857 (PANTHER), SSF53300 (SUPERFAMILY)
Homo sapiens	igha1_human ame: full=ig alpha-1 chain c region	4	P:GO:0018298; P:GO:0006955; F:GO:0003823; F:GO:0005515	-		IPR003597; IPR007110; IPR013783; PTHR23266 (PANTHER), PTHR23266:SF11 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis briggsae	ring finger protein 141	1	F:GO:0005488	-		IPR001841; IPR013083; IPR017907; IPR018957; PTHR22938 (PANTHER), SSF57850 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	rab11 interacting isoform b	1	P:GO:0040018	-		-
Caenorhabditis elegans	rab11 interacting isoform b	1	P:GO:0040018	-		-
Caenorhabditis briggsae	mbr family protein	2	F:GO:0004872; C:GO:0016021	-		-
	-	0				SignalP (SIGNALP)
Brugia malayi	histone h2b	11	P:GO:0040010; C:GO:0000786; P:GO:0018991; P:GO:0040035; F:GO:0043565; C:GO:0035267; P:GO:0002119; P:GO:0040011; P:GO:0006334; P:GO:0009792; C:GO:0005811	-		IPR000558; IPR007125; IPR009072

Brugia malayi	histone h2b	11	P:GO:0040010; C:GO:0000786; P:GO:0018991; P:GO:0040035; F:GO:0043565; C:GO:0035267; P:GO:0002119; P:GO:0040011; P:GO:0006334; P:GO:0009792; C:GO:0005811	-		IPR000558; IPR007125; IPR009072
Brugia malayi	protein n-termi-l glutamine amidohydrolase	4	P:GO:0006464; F:GO:0005515; C:GO:0005634; C:GO:0005829	-		IPR019161; IPR023128; PTHR13035 (PANTHER)
Caenorhabditis elegans	eukaryotic translation initiation factor 3 subunit 9	12	P:GO:0006413; P:GO:0040010; P:GO:0008340; F:GO:0003676; P:GO:0000003; P:GO:0010171; P:GO:0019915; P:GO:0002119; P:GO:0040011; P:GO:0006898; P:GO:0009792; C:GO:0005737	-		IPR000504; IPR011400; IPR012677; SSF54928 (SUPERFAMILY)
Brugia malayi	phd finger protein 5a	10	C:GO:0016363; C:GO:0005730; C:GO:0071011; C:GO:0005686; F:GO:0003677; P:GO:0002119; F:GO:0003700; P:GO:0000398; C:GO:0071013; P:GO:0045893	-		-
	-	0				-
Caenorhabditis briggsae	atf (camp-dependent transciption factor) family member (atf-7)	5	P:GO:0048519; P:GO:0048518; F:GO:0005515; P:GO:0045088; P:GO:0010551	-		IPR000408; IPR004827; IPR011700; G3DSA:1.20.5.170 (GENE3D), PTHR13044 (PANTHER)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-frm-10 protein	1	P:GO:0030178	-		PTHR13283 (PANTHER)
	-	0				-
	-	0				-

Caenorhabditis elegans	valyl-tr- synthetase	8	F:GO:0004832; P:GO:0006438; C:GO:0005739; P:GO:0006333; F:GO:0005524; C:GO:0000785; F:GO:0003682; C:GO:0005634	-	EC:6.1.1.9	IPR002300; IPR002303; IPR009008; G3DSA:3.90.740.10 (GENE3D), PTHR11946 (PANTHER)
	-	0				SignalP (SIGNALP)
Brugia malayi	hypothetical protein Bm1_47635 [Brugia malayi]	0				-
Caenorhabditis briggsae	metaxin 2	3	P:GO:0006626; F:GO:0005515; C:GO:0005739	-		IPR004046; IPR010987; PTHR12289 (PANTHER), PTHR12289:SF11 (PANTHER), PF11801 (PFAM)
Caenorhabditis elegans	aha-1	19	P:GO:0040010; P:GO:0048813; P:GO:0009410; P:GO:0040017; P:GO:0010552; P:GO:0007517; F:GO:0016563; F:GO:0046982; F:GO:0003702; P:GO:0007420; F:GO:0043565; C:GO:0043234; P:GO:0007165; P:GO:0002119; P:GO:0030522; F:GO:0003700; P:GO:0010171; F:GO:0004872; C:GO:0005634	-		-
	-	0				-

Caenorhabditis briggsae	proprotein convertase subtilisin kexin type 1	38	P:GO:0009745; P:GO:0032496; F:GO:0051087; C:GO:0005802; P:GO:0031016; F:GO:0004252; F:GO:0043559; P:GO:0010157; P:GO:0040010; C:GO:0043679; P:GO:0051592; P:GO:0040011; P:GO:0070542; C:GO:0005615; P:GO:0021983; P:GO:0051384; P:GO:0016540; C:GO:0030425; P:GO:0043434; C:GO:0043025; P:GO:0043278; P:GO:0009792; P:GO:0050714; P:GO:0048678; P:GO:0002119; P:GO:0051789; P:GO:0042493; P:GO:0016486;	-		EC:3.4.21.0	-
Caenorhabditis elegans	briggsae cbr-spat-1 protein	1	P:GO:0009987	-			-
Caenorhabditis briggsae	chromatin modifying protein 1b	9	P:GO:0009792; P:GO:0002119; C:GO:0005768; F:GO:0019904; P:GO:0040010; P:GO:0040011; P:GO:0009987; C:GO:0016020; P:GO:0015031	-			-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	F:GO:0016301	-			IPR003598; IPR003599; IPR007110; IPR013098; IPR013783; PTHR10489 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	g patch domain and kow motifs	8	P:GO:0009792; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0040010; P:GO:0000003; P:GO:0040011; P:GO:0006898	-			IPR000467; IPR005824; IPR008991; IPR014722; PTHR15818 (PANTHER)
Caenorhabditis briggsae	deoxyribonuclease ii family protein	3	C:GO:0005737; C:GO:0005576; F:GO:0004520	-			IPR004947; SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0					SignalP (SIGNALP)

Caenorhabditis elegans	pre-mr--splicing factor rbm22	7	F:GO:0003729; F:GO:0008270; C:GO:0071011; P:GO:0000381; F:GO:0000166; C:GO:0071013; P:GO:0009790	-		PTHR14089 (PANTHER), PTHR14089:SF4 (PANTHER)
Loa loa	mr- cleavage stimulating 50kd-	7	P:GO:0009792; P:GO:0002119; P:GO:0001703; P:GO:0040010; P:GO:0040011; P:GO:0006898; P:GO:0048477	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR22840 (PANTHER), PTHR22840:SF5 (PANTHER)
Caenorhabditis elegans	splicing factor 3b subunit 3	7	P:GO:0006461; F:GO:0003676; C:GO:0005681; F:GO:0005515; P:GO:0000375; C:GO:0030532; P:GO:0006397	-		PTHR10644 (PANTHER), PTHR10644:SF1 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-cpg-4 protein	0				SignalP (SIGNALP)
Haemonchus contortus	enolase	12	P:GO:0040010; P:GO:0008340; P:GO:0040035; C:GO:0000015; C:GO:0009986; P:GO:0002119; F:GO:0000287; P:GO:0006096; P:GO:0006898; P:GO:0009792; P:GO:0040018; F:GO:0004634	-	EC:4.2.1.11	IPR000941; IPR020809; IPR020810; G3DSA:3.20.20.120 (GENE3D), PTHR11902 (PANTHER), PS51257 (PROFILE), SignalP (SIGNALP), SSF51604 (SUPERFAMILY), SSF54826 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Haemonchus contortus	enolase	12	P:GO:0040010; P:GO:0008340; P:GO:0040035; C:GO:0000015; C:GO:0009986; P:GO:0002119; F:GO:0000287; P:GO:0006096; P:GO:0006898; P:GO:0009792; P:GO:0040018; F:GO:0004634	-	EC:4.2.1.11	IPR000941; IPR020809; IPR020810; G3DSA:3.20.20.120 (GENE3D), PTHR11902 (PANTHER), PS51257 (PROFILE), SSF51604 (SUPERFAMILY), SSF54826 (SUPERFAMILY)

Haemonchus contortus	enolase	12	P:GO:0040010; P:GO:0008340; P:GO:0040035; C:GO:0000015; C:GO:0009986; P:GO:0002119; F:GO:0000287; P:GO:0006096; P:GO:0006898; P:GO:0009792; P:GO:0040018; F:GO:0004634	-	EC:4.2.1.11	IPR000941; IPR020809; IPR020810; G3DSA:3.20.20.120 (GENE3D), PTHR11902 (PANTHER), PS51257 (PROFILE), SignalP (SIGNALP), SSF51604 (SUPERFAMILY), SSF54826 (SUPERFAMILY)
	-	0				-
Loa loa	protein c1orf9-like protein	1	P:GO:0032502	-		SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	ain family member (clp-1)	3	C:GO:0044464; P:GO:0008219; F:GO:0004197	-	EC:3.4.22.0	-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				G3DSA:2.10.60.10 (GENE3D), PTHR21749 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	ankyrin repeat protein	6	P:GO:0033036; P:GO:0023033; P:GO:0048518; P:GO:0050896; P:GO:0048523; F:GO:0005488	-		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF290 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-ttr-33 protein	0				IPR001534; SignalP (SIGNALP)
Caenorhabditis sp. PS1010	briggsae cbr-dnj-18 protein	2	P:GO:0009792; F:GO:0005488	-		-
	-	0				-
Caenorhabditis elegans	bromodomain containing protein	2	F:GO:0008270; P:GO:0040011	-		IPR018501; SignalP (SIGNALP)
Brugia malayi	recombining binding protein suppressor of hairless	5	F:GO:0003700; F:GO:0003677; F:GO:0005515; C:GO:0005634; P:GO:0006355	-		IPR002909; IPR008967; IPR013783; IPR014756; IPR015350; IPR015351; G3DSA:2.80.10.50 (GENE3D), PTHR10665 (PANTHER)
Brugia malayi	recombining binding protein suppressor of hairless	5	F:GO:0003700; F:GO:0003677; F:GO:0005515; C:GO:0005634; P:GO:0006355	-		IPR002909; IPR008967; IPR013783; IPR014756; IPR015350; IPR015351; G3DSA:2.80.10.50 (GENE3D), PTHR10665 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	ypc1_caeel ame: full=uncharacterized protein	1	F:GO:0003677	-		IPR017956
Caenorhabditis elegans	suppression of tumorigenicity	5	C:GO:0016020; P:GO:0040018; P:GO:0000003; P:GO:0010171; P:GO:0002119	-		-
Caenorhabditis elegans	hypothetical protein F53H1.4 [Caenorhabditis elegans]	2	P:GO:0040010; P:GO:0006898	-		-

Caenorhabditis briggsae	malate cytoplasmic	7	P:GO:0009056; P:GO:0044262; F:GO:0016615; P:GO:0044281; F:GO:0016616; C:GO:0005829; P:GO:0006091	-	EC:1.1.1.0	-
Caenorhabditis briggsae	cwf19-like protein 1	1	F:GO:0003824	-		-
	-	0				-
	-	0				-
Loa loa	myb binding protein 1a	5	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0040010; P:GO:0006898	-		IPR007015; PTHR13213:SF5 (PANTHER)
Caenorhabditis briggsae	guanylate ki-se	7	P:GO:0040010; P:GO:0040035; F:GO:0004385; F:GO:0000166; P:GO:0040011; P:GO:0006898; P:GO:0006163	-	EC:2.7.4.8	-
Caenorhabditis briggsae	guanylate ki-se	7	P:GO:0040010; P:GO:0040035; F:GO:0004385; F:GO:0000166; P:GO:0040011; P:GO:0006898; P:GO:0006163	-	EC:2.7.4.8	-
Caenorhabditis sp. PS1010	briggsae cbr-cdh-4 protein	5	P:GO:0007411; P:GO:0007163; P:GO:0007155; P:GO:0007413; C:GO:0016020	-		IPR000742; IPR001791; IPR006210; IPR008985; IPR012680; IPR013032; IPR013320; G3DSA:2.10.25.10 (GENE3D), PTHR10574 (PANTHER), PTHR10574:SF17 (PANTHER), SSF57196 (SUPERFAMILY)
Caenorhabditis elegans	aldehyde dehydroge-se family subfamily a2	11	F:GO:0004028; F:GO:0004030; C:GO:0005743; P:GO:0008218; P:GO:0046292; P:GO:0055114; C:GO:0016021; C:GO:0005634; C:GO:0005829; C:GO:0042406; P:GO:0000302	-	EC:1.2.1.5	IPR012394; IPR015590; IPR016161; IPR016162; IPR016163
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0004871; C:GO:0016021; P:GO:0007165; F:GO:0003774; C:GO:0016459; F:GO:0005515		PD936484 (PRODOM)

Caenorhabditis briggsae	ankyrin unc44	0		F:GO:0004672; P:GO:0006915; P:GO:0006468; F:GO:0000166; F:GO:0017111; F:GO:0005524; P:GO:0016567; F:GO:0004842; C:GO:0000151; F:GO:0005488		-
Caenorhabditis elegans	abnormal dauer formation family member (daf-12)	6	F:GO:0003700; F:GO:0043565; F:GO:0003707; C:GO:0005634; F:GO:0008270; P:GO:0006355	-		-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Brugia malayi	briggsae cbr-tag-335 protein	9	P:GO:0009792; P:GO:0002119; F:GO:0005525; P:GO:0009058; F:GO:0004475; P:GO:0000003; P:GO:0008340; P:GO:0040007; P:GO:0006898	-	EC:2.7.7.13	IPR001451; IPR005835; IPR018357; G3DSA:2.160.10.10 (GENE3D), G3DSA:3.90.550.10 (GENE3D), PTHR22572 (PANTHER), PTHR22572:SF15 (PANTHER), SignalP (SIGNALP), SSF53448 (SUPERFAMILY)
Brugia malayi	briggsae cbr-tag-335 protein	9	P:GO:0009792; P:GO:0002119; F:GO:0005525; P:GO:0009058; F:GO:0004475; P:GO:0000003; P:GO:0008340; P:GO:0040007; P:GO:0006898	-	EC:2.7.7.13	IPR001451; IPR005835; IPR018357; G3DSA:2.160.10.10 (GENE3D), G3DSA:3.90.550.10 (GENE3D), PTHR22572 (PANTHER), PTHR22572:SF15 (PANTHER), SignalP (SIGNALP), SSF53448 (SUPERFAMILY)
Caenorhabditis elegans	translation initiation factor eif-2b subunit alpha	1	F:GO:0005515	-		IPR000649; G3DSA:3.40.50.10470 (GENE3D), PTHR10233:SF7 (PANTHER), SSF100950 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	charged multivesicular body protein 4b	3	P:GO:0015031; C:GO:0005829; C:GO:0031902	-		-
Caenorhabditis briggsae	charged multivesicular body protein 4b	3	P:GO:0015031; C:GO:0005829; C:GO:0031902	-		-
Caenorhabditis elegans	ubiquitin carboxyl-termi-l hydrolase family protein	3	F:GO:0008233; P:GO:0006511; F:GO:0005488	-		IPR001394; PTHR10420 (PANTHER), PTHR10420:SF36 (PANTHER), SSF54001 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG05711 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	polymerase iii (d- directed) polypeptide 39 kda	1	P:GO:0000003	-		-

	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	lethal family member (let-805)	8	P:GO:0018996; P:GO:0009792; P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		PTHR19143 (PANTHER), PTHR19143:SF4 (PANTHER)
Caenorhabditis elegans	transcription factor iiia	0		P:GO:0040027; C:GO:0005634; F:GO:0003677; F:GO:0003676; F:GO:0008270; F:GO:0003674; F:GO:0003723; P:GO:0009303; P:GO:0006383; F:GO:0005515; C:GO:0005622; F:GO:0046872; F:GO:0003709; P:GO:0045449		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		-
						IPR003598; IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF11 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	wapl (drosophila wings apart-like cohesin interactor) family member (wapl-1)	5	P:GO:0009636; P:GO:0018991; P:GO:0040010; P:GO:0040011; C:GO:0000795	-		IPR012502; IPR022771; PTHR22100 (PANTHER), PTHR22100:SF7 (PANTHER)
Homo sapiens	ubiquitously-expressed transcript	11	F:GO:0008017; P:GO:0047497; P:GO:0006457; F:GO:0051015; C:GO:0005813; P:GO:0051297; F:GO:0051082; F:GO:0048487; C:GO:0016272; C:GO:0000930; C:GO:0005634	-		SignalP (SIGNALP)
Caenorhabditis elegans	cell adhesion	8	P:GO:0009792; P:GO:0002119; P:GO:0018996; F:GO:0005515; P:GO:0000003; P:GO:0008340; P:GO:0040011; P:GO:0006898	-		IPR003961; IPR008957; IPR013783; PTHR19900 (PANTHER), PTHR19900:SF3 (PANTHER)

Caenorhabditis elegans	phosphoenolpyruvate carboxyki-se	6	C:GO:0005737; P:GO:0006094; F:GO:0046872; F:GO:0005525; F:GO:0016301; F:GO:0004613	-	EC:4.1.1.32	IPR008209; IPR008210
Caenorhabditis briggsae	phosphatidylinositol-4-phosphate 5-ki-se type i	2	P:GO:0046488; F:GO:0016307	-		IPR002498; G3DSA:3.30.810.10 (GENE3D), PTHR23086:SF5 (PANTHER), SSF56104 (SUPERFAMILY)
	-	0				-
Oryctolagus cuniculus	ribosomal protein s8	4	F:GO:0003735; F:GO:0005515; C:GO:0022627; P:GO:0006414	-		IPR022309; PTHR10394 (PANTHER), PTHR10394:SF1 (PANTHER)
	-	0				-
Caenorhabditis briggsae	atp-dependent transporter	2	F:GO:0016887; F:GO:0005524	-		G3DSA:3.40.50.300 (GENE3D), PTHR19222 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Brugia malayi	hypothetical protein Bm1_05610 [Brugia malayi]	0				PF05536 (PFAM)
	-	0				-
Caenorhabditis elegans	ubiquinol-cytochrome c rieske iron-sulfur polypeptide 1	12	C:GO:0005875; P:GO:0009725; F:GO:0008121; F:GO:0051537; P:GO:0046677; F:GO:0046872; C:GO:0005750; P:GO:0006811; F:GO:0032403; P:GO:0006122; P:GO:0042493; P:GO:0007040	-	EC:1.10.2.2	IPR004192; IPR005805; IPR006317; IPR014349; IPR017941
Caenorhabditis elegans	h+ lysosomal v1 subunit d	10	C:GO:0016471; P:GO:0015986; P:GO:0040007; P:GO:0006200; P:GO:0002119; F:GO:0005515; F:GO:0046961; P:GO:0009792; C:GO:0005634; C:GO:0033178	-	EC:3.6.3.14	IPR002699
Caenorhabditis briggsae	atp synthase b	10	P:GO:0008340; C:GO:0005929; P:GO:0040027; P:GO:0040010; F:GO:0015078; P:GO:0034606; P:GO:0009792; P:GO:0015986; P:GO:0007281; C:GO:0000276	-		IPR008688; IPR013837
Caenorhabditis elegans	elav-type r- binding protein family member (etr-1)	4	F:GO:0003729; F:GO:0005515; P:GO:0017148; F:GO:0000166	-		-
	-	0				-

Brugia malayi	presenilin spe-4	0		C:GO:0016021		IPR001108; PTHR10202:SF1 (PANTHER)
Caenorhabditis elegans	step ii splicing factor slu7	12	P:GO:0008340; F:GO:0008270; F:GO:0003676; P:GO:0040007; P:GO:0000003; P:GO:0018996; P:GO:0002119; P:GO:0040011; P:GO:0000398; C:GO:0030529; C:GO:0044428; P:GO:0009792	-		IPR001878; IPR021715; PTHR12942 (PANTHER)
Caenorhabditis elegans	cystathionine gamma-synthase	3	F:GO:0030170; P:GO:0006520; F:GO:0003824	-		-
	-	0				IPR006909; IPR023093; SSF46785 (SUPERFAMILY)
	-	0				IPR000436; IPR016060
	-	0				-
Caenorhabditis elegans	btb poz domain containing protein	1	F:GO:0005515	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	subfamily member 13	1	F:GO:0031072	-		IPR001623
Caenorhabditis elegans	subfamily member 13	1	F:GO:0031072	-		IPR001623
Caenorhabditis elegans	subfamily member 13	3	P:GO:0006457; F:GO:0031072; F:GO:0051082	-		-
Caenorhabditis elegans	subfamily member 13	1	F:GO:0031072	-		IPR001623
Caenorhabditis elegans	subfamily member 13	1	F:GO:0031072	-		IPR001623
Loa loa	protein-tyrosine phosphatase containing protein	4	F:GO:0004725; P:GO:0006470; P:GO:0009792; P:GO:0000003	-	EC:3.1.3.48	IPR000242; IPR000387; IPR016130; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
Physarum polycephalum	d--topoisomerase ii	0		F:GO:0003918; F:GO:0003916; P:GO:0006265; C:GO:0005694; F:GO:0003700; P:GO:0006259; F:GO:0003677; F:GO:0000166; F:GO:0005524; P:GO:0006355; F:GO:0016853		-
Caenorhabditis elegans	syntaxin 6	4	P:GO:0046907; F:GO:0005515; P:GO:0016081; C:GO:0016020	-		-
Caenorhabditis elegans	yhb8_caeel ame: full=uncharacterized protein flags: precursor	0				-
	-	0				-

Caenorhabditis briggsae	mammalian fe65 homolog family member (feh-1)	0		F:GO:0005515		IPR001202; G3DSA:2.20.70.10 (GENE3D), PTHR14058 (PANTHER), PTHR14058:SF9 (PANTHER)
Loa loa	microtubule associated calponin and lim domain containing 2	2	F:GO:0003824; F:GO:0005488	-		PTHR11915 (PANTHER), PTHR11915:SF1 (PANTHER)
Caenorhabditis elegans	shc (src homology domain c-termi-l) adaptor homolog family member (shc-1)	0		F:GO:0005515		IPR011993; SignalP (SIGNALP), SSF50729 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-shc-1 protein	1	F:GO:0005515	-		IPR006020; IPR011993; PTHR10337 (PANTHER), SSF50729 (SUPERFAMILY)
Loa loa	swi snf matrix actin dependent regulator of subfamily member 2	12	C:GO:0071564; C:GO:0071565; P:GO:0006357; C:GO:0017053; C:GO:0005730; F:GO:0042802; F:GO:0003677; C:GO:0016514; F:GO:0003713; P:GO:0045892; P:GO:0045893; P:GO:0006338	-		-
Loa loa	swi snf matrix actin dependent regulator of subfamily member 2	12	C:GO:0071564; C:GO:0071565; P:GO:0006357; C:GO:0017053; C:GO:0005730; F:GO:0042802; F:GO:0003677; C:GO:0016514; F:GO:0003713; P:GO:0045892; P:GO:0045893; P:GO:0006338	-		-
Caenorhabditis elegans	msf1-like conserved region family protein	4	P:GO:0030432; C:GO:0005739; P:GO:0030537; P:GO:0007283	-		IPR006797; PTHR11158 (PANTHER), PTHR11158:SF15 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-apl-1 protein	9	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0042395; P:GO:0040018; F:GO:0003723; P:GO:0018991; P:GO:0040017; C:GO:0031410	-		IPR008155; IPR019543; PTHR23103 (PANTHER), PTHR23103:SF3 (PANTHER), SSF109843 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-puf-12 protein	2	P:GO:0018991; F:GO:0003723	-		-

Caenorhabditis briggsae	briggsae cbr-apl-1 protein	15	P:GO:0000003; P:GO:0042395; C:GO:0031410; P:GO:0048812; P:GO:0010171; P:GO:0002119; P:GO:0007422; F:GO:0005515; P:GO:0050808; P:GO:0040017; P:GO:0048678; C:GO:0005576; P:GO:0009792; P:GO:0040018; C:GO:0005886	-		IPR008154; IPR008155; IPR011178; IPR015849; IPR019543; IPR019744; PTHR23103 (PANTHER), PTHR23103:SF3 (PANTHER), SignalP (SIGNALP), SSF109843 (SUPERFAMILY)
Caenorhabditis briggsae	26s proteasome non-atpase regulatory subunit 12	1	P:GO:0000003	-		PTHR10855 (PANTHER), PTHR10855:SF1 (PANTHER)
Ancylostoma caninum	cysteine-rich secretory protein-buccal gland	0		P:GO:0006898; C:GO:0005576		IPR001283; IPR014044; IPR018244; PTHR10334:SF11 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-npp-15 protein	0		F:GO:0003674; C:GO:0016021; P:GO:0040010		IPR007187; PTHR13405 (PANTHER), PTHR13405:SF6 (PANTHER)
	-	0				-
Caenorhabditis elegans	novel protein vertebrate alpha 6	5	F:GO:0004872; P:GO:0007229; F:GO:0005515; P:GO:0007155; C:GO:0008305	-		IPR000413; IPR013517; IPR013519; G3DSA:2.130.10.130 (GENE3D), PTHR23220 (PANTHER), PTHR23220:SF11 (PANTHER), PS51470 (PROFILE), SSF69318 (SUPERFAMILY)
Caenorhabditis elegans	novel protein vertebrate alpha 6	1	C:GO:0016021	-		IPR000413; IPR013517; IPR013519; G3DSA:2.130.10.130 (GENE3D), PTHR23220 (PANTHER), PTHR23220:SF11 (PANTHER), PS51470 (PROFILE), SSF69318 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	briggsae cbr-i--1 protein	4	F:GO:0005515; P:GO:0009987; C:GO:0016021; P:GO:0023052	-		IPR000413; IPR013517; IPR013519; G3DSA:2.130.10.130 (GENE3D), PTHR23220 (PANTHER), PTHR23220:SF11 (PANTHER), PS51470 (PROFILE), SignalP (SIGNALP), SSF69318 (SUPERFAMILY)
Brugia malayi	hypothetical protein Bm1_14505 [Brugia malayi]	0				-
Caenorhabditis elegans	gtpase activating protein family member (gap-2)	5	C:GO:0005737; P:GO:0046580; P:GO:0040010; P:GO:0000003; F:GO:0005099	-		IPR001936; IPR008936; IPR023152; PTHR10194 (PANTHER), PTHR10194:SF25 (PANTHER)
Caenorhabditis elegans	gtpase activating protein family member (gap-2)	5	C:GO:0005737; P:GO:0046580; P:GO:0040010; P:GO:0000003; F:GO:0005099	-		IPR001936; IPR008936; IPR023152; PTHR10194 (PANTHER), PTHR10194:SF25 (PANTHER)

Caenorhabditis elegans	tfiih basal transcription factor complex helicase xpb subunit	32	P:GO:0000718; P:GO:0006468; P:GO:0009650; C:GO:0000441; P:GO:0000075; F:GO:0003684; F:GO:0008022; P:GO:0006283; F:GO:0047485; F:GO:0005525; P:GO:0006265; P:GO:0000717; C:GO:0005675; P:GO:0009792; F:GO:0032564; P:GO:0001666; P:GO:0008104; P:GO:0006917; P:GO:0033683; P:GO:0006368; F:GO:0042277; P:GO:0045944; F:GO:0008353; F:GO:0004003; P:GO:0006200; F:GO:0008134; F:GO:0005524;	-	EC:2.7.11.23	IPR001161; IPR001650; IPR006935; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR11274 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	tfiih basal transcription factor complex helicase xpb subunit	32	P:GO:0000718; P:GO:0006468; P:GO:0009650; C:GO:0000441; P:GO:0000075; F:GO:0003684; F:GO:0008022; P:GO:0006283; F:GO:0047485; F:GO:0005525; P:GO:0006265; P:GO:0000717; C:GO:0005675; P:GO:0009792; F:GO:0032564; P:GO:0001666; P:GO:0008104; P:GO:0006917; P:GO:0033683; P:GO:0006368; F:GO:0042277; P:GO:0045944; F:GO:0008353; F:GO:0004003; P:GO:0006200; F:GO:0008134;	-	EC:2.7.11.23	IPR001161; IPR001650; IPR006935; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR11274 (PANTHER), SSF52540 (SUPERFAMILY)

Caenorhabditis elegans	tfiih basal transcription factor complex helicase xpb subunit	32	P:GO:0000718; P:GO:0006468; P:GO:0009650; C:GO:0000441; P:GO:0000075; F:GO:0003684; F:GO:0008022; P:GO:0006283; F:GO:0047485; F:GO:0005525; P:GO:0006265; P:GO:0000717; C:GO:0005675; P:GO:0009792; F:GO:0032564; P:GO:0001666; P:GO:0008104; P:GO:0006917; P:GO:0033683; P:GO:0006368; F:GO:0042277; P:GO:0045944; F:GO:0008353; F:GO:0004003; P:GO:0006200; F:GO:0008134; F:GO:0005524;	-	EC:2.7.11.23	IPR001161; IPR001650; IPR006935; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR11274 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	tfiih basal transcription factor complex helicase xpb subunit	32	P:GO:0000718; P:GO:0006468; P:GO:0009650; C:GO:0000441; P:GO:0000075; F:GO:0003684; F:GO:0008022; P:GO:0006283; F:GO:0047485; F:GO:0005525; P:GO:0006265; P:GO:0000717; C:GO:0005675; P:GO:0009792; F:GO:0032564; P:GO:0001666; P:GO:0008104; P:GO:0006917; P:GO:0033683; P:GO:0006368; F:GO:0042277; P:GO:0045944; F:GO:0008353; F:GO:0004003; P:GO:0006200; F:GO:0008134; F:GO:0005524;	-	EC:2.7.11.23	IPR001161; IPR001650; IPR006935; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR11274 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-cpg-4 protein	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-cpg-4 protein	0				SignalP (SIGNALP)
	-	0				-

Caenorhabditis briggsae	aurin family member (cnt-2)	5	C:GO:0005622; P:GO:0000003; F:GO:0005515; P:GO:0050794; P:GO:0009792	-		IPR001164; IPR002110; IPR020683; PTHR23180 (PANTHER), PTHR23180:SF21 (PANTHER)
Caenorhabditis briggsae	exocyst complex component 7	2	C:GO:0044444; C:GO:0044446	-		IPR004140; IPR016159; PTHR12542:SF7 (PANTHER)
Caenorhabditis elegans	apical junction molecule family member (ajm-1)	7	P:GO:0009792; C:GO:0043296; P:GO:0045216; F:GO:0008092; C:GO:0005913; P:GO:0040010; P:GO:0040011	-		PR01217 (PRINTS), PTHR23202 (PANTHER), PTHR23202:SF3 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	u3 small nucleolar r--associated protein 15 homolog	1	C:GO:0005737	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; IPR020472; PTHR19924 (PANTHER), PTHR19924:SF2 (PANTHER)
Caenorhabditis elegans	squamous cell carcinoma antigen recognized by t cells	10	C:GO:0015030; P:GO:0040007; P:GO:0006397; P:GO:0040011; C:GO:0005737; P:GO:0018996; P:GO:0008380; P:GO:0002119; P:GO:0045585; P:GO:0040035	-		IPR005011
Caenorhabditis elegans	vacuolar h	11	P:GO:0016337; F:GO:0008553; F:GO:0046933; C:GO:0000221; P:GO:0008219; P:GO:0015986; C:GO:0005769; F:GO:0005524; P:GO:0015988; F:GO:0046961; C:GO:0005886	-	EC:3.6.3.6; EC:3.6.3.14	IPR000194; IPR000793; IPR004100; IPR005723; IPR020003; G3DSA:3.40.50.300 (GENE3D), PTHR15184 (PANTHER), PTHR15184:SF11 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	wd repeat and fyve domain containing 2	3	P:GO:0006897; F:GO:0008270; F:GO:0005515	-		-
	-	0				-
Caenorhabditis briggsae	y92h3_caeel ame: full=uncharacterized protein	0		F:GO:0003735; P:GO:0006412; C:GO:0015934		-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		C:GO:0016021		-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				IPR004988
Caenorhabditis briggsae	briggsae cbr-ttr-8 protein	0				-
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis briggsae	developmentally regulated gtp binding protein 1	12	C:GO:0016021; P:GO:0040007; P:GO:0015684; P:GO:0040035; F:GO:0015093; C:GO:0045111; P:GO:0002119; F:GO:0005515; P:GO:0009792; C:GO:0005737; C:GO:0005634; F:GO:0005525	-		IPR002917; IPR004095; IPR005225; IPR006073; IPR006074; IPR012676; G3DSA:3.40.50.300 (GENE3D), PTHR11702 (PANTHER), PTHR11702:SF8 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Apis mellifera	nuclear membrane protein xman1	0				IPR003887; IPR011015
Caenorhabditis briggsae	Hypothetical protein CBG22717 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	heterogeneous nuclear ribonucleoprotein	3	F:GO:0003676; P:GO:0000003; F:GO:0000166	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF7 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-nhr-17 protein	6	F:GO:0003700; F:GO:0043565; F:GO:0003707; C:GO:0005634; F:GO:0008270; P:GO:0006355	-		-
Ustilago maydis 521	hypothetical protein UM00480.1 [Ustilago maydis 521]	0				-
Ustilago maydis 521	hypothetical protein UM00480.1 [Ustilago maydis 521]	0				-
Caenorhabditis elegans	probable dolichol-phosphate mannosyltransferase subunit	3	P:GO:0040018; P:GO:0000003; C:GO:0016020	-		IPR013174; SignalP (SIGNALP)
	-	0				-
Nematostella vectensis	p63-like transcription factor	25	P:GO:0006461; P:GO:0006281; P:GO:0009607; P:GO:0006996; C:GO:0043234; C:GO:0043232; P:GO:0008104; P:GO:0051336; P:GO:0051128; C:GO:0016604; P:GO:0045944; P:GO:0040007; P:GO:0010212; P:GO:0030330; P:GO:0007050; P:GO:0008629; F:GO:0003677; P:GO:0030154; P:GO:0065008; P:GO:0008283; P:GO:0007154; F:GO:0046914; F:GO:0019899; C:GO:0044444; P:GO:0048731	-		IPR008967; IPR011615; IPR012346; IPR015551; PTHR11447:SF9 (PANTHER)
	-	0				-
	-	0				-
	-	0				-

Taeniopygia guttata	ribosomal protein s9	8	C:GO:0005730; F:GO:0045182; P:GO:0008284; F:GO:0003735; F:GO:0005515; C:GO:0022627; F:GO:0019843; P:GO:0006414	-		IPR001912; IPR002942; IPR005710; IPR018079; IPR022801; G3DSA:3.10.290.10 (GENE3D), PTHR11831:SF3 (PANTHER), SSF55174 (SUPERFAMILY)
Ancylostoma ceylanicum	secreted protein asp-2	0		P:GO:0040011; P:GO:0006898; C:GO:0005576		IPR001283; IPR014044; SignalP (SIGNALP)
Caenorhabditis elegans	plexin a	5	C:GO:0016021; P:GO:0007165; P:GO:0007275; F:GO:0004872; C:GO:0005622	-		PTHR22625 (PANTHER), PTHR22625:SF11 (PANTHER)
Caenorhabditis briggsae	mitochondrial carnitine acylcarnitine carrier protein	7	P:GO:0009792; F:GO:0005488; C:GO:0005743; P:GO:0055085; P:GO:0006839; C:GO:0016021; F:GO:0005215	-		-
Caenorhabditis briggsae	briggsae cbr-tag-174 protein	2	C:GO:0016020; C:GO:0005739	-		-
Caenorhabditis elegans	stromal cell derived factor 4	1	F:GO:0005515	-		IPR011992; IPR018247; IPR018249; PTHR10827 (PANTHER), PTHR10827:SF13 (PANTHER), SSF47473 (SUPERFAMILY)
Caenorhabditis briggsae	phosphoglucose isomerase	5	P:GO:0009792; F:GO:0005515; P:GO:0006006; P:GO:0008340; F:GO:0016853	-		IPR001672; G3DSA:3.40.50.10490 (GENE3D), PS51463 (PROFILE), SSF53697 (SUPERFAMILY)
Caenorhabditis briggsae	vesicle protein sorting-associated	9	P:GO:0031101; P:GO:0000003; P:GO:0018996; F:GO:0005515; P:GO:0048193; P:GO:0006898; C:GO:0044431; P:GO:0006904; C:GO:0016020	-		IPR001619; G3DSA:1.25.40.60 (GENE3D), G3DSA:3.40.50.1910 (GENE3D), G3DSA:3.40.50.2060 (GENE3D), G3DSA:3.90.830.10 (GENE3D), PTHR11679:SF2 (PANTHER)
	-	0				SignalP (SIGNALP)
Macaca mulatta	ribosomal protein l36	5	C:GO:0005730; F:GO:0003735; F:GO:0005515; C:GO:0022625; P:GO:0006414	-		-
Homo sapiens	cytochrome b	0				-
	-	0				-
Caenorhabditis briggsae	mgc69286 protein	0				PTHR12460 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-

Macaca mulatta	PREDICTED: hypothetical protein LOC718269 [Macaca mulatta]	0				SignalP (SIGNALP)
Brugia malayi	pre-b-cell colony-enhancing factor	10	F:GO:0008144; F:GO:0047280; P:GO:0007049; F:GO:0004514; P:GO:0009435; F:GO:0005125; F:GO:0042803; C:GO:0005737; P:GO:0048661; C:GO:0005634	-	EC:2.4.2.12; EC:2.4.2.19	IPR002638; IPR015977; G3DSA:3.20.140.10 (GENE3D), PTHR11098 (PANTHER), PTHR11098:SF2 (PANTHER), SignalP (SIGNALP)
Brugia malayi	nicoti-mide phosphoribosyltransferase-like	9	F:GO:0008144; F:GO:0047280; P:GO:0007049; P:GO:0009435; F:GO:0005125; F:GO:0042803; C:GO:0005737; P:GO:0048661; C:GO:0005634	-	EC:2.4.2.12	IPR002638; IPR015977; PTHR11098 (PANTHER), PTHR11098:SF2 (PANTHER)
Loa loa	structural mainte-nce of chromosomes protein 5	1	P:GO:0007126	-		PTHR19306 (PANTHER), PTHR19306:SF1 (PANTHER)
Loa loa	structural mainte-nce of chromosomes protein 5	1	P:GO:0007126	-		PTHR19306 (PANTHER), PTHR19306:SF1 (PANTHER)
	-	0				PR00211 (PRINTS), SignalP (SIGNALP)
Caenorhabditis elegans	cytochrome p450 family protein	4	F:GO:0020037; P:GO:0055114; F:GO:0004497; F:GO:0009055	-		IPR001128; IPR017972; PTHR19383:SF165 (PANTHER)
Caenorhabditis briggsae	nuclear export factor crm1	6	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040010; P:GO:0040011; P:GO:0051301	-		PTHR11223 (PANTHER)
Brugia malayi	btb poz domain-containing protein 9	5	P:GO:0045132; P:GO:0009792; P:GO:0040007; F:GO:0042802; P:GO:0002119	-		IPR011705; IPR013089; PTHR23230:SF181 (PANTHER)
	-	0				IPR009057
Caenorhabditis elegans	phospholipase activating protein	1	P:GO:0040010	-		-
Caenorhabditis briggsae	briggsae cbr-lin-66 protein	4	P:GO:0040017; P:GO:0040035; F:GO:0005515; P:GO:0002119	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		IPR017853; PTHR23208 (PANTHER), PTHR23208:SF13 (PANTHER)
Caenorhabditis elegans	briggsae cbr-ssq-2 protein	0		F:GO:0008061; P:GO:0006030; P:GO:0044419; P:GO:0006350; P:GO:0016032; P:GO:0045449; C:GO:0005576; C:GO:0042025		-

	-	0				-
Brugia malayi	moz sas family protein	2	F:GO:0016747; F:GO:0005488	-	EC:2.3.1.0	IPR002717; IPR016181; G3DSA:3.30.60.60 (GENE3D), PTHR10615 (PANTHER), PTHR10615:SF28 (PANTHER)
Ciona intestinalis	matrix metalloprotei-se e	0				IPR003582; PTHR21724 (PANTHER), SSF57546 (SUPERFAMILY)
	-	0				-
Loa loa	troponin i	1	F:GO:0005515	-		SignalP (SIGNALP)
Brugia malayi	ribonuclease 3 isoform 1	3	P:GO:0009987; F:GO:0005488; P:GO:0043170	-		-
Brugia malayi	leucine carboxyl methyltransferase	2	P:GO:0040010; F:GO:0016740	-		IPR007213; IPR016651; IPR021121; SSF53335 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	oxysterol binding protein related family member (obr-1)	2	P:GO:0009792; P:GO:0006810	-		-
Caenorhabditis briggsae	oxysterol-binding protein	2	P:GO:0009792; P:GO:0006810	-		-
	-	0				-
Oesophagostomum dentatum	ubiquitin-conjugating enzyme e2d 3 (ubc4 5 yeast) isoform cra_a	24	P:GO:0000209; P:GO:0008054; P:GO:0070979; F:GO:0005515; P:GO:0070936; P:GO:0045676; P:GO:0031647; P:GO:0048132; P:GO:0006513; P:GO:0051246; P:GO:0051276; P:GO:0007067; F:GO:0004842; P:GO:0007286; P:GO:0006915; P:GO:0007140; C:GO:0005875; P:GO:0030718; P:GO:0016322; C:GO:0005886; P:GO:0030509; F:GO:0005524; C:GO:0010008; P:GO:0006281	-	EC:6.3.2.19	-
Drosophila yakuba	cell division cycle like	6	P:GO:0007498; F:GO:0005488; P:GO:0008360; P:GO:0007298; P:GO:0007155; P:GO:0006974	-		IPR001806; IPR013753; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF286 (PANTHER), SSF52540 (SUPERFAMILY)
Drosophila yakuba	cell division cycle like	6	P:GO:0007498; F:GO:0005488; P:GO:0008360; P:GO:0007298; P:GO:0007155; P:GO:0006974	-		IPR001806; IPR013753; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF286 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	upf0378 protein kiaa0100	0				IPR019441
	-	0				-

	-	0				-
Caenorhabditis elegans	palmitoyl-protein thioesterase 1	36	C:GO:0045121; P:GO:0044257; P:GO:0048666; P:GO:0050803; F:GO:0008474; P:GO:0051181; P:GO:0007269; P:GO:0007625; C:GO:0005624; P:GO:0006309; P:GO:0048167; C:GO:0005615; C:GO:0005764; P:GO:0048549; P:GO:0015031; P:GO:0008306; C:GO:0005794; C:GO:0005829; P:GO:0043524; C:GO:0030425; P:GO:0007042; P:GO:0007420; C:GO:0043025; P:GO:0007601; P:GO:0048260; P:GO:0030308; P:GO:0002084; C:GO:0030424;	-	EC:3.1.2.22; EC:3.1.2.2	IPR002472; G3DSA:3.40.50.1820 (GENE3D), PTHR11247 (PANTHER), PTHR11247:SF8 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	lethal neo18	2	P:GO:0009792; F:GO:0016491	-		IPR019173; PTHR13178 (PANTHER), SignalP (SIGNALP)
Caenorhabditis sp. PS1010	briggsae cbr-cdh-4 protein	8	P:GO:0007163; F:GO:0005488; P:GO:0016337; C:GO:0005886; P:GO:0007411; C:GO:0044425; C:GO:0042995; P:GO:0007413	-		IPR002126; IPR015919; IPR020894; PTHR10596 (PANTHER), PTHR10596:SF76 (PANTHER)
Caenorhabditis elegans	exosome component 6	1	F:GO:0016787	-		-
Caenorhabditis elegans	endoplasmic reticulum-golgi intermediate compartment protein 3	3	C:GO:0016020; C:GO:0044444; C:GO:0043231	-		IPR012936; PTHR10984 (PANTHER), PTHR10984:SF6 (PANTHER)
Caenorhabditis elegans	endoplasmic reticulum-golgi intermediate compartment protein 3	3	C:GO:0016020; C:GO:0044444; C:GO:0043231	-		IPR012936; PTHR10984 (PANTHER), PTHR10984:SF6 (PANTHER)
Brugia malayi	flightless i homolog	8	C:GO:0005730; P:GO:0051014; C:GO:0005813; P:GO:0030036; F:GO:0003779; P:GO:0007275; P:GO:0006350; P:GO:0006936	-		IPR001611; PR00019 (PRINTS), G3DSA:3.80.10.10 (GENE3D), PTHR23155 (PANTHER), SSF52058 (SUPERFAMILY)

Caenorhabditis elegans	yeats domain containing 4	7	P:GO:0043967; P:GO:0043968; P:GO:0006355; F:GO:0008022; F:GO:0003677; C:GO:0035267; F:GO:0003700	-		-
Caenorhabditis elegans	mflj00229 protein	0		F:GO:0005524		IPR012860
Caenorhabditis elegans	mflj00229 protein	0		F:GO:0005524		IPR012860
Caenorhabditis elegans	mflj00229 protein	0		F:GO:0005524		IPR012860
Caenorhabditis briggsae	b-box zinc finger family protein	3	F:GO:0008270; C:GO:0005622; F:GO:0005515	-		SignalP (SIGNALP)
Caenorhabditis briggsae	b-box type zinc-finger protein ncl-1	5	C:GO:0005622; P:GO:0007126; F:GO:0005515; P:GO:0007281; F:GO:0008270	-		SignalP (SIGNALP)
Caenorhabditis briggsae	ecdysone-induced protein isoform h	10	P:GO:0001700; P:GO:0006468; P:GO:0007552; P:GO:0048589; F:GO:0020037; F:GO:0005524; P:GO:0002168; F:GO:0004693; F:GO:0030332; P:GO:0002009	-	EC:2.7.11.22	IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF95 (PANTHER)
	-	0				-
	-	0				IPR001841; IPR013083; PTHR12183 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein F10D7.5 [Caenorhabditis elegans]	0		P:GO:0000003; F:GO:0008270; P:GO:0009792		IPR001841; IPR013083; PTHR12183 (PANTHER), SSF57850 (SUPERFAMILY)
Brugia malayi	tho complex subunit 6 homolog	0		F:GO:0003723; P:GO:0051028; P:GO:0008380; P:GO:0006397; P:GO:0006810		IPR015943
Caenorhabditis elegans	sy-ptobrevin homolog ykt6	15	P:GO:0042147; F:GO:0019706; P:GO:0006903; F:GO:0005484; C:GO:0005768; C:GO:0031410; C:GO:0044446; C:GO:0031090; P:GO:0006888; C:GO:0012505; C:GO:0031201; P:GO:0006904; C:GO:0005783; C:GO:0005794; C:GO:0005887	-		IPR001388; IPR010908; IPR011012; G3DSA:1.20.5.110 (GENE3D), PTHR21136 (PANTHER), PTHR21136:SF5 (PANTHER)
Caenorhabditis elegans	mannosyl-oligosaccharide -alpha-mannosidase ib	3	C:GO:0016020; F:GO:0004571; F:GO:0005509	-	EC:3.2.1.113	IPR001382; PTHR11742:SF10 (PANTHER), SignalP (SIGNALP)

Caenorhabditis elegans	mannosyl-oligosaccharide -alpha-mannosidase ib	3	C:GO:0016020; F:GO:0004571; F:GO:0005509	-	EC:3.2.1.113	IPR001382; PTHR11742:SF10 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	tfiih basal transcription factor complex helicase subunit	43	P:GO:0043249; P:GO:0001701; F:GO:0047485; F:GO:0008022; F:GO:0004003; P:GO:0030282; P:GO:0043588; P:GO:0021510; N:GO:0071817; F:GO:0008353; P:GO:0006283; P:GO:0048820; P:GO:0007059; F:GO:0046872; P:GO:0009791; P:GO:0035264; P:GO:0006368; C:GO:0005675; P:GO:0009650; P:GO:0000718; P:GO:0040016; P:GO:0006979; P:GO:0045944; P:GO:0007568; C:GO:0005737; C:GO:0019907; P:GO:0043066;	-	EC:2.7.11.23	IPR001945; IPR006555; PTHR11472 (PANTHER), PTHR11472:SF1 (PANTHER)
Brugia malayi	down-regulated by ctnnb1 protein	4	P:GO:0008340; P:GO:0040035; P:GO:0040039; P:GO:0002119	-		IPR018619
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				IPR001680; IPR017986; IPR019782
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				IPR001680; IPR017986; IPR019782
Brugia malayi	wd repeat-containing protein 48	3	P:GO:0016579; F:GO:0005515; C:GO:0005634	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	kinesin k39	8	F:GO:0005515; F:GO:0017111; C:GO:0044430; P:GO:0048513; P:GO:0051179; P:GO:0016043; P:GO:0007399; P:GO:0009987	-	EC:3.6.1.15	IPR009053; PD968187 (PRODOM)
Ascaris suum	spliced leader 175 kda protein	3	P:GO:0000003; P:GO:0007275; P:GO:0040007	-		-
Caenorhabditis briggsae	briggsae cbr-s--2 protein	3	P:GO:0040010; P:GO:0040035; P:GO:0002119	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	4	P:GO:0009792; P:GO:0040007; P:GO:0040035; P:GO:0002119	-		SignalP (SIGNALP)

Caenorhabditis briggsae	isoform cra_a	6	C:GO:0005829; F:GO:0003723; C:GO:0030529; C:GO:0005634; F:GO:0003677; P:GO:0016071	-		IPR004087; IPR004088; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR10288 (PANTHER), PTHR10288:SF48 (PANTHER), SSF54791 (SUPERFAMILY)
Caenorhabditis briggsae	m-rdgb2 reti-l degeneration protein b	3	C:GO:0005622; P:GO:0006810; F:GO:0046872	-		IPR001666; IPR013209; G3DSA:3.40.50.1000 (GENE3D), PTHR10658:SF6 (PANTHER), SSF56784 (SUPERFAMILY)
Caenorhabditis elegans	nuclear pore complex protein nup205	0				IPR021827
Loa loa	zinc finger protein 291	0		F:GO:0046872; C:GO:0005783; F:GO:0008270; C:GO:0005634; C:GO:0005622		-
Caenorhabditis elegans	probable protein brick1	6	C:GO:0005856; C:GO:0005737; P:GO:0008340; P:GO:0040010; F:GO:0005515; P:GO:0002119	-		-
Caenorhabditis elegans	chromosome 3 open reading frame 10	3	P:GO:0008340; P:GO:0040010; P:GO:0002119	-		-
Caenorhabditis elegans	mak16 protein	4	P:GO:0040035; C:GO:0005730; P:GO:0002119; P:GO:0040010	-		SignalP (SIGNALP)
	-	0				-
Mus musculus	ribosomal protein s6	22	P:GO:0006924; P:GO:0007369; F:GO:0005515; C:GO:0005844; P:GO:0000028; P:GO:0048821; P:GO:0006414; P:GO:0031929; P:GO:0001890; C:GO:0005730; P:GO:0002309; P:GO:0022605; P:GO:0007067; P:GO:0033077; F:GO:0003735; P:GO:0031575; C:GO:0048471; P:GO:0006364; P:GO:0043066; P:GO:0042593; P:GO:0043065; C:GO:0022627	-		IPR001377; IPR014401; IPR018282
Loa loa	tho complex 3	0		F:GO:0003674; F:GO:0008415; F:GO:0016740; F:GO:0004402; C:GO:0005575		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR22839 (PANTHER)

Caenorhabditis briggsae	reticulon 4 interacting protein 1	3	P:GO:0055114; F:GO:0016491; F:GO:0008270	-		IPR002085; IPR016040; PTHR11695:SF34 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	26s protease regulatory subunit 6a	16	P:GO:0006310; P:GO:0008340; P:GO:0006281; F:GO:0004175; C:GO:0008540; P:GO:0000003; P:GO:0006508; F:GO:0005524; P:GO:0002119; F:GO:0016887; F:GO:0005515; P:GO:0001824; F:GO:0009378; P:GO:0030163; C:GO:0005737; C:GO:0005634	-		IPR003593; IPR003959; IPR003960; IPR005937; G3DSA:1.10.8.60 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23073 (PANTHER), PTHR23073:SF7 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	26s protease regulatory subunit 6a	16	P:GO:0006310; P:GO:0008340; P:GO:0006281; F:GO:0004175; C:GO:0008540; P:GO:0000003; P:GO:0006508; F:GO:0005524; P:GO:0002119; F:GO:0016887; F:GO:0005515; P:GO:0001824; F:GO:0009378; P:GO:0030163; C:GO:0005737; C:GO:0005634	-		IPR003593; IPR003959; IPR003960; IPR005937; G3DSA:1.10.8.60 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23073 (PANTHER), PTHR23073:SF7 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	protein ki-se domain containing protein	7	P:GO:0002119; P:GO:0040022; F:GO:0004672; P:GO:0040011; P:GO:0040007; P:GO:0051729; F:GO:0000166	-		IPR000719; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-fl--1 protein	0		P:GO:0009612		IPR001298; IPR013783; IPR014756; IPR017868; PTHR11915 (PANTHER), PTHR11915:SF55 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	6	P:GO:0002009; P:GO:0018996; P:GO:0008340; P:GO:0000003; P:GO:0040010; P:GO:0002119	-		IPR000276; SignalP (SIGNALP)
Caenorhabditis briggsae	cg7289 cg7289-pa	0				-
Caenorhabditis elegans	chiti-se 7	1	F:GO:0003824	-		IPR001223; IPR011583; IPR013781; IPR017853; PTHR11177 (PANTHER), PTHR11177:SF5 (PANTHER), SignalP (SIGNALP)

Caenorhabditis elegans	chiti-se 7	1	F:GO:0003824	-		IPR001223; IPR011583; IPR013781; IPR017853; PTHR11177 (PANTHER), PTHR11177:SF5 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	chiti-se 7	1	F:GO:0003824	-		IPR001223; IPR011583; IPR013781; IPR017853; PTHR11177 (PANTHER), PTHR11177:SF5 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG17874 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	briggsae cbr-nsy-4 protein	2	P:GO:0009792; C:GO:0016021	-		IPR010761; SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0045449; F:GO:0003677		IPR018586
Taeniopygia guttata	dek oncogene (d- binding)	0		F:GO:0003676; F:GO:0042393; F:GO:0003674; P:GO:0008150; P:GO:0051789; C:GO:0005634; F:GO:0003677; C:GO:0005575		IPR014876; SSF109715 (SUPERFAMILY)
Caenorhabditis elegans	helix loop helix family member (hlh-30)	0		P:GO:0000003; P:GO:0045449; F:GO:0030528; P:GO:0019915; C:GO:0005634		-
Caenorhabditis elegans	helix loop helix family member (hlh-30)	0		P:GO:0000003; P:GO:0045449; P:GO:0019915; C:GO:0005634		-
Caenorhabditis briggsae	lon protease mitochondrial precursor	19	P:GO:0034619; F:GO:0004252; F:GO:0004176; F:GO:0070361; F:GO:0070363; F:GO:0070362; P:GO:0070407; F:GO:0003697; C:GO:0042645; F:GO:0003727; C:GO:0005777; P:GO:0006515; F:GO:0070364; P:GO:0001666; P:GO:0007005; P:GO:0051260; P:GO:0006200; F:GO:0005524; P:GO:0034599	-	EC:3.4.21.0	IPR003111; IPR003959; G3DSA:3.40.50.300 (GENE3D), PTHR10046 (PANTHER), SSF52540 (SUPERFAMILY)

Caenorhabditis briggsae	atp-dependent lon	14	P:GO:0001666; F:GO:0003727; P:GO:0051260; C:GO:0042645; F:GO:0004176; P:GO:0034599; F:GO:0005524; P:GO:0007005; P:GO:0070407; F:GO:0003697; F:GO:0004252; F:GO:0070361; P:GO:0006515; P:GO:0034619	-	EC:3.4.21.0	IPR003111; IPR003959; G3DSA:3.40.50.300 (GENE3D), PTHR10046 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-cogc-5 protein	0		F:GO:0050662; P:GO:0006414; F:GO:0000166; F:GO:0005525; C:GO:0019867; P:GO:0009792; F:GO:0016491; F:GO:0003824; F:GO:0003746; C:GO:0005622; P:GO:0040039; F:GO:0004308; P:GO:0009405; P:GO:0008152; F:GO:0003924		IPR012677; IPR019825; PTHR14127 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-cogc-5 protein	0		F:GO:0050662; P:GO:0006414; F:GO:0000166; F:GO:0005525; C:GO:0019867; P:GO:0009792; F:GO:0016491; F:GO:0003824; F:GO:0003746; C:GO:0005622; P:GO:0040039; F:GO:0004308; P:GO:0009405; P:GO:0008152; F:GO:0003924		IPR012677; IPR019825; PTHR14127 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-

Brugia malayi	metastasis associated isoform cra_c	14	P:GO:0008340; P:GO:0018991; P:GO:0040027; P:GO:0040010; P:GO:0006898; P:GO:0040011; C:GO:0005737; C:GO:0005730; F:GO:0003676; P:GO:0009792; P:GO:0002009; P:GO:0007165; P:GO:0010171; P:GO:0040035	-			IPR000679; IPR000949; IPR001005; IPR001025; IPR009057; IPR017884; PTHR10865 (PANTHER), PTHR10865:SF3 (PANTHER)
Brugia malayi	metastasis associated isoform cra_c	14	P:GO:0008340; P:GO:0018991; P:GO:0040027; P:GO:0040010; P:GO:0006898; P:GO:0040011; C:GO:0005737; C:GO:0005730; F:GO:0003676; P:GO:0009792; P:GO:0002009; P:GO:0007165; P:GO:0010171; P:GO:0040035	-			IPR000679; IPR000949; IPR001005; IPR001025; IPR009057; IPR017884; PTHR10865 (PANTHER), PTHR10865:SF3 (PANTHER)
Brugia malayi	metastasis associated isoform cra_c	14	P:GO:0008340; P:GO:0018991; P:GO:0040027; P:GO:0040010; P:GO:0006898; P:GO:0040011; C:GO:0005737; C:GO:0005730; F:GO:0003676; P:GO:0009792; P:GO:0002009; P:GO:0007165; P:GO:0010171; P:GO:0040035	-			IPR000679; IPR000949; IPR001005; IPR001025; IPR009057; IPR017884; PTHR10865 (PANTHER), PTHR10865:SF3 (PANTHER)
	-	0					-
Angiostrongylus cantonensis	elegans protein confirmed by transcript evidence	1	P:GO:0009792	-			IPR002486; IPR008160; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER)
Angiostrongylus cantonensis	elegans protein confirmed by transcript evidence	1	F:GO:0042302	-			IPR002486; IPR008160; PTHR10499 (PANTHER)
Angiostrongylus cantonensis	elegans protein confirmed by transcript evidence	1	P:GO:0009792	-			IPR002486; IPR008160; PTHR10499 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0					SignalP (SIGNALP)
Caenorhabditis briggsae	gtp-binding protein guf1 homolog	3	F:GO:0005525; C:GO:0005739; F:GO:0003924	-		EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000640; IPR004161; IPR009000; IPR009022; IPR013842; G3DSA:2.40.30.10 (GENE3D), G3DSA:3.30.70.870 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF40 (PANTHER)

Caenorhabditis elegans	phd finger protein 10	0		F:GO:0046872; P:GO:0007399; P:GO:0006350; P:GO:0045449; F:GO:0008270; F:GO:0005515; C:GO:0005634		IPR001965; IPR011011; IPR013083; IPR019787; PTHR10615 (PANTHER), PTHR10615:SF8 (PANTHER)
Caenorhabditis elegans	hypothetical protein D1007.15 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	r- family protein	0		F:GO:0003723; F:GO:0008168; P:GO:0045454; F:GO:0005488; F:GO:0016740; P:GO:0006396; F:GO:0008173; F:GO:0016853		-
Caenorhabditis elegans	neuro-l igcam family member (rig-1)	2	P:GO:0009792; P:GO:0000003	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	C:GO:0016021; F:GO:0005272; P:GO:0006814	-		-
Strongylocentrotus purpuratus	ensangp00000010363	0				PTHR22930 (PANTHER)
Caenorhabditis briggsae	vacuolar atp synthase 21 kda proteolipid subunit	4	F:GO:0015078; P:GO:0048066; P:GO:0015986; C:GO:0033179	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	endonuclease-reverse transcriptase	0		F:GO:0003723; P:GO:0006278; F:GO:0004519; F:GO:0003964		IPR000477; IPR015706; PTHR19446:SF100 (PANTHER), SSF56672 (SUPERFAMILY)
Caenorhabditis elegans	endonuclease-reverse transcriptase	0		F:GO:0003723; P:GO:0006278; F:GO:0004519; F:GO:0003964		IPR000477; IPR015706; PTHR19446:SF100 (PANTHER), SSF56672 (SUPERFAMILY)
Caenorhabditis elegans	endonuclease-reverse transcriptase	1	F:GO:0003824	-		IPR000477; IPR015706; PTHR19446:SF100 (PANTHER), SSF56672 (SUPERFAMILY)
Caenorhabditis elegans	endonuclease-reverse transcriptase	0		F:GO:0003723; P:GO:0006278; F:GO:0004519; F:GO:0003964		IPR000477; IPR015706; PTHR19446:SF100 (PANTHER), SSF56672 (SUPERFAMILY)
Caenorhabditis elegans	endonuclease-reverse transcriptase	0		F:GO:0003723; P:GO:0006278; F:GO:0004519; F:GO:0003964		IPR000477; IPR015706; PTHR19446:SF100 (PANTHER), SSF56672 (SUPERFAMILY)
Caenorhabditis elegans	endonuclease-reverse transcriptase	1	F:GO:0003824	-		
Caenorhabditis elegans	endonuclease-reverse transcriptase	0		F:GO:0003723; P:GO:0006278; F:GO:0004519; F:GO:0003964		IPR000477; IPR015706; PTHR19446:SF100 (PANTHER), SSF56672 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	endonuclease-reverse transcriptase	0		F:GO:0003723; P:GO:0006278; F:GO:0004519; F:GO:0003964		IPR000477; IPR015706; PTHR19446:SF100 (PANTHER), SSF56672 (SUPERFAMILY)
Caenorhabditis elegans	skeletal muscle cells re-entry induced	2	P:GO:0018991; P:GO:0040011	-		-
Caenorhabditis elegans	skeletal muscle cells re-entry induced	2	P:GO:0018991; P:GO:0040011	-		-
Caenorhabditis elegans	skeletal muscle cells re-entry induced	2	P:GO:0018991; P:GO:0040011	-		-
Caenorhabditis elegans	briggsae cbr-osm-11 protein	0				-
	-	0				-
Caenorhabditis elegans	amop domain containing protein	1	P:GO:0007160	-		IPR005533; PTHR13802 (PANTHER), PTHR13802:SF2 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	C:GO:0016021; P:GO:0007160	-		IPR005533; PTHR13802 (PANTHER), PTHR13802:SF2 (PANTHER)
Caenorhabditis briggsae	histidyl-tr- synthetase	4	P:GO:0006427; F:GO:0005524; C:GO:0005829; F:GO:0004821	-	EC:6.1.1.21	IPR000738; IPR002314; IPR004516; IPR006195; IPR009068; G3DSA:3.30.930.10 (GENE3D), SSF55681 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	tgf beta-inducible nuclear protein 1	2	C:GO:0005634; P:GO:0040035	-		IPR022309; PTHR12642 (PANTHER)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG04315 [Caenorhabditis briggsae]	0				-
	-	0				-
Caenorhabditis elegans	transmembrane emp24 domain trafficking protein 2	11	C:GO:0012507; P:GO:0006903; C:GO:0016021; C:GO:0005793; C:GO:0005792; F:GO:0005515; C:GO:0030663; P:GO:0006888; F:GO:0005215; C:GO:0042589; P:GO:0006886	-		IPR000348; IPR009038; PTHR22811 (PANTHER), PTHR22811:SF11 (PANTHER), SignalP (SIGNALP), SSF101576 (SUPERFAMILY)
Brugia malayi	posterior sex combs	13	P:GO:0030097; F:GO:0005515; P:GO:0016570; P:GO:0048706; P:GO:0003002; P:GO:0016567; C:GO:0044428; C:GO:0043234; P:GO:0045449; P:GO:0007399; P:GO:0050671; F:GO:0003824; P:GO:0048523	-		IPR001841; IPR013083; IPR017907; PTHR10825 (PANTHER), PTHR10825:SF19 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis briggsae	fshd region gene 1	2	C:GO:0031981; P:GO:0006396	-		IPR010414
	-	0				-
	-	0				-

Caenorhabditis elegans	dcun1d1 protein	5	C:GO:0005737; F:GO:0043130; C:GO:0000151; C:GO:0005634; P:GO:0045116	-		IPR005176; IPR009060; IPR014764; G3DSA:1.10.8.10 (GENE3D)
	-	0				-
Caenorhabditis elegans	fanci (fanconi anemia complex component i) homolog family member (fnci-1)	0				-
	-	0				-
Caenorhabditis elegans	4-nitrophenylphosphatase isoform 2	2	P:GO:0008152; F:GO:0016791	-	EC:3.1.3.0	IPR005834; G3DSA:3.40.50.1000 (GENE3D), G3DSA:3.40.50.10410 (GENE3D), PTHR19288 (PANTHER), PTHR19288:SF11 (PANTHER), SSF56784 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-atn-1 protein	13	P:GO:0040010; C:GO:0030018; P:GO:0007016; F:GO:0005509; P:GO:0007629; C:GO:0055120; P:GO:0051017; P:GO:0031532; F:GO:0051015; F:GO:0042802; C:GO:0005925; P:GO:0007067; P:GO:0009792	-		IPR002017; IPR011992; IPR018159; IPR018249; G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF47 (PANTHER), SSF46966 (SUPERFAMILY)
Caenorhabditis elegans	sphingosine-1-phosphate lyase 1	20	P:GO:0030097; P:GO:0008340; P:GO:0060021; P:GO:0001822; P:GO:0040010; P:GO:0008210; P:GO:0010761; P:GO:0008209; P:GO:0007283; P:GO:0006807; P:GO:0060325; P:GO:0009791; F:GO:0016830; C:GO:0044425; P:GO:0001553; P:GO:0048008; P:GO:0048705; P:GO:0033327; P:GO:0040014; P:GO:0001570	-		IPR015421; IPR015424
Haemonchus contortus	parasitic stage specific protein 2	0				-
Haemonchus contortus	parasitic stage specific protein 2	0				-
Haemonchus contortus	transmembrane domain-containing	0		C:GO:0009536; C:GO:0016021		-
Haemonchus contortus	transmembrane domain-containing	0		C:GO:0009536; C:GO:0016021		-
Haemonchus contortus	parasitic stage specific protein 2	0				-
Haemonchus contortus	parasitic stage specific protein 2	0				-
Haemonchus contortus	transmembrane domain-containing	0		C:GO:0009536; C:GO:0016021		-

Caenorhabditis briggsae	wd repeat phosphoinositide interacting 1	1	C:GO:0044444	-		IPR001680; IPR011046; IPR015943; IPR019781; PTHR11227 (PANTHER), PTHR11227:SF17 (PANTHER)
Brugia malayi	85 kda calcium-independent phospholipase a2	2	F:GO:0016787; P:GO:0016042	-		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF81 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	bcr-associated bap	1	C:GO:0044464	-		IPR008417; PTHR12701:SF3 (PANTHER), SignalP (SIGNALP)
Brugia malayi	variant sh3 domain containing protein	1	F:GO:0005509	-		IPR000108; IPR001452; G3DSA:2.30.30.40 (GENE3D), PTHR11216 (PANTHER), PTHR11216:SF24 (PANTHER)
Brugia malayi	variant sh3 domain containing protein	1	F:GO:0005509	-		-
Brugia malayi	variant sh3 domain containing protein	1	F:GO:0005509	-		-
Brugia malayi	transcription factor iib	0		F:GO:0003674; C:GO:0005575		IPR007714
Angiostrongylus cantonensis	large subunit ribosomal protein 34	7	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; P:GO:0040010; P:GO:0008340; P:GO:0006412	-	EC:3.6.5.3	IPR008195
Caenorhabditis elegans	lysyl-tr- synthetase	11	C:GO:0005829; C:GO:0017101; F:GO:0004824; P:GO:0015966; F:GO:0005524; F:GO:0005515; F:GO:0000287; C:GO:0005759; F:GO:0016597; P:GO:0006430; F:GO:0000049	-	EC:6.1.1.6	IPR002313; IPR004364; IPR004365; IPR006195; IPR012340; IPR016027; IPR018149; IPR018150; G3DSA:3.30.930.10 (GENE3D), SSF55681 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Loa loa	topoisomerase i	17	P:GO:0012501; P:GO:0040016; P:GO:0006268; C:GO:0000228; C:GO:0005730; F:GO:0003917; F:GO:0005524; F:GO:0005515; F:GO:0003918; P:GO:0016310; P:GO:0042493; P:GO:0044419; C:GO:0005654; P:GO:0006265; C:GO:0005737; F:GO:0003682; C:GO:0043204	-	EC:5.99.1.2; EC:5.99.1.3	IPR001631; IPR008336; IPR011010; IPR013030; IPR013034; IPR013499; IPR013500; IPR014711; PTHR10290 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	potassium channel tetramerisation domain containing 5	5	F:GO:0042802; C:GO:0008076; F:GO:0005249; P:GO:0006813; C:GO:0005829	-		IPR000210; IPR003131; IPR011333; PTHR14958 (PANTHER)
Loa loa	protein phosphatase regulatory subunit 7	7	C:GO:0005737; P:GO:0040035; P:GO:0009792; F:GO:0005515; F:GO:0008599; P:GO:0040011; P:GO:0006898	-		IPR003603; G3DSA:3.80.10.10 (GENE3D), SSF52058 (SUPERFAMILY)
Brugia malayi	endothelin converting enzyme-like 1	1	F:GO:0016787	-		IPR000718; IPR008753; G3DSA:1.10.1380.10 (GENE3D), SSF55486 (SUPERFAMILY)
Brugia malayi	nuclear receptor nhr-88	9	P:GO:0008340; F:GO:0008270; P:GO:0006355; F:GO:0043565; P:GO:0019915; F:GO:0005515; F:GO:0003700; F:GO:0003707; C:GO:0005634	-		IPR001628; IPR008946; IPR013088; PR00350 (PRINTS), PTHR11865 (PANTHER), PTHR11865:SF197 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis elegans	nuclear receptor nhr-88	7	F:GO:0008270; P:GO:0006355; F:GO:0043565; P:GO:0019915; F:GO:0003700; F:GO:0003707; C:GO:0005634	-		IPR000536; IPR001628; IPR008946; IPR013088; PR00350 (PRINTS), PTHR11865 (PANTHER), PTHR11865:SF197 (PANTHER), SSF57716 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	hypothetical bps2 protein	0		F:GO:0005515		-
Caenorhabditis elegans	cytoplasmic dynein 1 heavy chain 1	9	F:GO:0003777; P:GO:0006810; C:GO:0030286; C:GO:0005874; P:GO:0006200; F:GO:0005524; P:GO:0007018; F:GO:0016887; F:GO:0005515	-		IPR013602
Oryctolagus cuniculus	b chain activator-bound structure of human pyruvate ki-se m2	11	F:GO:0004743; C:GO:0019861; F:GO:0005515; F:GO:0030955; F:GO:0005524; F:GO:0000287; P:GO:0006096; P:GO:0012501; C:GO:0005634; C:GO:0005829; C:GO:0005739	-	EC:2.7.1.40	-

Caenorhabditis briggsae	briggsae cbr-ced-9 protein	6	P:GO:0009792; C:GO:0005624; F:GO:0005515; P:GO:0006916; C:GO:0005741; C:GO:0048471	-		IPR000712; IPR002475; IPR003093; G3DSA:1.10.437.10 (GENE3D), SSF56854 (SUPERFAMILY)
Trichostrongylus colubriformis	globin	3	C:GO:0005576; F:GO:0005506; P:GO:0006810	-		IPR000971; IPR009050; IPR012292
Trichostrongylus colubriformis	globin	6	F:GO:0020037; C:GO:0005576; C:GO:0005737; F:GO:0005344; P:GO:0015671; F:GO:0019825	-		IPR009548
Trichostrongylus colubriformis	globin	6	F:GO:0020037; C:GO:0005576; C:GO:0005737; F:GO:0005344; P:GO:0015671; F:GO:0019825	-		IPR009548
Trichostrongylus colubriformis	globin	6	F:GO:0020037; C:GO:0005576; C:GO:0005737; F:GO:0005344; P:GO:0015671; F:GO:0019825	-		IPR009548
Trichostrongylus colubriformis	globin	6	F:GO:0020037; C:GO:0005615; C:GO:0005737; F:GO:0005344; P:GO:0015671; F:GO:0019825	-		IPR000971; IPR009050; IPR012292
Trichostrongylus colubriformis	globin	6	F:GO:0020037; C:GO:0005576; C:GO:0005737; F:GO:0005344; P:GO:0015671; F:GO:0019825	-		IPR000971; IPR009050; IPR012292
Brugia malayi	no mechanoreceptor potential isoform d	0		F:GO:0005216; C:GO:0000785; P:GO:0006816; C:GO:0016021; C:GO:0016020; F:GO:0003682; P:GO:0006811; C:GO:0005634; F:GO:0003677; P:GO:0006810; P:GO:0006306; P:GO:0006333; F:GO:0005262; P:GO:0055085		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF294 (PANTHER)
	-	0				-

Caenorhabditis elegans	fatty acid binding protein muscle and heart	8	P:GO:0006810; P:GO:0008340; P:GO:0006656; F:GO:0008289; F:GO:0005515; C:GO:0044444; P:GO:0040011; F:GO:0005215	-		IPR000463; IPR000566; IPR011038; IPR012674
	-	0				-
Caenorhabditis briggsae	temporarily assigned gene -me family member (tag-163)	0		F:GO:0005515		PTHR12583 (PANTHER), PTHR12583:SF1 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	transmembrane protein 66	1	C:GO:0016021	-		IPR009567; SignalP (SIGNALP)
	-	0				-
Phragmatopoma californica	cement precursor protein 3b variant 1	0				-
	-	0				-
Caenorhabditis briggsae	hydroxypyruvate reductase	1	F:GO:0003824	-		IPR007835; G3DSA:3.40.1480.10 (GENE3D), G3DSA:3.40.50.10180 (GENE3D), PTHR12227 (PANTHER), SSF82544 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	11	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040002; P:GO:0040011; C:GO:0016021; C:GO:0005576; P:GO:0019915; P:GO:0040007; P:GO:0006898; F:GO:0042302	-		IPR002486; IPR008160; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	hydroxyacyl-coenzyme a dehydroge-se 3-ketoacyl-coenzyme a thiolase enoyl-coenzyme a hydratase (trifunctio-l protein) alpha subunit	19	F:GO:0003985; F:GO:0016508; F:GO:0000062; F:GO:0003988; C:GO:0005743; P:GO:0055114; P:GO:0040007; C:GO:0016507; C:GO:0042645; F:GO:0051287; P:GO:0019915; F:GO:0003857; P:GO:0002119; P:GO:0006635; P:GO:0042493; P:GO:0006898; F:GO:0016509; P:GO:0009792; F:GO:0004300	-	EC:2.3.1.9; EC:4.2.1.74; EC:2.3.1.16; EC:1.1.1.35; EC:1.1.1.211 ; EC:4.2.1.17	IPR006108; IPR008927; IPR013328; PTHR23309 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-tmd-1 protein	4	C:GO:0045169; C:GO:0005856; P:GO:0000003; F:GO:0005523	-		IPR004934; G3DSA:3.80.10.10 (GENE3D), PTHR10901:SF7 (PANTHER), SSF52047 (SUPERFAMILY)

Caenorhabditis elegans	subfamily member 12	5	P:GO:0006457; C:GO:0005783; F:GO:0051082; F:GO:0031072; P:GO:0040011	-		IPR001623; IPR003095; IPR015399; IPR015609; IPR018253; PTHR11821:SF17 (PANTHER)
Caenorhabditis elegans	subfamily member 12	5	P:GO:0006457; C:GO:0005783; F:GO:0051082; F:GO:0031072; P:GO:0040011	-		IPR001623; IPR003095; IPR015399; IPR015609; IPR018253; PTHR11821:SF17 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis briggsae	transmembrane protein 41a	0		F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150; C:GO:0005575		PTHR12677 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0003674; C:GO:0016021; C:GO:0016020		SignalP (SIGNALP)
Caenorhabditis elegans	transmembrane protein 41a	1	P:GO:0010171	-		IPR015414; PTHR12677 (PANTHER)
Caenorhabditis briggsae	mtch1 protein	9	F:GO:0005488; P:GO:0008340; C:GO:0005739; P:GO:0042981; P:GO:0040007; P:GO:0019915; P:GO:0002119; P:GO:0009792; C:GO:0016020	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR10780 (PANTHER), PTHR10780:SF1 (PANTHER)
Caenorhabditis briggsae	mtch1 protein	9	F:GO:0005488; P:GO:0008340; C:GO:0005739; P:GO:0042981; P:GO:0040007; P:GO:0019915; P:GO:0002119; P:GO:0009792; C:GO:0016020	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR10780 (PANTHER), PTHR10780:SF1 (PANTHER)
Caenorhabditis elegans	sphingolipid delta 4 desaturase c-4 hydroxylase protein des2	5	P:GO:0006633; F:GO:0005515; P:GO:0055114; F:GO:0016705; C:GO:0016021	-		IPR005804; IPR011388; IPR013866; PTHR12879 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	high temperature-induced dauer formation family member (hid-1)	0				PTHR21575 (PANTHER), PTHR21575:SF9 (PANTHER)
Loa loa	pre-mr- splicing	11	P:GO:0000003; F:GO:0005515; P:GO:0040010; P:GO:0040015; P:GO:0006898; C:GO:0030532; P:GO:0018996; P:GO:0040039; P:GO:0000398; P:GO:0009792; P:GO:0002119	-		IPR003107; IPR010491; IPR011990; IPR013026; IPR019734; PTHR11246 (PANTHER), PTHR11246:SF1 (PANTHER), SignalP (SIGNALP), SSF48452 (SUPERFAMILY)
Loa loa	tcf3 fusion partner-like	0		F:GO:0003677; C:GO:0005634		-

Caenorhabditis briggsae	briggsae cbr-ergo- protein	0		F:GO:0003676; F:GO:0005509; P:GO:0007156; F:GO:0005544; P:GO:0007155; C:GO:0008305; C:GO:0016020; F:GO:0005515		-
Brugia malayi	elegans protein confirmed by transcript evidence	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		IPR007087; IPR015880; PTHR23228 (PANTHER), PTHR23228:SF45 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis elegans	5 -3 exoribonuclease 1	5	C:GO:0005737; P:GO:0044260; F:GO:0003676; P:GO:0090304; F:GO:0008409	-		IPR004859
Caenorhabditis briggsae	cathepsin a	6	F:GO:0008047; F:GO:0004180; F:GO:0005515; P:GO:0006886; P:GO:0019915; C:GO:0005783	-		IPR001563; IPR018202; IPR019775; G3DSA:3.40.50.1820 (GENE3D), PTHR11802:SF9 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
Oryctolagus cuniculus	beta	20	C:GO:0042612; P:GO:0019882; P:GO:0042267; C:GO:0045298; P:GO:0006928; F:GO:0005525; F:GO:0042288; C:GO:0016021; P:GO:0006184; P:GO:0051225; C:GO:0005829; C:GO:0005874; P:GO:0051258; P:GO:0007067; F:GO:0042277; F:GO:0032403; F:GO:0003924; P:GO:0007018; F:GO:0005200; P:GO:0030182	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000217; IPR002453; IPR003008; IPR008280; IPR018316
Caenorhabditis elegans	briggsae cbr-max-1 protein	4	C:GO:0005856; P:GO:0008340; F:GO:0005488; P:GO:0040010	-		-
Caenorhabditis briggsae	3-oxoacid transferase 1	4	F:GO:0008260; C:GO:0005759; P:GO:0046952; F:GO:0042803	-	EC:2.8.3.5	IPR004164; IPR004165; IPR012791; G3DSA:3.40.1080.10 (GENE3D), G3DSA:3.40.810.20 (GENE3D), PTHR13707:SF1 (PANTHER), SSF100950 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0005515		IPR011333; IPR013069
Caenorhabditis briggsae	cysteine and histidine-rich domain-containing protein 1	4	P:GO:0040035; F:GO:0042802; P:GO:0002119; P:GO:0006898	-		IPR007051; IPR007052; IPR008978; IPR017447; G3DSA:2.60.40.790 (GENE3D), PTHR12621 (PANTHER), PTHR12621:SF3 (PANTHER)
	-	0				-

Caenorhabditis briggsae	briggsae cbr-rha-2 protein	23	P:GO:0008340; P:GO:0000003; P:GO:0016246; F:GO:0000166; F:GO:0008026; F:GO:0004687; P:GO:0040010; P:GO:0006898; P:GO:0007076; P:GO:0040011; P:GO:0007498; P:GO:0045214; P:GO:0007520; F:GO:0003779; F:GO:0008307; P:GO:0009792; P:GO:0016203; P:GO:0007519; P:GO:0002119; C:GO:0005875; C:GO:0000794; C:GO:0030018; P:GO:0007062	-	EC:2.7.11.18	IPR001650; IPR002464; IPR011545; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR18934 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	protein ki-se domain containing protein	8	P:GO:0006007; F:GO:0005516; P:GO:0048598; F:GO:0004689; F:GO:0005524; C:GO:0005964; P:GO:0005978; P:GO:0006468	-	EC:2.7.11.19	IPR000719; IPR002291; IPR008271; IPR011009; IPR017442; IPR020636; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
Caenorhabditis elegans	phosphorylase gamma 2	7	F:GO:0005516; P:GO:0048598; F:GO:0004689; F:GO:0005524; C:GO:0005964; P:GO:0005978; P:GO:0006468	-	EC:2.7.11.19	IPR000719; IPR002291; IPR008271; IPR011009; IPR017442; IPR020636; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
Caenorhabditis elegans	ke (drosophila actin-binding) homolog family member (ketn-1)	1	P:GO:0000003	-		IPR007110; IPR013783; PTHR10489 (PANTHER), PTHR10489:SF27 (PANTHER), SSF48726 (SUPERFAMILY)
Brugia malayi	protein ki-se domain containing protein	0		F:GO:0016301; F:GO:0004672; F:GO:0005524; P:GO:0006468; F:GO:0004674		-
	-	0				-
Ancylostoma caninum	venom-allergen-like protein family member (vap-1)	0		F:GO:0009055; P:GO:0019646; P:GO:0040011; C:GO:0005576		IPR001283; IPR002172; IPR014044; PTHR10334:SF11 (PANTHER), SSF57059 (SUPERFAMILY)
Brugia malayi	domain containing protein	0		F:GO:0005089; P:GO:0035023; C:GO:0005622		IPR001357; G3DSA:3.40.50.10190 (GENE3D)

Caenorhabditis elegans	fad-dependent oxidoreductase domain-containing protein 1	5	P:GO:0009792; F:GO:0016491; P:GO:0040010; C:GO:0044464; P:GO:0000003	-		IPR006076; G3DSA:3.50.50.60 (GENE3D), PTHR13847 (PANTHER), PTHR13847:SF12 (PANTHER), SSF51905 (SUPERFAMILY)
Caenorhabditis elegans	-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)	4	F:GO:0016874; P:GO:0006760; F:GO:0005488; C:GO:0044464	-		IPR002698; PTHR23407 (PANTHER), SSF100950 (SUPERFAMILY)
Loa loa	ephrin efn-4	0				IPR001799; IPR008972; PTHR11304:SF23 (PANTHER)
Brugia malayi	elegans protein confirmed by transcript evidence	0				IPR019361; PTHR13386 (PANTHER)
Caenorhabditis briggsae	ypd7_caeel ame: full=uncharacterized protein	1	P:GO:0006629	-		-
Caenorhabditis briggsae	Hypothetical protein CBG06964 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG06964 [Caenorhabditis briggsae]	0				-
Brugia malayi	ac1147-like protein	0				-
Brugia malayi	ac1147-like protein	0				-
Brugia malayi	ac1147-like protein	0				-
Caenorhabditis briggsae	myosin ie	15	F:GO:0005516; P:GO:0001570; P:GO:0048008; F:GO:0000146; C:GO:0016459; F:GO:0042623; F:GO:0032403; P:GO:0035166; P:GO:0006508; F:GO:0005524; F:GO:0003779; P:GO:0006807; P:GO:0001822; P:GO:0030048; P:GO:0001701	-		IPR000169; IPR001609; PTHR13140 (PANTHER), PTHR13140:SF31 (PANTHER), SSF52540 (SUPERFAMILY)
Angiostrongylus cantonensis	briggsae cbr-pod-1 protein	0		F:GO:0008415; F:GO:0016740; F:GO:0004402		IPR015049; IPR015505
Caenorhabditis briggsae	eukaryotic initiation factor gamma subunit family protein	0		P:GO:0006413; P:GO:0006446; F:GO:0003743; C:GO:0005575		IPR007316
	-	0				-
Bombyx mori	annexin b13	0		F:GO:0005509; F:GO:0005544		-
Caenorhabditis elegans	iron regulatory protein	13	C:GO:0005829; F:GO:0030350; P:GO:0006447; P:GO:0010040; P:GO:0006879; P:GO:0006099; F:GO:0051539; F:GO:0005515; F:GO:0003994; F:GO:0005506; C:GO:0005794; P:GO:0006101; C:GO:0005783	-	EC:4.2.1.3	IPR000573; IPR015928; IPR015934; IPR015937
Caenorhabditis elegans	wd repeat domain 24	1	P:GO:0009987	-		PTHR16453 (PANTHER), PTHR16453:SF2 (PANTHER)

Loa loa	expressed sequence aw209491	0		F:GO:0003674; P:GO:0008150; C:GO:0005575		IPR010733
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	d- polymerase family exonuclease domain containing protein	7	F:GO:0005488; P:GO:0040035; F:GO:0016740; P:GO:0040011; P:GO:0006997; P:GO:0002009; P:GO:0009792	-		IPR013697; PTHR10670 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG15176 [Caenorhabditis briggsae]	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		-
	-	0				-
Caenorhabditis briggsae	eukaryotic initiation factor 4a	10	P:GO:0009792; P:GO:0002119; F:GO:0008026; P:GO:0040010; F:GO:0005524; P:GO:0000003; P:GO:0008340; P:GO:0040011; F:GO:0003743; P:GO:0019915	-		IPR000629; IPR001650; IPR011545; IPR014001; IPR014014; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF2 (PANTHER), SSF52540 (SUPERFAMILY)
Ailuropoda melanoleuca	cytoplasmic 1	19	C:GO:0005829; C:GO:0030863; P:GO:0045214; C:GO:0030424; C:GO:0005625; F:GO:0019894; C:GO:0030016; F:GO:0042802; C:GO:0035267; F:GO:0005524; P:GO:0007409; F:GO:0050998; P:GO:0006928; C:GO:0031941; F:GO:0019901; F:GO:0005200; C:GO:0030529; C:GO:0070688; P:GO:0051592	-		IPR004000; IPR004001; IPR020902; G3DSA:2.30.36.70 (GENE3D), G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), SSF53067 (SUPERFAMILY)
Ancylostoma ceylanicum	elegans protein partially confirmed by transcript evidence	2	F:GO:0046872; F:GO:0008237	-		IPR001506; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
Ancylostoma ceylanicum	metalloprotease 1 precursor	2	F:GO:0046872; F:GO:0008237	-		IPR000859; IPR001506; IPR006026; IPR013032; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
Ancylostoma ceylanicum	metalloprotease 1 precursor	2	F:GO:0046872; F:GO:0008237	-		IPR000859; IPR001506; IPR006026; IPR013032; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)

Ancylostoma ceylanicum	metalloprotease 1 precursor	2	F:GO:0046872; F:GO:0008237	-		IPR000859; IPR001506; IPR006026; IPR013032; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis briggsae	acyl- thioesterase 8	5	P:GO:0006637; C:GO:0005777; F:GO:0005515; P:GO:0033540; F:GO:0016291	-		IPR003703; G3DSA:3.10.129.10 (GENE3D), PTHR11066:SF7 (PANTHER), SSF54637 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	-dh-ubiquinone oxidoreductase 39 kda subunit	10	P:GO:0009792; P:GO:0002119; P:GO:0006694; F:GO:0003854; P:GO:0045226; P:GO:0040010; P:GO:0008340; F:GO:0050662; P:GO:0006898; F:GO:0008831	-	EC:1.1.1.145 ; EC:1.1.1.133	IPR001509; IPR016040; PTHR12126 (PANTHER), PTHR12126:SF1 (PANTHER), SignalP (SIGNALP), SSF51735 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-mppb-1 protein	11	C:GO:0005875; F:GO:0008121; F:GO:0008270; C:GO:0005750; P:GO:0031122; F:GO:0004222; P:GO:0006508; P:GO:0006122; C:GO:0005759; P:GO:0016485; C:GO:0005811	-	EC:1.10.2.2; EC:3.4.24.0	IPR001431; IPR007863; IPR011237; IPR011249; IPR011765; PTHR11851 (PANTHER), PTHR11851:SF58 (PANTHER)
Loa loa	nuclear pore complex protein family member (npp-1)	4	P:GO:0046907; C:GO:0005635; C:GO:0016020; P:GO:0015031	-		PTHR13000 (PANTHER)
Caenorhabditis briggsae	r--binding protein 28	1	F:GO:0005488	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF50 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
Brugia malayi	domain containing protein	4	P:GO:0018991; F:GO:0005515; P:GO:0040011; P:GO:0006898	-		-
	-	0				-
Caenorhabditis elegans	ras association domain family 1 isoform a	4	F:GO:0042802; P:GO:0009987; P:GO:0023052; C:GO:0044424	-		-
Caenorhabditis elegans	ras association domain family 1 isoform a	4	F:GO:0042802; P:GO:0009987; P:GO:0023052; C:GO:0044424	-		-

Caenorhabditis elegans	ras association domain family 1 isoform a	4	F:GO:0042802; P:GO:0009987; P:GO:0023052; C:GO:0044424	-		-
Caenorhabditis elegans	sorting nexin 6	3	P:GO:0048523; F:GO:0005515; P:GO:0007154	-		IPR015404; PTHR10555 (PANTHER), PTHR10555:SF7 (PANTHER)
Caenorhabditis elegans	protein transport protein sec31	2	C:GO:0043231; C:GO:0044444	-		IPR001680; IPR011046; IPR015943; IPR019781; PTHR13923 (PANTHER), PTHR13923:SF1 (PANTHER)
Caenorhabditis elegans	1-aminocyclopropane-1-carboxylate synthase homolog (non-functio-l)	0		P:GO:0009058; F:GO:0003674; F:GO:0016847; F:GO:0003824; P:GO:0042218; P:GO:0008150; F:GO:0030170; F:GO:0016769		-
Caenorhabditis elegans	briggsae cbr-wrs-2 protein	3	P:GO:0006412; F:GO:0005488; F:GO:0016874	-	EC:3.6.5.3	-
Haemonchus contortus	multidrug resistance protein	9	C:GO:0009986; F:GO:0042626; C:GO:0005624; P:GO:0042493; C:GO:0005886; F:GO:0005515; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		IPR001140; IPR003439; IPR011527; IPR017871; IPR017940; G3DSA:1.20.1560.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF96 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	tr--dihydrouridine synthase 1-like	4	P:GO:0055114; F:GO:0050660; F:GO:0017150; P:GO:0008033	-		IPR001269; IPR013785; IPR018517; PTHR11082:SF5 (PANTHER), SSF51395 (SUPERFAMILY)
Caenorhabditis briggsae	5-methyltetrahydrofolate-homocysteine methyltransferase	14	P:GO:0046653; C:GO:0005829; P:GO:0009086; F:GO:0008705; F:GO:0008270; C:GO:0005625; F:GO:0005542; P:GO:0032940; P:GO:0007399; F:GO:0008898; F:GO:0005515; P:GO:0006479; P:GO:0050667; F:GO:0031419	-	EC:2.1.1.13; EC:2.1.1.10	IPR000489; IPR003726; IPR003759; IPR004223; IPR006158; IPR011005; IPR011822; PTHR21091 (PANTHER), PTHR21091:SF9 (PANTHER)

Caenorhabditis briggsae	5-methyltetrahydrofolate-homocysteine methyltransferase	14	P:GO:0046653; C:GO:0005829; P:GO:0009086; F:GO:0008705; F:GO:0008270; C:GO:0005625; F:GO:0005542; P:GO:0032940; P:GO:0007399; F:GO:0008898; F:GO:0005515; P:GO:0006479; P:GO:0050667; F:GO:0031419	-	EC:2.1.1.13; EC:2.1.1.10	IPR000489; IPR003726; IPR003759; IPR004223; IPR006158; IPR011005; IPR011822; PTHR21091 (PANTHER), PTHR21091:SF9 (PANTHER)
Loa loa	dis3-like exonuclease 2	1	F:GO:0004518	-		IPR001900; IPR022966; PTHR23355 (PANTHER), PTHR23355:SF10 (PANTHER)
Loa loa	dis3-like exonuclease 2	1	F:GO:0004518	-		IPR001900; IPR022966; PTHR23355 (PANTHER), PTHR23355:SF10 (PANTHER)
Loa loa	dis3-like exonuclease 2	1	F:GO:0004518	-		IPR001900; IPR022966; PTHR23355 (PANTHER), PTHR23355:SF10 (PANTHER)
Caenorhabditis briggsae	calcium voltage- alpha2 delta subunit 3	5	F:GO:0005262; P:GO:0006816; P:GO:0034220; F:GO:0005244; C:GO:0016021	-		IPR002035; G3DSA:3.40.50.410 (GENE3D), PTHR10166 (PANTHER), PTHR10166:SF5 (PANTHER), SSF53300 (SUPERFAMILY)
Caenorhabditis elegans	ubiquitin-conjugating enzyme e2 l3	16	P:GO:0006511; P:GO:0000209; P:GO:0070979; P:GO:0071385; P:GO:0051246; F:GO:0019899; P:GO:0007090; F:GO:0004842; F:GO:0005524; C:GO:0000151; F:GO:0050662; F:GO:0003713; P:GO:0008283; C:GO:0005737; C:GO:0005634; P:GO:0032583	-	EC:6.3.2.19	IPR000608; IPR016135; PTHR11621 (PANTHER), PTHR11621:SF23 (PANTHER)
Caenorhabditis elegans	ring finger and spry domain containing 1	1	F:GO:0046872	-		IPR001841; IPR001870; IPR003877; IPR008985; IPR013083; IPR018355; PTHR13363 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis elegans	ring finger and spry domain containing 1	1	F:GO:0046872	-		IPR001841; IPR001870; IPR003877; IPR008985; IPR013083; IPR018355; PTHR13363 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				PTHR21724 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-

Caenorhabditis briggsae	ubx domain-containing protein 4	0		C:GO:0005789; P:GO:0006986; C:GO:0005783; C:GO:0016020; F:GO:0005515; C:GO:0005635; C:GO:0005634		PTHR13020 (PANTHER), PTHR13020:SF5 (PANTHER)
Caenorhabditis briggsae	ubx domain-containing protein 4	0		C:GO:0005789; P:GO:0006986; C:GO:0005783; C:GO:0016020; F:GO:0005515; C:GO:0005635; C:GO:0005634		PTHR13020 (PANTHER), PTHR13020:SF5 (PANTHER)
Loa loa	tripartite motif-containing 33	4	P:GO:0009987; P:GO:0050789; C:GO:0005622; F:GO:0005515	-		IPR001487; IPR001965; IPR011011; IPR013083; IPR013090; IPR019787; PTHR13712 (PANTHER), PTHR13712:SF18 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	adam metallopeptidase domain 32	3	F:GO:0004222; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	IPR002870; PTHR11905 (PANTHER), PTHR11905:SF11 (PANTHER)
Caenorhabditis elegans	fad-dependent pyridine nucleotide-disulfide oxidoreductase	2	F:GO:0016491; P:GO:0055114	-		-
Brugia malayi	actin	18	P:GO:0007126; P:GO:0007108; P:GO:0040007; P:GO:0007517; P:GO:0000281; P:GO:0040035; P:GO:0030036; C:GO:0005865; F:GO:0005524; C:GO:0005938; P:GO:0002119; F:GO:0016887; F:GO:0005515; C:GO:0005884; F:GO:0005200; P:GO:0040039; P:GO:0006898; P:GO:0009792	-		-
Nematostella vectensis	coiled-coil domain containing 88a	4	P:GO:0009950; P:GO:0060071; P:GO:0007257; P:GO:0060070	-		PTHR18947 (PANTHER), PTHR18947:SF4 (PANTHER), SSF116907 (SUPERFAMILY)
	-	0				-

Volvox carteri f. nagariensis	hypothetical protein VOLCADRAFT_118487 [Volvox carteri f. - gariensis]	0		F:GO:0003702; F:GO:0003677; C:GO:0005634; F:GO:0030528; F:GO:0003676; F:GO:0008270; F:GO:0003746; P:GO:0006355; P:GO:0006354; F:GO:0005515; P:GO:0006350		-
Caenorhabditis elegans	hypothetical protein F56H1.7 [Caenorhabditis elegans]	0				PF10937 (PFAM)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	fyve zinc finger family protein	1	F:GO:0046872	-		IPR021565; SSF140125 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein F40F4.6 [Caenorhabditis elegans]	1	P:GO:0040010	-		-
Caenorhabditis briggsae	odd oz protein	0		P:GO:0006629; F:GO:0016740; F:GO:0030246; F:GO:0004714; C:GO:0016021; F:GO:0004629; C:GO:0016020		IPR006530; PTHR11219 (PANTHER), PTHR11219:SF4 (PANTHER)
Glossina morsitans morsitans	chromobox protein 5	1	C:GO:0043229	-		IPR000953; IPR016197; IPR017984; G3DSA:2.40.50.40 (GENE3D), PTHR22812 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				G3DSA:3.40.50.1980 (GENE3D)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	2	P:GO:0009792; P:GO:0000003	-		-
Caenorhabditis elegans	cell death abnormality family member (ced-1)	14	P:GO:0012501; P:GO:0043652; P:GO:0008340; C:GO:0030670; P:GO:0042742; P:GO:0034620; P:GO:0031532; P:GO:0045184; P:GO:0043654; C:GO:0031260; C:GO:0009986; F:GO:0005515; F:GO:0005044; P:GO:0001845	-		IPR000742; IPR002049; IPR006210; IPR009030; IPR013032; PR00011 (PRINTS), G3DSA:2.10.25.10 (GENE3D), G3DSA:2.170.300.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF221 (PANTHER), SSF57196 (SUPERFAMILY)

Caenorhabditis elegans	cell death abnormality family member (ced-1)	14	P:GO:0012501; P:GO:0043652; P:GO:0008340; C:GO:0030670; P:GO:0042742; P:GO:0034620; P:GO:0031532; P:GO:0045184; P:GO:0043654; C:GO:0031260; C:GO:0009986; F:GO:0005515; F:GO:0005044; P:GO:0001845	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	cell death abnormality family member (ced-1)	14	P:GO:0012501; P:GO:0043652; P:GO:0008340; C:GO:0030670; P:GO:0042742; P:GO:0034620; P:GO:0031532; P:GO:0045184; P:GO:0043654; C:GO:0031260; C:GO:0009986; F:GO:0005515; F:GO:0005044; P:GO:0001845	-		IPR000742; IPR002049; IPR006210; IPR009030; IPR013032; PR00011 (PRINTS), G3DSA:2.10.25.10 (GENE3D), G3DSA:2.170.300.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF221 (PANTHER), SSF57196 (SUPERFAMILY)
Caenorhabditis elegans	cell death abnormality family member (ced-1)	14	P:GO:0012501; P:GO:0043652; P:GO:0008340; C:GO:0030670; P:GO:0042742; P:GO:0034620; P:GO:0031532; P:GO:0045184; P:GO:0043654; C:GO:0031260; C:GO:0009986; F:GO:0005515; F:GO:0005044; P:GO:0001845	-		IPR000742; IPR002049; IPR006210; IPR009030; IPR013032; PR00011 (PRINTS), G3DSA:2.10.25.10 (GENE3D), G3DSA:2.170.300.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF221 (PANTHER), SSF57196 (SUPERFAMILY)
Caenorhabditis briggsae	ovarian cancer-associated gene 2 protein homolog	0		F:GO:0003674; P:GO:0008150; C:GO:0005575		IPR005645; G3DSA:3.40.50.1820 (GENE3D), PTHR22778 (PANTHER), SSF53474 (SUPERFAMILY)
Caenorhabditis briggsae	ovca2 protein	0		F:GO:0003674; P:GO:0008150		IPR005645; PTHR22778 (PANTHER)
Caenorhabditis briggsae	hypothetical kda protein in pop4-shm1 intergenic	8	P:GO:0016477; P:GO:0007411; P:GO:0006480; P:GO:0043050; F:GO:0016740; P:GO:0002119; P:GO:0009792; P:GO:0008406	-		IPR008576; G3DSA:3.40.50.150 (GENE3D), SignalP (SIGNALP), SSF53335 (SUPERFAMILY)
	-	0				-

Caenorhabditis elegans	sac3 domain containing 1	4	P:GO:0000226; C:GO:0044430; P:GO:0000279; C:GO:0015630	-		IPR005062; PTHR12436 (PANTHER)
Caenorhabditis briggsae	leucine rich repeat family protein	1	F:GO:0005515	-		IPR001806; IPR008467; IPR022780; G3DSA:3.40.50.300 (GENE3D), SSF52540 (SUPERFAMILY)
Caenorhabditis remanei	briggsae cbr-itsn-1 protein	0		F:GO:0005509		PTHR11216 (PANTHER), PTHR11216:SF24 (PANTHER)
Loa loa	zinc finger swim domain-containing protein kiaa0913	0		F:GO:0046872; F:GO:0008270		-
Caenorhabditis elegans	plexin a	4	P:GO:0016199; F:GO:0005515; C:GO:0044464; F:GO:0004888	-		IPR001627; IPR015943; PTHR22625 (PANTHER), PTHR22625:SF11 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	plexin a	4	P:GO:0016199; F:GO:0005515; C:GO:0044464; F:GO:0004888	-		IPR001627; IPR015943; PTHR22625 (PANTHER), PTHR22625:SF11 (PANTHER), SignalP (SIGNALP)
Homo sapiens	igh@ protein	4	P:GO:0018298; P:GO:0006955; F:GO:0003823; F:GO:0005515	-		-
Caenorhabditis briggsae	ribosomal protein l16 containing protein	8	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; F:GO:0005515; P:GO:0040010; P:GO:0006412; F:GO:0019843	-	EC:3.6.5.3	IPR000114; PTHR12220:SF12 (PANTHER)
Brugia malayi	cytoskeletal structural protein	0		P:GO:0007165		IPR000159
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; P:GO:0007186		-
Caenorhabditis briggsae	briggsae cbr-mac-1 protein	2	F:GO:0017111; F:GO:0005524	-	EC:3.6.1.15	IPR015415; G3DSA:1.10.8.60 (GENE3D), PTHR23077 (PANTHER), PTHR23077:SF16 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-gad-1 protein	3	F:GO:0005515; F:GO:0004672; F:GO:0000166	-		IPR001680; IPR011046; IPR015943; IPR019781; PTHR16017 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0003676; C:GO:0005622		IPR000253; IPR008984; PTHR23106 (PANTHER), PTHR23106:SF1 (PANTHER)
	-	0				-
Pan troglodytes	tumor necrosis factor receptor member 10c	0		F:GO:0004888; P:GO:0006915; P:GO:0007165; C:GO:0005887; C:GO:0031225; C:GO:0005886		-

Caenorhabditis briggsae	ubiquitin protein ligase e3 component n-recognin 4	0		F:GO:0016874; C:GO:0016021; C:GO:0016020; C:GO:0005634; P:GO:0006260; F:GO:0008270; P:GO:0016567; F:GO:0005516; F:GO:0004842; F:GO:0046872; P:GO:0008152; C:GO:0005856		PTHR21725 (PANTHER)
	-	0				-
Dictyocaulus viviparus	paramyosin	4	C:GO:0030016; C:GO:0032982; F:GO:0003774; F:GO:0005515	-		IPR002928; IPR009053; IPR010978; PD936484 (PRODOM), PTHR13140 (PANTHER), PTHR13140:SF11 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR001534; SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	myotonin-protein ki-se	6	F:GO:0005083; P:GO:0006468; F:GO:0046872; P:GO:0023034; F:GO:0004697; F:GO:0005524	-	EC:2.7.11.13	IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22988 (PANTHER), PTHR22988:SF2 (PANTHER)
Caenorhabditis elegans	wingless-type mmtv integration site member 7b	48	C:GO:0009986; P:GO:0050768; F:GO:0005109; P:GO:0032364; P:GO:0060560; P:GO:0060710; P:GO:0008284; P:GO:0060669; P:GO:0072060; P:GO:0045669; P:GO:0051384; C:GO:0005615; P:GO:0032536; P:GO:0072089; P:GO:0032583; P:GO:0048864; P:GO:0060428; P:GO:0072205; P:GO:0003338; P:GO:0060482; C:GO:0005886; C:GO:0005737; P:GO:0071300; P:GO:0050808; P:GO:0072061; P:GO:0048812; P:GO:0051145;	-		IPR005816; IPR005817; IPR018161; PTHR12027:SF3 (PANTHER)

Desulfovibrio fructosovorans JJ	adenylate cyclase	0		F:GO:0004651; C:GO:0016021; P:GO:0006370; C:GO:0016020; P:GO:0006810; F:GO:0016829; P:GO:0006171; F:GO:0005515; P:GO:0055085; F:GO:0004016; C:GO:0031533; F:GO:0005488		IPR004206; IPR008172; PD009560 (PRODOM), G3DSA:2.40.320.10 (GENE3D), PTHR21028 (PANTHER)
Caenorhabditis elegans	regulator of g protein sig-ling	3	P:GO:0007186; F:GO:0004871; C:GO:0005834	-	EC:3.6.5.1	IPR000342; IPR000591; IPR011991; IPR015898; IPR016137; G3DSA:1.10.167.10 (GENE3D), G3DSA:1.10.196.10 (GENE3D), PTHR10845 (PANTHER), PTHR10845:SF24 (PANTHER), SignalP (SIGNALP), SSF46785 (SUPERFAMILY)
Caenorhabditis elegans	regulator of g protein sig-ling	3	P:GO:0007186; F:GO:0004871; C:GO:0005834	-	EC:3.6.5.1	IPR000342; IPR000591; IPR011991; IPR015898; IPR016137; G3DSA:1.10.167.10 (GENE3D), G3DSA:1.10.196.10 (GENE3D), PTHR10845 (PANTHER), PTHR10845:SF24 (PANTHER), SignalP (SIGNALP), SSF46785 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Pristionchus uniformis	large subunit ribosomal protein 1	10	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; F:GO:0003723; F:GO:0005515; P:GO:0040010; P:GO:0000003; P:GO:0006412; P:GO:0006396	-	EC:3.6.5.3	IPR002143; IPR016094; IPR016095; PTHR23105 (PANTHER), PTHR23105:SF4 (PANTHER)
Pristionchus lheritieri	large subunit ribosomal protein 1	5	C:GO:0005840; F:GO:0003735; F:GO:0003723; P:GO:0006412; P:GO:0006396	-	EC:3.6.5.3	SignalP (SIGNALP)
Caenorhabditis briggsae	zinc finger protein	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		IPR007087; IPR015880
	-	0				IPR007087; IPR015880
Caenorhabditis elegans	alpha- -mannosyltransferase alg12	4	C:GO:0031224; P:GO:0006488; F:GO:0000009; C:GO:0005783	-		-
	-	0				-

Brugia malayi	protein ki-se n2	2	F:GO:0005488; F:GO:0004674	-	EC:2.7.11.0	IPR008973; G3DSA:2.60.40.150 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22985 (PANTHER), PTHR22985:SF54 (PANTHER), SignalP (SIGNALP)
Brugia malayi	protein ki-se c	1	F:GO:0016301	-		IPR008973; G3DSA:2.60.40.150 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22985 (PANTHER), PTHR22985:SF54 (PANTHER), SignalP (SIGNALP)
Ciona intestinalis	astacin family metalloendopeptidase farm-1	1	F:GO:0016787	-		IPR003582; PTHR21724 (PANTHER), SSF57546 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG22158 [Caenorhabditis briggsae]	0		C:GO:0005634		PTHR15565 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG22158 [Caenorhabditis briggsae]	0		C:GO:0005634		PTHR15565 (PANTHER)
Caenorhabditis elegans	briggsae cbr-ceh-20 protein	0		P:GO:0016477; P:GO:0009952; F:GO:0003677; C:GO:0005634; P:GO:0040027; P:GO:0042692; F:GO:0030528; P:GO:0006355; P:GO:0007498; P:GO:0008340; P:GO:0006898; P:GO:0009792; F:GO:0003700; P:GO:0010171; P:GO:0045449; F:GO:0043565; F:GO:0005515; P:GO:0040011; P:GO:0007501; P:GO:0040010; P:GO:0018991		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	sjoegren syndrome scleroderma autoantigen 1 homolog	0		F:GO:0003674; P:GO:0008150		IPR009563
Caenorhabditis briggsae	sjoegren syndrome scleroderma autoantigen 1 homolog	0		F:GO:0003674; P:GO:0008150		IPR009563
Loa loa	gmp synthase	5	P:GO:0006541; F:GO:0003922; F:GO:0005524; F:GO:0005515; P:GO:0006177	-	EC:6.3.5.2	IPR001674; G3DSA:3.30.300.10 (GENE3D), PTHR11922 (PANTHER), PTHR11922:SF2 (PANTHER), SSF54810 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				IPR013032
Caenorhabditis elegans	ras gtp exchange son of sevenless	2	P:GO:0009987; C:GO:0005622	-		IPR000651; IPR001849; IPR008937; IPR011993; IPR015759; G3DSA:1.20.870.10 (GENE3D), SSF50729 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Angiostrongylus cantonensis	proton-coupled amino acid transporter 1	1	C:GO:0016021	-		-

Ostreococcus tauri	dentin sialophosphoprotein precursor	0		F:GO:0016740; C:GO:0009986; F:GO:0003677; P:GO:0071460; C:GO:0005578; C:GO:0031012; F:GO:0016779; C:GO:0005618; P:GO:0006350; P:GO:0031214; F:GO:0003899		-
Ostreococcus tauri	d--directed r- polymerase	0		F:GO:0016779; F:GO:0003899; F:GO:0016740; P:GO:0006350; F:GO:0003677		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0046872; C:GO:0016021; C:GO:0016020; P:GO:0023034; F:GO:0005515		IPR002219; G3DSA:3.30.60.20 (GENE3D), SSF57889 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0046872; C:GO:0016021; C:GO:0016020; P:GO:0023034; F:GO:0005515		IPR002219; G3DSA:3.30.60.20 (GENE3D), SSF57889 (SUPERFAMILY)
Caenorhabditis elegans	zip zinc transporter family protein	2	P:GO:0009792; P:GO:0006810	-		IPR003689; PTHR11040 (PANTHER), PTHR11040:SF8 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	zip zinc transporter family protein	5	P:GO:0030001; C:GO:0016021; P:GO:0009792; F:GO:0046873; P:GO:0055085	-		IPR003689; PTHR11040 (PANTHER), PTHR11040:SF8 (PANTHER)
Caenorhabditis elegans	zip zinc transporter family protein	2	C:GO:0016020; P:GO:0006810	-		IPR003689; PTHR11040 (PANTHER), PTHR11040:SF8 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	tryptophanyl-tr- synthetase	5	C:GO:0005737; F:GO:0004830; P:GO:0006436; F:GO:0005524; P:GO:0007040	-	EC:6.1.1.2	IPR001412; IPR002305; IPR002306; IPR014729; G3DSA:1.10.240.10 (GENE3D), SSF52374 (SUPERFAMILY)
Caenorhabditis briggsae	unconventio-l s-re in the er 1 homolog	5	P:GO:0046907; F:GO:0005488; C:GO:0043231; C:GO:0044444; P:GO:0016192	-		IPR019150; PTHR13050 (PANTHER)
	-	0				-
Brugia malayi	ubiquitin-activating enzyme e1	3	F:GO:0008641; P:GO:0006464; F:GO:0008134	-		IPR000594; IPR009036; IPR016040; IPR018074; IPR019572; G3DSA:1.10.3240.10 (GENE3D), PTHR10953 (PANTHER), PTHR10953:SF5 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-

	-	0				-
Caenorhabditis elegans	briggsae cbr-ccdc-55 protein	4	P:GO:0002119; P:GO:0040010; P:GO:0006898; P:GO:0040039	-		IPR018612; PTHR22908 (PANTHER), PTHR22908:SF4 (PANTHER)
Loa loa	agap010322 protein	7	P:GO:0045944; F:GO:0016564; P:GO:0000122; F:GO:0016563; F:GO:0005515; C:GO:0005634; F:GO:0003702	-		IPR009072; PTHR11064 (PANTHER), PTHR11064:SF8 (PANTHER)
Caenorhabditis elegans	protein fam69c-like	0		F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150		IPR022049; PTHR21093 (PANTHER)
	-	0				-
Loa loa	kinesin-like protein at 3a-like	2	F:GO:0005488; C:GO:0043232	-		PTHR16012 (PANTHER), PTHR16012:SF119 (PANTHER)
Loa loa	kinesin-like protein at 3a-like	2	F:GO:0005488; C:GO:0043232	-		PTHR16012 (PANTHER), PTHR16012:SF119 (PANTHER)
Caenorhabditis briggsae	outer membrane protein	1	F:GO:0005515	-		IPR011935
Caenorhabditis briggsae	mucoidy inhibitor a	1	F:GO:0005515	-		-
Caenorhabditis briggsae	mucoidy inhibitor a	1	F:GO:0005515	-		IPR011935
Caenorhabditis briggsae	outer membrane protein	1	F:GO:0005515	-		IPR011935
	-	0				-
	-	0				-
Caenorhabditis briggsae	outer membrane protein	1	F:GO:0005515	-		-
Caenorhabditis briggsae	outer membrane protein	1	F:GO:0005515	-		IPR011935
Caenorhabditis briggsae	mucoidy inhibitor a	1	F:GO:0005515	-		
Caenorhabditis briggsae	outer membrane protein	1	F:GO:0005515	-		-
Caenorhabditis briggsae	outer membrane protein	1	F:GO:0005515	-		IPR011935
Caenorhabditis briggsae	mucoidy inhibitor a	1	F:GO:0005515	-		-
	-	0				-
Caenorhabditis elegans	mitochondrial ribosomal protein l46	0		F:GO:0003735; F:GO:0016787		IPR000086; IPR015797; IPR021757; PTHR13124 (PANTHER), PTHR13124:SF11 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	salt tolerance protein	6	P:GO:0008380; F:GO:0003729; P:GO:0006915; F:GO:0005515; P:GO:0006950; C:GO:0005634	-		IPR004882; PTHR12375:SF17 (PANTHER)
Caenorhabditis briggsae	hydroxysteroid (17-beta) dehydroge-se isoform cra_a	14	P:GO:0006952; P:GO:0000038; P:GO:0060009; P:GO:0008340; C:GO:0005739; F:GO:0033989; P:GO:0033540; F:GO:0015248; F:GO:0042802; F:GO:0030283; P:GO:0019915; F:GO:0003857; F:GO:0004303; C:GO:0005782	-	EC:4.2.1.107; EC:1.1.1.51; EC:1.1.1.35; EC:1.1.1.62	-

	-	0				-
Loa loa	vacuolar protein sorting-associated protein 33b	7	P:GO:0016192; C:GO:0005764; P:GO:0051640; C:GO:0005774; C:GO:0005770; F:GO:0019905; P:GO:0016043	-		IPR001619; G3DSA:3.40.50.1910 (GENE3D), G3DSA:3.90.830.10 (GENE3D), PTHR11679:SF1 (PANTHER)
Caenorhabditis briggsae	vacuolar protein sorting 35	4	C:GO:0005768; F:GO:0005515; P:GO:0006810; C:GO:0005829	-		-
Caenorhabditis elegans	rho gtpase activating protein 29	3	F:GO:0046872; P:GO:0007165; C:GO:0005622	-		IPR000198; IPR002219; IPR008936; G3DSA:3.30.60.20 (GENE3D), PTHR15228 (PANTHER), PTHR15228:SF1 (PANTHER), SSF57889 (SUPERFAMILY)
Caenorhabditis briggsae	adipokinetic hormone receptor	4	P:GO:0007186; C:GO:0016021; P:GO:0007165; F:GO:0005000	-		IPR000276; IPR017452; G3DSA:1.20.1070.10 (GENE3D), PTHR19264 (PANTHER), PTHR19264:SF50 (PANTHER), SignalP (SIGNALP), SSF81321 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG13933 [Caenorhabditis briggsae]	2	P:GO:0040010; P:GO:0006898	-		-
Caenorhabditis briggsae	bromodomain adjacent to zinc finger 1b	7	F:GO:0005515; P:GO:0010468; F:GO:0016740; P:GO:0006350; C:GO:0044446; C:GO:0005634; P:GO:0016568	-		IPR001965; IPR011011; IPR013083; IPR019786; IPR019787; PTHR22880 (PANTHER), PTHR22880:SF4 (PANTHER)
Caenorhabditis briggsae	bromodomain adjacent to zinc finger 1b	7	F:GO:0005515; P:GO:0010468; F:GO:0016740; P:GO:0006350; C:GO:0044446; C:GO:0005634; P:GO:0016568	-		-
	-	0				-
Caenorhabditis briggsae	bromodomain adjacent to zinc finger 1b	8	P:GO:0044260; P:GO:0010467; F:GO:0016740; P:GO:0044238; P:GO:0050789; C:GO:0043229; F:GO:0005488; P:GO:0006325	-		IPR001965; IPR011011; IPR013083; IPR019786; IPR019787; PTHR22880 (PANTHER), PTHR22880:SF4 (PANTHER)
Brugia malayi	alpha 1b	8	F:GO:0005200; P:GO:0007018; F:GO:0005525; F:GO:0005515; P:GO:0000226; P:GO:0051258; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000217; IPR002452; IPR003008; IPR008280; IPR017975; IPR018316; IPR023123

Loa loa	bromodomain containing protein	12	P:GO:0000117; F:GO:0008270; P:GO:0006367; P:GO:0051726; P:GO:0045944; F:GO:0016251; F:GO:0035174; F:GO:0043565; F:GO:0016563; F:GO:0005515; P:GO:0016573; C:GO:0005669	-		IPR022591; PTHR13900 (PANTHER)
Caenorhabditis elegans	bifunctio-l coenzyme a synthase	7	F:GO:0016779; P:GO:0007303; P:GO:0007297; P:GO:0009058; P:GO:0070328; P:GO:0007476; F:GO:0016301	-	EC:2.7.7.0	IPR001977; IPR004820; IPR004821; IPR014729; G3DSA:3.40.50.300 (GENE3D), PTHR10695 (PANTHER), SSF52374 (SUPERFAMILY), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Loa loa	iron-sulfur cluster assembly accessory protein	1	F:GO:0005488	-		IPR010304; IPR018351; G3DSA:2.30.30.140 (GENE3D), PTHR12664 (PANTHER), SSF63748 (SUPERFAMILY)
Caenorhabditis briggsae	protein mago -shi	20	P:GO:0008340; P:GO:0016246; P:GO:0008103; P:GO:0007267; F:GO:0005515; P:GO:0006406; P:GO:0040010; C:GO:0071011; P:GO:0040011; P:GO:0007318; P:GO:0007317; C:GO:0071013; P:GO:0046594; P:GO:0000398; C:GO:0045495; P:GO:0009792; P:GO:0002119; P:GO:0010171; P:GO:0040022; P:GO:0001703	-		IPR004023

Caenorhabditis briggsae	protein mago -shi	20	P:GO:0008340; P:GO:0016246; P:GO:0008103; P:GO:0007267; F:GO:0005515; P:GO:0006406; P:GO:0040010; C:GO:0071011; P:GO:0040011; P:GO:0007318; P:GO:0007317; C:GO:0071013; P:GO:0046594; P:GO:0000398; C:GO:0045495; P:GO:0009792; P:GO:0002119; P:GO:0010171; P:GO:0040022; P:GO:0001703	-		IPR004023
Caenorhabditis briggsae	protein mago -shi	20	P:GO:0008340; P:GO:0016246; P:GO:0008103; P:GO:0007267; F:GO:0005515; P:GO:0006406; P:GO:0040010; C:GO:0071011; P:GO:0040011; P:GO:0007318; P:GO:0007317; C:GO:0071013; P:GO:0046594; P:GO:0000398; C:GO:0045495; P:GO:0009792; P:GO:0002119; P:GO:0010171; P:GO:0040022; P:GO:0001703	-		IPR004023
Caenorhabditis briggsae	protein phosphatase regulatory subunit 1	1	P:GO:0000003	-		IPR011989; IPR016024; IPR021133; PTHR10648 (PANTHER)
	-	0				-
Caenorhabditis briggsae	rcc1 protein	0		C:GO:0005737; P:GO:0007049; P:GO:0051301; P:GO:0007067; F:GO:0005085; C:GO:0005634		PS51257 (PROFILE), SignalP (SIGNALP)
Caenorhabditis briggsae	rcc1 protein	0		C:GO:0005737; P:GO:0007049; P:GO:0051301; P:GO:0007067; F:GO:0005085; C:GO:0005634		-
	-	0				-
	-	0				-

Loa loa	unc-119 homolog b	3	F:GO:0004114; F:GO:0005515; P:GO:0007275	-	EC:3.1.4.17	IPR008015; IPR014756; PTHR12951 (PANTHER), PTHR12951:SF1 (PANTHER)
Caenorhabditis elegans	protein rer1	2	P:GO:0006890; C:GO:0030173	-		IPR004932; SignalP (SIGNALP)
Caenorhabditis elegans	lung seven transmembrane receptor family protein	1	C:GO:0016021	-		-
Caenorhabditis elegans	deah (asp-glu-ala-his) box polypeptide 35	4	F:GO:0008026; F:GO:0003676; F:GO:0005524; P:GO:0006396	-		IPR002464; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR18934 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	cmc1_caeel ame: full=probable calcium-binding mitochondrial carrier	3	F:GO:0005488; P:GO:0006810; C:GO:0016020	-		-
Caenorhabditis briggsae	salivary secreted ribonuclease	6	P:GO:0009792; P:GO:0002119; P:GO:0018996; F:GO:0004518; P:GO:0000003; P:GO:0006898	-		SignalP (SIGNALP)
Caenorhabditis briggsae	salivary secreted ribonuclease	6	P:GO:0009792; P:GO:0002119; P:GO:0018996; F:GO:0004518; P:GO:0000003; P:GO:0006898	-		SignalP (SIGNALP)
Caenorhabditis elegans	rgp1 retrograde golgi transport homolog	0		F:GO:0003674; P:GO:0008150; C:GO:0005575		IPR014848; PTHR12507 (PANTHER)
Caenorhabditis elegans	cell division cycle 40 homolog	10	P:GO:0040007; P:GO:0000003; P:GO:0008380; P:GO:0010171; P:GO:0002119; P:GO:0040039; P:GO:0002009; P:GO:0001703; C:GO:0005634; P:GO:0016246	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; IPR020472; PTHR19852 (PANTHER), PTHR19852:SF7 (PANTHER)
Caenorhabditis briggsae	transmembrane protein 180-like	2	C:GO:0016021; P:GO:0008340	-		IPR016196
Brugia malayi	cutaneous t-cell lymphoma tumor antigen se70-2	3	P:GO:0010171; F:GO:0005488; P:GO:0040010	-		IPR000504; IPR000571; IPR012677; G3DSA:4.10.1000.10 (GENE3D), PTHR14398 (PANTHER), SSF54928 (SUPERFAMILY)
Clavispora lusitaniae ATCC 42720	proteophosphoglycan ppg4	0		F:GO:0005524; F:GO:0004479; P:GO:0006412; F:GO:0003774; C:GO:0016459		-
Caenorhabditis elegans	uncoordi-ted family member (unc-22)	5	C:GO:0030018; F:GO:0008307; P:GO:0007498; F:GO:0004674; F:GO:0000166	-	EC:2.7.11.0	-

Caenorhabditis elegans	myosin regulatory light chain	7	C:GO:0005856; F:GO:0005509; C:GO:0030016; P:GO:0055003; F:GO:0005515; P:GO:0042694; P:GO:0060048	-		-
Nasonia vitripennis	histone	16	P:GO:0040010; C:GO:0000786; P:GO:0008340; P:GO:0009725; P:GO:0008360; P:GO:0007420; F:GO:0003677; C:GO:0005700; P:GO:0010171; P:GO:0007155; P:GO:0002119; P:GO:0006334; P:GO:0009792; P:GO:0007140; C:GO:0005634; P:GO:0006974	-		IPR000164; IPR007125; IPR009072
Caenorhabditis briggsae	atpase 7b	33	P:GO:0006915; P:GO:0035434; C:GO:0005923; C:GO:0005802; F:GO:0005507; P:GO:0042415; P:GO:0007420; P:GO:0043085; P:GO:0048552; P:GO:0009072; P:GO:0044283; F:GO:0043682; P:GO:0006464; P:GO:0007005; P:GO:0006586; P:GO:0010043; P:GO:0008544; P:GO:0009101; C:GO:0042995; P:GO:0021954; P:GO:0046688; F:GO:0008270; P:GO:0048812; P:GO:0050794; P:GO:0030198; P:GO:0051591; P:GO:0030005;	-		IPR001757; IPR006121; IPR006403; IPR017969; G3DSA:3.30.70.100 (GENE3D), PTHR11939:SF38 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Culex quinquefasciatus	conserved hypothetical protein [Culex quinquefasciatus]	0				-
Caenorhabditis elegans	riken cd- 2400010d15	1	F:GO:0005515	-		IPR000532; PTHR12897 (PANTHER)
	-	0				IPR022353; SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	small nuclear ribonucleoprotein polypeptide a	5	C:GO:0005686; F:GO:0003676; C:GO:0005681; F:GO:0005515; P:GO:0000398	-		-
Caenorhabditis briggsae	suppressor with morphological effect on genitalia family member (smg-6)	0				-
Caenorhabditis elegans	tld family protein	1	F:GO:0005515	-		-
	briggsae cbr-crn-5 protein	3	F:GO:0005488; F:GO:0016787; C:GO:0044424	-		IPR001247; IPR015847; IPR020568; PTHR11953 (PANTHER)
	exosome component 5	3	F:GO:0005488; F:GO:0016787; C:GO:0044424	-		-
	briggsae cbr-crn-5 protein	3	F:GO:0005488; F:GO:0016787; C:GO:0044424	-		IPR001247; IPR015847; IPR020568; PTHR11953 (PANTHER)
Caenorhabditis elegans	hypothetical protein C50F2.3 [Caenorhabditis elegans]	0		P:GO:0000910; P:GO:0006396; P:GO:0000003; P:GO:0051301; P:GO:0002119; P:GO:0009792; P:GO:0009790; P:GO:0001703; P:GO:0040010; P:GO:0007369; P:GO:0040007; F:GO:0005488		-
Loa loa	hypothetical protein LOAG_10592 [Loa loa]	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	P:GO:0002119	-		-
Loa loa	kiaa1530 protein	0				-
	-	0				IPR001111; SignalP (SIGNALP)
Caenorhabditis briggsae	chl1 potential helicase	6	F:GO:0003676; F:GO:0008026; P:GO:0000003; F:GO:0000166; P:GO:0006139; P:GO:0009792	-		IPR010614; IPR014013; PTHR11472 (PANTHER), PTHR11472:SF5 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	activating sig-l cointegrator 1 complex subunit 1	2	F:GO:0005488; P:GO:0050789	-		IPR004087; IPR004088; IPR009210; IPR018111; IPR019510; G3DSA:3.30.1370.10 (GENE3D), G3DSA:3.90.1140.10 (GENE3D), PTHR11208 (PANTHER), PTHR11208:SF7 (PANTHER), SSF54791 (SUPERFAMILY)
Caenorhabditis briggsae	activating sig-l cointegrator 1 complex subunit 1	2	F:GO:0005488; P:GO:0050789	-		IPR004087; IPR004088; IPR009097; IPR009210; IPR018111; IPR019510; G3DSA:3.30.1370.10 (GENE3D), G3DSA:3.90.1140.10 (GENE3D), PTHR11208 (PANTHER), PTHR11208:SF7 (PANTHER), SSF54791 (SUPERFAMILY)
Loa loa	thioredoxin domain-containing protein 11	1	C:GO:0016020	-		IPR012335; IPR012336

	-	0				PS51257 (PROFILE), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	membrane protein tms1d	3	P:GO:0018991; C:GO:0016021; P:GO:0040010	-		IPR005016; IPR015461; SignalP (SIGNALP)
Caenorhabditis elegans	tde2 protein	3	P:GO:0018991; C:GO:0016021; P:GO:0040010	-		IPR005016; IPR015461; SignalP (SIGNALP)
Caenorhabditis elegans	membrane protein tms1d	3	P:GO:0018991; C:GO:0016021; P:GO:0040010	-		IPR005016; IPR015461; SignalP (SIGNALP)
Caenorhabditis elegans	membrane protein tms1d	3	P:GO:0018991; C:GO:0016021; P:GO:0040010	-		IPR005016; IPR015461; SignalP (SIGNALP)
Caenorhabditis elegans	membrane protein tms1d	3	P:GO:0018991; C:GO:0016021; P:GO:0040010	-		IPR005016; IPR015461; SignalP (SIGNALP)
Caenorhabditis elegans	membrane protein tms1d	3	P:GO:0018991; C:GO:0016021; P:GO:0040010	-		IPR005016; IPR015461; SignalP (SIGNALP)
Loa loa	hypothetical protein LOAG_06660 [Loa loa]	0				-
Caenorhabditis briggsae	tissue factor pathway inhibitor 2	1	F:GO:0004867	-		-
Caenorhabditis briggsae	tissue factor pathway inhibitor 2	1	F:GO:0004867	-		-
Caenorhabditis briggsae	phosphoenolpyruvate carboxyki-se	6	C:GO:0005737; P:GO:0006094; F:GO:0046872; F:GO:0005525; F:GO:0016301; F:GO:0004613	-	EC:4.1.1.32	IPR008209; IPR008210; IPR013035; IPR018091; G3DSA:2.170.8.10 (GENE3D), SSF53795 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-kbp-2 protein	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		-
	-	0				-
Caenorhabditis elegans	rab proteins geranylgeranyltransferase component a 2	4	P:GO:0060042; P:GO:0050910; P:GO:0048798; P:GO:0050935	-		IPR002005; IPR016664; IPR018203; G3DSA:1.10.405.10 (GENE3D), G3DSA:3.30.519.10 (GENE3D), G3DSA:3.50.50.60 (GENE3D), SSF51905 (SUPERFAMILY)
Caenorhabditis elegans	rab escort protein homolog family member (rep-1)	2	P:GO:0009987; F:GO:0017137	-		IPR002005; IPR016664; IPR018203; G3DSA:1.10.405.10 (GENE3D), G3DSA:3.30.519.10 (GENE3D), G3DSA:3.50.50.60 (GENE3D), SSF51905 (SUPERFAMILY)
Caenorhabditis elegans	protein fem-1 homolog c	1	F:GO:0005515	-		PTHR18958 (PANTHER), PTHR18958:SF131 (PANTHER), SignalP (SIGNALP)
Loa loa	geranylgeranyl pyrophosphate synthetase	11	F:GO:0004337; P:GO:0000022; P:GO:0008354; F:GO:0003735; F:GO:0004161; F:GO:0004311; P:GO:0035050; C:GO:0043025; C:GO:0005811; C:GO:0022625; P:GO:0008299	-	EC:2.5.1.10; EC:2.5.1.1; EC:2.5.1.29	IPR000092; IPR008949; IPR017446; PTHR12001:SF5 (PANTHER)

Caenorhabditis briggsae	lipoyltransferase mitochondrial precursor	4	P:GO:0006629; P:GO:0006464; F:GO:0005515; F:GO:0003824	-		IPR004143; G3DSA:3.90.1550.10 (GENE3D), PTHR12561 (PANTHER), SSF55681 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	myb-like d--binding domain containing protein	1	F:GO:0005488	-		IPR000949; IPR001005; IPR009057; IPR014778; IPR017884; PTHR16089 (PANTHER), PTHR16089:SF1 (PANTHER)
Caenorhabditis elegans	dense body family member (deb-1)	6	F:GO:0005200; C:GO:0005856; C:GO:0005912; P:GO:0007016; F:GO:0005515; P:GO:0006911	-		IPR006077; G3DSA:1.20.120.230 (GENE3D)
	-	0				-
Caenorhabditis briggsae	thioredoxin	0		P:GO:0045454; F:GO:0016491; F:GO:0016209; C:GO:0005575		IPR012335; IPR012336; IPR013766; IPR017936; PTHR13871 (PANTHER), PTHR13871:SF5 (PANTHER)
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	2	P:GO:0042981; C:GO:0005622	-		IPR001315; IPR011029
	-	0				-
Lepeophtheirus salmonis	yippee-like 5	0		P:GO:0055114; F:GO:0003674; F:GO:0008113; C:GO:0005575		IPR004910; PTHR13847 (PANTHER), PTHR13847:SF1 (PANTHER)
Caenorhabditis elegans	uncoordi-ted family member (unc-52)	0		F:GO:0003674; C:GO:0005578; P:GO:0030239		IPR007110; IPR013783; PTHR10489 (PANTHER), PTHR10489:SF20 (PANTHER)
Caenorhabditis elegans	39s ribosomal protein mitochondrial	2	C:GO:0044444; C:GO:0043229	-		IPR010793; PTHR15889 (PANTHER)
Caenorhabditis elegans	mitochondrial ribosomal protein l37	2	C:GO:0044444; C:GO:0043229	-		IPR010793; PTHR15889 (PANTHER)
Caenorhabditis briggsae	ribosomal protein l13 containing protein	5	F:GO:0005488; P:GO:0055085; P:GO:0008340; C:GO:0016021; F:GO:0005215	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF23 (PANTHER)
	-	0				-
Caenorhabditis elegans	hypothetical protein T05C1.1 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical tyrosi-se-like protein in chromosome	4	F:GO:0005515; F:GO:0046872; P:GO:0008152; F:GO:0016491	-		IPR002227; IPR008922
Caenorhabditis elegans	hypothetical tyrosi-se-like protein in chromosome	4	F:GO:0005515; F:GO:0046872; P:GO:0008152; F:GO:0016491	-		IPR002227; IPR008922
	-	0				-
Ancylostoma caninum	secreted protein asp-2	0		P:GO:0040011; C:GO:0005576		IPR014044
	-	0				-

Caenorhabditis elegans	ferm domain (-ezrin-radixin-moesin) family member (frm-1)	0		F:GO:0004386; P:GO:0006030; F:GO:0003677; C:GO:0005634; F:GO:0003676; F:GO:0005524; F:GO:0005198; F:GO:0008061; F:GO:0008092; C:GO:0019898; F:GO:0003682; C:GO:0005737; C:GO:0000785; F:GO:0005488; F:GO:0003779; P:GO:0006333; C:GO:0005856; F:GO:0005515; C:GO:0005576		-
Caenorhabditis elegans	autophagy-related protein 2 homolog b-like	0				PTHR13190 (PANTHER), PTHR13190:SF2 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	u1 small nuclear ribonucleoprotein a	4	P:GO:0002119; F:GO:0005488; P:GO:0016246; P:GO:0040007	-		IPR000504; IPR012677; PTHR10501 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	hypothetical kda protein in mob1-sga1 intergenic	4	C:GO:0044424; P:GO:0000003; P:GO:0040010; P:GO:0002119	-		IPR002728; PTHR10762:SF1 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	C:GO:0005739	-		IPR003593; IPR011704; G3DSA:3.40.50.300 (GENE3D), PTHR21610 (PANTHER), PTHR21610:SF1 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	adenylate ki-se 2	14	P:GO:0046939; P:GO:0040010; F:GO:0004017; C:GO:0005743; P:GO:0040035; P:GO:0035046; C:GO:0005758; F:GO:0005524; P:GO:0002119; P:GO:0009792; C:GO:0005811; P:GO:0040018; P:GO:0006172; F:GO:0046899	-	EC:2.7.4.3; EC:2.7.4.10	IPR000850; IPR006259; IPR007862; G3DSA:3.40.50.300 (GENE3D), PTHR23359:SF22 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)

Mus musculus	nuclear transport factor 2	5	C:GO:0005643; P:GO:0006606; F:GO:0005515; F:GO:0008565; C:GO:0005829	-		-
Brugia malayi	fas apoptotic inhibitory molecule 2	3	P:GO:0006915; F:GO:0005515; C:GO:0044425	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Brugia malayi	fas apoptotic inhibitory molecule 2	3	P:GO:0006915; F:GO:0005515; C:GO:0016021	-		IPR006214; PTHR23291:SF14 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	phospholipase c gamma	10	P:GO:0051239; P:GO:0048514; F:GO:0004435; P:GO:0009395; F:GO:0004871; P:GO:0048646; P:GO:0030154; F:GO:0005515; P:GO:0007165; P:GO:0007275	-	EC:3.1.4.11	IPR000980; IPR001452; G3DSA:2.30.30.40 (GENE3D), PTHR22820 (PANTHER), PTHR22820:SF14 (PANTHER), SSF55550 (SUPERFAMILY)
Caenorhabditis elegans	-dc (-+-coupled dicarboxylate transporter) family member (-c-3)	5	P:GO:0055085; P:GO:0006814; C:GO:0030054; F:GO:0015362; C:GO:0005813	-		IPR001898; PTHR10283 (PANTHER), PTHR10283:SF15 (PANTHER), SignalP (SIGNALP)
Strongylocentrotus purpuratus	spen transcriptio-l regulator	7	P:GO:0006357; F:GO:0003714; F:GO:0016563; F:GO:0003700; F:GO:0003697; P:GO:0045892; C:GO:0005634	-		IPR010912; IPR012921; IPR016194; G3DSA:2.40.290.10 (GENE3D)
Strongylocentrotus purpuratus	spen transcriptio-l regulator	7	P:GO:0006357; F:GO:0003714; F:GO:0016563; F:GO:0003700; F:GO:0003697; P:GO:0045892; C:GO:0005634	-		IPR010912; IPR012921; IPR016194; G3DSA:2.40.290.10 (GENE3D)
Caenorhabditis briggsae	3 -5 exonuclease family protein	9	P:GO:0006139; F:GO:0003676; C:GO:0005622; F:GO:0005515; P:GO:0018996; F:GO:0008408; P:GO:0000003; P:GO:0040011; P:GO:0002009	-		IPR002355; IPR002562; IPR012337; G3DSA:3.30.420.10 (GENE3D)
Ancylostoma caninum	secreted protein asp-2	0		C:GO:0005576		IPR001283; IPR014044; PTHR10334:SF11 (PANTHER)

Caenorhabditis elegans	acid phosphatase tartrate resistant	6	P:GO:0048519; C:GO:0044464; F:GO:0016787; P:GO:0050896; F:GO:0046872; P:GO:0032501	-		IPR004843; G3DSA:3.60.21.10 (GENE3D), PTHR10161 (PANTHER), PTHR10161:SF3 (PANTHER), SSF56300 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-him-17 protein	0				IPR006612
Caenorhabditis elegans	pp-loop domain protein	6	P:GO:0006357; F:GO:0016455; F:GO:0000166; C:GO:0016592; F:GO:0003824; F:GO:0030170	-		PTHR11807 (PANTHER), PTHR11807:SF4 (PANTHER), SSF52402 (SUPERFAMILY)
Caenorhabditis briggsae	solute carrier family member 46	1	C:GO:0016020	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR21252 (PANTHER)
Caenorhabditis briggsae	solute carrier family member 46	1	C:GO:0016020	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR21252 (PANTHER)
Caenorhabditis briggsae	benzodiazapine receptor associated protein 1	1	C:GO:0005737	-		IPR001452; IPR011511; G3DSA:2.30.30.40 (GENE3D), PTHR14234 (PANTHER), PTHR14234:SF1 (PANTHER)
Caenorhabditis briggsae	succi-te dehydroge-se	12	P:GO:0040010; P:GO:0022900; P:GO:0018991; C:GO:0005749; F:GO:0009055; P:GO:0006099; P:GO:0010171; P:GO:0002119; F:GO:0008177; F:GO:0050660; P:GO:0009792; F:GO:0004776	-	EC:1.3.5.1; EC:6.2.1.4	-
Ornithorhynchus anatinus	microspherule protein 1	1	C:GO:0005654	-		PTHR13233 (PANTHER)
Tetraodon nigroviridis	microspherule protein 1	0				PTHR13233 (PANTHER)
Caenorhabditis elegans	ubiquitin-conjugating enzyme e2w	6	P:GO:0006513; F:GO:0005515; F:GO:0005524; F:GO:0004842; P:GO:0051246; P:GO:0070979	-	EC:6.3.2.19	IPR000608; IPR016135; PTHR11621 (PANTHER), PTHR11621:SF16 (PANTHER)
Caenorhabditis elegans	thyroid hormone receptor interactor 11	2	F:GO:0005515; C:GO:0043229	-		-
Brugia malayi	argo-ute-like protein	1	P:GO:0016246	-		IPR003165; IPR012337; PTHR22891 (PANTHER)
Caenorhabditis elegans	dystrophin	7	P:GO:0007271; F:GO:0005515; P:GO:0040017; C:GO:0016010; F:GO:0005277; P:GO:0015870; P:GO:0046716	-		IPR015153; PTHR11915 (PANTHER), PTHR11915:SF57 (PANTHER), SSF47473 (SUPERFAMILY)

Brugia malayi	dead box atp-dependent r- helicase	7	F:GO:0003676; F:GO:0008026; F:GO:0005524; F:GO:0005515; P:GO:0006406; C:GO:0005635; C:GO:0016020	-		IPR011545; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF3 (PANTHER), SSF52540 (SUPERFAMILY)
Brugia malayi	dead box atp-dependent r- helicase	7	F:GO:0003676; F:GO:0008026; F:GO:0005524; F:GO:0005515; P:GO:0006406; C:GO:0005635; C:GO:0016020	-		IPR011545; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF3 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elac homolog 2 (coli)	3	F:GO:0005488; F:GO:0016787; C:GO:0005739	-		IPR001279; G3DSA:3.60.15.10 (GENE3D), PTHR12553 (PANTHER), PTHR12553:SF3 (PANTHER), SSF56281 (SUPERFAMILY)
Caenorhabditis elegans	elac homolog 2 (coli)	3	F:GO:0005488; F:GO:0016787; C:GO:0005739	-		IPR001279; G3DSA:3.60.15.10 (GENE3D), PTHR12553 (PANTHER), PTHR12553:SF3 (PANTHER), SSF56281 (SUPERFAMILY)
Brugia malayi	r- binding motif protein 21	0		F:GO:0003676; F:GO:0000166		IPR000504; IPR002934; G3DSA:3.30.460.10 (GENE3D), SSF81301 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	translation initiation factor if-2	14	F:GO:0003743; F:GO:0016779; F:GO:0003746; P:GO:0040010; C:GO:0005739; C:GO:0016021; P:GO:0007264; F:GO:0043024; P:GO:0015684; F:GO:0015093; F:GO:0003924; P:GO:0006446; P:GO:0006898; F:GO:0005525	-	EC:2.7.7.0; EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Caenorhabditis elegans	briggsae cbr-taf-1 protein	1	F:GO:0005515	-		-
	-	0				-
	-	0				IPR005479
Caenorhabditis briggsae	trehalase family protein	5	P:GO:0009792; P:GO:0002119; F:GO:0004553; P:GO:0044262; P:GO:0040007	-	EC:3.2.1.0	IPR001661; IPR008928; PTHR23403:SF1 (PANTHER)
	-	0				IPR013783; SSF48726 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0016787	-		IPR002921; G3DSA:3.40.50.1820 (GENE3D), SSF53474 (SUPERFAMILY)

Haemonchus contortus	ilin (drosophila ecm protein) homolog family member (ppn-1)	6	P:GO:0009987; F:GO:0004867; F:GO:0008270; F:GO:0004222; F:GO:0005515; C:GO:0005578	-	EC:3.4.24.0	SignalP (SIGNALP)
Haemonchus contortus	ilin (drosophila ecm protein) homolog family member (ppn-1)	6	P:GO:0009987; F:GO:0004867; F:GO:0008270; F:GO:0004222; F:GO:0005515; C:GO:0005578	-	EC:3.4.24.0	IPR000884; IPR002223; IPR020901; PTHR13723 (PANTHER), PTHR13723:SF18 (PANTHER)
Caenorhabditis elegans	cral trio domain containing protein	0		F:GO:0005215; C:GO:0005634; P:GO:0006810; C:GO:0005737; F:GO:0003674; C:GO:0005575; F:GO:0008289; C:GO:0005622; P:GO:0008150; P:GO:0045449		-
Saccoglossus kowalevskii	cut-like homeobox 1	0		F:GO:0003677; C:GO:0005634; P:GO:0042491; P:GO:0006357; P:GO:0030324; F:GO:0030528; P:GO:0006355; C:GO:0016021; P:GO:0000122; C:GO:0016020; F:GO:0016564; P:GO:0006350; F:GO:0003702; F:GO:0003700; P:GO:0006891; C:GO:0000139; P:GO:0007275; F:GO:0003682; F:GO:0030674; P:GO:0045449; C:GO:0005794; F:GO:0043565; P:GO:0000301; P:GO:0006810; C:GO:0030173		-
Caenorhabditis elegans	g-patch domain containing protein	2	F:GO:0005488; P:GO:0019915	-		IPR000467; IPR000571; G3DSA:4.10.1000.10 (GENE3D), PTHR23329 (PANTHER), PTHR23329:SF2 (PANTHER)

Caenorhabditis briggsae	lipoic acid mitochondrial precursor	8	P:GO:0040010; C:GO:0005739; F:GO:0046872; P:GO:0009107; F:GO:0051539; P:GO:0002119; P:GO:0009792; F:GO:0016992	-	EC:2.8.1.8	IPR013785; PTHR10949 (PANTHER), SSF102114 (SUPERFAMILY)
Caenorhabditis briggsae	programmed cell death 6-interacting protein	0				IPR004328; G3DSA:1.20.120.560 (GENE3D), G3DSA:1.25.40.280 (GENE3D), PTHR23030 (PANTHER), PTHR23030:SF11 (PANTHER)
Caenorhabditis elegans	rw1 protein	1	F:GO:0005515	-		IPR022113; PTHR22050 (PANTHER), SignalP (SIGNALP)
Brugia malayi	related to oncogene abl family member (abl-1)	7	F:GO:0004715; F:GO:0030145; F:GO:0005515; P:GO:0018108; F:GO:0005524; F:GO:0000287; P:GO:0007165	-	EC:2.7.10.2	IPR000719; IPR000980; IPR001245; IPR001452; IPR017441; IPR020685; IPR020700; G3DSA:2.30.30.40 (GENE3D), G3DSA:3.30.200.20 (GENE3D), SSF55550 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	uncoordi-ted protein isoform partially confirmed by transcript evidence	0		F:GO:0004672; F:GO:0005524; F:GO:0000166; P:GO:0006468; F:GO:0004674		-
Caenorhabditis briggsae	ornithine aminotransferase	4	F:GO:0030170; C:GO:0005739; F:GO:0008483; F:GO:0005515	-	EC:2.6.1.0	IPR005814; IPR010164; IPR015421; IPR015422; IPR015424
Ixodes scapularis	tpa: zinc finger protein	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		-
	-	0				-
Caenorhabditis elegans	universal minicircle sequence binding protein	6	P:GO:0009792; P:GO:0002119; F:GO:0005488; P:GO:0000003; P:GO:0040011; P:GO:0040007	-		-
Caenorhabditis briggsae	coenzyme q10 homolog b (cerevisiae)	1	C:GO:0005739	-		IPR007087; IPR015880
Caenorhabditis elegans	briggsae cbr-sel-2 protein	4	C:GO:0005737; P:GO:0008104; F:GO:0051018; P:GO:0042675	-		IPR000409; IPR010508; PD329443 (PRODOM), G3DSA:2.30.29.40 (GENE3D), PTHR13743 (PANTHER), SSF50729 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Loa loa	cdc2l5 protein ki-se	6	P:GO:0006468; P:GO:0008284; P:GO:0007275; P:GO:0007088; F:GO:0005524; F:GO:0004693	-	EC:2.7.11.22	IPR000719; IPR011009; IPR017441; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF112 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG09770 [Caenorhabditis briggsae]	0				-

Caenorhabditis elegans	rilp-like protein	0				IPR019143; IPR021563; PD936484 (PRODOM)
Caenorhabditis briggsae	rilp-like protein	0		F:GO:0003674; C:GO:0005575		IPR019143; IPR021563; PD936484 (PRODOM)
Ostertagia ostertagi	metalloprotease 1 precursor	2	F:GO:0046872; F:GO:0008237	-		IPR001506; IPR006026; IPR013032; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SignalP (SIGNALP), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	receptor mediated endocytosis family member (rme-1)	9	P:GO:0007291; F:GO:0005509; F:GO:0005515; P:GO:0007474; P:GO:0006897; F:GO:0003924; P:GO:0048477; P:GO:0008587; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
	-	0				-
Caenorhabditis briggsae	ras-related gtp-binding protein a	4	C:GO:0005737; F:GO:0005525; C:GO:0005634; P:GO:0007264	-		IPR006762; PTHR11259:SF1 (PANTHER)
Brugia malayi	insulin-like growth factor 1 receptor	5	P:GO:0009987; F:GO:0004872; F:GO:0004713; F:GO:0005515; C:GO:0016020	-	EC:2.7.10.0	IPR000494; IPR003961; IPR006211; IPR006212; IPR008957; IPR009030; IPR013783; IPR017441; IPR017896; IPR020685; IPR020772; G3DSA:2.10.220.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), G3DSA:3.80.20.20 (GENE3D), SSF52058 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG07001 [Caenorhabditis briggsae]	0		P:GO:0040017; P:GO:0000003; P:GO:0040035; P:GO:0006898; P:GO:0009792		-
Caenorhabditis elegans	jnk1 mapk8-associated membrane protein	1	P:GO:0000003	-		IPR008485; SignalP (SIGNALP)
Caenorhabditis elegans	jnk1 mapk8-associated membrane protein	1	P:GO:0000003	-		IPR008485; SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	deah (asp-glu-ala-his) box polypeptide 8	8	F:GO:0003723; F:GO:0004004; C:GO:0005681; P:GO:0006200; P:GO:0008380; F:GO:0005524; F:GO:0005515; P:GO:0006397	-		IPR001650; IPR002464; IPR011545; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR18934 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	bess motif family protein	0		F:GO:0046872; F:GO:0008270; F:GO:0005515; F:GO:0003677		-

Caenorhabditis briggsae	bess motif family protein	0		F:GO:0046872; F:GO:0008270; F:GO:0005515; F:GO:0003677		-
Aedes aegypti	cysteine-rich venom	0				IPR002919; G3DSA:2.10.25.10 (GENE3D), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	illin homolo family member (pxl-1)	4	P:GO:0009792; P:GO:0040010; F:GO:0008270; P:GO:0002119	-		IPR001781; PTHR18973 (PANTHER), PTHR18973:SF96 (PANTHER), SSF57716 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	3-hydroxyisobutyrate dehydroge-se	8	F:GO:0008442; P:GO:0006098; P:GO:0006813; P:GO:0055114; P:GO:0006573; F:GO:0051287; C:GO:0005759; F:GO:0004616	-	EC:1.1.1.31; EC:1.1.1.44	IPR002204; IPR006115; IPR008927; IPR011548; IPR013328; IPR015815; IPR016040; PTHR22981:SF7 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	3-hydroxyisobutyrate dehydroge-se	8	F:GO:0008442; P:GO:0006098; P:GO:0006813; P:GO:0055114; P:GO:0006573; F:GO:0051287; C:GO:0005759; F:GO:0004616	-	EC:1.1.1.31; EC:1.1.1.44	-
Caenorhabditis elegans	3-hydroxyisobutyrate dehydroge-se	8	F:GO:0008442; P:GO:0006098; P:GO:0006813; P:GO:0055114; P:GO:0006573; F:GO:0051287; C:GO:0005759; F:GO:0004616	-	EC:1.1.1.31; EC:1.1.1.44	-
Loa loa	kinesin family member 4	6	P:GO:0006996; C:GO:0005876; F:GO:0003774; F:GO:0005515; P:GO:0008089; F:GO:0000166	-		IPR001752; IPR019821; PTHR16012 (PANTHER), PTHR16012:SF119 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	h aca ribonucleoprotein complex subunit 1	5	F:GO:0009982; C:GO:0001651; F:GO:0030515; C:GO:0031429; P:GO:0006364	-	EC:5.4.99.12	IPR007504; IPR009000; IPR021154
Loa loa	hypothetical protein LOAG_05186 [Loa loa]	0				-
Loa loa	hypothetical protein LOAG_05186 [Loa loa]	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	prion-like-(q n-rich)-domain-bearing protein protein partially confirmed by transcript evidence	0		P:GO:0009792; F:GO:0005515		-
Caenorhabditis elegans	transcription termi-tion r- polymerase ii	3	F:GO:0005488; P:GO:0006139; F:GO:0016787	-		IPR010916; PTHR10799 (PANTHER), PTHR10799:SF63 (PANTHER)

	-	0				-
						-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0003840	-	EC:2.3.2.2	-
Homo sapiens	-dh dehydroge-se subunit 2	6	P:GO:0006120; C:GO:0005743; C:GO:0070469; F:GO:0008137; P:GO:0006810; C:GO:0016021	-	EC:1.6.5.3	-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG10904 [Caenorhabditis briggsae]	0				-
Loa loa	loc431806 protein	0		F:GO:0000049; C:GO:0005737; P:GO:0008033; C:GO:0005829; P:GO:0008150; P:GO:0002098; P:GO:0034227		-
Brugia malayi	tyrosyl-d- phosphodiesterase 1	7	C:GO:0005737; P:GO:0000012; F:GO:0005515; F:GO:0003697; F:GO:0017005; P:GO:0006302; F:GO:0003690	-		IPR010347; G3DSA:3.30.870.20 (GENE3D), SSF56024 (SUPERFAMILY)
Caenorhabditis briggsae	lim domain family member (lim-8)	1	F:GO:0005515	-		-
Caenorhabditis briggsae	lim domain family member (lim-8)	1	F:GO:0005515	-		-
Caenorhabditis elegans	hypothetical protein F01F1.3 [Caenorhabditis elegans]	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	mitochondrial ribosomal protein l17	3	C:GO:0005840; F:GO:0003735; P:GO:0006412	-	EC:3.6.5.3	IPR000456; PTHR14413:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis elegans	: shorter than wild-type family member (dpy-23)	4	C:GO:0030122; F:GO:0005515; P:GO:0016192; P:GO:0006886	-		IPR011012; IPR015629; G3DSA:3.30.450.60 (GENE3D), PTHR11998 (PANTHER)
Caenorhabditis briggsae	d- topoisomerase iii	5	P:GO:0006259; P:GO:0007276; P:GO:0007126; P:GO:0071103; F:GO:0003916	-		IPR000380; IPR006171; G3DSA:3.40.50.140 (GENE3D)
Caenorhabditis briggsae	peptidase s9 prolyl oligopeptidase active site domain protein	2	P:GO:0008152; F:GO:0008236	-		IPR001375; IPR015943; G3DSA:3.40.50.1820 (GENE3D), PTHR11731 (PANTHER), PTHR11731:SF7 (PANTHER), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	ubiquitin-conjugating enzyme e2r	3	P:GO:0051246; F:GO:0019787; P:GO:0043687	-		IPR000608; IPR016135; PTHR11621 (PANTHER), PTHR11621:SF37 (PANTHER)
Loa loa	fidipidine	0				PD936484 (PRODOM), PTHR16441 (PANTHER)
Caenorhabditis elegans	lysosomal acid lipase cholesteryl ester hydrolase	3	F:GO:0016788; P:GO:0032501; P:GO:0001666	-		IPR000073; IPR006693; G3DSA:3.40.50.1820 (GENE3D), PTHR11005 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)

Oryctolagus cuniculus	beta	20	C:GO:0042612; P:GO:0019882; P:GO:0042267; C:GO:0045298; P:GO:0006928; F:GO:0005525; F:GO:0042288; C:GO:0016021; P:GO:0006184; P:GO:0051225; C:GO:0005829; C:GO:0005874; P:GO:0051258; P:GO:0007067; F:GO:0042277; F:GO:0032403; F:GO:0003924; P:GO:0007018; F:GO:0005200; P:GO:0030182	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000217; IPR002453; IPR008280; IPR018316; IPR023123
Caenorhabditis elegans	sensory axon guidance family member (sax-7)	16	P:GO:0007158; P:GO:0016319; P:GO:0019991; P:GO:0048813; C:GO:0030175; F:GO:0005509; P:GO:0007173; P:GO:0035151; P:GO:0048675; C:GO:0005919; P:GO:0021682; P:GO:0050808; P:GO:0008366; P:GO:0007560; P:GO:0035011; P:GO:0060857	-		-
Caenorhabditis briggsae	phosphoribosylaminoimidazolecarboxamide formyltransferase imp cyclohydrolase	3	F:GO:0004643; F:GO:0003937; P:GO:0006188	-	EC:2.1.2.3; EC:3.5.4.10	-
Caenorhabditis elegans	hypothetical protein Y57E12AL.6 [Caenorhabditis elegans]	2	P:GO:0002119; P:GO:0009792	-		-
Caenorhabditis elegans	hypothetical protein Y57E12AL.6 [Caenorhabditis elegans]	2	P:GO:0002119; P:GO:0009792	-		-
	-	0				IPR007087; IPR015880; PTHR11389 (PANTHER)
	-	0				-
Caenorhabditis elegans	28s ribosomal protein mitochondrial	4	P:GO:0000003; P:GO:0040007; P:GO:0006898; P:GO:0002119	-		IPR019266; SignalP (SIGNALP)
Caenorhabditis elegans	amylase 2- pancreatic	5	C:GO:0005615; F:GO:0031404; F:GO:0004556; P:GO:0016052; F:GO:0005509	-	EC:3.2.1.1	IPR006046; IPR006047; IPR013781; IPR017853; PTHR10357 (PANTHER), PTHR10357:SF26 (PANTHER)

Oryctolagus cuniculus	zinc finger protein 701-like	5	F:GO:0003676; C:GO:0005622; F:GO:0005515; F:GO:0008270; P:GO:0006355	-		-
Oryctolagus cuniculus	zinc finger protein 701-like	5	F:GO:0003676; C:GO:0005622; F:GO:0005515; F:GO:0008270; P:GO:0006355	-		-
Brugia malayi	d--directed r- polymerases and iii subunit rpabc2	11	F:GO:0003899; F:GO:0004672; P:GO:0006367; C:GO:0005730; P:GO:0000003; P:GO:0008380; C:GO:0005665; F:GO:0003677; P:GO:0006368; P:GO:0006898; P:GO:0009792	-	EC:2.7.7.6	IPR006110; IPR006111; IPR012293; IPR020708; PTHR10773:SF8 (PANTHER)
Brugia malayi	d--directed r- polymerases and iii subunit rpabc2	11	F:GO:0003899; F:GO:0004672; P:GO:0006367; C:GO:0005730; P:GO:0000003; P:GO:0008380; C:GO:0005665; F:GO:0003677; P:GO:0006368; P:GO:0006898; P:GO:0009792	-	EC:2.7.7.6	SignalP (SIGNALP)
Brugia malayi	d--directed r- polymerases and iii subunit rpabc2	11	F:GO:0003899; F:GO:0004672; P:GO:0006367; C:GO:0005730; P:GO:0000003; P:GO:0008380; C:GO:0005665; F:GO:0003677; P:GO:0006368; P:GO:0006898; P:GO:0009792	-	EC:2.7.7.6	IPR006110; IPR006111; IPR012293; IPR020708; PTHR10773:SF8 (PANTHER)
Cooperia oncophora	briggsae cbr-lat-1 protein	6	P:GO:0007218; C:GO:0016021; P:GO:0007165; C:GO:0005886; F:GO:0005529; F:GO:0004930	-		IPR000203; IPR000922; IPR001879; IPR022624; PTHR12011 (PANTHER), PTHR12011:SF55 (PANTHER), SignalP (SIGNALP), SSF111418 (SUPERFAMILY)
Caenorhabditis briggsae	eukaryotic translation initiation factor 3 subunit k	6	C:GO:0005852; F:GO:0005515; P:GO:0006446; F:GO:0003743; C:GO:0005634; F:GO:0043022	-		IPR005062; IPR009374; IPR011991; IPR016020; IPR016024; SignalP (SIGNALP), SSF46785 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	Hypothetical protein C25H3.17 [Caenorhabditis elegans]	0				SignalP (SIGNALP)

Loa loa	paz piwi domain-containing family member (ppw-1)	0		P:GO:0000003; F:GO:0003676; P:GO:0016246		G3DSA:2.170.260.10 (GENE3D), SSF101690 (SUPERFAMILY)
Caenorhabditis elegans	protein ki-se isoform cra_a	35	P:GO:0008340; P:GO:0000003; P:GO:0009749; P:GO:0043410; P:GO:0042542; C:GO:0016020; F:GO:0019901; P:GO:0046777; P:GO:0045471; P:GO:0009612; C:GO:0005624; P:GO:0016064; P:GO:0014070; F:GO:0046872; P:GO:0050732; P:GO:0009792; P:GO:0042100; F:GO:0043560; P:GO:0015810; P:GO:0043406; P:GO:0001666; P:GO:0006917; P:GO:0042493; P:GO:0043200; P:GO:0042149; P:GO:0032615; P:GO:0009408;	-		IPR000719; IPR000961; IPR002219; IPR002290; IPR008271; IPR011009; IPR015745; IPR017441; IPR017442; IPR017892; IPR020454; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), G3DSA:3.30.60.20 (GENE3D), PTHR22985 (PANTHER), SSF57889 (SUPERFAMILY)
Caenorhabditis briggsae	tripartite motif protein trim9	2	P:GO:0008340; F:GO:0005488	-		IPR001841; IPR013083; PTHR13712 (PANTHER), PTHR13712:SF62 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG04315 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	nuclear transcription x-box binding 1	3	F:GO:0003676; F:GO:0046872; P:GO:0006355	-		IPR000967; IPR001841; IPR018271; PTHR12360 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis elegans	genghis khan	3	P:GO:0009987; F:GO:0005488; F:GO:0016301	-		PTHR22988 (PANTHER), PTHR22988:SF2 (PANTHER)
Caenorhabditis elegans	genghis khan	3	P:GO:0009987; F:GO:0005488; F:GO:0016301	-		PTHR22988 (PANTHER), PTHR22988:SF2 (PANTHER)
	-	0				-

Caenorhabditis elegans	ubiquinone biosynthesis protein coq7 homolog	22	P:GO:0070584; F:GO:0046914; P:GO:0008340; P:GO:0000003; P:GO:0051094; P:GO:0001841; C:GO:0016020; P:GO:0040010; P:GO:0006744; P:GO:0001306; P:GO:0006355; P:GO:0030534; F:GO:0016491; P:GO:0048520; P:GO:0042775; P:GO:0042493; P:GO:0022008; C:GO:0005634; P:GO:0034599; P:GO:0001701; C:GO:0005739; P:GO:0019538	-		-
Caenorhabditis elegans	dynein heavy chain	5	P:GO:0007018; C:GO:0030286; F:GO:0016887; F:GO:0005524; F:GO:0003777	-		IPR003593; IPR011704; IPR013602; G3DSA:3.40.50.300 (GENE3D), PTHR10676 (PANTHER), PTHR10676:SF28 (PANTHER), SSF52540 (SUPERFAMILY)
Tribolium castaneum	isoform d	8	P:GO:0016321; F:GO:0004672; P:GO:0051225; P:GO:0007348; P:GO:0051299; P:GO:0000077; F:GO:0031151; C:GO:0005634	-		-
Caenorhabditis briggsae	suppressor of variegation 4-20 homolog 1	5	P:GO:0000003; F:GO:0042799; C:GO:0000780; P:GO:0006350; P:GO:0016571	-		-
Caenorhabditis briggsae	suppressor of variegation 4-20 homolog 1	5	P:GO:0000003; F:GO:0042799; C:GO:0000780; P:GO:0006350; P:GO:0016571	-		-
	-	0				-
Brugia malayi	negative elongation factor b homolog	0		F:GO:0003746; P:GO:0016481; C:GO:0005634		IPR010405; PTHR13503:SF1 (PANTHER)

Caenorhabditis briggsae	briggsae cbr-glit-1 protein	20	P:GO:0048666; F:GO:0030528; P:GO:0035220; P:GO:0007448; P:GO:0008544; P:GO:0006357; P:GO:0040010; P:GO:0007424; C:GO:0044424; P:GO:0030030; C:GO:0043234; P:GO:0007350; P:GO:0048522; P:GO:0009887; P:GO:0022403; P:GO:0048477; P:GO:0030855; P:GO:0007346; C:GO:0005886; F:GO:0005488	-		IPR002018; IPR019819; G3DSA:3.40.50.1820 (GENE3D), PTHR11559:SF32 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-bag-1 protein	4	P:GO:0006457; P:GO:0016049; P:GO:0006950; F:GO:0051087	-		IPR003103; G3DSA:1.20.58.120 (GENE3D), SSF63491 (SUPERFAMILY)
Caenorhabditis briggsae	translocase of inner mitochondrial membrane 22 homolog	6	P:GO:0009792; C:GO:0005743; F:GO:0005515; F:GO:0008565; C:GO:0016021; P:GO:0015031	-		IPR003397; PTHR14110 (PANTHER)
Caenorhabditis briggsae	translocase of inner mitochondrial membrane 22 homolog	6	P:GO:0009792; C:GO:0005743; F:GO:0005515; F:GO:0008565; C:GO:0016021; P:GO:0015031	-		-
Caenorhabditis briggsae	solute carrier family 35 member c2	4	C:GO:0016021; F:GO:0016491; F:GO:0008270; P:GO:0055085	-		IPR004853; IPR020904; PTHR11132 (PANTHER), SignalP (SIGNALP), SSF103481 (SUPERFAMILY)
Caenorhabditis briggsae	solute carrier family 35 member c2	4	C:GO:0016021; F:GO:0016491; F:GO:0008270; P:GO:0055085	-		IPR004853; IPR020904; PTHR11132 (PANTHER), SignalP (SIGNALP), SSF103481 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	P:GO:0009987	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		C:GO:0005666; P:GO:0006898; F:GO:0003677; P:GO:0002119; P:GO:0009792; P:GO:0016246; P:GO:0006383; P:GO:0040007; F:GO:0003899		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	spindle pole body	2	C:GO:0044444; F:GO:0005515	-		IPR005061; PTHR12161 (PANTHER), PTHR12161:SF3 (PANTHER)
	-	0				-

	-	0				SignalP (SIGNALP)
Canis familiaris	ribosomal protein l18a	5	F:GO:0003735; F:GO:0003723; F:GO:0005515; C:GO:0022625; P:GO:0006414	-		IPR002670; IPR021138; G3DSA:3.10.20.10 (GENE3D), PTHR10052 (PANTHER)
	-	0				-
Loa loa	bess motif family protein	3	F:GO:0008270; F:GO:0005515; F:GO:0003677	-		IPR006578
Loa loa	bess motif family protein	3	F:GO:0008270; F:GO:0005515; F:GO:0003677	-		IPR006578
Caenorhabditis briggsae	atp-dependent protease la	25	P:GO:0034619; F:GO:0004252; F:GO:0004176; F:GO:0070361; F:GO:0070363; F:GO:0070362; P:GO:0007568; P:GO:0010044; F:GO:0043531; P:GO:0070407; F:GO:0003697; C:GO:0042645; F:GO:0003727; C:GO:0005777; P:GO:0006515; F:GO:0070364; P:GO:0001666; F:GO:0070182; F:GO:0051880; P:GO:0007005; P:GO:0051260; P:GO:0006200; P:GO:0009725; F:GO:0005524; P:GO:0034599	-	EC:3.4.21.0	IPR001984; IPR008268; IPR008269; IPR020568; G3DSA:1.10.8.60 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR10046 (PANTHER), SSF52540 (SUPERFAMILY)
Loa loa	r--binding protein 12 (sh3 ww domain anchor protein in the nucleus)	1	F:GO:0005515	-		PTHR13976 (PANTHER), PTHR13976:SF1 (PANTHER), SignalP (SIGNALP), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; C:GO:0016020; F:GO:0008375		IPR003406; PTHR19297:SF3 (PANTHER)
	-	0				PR01217 (PRINTS)
Caenorhabditis elegans	lipopolysaccharide-induced tumor necrosis factor-alpha factor homolog	0				-
Caenorhabditis elegans	double-stranded r- binding motif family protein	2	P:GO:0007126; P:GO:0009792	-		IPR001159; IPR014720; PTHR10910 (PANTHER), PTHR10910:SF2 (PANTHER), SSF54768 (SUPERFAMILY)
Caenorhabditis elegans	double-stranded r- binding motif family protein	2	P:GO:0007126; P:GO:0009792	-		IPR001159; IPR014720; PTHR10910 (PANTHER), PTHR10910:SF2 (PANTHER), SSF54768 (SUPERFAMILY)
Caenorhabditis elegans	transcription factor mitochondrial	4	P:GO:0000154; C:GO:0042645; F:GO:0000179; F:GO:0005515	-		IPR001737; IPR020598; IPR023165; G3DSA:3.40.50.150 (GENE3D), SSF53335 (SUPERFAMILY)

Caenorhabditis briggsae	adipor-like receptor	6	F:GO:0042562; C:GO:0016021; F:GO:0004872; P:GO:0009755; P:GO:0050794; P:GO:0019395	-		IPR004254; PTHR20855:SF13 (PANTHER)
Caenorhabditis briggsae	adipor-like receptor	6	F:GO:0042562; C:GO:0016021; F:GO:0004872; P:GO:0009755; P:GO:0050794; P:GO:0019395	-		IPR004254; PTHR20855:SF13 (PANTHER)
	-	0				-
Caenorhabditis elegans	subfamily member 10	2	F:GO:0005515; P:GO:0009987	-		IPR005746; IPR012335; IPR012336; IPR013766; IPR015609; IPR017936; IPR017937; PTHR11821:SF16 (PANTHER)
Caenorhabditis elegans	integrin-linked protein ki-se	7	P:GO:0006468; P:GO:0007229; F:GO:0005515; F:GO:0016787; F:GO:0005524; P:GO:0009966; F:GO:0004674	-	EC:2.7.11.0	IPR002110; IPR020683; PTHR18958 (PANTHER)
Caenorhabditis elegans	zinc and double phd fingers family 2	3	F:GO:0046872; F:GO:0005515; C:GO:0005634	-		IPR001841; IPR001965; IPR007087; IPR011011; IPR013083; IPR015880; IPR019786; IPR019787; PTHR10615 (PANTHER), PTHR10615:SF9 (PANTHER)
Caenorhabditis briggsae	zinc and double phd fingers family 2	5	F:GO:0046872; P:GO:0045449; P:GO:0048644; F:GO:0005515; C:GO:0005634	-		PTHR10615 (PANTHER), PTHR10615:SF9 (PANTHER)
Caenorhabditis elegans	zinc and double phd fingers family 2	3	F:GO:0046872; F:GO:0005515; C:GO:0005634	-		-
Caenorhabditis elegans	clathrin coat assembly protein ap19	13	F:GO:0008565; P:GO:0006901; C:GO:0030130; C:GO:0008021; P:GO:0040007; P:GO:0000003; C:GO:0030131; P:GO:0002119; P:GO:0007269; F:GO:0005515; P:GO:0040011; P:GO:0006886; P:GO:0009792	-		IPR000804; IPR011012; IPR015604; IPR016635; IPR022775; G3DSA:3.30.450.60 (GENE3D), PTHR11753 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	zinc and double phd fingers family 2	3	F:GO:0046872; F:GO:0005515; C:GO:0005634	-		IPR001841; IPR001965; IPR007087; IPR011011; IPR013083; IPR015880; IPR019786; IPR019787; PTHR10615 (PANTHER), PTHR10615:SF9 (PANTHER)
Caenorhabditis elegans	chromosome 6 open reading frame 211	1	F:GO:0005515	-		IPR002791; PTHR12260 (PANTHER)
Caenorhabditis elegans	chromosome 6 open reading frame 211	1	F:GO:0005515	-		IPR002791; PTHR12260 (PANTHER)

Caenorhabditis elegans	bis(5 -nucleosyl)-tetraphosphatase	2	P:GO:0006917; F:GO:0004081	-	EC:3.6.1.17	IPR000086; IPR003565; IPR015797; IPR020084; PTHR21340 (PANTHER), PS51462 (PROFILE)
Caenorhabditis elegans	tgf-beta resistance-associated protein trag	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	phospholipase d1	11	P:GO:0001525; P:GO:0007265; F:GO:0004630; P:GO:0016042; C:GO:0044431; C:GO:0031090; P:GO:0006935; C:GO:0005768; P:GO:0008654; P:GO:0050830; F:GO:0005488	-	EC:3.1.4.4	SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-pld-1 protein	0		F:GO:0035091; P:GO:0008152; F:GO:0003824; P:GO:0007154; F:GO:0005515		IPR015679; PTHR18896:SF6 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-vit-4 protein	0		P:GO:0006869; F:GO:0005319; P:GO:0040010; P:GO:0009792; P:GO:0008340; F:GO:0005515		IPR015816; PTHR23345 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-vit-4 protein	0		P:GO:0006869; F:GO:0005319; P:GO:0040010; P:GO:0009792; P:GO:0008340; F:GO:0005515		IPR015816; PTHR23345 (PANTHER)
Callithrix jacchus	chromosome segregation protein smc	4	F:GO:0005488; C:GO:0043232; P:GO:0032501; N:GO:0071842	-		PD936484 (PRODOM)
Angiostrongylus cantonensis	pleiotropic regulator 1	5	P:GO:0018996; P:GO:0000003; P:GO:0040007; P:GO:0002119; P:GO:0040011	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR19923 (PANTHER)
Angiostrongylus cantonensis	pleiotropic regulator 1	5	P:GO:0002119; P:GO:0018996; P:GO:0000003; P:GO:0040007; P:GO:0040011	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR19923 (PANTHER)
Caenorhabditis briggsae	transcription elongation factor spt5	2	P:GO:0000003; P:GO:0007275	-		PTHR11125 (PANTHER)
Caenorhabditis elegans	rrn3 r- polymerase i transcription factor homolog	4	P:GO:0009987; P:GO:0008340; C:GO:0031981; P:GO:0000003	-		IPR007991
Caenorhabditis elegans	tb2 hva22 family protein	1	F:GO:0005515	-		IPR004345; PTHR12300:SF13 (PANTHER)
Caenorhabditis elegans	tb2 hva22 family protein	0		C:GO:0016021; C:GO:0016020		IPR004345; PTHR12300:SF13 (PANTHER)

Caenorhabditis briggsae	briggsae cbr-sec-8 protein	0		P:GO:0006904; C:GO:0000145; P:GO:0015031		-
Caenorhabditis elegans	briggsae cbr-gly-7 protein	5	F:GO:0004653; F:GO:0005529; C:GO:0005795; P:GO:0009312; C:GO:0016021	-	EC:2.4.1.41	IPR000772; IPR001173; IPR008997; G3DSA:2.80.10.50 (GENE3D), G3DSA:3.90.550.10 (GENE3D), PTHR11675 (PANTHER), SignalP (SIGNALP), SSF53448 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-gly-7 protein	5	F:GO:0004653; F:GO:0005529; C:GO:0005795; P:GO:0009312; C:GO:0016021	-	EC:2.4.1.41	IPR000772; IPR001173; IPR008997; G3DSA:2.80.10.50 (GENE3D), G3DSA:3.90.550.10 (GENE3D), PTHR11675 (PANTHER), SignalP (SIGNALP), SSF53448 (SUPERFAMILY)
Caenorhabditis elegans	s-phase ki-se-associated protein 2	0		F:GO:0016301; P:GO:0006511		IPR001810; G3DSA:3.80.10.10 (GENE3D), PTHR23125 (PANTHER), PTHR23125:SF34 (PANTHER), SSF52047 (SUPERFAMILY)
Caenorhabditis elegans	s-phase ki-se-associated protein 2	0		F:GO:0016301; P:GO:0006511		IPR001810; G3DSA:3.80.10.10 (GENE3D), PTHR23125 (PANTHER), PTHR23125:SF34 (PANTHER), SSF52047 (SUPERFAMILY)
Caenorhabditis briggsae	-dh dehydroge-se	5	F:GO:0008137; C:GO:0005747; P:GO:0055114; P:GO:0006091; P:GO:0001932	-	EC:1.6.5.3	IPR006885; G3DSA:3.30.160.190 (GENE3D), PTHR12219:SF7 (PANTHER)
Caenorhabditis elegans	r- binding motif protein 22	10	F:GO:0003723; C:GO:0005681; F:GO:0008270; C:GO:0005730; P:GO:0000060; P:GO:0008380; F:GO:0048306; F:GO:0000166; P:GO:0006397; C:GO:0005737	-		IPR000504; IPR012677; PTHR14089 (PANTHER), PTHR14089:SF4 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	sec23 protein	16	P:GO:0040010; P:GO:0030421; F:GO:0008270; C:GO:0000139; P:GO:0048821; P:GO:0032940; P:GO:0018996; P:GO:0002119; F:GO:0005515; C:GO:0030127; P:GO:0006888; C:GO:0048471; P:GO:0006898; P:GO:0006886; P:GO:0048477; P:GO:0048702	-		IPR006896; IPR006900; IPR007123; IPR012990; G3DSA:3.40.50.410 (GENE3D), PTHR11141 (PANTHER), SSF53300 (SUPERFAMILY), SSF81995 (SUPERFAMILY), SSF82754 (SUPERFAMILY)
	-	0				-
	-	0				-

Caenorhabditis elegans	39s ribosomal protein mitochondrial	9	P:GO:0009792; P:GO:0010171; P:GO:0002119; C:GO:0005761; F:GO:0003735; P:GO:0040010; P:GO:0000003; P:GO:0008340; P:GO:0006412	-	EC:3.6.5.3	IPR010729; PTHR21183:SF12 (PANTHER)
Caenorhabditis elegans	39s ribosomal protein mitochondrial	9	P:GO:0009792; P:GO:0010171; P:GO:0002119; C:GO:0005761; F:GO:0003735; P:GO:0040010; P:GO:0000003; P:GO:0008340; P:GO:0006412	-	EC:3.6.5.3	IPR010729; PTHR21183:SF12 (PANTHER)
Caenorhabditis briggsae	kiaa1688 protein	3	C:GO:0005856; P:GO:0007165; F:GO:0005515	-		IPR000198; IPR008936; PTHR23177 (PANTHER), PTHR23177:SF1 (PANTHER)
	-	0				-
Caenorhabditis elegans	rapamycin and fkbp12 target-1 partial	1	F:GO:0016740	-		IPR003151; IPR011989; IPR014009; IPR016024; PTHR11139 (PANTHER), PTHR11139:SF9 (PANTHER)
Caenorhabditis elegans	start domain containing 3	2	P:GO:0006629; C:GO:0044464	-		IPR000799; IPR002913; IPR019498; G3DSA:3.30.530.20 (GENE3D), PTHR12136 (PANTHER), PTHR12136:SF3 (PANTHER), SignalP (SIGNALP), SSF55961 (SUPERFAMILY)
Streptomyces avermitilis MA-4680	briggsae cbr-dao-5 protein	0		P:GO:0001503; C:GO:0005882; P:GO:0030261; F:GO:0003677; F:GO:0003924; F:GO:0005525; P:GO:0007155; F:GO:0005198; C:GO:0019867; P:GO:0007010; P:GO:0006413; P:GO:0006412; P:GO:0009405; F:GO:0000166; C:GO:0005737; F:GO:0003779; F:GO:0003743; C:GO:0005622		IPR017956
Caenorhabditis briggsae	-dh dehydroge-se 1 alpha subcomplex 2 variant 1	2	C:GO:0016020; C:GO:0005739	-		IPR007741; IPR012336; PTHR12878 (PANTHER)

Pongo abelii	low quality protein: guanine nucleotide-binding protein subunit beta-2-like 1-like	9	P:GO:0023034; P:GO:0008104; F:GO:0019903; C:GO:0005737; C:GO:0043025; F:GO:0004872; F:GO:0005102; F:GO:0005080; C:GO:0005886	-		IPR001680; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR19868 (PANTHER), SSF101908 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein F48E3.4 [Caenorhabditis elegans]	0		F:GO:0003824		IPR001254; IPR009003; G3DSA:2.40.10.10 (GENE3D), PTHR19355 (PANTHER), PTHR19355:SF135 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	ribosomal protein s17	13	P:GO:0006413; P:GO:0040010; P:GO:0006364; F:GO:0003735; P:GO:0034101; P:GO:0000003; P:GO:0006414; C:GO:0022627; P:GO:0042274; P:GO:0010171; P:GO:0002119; P:GO:0009792; P:GO:0040018	-		IPR001210; IPR018273; SSF116820 (SUPERFAMILY)
Caenorhabditis elegans	orotate phosphoribosyltransferase family protein	5	P:GO:0034404; C:GO:0005875; F:GO:0005515; P:GO:0046483; F:GO:0004588	-	EC:2.4.2.10	IPR000836; IPR004467; G3DSA:3.40.50.2020 (GENE3D), SSF53271 (SUPERFAMILY)
Caenorhabditis briggsae	upf0402 protein cg32590	0		F:GO:0003674; C:GO:0005575		-
Caenorhabditis elegans	hypothetical protein F29C12.3 [Caenorhabditis elegans]	0				PTHR13298 (PANTHER), PTHR13298:SF2 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG20694 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	Hypothetical protein CBG20694 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	Hypothetical protein CBG20694 [Caenorhabditis briggsae]	0				-
	-	0				-
Caenorhabditis brenneri	f-box lrr-repeat protein 20	0		F:GO:0005515; C:GO:0005575		G3DSA:3.80.10.10 (GENE3D), PTHR23125 (PANTHER), PTHR23125:SF32 (PANTHER), SSF52047 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein F32B5.6 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	hypothetical protein F32B5.6 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	F:GO:0005488; F:GO:0016301	-		IPR000719; IPR011009; IPR017441; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR22971 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	ethanolamine-phosphate cytidylyltransferase	3	P:GO:0006646; F:GO:0005515; F:GO:0004306	-	EC:2.7.7.14	-

Caenorhabditis briggsae	Hypothetical protein CBG12107 [Caenorhabditis briggsae]	0				-
Ostertagia ostertagi	two-domain activation associated secreted protein asp4 precursor	0		C:GO:0005576		-
Caenorhabditis briggsae	small nuclear ribonucleoprotein e	8	C:GO:0005683; C:GO:0005654; P:GO:0000387; C:GO:0005681; F:GO:0003723; F:GO:0005515; C:GO:0005829; P:GO:0000245	-		IPR001163; IPR006649; IPR010920; G3DSA:2.30.30.100 (GENE3D), PTHR11193 (PANTHER)
Loa loa	3-phosphoinositide dependent protein ki-se-1	1	F:GO:0016301	-		IPR000719; IPR011009; IPR015746; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22985 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Loa loa	nuclear receptor nhr-88	6	F:GO:0046872; F:GO:0004879; F:GO:0003677; P:GO:0045449; F:GO:0005515; P:GO:0019915	-		IPR001628; IPR008946; IPR013088; PR00350 (PRINTS), PTHR11865 (PANTHER), PTHR11865:SF197 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	C:GO:0044425	-		IPR002490; PTHR11629:SF23 (PANTHER)
Caenorhabditis elegans	glycyl-tr- synthetase	7	C:GO:0016021; P:GO:0006426; P:GO:0015966; F:GO:0005524; F:GO:0046983; C:GO:0005737; F:GO:0004820	-	EC:6.1.1.14	IPR000738; IPR002314; IPR002315; IPR009068; G3DSA:3.30.930.10 (GENE3D), SSF55681 (SUPERFAMILY)
Caenorhabditis elegans	vamp (vesicle-associated membrane protein)-associated protein like	8	C:GO:0005923; F:GO:0004871; P:GO:0043123; C:GO:0031982; P:GO:0006944; C:GO:0048471; F:GO:0046982; C:GO:0005789	-		IPR000535; IPR008962; PTHR10809 (PANTHER)
Brugia malayi	hypothetical protein Bm1_31440 [Brugia malayi]	0				-
	-	0				-
Haemonchus contortus	atp-binding sub-family b (mdr tap) member 4	12	P:GO:0055085; P:GO:0006629; F:GO:0008559; C:GO:0046581; C:GO:0000139; C:GO:0005624; F:GO:0005524; P:GO:0051384; F:GO:0005515; P:GO:0042493; C:GO:0016324; C:GO:0005887	-	EC:3.6.3.44	-

Caenorhabditis elegans	mevalo-te ki-se	16	C:GO:0005829; F:GO:0003729; P:GO:0017148; P:GO:0008340; C:GO:0005777; C:GO:0005625; P:GO:0019287; P:GO:0040007; F:GO:0042802; F:GO:0005524; P:GO:0002119; P:GO:0016310; P:GO:0040011; P:GO:0009792; F:GO:0004496; P:GO:0016126	-	EC:2.7.1.36	IPR006205; G3DSA:3.30.70.890 (GENE3D), PTHR10457 (PANTHER), SSF55060 (SUPERFAMILY)
Caenorhabditis elegans	lipb_caeel ame: full=liprin-beta ame: full=lar-interacting protein beta	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein C09D4.4 [Caenorhabditis elegans]	0		F:GO:0016788; P:GO:0006886; C:GO:0031227		-
Gallus gallus	PREDICTED: hypothetical protein [Gallus gallus]	0				-
Caenorhabditis briggsae	hypothetical kda protein in chromosome	0		P:GO:0000003; P:GO:0006898		SignalP (SIGNALP)
Caenorhabditis elegans	kiaa0564 protein	3	C:GO:0005622; F:GO:0017111; F:GO:0000166	-	EC:3.6.1.15	PTHR21610 (PANTHER), PTHR21610:SF3 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	propionyl- carboxylase	9	P:GO:0009792; P:GO:0002119; F:GO:0003723; F:GO:0004485; P:GO:0040010; F:GO:0004525; F:GO:0016740; F:GO:0004658; P:GO:0006396	-	EC:6.4.1.4; EC:3.1.26.3; EC:6.4.1.3	IPR000022; IPR011763; G3DSA:3.90.226.10 (GENE3D), PTHR22855 (PANTHER), PTHR22855:SF13 (PANTHER), SSF52096 (SUPERFAMILY)
Brugia malayi	bromodomain containing protein	0				PTHR22880 (PANTHER), PTHR22880:SF21 (PANTHER)
	-	0				-
Laccaria bicolor S238N-H82	protein	0				-
Caenorhabditis elegans	-d dehydroge-se	4	C:GO:0005737; P:GO:0006546; F:GO:0016491; F:GO:0004047	-	EC:2.1.2.10	IPR006076; IPR006222; G3DSA:3.50.50.60 (GENE3D), PTHR13847 (PANTHER), PTHR13847:SF16 (PANTHER), SSF103025 (SUPERFAMILY), SSF51905 (SUPERFAMILY), SSF54373 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein T27C4.1 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
Caenorhabditis elegans	a in (actin filament binding protein) homolog family member (afd-1)	3	C:GO:0030054; F:GO:0005515; P:GO:0040010	-		IPR000253; IPR001478; IPR002710; IPR008984; IPR018444; G3DSA:2.30.42.10 (GENE3D), PTHR10398 (PANTHER)
Caenorhabditis elegans	a in (actin filament binding protein) homolog family member (afd-1)	3	C:GO:0030054; F:GO:0005515; P:GO:0040010	-		IPR000253; IPR001478; IPR002710; IPR008984; IPR018444; G3DSA:2.30.42.10 (GENE3D), PTHR10398 (PANTHER)

Caenorhabditis elegans	a in (actin filament binding protein) homolog family member (afd-1)	3	C:GO:0030054; F:GO:0005515; P:GO:0040010	-		IPR000253; IPR001478; IPR002710; IPR008984; IPR018444; G3DSA:2.30.42.10 (GENE3D), PTHR10398 (PANTHER)
Caenorhabditis elegans	a in (actin filament binding protein) homolog family member (afd-1)	3	C:GO:0030054; F:GO:0005515; P:GO:0040010	-		IPR000253; IPR001478; IPR002710; IPR008984; IPR018444; G3DSA:2.30.42.10 (GENE3D), PTHR10398 (PANTHER)
Caenorhabditis elegans	a in (actin filament binding protein) homolog family member (afd-1)	3	C:GO:0030054; F:GO:0005515; P:GO:0040010	-		IPR000253; IPR001478; IPR002710; IPR008984; IPR018444; G3DSA:2.30.42.10 (GENE3D), PTHR10398 (PANTHER)
Caenorhabditis elegans	a in (actin filament binding protein) homolog family member (afd-1)	3	C:GO:0030054; F:GO:0005515; P:GO:0040010	-		IPR000253; IPR001478; IPR002710; IPR008984; IPR018444; G3DSA:2.30.42.10 (GENE3D), PTHR10398 (PANTHER)
Caenorhabditis briggsae	te-scin precursor	2	P:GO:0032501; C:GO:0044421	-		IPR000742; IPR002049; IPR006210; IPR013032; PR00011 (PRINTS), G3DSA:2.170.300.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF147 (PANTHER), SSF57196 (SUPERFAMILY)
Caenorhabditis elegans	beta chain spectrin	2	F:GO:0003779; C:GO:0044444	-		IPR001452; IPR002017; IPR018159; G3DSA:1.20.58.60 (GENE3D), G3DSA:2.30.30.40 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF48 (PANTHER), SSF46966 (SUPERFAMILY)
Loa loa	transmembrane protein 106b	0		F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150; C:GO:0005575		IPR009790
Loa loa	transmembrane protein 106b	0		F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150; C:GO:0005575		IPR009790
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Macaca mulatta	translocon-associated protein subunit beta precursor	4	C:GO:0005789; F:GO:0005048; P:GO:0006613; C:GO:0016021	-		IPR008856
	-	0				-
Caenorhabditis elegans	insulin-degrading enzyme	9	P:GO:0010815; F:GO:0008270; C:GO:0005777; F:GO:0004222; P:GO:0050435; P:GO:0006508; P:GO:0065007; F:GO:0042803; F:GO:0005524	-	EC:3.4.24.0	IPR007863; IPR011249; PTHR11851 (PANTHER), PTHR11851:SF64 (PANTHER)

Caenorhabditis briggsae	ap-2 complex subunit mu-1	9	P:GO:0016192; C:GO:0005829; F:GO:0008289; C:GO:0005778; P:GO:0050690; C:GO:0030122; F:GO:0005515; F:GO:0005215; P:GO:0006886	-		IPR001392; IPR008968; IPR015629; IPR018240; G3DSA:2.60.40.1170 (GENE3D), PTHR11998 (PANTHER)
Caenorhabditis briggsae	adenylosucci-te lyase	18	C:GO:0005829; F:GO:0004018; P:GO:0040010; P:GO:0018991; C:GO:0005625; C:GO:0005739; P:GO:0007584; P:GO:0040035; P:GO:0009168; P:GO:0010171; P:GO:0009060; P:GO:0002119; F:GO:0070626; P:GO:0040011; P:GO:0006997; P:GO:0006898; P:GO:0002009; P:GO:0009792	-	EC:4.3.2.2	IPR000362; IPR008948; IPR019468; IPR020557; IPR022761; G3DSA:1.20.200.10 (GENE3D), PTHR11444 (PANTHER), PTHR11444:SF2 (PANTHER)
Xenopus laevis	member ras oncogene family	15	C:GO:0005768; C:GO:0031410; F:GO:0019003; C:GO:0044446; F:GO:0005515; C:GO:0031090; P:GO:0046907; F:GO:0003924; P:GO:0007165; C:GO:0012505; P:GO:0009792; P:GO:0015031; C:GO:0005794; C:GO:0005783; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001806; IPR003579; IPR005225; IPR013753; IPR015601; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), SSF52540 (SUPERFAMILY)
Oryctolagus cuniculus	zinc finger protein 384	0		C:GO:0005925; F:GO:0003677; C:GO:0005634; F:GO:0003676; P:GO:0045941; F:GO:0008270; P:GO:0006913; C:GO:0005730; C:GO:0005622; F:GO:0046872; F:GO:0042156; P:GO:0045449; F:GO:0017124		-
	-	0				-
Caenorhabditis briggsae	lin-48 expression abnormal family member (lex-1)	1	P:GO:0009987	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR009673; SignalP (SIGNALP)

Caenorhabditis briggsae	Hypothetical protein CBG01085 [Caenorhabditis briggsae]	0		C:GO:0016021; C:GO:0016020		IPR007514
Loa loa	deoxycytidylate deami-se	2	F:GO:0008270; F:GO:0004132	-	EC:3.5.4.12	IPR002125; IPR015517; IPR016192; IPR016193; G3DSA:3.40.140.10 (GENE3D), PTHR11086:SF2 (PANTHER)
Caenorhabditis elegans	protein-tyrosine phosphatase containing protein	3	F:GO:0004725; P:GO:0006470; F:GO:0008138	-	EC:3.1.3.48	IPR000242; IPR000387; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF26 (PANTHER), SSF52799 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	swi snf-related matrix-associated actin-dependent regulator of chromatin subfamily a-like protein 1	8	P:GO:0016568; F:GO:0003678; P:GO:0006357; P:GO:0006259; F:GO:0003677; F:GO:0005524; F:GO:0008094; C:GO:0005634	-		-
Caenorhabditis elegans	swi snf-related matrix-associated actin-dependent regulator of chromatin subfamily a-like protein 1	8	P:GO:0016568; F:GO:0003678; P:GO:0006357; P:GO:0006259; F:GO:0003677; F:GO:0005524; F:GO:0008094; C:GO:0005634	-		PTHR10799 (PANTHER), PTHR10799:SF43 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				IPR000436; IPR016060; SignalP (SIGNALP)
Brugia malayi	ubiquitin-conjugating enzyme e2q family member 1	3	F:GO:0005515; P:GO:0070936; F:GO:0004842	-	EC:6.3.2.19	IPR016135; PTHR11621 (PANTHER), PTHR11621:SF6 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-ego-1 protein	1	F:GO:0005515	-		-
Caenorhabditis elegans	galactoside- 9	0		C:GO:0005737; F:GO:0005534; P:GO:0043123; F:GO:0004871; F:GO:0005529; C:GO:0005576		IPR001079; IPR008985; IPR013320
Caenorhabditis elegans	galactoside- 9	0		C:GO:0005737; F:GO:0005534; P:GO:0043123; F:GO:0004871; F:GO:0005529; C:GO:0005576		IPR001079; IPR008985; IPR013320
Caenorhabditis elegans	arp2 3 complex 20 kd subunit	11	P:GO:0043652; P:GO:0040010; C:GO:0005856; P:GO:0008360; P:GO:0016331; P:GO:0010631; P:GO:0030041; P:GO:0030866; F:GO:0003779; P:GO:0009792; P:GO:0030031	-		IPR008384; G3DSA:3.30.1460.20 (GENE3D), SSF69645 (SUPERFAMILY)

Caenorhabditis elegans	arp2 3 complex 20 kd subunit	11	P:GO:0043652; P:GO:0040010; C:GO:0005856; P:GO:0008360; P:GO:0016331; P:GO:0010631; P:GO:0030041; P:GO:0030866; F:GO:0003779; P:GO:0009792; P:GO:0030031	-		IPR008384; G3DSA:3.30.1460.20 (GENE3D), SSF69645 (SUPERFAMILY)
Loa loa	enhancer of yellow 2 transcription factor homolog	5	P:GO:0006810; C:GO:0000124; F:GO:0030374; P:GO:0016578; P:GO:0045893	-		IPR018783
Loa loa	sphingomyelin synthase-related 1	2	C:GO:0016021; P:GO:0006686	-		PTHR21290 (PANTHER), PTHR21290:SF7 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	thioredoxin domain-containing protein 15	0		F:GO:0003674; P:GO:0045454; C:GO:0016021; C:GO:0016020; C:GO:0005575; F:GO:0016853		IPR005746; IPR012335; IPR012336; IPR013766; PTHR10438:SF5 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	C:GO:0016021; F:GO:0005272; P:GO:0006814	-		-
Caenorhabditis elegans	sig-l recognition particle receptor alpha subunit	12	F:GO:0003729; C:GO:0005785; C:GO:0016021; F:GO:0004872; P:GO:0050708; F:GO:0005515; P:GO:0007409; F:GO:0003924; P:GO:0006614; C:GO:0005811; F:GO:0005525; F:GO:0005047	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000897; IPR003593; IPR013822; G3DSA:3.40.50.300 (GENE3D), PTHR11564 (PANTHER), PTHR11564:SF8 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	cleavage and polyadenylation specificity factor subunit 1	4	P:GO:0006378; C:GO:0005847; F:GO:0003723; P:GO:0006379	-		PTHR10644 (PANTHER), PTHR10644:SF2 (PANTHER)
Loa loa	der1-like domain member 1	7	P:GO:0030433; C:GO:0030176; F:GO:0042288; F:GO:0004872; P:GO:0019060; P:GO:0030968; P:GO:0030970	-		IPR007599
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0045132; F:GO:0003677; C:GO:0005634		PTHR19932 (PANTHER), PTHR19932:SF2 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0045132; F:GO:0003677; C:GO:0005634		PTHR19932 (PANTHER), PTHR19932:SF2 (PANTHER)

Caenorhabditis elegans	serine threonine-protein phosphatase pp1-beta catalytic subunit	18	P:GO:0005981; P:GO:0000003; F:GO:0005515; F:GO:0017018; P:GO:0051301; C:GO:0000164; C:GO:0005730; F:GO:0046872; P:GO:0009792; P:GO:0007067; P:GO:0005979; P:GO:0007126; P:GO:0002119; C:GO:0070688; P:GO:0006470; P:GO:0001889; P:GO:0016568; C:GO:0042587	-		IPR004843; IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF19 (PANTHER), SSF56300 (SUPERFAMILY)
Caenorhabditis elegans	serine threonine-protein phosphatase pp1-beta catalytic subunit	18	P:GO:0005981; P:GO:0000003; F:GO:0005515; F:GO:0017018; P:GO:0051301; C:GO:0000164; C:GO:0005730; F:GO:0046872; P:GO:0009792; P:GO:0007067; P:GO:0005979; P:GO:0007126; P:GO:0002119; C:GO:0070688; P:GO:0006470; P:GO:0001889; P:GO:0016568; C:GO:0042587	-		SignalP (SIGNALP)
Caenorhabditis elegans	serine threonine-protein phosphatase pp1-beta catalytic subunit	18	P:GO:0005981; P:GO:0000003; F:GO:0005515; F:GO:0017018; P:GO:0051301; C:GO:0000164; C:GO:0005730; F:GO:0046872; P:GO:0009792; P:GO:0007067; P:GO:0005979; P:GO:0007126; P:GO:0002119; C:GO:0070688; P:GO:0006470; P:GO:0001889; P:GO:0016568; C:GO:0042587	-		IPR004843; IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF19 (PANTHER), SSF56300 (SUPERFAMILY)

Caenorhabditis elegans	rap ran-gap family protein	5	F:GO:0005099; C:GO:0005622; P:GO:0051056; F:GO:0005515; P:GO:0007265	-		IPR000331; PTHR15711 (PANTHER), SSF111347 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0003674; P:GO:0008150; C:GO:0005575		IPR010342
Angiostrongylus cantonensis	osta2_caeel ame: full=organic solute transporter alpha-like protein	3	C:GO:0016021; P:GO:0006810; F:GO:0005215	-		-
Angiostrongylus cantonensis	organic solute transporter subunit alpha-like	3	C:GO:0016021; P:GO:0006810; F:GO:0005215	-		-
Angiostrongylus cantonensis	organic solute transporter subunit alpha-like	3	C:GO:0016021; P:GO:0006810; F:GO:0005215	-		-
Angiostrongylus cantonensis	organic solute transporter subunit alpha-like	3	C:GO:0016021; P:GO:0006810; F:GO:0005215	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	steroid dehydroge-se	8	F:GO:0001968; F:GO:0016491; P:GO:0010811; F:GO:0005518; P:GO:0008152; C:GO:0031012; F:GO:0008201; P:GO:0030198	-		IPR002198; IPR002347; IPR016040; IPR020904; PTHR19410:SF38 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	P:GO:0006810; C:GO:0016020	-		IPR011701; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11662 (PANTHER), PTHR11662:SF11 (PANTHER)
Caenorhabditis elegans	briggsae cbr-swan-1 protein	0				IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR19919 (PANTHER)
Dictyocaulus viviparus	acetylcholinesterase 2	6	F:GO:0004104; P:GO:0001507; F:GO:0003990; C:GO:0005623; P:GO:0040012; F:GO:0042803	-	EC:3.1.1.8; EC:3.1.1.7	IPR000997; IPR002018; IPR019826; G3DSA:3.40.50.1820 (GENE3D), PTHR11559:SF33 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)

Caenorhabditis elegans	d- polymerase alpha catalytic subunit	20	C:GO:0016363; P:GO:0000084; C:GO:0005730; F:GO:0003887; P:GO:0006303; F:GO:0003896; F:GO:0003677; P:GO:0006272; P:GO:0000731; C:GO:0000785; F:GO:0005515; P:GO:0006270; F:GO:0000166; C:GO:0005635; C:GO:0005658; P:GO:0006273; C:GO:0005654; P:GO:0008283; C:GO:0005737; F:GO:0003682	-	EC:2.7.7.7	IPR006134; IPR015088; IPR017964; G3DSA:3.90.1600.10 (GENE3D), PTHR10322 (PANTHER), PTHR10322:SF3 (PANTHER), SSF56672 (SUPERFAMILY)
Caenorhabditis elegans	ys44_caeel ame: full=uncharacterized protein	0				IPR017969
Caenorhabditis elegans	ys44_caeel ame: full=uncharacterized protein	0				IPR017969
Caenorhabditis elegans	tbc1 domain member 9 (with gram domain)	4	F:GO:0005097; F:GO:0005509; C:GO:0005622; P:GO:0032313	-		IPR000195; IPR011992; IPR018247; G3DSA:1.10.8.270 (GENE3D), PTHR22957 (PANTHER), PTHR22957:SF48 (PANTHER)
Caenorhabditis elegans	ancient ubiquitous protein 1	1	C:GO:0016020	-		IPR002123; PTHR15486 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0005515		-
Caenorhabditis elegans	chaperonin containing subunit 4	13	C:GO:0005737; P:GO:0009792; P:GO:0002119; P:GO:0006457; F:GO:0005524; P:GO:0000003; P:GO:0008340; F:GO:0051082; P:GO:0001666; P:GO:0040007; P:GO:0006898; P:GO:0040032; P:GO:0002009	-		IPR002423; IPR012717; IPR017998; G3DSA:1.10.560.10 (GENE3D), G3DSA:3.50.7.10 (GENE3D), SSF52029 (SUPERFAMILY)
Brugia malayi	germ cell-less homolog 1	3	P:GO:0009987; F:GO:0042802; C:GO:0044428	-		IPR011333; IPR011705; IPR013069; PTHR23231 (PANTHER), PTHR23231:SF2 (PANTHER)
Caenorhabditis briggsae	n-acetylglucosamine-6-phosphate deacetylase	3	P:GO:0005975; F:GO:0016810; F:GO:0005515	-		IPR006680; IPR011059; G3DSA:2.30.40.10 (GENE3D), G3DSA:3.20.20.140 (GENE3D), PTHR11113 (PANTHER), SSF51556 (SUPERFAMILY)
Callithrix jacchus	60s ribosomal protein l37a	6	C:GO:0005840; F:GO:0046872; F:GO:0003735; F:GO:0005515; C:GO:0005829; P:GO:0006414	-		-

Caenorhabditis elegans	major allergen	0				-
Brugia malayi	zinc c2h2 type family protein	1	F:GO:0005488	-		IPR007087; IPR015880
Brugia malayi	paz piwi domain-containing family member (ppw-1)	1	P:GO:0000003	-		-
Brugia malayi	briggsae cbr-pqn-85 protein	0		F:GO:0005488; P:GO:0034088; C:GO:0032116		-
Ostertagia ostertagi	cysteine synthase	12	C:GO:0005829; P:GO:0006565; P:GO:0019448; P:GO:0043418; C:GO:0005730; F:GO:0031625; F:GO:0004122; F:GO:0020037; P:GO:0070814; F:GO:0042803; F:GO:0030170; P:GO:0019344	-	EC:4.2.1.22	IPR001926; G3DSA:3.40.50.1100 (GENE3D), PTHR10314 (PANTHER), PTHR10314:SF8 (PANTHER)
	-	0				-
Homo sapiens	glutathione s-transferase pi	10	C:GO:0005737; P:GO:0007417; F:GO:0004364; P:GO:0006805; F:GO:0005515; P:GO:0006749; F:GO:0008144; P:GO:0006916; C:GO:0005634; F:GO:0043295	-	EC:2.5.1.18	IPR004046; IPR010987; IPR017933; PTHR11571 (PANTHER), PTHR11571:SF2 (PANTHER)
Brugia malayi	elegans protein partially confirmed by transcript evidence	6	P:GO:0040010; F:GO:0005488; P:GO:0008340; F:GO:0004672; P:GO:0040017; C:GO:0016020	-		IPR000719; IPR001245; IPR008266; IPR011009; IPR017441; IPR020635; IPR020685; IPR020733; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
Caenorhabditis elegans	b chain reactivity modulation of human branched-chain alpha- ketoacid dehydroge-se by an inter-l molecular switch	15	F:GO:0003826; P:GO:0040010; P:GO:0009083; C:GO:0005743; F:GO:0003863; P:GO:0055114; P:GO:0007584; P:GO:0000003; F:GO:0032403; P:GO:0051384; P:GO:0040011; C:GO:0005947; P:GO:0009792; F:GO:0016831; P:GO:0051591	-	EC:1.2.4.4; EC:4.1.1.0	IPR005475; IPR005476; IPR009014; IPR015941; G3DSA:3.40.50.970 (GENE3D), PTHR11624 (PANTHER), PTHR11624:SF21 (PANTHER), SSF52518 (SUPERFAMILY)
Caenorhabditis briggsae	zinc finger protein 706	3	C:GO:0005622; P:GO:0040010; F:GO:0008270	-		-
Caenorhabditis elegans	gpi mannosyltransferase 1	5	P:GO:0000003; P:GO:0016254; F:GO:0016758; C:GO:0005783; C:GO:0044425	-	EC:2.4.1.0	IPR007704; SignalP (SIGNALP)

	-	0				SignalP (SIGNALP)
Brugia malayi	hypothetical protein [Brugia malayi]	4	P:GO:0040007; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		PTHR21663 (PANTHER)
Brugia malayi	family with sequence similarity member a	2	P:GO:0000003; P:GO:0008340	-		IPR018797
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		-
Brugia malayi	t-complex 11 like 1	0				IPR008862; PTHR12832:SF6 (PANTHER)
Brugia malayi	cell division protein ki-se 13-like	6	P:GO:0006468; P:GO:0008284; P:GO:0007275; P:GO:0007088; F:GO:0005524; F:GO:0004693	-	EC:2.7.11.22	IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF112 (PANTHER)
Brugia malayi	microtubule binding protein	1	F:GO:0008017	-		IPR001715; PTHR10623 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	tubulin folding cofactor e-like protein family member (coel-1)	0				-
Caenorhabditis elegans	tubulin folding cofactor e-like	0		F:GO:0003674; C:GO:0005737; C:GO:0005856; P:GO:0008150; C:GO:0005575		G3DSA:3.80.10.10 (GENE3D), PTHR15140 (PANTHER), SSF52058 (SUPERFAMILY)
Caenorhabditis elegans	arginine ki-se	3	C:GO:0016021; F:GO:0005524; F:GO:0004054	-	EC:2.7.3.3	IPR000749; IPR014746; IPR022413; IPR022414; PTHR11547:SF13 (PANTHER), SignalP (SIGNALP), SSF55931 (SUPERFAMILY)
Caenorhabditis briggsae	trafficking protein particle complex 3	11	C:GO:0005829; F:GO:0004383; C:GO:0000139; C:GO:0030008; P:GO:0000003; F:GO:0005515; P:GO:0006888; F:GO:0020037; P:GO:0009792; C:GO:0005783; P:GO:0006182	-	EC:4.6.1.2	IPR007194; IPR011644; G3DSA:3.30.1380.20 (GENE3D), PTHR13048 (PANTHER)
Caenorhabditis elegans	cardiac calsequestrin	1	F:GO:0005509	-		IPR001393; IPR012335; IPR012336
Caenorhabditis elegans	wd40 protein	3	P:GO:0009792; P:GO:0040035; F:GO:0005515	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR22847 (PANTHER), PTHR22847:SF44 (PANTHER)
Caenorhabditis elegans	wd40 protein	3	P:GO:0009792; P:GO:0040035; F:GO:0005515	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR22847 (PANTHER), PTHR22847:SF44 (PANTHER)
Caenorhabditis elegans	wd40 protein	3	P:GO:0009792; P:GO:0040035; F:GO:0005515	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR22847 (PANTHER), PTHR22847:SF44 (PANTHER)
	-	0				-
	-	0				-

Caenorhabditis briggsae	briggsae cbr-fhod-1 protein	0		F:GO:0005488; F:GO:0003779; P:GO:0016043; P:GO:0030036		PTHR23213 (PANTHER), PTHR23213:SF3 (PANTHER)
	-	0				-
Loa loa	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		PTHR13976 (PANTHER), PTHR13976:SF1 (PANTHER)
Brugia malayi	ran gtpase activating protein 1	4	C:GO:0005643; C:GO:0005625; C:GO:0000776; F:GO:0005515	-		G3DSA:3.80.10.10 (GENE3D), PTHR13824 (PANTHER), PTHR13824:SF8 (PANTHER), SSF52047 (SUPERFAMILY)
Brugia malayi	ran gtpase activating protein 1	4	C:GO:0005643; C:GO:0005625; C:GO:0000776; F:GO:0005515	-		G3DSA:3.80.10.10 (GENE3D), PTHR13824 (PANTHER), PTHR13824:SF8 (PANTHER), SSF52047 (SUPERFAMILY)
synthetic construct	beta-2-microglobulin	12	C:GO:0031901; P:GO:0002474; C:GO:0009897; C:GO:0000139; C:GO:0005615; P:GO:0002481; F:GO:0005515; P:GO:0002237; P:GO:0001916; P:GO:0042493; P:GO:0046686; C:GO:0042612	-		IPR003006; IPR003597; IPR007110; IPR013783; IPR015707; PTHR19944 (PANTHER), SignalP (SIGNALP), SSF48726 (SUPERFAMILY)
Caenorhabditis briggsae	polymerase iii (d- directed) polypeptide e	7	P:GO:0040010; P:GO:0000003; P:GO:0002119; P:GO:0040011; P:GO:0006898; P:GO:0009792; P:GO:0016246	-		IPR006886; PTHR12069 (PANTHER)
Caenorhabditis elegans	hypothetical protein C04E6.11 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	conserved hypothetical atp binding protein	2	F:GO:0005515; F:GO:0000166	-		-
Caenorhabditis sp. PS1010	gtp-binding protein alpha g-	14	P:GO:0016199; F:GO:0004871; P:GO:0043052; P:GO:0007602; P:GO:0002385; P:GO:0007202; C:GO:0005834; P:GO:0016056; C:GO:0016027; F:GO:0005525; P:GO:0006471; P:GO:0046673; F:GO:0003924; P:GO:0007608	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000654; IPR001019; IPR011025; G3DSA:3.40.50.300 (GENE3D), PTHR10218:SF84 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	heat shock 10kd protein 1	5	P:GO:0009792; P:GO:0006457; P:GO:0006950; C:GO:0005759; F:GO:0005524	-		IPR011032; IPR018369; IPR020818

Loa loa	atp synthase subunit mitochondrial	5	P:GO:0040010; P:GO:0000003; P:GO:0002119; P:GO:0040039; P:GO:0009792	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR000859; PTHR10127 (PANTHER), PTHR10127:SF33 (PANTHER)
Caenorhabditis elegans	calcineurin b	11	P:GO:0006470; C:GO:0005829; P:GO:0008633; F:GO:0005516; P:GO:0001837; P:GO:0060487; F:GO:0005509; P:GO:0034504; P:GO:0007507; C:GO:0005955; F:GO:0004723	-		IPR001125; IPR002048; IPR011992; IPR018247; IPR018248; IPR018249; PTHR23056 (PANTHER), PTHR23056:SF4 (PANTHER), SSF47473 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-npp-19 protein	0				PTHR21527 (PANTHER), PTHR21527:SF1 (PANTHER)
	-	0				-
Brugia malayi	cytoplasmic polyadenylation element binding protein	0		F:GO:0003723; F:GO:0003676; P:GO:0030154; P:GO:0007275; F:GO:0000166; P:GO:0007283		IPR000504; IPR012677; PTHR12566 (PANTHER), SSF54928 (SUPERFAMILY)
Tribolium castaneum	chromobox protein	0		F:GO:0003682; C:GO:0000785; P:GO:0006333; C:GO:0005634		G3DSA:2.40.50.40 (GENE3D)
	-	0				G3DSA:2.40.50.40 (GENE3D)
Tribolium castaneum	chromobox protein	0		F:GO:0003682; C:GO:0000785; P:GO:0006333; C:GO:0005634		G3DSA:2.40.50.40 (GENE3D)
Loa loa	briggsae cbr-sym-2 protein	2	F:GO:0003676; P:GO:0006396	-		IPR000504; IPR012677; PTHR13976 (PANTHER), PTHR13976:SF2 (PANTHER), SSF54928 (SUPERFAMILY)
Ostertagia ostertagi	l3 es protein	0				SignalP (SIGNALP)
	-	0				-
Danio rerio	hla-b-associated transcript 3-like	0		F:GO:0005515		-
	-	0				-
Caenorhabditis elegans	aminopeptidase n	0		C:GO:0043231; F:GO:0051537		IPR006622; IPR018967
Drosophila ananassae	b chain crystal structure of a pyrimidine degrading enzyme from drosophila melanogaster	3	F:GO:0003837; P:GO:0006208; P:GO:0006207	-	EC:3.5.1.6	-

Caenorhabditis elegans	member of ras oncogene family	11	P:GO:0030336; C:GO:0055038; F:GO:0005515; P:GO:0034613; C:GO:0005829; P:GO:0045184; P:GO:0031954; P:GO:0031532; F:GO:0003924; P:GO:0048814; P:GO:0046328	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001806; IPR013753; IPR020849; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF304 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	3	P:GO:0019915; P:GO:0008152; F:GO:0016740	-		IPR002213; G3DSA:3.40.50.2000 (GENE3D), PTHR11926:SF3 (PANTHER), SSF53756 (SUPERFAMILY)
Ixodes scapularis	f-box only protein 28	0				IPR001810; IPR022364; G3DSA:1.20.1280.50 (GENE3D), PTHR13252 (PANTHER), PTHR13252:SF2 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG11709 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	hypothetical protein F09E10.6 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	briggsae cbr-sdn-1 protein	2	F:GO:0008092; C:GO:0016021	-		SignalP (SIGNALP)
Caenorhabditis briggsae	u4 tri-snrnp-associated protein 2	13	P:GO:0006396; P:GO:0006511; F:GO:0004221; F:GO:0008270; C:GO:0005622; P:GO:0040007; P:GO:0040035; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0006898; P:GO:0002009; P:GO:0009792	-	EC:3.1.2.15	-
Caenorhabditis elegans	calcium atpase	6	F:GO:0005388; P:GO:0006754; F:GO:0005524; F:GO:0005515; P:GO:0006816; C:GO:0005887	-	EC:3.6.3.8	-
	-	0				-
Caenorhabditis elegans	er degradation mannosidase alpha-like 1	7	P:GO:0030433; C:GO:0030176; F:GO:0005509; F:GO:0051787; F:GO:0004571; P:GO:0006986; F:GO:0004559	-	EC:3.2.1.113; EC:3.2.1.24	IPR001382; PTHR11742:SF11 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	-dph-cytochrome p450 reductase	6	F:GO:0005488; F:GO:0003958; P:GO:0044237; P:GO:0032770; P:GO:0055114; C:GO:0005783	-	EC:1.6.2.4	IPR001094; IPR001433; IPR001709; IPR003097; IPR008254; IPR015702; IPR017927; IPR017938; IPR023173; G3DSA:2.40.30.10 (GENE3D), G3DSA:3.40.50.360 (GENE3D), G3DSA:3.40.50.80 (GENE3D), PTHR19384 (PANTHER), SSF52218 (SUPERFAMILY), SSF52343 (SUPERFAMILY)

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				PTHR13167 (PANTHER), PTHR13167:SF6 (PANTHER)
Caenorhabditis elegans	variable abnormal morphology family member (vab-10)	11	P:GO:0000226; P:GO:0007424; P:GO:0065008; P:GO:0007409; P:GO:0007517; C:GO:0005874; F:GO:0008092; P:GO:0035239; P:GO:0051128; P:GO:0048523; C:GO:0044444	-		G3DSA:1.20.58.60 (GENE3D), SSF46966 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	wd-40 repeat protein	0		F:GO:0004252; P:GO:0006952; C:GO:0016020; F:GO:0043565; F:GO:0003677; C:GO:0005634; F:GO:0030528; P:GO:0006915; F:GO:0005524; F:GO:0003824; P:GO:0006508; F:GO:0003743; P:GO:0045449		SignalP (SIGNALP)
Loa loa	transcriptio-l sir2 family protein	14	F:GO:0070403; F:GO:0008270; P:GO:0045843; P:GO:0007049; P:GO:0006476; F:GO:0035035; C:GO:0005874; F:GO:0042903; F:GO:0043130; F:GO:0017136; F:GO:0008134; P:GO:0016481; C:GO:0005737; F:GO:0042826	-		IPR003000; G3DSA:3.30.1600.10 (GENE3D), G3DSA:3.40.50.1220 (GENE3D), SSF52467 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-cul-5 protein	6	P:GO:0006511; P:GO:0007528; C:GO:0031461; F:GO:0031625; P:GO:0016360; F:GO:0016931	-		IPR001373; IPR011991; IPR016158; G3DSA:4.10.1030.10 (GENE3D), PTHR11932 (PANTHER), PTHR11932:SF16 (PANTHER)
Caenorhabditis briggsae	tb2 hva22 family protein	1	F:GO:0005515	-		IPR004345; PTHR12300:SF13 (PANTHER)
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
	-	0				-

Caenorhabditis elegans	neurotransmitter-gated ion-channel ligand binding domain containing protein	5	C:GO:0016021; C:GO:0030054; C:GO:0045211; F:GO:0005230; P:GO:0006811	-		IPR006028; IPR006029; IPR006201; IPR006202; IPR018000; G3DSA:1.20.120.370 (GENE3D), PTHR18945:SF12 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	sb:cb283 protein	0		P:GO:0006508; F:GO:0004177; C:GO:0005622		IPR000819; G3DSA:3.40.630.10 (GENE3D), PTHR11963 (PANTHER), PTHR11963:SF2 (PANTHER), SignalP (SIGNALP), SSF53187 (SUPERFAMILY)
Caenorhabditis elegans	sb:cb283 protein	0		P:GO:0006508; F:GO:0004177; C:GO:0005622		IPR000819; G3DSA:3.40.630.10 (GENE3D), PTHR11963 (PANTHER), PTHR11963:SF2 (PANTHER), SignalP (SIGNALP), SSF53187 (SUPERFAMILY)
Caenorhabditis elegans	sb:cb283 protein	0		P:GO:0006508; F:GO:0004177; C:GO:0005622		IPR000819; G3DSA:3.40.630.10 (GENE3D), PTHR11963 (PANTHER), PTHR11963:SF2 (PANTHER), SignalP (SIGNALP), SSF53187 (SUPERFAMILY)
	-	0				-
	-	0				-
Tribolium castaneum	r- polymerase-associated protein leo1	10	P:GO:0030318; P:GO:0033523; P:GO:0010390; P:GO:0007507; C:GO:0016593; P:GO:0050936; P:GO:0021782; P:GO:0014032; F:GO:0005515; P:GO:0006350	-		IPR007149; PTHR23146 (PANTHER)
Caenorhabditis brenneri	myelinprotein expression factor	3	F:GO:0003729; F:GO:0005515; C:GO:0044424	-		-
Caenorhabditis elegans	leucine-rich repeat serine threonine-protein ki-se 1	2	F:GO:0016301; F:GO:0000166	-		-
Caenorhabditis briggsae	protein ki-se domain containing protein	4	P:GO:0006468; F:GO:0005524; P:GO:0040011; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
	-	0				-
Caenorhabditis elegans	hypothetical protein F52E1.9 [Caenorhabditis elegans]	0				-
Equus caballus	fibrous sheath cabyr binding protein	0		C:GO:0005882		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	ph domain containing protein	2	C:GO:0005886; F:GO:0005488	-		IPR001849; IPR011993; SSF50729 (SUPERFAMILY)

Caenorhabditis elegans	briggsae cbr-apb-1 protein	21	P:GO:0000003; P:GO:0007522; F:GO:0005515; P:GO:0040007; P:GO:0006898; P:GO:0007269; F:GO:0008565; P:GO:0007507; P:GO:0016183; P:GO:0007494; P:GO:0006886; P:GO:0009792; F:GO:0003705; F:GO:0043565; P:GO:0010551; P:GO:0002119; C:GO:0008021; P:GO:0007501; C:GO:0030121; C:GO:0005886; C:GO:0005634	-		IPR002553; IPR011989; IPR016024; PTHR11134 (PANTHER), PTHR11134:SF3 (PANTHER)
Caenorhabditis briggsae	rain ki-se homolog family member (mbk-2)	9	P:GO:0006468; P:GO:0050896; F:GO:0005515; P:GO:0007275; F:GO:0004713; C:GO:0005938; F:GO:0005524; P:GO:0007608; F:GO:0004674	-	EC:2.7.10.0; EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF22 (PANTHER)
Caenorhabditis briggsae	rain ki-se homolog family member (mbk-2)	13	F:GO:0030145; P:GO:0006468; P:GO:0045725; F:GO:0005515; P:GO:0007275; F:GO:0004713; P:GO:0042771; F:GO:0004674; F:GO:0000287; C:GO:0005634; F:GO:0005524; P:GO:0007608; C:GO:0005938	-	EC:2.7.10.0; EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF22 (PANTHER)
Caenorhabditis briggsae	rain ki-se homolog family member (mbk-2)	9	P:GO:0006468; P:GO:0050896; F:GO:0005515; P:GO:0007275; F:GO:0004713; C:GO:0005938; F:GO:0005524; P:GO:0007608; F:GO:0004674	-	EC:2.7.10.0; EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF22 (PANTHER)
Caenorhabditis elegans	glycosylation related family member (gly-5)	1	F:GO:0005515	-		SignalP (SIGNALP)

Caenorhabditis elegans	nucleolar protein 14	8	P:GO:0000462; C:GO:0005730; P:GO:0000479; C:GO:0030686; P:GO:0002119; C:GO:0044444; P:GO:0006898; P:GO:0009792	-		IPR007276
Caenorhabditis elegans	protein ki-se	5	P:GO:0009987; F:GO:0004674; F:GO:0005515; F:GO:0000166; C:GO:0044424	-	EC:2.7.11.0	IPR000719; IPR008266; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11042 (PANTHER), PTHR11042:SF4 (PANTHER)
Caenorhabditis elegans	ring finger-containing	2	F:GO:0046872; C:GO:0005622	-		IPR000315; IPR001298; IPR001841; IPR011042; IPR013083; IPR013783; IPR014756; IPR017868; IPR017907; PTHR13712 (PANTHER), PTHR13712:SF61 (PANTHER), SSF101898 (SUPERFAMILY), SSF57850 (SUPERFAMILY)
	-	0				PR01217 (PRINTS), SignalP (SIGNALP)
	-	0				PR01217 (PRINTS), SignalP (SIGNALP)
Loa loa	homeodomain interacting protein ki-se protein isoform	0		F:GO:0016301; F:GO:0004672; F:GO:0005524; F:GO:0000166; P:GO:0006468; F:GO:0003677; F:GO:0004674		-
Loa loa	hypothetical protein LOAG_00607 [Loa loa]	0				-
Caenorhabditis briggsae	transmembrane and coiled-coil domains 4	1	C:GO:0016020	-		IPR007941; G3DSA:3.40.50.1820 (GENE3D), SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-mog-4 protein	7	F:GO:0004004; F:GO:0003676; F:GO:0005515; C:GO:0071011; F:GO:0005524; P:GO:0000398; C:GO:0071013	-		-
Caenorhabditis elegans	acyl ydroge-se family member (acdh-13)	6	P:GO:0009792; F:GO:0016491; P:GO:0040010; P:GO:0000003; P:GO:0008152; P:GO:0006898	-		IPR009075; IPR009100; PTHR10909 (PANTHER), PTHR10909:SF9 (PANTHER)
Loa loa	small family member (sma-9)	1	F:GO:0005515	-		IPR007087; IPR013087; IPR015880; PTHR23233 (PANTHER), PTHR23233:SF13 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG18472 [Caenorhabditis briggsae]	0				-
	-	0				SignalP (SIGNALP)
	-	0				IPR003582
Caenorhabditis elegans	gastric cancer antigen zg14 homolog	0		F:GO:0003723; F:GO:0003676; C:GO:0005737; F:GO:0000166; C:GO:0005634		PTHR13191 (PANTHER), SignalP (SIGNALP)
	-	0				-

Ancylostoma ceylanicum	tissue factor pathway inhibitor	1	F:GO:0030414	-		IPR002223; IPR020901; PTHR10083 (PANTHER), PTHR10083:SF39 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-csn-3 protein	0				-
	-	0				-
Necator americanus	briggsae cbr-gst- protein	4	P:GO:0008340; P:GO:0040010; F:GO:0005515; F:GO:0016740	-		IPR004045; IPR012335; IPR012336; PTHR11571 (PANTHER), PTHR11571:SF6 (PANTHER)
	-	0				-
Caenorhabditis elegans	prion-like-(q n-rich)-domain-bearing protein family member (pqn-52)	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	prion-like-(q n-rich)-domain-bearing protein family member (pqn-52)	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Ornithorhynchus anatinus	ribosomal protein s15	11	F:GO:0003723; P:GO:0006364; F:GO:0003735; P:GO:0006414; C:GO:0022627; P:GO:0000056; F:GO:0003677; F:GO:0005515; P:GO:0000028; C:GO:0005654; P:GO:0009790	-		-
	-	0				-
Micromonas pusilla CCMP1545	mkiaa0176 protein	0		F:GO:0005249; C:GO:0016020; P:GO:0006813; F:GO:0005515; C:GO:0008076		IPR003131; IPR011333; PTHR11145 (PANTHER)
Caenorhabditis elegans	epsin 2	9	P:GO:0009792; P:GO:0002119; F:GO:0005515; P:GO:0040017; P:GO:0040010; P:GO:0000003; P:GO:0019915; P:GO:0006898; P:GO:0051729	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR016181
Caenorhabditis briggsae	iator family member (mdt-28)	0				IPR021640
Caenorhabditis elegans	lysozyme	5	C:GO:0005576; P:GO:0050830; P:GO:0009792; F:GO:0003796; P:GO:0050829	-	EC:3.2.1.17	IPR008597; PTHR11195:SF7 (PANTHER), SignalP (SIGNALP), SSF53955 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-tag-141 protein	0		C:GO:0016021; C:GO:0016020; P:GO:0055085; P:GO:0030001; F:GO:0046873		IPR003689; PTHR16950 (PANTHER), PTHR16950:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	zinc transporter zip6-like	3	C:GO:0005768; C:GO:0016020; P:GO:0030001	-		IPR003689; PTHR16950 (PANTHER), PTHR16950:SF1 (PANTHER), SignalP (SIGNALP)
	-	0				-

	-	0				-
Saccoglossus kowalevskii	cyclin-dependent ki-se 3	17	P:GO:0000278; P:GO:0000003; F:GO:0005515; F:GO:0000166; P:GO:0040018; P:GO:0040011; P:GO:0008283; P:GO:0040002; P:GO:0018996; P:GO:0009792; P:GO:0002009; F:GO:0004674; P:GO:0002119; C:GO:0043229; P:GO:0022403; P:GO:0010171; P:GO:0048523	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF109 (PANTHER)
Ciona intestinalis	PREDICTED: similar to F36H2.3 [Cio- intesti-lis]	0				IPR000436; IPR016060
Caenorhabditis elegans	trimethylguanosine synthase-like	12	C:GO:0030532; P:GO:0001510; P:GO:0040010; P:GO:0000387; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0071167; F:GO:0071164; P:GO:0009792; C:GO:0005737; P:GO:0016246	-		IPR019012; G3DSA:3.40.50.150 (GENE3D), PTHR14741 (PANTHER), PTHR14741:SF4 (PANTHER), SSF53335 (SUPERFAMILY)
	-	0				-
Burkholderia phymatum STM815	hypothetical protein Bphy_1520 [Burkholderia phymatum STM815]	0				-
	-	0				-
Caenorhabditis elegans	pq-loop repeat-containing protein 1	1	P:GO:0019915	-		PTHR14856 (PANTHER), PTHR14856:SF5 (PANTHER), PF04193 (PFAM), SignalP (SIGNALP)
Homo sapiens	PREDICTED: hypothetical protein [Homo sapiens]	0				-
	-	0				-
	-	0				IPR016186
Angiostrongylus cantonensis	trafficking protein particle complex subunit 6b	3	P:GO:0006182; F:GO:0020037; F:GO:0004383	-	EC:4.6.1.2	IPR007194; IPR011644; G3DSA:3.30.1380.20 (GENE3D), PTHR12817 (PANTHER)
Loa loa	hypothetical protein LOAG_09794 [Loa loa]	0				SignalP (SIGNALP)
Caenorhabditis elegans	acyl- synthetase long-chain family member 4	7	P:GO:0060136; P:GO:0050896; P:GO:0006631; F:GO:0004467; C:GO:0031090; C:GO:0044446; C:GO:0005739	-	EC:6.2.1.3	IPR000873; IPR020459; IPR020845; G3DSA:3.40.50.980 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF8 (PANTHER), SignalP (SIGNALP), SSF56801 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG18375 [Caenorhabditis briggsae]	0		C:GO:0016020; F:GO:0008158		-
Caenorhabditis briggsae	resistance-nodulation-cell division superfamily transporter	2	F:GO:0008158; C:GO:0016020	-		PTHR10796 (PANTHER), PTHR10796:SF13 (PANTHER), SSF82866 (SUPERFAMILY)
	-	0				-

Caenorhabditis briggsae	Hypothetical protein CBG18375 [Caenorhabditis briggsae]	0		C:GO:0016020; F:GO:0008158		-
Caenorhabditis briggsae	resistance-nodulation-cell division superfamily transporter	0		C:GO:0016021; P:GO:0051301; C:GO:0016020; F:GO:0005215; P:GO:0006810; F:GO:0008158		PTHR10796 (PANTHER), PTHR10796:SF13 (PANTHER), SSF82866 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG18375 [Caenorhabditis briggsae]	0		C:GO:0016020; F:GO:0008158		-
Loa loa	cxxc zinc finger family protein	8	P:GO:0016568; F:GO:0046872; P:GO:0006355; F:GO:0018024; P:GO:0040029; F:GO:0005515; P:GO:0043414; C:GO:0005634	-	EC:2.1.1.43	IPR001525; IPR002857; PTHR10629:SF6 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	protein geranylgeranyltransferase type beta subunit	13	F:GO:0004662; F:GO:0008144; F:GO:0042277; P:GO:0045787; P:GO:0051789; F:GO:0008270; P:GO:0051774; C:GO:0005953; F:GO:0005515; P:GO:0034097; P:GO:0008284; P:GO:0018348; F:GO:0019840	-	EC:2.5.1.59	IPR001330; IPR008930; G3DSA:1.50.10.20 (GENE3D), PTHR11774 (PANTHER), PTHR11774:SF4 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-ani-2 protein	0		F:GO:0005515		-
Caenorhabditis briggsae	briggsae cbr-ani-2 protein	0		F:GO:0005515		-
Caenorhabditis briggsae	briggsae cbr-ani-2 protein	0		F:GO:0005515		-
Caenorhabditis elegans	survival of motor neuron-related-splicing factor 30	1	P:GO:0000003	-		PTHR12664 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	4930438o05rik protein	0		F:GO:0003674; F:GO:0005488; P:GO:0008150; C:GO:0005575		-
	-	0				-
Caenorhabditis elegans	set and mynd domain-containing protein 1	0		P:GO:0006338; F:GO:0003677; C:GO:0005634; C:GO:0005737; F:GO:0008270; P:GO:0007507; F:GO:0005515; F:GO:0003714; F:GO:0046872; P:GO:0006350; P:GO:0016481; P:GO:0045449		PTHR12197 (PANTHER), PTHR12197:SF9 (PANTHER)

Loa loa	ero1-like beta (cerevisiae)	10	C:GO:0005789; P:GO:0006467; P:GO:0002119; F:GO:0016671; F:GO:0005515; P:GO:0055114; P:GO:0000003; P:GO:0008340; F:GO:0050660; P:GO:0040007	-	EC:1.8.4.0	IPR007266
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	2	P:GO:0008104; F:GO:0003676	-		SignalP (SIGNALP)
Caenorhabditis briggsae	atp-binding cassette sub-family e member 1	11	P:GO:0040035; P:GO:0009792; P:GO:0010171; P:GO:0002119; F:GO:0016887; F:GO:0051536; F:GO:0009055; P:GO:0040010; F:GO:0005524; P:GO:0040011; C:GO:0005739	-		IPR001450; IPR003439; IPR003593; IPR013283; IPR017896; IPR017900; G3DSA:3.30.70.20 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR19248 (PANTHER), PTHR19248:SF5 (PANTHER), SSF52540 (SUPERFAMILY), SSF54862 (SUPERFAMILY)
Loa loa	elegans protein confirmed by transcript evidence	2	P:GO:0040010; P:GO:0002119	-		-
Brugia malayi	denn domain-containing protein 2a-like	0		F:GO:0003674; P:GO:0008150		IPR001194; IPR005112; IPR005113; PTHR15288 (PANTHER)
	-	0				-
Caenorhabditis elegans	yuqp_caeel ame: full=cral-trio domain-containing protein	0				PTHR23324 (PANTHER), PTHR23324:SF3 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				PTHR23324 (PANTHER), PTHR23324:SF3 (PANTHER)
Caenorhabditis elegans	ric1 protein	1	C:GO:0016021	-		-
Caenorhabditis elegans	cysteine synthase	6	C:GO:0005737; F:GO:0050461; F:GO:0030170; F:GO:0004124; P:GO:0006535; F:GO:0047458	-	EC:2.5.1.52; EC:2.5.1.47; EC:2.5.1.51	IPR001216; IPR001926; IPR005856; IPR005859; G3DSA:3.40.50.1100 (GENE3D), PTHR10314 (PANTHER), PTHR10314:SF8 (PANTHER)
Caenorhabditis elegans	transmembrane 9 superfamily protein member 4	3	P:GO:0035010; P:GO:0050829; P:GO:0006911	-		IPR004240; PTHR10766:SF12 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	-dph:adrenodoxin mitochondrial	0		P:GO:0055114; F:GO:0005488; P:GO:0008152; F:GO:0003824		IPR016040; PTHR11938 (PANTHER), PTHR11938:SF4 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	novel trtraspanin family protein	0		C:GO:0016021; C:GO:0016020; F:GO:0005515		IPR000301; IPR008952; IPR018499; PTHR19282 (PANTHER), PTHR19282:SF38 (PANTHER), SignalP (SIGNALP)

Caenorhabditis briggsae	cytochrome b5	8	F:GO:0005488; C:GO:0005625; P:GO:0040007; C:GO:0005792; P:GO:0002119; P:GO:0009792; P:GO:0046686; C:GO:0005789	-		IPR001199; IPR018506; PTHR19359 (PANTHER)
Caenorhabditis briggsae	armet-like protein precursor	0		P:GO:0007275; C:GO:0005576		IPR019345; SignalP (SIGNALP), SSF68906 (SUPERFAMILY)
Caenorhabditis briggsae	adp-ribosylation factor	7	C:GO:0005737; F:GO:0005525; F:GO:0004871; P:GO:0006886; P:GO:0007186; C:GO:0005634; P:GO:0007264	-		-
Caenorhabditis briggsae	cg7039 protein	7	C:GO:0005737; F:GO:0005525; F:GO:0004871; P:GO:0006886; P:GO:0007186; C:GO:0005634; P:GO:0007264	-		IPR006689; G3DSA:3.40.50.300 (GENE3D), PTHR11711:SF19 (PANTHER), PS51417 (PROFILE), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	cg7039 protein	7	C:GO:0005737; F:GO:0005525; F:GO:0004871; P:GO:0006886; P:GO:0007186; C:GO:0005634; P:GO:0007264	-		-
	-	0				-
Caenorhabditis elegans	s4 domain containing protein	0		F:GO:0003723		IPR002942; G3DSA:3.10.290.10 (GENE3D), SSF55174 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	talin 2	5	F:GO:0005200; P:GO:0007016; F:GO:0005515; C:GO:0005925; C:GO:0001726	-		IPR015710; G3DSA:1.20.1410.10 (GENE3D), SSF109885 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	sec24 related gene member c (cerevisiae)	9	F:GO:0008270; P:GO:0040007; P:GO:0000003; P:GO:0002119; F:GO:0005515; C:GO:0030127; P:GO:0006888; P:GO:0006898; P:GO:0006886	-		IPR006895; IPR006896; IPR006900; IPR007123; IPR012990; IPR015880; G3DSA:3.40.50.410 (GENE3D), PTHR13803 (PANTHER), SSF53300 (SUPERFAMILY), SSF81995 (SUPERFAMILY), SSF82754 (SUPERFAMILY)

Caenorhabditis elegans	carbamoyl-phosphate synthase large chain	8	F:GO:0004086; P:GO:0006541; F:GO:0016812; F:GO:0005524; F:GO:0004070; F:GO:0016597; P:GO:0060041; P:GO:0006207	-	EC:3.5.2.0; EC:2.1.3.2	IPR002082; IPR006130; IPR006131; IPR006132; G3DSA:3.40.50.1370 (GENE3D), PTHR11405 (PANTHER), PTHR11405:SF3 (PANTHER)
Caenorhabditis elegans	sorting nexin	3	F:GO:0035091; F:GO:0005515; P:GO:0007154	-		IPR001683; PTHR10555 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-vit-6 protein	3	P:GO:0006810; F:GO:0022892; P:GO:0033036	-		-
Caenorhabditis briggsae	briggsae cbr-vit-6 protein	3	P:GO:0006810; F:GO:0022892; P:GO:0033036	-		-
Caenorhabditis briggsae	briggsae cbr-vit-6 protein	3	P:GO:0006810; F:GO:0022892; P:GO:0033036	-		-
Apis mellifera	forkhead box n4	27	F:GO:0016566; C:GO:0000785; P:GO:0008016; P:GO:0048813; P:GO:0043193; C:GO:0005701; P:GO:0007389; P:GO:0007517; P:GO:0007400; F:GO:0003704; C:GO:0005730; F:GO:0016563; C:GO:0005667; P:GO:0007391; P:GO:0048663; P:GO:0008105; F:GO:0003705; P:GO:0010551; P:GO:0048749; P:GO:0051090; F:GO:0003690; F:GO:0003682; F:GO:0008301; F:GO:0010843; F:GO:0008134; P:GO:0007476; P:GO:0006325	-		IPR001766; IPR011991; IPR018122; SSF46785 (SUPERFAMILY)
Caenorhabditis briggsae	filamin-b isoform 3	10	P:GO:0007016; C:GO:0016021; P:GO:0030036; F:GO:0003779; C:GO:0015629; C:GO:0044444; P:GO:0007165; P:GO:0007275; F:GO:0016787; C:GO:0005886	-		IPR001715; PTHR11915 (PANTHER), PTHR11915:SF24 (PANTHER), SignalP (SIGNALP)

Caenorhabditis briggsae	nedd8-activating enzyme e1 catalytic subunit	4	F:GO:0008641; P:GO:0045116; F:GO:0016881; F:GO:0005524	-	EC:6.3.2.0	IPR000127; IPR000594; IPR009036; IPR014929; IPR016040; IPR018074; IPR019572; G3DSA:1.10.10.520 (GENE3D), G3DSA:3.10.20.260 (GENE3D), PTHR10953 (PANTHER), PTHR10953:SF6 (PANTHER)
Ancylostoma duodenale	ancylostoma-secreted protein 1 precursor	0		C:GO:0005576		IPR014044
Brugia malayi	hypothetical protein Bm1_56010 [Brugia malayi]	0				SignalP (SIGNALP)
Harpegnathos saltator	pantothe-te ki-se 4	1	F:GO:0016740	-		IPR011602; PTHR12280 (PANTHER), PTHR12280:SF10 (PANTHER)
Caenorhabditis elegans	Hypothetical protein ZC404.15 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
Hyalomma marginatum rufipes	ubiquitin c	2	C:GO:0005634; C:GO:0005737	-		IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), PTHR10666:SF9 (PANTHER), SSF54236 (SUPERFAMILY)
Homo sapiens	ubiquitin c	2	C:GO:0005634; C:GO:0005737	-		IPR000626; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), PTHR10666:SF9 (PANTHER), SSF54236 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	db module family protein	0				IPR002602; PTHR21679 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-lpd-6 protein	2	P:GO:0009987; C:GO:0044464	-		IPR007109; PTHR12661 (PANTHER), PTHR12661:SF1 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-pqn-55 protein	0		F:GO:0008270		-
Caenorhabditis briggsae	briggsae cbr-sym-3 protein	0		F:GO:0003674; C:GO:0005575		IPR019448; PTHR21456 (PANTHER)
Loa loa	rap ran-gap family protein	0		F:GO:0005096; P:GO:0051056; F:GO:0005488; C:GO:0005622; P:GO:0043547		IPR018515
Caenorhabditis elegans	vps53- n-termi-l family protein	0				IPR007234; PTHR12820 (PANTHER)
Caenorhabditis brenneri	ubiquitin	16	P:GO:0006412; C:GO:0005875; P:GO:0006511; P:GO:0006355; P:GO:0040007; F:GO:0003735; P:GO:0000003; P:GO:0002119; P:GO:0042254; F:GO:0005515; P:GO:0006325; C:GO:0005811; P:GO:0006950; C:GO:0022625; C:GO:0005634; P:GO:0006464	-	EC:3.6.5.3	IPR000626; IPR001975; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), PTHR10666:SF9 (PANTHER), SSF54236 (SUPERFAMILY)

Caenorhabditis brenneri	ubiquitin	16	P:GO:0006412; C:GO:0005875; P:GO:0006511; P:GO:0006355; P:GO:0040007; F:GO:0003735; P:GO:0000003; P:GO:0002119; P:GO:0042254; F:GO:0005515; P:GO:0006325; C:GO:0005811; P:GO:0006950; C:GO:0022625; C:GO:0005634; P:GO:0006464	-	EC:3.6.5.3	IPR000626; IPR001975; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), PTHR10666:SF9 (PANTHER), SSF54236 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	protein-tyrosine phosphatase containing protein	2	F:GO:0016791; P:GO:0040011	-	EC:3.1.3.0	-
Caenorhabditis elegans	carnitine o-acyltransferase	1	F:GO:0008415	-		-
Caenorhabditis elegans	protein kiaa0103 homolog	6	C:GO:0005875; F:GO:0005515; P:GO:0040017; P:GO:0040010; P:GO:0000003; P:GO:0006898	-		IPR011990; IPR013026; PTHR12760 (PANTHER), SSF48452 (SUPERFAMILY)
Angiostrongylus cantonensis	galectin protein 10	2	F:GO:0005515; P:GO:0009792	-		IPR001079; IPR008985; IPR013320; PTHR11346:SF4 (PANTHER)
	-	0				-
Caenorhabditis elegans	delta chain (clathrin associated complex) family member (apd-3)	16	C:GO:0030117; C:GO:0005802; C:GO:0000139; F:GO:0005515; P:GO:0006726; P:GO:0040007; F:GO:0008565; P:GO:0061088; P:GO:0006886; P:GO:0016192; P:GO:0009792; P:GO:0002119; P:GO:0048007; P:GO:0006829; P:GO:0010171; P:GO:0051138	-		-
Caenorhabditis briggsae	gns1 sur4 family protein	2	P:GO:0040010; C:GO:0016021	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	inositol polyphosphate-4- type 1 isoform 2	0				PTHR12187 (PANTHER), PTHR12187:SF2 (PANTHER)
	-	0				SignalP (SIGNALP)

Haemonchus contortus	briggsae cbr-vit-2 protein	6	P:GO:0006869; F:GO:0005319; P:GO:0009792; P:GO:0008340; P:GO:0040010; F:GO:0005515	-		IPR000372
Haemonchus contortus	briggsae cbr-vit-2 protein	6	P:GO:0006869; F:GO:0005319; P:GO:0009792; P:GO:0008340; P:GO:0040010; F:GO:0005515	-		IPR000372
Haemonchus contortus	briggsae cbr-vit-6 protein	6	P:GO:0009792; F:GO:0005319; F:GO:0005515; P:GO:0040010; P:GO:0006869; P:GO:0008340	-		IPR015255
Haemonchus contortus	briggsae cbr-vit-6 protein	3	P:GO:0006869; F:GO:0005319; F:GO:0005515	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0016301; F:GO:0005515		IPR001202; IPR001478; G3DSA:2.20.70.10 (GENE3D), G3DSA:2.30.42.10 (GENE3D), PTHR10316 (PANTHER), PTHR10316:SF7 (PANTHER)
Loa loa	nurf (nucleosome remodeling factor) complex homolog family member (nurf-1)	7	P:GO:0009987; P:GO:0040010; F:GO:0005488; P:GO:0000003; P:GO:0007492; P:GO:0001892; P:GO:0009952	-		IPR001487; IPR018359; PTHR22880 (PANTHER), PTHR22880:SF6 (PANTHER)
Caenorhabditis elegans	briggsae cbr-acy-4 protein	1	F:GO:0016849	-		IPR001054; IPR018297; PTHR11920 (PANTHER), PTHR11920:SF14 (PANTHER)
Dictyocaulus viviparus	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	cofactor required for sp1 transcriptio-l subunit 3	3	P:GO:0044260; P:GO:0090304; P:GO:0010467	-		IPR021629; PTHR12691 (PANTHER), PTHR12691:SF3 (PANTHER)
Caenorhabditis elegans	histone deacetylase	6	F:GO:0004407; P:GO:0045449; P:GO:0016575; P:GO:0006099; P:GO:0022904; C:GO:0005737	-		IPR000286; IPR001607; IPR013083; PTHR10625:SF19 (PANTHER), SSF52768 (SUPERFAMILY)
Caenorhabditis briggsae	transmembrane protein 120b	0		C:GO:0016021		IPR012926
Caenorhabditis elegans	myelin proteolipid	0				IPR001614; PTHR11683:SF1 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	msp-domain protein 1 variant	6	C:GO:0044297; P:GO:0019915; P:GO:0040018; P:GO:0000003; F:GO:0005198; C:GO:0031143	-		IPR000535; IPR008962; PTHR22947 (PANTHER)

Caenorhabditis elegans	alkylation repair homolog 1	0				-
Caenorhabditis briggsae	transmembrane protein 194a	1	F:GO:0005515	-		IPR019358; PTHR13598 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	transmembrane protein 194a	1	F:GO:0005515	-		IPR019358; PTHR13598 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	glycosyltransferase 25 family member	5	P:GO:0040035; F:GO:0005515; P:GO:0040010; P:GO:0040011; P:GO:0002009	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-png-1 protein	3	F:GO:0005488; F:GO:0016787; C:GO:0044444	-		IPR006588; IPR008979; PTHR12143 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-png-1 protein	3	F:GO:0005488; F:GO:0016787; C:GO:0044444	-		IPR006588; IPR008979; PTHR12143 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-png-1 protein	3	F:GO:0005488; F:GO:0016787; C:GO:0044444	-		IPR006588; IPR008979; PTHR12143 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-try-10 protein	1	P:GO:0019915	-		IPR007621
Homo sapiens	mhc class ii antigen	10	C:GO:0005789; C:GO:0005887; C:GO:0042613; C:GO:0005794; P:GO:0002504; C:GO:0031902; P:GO:0007165; C:GO:0005765; F:GO:0032395; P:GO:0006955	-		SignalP (SIGNALP)
Homo sapiens	mhc class ii antigen	10	C:GO:0005789; C:GO:0005887; C:GO:0042613; C:GO:0005794; P:GO:0002504; C:GO:0031902; P:GO:0007165; C:GO:0005765; F:GO:0032395; P:GO:0006955	-		IPR000353; IPR003006; IPR003597; IPR007110; IPR011162; IPR013783; IPR014745; PTHR19944 (PANTHER), PTHR19944:SF26 (PANTHER), SignalP (SIGNALP), SSF48726 (SUPERFAMILY)
Homo sapiens	mhc class ii antigen	10	C:GO:0005789; C:GO:0005887; C:GO:0042613; C:GO:0005794; P:GO:0002504; C:GO:0031902; P:GO:0007165; C:GO:0005765; F:GO:0032395; P:GO:0006955	-		IPR000353; IPR003006; IPR003597; IPR007110; IPR011162; IPR013783; IPR014745; PTHR19944 (PANTHER), PTHR19944:SF26 (PANTHER), SSF48726 (SUPERFAMILY)

Homo sapiens	mhc class ii antigen	10	C:GO:0005789; C:GO:0005887; C:GO:0042613; C:GO:0005794; P:GO:0002504; C:GO:0031902; P:GO:0007165; C:GO:0005765; F:GO:0032395; P:GO:0006955	-		IPR000353; IPR003006; IPR003597; IPR007110; IPR011162; IPR013783; IPR014745; PTHR19944 (PANTHER), PTHR19944:SF26 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	zinc finger swim domain-containing protein kiaa0913	0		F:GO:0046872; F:GO:0003674; P:GO:0008150; F:GO:0008270; C:GO:0005575		PTHR22619 (PANTHER)
Caenorhabditis elegans	aquarius homolog	5	F:GO:0008026; F:GO:0003676; F:GO:0005524; C:GO:0005634; P:GO:0006396	-		G3DSA:3.40.50.300 (GENE3D), PTHR10887 (PANTHER), PTHR10887:SF5 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	formin homology 2 domain containing 1	2	P:GO:0030036; F:GO:0003779	-		IPR015425; PTHR23213 (PANTHER), PTHR23213:SF3 (PANTHER)
	-	0				-
Brugia malayi	nonmuscle myosin-ii heavy chain	32	P:GO:0045200; C:GO:0016461; P:GO:0035159; P:GO:0031036; C:GO:0016460; P:GO:0007409; P:GO:0035072; P:GO:0007443; P:GO:0007395; P:GO:0045214; P:GO:0035017; C:GO:0016021; P:GO:0006936; P:GO:0007297; P:GO:0046663; F:GO:0003779; P:GO:0001736; F:GO:0032027; P:GO:0008258; P:GO:0051259; P:GO:0016203; C:GO:0032154; C:GO:0045179; F:GO:0003774; P:GO:0045184; P:GO:0035317; C:GO:0030018;	-		IPR000048; IPR001609; G3DSA:4.10.270.10 (GENE3D), PTHR13140 (PANTHER), PTHR13140:SF23 (PANTHER), SSF52540 (SUPERFAMILY)

Pongo abelii	glycosylphosphatidylinositol anchor attachment protein 1 homolog	8	C:GO:0042765; P:GO:0016255; P:GO:0006461; F:GO:0034235; F:GO:0015631; P:GO:0006621; C:GO:0005887; F:GO:0003923	-		-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	P:GO:0040010	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	P:GO:0040010	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0040010		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0040010		-
Caenorhabditis elegans	cdc45 cell division cycle 45-like (cerevisiae)	2	C:GO:0043229; P:GO:0006260	-		-
Brugia malayi	dead box atp-dependent r- helicase	7	F:GO:0003676; F:GO:0008026; P:GO:0000245; P:GO:0001700; P:GO:0042254; F:GO:0000166; P:GO:0006446	-		IPR008985; IPR011545; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF44 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-unc-5 protein	4	P:GO:0009987; P:GO:0050789; P:GO:0048856; P:GO:0007275	-		IPR000488; IPR011029; PTHR12582 (PANTHER), PTHR12582:SF2 (PANTHER)
Caenorhabditis elegans	carnitine palmitoyltransferase ii	5	P:GO:0006853; P:GO:0046320; C:GO:0005743; F:GO:0004095; P:GO:0009792	-	EC:2.3.1.21	IPR000542; PTHR22589:SF16 (PANTHER), SSF52777 (SUPERFAMILY)
Caenorhabditis briggsae	d- directed r- polymerase ii polypeptide d	5	F:GO:0003899; C:GO:0005665; F:GO:0004672; P:GO:0006366; F:GO:0000166	-	EC:2.7.7.6	IPR005574; IPR006590; IPR010997; PTHR21297 (PANTHER)
	-	0				-
	-	0				-
Angiostrongylus cantonensis	nematode cuticle collagen n-termi-l domain containing protein	2	F:GO:0042302; C:GO:0016021	-		IPR002486; IPR008160; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-cht-1 protein	3	P:GO:0009792; F:GO:0016787; P:GO:0008152	-		IPR002557; G3DSA:2.170.140.10 (GENE3D), PTHR11177 (PANTHER), PTHR11177:SF31 (PANTHER)
Ciona intestinalis	transcription factor ap-2 gamma	8	P:GO:0006357; P:GO:0007267; P:GO:0008584; F:GO:0003677; P:GO:0030154; F:GO:0046983; F:GO:0003700; C:GO:0005634	-		-
Caenorhabditis briggsae	upf0493 protein kiaa1632-like	1	P:GO:0040017	-		-

Brugia malayi	coiled-coil domain-containing protein 6	0		F:GO:0003674; F:GO:0005515; C:GO:0005575		IPR019152; PD968187 (PRODOM)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Loa loa	pab-dependent poly -specific ribonuclease subunit 3	8	C:GO:0005737; P:GO:0006468; F:GO:0003676; F:GO:0005515; F:GO:0004672; P:GO:0006397; F:GO:0005524; F:GO:0008270	-		SignalP (SIGNALP)
Caenorhabditis briggsae	alpha mannosidase	5	C:GO:0000139; F:GO:0004571; P:GO:0006487; P:GO:0008340; P:GO:0042221	-	EC:3.2.1.113	IPR001382; PTHR11742:SF6 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	adp-ribosylation factor	1	F:GO:0005488	-		IPR005225; IPR006689; G3DSA:3.40.50.300 (GENE3D), PTHR11711:SF17 (PANTHER), PS51417 (PROFILE), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	ring finger protein 139	1	F:GO:0046872	-		IPR001841; IPR013083; IPR018957; PTHR12477 (PANTHER), PTHR12477:SF9 (PANTHER), SSF57850 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	pre-mr--splicing factor syf2	3	P:GO:0006397; C:GO:0005634; P:GO:0008380	-		IPR013260
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	4	P:GO:0002119; P:GO:0009792; P:GO:0000003; P:GO:0040007	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	3	P:GO:0040017; F:GO:0005198; F:GO:0005515	-		IPR000535; IPR008962; PTHR22947 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	3	C:GO:0034703; F:GO:0005261; P:GO:0055080	-		-
Caenorhabditis elegans	aldo keto reductase family protein	2	P:GO:0043050; P:GO:0040011	-		SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-nlp-14 protein	4	C:GO:0005576; C:GO:0016020; F:GO:0005488; P:GO:0055085	-		PTHR22283 (PANTHER)
Caenorhabditis elegans	ring finger protein 43	2	F:GO:0046872; C:GO:0044464	-		IPR001841; IPR013083; IPR018957; PTHR14155 (PANTHER), PTHR14155:SF2 (PANTHER), SignalP (SIGNALP), SSF57850 (SUPERFAMILY)

Caenorhabditis elegans	ring finger protein 43	1	F:GO:0046872	-		IPR001841; IPR013083; IPR018957; PTHR14155 (PANTHER), PTHR14155:SF2 (PANTHER), SignalP (SIGNALP), SSF57850 (SUPERFAMILY)
Caenorhabditis elegans	ring finger protein 43	2	F:GO:0046872; C:GO:0044464	-		IPR001841; IPR013083; IPR018957; PTHR14155 (PANTHER), PTHR14155:SF2 (PANTHER), SignalP (SIGNALP), SSF57850 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-twk-25 protein	1	P:GO:0006810	-		IPR013099; G3DSA:1.10.287.70 (GENE3D), PTHR11003 (PANTHER), PTHR11003:SF7 (PANTHER), SSF81324 (SUPERFAMILY)
Caenorhabditis elegans	autophagy-related protein 3	3	P:GO:0015031; C:GO:0005737; P:GO:0006914	-		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0000003; P:GO:0016311; F:GO:0016791; P:GO:0006470; F:GO:0016787; F:GO:0008138; F:GO:0004725; F:GO:0004721		-
Caenorhabditis briggsae	briggsae cbr-tag-301 protein	4	P:GO:0016337; C:GO:0005913; P:GO:0035147; P:GO:0035156	-		IPR008144; G3DSA:3.40.50.300 (GENE3D), PTHR13865 (PANTHER), PTHR13865:SF7 (PANTHER)
	-	0				-
Caenorhabditis briggsae	g1 to s phase transition 1	8	F:GO:0003746; P:GO:0006479; P:GO:0006415; F:GO:0005525; F:GO:0004781; F:GO:0005515; F:GO:0003747; F:GO:0003924	-	EC:2.7.7.4; EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR004160; IPR009001; G3DSA:2.40.30.10 (GENE3D)
Caenorhabditis briggsae	regulator of g-protein sig-ling 7	6	F:GO:0004871; P:GO:0007186; C:GO:0005834; F:GO:0005515; P:GO:0050794; F:GO:0005096	-	EC:3.6.5.1	IPR000342; IPR015898; IPR016137; G3DSA:1.10.196.10 (GENE3D), PTHR10845 (PANTHER), PTHR10845:SF22 (PANTHER)
Caenorhabditis briggsae	protein phosphatase 2 (formerly 2a) regulatory subunit	1	F:GO:0005515	-		IPR011992; IPR018247; PTHR14095 (PANTHER), SSF47473 (SUPERFAMILY)
Macaca mulatta	ribosomal protein l7	9	P:GO:0042273; F:GO:0003729; F:GO:0030528; F:GO:0003677; F:GO:0003735; P:GO:0006364; C:GO:0022625; F:GO:0042803; P:GO:0006414	-		IPR005998; IPR012988; IPR016082; IPR018038; PTHR11524 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-ztf-8 protein	1	F:GO:0005488	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0005515		-

	-	0				-
Caenorhabditis elegans	transmembrane protein 180-like	1	P:GO:0008340	-		IPR016196; SignalP (SIGNALP)
Brugia malayi	threonine aspartase 1	1	F:GO:0016787	-		IPR000246; PTHR10188:SF8 (PANTHER), SSF56235 (SUPERFAMILY)
Brugia malayi	thyroid hormone receptor interactor 10	3	F:GO:0005488; C:GO:0044444; P:GO:0009987	-		IPR001060; IPR001452; G3DSA:2.30.30.40 (GENE3D), PTHR12602 (PANTHER), PTHR12602:SF4 (PANTHER)
Caenorhabditis elegans	uncharacterized protein cg1161	0		C:GO:0016021		IPR008853; PTHR13064:SF4 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	uncharacterized protein cg1161	0		C:GO:0016021		IPR008853; PTHR13064:SF4 (PANTHER), SignalP (SIGNALP)
Brugia malayi	ubiquitin fusion degradation (yeast ufd homolog) family member (ufd-2)	6	P:GO:0006915; P:GO:0042787; F:GO:0005515; F:GO:0004842; P:GO:0009411; C:GO:0000151	-	EC:6.3.2.19	IPR003613; IPR013083; IPR019474; PTHR13931 (PANTHER), PTHR13931:SF2 (PANTHER), SSF57850 (SUPERFAMILY)
Brugia malayi	ubiquitin fusion degradation (yeast ufd homolog) family member (ufd-2)	6	P:GO:0006915; P:GO:0042787; F:GO:0005515; F:GO:0004842; P:GO:0009411; C:GO:0000151	-	EC:6.3.2.19	IPR003613; IPR013083; IPR019474; PTHR13931 (PANTHER), PTHR13931:SF2 (PANTHER), SSF57850 (SUPERFAMILY)
Brugia malayi	ubiquitin conjugation factor e4 b	5	P:GO:0006915; P:GO:0016567; P:GO:0006511; P:GO:0009411; C:GO:0044424	-		IPR003613; IPR013083; IPR019474; PTHR13931 (PANTHER), PTHR13931:SF2 (PANTHER), SSF57850 (SUPERFAMILY)
Brugia malayi	ubiquitin conjugation factor e4 b	5	P:GO:0006915; P:GO:0016567; P:GO:0006511; P:GO:0009411; C:GO:0044424	-		IPR003613; IPR013083; IPR019474; PTHR13931 (PANTHER), PTHR13931:SF2 (PANTHER), SSF57850 (SUPERFAMILY)
Bos taurus	PREDICTED: hypothetical protein [Bos taurus]	0				-
Caenorhabditis briggsae	subfamily member 9	2	F:GO:0005515; P:GO:0040011	-		IPR001623; IPR015609; IPR018253; PTHR11821:SF31 (PANTHER)
Bos taurus	PREDICTED: hypothetical protein [Bos taurus]	0				-
Monodelphis domestica	subfamily member 9	2	F:GO:0005515; P:GO:0040011	-		IPR001623; IPR015609; IPR018253; PTHR11821:SF31 (PANTHER)
Bos taurus	PREDICTED: hypothetical protein [Bos taurus]	0				-
Ascaris suum	MFP3 [Ascaris suum]	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-swm-1 protein	0				PTHR23259 (PANTHER)
Caenorhabditis elegans	briggsae cbr-swm-1 protein	0				-
Caenorhabditis elegans	briggsae cbr-swm-1 protein	0		C:GO:0031093; P:GO:0010951; F:GO:0004869; P:GO:0008150; F:GO:0004867; C:GO:0005576; P:GO:0051918; C:GO:0005575		-
Caenorhabditis elegans	briggsae cbr-swm-1 protein	0				-
Caenorhabditis elegans	briggsae cbr-swm-1 protein	0				-

Caenorhabditis elegans	briggsae cbr-swm-1 protein	0		C:GO:0031093; P:GO:0010951; F:GO:0004869; P:GO:0008150; F:GO:0004867; C:GO:0005576; P:GO:0051918; C:GO:0005575		-
Caenorhabditis elegans	briggsae cbr-swm-1 protein	0				PTHR23259 (PANTHER)
Caenorhabditis elegans	briggsae cbr-swm-1 protein	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Brugia malayi	alkbh protein	0				-
Caenorhabditis elegans	histone-lysine n-	7	F:GO:0005488; P:GO:0048856; F:GO:0018024; P:GO:0007275; C:GO:0005694; P:GO:0048477; P:GO:0016571	-	EC:2.1.1.43	IPR001739; IPR007728; IPR016177; G3DSA:2.170.270.10 (GENE3D), PTHR22884 (PANTHER), PTHR22884:SF24 (PANTHER), SSF82199 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-ced-12 protein	14	P:GO:0043652; F:GO:0070064; P:GO:0007015; P:GO:0031532; F:GO:0032403; F:GO:0019899; P:GO:0030334; P:GO:0060097; P:GO:0040025; C:GO:0044444; P:GO:0040039; P:GO:0009792; P:GO:0035262; C:GO:0005886	-		IPR006816; PTHR12771 (PANTHER), PTHR12771:SF5 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0006355; F:GO:0043565; F:GO:0046983; F:GO:0003677; F:GO:0003700; C:GO:0005634		IPR004827; IPR011700; G3DSA:1.20.5.170 (GENE3D), PS51257 (PROFILE)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	F:GO:0005525; P:GO:0044237; P:GO:0044238; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000640; IPR005517; IPR009022; IPR014721; IPR020568; PTHR23115 (PANTHER), PTHR23115:SF3 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-mtm-3 protein	0		F:GO:0046872; P:GO:0016311; F:GO:0016791; F:GO:0004725; F:GO:0008270		IPR000306; IPR011011; IPR013083; IPR017455; PTHR10807 (PANTHER), PTHR10807:SF6 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-

Brugia malayi	talin 1	18	C:GO:0005829; F:GO:0005158; C:GO:0043231; C:GO:0001726; P:GO:0007016; F:GO:0017166; F:GO:0030274; P:GO:0007044; C:GO:0005813; P:GO:0007155; C:GO:0005925; P:GO:0030866; F:GO:0003779; C:GO:0015629; F:GO:0005178; F:GO:0005200; C:GO:0005576; P:GO:0006936	-		IPR002558; IPR015710; IPR015711; G3DSA:1.20.1410.10 (GENE3D), SSF109885 (SUPERFAMILY)
Caenorhabditis elegans	small ubiquitin-related modifier precursor	1	F:GO:0005515	-		IPR019955; IPR022617; G3DSA:3.10.20.90 (GENE3D), PTHR10562 (PANTHER), SSF54236 (SUPERFAMILY)
Caenorhabditis elegans	deoxyhypusine synthase	6	P:GO:0009792; F:GO:0034038; F:GO:0005515; P:GO:0008612; P:GO:0050983; P:GO:0051289	-	EC:2.5.1.46	-
Caenorhabditis elegans	deoxyhypusine synthase	6	P:GO:0009792; F:GO:0034038; F:GO:0005515; P:GO:0008612; P:GO:0050983; P:GO:0051289	-	EC:2.5.1.46	-
	-	0				-
Caenorhabditis briggsae	lipase maturation factor 2	0				-
Caenorhabditis elegans	dedicator of cytokinesis family protein	0		F:GO:0005525; F:GO:0051020; F:GO:0005488; F:GO:0005085		PTHR23317 (PANTHER), PTHR23317:SF26 (PANTHER)
	-	0				-
Caenorhabditis briggsae	hira_caeel ame: full=protein hira homolog	1	P:GO:0050789	-		-
Caenorhabditis elegans	loechrig isoform vii	4	P:GO:0042632; P:GO:0006468; P:GO:0045787; F:GO:0004679	-		-
Caenorhabditis elegans	nuclear receptor binding protein	6	F:GO:0004672; F:GO:0005524; P:GO:0006888; C:GO:0012505; C:GO:0048471; F:GO:0042803	-		IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR13902 (PANTHER), PTHR13902:SF9 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	nuclear receptor binding protein	3	C:GO:0012505; F:GO:0005515; P:GO:0006888	-		IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR13902 (PANTHER), PTHR13902:SF9 (PANTHER), SignalP (SIGNALP)

Haemonchus contortus	heat shock protein 90	7	F:GO:0042802; P:GO:0006457; P:GO:0006950; P:GO:0007049; F:GO:0005524; F:GO:0051082; C:GO:0048471	-		-
Haemonchus contortus	heat shock protein 90	7	F:GO:0042802; P:GO:0006457; P:GO:0006950; P:GO:0007049; F:GO:0005524; F:GO:0051082; C:GO:0048471	-		-
Haemonchus contortus	heat shock protein 90	7	F:GO:0042802; P:GO:0006457; P:GO:0006950; P:GO:0007049; F:GO:0005524; F:GO:0051082; C:GO:0048471	-		IPR001404; IPR003594; IPR019805; IPR020575; IPR020576
Haemonchus contortus	heat shock protein 90	7	F:GO:0042802; P:GO:0006457; P:GO:0006950; P:GO:0007049; F:GO:0005524; F:GO:0051082; C:GO:0048471	-		IPR001404; IPR003594; IPR019805; IPR020575; IPR020576
Haemonchus contortus	heat shock protein 90	7	F:GO:0042802; P:GO:0006457; P:GO:0006950; P:GO:0007049; F:GO:0005524; F:GO:0051082; C:GO:0048471	-		IPR001404; IPR003594; IPR019805; IPR020568; IPR020575; IPR020576
Haemonchus contortus	heat shock protein 90	7	F:GO:0042802; P:GO:0006457; P:GO:0006950; P:GO:0007049; F:GO:0005524; F:GO:0051082; C:GO:0048471	-		IPR001404; IPR003594; IPR019805; IPR020568; IPR020575; IPR020576
Haemonchus contortus	heat shock protein 90	7	F:GO:0042802; P:GO:0006457; P:GO:0006950; P:GO:0007049; F:GO:0005524; F:GO:0051082; C:GO:0048471	-		-
Haemonchus contortus	heat shock protein 90	7	F:GO:0042802; P:GO:0006457; P:GO:0006950; P:GO:0007049; F:GO:0005524; F:GO:0051082; C:GO:0048471	-		-

Loa loa	d- repair protein rad51 homolog 1	17	F:GO:0043142; F:GO:0003684; F:GO:0003690; P:GO:0006268; P:GO:0051106; C:GO:0005739; P:GO:0051260; F:GO:0008022; P:GO:0000724; F:GO:0042802; P:GO:0006312; F:GO:0005524; C:GO:0016605; P:GO:0007131; C:GO:0048471; F:GO:0003697; C:GO:0000800	-		-
Caenorhabditis elegans	angiopoietin-like 6	4	P:GO:0009792; F:GO:0005488; P:GO:0009987; C:GO:0005576	-		IPR002181; IPR014715; IPR014716; IPR020837; PTHR19143 (PANTHER), PTHR19143:SF28 (PANTHER)
Caenorhabditis elegans	alix (apoptosis-linked gene 2 interacting protein x) homolog family member (alx-1)	0				-
Brugia malayi	numb related family member (num-1)	6	C:GO:0005737; C:GO:0005887; F:GO:0019904; F:GO:0005069; F:GO:0005080; P:GO:0006612	-		IPR006020; IPR011993; PTHR11232 (PANTHER), PTHR11232:SF1 (PANTHER), SSF50729 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	isoform b	0		C:GO:0016021		IPR006838; PTHR10989 (PANTHER), SignalP (SIGNALP)
Homo sapiens	histone acetyltransferase myst3	11	P:GO:0045941; F:GO:0004402; P:GO:0006323; P:GO:0035162; C:GO:0070776; P:GO:0035019; F:GO:0046872; F:GO:0003713; P:GO:0030099; P:GO:0043966; P:GO:0016481	-	EC:2.3.1.48	IPR002717; IPR016181; G3DSA:3.30.60.60 (GENE3D), PTHR10615 (PANTHER), PTHR10615:SF26 (PANTHER)
Brugia malayi	nitric oxide synthase-interacting protein	4	P:GO:0051001; C:GO:0005829; C:GO:0005634; F:GO:0005515	-		IPR013083; PTHR13063 (PANTHER), PTHR13063:SF4 (PANTHER), SSF57850 (SUPERFAMILY)
Brugia malayi	prp39 pre-mr- processing factor 39 homolog	0				PTHR17204 (PANTHER), PTHR17204:SF9 (PANTHER)
	-	0				-
Brugia malayi	associated with tfs and helicases family protein	1	F:GO:0005488	-		IPR006576
Caenorhabditis briggsae	ubiquitin associated and sh3 domain a short form	1	C:GO:0005737	-		-

Caenorhabditis elegans	slit-robo rho gtpase-activating protein 1	6	F:GO:0005100; P:GO:0016477; P:GO:0007266; C:GO:0005622; P:GO:0045132; F:GO:0017048	-		IPR001060; PTHR14166 (PANTHER), PTHR14166:SF1 (PANTHER)
Caenorhabditis briggsae	probable nucleolar gtp-binding protein	21	P:GO:0008156; P:GO:0000003; P:GO:0030336; F:GO:0005515; F:GO:0015093; P:GO:0015684; P:GO:0040010; P:GO:0050821; F:GO:0005525; C:GO:0016021; P:GO:0000079; C:GO:0005730; P:GO:0008285; P:GO:0022408; P:GO:0009792; P:GO:0002119; P:GO:0031397; C:GO:0048471; F:GO:0003924; P:GO:0033342; P:GO:0042254	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR006073; IPR010674; G3DSA:3.40.50.300 (GENE3D), PTHR11702 (PANTHER), PTHR11702:SF4 (PANTHER), SSF52540 (SUPERFAMILY)
Loa loa	tb2 hva22 family protein	0		C:GO:0005856; F:GO:0005198		IPR000535; IPR008962
Caenorhabditis briggsae	ph domain containing protein	0		F:GO:0016740; P:GO:0008152; F:GO:0016758; F:GO:0016757		IPR001849; IPR011993; SSF50729 (SUPERFAMILY)
Caenorhabditis elegans	lim domain containing protein	2	F:GO:0046872; C:GO:0043232	-		IPR001781; PTHR18973 (PANTHER), PTHR18973:SF98 (PANTHER), SSF57716 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG02308 [Caenorhabditis briggsae]	0		F:GO:0003824; F:GO:0004721		-
Loa loa	tbc1 domain member 7	0		F:GO:0005096; F:GO:0003674; P:GO:0032313; P:GO:0008150; C:GO:0005575; F:GO:0005097; C:GO:0005622		IPR013090

Caenorhabditis elegans	c family member (clr-1)	11	P:GO:0006470; P:GO:0040037; P:GO:0040010; P:GO:0018991; P:GO:0040002; P:GO:0010171; P:GO:0002119; P:GO:0040017; F:GO:0005001; P:GO:0002009; C:GO:0005886	-		IPR000242; IPR000387; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF43 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis elegans	aspartyl protease family member (asp-2)	4	P:GO:0008219; F:GO:0016787; F:GO:0005515; P:GO:0040011	-		-
Caenorhabditis briggsae	briggsae cbr-asp-2 protein	6	C:GO:0016021; P:GO:0008219; P:GO:0006508; F:GO:0004190; F:GO:0005515; P:GO:0040011	-	EC:3.4.23.0	-
Caenorhabditis elegans	aspartyl protease family member (asp-2)	4	P:GO:0008219; F:GO:0005515; P:GO:0040011; F:GO:0008233	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	protein phosphatase 2a (two a) regulatory subunit family member (pptr-2)	7	P:GO:0009792; C:GO:0000159; P:GO:0007165; P:GO:0040007; F:GO:0005488; F:GO:0008601; P:GO:0002119	-		IPR002554; IPR016024
Caenorhabditis briggsae	protein phosphatase 2a (two a) regulatory subunit family member (pptr-2)	3	P:GO:0009792; P:GO:0040007; P:GO:0002119	-		-
Brugia malayi	pecanex-like protein 1	2	C:GO:0016020; P:GO:0040011	-		PTHR12372 (PANTHER)
Brugia malayi	pecanex-like protein 1	2	C:GO:0016020; P:GO:0040011	-		PTHR12372 (PANTHER)
	-	0				-
Angiostrongylus cantonensis	copper chaperone	2	F:GO:0046872; P:GO:0030001	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	F:GO:0016757; F:GO:0005515; C:GO:0016020	-		IPR000772; IPR001173; IPR008997; G3DSA:2.80.10.50 (GENE3D), G3DSA:3.90.550.10 (GENE3D), PTHR11675 (PANTHER), SignalP (SIGNALP), SSF53448 (SUPERFAMILY)
Loa loa	hypothetical protein LOAG_05685 [Loa loa]	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	leukocyte receptor cluster member	0		F:GO:0004872		IPR005062; PTHR12436 (PANTHER), PTHR12436:SF4 (PANTHER)
	-	0				-

Brugia malayi	myosin xviiia	4	F:GO:0005515; C:GO:0016459; F:GO:0005524; F:GO:0003774	-		PTHR13140 (PANTHER), PTHR13140:SF10 (PANTHER)
Caenorhabditis briggsae	hydroxyacyl-coenzyme a dehydroge-se 3-ketoacyl-coenzyme a thiolase enoyl-coenzyme a hydratase (trifunctio-l protein) alpha subunit	18	F:GO:0016508; F:GO:0000062; F:GO:0003988; C:GO:0005743; P:GO:0055114; P:GO:0040007; C:GO:0016507; C:GO:0042645; F:GO:0051287; P:GO:0019915; F:GO:0003857; P:GO:0002119; P:GO:0006635; P:GO:0042493; P:GO:0006898; F:GO:0016509; P:GO:0009792; F:GO:0004300	-	EC:4.2.1.74; EC:2.3.1.16; EC:1.1.1.35; EC:1.1.1.211 ; EC:4.2.1.17	IPR006108; IPR006176; IPR008927; IPR013328; IPR016040; PTHR23309 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	mitochondrial ribosomal protein s35	3	P:GO:0009792; P:GO:0040007; P:GO:0002119	-		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0004500; P:GO:0006548		IPR005018; PTHR23130 (PANTHER), PTHR23130:SF8 (PANTHER), SignalP (SIGNALP)
Loa loa	alpha- -mannosyl-glycoprotein 2-beta-n-acetylglucosaminyltransferase	2	P:GO:0009792; F:GO:0016740	-		IPR004139; G3DSA:3.90.550.10 (GENE3D), SSF53448 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	fructose-bisphosphate aldolase	3	P:GO:0006096; F:GO:0004332; F:GO:0042802	-	EC:4.1.2.13	IPR000741; IPR013785; SignalP (SIGNALP), SSF51569 (SUPERFAMILY)
	-	0				-
	-	0				-
Loa loa	smoothened protein	0		F:GO:0004888; C:GO:0016021; C:GO:0016020; F:GO:0004930; F:GO:0004926; P:GO:0007275; P:GO:0007166; P:GO:0007165; F:GO:0004872; F:GO:0004871; P:GO:0007186; P:GO:0016055		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	sy-ptojanin 2 binding protein	6	F:GO:0008022; P:GO:0006605; C:GO:0031307; P:GO:0030100; P:GO:0048312; P:GO:0007266	-		-

Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
Caenorhabditis elegans	sideroflexin 1	5	F:GO:0008324; P:GO:0055085; P:GO:0006812; C:GO:0016021; C:GO:0031966	-		IPR004686; PTHR11153:SF9 (PANTHER)
	-	0				-
Caenorhabditis briggsae	helicase ski2w	4	F:GO:0008026; F:GO:0003676; F:GO:0005515; F:GO:0000166	-		-
Caenorhabditis briggsae	antiviral helicase ski2	4	F:GO:0004004; F:GO:0003676; F:GO:0005515; F:GO:0000166	-		-
	-	0				-
	-	0				-
Caenorhabditis briggsae	intersectin 1 (sh3 domain protein)	9	F:GO:0005488; P:GO:0007264; P:GO:0042981; F:GO:0030234; P:GO:0048522; C:GO:0042995; C:GO:0044444; P:GO:0009966; P:GO:0035466	-		IPR000261; IPR002048; IPR011992; IPR018247; IPR018249; PTHR11216 (PANTHER), PTHR11216:SF24 (PANTHER), SSF47473 (SUPERFAMILY)
Caenorhabditis briggsae	intersectin 1 (sh3 domain protein)	9	F:GO:0005488; P:GO:0007264; P:GO:0042981; F:GO:0030234; P:GO:0048522; C:GO:0042995; C:GO:0044444; P:GO:0009966; P:GO:0035466	-		IPR000261; IPR002048; IPR011992; IPR018247; IPR018249; PTHR11216 (PANTHER), PTHR11216:SF24 (PANTHER), SSF47473 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0008276; C:GO:0005737; P:GO:0006479		-
Brugia malayi	peptidase m16 i-ctive domain containing protein	5	F:GO:0004222; P:GO:0016485; C:GO:0005759; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	IPR011237; IPR011765
Caenorhabditis briggsae	proteasome subunit beta type	14	P:GO:0008340; P:GO:0009401; P:GO:0040007; P:GO:0000003; F:GO:0004298; P:GO:0018996; P:GO:0051603; P:GO:0002119; P:GO:0040011; P:GO:0009792; C:GO:0005737; F:GO:0005351; C:GO:0005839; C:GO:0005634	-	EC:3.4.25.0	IPR000243; IPR001353; IPR002114; G3DSA:3.60.20.10 (GENE3D), PTHR11599 (PANTHER), PTHR11599:SF3 (PANTHER), PS51476 (PROFILE), SSF56235 (SUPERFAMILY)
	-	0				-

Homo sapiens	eukaryotic translation initiation factor 3 subunit k	8	C:GO:0005852; F:GO:0003723; F:GO:0005515; P:GO:0045948; F:GO:0003743; C:GO:0005634; C:GO:0005829; F:GO:0043022	-		IPR009374; IPR011991; IPR019280; SSF46785 (SUPERFAMILY)
Caenorhabditis elegans	krr1 small subunit processome component homolog	5	P:GO:0018991; F:GO:0003723; P:GO:0040007; P:GO:0010171; P:GO:0002119	-		IPR004087; G3DSA:3.30.1370.10 (GENE3D), PTHR12581 (PANTHER), SSF54791 (SUPERFAMILY)
Loa loa	ruvb-like 1	19	P:GO:0043967; P:GO:0010628; P:GO:0042127; F:GO:0017025; P:GO:0006310; P:GO:0051301; P:GO:0030111; F:GO:0003713; C:GO:0031011; C:GO:0005875; P:GO:0045449; C:GO:0035267; P:GO:0043968; F:GO:0008013; C:GO:0035060; F:GO:0005524; F:GO:0003678; P:GO:0007049; C:GO:0071339	-		IPR010339; IPR016027; G3DSA:3.40.50.300 (GENE3D), PTHR11093 (PANTHER), SSF52540 (SUPERFAMILY)
Loa loa	hypothetical protein LOAG_08700 [Loa loa]	0				-
Heligmosomoides polygyrus	briggsae cbr-gst- protein	2	F:GO:0005515; P:GO:0008340	-		IPR004045; IPR010987; IPR012335; IPR012336; IPR017933; PTHR11571 (PANTHER), PTHR11571:SF6 (PANTHER)
Heligmosomoides polygyrus	briggsae cbr-gst- protein	2	F:GO:0005515; P:GO:0008340	-		IPR004045; IPR010987; IPR012335; IPR012336; IPR017933; PTHR11571 (PANTHER), PTHR11571:SF6 (PANTHER)
Caenorhabditis briggsae	peptidoglycan- domain containing 3	1	C:GO:0016020	-		IPR002482; IPR018392; G3DSA:3.10.350.10 (GENE3D), PTHR20932 (PANTHER), SSF54106 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Haemonchus contortus	cytochrome c oxidase subunit ii	9	C:GO:0005743; F:GO:0005507; C:GO:0070469; F:GO:0009055; F:GO:0020037; P:GO:0006810; C:GO:0016021; P:GO:0022904; F:GO:0004129	-	EC:1.9.3.1	IPR002429; IPR008972
Loa loa	exchange factor for arf family member (efa-6)	0		P:GO:0032012; F:GO:0005086; C:GO:0005622		-

Loa loa	exchange factor for arf family member (efa-6)	0		P:GO:0032012; F:GO:0005086; C:GO:0005622		-
	-	0				-
	-	0				-
Caenorhabditis elegans	f-box and leucine-rich repeat protein 20	2	F:GO:0005515; C:GO:0005737	-		IPR001810; IPR022364; G3DSA:1.20.1280.50 (GENE3D), PTHR23125 (PANTHER), PTHR23125:SF69 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	ctn-2 protein	10	P:GO:0050789; C:GO:0005912; P:GO:0048667; P:GO:0007420; P:GO:0048812; P:GO:0007155; C:GO:0042995; F:GO:0005515; P:GO:0050877; C:GO:0044424	-		IPR001033; IPR006077; G3DSA:1.20.120.230 (GENE3D), PTHR18914 (PANTHER), PTHR18914:SF9 (PANTHER)
Loa loa	inhibitor of growth ing4	2	F:GO:0046872; P:GO:0009987	-		IPR001965; IPR011011; IPR013083; IPR019786; IPR019787; PTHR10333 (PANTHER)
Caenorhabditis briggsae	eukaryotic translation initiation factor 6	10	F:GO:0003743; P:GO:0040010; P:GO:0007229; C:GO:0005638; F:GO:0043022; P:GO:0002119; F:GO:0005515; P:GO:0006898; P:GO:0009792; P:GO:0042256	-		IPR002769; G3DSA:3.75.10.10 (GENE3D), SSF55909 (SUPERFAMILY)
Caenorhabditis briggsae	eukaryotic translation initiation factor 6	10	F:GO:0003743; P:GO:0040010; P:GO:0007229; C:GO:0005638; F:GO:0043022; P:GO:0002119; F:GO:0005515; P:GO:0006898; P:GO:0009792; P:GO:0042256	-		IPR002769; G3DSA:3.75.10.10 (GENE3D), SSF55909 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	orai (store-operated calcium channel) homolog protein isoform confirmed by transcript evidence	1	C:GO:0016021	-		IPR012446
Caenorhabditis elegans	orai (store-operated calcium channel) homolog protein isoform confirmed by transcript evidence	1	C:GO:0016021	-		IPR012446
Caenorhabditis elegans	orai (store-operated calcium channel) homolog protein isoform confirmed by transcript evidence	1	C:GO:0016021	-		IPR012446

Caenorhabditis briggsae	caax prenyl protease 1 homolog	6	P:GO:0006998; F:GO:0004222; P:GO:0030327; C:GO:0043231; C:GO:0044444; C:GO:0016021	-	EC:3.4.24.0	IPR001915; PTHR10120 (PANTHER), PTHR10120:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	endothelin converting enzyme 2	10	P:GO:0009987; C:GO:0030659; F:GO:0005488; P:GO:0016486; P:GO:0023052; F:GO:0004222; F:GO:0016740; P:GO:0048513; P:GO:0009792; C:GO:0005794	-	EC:3.4.24.0	IPR013216; G3DSA:3.40.50.150 (GENE3D), PTHR12176 (PANTHER), SSF53335 (SUPERFAMILY)
Caenorhabditis elegans	yp62_caeel ame: full= serine threonine-protein ki-se	0				-
Brugia malayi	protein ki-se domain containing protein	3	P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	PTHR11295 (PANTHER), PTHR11295:SF86 (PANTHER)
Caenorhabditis briggsae	n-acetylglucosaminyl-phosphatidylinositol biosynthetic	4	C:GO:0044432; P:GO:0045132; P:GO:0006506; C:GO:0016021	-		IPR001296; PTHR12526 (PANTHER), PTHR12526:SF37 (PANTHER), SSF53756 (SUPERFAMILY)
Caenorhabditis briggsae	n-acetylglucosaminyl-phosphatidylinositol biosynthetic	4	F:GO:0016757; P:GO:0006506; C:GO:0016021; P:GO:0045132	-		IPR001296; PTHR12526 (PANTHER), PTHR12526:SF37 (PANTHER), SSF53756 (SUPERFAMILY)
Brugia malayi	zinc c2h2 type family protein	7	F:GO:0008270; F:GO:0003676; P:GO:0046672; P:GO:0006099; P:GO:0046580; P:GO:0030536; C:GO:0005634	-		IPR007087; IPR013087; IPR015880; PR00048 (PRINTS), PTHR23229 (PANTHER), PTHR23229:SF13 (PANTHER), SSF57667 (SUPERFAMILY)
	-	0				-
	-	0				IPR008160; PTHR10499 (PANTHER), PTHR10499:SF112 (PANTHER)
Caenorhabditis elegans	a in (actin filament binding protein) homolog family member (afd-1)	2	P:GO:0040010; F:GO:0005515	-		PTHR10398 (PANTHER)
Caenorhabditis elegans	a in (actin filament binding protein) homolog family member (afd-1)	2	P:GO:0040010; F:GO:0005515	-		PTHR10398 (PANTHER)
Caenorhabditis elegans	a in (actin filament binding protein) homolog family member (afd-1)	2	P:GO:0040010; F:GO:0005515	-		PTHR10398 (PANTHER)
Caenorhabditis briggsae	coiled-coil domain-containing protein 47	1	F:GO:0005515	-		IPR012879
	-	0				-
Caenorhabditis elegans	nudix (nucleoside diphosphate linked moiety x)-type motif 3	5	P:GO:0044282; P:GO:0044238; F:GO:0046872; F:GO:0016787; P:GO:0044237	-		IPR000086; IPR015797; IPR020084; IPR020476; PTHR12629 (PANTHER), PS51462 (PROFILE), SignalP (SIGNALP)
Caenorhabditis briggsae	ankle2 protein	0		C:GO:0016021; C:GO:0016020; C:GO:0005635		PTHR20976 (PANTHER)
Caenorhabditis briggsae	prominin protein	0		C:GO:0016021		IPR008795; SignalP (SIGNALP)

Caenorhabditis briggsae	mitotic spindle assembly checkpoint protein mad1	8	C:GO:0016020; C:GO:0043231; C:GO:0005694; C:GO:0043234; C:GO:0044446; F:GO:0005488; C:GO:0044444; P:GO:0007049	-		IPR008672; PD936484 (PRODOM), PTHR23168 (PANTHER)
Caenorhabditis briggsae	mitotic spindle assembly checkpoint protein mad1	5	C:GO:0005737; C:GO:0044446; C:GO:0043232; F:GO:0005488; P:GO:0007049	-		IPR008672; PTHR23168 (PANTHER)
Caenorhabditis briggsae	mitotic spindle assembly checkpoint protein mad1	5	C:GO:0005737; C:GO:0044446; C:GO:0043232; F:GO:0005488; P:GO:0007049	-		IPR008672; PD936484 (PRODOM), PTHR23168 (PANTHER)
Caenorhabditis briggsae	mitotic spindle assembly checkpoint protein mad1	5	C:GO:0005737; C:GO:0044446; C:GO:0043232; F:GO:0005488; P:GO:0007049	-		IPR008672; PD936484 (PRODOM), PTHR23168 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	nuclear receptor nhr-31	5	F:GO:0046872; F:GO:0004879; F:GO:0003677; P:GO:0045449; F:GO:0005515	-		IPR001628; IPR008946; IPR015619; PTHR11865 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis elegans	ubiquitin-conjugating enzyme e2n	18	P:GO:0070534; P:GO:0033182; P:GO:0000724; F:GO:0043130; C:GO:0005829; P:GO:0006511; C:GO:0031372; P:GO:0043123; F:GO:0004842; P:GO:0031058; P:GO:0050852; P:GO:0051443; P:GO:0000729; P:GO:0006301; P:GO:0051092; C:GO:0005634; F:GO:0005524; P:GO:0045739	-	EC:6.3.2.19	IPR000608; IPR016135; PTHR11621 (PANTHER), PTHR11621:SF30 (PANTHER)
Brugia malayi	ankyrin repeat and sterile alpha motif domain containing 1a	1	F:GO:0005515	-		IPR002110; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER), PTHR18958:SF212 (PANTHER)
	-	0				-

Brugia malayi	transducin -like 1 x-linked	19	P:GO:0060070; F:GO:0042393; F:GO:0003714; P:GO:0007605; P:GO:0043161; F:GO:0008022; C:GO:0017053; P:GO:0043627; F:GO:0016563; P:GO:0045444; C:GO:0005667; F:GO:0019904; P:GO:0010553; C:GO:0000118; P:GO:0045944; C:GO:0005876; F:GO:0003682; F:GO:0008013; F:GO:0010843	-		-
Caenorhabditis briggsae	protein	9	P:GO:0009792; P:GO:0010171; P:GO:0002119; C:GO:0005840; P:GO:0042254; P:GO:0000003; P:GO:0040007; P:GO:0006898; P:GO:0006412	-	EC:3.6.5.3	IPR002415; IPR004037; IPR004038; IPR018492; G3DSA:3.30.1330.30 (GENE3D), PTHR23105 (PANTHER), PTHR23105:SF11 (PANTHER), SSF55315 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	phosphoenolpyruvate carboxyki-se	6	C:GO:0005737; P:GO:0006094; F:GO:0046872; F:GO:0005525; F:GO:0016301; F:GO:0004613	-	EC:4.1.1.32	IPR008209; IPR008210; IPR013035; IPR018091; G3DSA:2.170.8.10 (GENE3D), SSF53795 (SUPERFAMILY)
Caenorhabditis briggsae	carbamoyl-phosphate synthase large chain	8	F:GO:0004086; P:GO:0006541; F:GO:0016812; F:GO:0005524; F:GO:0004070; F:GO:0016597; P:GO:0060041; P:GO:0006207	-	EC:3.5.2.0; EC:2.1.3.2	IPR002195; IPR005479; IPR005481; IPR005483; IPR006680; IPR011607; IPR011761; IPR013815; IPR013816; IPR013817; IPR016185; G3DSA:3.20.20.140 (GENE3D), PTHR11405 (PANTHER), PTHR11405:SF3 (PANTHER), SSF51556 (SUPERFAMILY), SSF56059 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	rrp12-like protein	0		C:GO:0016021; C:GO:0016020; C:GO:0005634; F:GO:0003674; C:GO:0005575; C:GO:0031965; C:GO:0005730; F:GO:0005515; P:GO:0008150; F:GO:0005488		PTHR21576 (PANTHER), PTHR21576:SF2 (PANTHER)
Brugia malayi	uncharacterized protein kiaa0467	0				-

Caenorhabditis briggsae	kow motif family protein	8	P:GO:0009792; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0040010; P:GO:0000003; P:GO:0040011; P:GO:0006898	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Necator americanus	zinc metallopeptidase	2	P:GO:0008152; F:GO:0008237	-		IPR000718; IPR008753; G3DSA:1.10.1380.10 (GENE3D), PTHR11733:SF15 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	yip1 interacting factor homolog a (cerevisiae)	3	C:GO:0005793; C:GO:0005794; C:GO:0016021	-		IPR005578; SignalP (SIGNALP)
Caenorhabditis elegans	yip1 interacting factor homolog a (cerevisiae)	3	C:GO:0005793; C:GO:0005794; C:GO:0016021	-		SignalP (SIGNALP)
Caenorhabditis elegans	yip1 interacting factor homolog a (cerevisiae)	3	C:GO:0005793; C:GO:0005794; C:GO:0016021	-		-
Caenorhabditis briggsae	atp synthase subunit s-like protein	0		P:GO:0006355; F:GO:0003700		G3DSA:3.80.10.10 (GENE3D), PTHR13318 (PANTHER), SSF52047 (SUPERFAMILY)
Caenorhabditis briggsae	midasin (midas-containing protein)	0		C:GO:0005634; F:GO:0000166; F:GO:0008134; F:GO:0017111; F:GO:0005524; F:GO:0016887; P:GO:0006355; C:GO:0005622; P:GO:0043254		PTHR22908 (PANTHER), PTHR22908:SF13 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG15276 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	cgmp-dependent protein ki-se egl-4	3	P:GO:0006468; F:GO:0005524; F:GO:0004692	-	EC:2.7.11.12	-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	C:GO:0016021; F:GO:0005488	-		IPR005301; PTHR22599:SF3 (PANTHER)
Caenorhabditis elegans	ferm domain (-ezrin-radixin-moesin) family member (frm-1)	1	F:GO:0005488	-		-
Caenorhabditis briggsae	pecanex-like protein 1	0		C:GO:0016021		-
Caenorhabditis elegans	d- repair protein rad4 containing protein	0		F:GO:0003684; P:GO:0006289; C:GO:0005634		-
Caenorhabditis briggsae	lethal 37bb	7	F:GO:0008115; C:GO:0016020; P:GO:0009792; P:GO:0055114; P:GO:0000003; F:GO:0005488; P:GO:0040010	-	EC:1.5.3.1	IPR006076; G3DSA:3.50.50.60 (GENE3D), PTHR13847 (PANTHER), PTHR13847:SF12 (PANTHER), SSF51905 (SUPERFAMILY)

Caenorhabditis elegans	mitogen activated protein ki-se ki-se ki-se mekk5	4	P:GO:0006468; F:GO:0005515; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	-
	-	0				-
Loa loa	endoribonuclease dicer	5	F:GO:0003676; C:GO:0005622; P:GO:0035279; P:GO:0031054; F:GO:0016787	-		IPR005034; PTHR14950 (PANTHER), PTHR14950:SF3 (PANTHER)
Caenorhabditis briggsae	dihydroorotate dehydroge-se	7	P:GO:0043065; F:GO:0004158; C:GO:0005743; P:GO:0055114; P:GO:0006222; P:GO:0090140; P:GO:0006207	-	EC:1.3.3.1	IPR013785; PTHR11938 (PANTHER), PTHR11938:SF7 (PANTHER), SSF51395 (SUPERFAMILY)
Caenorhabditis elegans	fructose- -bisphosphatase	3	P:GO:0016051; C:GO:0005737; F:GO:0042132	-	EC:3.1.3.11	IPR000146; IPR020548; G3DSA:3.30.540.10 (GENE3D), G3DSA:3.40.190.80 (GENE3D), SSF56655 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-atp-3 protein	13	P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0040010; F:GO:0046933; P:GO:0019915; C:GO:0045261; P:GO:0009792; P:GO:0015986; P:GO:0002119; C:GO:0005811; F:GO:0003824; C:GO:0005886	-	EC:3.6.3.14	IPR000711
Caenorhabditis briggsae	briggsae cbr-atp-3 protein	13	P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0040010; F:GO:0046933; P:GO:0019915; C:GO:0045261; P:GO:0009792; P:GO:0015986; P:GO:0002119; C:GO:0005811; F:GO:0003824; C:GO:0005886	-	EC:3.6.3.14	IPR000711

Caenorhabditis briggsae	briggsae cbr-atp-3 protein	13	P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0040010; F:GO:0046933; P:GO:0019915; C:GO:0045261; P:GO:0009792; P:GO:0015986; P:GO:0002119; C:GO:0005811; F:GO:0003824; C:GO:0005886	-	EC:3.6.3.14	IPR000711
Pongo abelii	filamin a	28	F:GO:0004871; C:GO:0005802; P:GO:0043433; P:GO:0034394; C:GO:0015629; P:GO:0050821; P:GO:0051220; C:GO:0005576; C:GO:0005829; F:GO:0001948; P:GO:0051764; P:GO:0043123; F:GO:0051015; F:GO:0048365; P:GO:0045022; P:GO:0007195; F:GO:0042803; F:GO:0034989; P:GO:0031532; F:GO:0034988; C:GO:0005886; F:GO:0008134; P:GO:0042177; C:GO:0005634; P:GO:0042993; C:GO:0005938;	-		IPR013783; IPR014756; IPR017868; PTHR11915 (PANTHER), PTHR11915:SF24 (PANTHER)
	-	0				IPR010579; PTHR16675 (PANTHER), PTHR16675:SF53 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	egf-like domain containing protein	0		F:GO:0005509		IPR003582
Caenorhabditis briggsae	atp-binding cassette subfamily member 1	7	C:GO:0005875; C:GO:0005811; C:GO:0005759; P:GO:0055114; P:GO:0006635; F:GO:0003995; F:GO:0050660	-	EC:1.3.99.3	IPR006089; IPR006090; IPR006091; IPR006092; IPR009075; IPR009100; IPR013786; PTHR10909 (PANTHER), PTHR10909:SF10 (PANTHER)
Caenorhabditis briggsae	autophagocytosis associated c-termi-l domain containing protein	1	P:GO:0006810	-		IPR007135; PTHR12866 (PANTHER)

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		C:GO:0016021; P:GO:0016042; P:GO:0006644		IPR013090; IPR016090; SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0040010; P:GO:0002119; P:GO:0040011	-		SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-dut-1 protein	5	P:GO:0009792; F:GO:0004170; P:GO:0000910; P:GO:0000003; P:GO:0046080	-	EC:3.6.1.23	IPR008180; IPR008181; G3DSA:2.70.40.10 (GENE3D), PTHR11241 (PANTHER), SSF51283 (SUPERFAMILY)
Caenorhabditis briggsae	downstream of daf-16 (regulated by daf-16) family member (dod-3)	1	P:GO:0008340	-		-
Caenorhabditis elegans	nfs1 nitrogen fixation 1 homolog	10	C:GO:0005829; P:GO:0006777; P:GO:0018283; P:GO:0006461; F:GO:0031071; C:GO:0005759; F:GO:0042803; F:GO:0030170; C:GO:0005634; P:GO:0006534	-	EC:2.8.1.7	IPR000192; IPR015421; IPR015424; PTHR11601 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Xenopus laevis	5 - cytosolic iii-like	0		F:GO:0008253; P:GO:0009117; F:GO:0046872; C:GO:0005737; F:GO:0000287; F:GO:0016740; F:GO:0000166; F:GO:0016787		IPR006434; PF05822 (PFAM), SignalP (SIGNALP), SSF56784 (SUPERFAMILY)
Caenorhabditis briggsae	-dh dehydroge-se	15	P:GO:0006979; P:GO:0006810; P:GO:0040010; P:GO:0008340; P:GO:0019684; F:GO:0008137; C:GO:0005747; F:GO:0009055; F:GO:0051539; P:GO:0006120; P:GO:0002119; P:GO:0042493; P:GO:0032981; P:GO:0009792; F:GO:0005506	-	EC:1.6.5.3	IPR001450; IPR010226; IPR012285; IPR017896; IPR017900; PTHR10849 (PANTHER), SignalP (SIGNALP), SSF54862 (SUPERFAMILY)
Caenorhabditis elegans	ankyrin repeat domain-containing protein 17	0				IPR002110; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER), PTHR18958:SF263 (PANTHER)
Haemonchus contortus	af305962_1 protein	2	P:GO:0009790; P:GO:0009653	-		SignalP (SIGNALP)

Saccoglossus kowalevskii	neurogenic locus notch homolog protein 2-like	0		P:GO:0006508; F:GO:0005488; F:GO:0004252; P:GO:0007155; F:GO:0003824; F:GO:0008233		IPR000436; IPR016060; SignalP (SIGNALP)
Loa loa	elegans protein partially confirmed by transcript evidence	0		F:GO:0016787; P:GO:0001701; F:GO:0043499; C:GO:0005634; C:GO:0016021; P:GO:0007155; C:GO:0016020; P:GO:0030449; F:GO:0008201; C:GO:0005615; F:GO:0004872; P:GO:0006958; P:GO:0045916; P:GO:0007275; P:GO:0006956; C:GO:0005737; F:GO:0005488; C:GO:0009897; F:GO:0005515; P:GO:0007565; C:GO:0005886; P:GO:0045087		IPR000436; IPR016060; PTHR19325 (PANTHER), PTHR19325:SF25 (PANTHER)
Caenorhabditis elegans	complement factor h	2	P:GO:0006956; C:GO:0044464	-		-
Loa loa	complement factor h	2	P:GO:0006956; C:GO:0044464	-		IPR000436; IPR016060; PTHR19325 (PANTHER), PTHR19325:SF25 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	complement factor h	2	P:GO:0006956; C:GO:0044464	-		IPR000436; IPR016060; PTHR19325 (PANTHER), PTHR19325:SF25 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	dehydroge-se e1 and transketolase domain containing 1	5	F:GO:0004591; P:GO:0055114; P:GO:0006096; F:GO:0030976; C:GO:0005739	-	EC:1.2.4.2	IPR005475; IPR011603; G3DSA:3.40.50.970 (GENE3D), SSF52518 (SUPERFAMILY)
Brugia malayi	-like 1	17	P:GO:0043967; F:GO:0005515; C:GO:0016020; C:GO:0005815; P:GO:0006357; P:GO:0006310; P:GO:0007283; P:GO:0051301; P:GO:0040008; P:GO:0007067; C:GO:0016363; C:GO:0035267; F:GO:0016887; P:GO:0043968; F:GO:0005524; F:GO:0003678; C:GO:0071339	-		IPR010339; G3DSA:1.10.8.60 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR11093 (PANTHER), SSF52540 (SUPERFAMILY)

Pan troglodytes	heavy polypeptide 1	12	C:GO:0008043; C:GO:0005829; F:GO:0008199; P:GO:0006892; P:GO:0055114; F:GO:0004322; P:GO:0016044; P:GO:0006955; P:GO:0008285; P:GO:0006880; P:GO:0006826; F:GO:0005515	-	EC:1.16.3.1	IPR001519; IPR008331; IPR009040; IPR009078; IPR012347; IPR014034; PTHR11431:SF14 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0003674; P:GO:0008150		IPR007529; PTHR15555 (PANTHER)
Caenorhabditis elegans	major facilitator superfamily protein	5	C:GO:0016021; P:GO:0000003; P:GO:0040010; P:GO:0006898; P:GO:0055085	-		PTHR10924 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	aha-1	28	F:GO:0042789; P:GO:0001938; F:GO:0004871; P:GO:0040010; P:GO:0001892; P:GO:0009410; P:GO:0043193; P:GO:0040017; F:GO:0017162; C:GO:0005737; P:GO:0043619; F:GO:0046982; C:GO:0005667; P:GO:0045821; F:GO:0003705; F:GO:0003713; P:GO:0001666; F:GO:0043565; P:GO:0007165; P:GO:0002119; P:GO:0010575; P:GO:0033235; P:GO:0030522; P:GO:0045648; P:GO:0010171; P:GO:0045944; P:GO:0046886; P:GO:0030949	-		IPR011598; PTHR23042 (PANTHER), PTHR23042:SF7 (PANTHER)
Caenorhabditis briggsae	leukocyte receptor cluster member 1	0		F:GO:0003674; F:GO:0004872; P:GO:0008150		IPR019339; PTHR22093 (PANTHER)
	-	0				-

Caenorhabditis elegans	briggsae cbr-csnk-1 protein	11	P:GO:0040010; P:GO:0018991; F:GO:0004674; P:GO:0040035; F:GO:0005524; P:GO:0010171; P:GO:0002119; P:GO:0040011; P:GO:0009792; P:GO:0040018; P:GO:0006468	-	EC:2.7.11.0	G3DSA:3.30.200.20 (GENE3D)
Caenorhabditis elegans	vacuolar assembly sorting protein	1	C:GO:0005737	-		-
	-	0				-
Caenorhabditis elegans	polynucleotide ki-se 3 -phosphatase	20	P:GO:0009314; P:GO:0000718; P:GO:0006979; F:GO:0046404; P:GO:0046939; F:GO:0019201; F:GO:0003684; F:GO:0003690; P:GO:0008340; P:GO:0042769; F:GO:0004519; C:GO:0005730; P:GO:0016311; P:GO:0040007; F:GO:0046403; P:GO:0006261; F:GO:0005524; P:GO:0019915; P:GO:0002119; F:GO:0005515	-	EC:2.7.1.78; EC:3.1.3.32	IPR013954; IPR015636; G3DSA:3.40.50.1000 (GENE3D), SSF56784 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-cgh-1 protein	20	P:GO:0008340; P:GO:0017148; F:GO:0005515; P:GO:0040010; P:GO:0006898; P:GO:0006916; P:GO:0009792; P:GO:0002009; C:GO:0043186; P:GO:0002119; C:GO:0005875; F:GO:0003723; P:GO:0007276; C:GO:0000932; P:GO:0051729; P:GO:0016071; F:GO:0004004; F:GO:0005524; P:GO:0033962; P:GO:0040035	-		IPR000629; IPR001650; IPR011545; IPR014001; IPR014014; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF6 (PANTHER), SSF52540 (SUPERFAMILY)
Loa loa	gro-1 operon gene protein 1	0				IPR019155; PTHR21481 (PANTHER)

Caenorhabditis elegans	cytokine induced apoptosis inhibitor 1	7	P:GO:0030097; C:GO:0005737; C:GO:0005730; P:GO:0009792; P:GO:0000003; P:GO:0006916; P:GO:0006898	-		IPR007785; PTHR13273:SF10 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	zinc cchc domain containing 11	8	F:GO:0016779; P:GO:0016070; P:GO:0010468; F:GO:0005515; P:GO:0050794; P:GO:0007166; C:GO:0044424; P:GO:0001816	-	EC:2.7.7.0	IPR001878; G3DSA:3.30.460.10 (GENE3D), PTHR12271 (PANTHER), PTHR12271:SF15 (PANTHER), SSF81301 (SUPERFAMILY), SSF81631 (SUPERFAMILY)
Caenorhabditis elegans	zinc cchc domain containing 11	8	F:GO:0016779; P:GO:0016070; P:GO:0010468; F:GO:0005515; P:GO:0050794; P:GO:0007166; C:GO:0044424; P:GO:0001816	-	EC:2.7.7.0	IPR001878; G3DSA:3.30.460.10 (GENE3D), PTHR12271 (PANTHER), PTHR12271:SF15 (PANTHER), SSF81301 (SUPERFAMILY), SSF81631 (SUPERFAMILY)
Loa loa	protein	0		P:GO:0051301		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR19918 (PANTHER)
Caenorhabditis elegans	ring finger protein 157	7	P:GO:0040035; P:GO:0010171; F:GO:0046872; P:GO:0018996; P:GO:0040010; P:GO:0008340; P:GO:0040011	-		SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG19140 [Caenorhabditis briggsae]	2	P:GO:0040010; P:GO:0040017	-		-
Brugia malayi	d--directed r- polymerase iii subunit rpc8	7	F:GO:0003899; P:GO:0040010; P:GO:0006383; P:GO:0040035; P:GO:0002119; P:GO:0006898; C:GO:0005666	-	EC:2.7.7.6	PS51257 (PROFILE)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	4	F:GO:0016788; P:GO:0019915; C:GO:0016020; P:GO:0006629	-		IPR001087; PTHR21325 (PANTHER)

Caenorhabditis briggsae	atp-binding sub-family d member 2	12	P:GO:0055085; C:GO:0005779; P:GO:0007031; F:GO:0005325; C:GO:0005739; F:GO:0042626; P:GO:0033540; F:GO:0042802; C:GO:0043190; F:GO:0005524; P:GO:0015919; C:GO:0005887	-	EC:3.6.3.47	IPR003439; IPR003593; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR11384 (PANTHER), PTHR11384:SF12 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein F29B9.11 [Caenorhabditis elegans]	5	P:GO:0019915; P:GO:0009792; P:GO:0000003; P:GO:0040010; P:GO:0002119	-		SignalP (SIGNALP)
Caenorhabditis briggsae	transmembrane and coiled-coil domain family 1	1	F:GO:0005515	-		IPR019394; PTHR17613 (PANTHER)
	-	0				-
	-	0				PTHR10499 (PANTHER)
Caenorhabditis briggsae	nucleotide-sugar transporter	6	C:GO:0000139; P:GO:0006047; P:GO:0015788; F:GO:0005351; C:GO:0016021; F:GO:0005462	-		IPR007271; PTHR10231:SF15 (PANTHER)
	-	0				-
Heligmosomoides polygyrus	glutathione s-transferase	3	P:GO:0008340; P:GO:0040010; F:GO:0016740	-		IPR004045; IPR012335; IPR012336; PTHR11571 (PANTHER), PTHR11571:SF6 (PANTHER)
Caenorhabditis elegans	family with sequence similarity member a	4	P:GO:0040035; P:GO:0002119; P:GO:0008340; P:GO:0040039	-		IPR018619
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	tumor suppressor candidate 3	8	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0018996; C:GO:0008250; P:GO:0040007; P:GO:0006898; C:GO:0005739	-		IPR006844; IPR012335; IPR012336; IPR021149; SignalP (SIGNALP)
Brugia malayi	beta -galactosyltransferase-like	1	C:GO:0044464	-		IPR003378; PTHR10811 (PANTHER), PTHR10811:SF2 (PANTHER)
Caenorhabditis briggsae	d- repair protein rad50	5	P:GO:0040010; P:GO:0045132; P:GO:0006915; P:GO:0000003; P:GO:0009792	-		G3DSA:3.40.50.300 (GENE3D), PTHR18867 (PANTHER), PTHR18867:SF11 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
	-	0				-

Caenorhabditis briggsae	d- polymerase delta catalytic subunit	14	C:GO:0005875; P:GO:0000910; F:GO:0003887; F:GO:0008310; C:GO:0043625; F:GO:0003677; P:GO:0006272; P:GO:0035188; P:GO:0002119; F:GO:0000166; P:GO:0006898; P:GO:0006273; P:GO:0009792; P:GO:0006974	-	EC:2.7.7.7	IPR006134; PTHR10322 (PANTHER), PTHR10322:SF4 (PANTHER), SSF56672 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
NADP, mitochondrial-like isoform 3	isocitrate dehydroge-se	9	F:GO:0051287; F:GO:0004450; P:GO:0006103; P:GO:0055114; F:GO:0000287; P:GO:0006099; P:GO:0006102; C:GO:0005739; P:GO:0006097	-	EC:1.1.1.42	-
Brugia malayi	centromere kinetochore protein zw10 homolog	9	P:GO:0051649; P:GO:0006996; P:GO:0016192; C:GO:0005694; C:GO:0005856; P:GO:0050789; C:GO:0044446; P:GO:0000087; F:GO:0005488	-		IPR009361; PTHR12205 (PANTHER)
	-	0				-
Caenorhabditis elegans	transmembrane protein 53	1	F:GO:0005515	-		IPR008547
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		SignalP (SIGNALP)
Caenorhabditis briggsae	bed zinc finger family protein	2	F:GO:0005515; F:GO:0003677	-		IPR003656; PTHR21709 (PANTHER)
Homo sapiens	ribosomal p0	7	F:GO:0003735; F:GO:0003723; F:GO:0005515; P:GO:0042254; C:GO:0022625; P:GO:0044419; P:GO:0006414	-		IPR001790; IPR001813; PTHR21141 (PANTHER)
Canis familiaris	rplp0 protein	7	F:GO:0003735; F:GO:0003723; F:GO:0005515; P:GO:0042254; C:GO:0022625; P:GO:0044419; P:GO:0006414	-		IPR001790; IPR001813; PTHR21141 (PANTHER)
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	casein ki-se	14	P:GO:0040010; P:GO:0016055; P:GO:0018991; F:GO:0004674; P:GO:0008347; P:GO:0040035; P:GO:0007283; F:GO:0005524; P:GO:0010171; P:GO:0002119; P:GO:0009792; P:GO:0040018; C:GO:0005886; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF18 (PANTHER)
	-	0				SSF56672 (SUPERFAMILY)
Caenorhabditis elegans	osteoclast stimulating factor 1	2	F:GO:0017124; F:GO:0042802	-		IPR000108; IPR001452; IPR002110; IPR020683; G3DSA:2.30.30.40 (GENE3D), PTHR18958 (PANTHER), PTHR18958:SF213 (PANTHER)
	-	0				-
	-	0				-
Bos taurus	family with sequence similarity member a1	0		F:GO:0003674; C:GO:0005575		-
Caenorhabditis elegans	serine active site containing 1	4	P:GO:0009792; F:GO:0016788; P:GO:0006886; C:GO:0031227	-		IPR012908; G3DSA:3.40.50.1820 (GENE3D), PTHR22731 (PANTHER), SSF53474 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	4	F:GO:0005515; P:GO:0044237; P:GO:0040010; F:GO:0003824	-		IPR002198; IPR002347; IPR016040; IPR020904; PTHR19410:SF76 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	c-type lectin family member (clec-88)	0		F:GO:0005488; F:GO:0003674; C:GO:0016021; F:GO:0005529; P:GO:0008150; C:GO:0005575		-
Caenorhabditis elegans	c-type lectin family member (clec-88)	0		F:GO:0005488; F:GO:0003674; C:GO:0016021; F:GO:0005529; P:GO:0008150; C:GO:0005575		-

Caenorhabditis briggsae	laminin receptor 1	17	P:GO:0040010; P:GO:0016337; F:GO:0003735; C:GO:0005604; F:GO:0005055; P:GO:0040035; P:GO:0006414; P:GO:0018996; C:GO:0022627; F:GO:0043022; C:GO:0005624; P:GO:0002119; F:GO:0043236; P:GO:0030855; C:GO:0043025; P:GO:0009792; C:GO:0016020	-		IPR001865; IPR005707; IPR018130
Caenorhabditis briggsae	laminin receptor 1	17	P:GO:0040010; P:GO:0016337; F:GO:0003735; C:GO:0005604; F:GO:0005055; P:GO:0040035; P:GO:0006414; P:GO:0018996; C:GO:0022627; F:GO:0043022; C:GO:0005624; P:GO:0002119; F:GO:0043236; P:GO:0030855; C:GO:0043025; P:GO:0009792; C:GO:0016020	-		IPR001865; IPR005707; IPR018130
	-	0				-
Teladorsagia circumcincta	calcium activated nucleotidase isoform cra_b	9	P:GO:0040010; C:GO:0043231; P:GO:0008340; F:GO:0004871; P:GO:0043123; F:GO:0005515; C:GO:0044444; F:GO:0016787; C:GO:0016020	-		IPR009283; SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	4	F:GO:0005097; C:GO:0005622; P:GO:0000003; P:GO:0032313	-		IPR000195; G3DSA:1.10.8.270 (GENE3D), PTHR22957 (PANTHER), PTHR22957:SF46 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	4	F:GO:0005097; C:GO:0005622; P:GO:0000003; P:GO:0032313	-		IPR000195; G3DSA:1.10.8.270 (GENE3D), PTHR22957 (PANTHER), PTHR22957:SF46 (PANTHER)

Tribolium castaneum	ubiquitin carboxyl-termi-l hydrolase 14	13	F:GO:0004221; N:GO:0061136; F:GO:0004866; C:GO:0005625; P:GO:0050920; C:GO:0009986; F:GO:0004197; C:GO:0016023; F:GO:0004843; P:GO:0007268; F:GO:0070628; C:GO:0019717; F:GO:0008193	-	EC:3.1.2.15; EC:3.4.22.0	SignalP (SIGNALP)
Loa loa	ubiquitin-conjugating enzyme e2 j2	3	P:GO:0051246; F:GO:0019787; P:GO:0043687	-		IPR000608; IPR016135; PTHR11621 (PANTHER), PTHR11621:SF14 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	abhydrolase domain containing 5	4	P:GO:0050789; P:GO:0008152; C:GO:0005811; F:GO:0016787	-		IPR000073; G3DSA:3.40.50.1820 (GENE3D), PTHR10992 (PANTHER), PTHR10992:SF19 (PANTHER), SSF53474 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	ubiquinol-cytochrome c reductase hinge protein variant 1	2	P:GO:0006122; F:GO:0008121	-	EC:1.10.2.2	IPR003422; IPR023184
Caenorhabditis elegans	illin homolo family member (pxl-1)	3	P:GO:0009792; P:GO:0040010; P:GO:0002119	-		-
Caenorhabditis briggsae	cytoplasmic dynein 1 intermediate chain 2	7	P:GO:0002119; P:GO:0035046; C:GO:0005869; F:GO:0005515; P:GO:0040007; P:GO:0006898; C:GO:0005868	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR12442 (PANTHER), PTHR12442:SF22 (PANTHER)
Caenorhabditis briggsae	cytoplasmic dynein 1 intermediate chain 2	7	P:GO:0002119; P:GO:0035046; C:GO:0005869; F:GO:0005515; P:GO:0040007; P:GO:0006898; C:GO:0005868	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR12442 (PANTHER), PTHR12442:SF22 (PANTHER)
Caenorhabditis briggsae	member ras oncogene family	13	P:GO:0007049; C:GO:0005739; P:GO:0007264; P:GO:0048169; C:GO:0030133; P:GO:0051223; F:GO:0019003; P:GO:0006184; C:GO:0055037; C:GO:0005802; F:GO:0003924; F:GO:0005525; C:GO:0005886	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001806; IPR002078; IPR003579; IPR005225; IPR013753; IPR015595; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-

Caenorhabditis elegans	excitatory amino acid transporter 2	17	P:GO:0031668; C:GO:0016021; P:GO:0009611; P:GO:0046326; P:GO:0051938; P:GO:0007632; P:GO:0035264; P:GO:0010259; P:GO:0070779; F:GO:0015501; P:GO:0021537; F:GO:0017153; P:GO:0006835; P:GO:0042493; C:GO:0030673; P:GO:0043200; P:GO:0030534	-		IPR001991; IPR018107; PTHR11958:SF23 (PANTHER), SignalP (SIGNALP), SSF118215 (SUPERFAMILY)
Caenorhabditis elegans	yol4_caeel ame: full=uncharacterized nte family protein	0		C:GO:0005789; P:GO:0006629; C:GO:0016021; P:GO:0046470		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	katanin p80 wd40-containing subunit b1	5	F:GO:0005515; C:GO:0044430; C:GO:0015630; P:GO:0016043; P:GO:0050794	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; PTHR19845 (PANTHER)
Caenorhabditis elegans	katanin p80 wd40-containing subunit b1	5	F:GO:0005515; C:GO:0044430; C:GO:0015630; P:GO:0016043; P:GO:0050794	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; PTHR19845 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-smf-1 protein	3	P:GO:0010467; C:GO:0016020; P:GO:0019725	-		IPR001046; PTHR11706:SF7 (PANTHER), SignalP (SIGNALP)
Loa loa	n-termi-l acetyltransferase complex ard1 subunit	9	C:GO:0005737; P:GO:0009792; P:GO:0002119; P:GO:0006474; F:GO:0005515; F:GO:0004596; P:GO:0000003; C:GO:0005634; F:GO:0043022	-	EC:2.3.1.88	IPR000182; IPR016181; PTHR23091 (PANTHER), PTHR23091:SF4 (PANTHER)
Caenorhabditis briggsae	methionine gamma-lyase	4	F:GO:0030170; F:GO:0016769; P:GO:0006520; P:GO:0009058	-		IPR000277; IPR015421; IPR015424; PTHR11808:SF19 (PANTHER)
Caenorhabditis briggsae	apoptosis-linked protein 2	1	F:GO:0005509	-		-
Caenorhabditis briggsae	apoptosis-linked protein 2	1	F:GO:0005509	-		-
Caenorhabditis elegans	hypothetical protein F40B5.2 [Caenorhabditis elegans]	0		F:GO:0016787; C:GO:0016021		SignalP (SIGNALP)
Caenorhabditis elegans	leucine rich repeat family protein	6	P:GO:0009792; P:GO:0002119; F:GO:0005488; P:GO:0018996; P:GO:0040017; P:GO:0040007	-		IPR001611; G3DSA:3.80.10.10 (GENE3D), PTHR23154 (PANTHER), PTHR23154:SF116 (PANTHER), SSF52058 (SUPERFAMILY)

Caenorhabditis briggsae	n-acetyltransferase 5	2	P:GO:0008152; F:GO:0004596	-	EC:2.3.1.88	-
Tribolium castaneum	coagulation factor xi	0		F:GO:0004252; C:GO:0001669; C:GO:0016020; F:GO:0016787; F:GO:0008236; C:GO:0043234; F:GO:0003824; C:GO:0005575; F:GO:0008233; P:GO:0006508; F:GO:0005515; P:GO:0007190; P:GO:0007339; P:GO:0007341; F:GO:0005537; P:GO:0007338; P:GO:0007340		IPR001254; IPR001314; IPR005514; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR19355 (PANTHER), PTHR19355:SF82 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	gpn-loop gtpase 1	7	P:GO:0040010; P:GO:0040035; P:GO:0002119; F:GO:0005515; P:GO:0006898; P:GO:0009792; F:GO:0005525	-		IPR004130; G3DSA:3.40.50.300 (GENE3D), PTHR21231 (PANTHER), PTHR21231:SF1 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Homo sapiens	transmembrane protein 147	2	F:GO:0005515; C:GO:0016021	-		IPR019164; PTHR12869 (PANTHER)
	-	0				-
Loa loa	lethal isoform k	6	F:GO:0000827; F:GO:0003993; F:GO:0000832; P:GO:0006020; F:GO:0033857; C:GO:0005829	-	EC:3.1.3.2; EC:2.7.4.24	PTHR12750 (PANTHER), PTHR12750:SF5 (PANTHER)
Caenorhabditis briggsae	phospholipase plb1	0		P:GO:0006629; F:GO:0016788; F:GO:0016787		PTHR21325 (PANTHER)
Caenorhabditis briggsae	peptidase d	6	F:GO:0030145; F:GO:0004181; P:GO:0007281; F:GO:0004177; P:GO:0006520; P:GO:0006508	-	EC:3.4.17.0; EC:3.4.11.0	IPR000994; IPR001131; IPR007865; G3DSA:3.40.350.10 (GENE3D), PTHR10804:SF17 (PANTHER), SSF53092 (SUPERFAMILY)
Brugia malayi	peptidase d	5	F:GO:0030145; F:GO:0008235; P:GO:0007281; F:GO:0004177; P:GO:0006508	-	EC:3.4.11.0	IPR007865; G3DSA:3.40.350.10 (GENE3D), SSF53092 (SUPERFAMILY)
Ancylostoma ceylanicum	kunitz type serine protease inhibitor	0		F:GO:0008233; F:GO:0004867		IPR002223; PTHR10083 (PANTHER), PTHR10083:SF17 (PANTHER)

Loa loa	adp-ribosylation factor 1	27	F:GO:0004871; P:GO:0008360; F:GO:0005515; P:GO:0007155; P:GO:0040010; P:GO:0007269; P:GO:0040011; F:GO:0005525; C:GO:0005794; P:GO:0006886; C:GO:0005829; P:GO:0006471; P:GO:0007264; P:GO:0009792; P:GO:0002009; P:GO:0016197; P:GO:0002119; P:GO:0007186; P:GO:0010883; C:GO:0012505; C:GO:0005783; P:GO:0048599; F:GO:0003924; C:GO:0005634; P:GO:0040035; C:GO:0030017; P:GO:0048488	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR006688; IPR006689; G3DSA:3.40.50.300 (GENE3D), PTHR11711:SF30 (PANTHER), PS51417 (PROFILE), SSF52540 (SUPERFAMILY)
Loa loa	adp-ribosylation factor 1	27	F:GO:0004871; P:GO:0008360; F:GO:0005515; P:GO:0007155; P:GO:0040010; P:GO:0007269; P:GO:0040011; F:GO:0005525; C:GO:0005794; P:GO:0006886; C:GO:0005829; P:GO:0006471; P:GO:0007264; P:GO:0009792; P:GO:0002009; P:GO:0016197; P:GO:0002119; P:GO:0007186; P:GO:0010883; C:GO:0012505; C:GO:0005783; P:GO:0048599; F:GO:0003924; C:GO:0005634; P:GO:0040035; C:GO:0030017; P:GO:0048488	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR006688; IPR006689; G3DSA:3.40.50.300 (GENE3D), PTHR11711:SF30 (PANTHER), PS51417 (PROFILE), SSF52540 (SUPERFAMILY)
Caenorhabditis brenneri	elegans protein confirmed by transcript evidence	0				IPR021869
Caenorhabditis briggsae	transmembrane protein 115	1	C:GO:0044464	-		IPR013861; PTHR13377 (PANTHER), SignalP (SIGNALP)

Caenorhabditis briggsae	transmembrane protein 115	0		F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150; C:GO:0005575		IPR013861; PTHR13377 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	chromatin modifying protein 5	8	C:GO:0005768; P:GO:0008333; F:GO:0005515; P:GO:0007040; C:GO:0016020; C:GO:0005634; P:GO:0001919; P:GO:0015031	-		IPR005024; PTHR22761 (PANTHER)
	-	0				-
Caenorhabditis briggsae	gamma-secretase subunit pen-2	21	F:GO:0004175; F:GO:0005515; P:GO:0043085; P:GO:0048542; P:GO:0016482; P:GO:0042332; P:GO:0031293; C:GO:0005794; P:GO:0008624; P:GO:0007291; P:GO:0006509; P:GO:0016485; P:GO:0007220; P:GO:0007301; C:GO:0005875; C:GO:0012505; P:GO:0042987; C:GO:0005783; C:GO:0005811; C:GO:0005887; P:GO:0006606	-		IPR019379; PTHR16318 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	had-superfamily hydrolase	0		C:GO:0009507; F:GO:0016787; P:GO:0008152; F:GO:0003824		IPR005834; G3DSA:3.40.50.1000 (GENE3D), PTHR18901 (PANTHER), SSF56784 (SUPERFAMILY)
Apis mellifera	protein tyrosine receptor a isoform 2	5	F:GO:0032403; P:GO:0048714; F:GO:0004725; C:GO:0005792; C:GO:0005886	-	EC:3.1.3.48	IPR000242; IPR000387; IPR016130; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), SignalP (SIGNALP), SSF52799 (SUPERFAMILY)
	-	0				IPR003195; PTHR11380:SF3 (PANTHER)
	-	0				-
	-	0				-
Oigolaimella attenuata	large subunit ribosomal protein 29	3	C:GO:0005840; F:GO:0003735; P:GO:0006412	-	EC:3.6.5.3	-
Loa loa	protein lsm12 homolog	0		F:GO:0003674; P:GO:0008150; F:GO:0005515; C:GO:0005575		IPR019181

Caenorhabditis elegans	subfamily member 10	5	P:GO:0006457; P:GO:0045454; F:GO:0031072; F:GO:0051082; C:GO:0005783	-		IPR001623; IPR012335; IPR012336; IPR013766; IPR015609; IPR017936; IPR018253; PTHR11821:SF16 (PANTHER)
Caenorhabditis elegans	u4 u6 small nuclear ribonucleoprotein prp3	4	C:GO:0044428; P:GO:0006898; C:GO:0030529; P:GO:0006396	-		IPR010541; IPR013881; PTHR14212 (PANTHER)
Caenorhabditis elegans	protein phosphatase pp2a regulatory subunit b	16	P:GO:0006470; F:GO:0008601; P:GO:0016055; P:GO:0007447; C:GO:0005875; P:GO:0007423; P:GO:0007088; P:GO:0007406; F:GO:0004722; P:GO:0001700; P:GO:0000090; P:GO:0045201; P:GO:0007165; C:GO:0000159; C:GO:0005737; C:GO:0005634	-		IPR000009; IPR001680; IPR011046; IPR015943; IPR018067; IPR019781
Caenorhabditis elegans	cohesin loading complex subunit scc4 homolog	3	P:GO:0007049; C:GO:0005634; C:GO:0044446	-		IPR019440; PTHR21394 (PANTHER)
Caenorhabditis elegans	hypothetical protein T23F2.2 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	sodium hydrogen exchanger 8	5	F:GO:0015385; P:GO:0055085; P:GO:0006812; P:GO:0006885; C:GO:0016021	-		IPR004709; IPR006153; IPR018407; IPR018422; SignalP (SIGNALP)
Caenorhabditis elegans	apurinic endonuclease apn1	7	P:GO:0009792; F:GO:0003677; C:GO:0005622; F:GO:0008833; F:GO:0016829; F:GO:0008270; P:GO:0006281	-	EC:3.1.21.2	IPR001719; IPR012307; IPR013022; IPR018246
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	2	P:GO:0006810; C:GO:0016020	-		-
	-	0				-
Ascaris lumbricoides	cytoplasmic intermediate filament protein	9	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0018991; P:GO:0018996; F:GO:0005515; P:GO:0040010; P:GO:0040011; P:GO:0006898	-		IPR001664; IPR016044; PD936484 (PRODOM), PTHR23239:SF13 (PANTHER)
Caenorhabditis briggsae	novel protein	2	P:GO:0040018; P:GO:0002119	-		IPR003890; IPR016021; PTHR18034 (PANTHER), PTHR18034:SF4 (PANTHER)

Caenorhabditis elegans	zinc carboxypeptidase family protein	0		P:GO:0006508; F:GO:0004181; F:GO:0004180; F:GO:0008270		-
Caenorhabditis elegans	hypothetical protein T23E7.2 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	Hypothetical protein CBG01887 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	hypothetical protein T23E7.2 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	hypothetical protein T23E7.2 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	briggsae cbr-unc-14 protein	0				-
Pan troglodytes	ribosomal protein l12	7	C:GO:0005730; C:GO:0005840; F:GO:0003735; F:GO:0003723; F:GO:0005515; C:GO:0005829; P:GO:0006414	-		IPR000911; IPR020783; IPR020784; IPR020785; PTHR11661:SF2 (PANTHER)
	-	0				-
Loa loa	taf3 r- polymerase tata box binding protein -associated factor	8	P:GO:0051457; F:GO:0008270; F:GO:0010843; P:GO:0030097; F:GO:0008134; C:GO:0005669; F:GO:0003702; P:GO:0006366	-		IPR001965; IPR011011; IPR013083; IPR019786; IPR019787; PTHR12321 (PANTHER)
Caenorhabditis briggsae	chid1 protein	0		F:GO:0004568; F:GO:0043169; F:GO:0003674; C:GO:0005764; P:GO:0005975; C:GO:0005576; F:GO:0003824; C:GO:0005575; F:GO:0004553; P:GO:0006032; P:GO:0008150		IPR001223; IPR013781; IPR017853; PTHR11177 (PANTHER), PTHR11177:SF6 (PANTHER)
	-	0				-
Salmo salar	ribosomal protein l38	6	P:GO:0009790; F:GO:0003735; F:GO:0003723; F:GO:0005515; C:GO:0022625; P:GO:0006414	-		-
Caenorhabditis briggsae	aldehyde dehydroge-se 4 member a1	11	P:GO:0040010; P:GO:0055114; P:GO:0000003; F:GO:0009055; P:GO:0040017; F:GO:0003842; C:GO:0005759; P:GO:0006898; P:GO:0006561; P:GO:0006562; F:GO:0004029	-	EC:1.5.1.12; EC:1.2.1.3	IPR005931; IPR015590; IPR016160; IPR016161; IPR016162; IPR016163; PTHR11699:SF52 (PANTHER)
Caenorhabditis briggsae	cathepsin f (c01 family)	4	F:GO:0004869; F:GO:0005515; F:GO:0004197; P:GO:0006508	-	EC:3.4.22.0	IPR000169; IPR000668; IPR013128; IPR013201; G3DSA:3.90.70.10 (GENE3D), PTHR12411:SF43 (PANTHER), SSF54001 (SUPERFAMILY)

Loa loa	c-termi-l binding protein	4	P:GO:0044238; F:GO:0016616; F:GO:0051287; F:GO:0016787	-	EC:1.1.1.0	IPR006140; IPR016040; PTHR10996 (PANTHER), PTHR10996:SF11 (PANTHER)
Caenorhabditis elegans	wd repeat-containing protein 91	0		F:GO:0003674; P:GO:0008150		-
	-	0				-
Caenorhabditis briggsae	ump synthase	6	F:GO:0004590; P:GO:0006222; P:GO:0009792; C:GO:0005737; C:GO:0005634; F:GO:0004588	-	EC:4.1.1.23; EC:2.4.2.10	IPR000836; IPR004467; G3DSA:3.40.50.2020 (GENE3D), SSF53271 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	2	P:GO:0040010; C:GO:0016020	-		G3DSA:1.20.1250.20 (GENE3D), PTHR11662 (PANTHER), PTHR11662:SF9 (PANTHER)
Caenorhabditis elegans	heat repeat containing 5b	4	P:GO:0040007; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		IPR011989; IPR016024; PTHR21663 (PANTHER)
Caenorhabditis elegans	heat repeat-containing protein 5b	4	P:GO:0040007; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		IPR011989; IPR016024; PTHR21663 (PANTHER)
Caenorhabditis briggsae	shwachman-bodian-diamond syndrome protein	9	F:GO:0005515; P:GO:0048513; P:GO:0007610; N:GO:0071840; P:GO:0002376; C:GO:0044446; C:GO:0043232; P:GO:0009987; C:GO:0005634	-		IPR002140; IPR018023; IPR018978; IPR019783; G3DSA:3.30.1250.10 (GENE3D), SSF109728 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Homo sapiens	s100 calcium binding protein a1	12	C:GO:0016529; C:GO:0005829; P:GO:0008016; C:GO:0043234; P:GO:0023034; F:GO:0005509; F:GO:0048154; F:GO:0048155; P:GO:0000122; F:GO:0051117; F:GO:0042803; C:GO:0005634	-		SignalP (SIGNALP)
Angiostrongylus cantonensis	msp-domain protein 4	3	C:GO:0005856; F:GO:0005198; P:GO:0040011	-		IPR000535; IPR008962; PTHR22947 (PANTHER)
	-	0				-
Caenorhabditis briggsae	mgc84524 protein	0		C:GO:0016021; C:GO:0016020		IPR018795
Caenorhabditis elegans	k2013_xentr ame: full=uncharacterized protein kiaa2013 homolog flags: precursor	0		C:GO:0016021; C:GO:0016020		IPR018795
Caenorhabditis briggsae	mgc84524 protein	0		C:GO:0016021; C:GO:0016020		IPR018795

Saccoglossus kowalevskii	forkhead box n1	0		C:GO:0005667; F:GO:0003677; C:GO:0005634; P:GO:0010551; P:GO:0006355; P:GO:0030216; F:GO:0016566; F:GO:0003705; P:GO:0007389; F:GO:0003704; P:GO:0006350; F:GO:0016563; P:GO:0009790; P:GO:0048538; P:GO:0051090; F:GO:0003700; F:GO:0010843; P:GO:0007275; P:GO:0045449; F:GO:0043565; F:GO:0008134; C:GO:0005575; F:GO:0003690; F:GO:0008301		-
Caenorhabditis elegans	isoform a	0				IPR011993; PTHR11232 (PANTHER), PTHR11232:SF2 (PANTHER), SSF50729 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	zinc finger transcription factor family member (ztf-23)	2	P:GO:0040015; F:GO:0005515	-		IPR007087; IPR015880
	-	0				-
Caenorhabditis briggsae	briggsae cbr-frm-10 protein	0		P:GO:0030178; F:GO:0005488; C:GO:0005856		IPR000299; IPR014352; IPR019748; PTHR13283 (PANTHER), PTHR13283:SF1 (PANTHER)
Caenorhabditis briggsae	high choriolytic enzyme 1 precursor	2	F:GO:0008233; P:GO:0007413	-		IPR001506; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF73 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis briggsae	pet191 polypeptide	0				IPR018793
Caenorhabditis briggsae	pet191 polypeptide	0				IPR018793
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-

Caenorhabditis elegans	eukaryotic translation initiation factor 2 gamma	27	P:GO:0006413; F:GO:0005515; F:GO:0008270; P:GO:0030702; P:GO:0051567; P:GO:0040010; F:GO:0046974; P:GO:0048132; P:GO:0040018; P:GO:0040011; F:GO:0005525; F:GO:0003743; C:GO:0005829; P:GO:0006306; C:GO:0000775; P:GO:0009792; C:GO:0000792; P:GO:0031507; P:GO:0002119; C:GO:0005850; P:GO:0010171; F:GO:0000049; P:GO:0070868; F:GO:0003682; F:GO:0003924; C:GO:0005634; P:GO:0006348	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000795; G3DSA:3.40.50.300 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF9 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-mtk-1 protein	2	P:GO:0009987; P:GO:0043170	-		-
	-	0				SignalP (SIGNALP)
Brugia malayi	hypothetical protein Bm1_28665 [Brugia malayi]	0				-
	-	0				-
Callithrix jacchus	heat shock protein 90kda beta member 1	23	P:GO:0030433; P:GO:0006457; C:GO:0005788; F:GO:0050750; P:GO:0031247; C:GO:0005792; C:GO:0042470; F:GO:0046790; F:GO:0005509; P:GO:0015031; C:GO:0005789; C:GO:0005829; P:GO:0006916; P:GO:0001666; F:GO:0051082; F:GO:0019903; F:GO:0003723; P:GO:0051208; C:GO:0048471; C:GO:0044459; P:GO:0071318; F:GO:0005524; P:GO:0043666	-		SignalP (SIGNALP)

Caenorhabditis briggsae	abnormal go-d development family member (gon-2)	6	P:GO:0007067; P:GO:0055085; P:GO:0006811; C:GO:0016021; P:GO:0008406; F:GO:0005216	-		PTHR13800 (PANTHER)
Caenorhabditis sp. PS1010	uncoordi-ted family member (unc-73)	1	F:GO:0005085	-		IPR001251; PTHR22826 (PANTHER), PTHR22826:SF39 (PANTHER)
Caenorhabditis briggsae	spectrin beta	1	F:GO:0003779	-		IPR001589; IPR001715; PTHR11915 (PANTHER), PTHR11915:SF48 (PANTHER)
Caenorhabditis elegans	snf related ki-se	5	P:GO:0006468; F:GO:0005524; F:GO:0000287; C:GO:0005634; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017441; IPR017442; IPR020636; IPR020661; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), SignalP (SIGNALP)
Caenorhabditis briggsae	cdc42 binding protein ki-se beta (dmpk-like)	10	F:GO:0005083; F:GO:0004674; C:GO:0005856; P:GO:0007163; F:GO:0046872; P:GO:0007010; F:GO:0005524; F:GO:0005515; P:GO:0007165; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR000961; IPR011009; IPR011993; IPR017442; IPR017892; G3DSA:1.10.510.10 (GENE3D), PTHR22988 (PANTHER), PTHR22988:SF2 (PANTHER)
Caenorhabditis elegans	hypothetical protein C15F1.2 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
Caenorhabditis elegans	golgi associated pdz and coiled-coil motif containing	14	C:GO:0044456; P:GO:0045176; C:GO:0030140; P:GO:0043004; C:GO:0019717; F:GO:0005083; P:GO:0007289; F:GO:0042802; P:GO:0006888; P:GO:0006914; C:GO:0042995; P:GO:0051260; C:GO:0005886; F:GO:0042980	-		IPR000408; G3DSA:2.30.42.10 (GENE3D), PTHR16528 (PANTHER)
Caenorhabditis sp. PS1010	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				IPR001611; PR00019 (PRINTS), G3DSA:3.80.10.10 (GENE3D), SSF52075 (SUPERFAMILY)
	-	0				-
Pan troglodytes	ribosomal protein l18	4	F:GO:0003735; F:GO:0003723; C:GO:0022625; P:GO:0006414	-		IPR000039; IPR021131; IPR021132; G3DSA:3.100.10.10 (GENE3D)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	P:GO:0002009; P:GO:0040010; P:GO:0040035; P:GO:0040011	-		-

Caenorhabditis elegans	beige beach domain containing protein	0		F:GO:0046872; F:GO:0005488; F:GO:0008270		-
Caenorhabditis elegans	hypothetical protein CC8.1 [Caenorhabditis elegans]	0		F:GO:0005515		-
Caenorhabditis elegans	wd repeat phosphoinositide interacting 1	5	C:GO:0043231; F:GO:0005102; C:GO:0016020; C:GO:0000407; C:GO:0044446	-		PTHR11227 (PANTHER), PTHR11227:SF17 (PANTHER)
Caenorhabditis elegans	wd repeat phosphoinositide interacting 1	5	C:GO:0043231; F:GO:0005102; C:GO:0016020; C:GO:0000407; C:GO:0044446	-		PTHR11227 (PANTHER), PTHR11227:SF17 (PANTHER)
Caenorhabditis elegans	wd repeat phosphoinositide interacting 1	5	C:GO:0043231; F:GO:0005102; C:GO:0016020; C:GO:0000407; C:GO:0044446	-		PTHR11227 (PANTHER), PTHR11227:SF17 (PANTHER)
Caenorhabditis briggsae	ykq9_caeel ame: full=uncharacterized protein	0		F:GO:0004553; P:GO:0005975; F:GO:0003824; F:GO:0043169		IPR003892; IPR009060
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	4	F:GO:0005097; C:GO:0005622; P:GO:0000003; P:GO:0032313	-		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	4	F:GO:0005097; C:GO:0005622; P:GO:0000003; P:GO:0032313	-		PTHR22957 (PANTHER), PTHR22957:SF46 (PANTHER)
Caenorhabditis elegans	nuclear receptor subfamily group member 3	13	P:GO:0060005; F:GO:0008270; P:GO:0045944; P:GO:0050885; P:GO:0048752; F:GO:0043565; F:GO:0016563; F:GO:0005515; F:GO:0003700; F:GO:0003707; P:GO:0001707; P:GO:0030534; C:GO:0005634	-		IPR001628; IPR013088; PR00350 (PRINTS), PTHR11865 (PANTHER), PTHR11865:SF168 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis elegans	nuclear receptor subfamily group member 3	7	F:GO:0003700; F:GO:0043565; F:GO:0005515; F:GO:0003707; C:GO:0005634; F:GO:0008270; P:GO:0006355	-		IPR001628; IPR013088; PR00350 (PRINTS), PTHR11865 (PANTHER), PTHR11865:SF168 (PANTHER), SSF57716 (SUPERFAMILY)
synthetic construct	parathymosin [synthetic construct]	4	C:GO:0005829; C:GO:0005634; C:GO:0005625; P:GO:0006260	-		-
	-	0				-
Ancylostoma duodenale	ancylostoma-secreted protein 1 precursor	0		C:GO:0005576		IPR014044; SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				IPR004988; SignalP (SIGNALP)

	-	0				G3DSA:3.10.370.10 (GENE3D)
Caenorhabditis elegans	abnormal embryogenesis family member (emb-27)	0		P:GO:0000003; P:GO:0040035; P:GO:0009792; P:GO:0007126; P:GO:0007067		-
Caenorhabditis elegans	yqoa_caeel ame: full= r--binding protein	1	F:GO:0005488	-		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	5	P:GO:0006732; F:GO:0005515; C:GO:0044444; P:GO:0006631; F:GO:0016291	-		IPR006862
	-	0				-
	-	0				PR01503 (PRINTS)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				IPR005069
Caenorhabditis briggsae	enoyl- mitochondrial	8	P:GO:0040010; C:GO:0005875; P:GO:0002119; P:GO:0006635; F:GO:0005515; C:GO:0005759; F:GO:0003824; C:GO:0005811	-		IPR001753; IPR014748; IPR018376; G3DSA:3.90.226.10 (GENE3D), PTHR11941 (PANTHER), SignalP (SIGNALP), SSF52096 (SUPERFAMILY)
Caenorhabditis briggsae	enoyl- mitochondrial	8	P:GO:0040010; C:GO:0005875; P:GO:0002119; P:GO:0006635; F:GO:0005515; C:GO:0005759; F:GO:0003824; C:GO:0005811	-		IPR001753; IPR014748; IPR018376; G3DSA:3.90.226.10 (GENE3D), PTHR11941 (PANTHER), SignalP (SIGNALP), SSF52096 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	d-j homolog subfamily c member 2	9	P:GO:0040010; P:GO:0034645; P:GO:0090304; P:GO:0000003; F:GO:0005515; P:GO:0008356; P:GO:0050794; P:GO:0010467; P:GO:0009792	-		IPR001005; IPR009057; IPR012287; IPR014778; IPR015609; IPR017877; PTHR11821:SF29 (PANTHER)
Caenorhabditis briggsae	tbc1 domain family member 2b	2	F:GO:0005515; F:GO:0005096	-		IPR000195; G3DSA:1.10.8.270 (GENE3D), PTHR22957 (PANTHER), PTHR22957:SF55 (PANTHER)

Caenorhabditis briggsae	purine nucleoside phosphorylase inosine and guanosine-specific	15	P:GO:0046124; P:GO:0006955; P:GO:0009165; P:GO:0042981; C:GO:0005737; P:GO:0043101; F:GO:0004731; P:GO:0045621; P:GO:0046130; P:GO:0050870; C:GO:0005634; F:GO:0005488; P:GO:0048584; P:GO:0009144; C:GO:0005576	-	EC:2.4.2.1	-
Caenorhabditis briggsae	ww domain-containing oxidoreductase	7	P:GO:0055114; P:GO:0030178; F:GO:0016491; F:GO:0046983; F:GO:0050662; P:GO:0008202; C:GO:0005794	-		IPR002198; IPR016040; PTHR19410:SF99 (PANTHER), SSF51735 (SUPERFAMILY)
Brugia malayi	rab gtpase activating protein 1	0		C:GO:0005875; F:GO:0015631; C:GO:0005815; C:GO:0005737; C:GO:0005813; C:GO:0005622; F:GO:0005097; F:GO:0005096; C:GO:0005829; P:GO:0007049; P:GO:0032313; C:GO:0005856		IPR000195; PTHR22957 (PANTHER), PTHR22957:SF44 (PANTHER)
Caenorhabditis elegans	translation initiation factor sui1 family protein	1	F:GO:0003676	-		IPR001950; PTHR12217 (PANTHER), PTHR12217:SF2 (PANTHER)
Caenorhabditis elegans	ligatin	1	F:GO:0005488	-		IPR001950; IPR002478; IPR004521; IPR015947; G3DSA:2.30.130.10 (GENE3D), PTHR12217 (PANTHER), PTHR12217:SF2 (PANTHER)
Caenorhabditis elegans	ligatin	1	F:GO:0005488	-		IPR001950; IPR002478; IPR004521; IPR015947; G3DSA:2.30.130.10 (GENE3D), PTHR12217 (PANTHER), PTHR12217:SF2 (PANTHER)
Caenorhabditis elegans	ligatin	1	F:GO:0005488	-		IPR001950; IPR002478; IPR004521; IPR015947; G3DSA:2.30.130.10 (GENE3D), PTHR12217 (PANTHER), PTHR12217:SF2 (PANTHER)
	-	0				-
Caenorhabditis briggsae	apolipoprotein a-i binding protein	0		C:GO:0005739; F:GO:0005515; C:GO:0005576		IPR004443; G3DSA:3.40.50.10260 (GENE3D), PTHR13232 (PANTHER), PTHR13232:SF3 (PANTHER)
Brugia malayi	lethal essential for life l2efl	1	F:GO:0042802	-		PS51257 (PROFILE)
Caenorhabditis elegans	homeobox family member (ceh-44)	5	F:GO:0005488; P:GO:0045449; P:GO:0007275; C:GO:0016020; C:GO:0005794	-		IPR012955; PD936484 (PRODOM), PTHR14043 (PANTHER), PTHR14043:SF2 (PANTHER)

Caenorhabditis elegans	cut-like 1	6	F:GO:0030528; P:GO:0006355; F:GO:0003677; P:GO:0048513; C:GO:0016020; C:GO:0005794	-		IPR012955; PTHR14043 (PANTHER), PTHR14043:SF2 (PANTHER)
Caenorhabditis elegans	alpha beta hydrolase fold-1 domain-containing protein	2	F:GO:0005488; C:GO:0044464	-		-
Caenorhabditis briggsae	sorting nexin 13	2	F:GO:0005515; P:GO:0007154	-		IPR000342; IPR016137; G3DSA:1.10.167.10 (GENE3D), PTHR22775 (PANTHER), PTHR22775:SF8 (PANTHER)
Caenorhabditis briggsae	isoform b	5	F:GO:0008607; F:GO:0016301; F:GO:0004339; P:GO:0005977; F:GO:0005516	-	EC:3.2.1.3	IPR008734; IPR008928; IPR011613; IPR012341; PTHR10749:SF3 (PANTHER), SignalP (SIGNALP)
Clavispora lusitaniae ATCC 42720	essential component of the nuclear pore which mediates nuclear import and export	0		C:GO:0005643; F:GO:0043169; P:GO:0046907; P:GO:0016998; P:GO:0006810; F:GO:0008270; P:GO:0005975; F:GO:0003824; F:GO:0017056; C:GO:0005622; P:GO:0009253; F:GO:0003796; F:GO:0005488		-
Caenorhabditis briggsae	leukotriene a4 hydrolase	5	P:GO:0006954; P:GO:0019370; P:GO:0006508; F:GO:0008270; F:GO:0008237	-		IPR001930; IPR014782; PTHR11533:SF4 (PANTHER), SSF55486 (SUPERFAMILY), SSF63737 (SUPERFAMILY)
Caenorhabditis elegans	serine threonine-protein phosphatase 5	14	P:GO:0006470; C:GO:0005829; P:GO:0051291; C:GO:0043005; F:GO:0004871; F:GO:0046872; P:GO:0043123; F:GO:0004722; P:GO:0007067; C:GO:0043025; F:GO:0019904; P:GO:0006350; P:GO:0043278; C:GO:0005634	-		IPR004843; IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF12 (PANTHER), SSF56300 (SUPERFAMILY)
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-

Caenorhabditis briggsae	transformation transcription domain-associated protein	9	P:GO:0043967; P:GO:0043968; P:GO:0016578; P:GO:0045449; C:GO:0035267; C:GO:0033276; C:GO:0030914; F:GO:0003713; P:GO:0007093	-		-
Caenorhabditis briggsae	briggsae cbr-apt-10 protein	1	P:GO:0016192	-		-
Loa loa	hypothetical protein LOAG_08693 [Loa loa]	0				-
	-	0				-
Loa loa	heavy unconventio-l myosin family member (hum-2)	4	C:GO:0016459; F:GO:0005515; F:GO:0005524; F:GO:0003774	-		IPR002710; IPR010916; IPR018444; PTHR13140 (PANTHER), PTHR13140:SF15 (PANTHER)
Caenorhabditis briggsae	heavy unconventio-l myosin family member (hum-2)	4	C:GO:0016459; F:GO:0005515; F:GO:0005524; F:GO:0003774	-		-
Brugia malayi	ftsj methyltransferase domain-containing protein 1	0		F:GO:0003676; F:GO:0008168; F:GO:0016740; C:GO:0016021; C:GO:0016020; P:GO:0032259		IPR002877; G3DSA:3.40.50.150 (GENE3D), PTHR16121 (PANTHER), SSF53335 (SUPERFAMILY)
Caenorhabditis elegans	adp-dependent glucoki-se	3	P:GO:0005975; F:GO:0016773; F:GO:0016301	-	EC:2.7.1.0	IPR007666; IPR019793; G3DSA:3.40.1190.20 (GENE3D), SignalP (SIGNALP), SSF53613 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	vacuolar protein sorting 11	8	P:GO:0009792; P:GO:0010171; F:GO:0005488; P:GO:0040018; P:GO:0018996; P:GO:0040010; P:GO:0000003; P:GO:0008219	-		IPR015943; PTHR23323 (PANTHER), PTHR23323:SF24 (PANTHER)
	-	0				IPR009539; PTHR20886:SF1 (PANTHER), SignalP (SIGNALP)
Loa loa	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	13	P:GO:0040010; C:GO:0008250; P:GO:0018279; C:GO:0005792; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0034097; P:GO:0042110; P:GO:0006496; P:GO:0009792; F:GO:0004579; P:GO:0040015	-	EC:2.4.1.119	IPR005013; SignalP (SIGNALP)
Caenorhabditis briggsae	phosphatidylinositol glycan anchor class q	2	F:GO:0016740; P:GO:0016254	-		IPR007720; PTHR21329 (PANTHER), PTHR21329:SF5 (PANTHER)

Caenorhabditis elegans	retinol dehydroge-se 12-like	2	P:GO:0008152; F:GO:0003824	-		IPR002198; IPR016040; PTHR19410:SF8 (PANTHER), SignalP (SIGNALP), SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein Y48G1A.1 [Caenorhabditis elegans]	0				IPR009091; SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-apd-3 protein	10	P:GO:0009792; P:GO:0010171; P:GO:0002119; C:GO:0005794; F:GO:0005515; C:GO:0030117; F:GO:0008565; P:GO:0016192; P:GO:0006886; P:GO:0040007	-		IPR000408; IPR002553; IPR011989; IPR016024; PTHR22781 (PANTHER), PTHR22781:SF9 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-apd-3 protein	10	P:GO:0009792; P:GO:0010171; P:GO:0002119; C:GO:0005794; F:GO:0005515; C:GO:0030117; F:GO:0008565; P:GO:0016192; P:GO:0006886; P:GO:0040007	-		IPR000408; IPR002553; IPR011989; IPR016024; PTHR22781 (PANTHER), PTHR22781:SF9 (PANTHER)
Caenorhabditis briggsae	universal minicircle sequence binding protein	2	F:GO:0005488; F:GO:0003824	-		-
Brugia malayi	universal minicircle sequence binding protein	7	F:GO:0005488; P:GO:0040007; P:GO:0000003; P:GO:0002119; P:GO:0040011; P:GO:0009792; F:GO:0016787	-		-
Caenorhabditis elegans	briggsae cbr-unc-36 protein	4	C:GO:0016021; F:GO:0005262; P:GO:0006816; F:GO:0005244	-		PTHR10166 (PANTHER), PTHR10166:SF5 (PANTHER)
Homo sapiens	ribosomal protein l4 variant	5	F:GO:0003735; F:GO:0003723; F:GO:0005515; C:GO:0022625; P:GO:0006414	-		IPR016160; PTHR19431 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	abnormal embryonic partitioning of cytoplasm family member (par-3)	8	C:GO:0005737; P:GO:0007163; P:GO:0040001; F:GO:0005515; P:GO:0007155; P:GO:0007369; C:GO:0016021; P:GO:0008406	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR16484 (PANTHER), PTHR16484:SF2 (PANTHER)
Caenorhabditis elegans	abnormal embryonic partitioning of cytoplasm family member (par-3)	1	P:GO:0009987	-		PTHR16484 (PANTHER), PTHR16484:SF2 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0045132; P:GO:0007126		-

Caenorhabditis elegans	briggsae cbr-nmy-1 protein	4	F:GO:0003779; C:GO:0016459; F:GO:0005524; F:GO:0003774	-		IPR001609; IPR004009; PTHR13140 (PANTHER), PTHR13140:SF23 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-gst-42 protein	2	F:GO:0042802; F:GO:0003824	-		IPR004045; IPR005955; IPR010987; IPR012335; IPR012336; IPR017933; PTHR11260 (PANTHER), PTHR11260:SF8 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-gst-42 protein	2	F:GO:0042802; F:GO:0003824	-		-
	-	0				SignalP (SIGNALP)
Brugia malayi	subfamily member 3	8	F:GO:0004860; C:GO:0005829; F:GO:0051087; F:GO:0051787; P:GO:0051603; C:GO:0031205; C:GO:0005788; P:GO:0030968	-		IPR001440; IPR001623; IPR011990; IPR013026; IPR013105; IPR015609; IPR019734; PTHR11821:SF68 (PANTHER), SignalP (SIGNALP), SSF48452 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG02464 [Caenorhabditis briggsae]	0				-
	-	0				-
Caenorhabditis elegans	spastin isoform 2	11	P:GO:0051013; P:GO:0031117; C:GO:0043231; P:GO:0034214; C:GO:0005874; P:GO:0051260; P:GO:0051301; F:GO:0005524; F:GO:0008568; C:GO:0048471; F:GO:0015631	-	EC:3.6.4.3	G3DSA:3.40.50.300 (GENE3D), PTHR23074 (PANTHER), PTHR23074:SF1 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein F31A3.5 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
Brugia malayi	transcription initiation factor iia gamma chain	4	P:GO:0006357; P:GO:0006367; C:GO:0005672; F:GO:0016251	-		IPR003194; IPR009083; IPR009088; IPR015871; IPR015872
Caenorhabditis briggsae	ubiquitin specific peptidase 19	3	P:GO:0051726; F:GO:0016787; C:GO:0005829	-		IPR001394; IPR018200; PTHR10420 (PANTHER), PTHR10420:SF73 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis briggsae	ubiquitin specific peptidase 19	3	P:GO:0051726; F:GO:0016787; C:GO:0005829	-		IPR001394; IPR002893; IPR018200; PTHR10420 (PANTHER), PTHR10420:SF73 (PANTHER), SSF144232 (SUPERFAMILY), SSF54001 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Brugia malayi	dedicator of cytokinesis 7	1	F:GO:0005488	-		-
	-	0				PR01217 (PRINTS)
	-	0				-
Caenorhabditis briggsae	lmbr1 domain containing 2	1	C:GO:0016021	-		IPR006876; PTHR21355 (PANTHER), SignalP (SIGNALP)
Brugia malayi	stromal antigen	1	F:GO:0005515	-		PTHR11199 (PANTHER)

Caenorhabditis briggsae	novel protein	0		C:GO:0005739; P:GO:0006200; F:GO:0000166; F:GO:0017111; F:GO:0003674; F:GO:0005524; F:GO:0016887; C:GO:0005576; P:GO:0008152; P:GO:0008150		-
Brugia malayi	eif4-gamma eif5 eif2-epsilon family protein	4	P:GO:0048856; P:GO:0000003; P:GO:0045927; P:GO:0007275	-		IPR001451; IPR011004; G3DSA:2.160.10.10 (GENE3D), PTHR22572 (PANTHER), PTHR22572:SF7 (PANTHER)
	-	0				-
	-	0				-
Loa loa	elegans protein confirmed by transcript evidence	7	F:GO:0003676; F:GO:0008026; F:GO:0005524; F:GO:0005515; P:GO:0006406; C:GO:0016020; C:GO:0005634	-		IPR001650; IPR011545; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF3 (PANTHER), SSF52540 (SUPERFAMILY)
Loa loa	elegans protein confirmed by transcript evidence	7	F:GO:0003676; F:GO:0008026; F:GO:0005524; F:GO:0005515; P:GO:0006406; C:GO:0016020; C:GO:0005634	-		-
Loa loa	elegans protein confirmed by transcript evidence	7	F:GO:0003676; F:GO:0008026; F:GO:0005524; F:GO:0005515; P:GO:0006406; C:GO:0016020; C:GO:0005634	-		IPR001650; IPR011545; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF3 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	pinin sdk mema protein conserved region containing protein	0				-
Caenorhabditis elegans	vacuolar protein sorting 16	14	P:GO:0006810; P:GO:0048565; P:GO:0008340; P:GO:0008219; P:GO:0040007; C:GO:0005768; P:GO:0010171; P:GO:0002119; C:GO:0044446; F:GO:0005515; C:GO:0031090; P:GO:0040011; P:GO:0009792; C:GO:0005773	-		IPR006926; PTHR12811 (PANTHER), SignalP (SIGNALP)

Caenorhabditis briggsae	briggsae cbr-mom-4 protein	2	F:GO:0005488; F:GO:0016740	-		IPR000719; IPR001245; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR23257 (PANTHER), PTHR23257:SF11 (PANTHER)
Caenorhabditis elegans	kiaa0020 protein	4	C:GO:0005730; F:GO:0003723; P:GO:0018991; C:GO:0005783	-		IPR001313; IPR011989; IPR016024; PTHR13389 (PANTHER)
synthetic construct	matrix gla protein	18	P:GO:0030324; C:GO:0043234; P:GO:0009725; F:GO:0005509; F:GO:0008147; P:GO:0007584; C:GO:0005615; P:GO:0030500; P:GO:0006461; P:GO:0030154; F:GO:0048306; P:GO:0001502; C:GO:0005578; F:GO:0005201; P:GO:0048754; C:GO:0005783; P:GO:0051592; P:GO:0009612	-		IPR000294; IPR002384; PTHR10109 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	motor axon guidance family member (max-2)	16	C:GO:0005925; P:GO:0007411; P:GO:0008340; P:GO:0006468; F:GO:0004702; P:GO:0008360; F:GO:0008270; P:GO:0050803; P:GO:0007155; F:GO:0003676; P:GO:0007391; P:GO:0007254; C:GO:0005856; P:GO:0016601; F:GO:0005524; P:GO:0050770	-		IPR000719; IPR011009; IPR015750; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22986 (PANTHER)
Camponotus floridanus	metastasis-associated protein mta1	6	C:GO:0005737; F:GO:0003700; F:GO:0043565; C:GO:0005634; F:GO:0008270; P:GO:0006355	-		-

Caenorhabditis elegans	at rich interactive domain 2 (rfx-like)	10	F:GO:0008270; C:GO:0005622; P:GO:0040007; P:GO:0040035; F:GO:0003677; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0006898; P:GO:0009792	-		IPR001606; PTHR22970 (PANTHER), PTHR22970:SF1 (PANTHER)
Caenorhabditis briggsae	transmembrane 9 superfamily member 2 precursor	3	C:GO:0005887; C:GO:0010008; P:GO:0006810	-		IPR004240; PTHR10766:SF13 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	inosine-5 -monophosphate dehydroge-se family protein	2	P:GO:0016070; F:GO:0003824	-		IPR020094; IPR020103
Caenorhabditis elegans	s-re domain containing protein	8	P:GO:0040010; P:GO:0040035; P:GO:0018996; P:GO:0002119; P:GO:0040011; P:GO:0006898; P:GO:0009792; P:GO:0016246	-		-
	-	0				-
Caenorhabditis elegans	ventricular zone expressed ph domain protein	3	P:GO:0007420; F:GO:0005488; C:GO:0005886	-		IPR011989; PTHR21630 (PANTHER), PTHR21630:SF6 (PANTHER)
Caenorhabditis elegans	heat repeat-containing protein 5b	4	P:GO:0040007; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		PTHR21663 (PANTHER)
Caenorhabditis briggsae	vacuolar protein sorting-associated protein 13d-like	0		P:GO:0008104		-
	-	0				-
Caenorhabditis elegans	tr- (nuclear export receptor for tr-s)	4	P:GO:0046907; F:GO:0003723; C:GO:0044428; P:GO:0033036	-		IPR011989; IPR013598; IPR016024; IPR018247; PTHR15952 (PANTHER), PTHR15952:SF11 (PANTHER)
Caenorhabditis elegans	briggsae cbr-smg-7 protein	0		F:GO:0005488		-
Loa loa	3 -5 exonuclease family protein	1	F:GO:0005515	-		IPR002562; IPR012337; G3DSA:3.30.420.10 (GENE3D)
Brugia malayi	protein angel homolog 2	0		F:GO:0004527; F:GO:0003674; F:GO:0004519; C:GO:0005575		-
Brugia malayi	protein angel homolog 2	0		F:GO:0004527; F:GO:0003674; F:GO:0004519; C:GO:0005575		-
	-	0				-
Caenorhabditis elegans	vacuolar-sorting protein snf8	8	P:GO:0006810; P:GO:0040010; P:GO:0008340; P:GO:0006357; C:GO:0005667; P:GO:0000003; F:GO:0008134; C:GO:0005737	-		IPR007286; IPR016689; SSF46785 (SUPERFAMILY)

Caenorhabditis elegans	vacuolar-sorting protein snf8	8	P:GO:0006810; P:GO:0040010; P:GO:0008340; P:GO:0006357; C:GO:0005667; P:GO:0000003; F:GO:0008134; C:GO:0005737	-		IPR007286; IPR016689; SSF46785 (SUPERFAMILY)
Loa loa	briggsae cbr-tag-203 protein	6	C:GO:0005686; F:GO:0003676; P:GO:0007052; C:GO:0071011; P:GO:0000398; C:GO:0071013	-		PTHR10644 (PANTHER), PTHR10644:SF1 (PANTHER)
Caenorhabditis briggsae	dead deah box helicase family protein	7	C:GO:0005737; F:GO:0008026; F:GO:0003677; F:GO:0005524; F:GO:0000287; F:GO:0004427; P:GO:0006796	-	EC:3.6.1.1	-
Caenorhabditis briggsae	ym65_caeel ame: full=uncharacterized protein	7	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0016246; P:GO:0040010; P:GO:0008340; P:GO:0006898	-		-
	-	0				SignalP (SIGNALP)
Loa loa	briggsae cbr-daf-15 protein	0		F:GO:0005488		IPR004083; PTHR12848:SF2 (PANTHER)
Caenorhabditis elegans	integrator complex subunit 5	0		C:GO:0032039; P:GO:0016180; C:GO:0016021; C:GO:0016020; P:GO:0055085; F:GO:0005515; P:GO:0006810; F:GO:0005215		-
Caenorhabditis briggsae	yot5_caeel ame: full=uncharacterized protein	0				-
Caenorhabditis elegans	caax beta	5	P:GO:0018347; C:GO:0005875; P:GO:0008284; F:GO:0004660; F:GO:0005515	-	EC:2.5.1.58	IPR000169; IPR001330; IPR008930; G3DSA:1.50.10.20 (GENE3D), PTHR11774 (PANTHER), PTHR11774:SF6 (PANTHER)
	-	0				-

Caenorhabditis elegans	brf1 subunit of r- polymerase iii transcription initiation factor iiib	24	P:GO:0006413; P:GO:0000003; P:GO:0045941; F:GO:0005515; F:GO:0008270; P:GO:0040007; P:GO:0006898; F:GO:0017091; P:GO:0006355; C:GO:0000126; P:GO:0000288; P:GO:0043488; F:GO:0003743; F:GO:0016563; C:GO:0005829; P:GO:0009303; P:GO:0006384; F:GO:0003709; P:GO:0006417; P:GO:0002119; P:GO:0009304; F:GO:0003700; F:GO:0003729; P:GO:0001570	-		IPR000812; IPR006670; IPR011028; IPR013137; IPR013150; IPR013763; G3DSA:2.20.25.10 (GENE3D), PTHR11618:SF4 (PANTHER), SSF57783 (SUPERFAMILY)
	-	0				-
Necator americanus	glutathione s-transferase	3	F:GO:0016740; F:GO:0005515; P:GO:0008340	-		IPR004046; IPR010987; IPR017933; PTHR11571 (PANTHER), PTHR11571:SF6 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	proteasome a-type and b-type family protein	13	P:GO:0008340; P:GO:0051436; P:GO:0051437; P:GO:0040007; P:GO:0000003; F:GO:0004298; P:GO:0031145; P:GO:0002119; P:GO:0040011; P:GO:0009792; C:GO:0005737; C:GO:0005839; C:GO:0005634	-	EC:3.4.25.0	IPR000243; IPR001353; G3DSA:3.60.20.10 (GENE3D), PTHR11599 (PANTHER), PTHR11599:SF1 (PANTHER), PS51476 (PROFILE), SSF56235 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0005524; C:GO:0005856; C:GO:0016459; F:GO:0003774		IPR001452; IPR011511; G3DSA:2.30.30.40 (GENE3D)
Caenorhabditis briggsae	protein ki-se domain containing protein	0		F:GO:0016301; F:GO:0004672; F:GO:0005524; F:GO:0000166; P:GO:0006468; P:GO:0040010; F:GO:0004674		PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)

Caenorhabditis briggsae	ef-1 guanine nucleotide exchange domain containing protein	5	F:GO:0005488; P:GO:0044238; P:GO:0044260; P:GO:0019915; P:GO:0010467	-		IPR002319; IPR019446; PTHR11538:SF1 (PANTHER)
Caenorhabditis briggsae	alveolar soft part sarcoma chromosome candidate 1	6	P:GO:0009987; P:GO:0006810; P:GO:0050789; C:GO:0005624; C:GO:0044425; C:GO:0044444	-		IPR021569; PTHR23153 (PANTHER), PTHR23153:SF1 (PANTHER), SSF54236 (SUPERFAMILY)
Caenorhabditis elegans	yse2_caeel ame: full=uncharacterized protein	0				-
Caenorhabditis elegans	guanine nucleotide exchange factor	1	P:GO:0000003	-		IPR000219; IPR001452; IPR001849; IPR011993; G3DSA:2.30.30.40 (GENE3D), PTHR12845 (PANTHER), SSF50729 (SUPERFAMILY)
Brugia malayi	elegans protein confirmed by transcript evidence	10	P:GO:0009948; P:GO:0007411; F:GO:0070016; P:GO:0032880; F:GO:0008022; P:GO:0030178; P:GO:0060070; C:GO:0005737; C:GO:0016020; C:GO:0005634	-		IPR000342; IPR001158; IPR016137; PTHR10845 (PANTHER), PTHR10845:SF10 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	vesicle-associated membrane protein 8	2	C:GO:0016020; P:GO:0016192	-		-
Angiostrongylus cantonensis	rho guanine nucleotide exchange factor 1	5	F:GO:0005089; C:GO:0005622; P:GO:0000003; P:GO:0035023; P:GO:0016043	-		IPR000219; IPR001849; IPR011993; SSF50729 (SUPERFAMILY)
	-	0				-
Loa loa	lanthionine synthetase c-like protein	0		F:GO:0003674; F:GO:0004872; F:GO:0003824; P:GO:0008150; P:GO:0007186; C:GO:0005575		IPR007822; IPR008928; IPR012341; IPR020464; PTHR12736 (PANTHER), PTHR12736:SF3 (PANTHER)
Loa loa	lanthionine synthetase c-like protein	0		F:GO:0003674; F:GO:0004872; F:GO:0003824; P:GO:0008150; P:GO:0007186; C:GO:0005575		IPR007822; IPR008928; IPR012341; IPR020464; PTHR12736 (PANTHER), PTHR12736:SF3 (PANTHER)
Caenorhabditis briggsae	ecotropic viral integration site	4	F:GO:0005097; C:GO:0005622; F:GO:0016491; P:GO:0032313	-		IPR000195; PTHR22957 (PANTHER), PTHR22957:SF44 (PANTHER)
Loa loa	briggsae cbr-pqn-27 protein	0		F:GO:0005488; P:GO:0016070; F:GO:0005515		-

Caenorhabditis briggsae	endonuclease exonuclease phosphatase family protein	1	P:GO:0000003	-		IPR005135; G3DSA:3.60.10.10 (GENE3D), PTHR11200 (PANTHER), PTHR11200:SF15 (PANTHER)
	-	0				-
Brugia malayi	mortality factor 4-like protein 1	0		F:GO:0003682; C:GO:0000785; P:GO:0006333; C:GO:0005634		IPR008676
	-	0				-
Caenorhabditis elegans	hypothetical protein Y42H9AR.4 [Caenorhabditis elegans]	0				-
Oesophagostomum dentatum	elegans protein confirmed by transcript evidence	1	P:GO:0007218	-		IPR002544; PTHR20986 (PANTHER), SignalP (SIGNALP)
	-	0				-
Loa loa	transcription elongation factor b polypeptide 1	10	C:GO:0005829; F:GO:0003746; P:GO:0006511; P:GO:0006357; F:GO:0004842; F:GO:0005515; F:GO:0003711; P:GO:0044419; C:GO:0005654; C:GO:0030891	-	EC:6.3.2.19	IPR001232; IPR011333; IPR016073; PTHR20648 (PANTHER), SignalP (SIGNALP)
Brugia malayi	alter-tive splicing defective family member (asd-2)	10	F:GO:0003730; P:GO:0008366; P:GO:0008078; P:GO:0007525; P:GO:0000381; P:GO:0008347; F:GO:0005515; P:GO:0007475; C:GO:0005634; P:GO:0007438	-		-
	-	0				-
Brugia malayi	elegans protein confirmed by transcript evidence	0		F:GO:0005515; F:GO:0003677		IPR006578
	-	0				-
	-	0				-
Loa loa	cation efflux family protein	9	P:GO:0046579; P:GO:0040010; F:GO:0016491; F:GO:0008324; P:GO:0019915; P:GO:0040026; P:GO:0010043; P:GO:0006812; C:GO:0005886	-		IPR002524; G3DSA:1.20.1510.10 (GENE3D), SignalP (SIGNALP)
Loa loa	heat shock transcription factor	0		P:GO:0006355; P:GO:0006950; F:GO:0043565; F:GO:0003677; F:GO:0003700; C:GO:0005634		PTHR10015 (PANTHER), PTHR10015:SF17 (PANTHER)
Caenorhabditis briggsae	downstream neighbor of son	3	P:GO:0009653; P:GO:0007275; P:GO:0000003	-		PTHR12972 (PANTHER)

Caenorhabditis elegans	vesicle-fusing atpase	10	P:GO:0009792; P:GO:0002119; F:GO:0005515; P:GO:0032940; F:GO:0005524; P:GO:0000003; P:GO:0040011; F:GO:0017111; P:GO:0040007; P:GO:0006898	-	EC:3.6.1.15	IPR003959; G3DSA:3.40.50.300 (GENE3D), PTHR23078 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	vesicular glutamate transporter 1	6	P:GO:0055085; C:GO:0016021; F:GO:0015319; C:GO:0045202; F:GO:0015321; P:GO:0006817	-		IPR011701; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11662 (PANTHER), PTHR11662:SF29 (PANTHER)
Caenorhabditis elegans	zinc c2h2 type family protein	2	P:GO:0009792; F:GO:0005515	-		IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis elegans	zinc c2h2 type family protein	2	P:GO:0009792; F:GO:0005515	-		IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis briggsae	ubiquitin-conjugating enzyme e2 g2	8	F:GO:0005515; F:GO:0005524; P:GO:0070936; F:GO:0004842; P:GO:0030433; P:GO:0051246; C:GO:0005829; C:GO:0005783	-	EC:6.3.2.19	IPR000608; IPR016135; PTHR11621 (PANTHER), PTHR11621:SF36 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-noah-1 protein	0				PTHR22963 (PANTHER), PTHR22963:SF1 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG16187 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	serine long chain base subunit 2	9	P:GO:0046511; C:GO:0005739; P:GO:0046512; F:GO:0004758; P:GO:0006686; F:GO:0016769; P:GO:0019915; C:GO:0017059; F:GO:0030170	-	EC:2.3.1.50	IPR001917; IPR004839; IPR015421; IPR015422; IPR015424; PTHR13693 (PANTHER), PTHR13693:SF3 (PANTHER)
Caenorhabditis elegans	60s acidic ribosomal protein p2	3	F:GO:0005515; C:GO:0030529; P:GO:0006412	-	EC:3.6.5.3	IPR001813; IPR001859; PTHR21141 (PANTHER), PTHR21141:SF5 (PANTHER)
Angiostrongylus cantonensis	iq calmodulin-binding motif domain protein	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	kex-2 proprotein convertase family member (kpc-1)	3	P:GO:0000003; P:GO:0006508; F:GO:0004252	-	EC:3.4.21.0	IPR000209; IPR009020; IPR015500; IPR022398; G3DSA:3.30.70.850 (GENE3D), PTHR10795:SF14 (PANTHER)
Caenorhabditis elegans	amop domain containing protein	2	C:GO:0016021; P:GO:0007160	-		IPR003886
Caenorhabditis elegans	amop domain containing protein	2	C:GO:0016021; P:GO:0007160	-		IPR003886

Caenorhabditis elegans	gtp-binding gtp1 obg domian containing protein	3	C:GO:0005622; P:GO:0000003; F:GO:0000166	-		IPR002917; IPR006073; IPR006169; IPR014100; G3DSA:3.40.50.300 (GENE3D), PTHR11702 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-hmp-2 protein	26	P:GO:0048526; P:GO:0003006; P:GO:0000902; P:GO:0014019; P:GO:0010552; P:GO:0007370; P:GO:0045186; C:GO:0016324; P:GO:0001709; P:GO:0035019; P:GO:0051179; F:GO:0003713; P:GO:0035153; C:GO:0005737; P:GO:0060232; P:GO:0003136; P:GO:0035147; P:GO:0046530; P:GO:0035017; P:GO:0060914; P:GO:0007391; P:GO:0008360; C:GO:0005634; P:GO:0048477; P:GO:0046667; C:GO:0005915	-		IPR000225; IPR011989; IPR013284; IPR016024; PTHR23315 (PANTHER), PTHR23315:SF10 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-hmp-2 protein	26	P:GO:0048526; P:GO:0003006; P:GO:0000902; P:GO:0014019; P:GO:0010552; P:GO:0007370; P:GO:0045186; C:GO:0016324; P:GO:0001709; P:GO:0035019; P:GO:0051179; F:GO:0003713; P:GO:0035153; C:GO:0005737; P:GO:0060232; P:GO:0003136; P:GO:0035147; P:GO:0046530; P:GO:0035017; P:GO:0060914; P:GO:0007391; P:GO:0008360; C:GO:0005634; P:GO:0048477; P:GO:0046667; C:GO:0005915	-		IPR000225; IPR011989; IPR013284; IPR016024; PTHR23315 (PANTHER), PTHR23315:SF10 (PANTHER)
Caenorhabditis briggsae	golgi golgin subfamily 7	1	C:GO:0044464	-		IPR019383; PTHR13254 (PANTHER)

Caenorhabditis elegans	sulfate transporter	0		P:GO:0008272; C:GO:0016021; F:GO:0008271; C:GO:0016020; P:GO:0055085; F:GO:0015116; F:GO:0005215; P:GO:0006810		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	novel protein containing mif4g and ma3 domains	7	F:GO:0003723; C:GO:0005681; P:GO:0048024; F:GO:0004713; F:GO:0005524; F:GO:0005515; P:GO:0006468	-	EC:2.7.10.0	IPR003890; IPR016021; IPR016024; PTHR18034 (PANTHER), PTHR18034:SF3 (PANTHER)
Caenorhabditis elegans	novel protein containing mif4g and ma3 domains	7	F:GO:0003723; C:GO:0005681; P:GO:0048024; F:GO:0004713; F:GO:0005524; F:GO:0005515; P:GO:0006468	-	EC:2.7.10.0	IPR003890; IPR016021; IPR016024; PTHR18034 (PANTHER), PTHR18034:SF3 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	4	P:GO:0010171; P:GO:0040010; P:GO:0002119; P:GO:0040011	-		IPR019013
Pongo abelii	protein phosphatase 1 regulatory subunit 14b	11	P:GO:0006468; F:GO:0005515; F:GO:0008599; F:GO:0004864; F:GO:0005524; P:GO:0050790; C:GO:0005634; F:GO:0008270; F:GO:0004674; P:GO:0042325; C:GO:0005739	-	EC:2.7.11.0	-
Caenorhabditis elegans	a ki-se anchor protein family member (aka-1)	0		F:GO:0046872; F:GO:0008270		IPR022557; PTHR22835 (PANTHER), PTHR22835:SF12 (PANTHER)
Loa loa	importin-beta n-termi-l domain containing protein	1	F:GO:0005488	-		IPR011989; IPR016024; PTHR10997 (PANTHER), PTHR10997:SF18 (PANTHER)
Loa loa	importin-beta n-termi-l domain containing protein	1	F:GO:0005488	-		IPR011989; IPR016024; PTHR10997 (PANTHER), PTHR10997:SF18 (PANTHER)
Angiostrongylus cantonensis	glycolipid transfer protein domain-containing protein 1	4	F:GO:0017089; C:GO:0005737; F:GO:0051861; P:GO:0046836	-		SignalP (SIGNALP)
Caenorhabditis briggsae	exportin 7	4	C:GO:0005737; C:GO:0005643; F:GO:0005049; P:GO:0006611	-		PTHR12596 (PANTHER), PTHR12596:SF2 (PANTHER)
Caenorhabditis elegans	aar2 protein	1	F:GO:0005515	-		IPR007946
Caenorhabditis elegans	aar2 protein	1	F:GO:0005515	-		IPR007946
Caenorhabditis elegans	hypothetical protein C52E12.4 [Caenorhabditis elegans]	0				-

	-	0				IPR001357; G3DSA:3.40.50.10190 (GENE3D)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				IPR003582; PTHR21724 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	succinyl- ligase	11	C:GO:0045244; P:GO:0006105; C:GO:0005743; F:GO:0003878; P:GO:0006104; P:GO:0006099; F:GO:0019003; F:GO:0004775; F:GO:0046982; F:GO:0004776; F:GO:0005525	-	EC:2.3.3.8; EC:6.2.1.5; EC:6.2.1.4	-
	-	0				-
Caenorhabditis elegans	pyruvate dehydroge-se	8	F:GO:0004739; P:GO:0040010; P:GO:0055114; P:GO:0006096; C:GO:0005759; P:GO:0006898; P:GO:0048477; P:GO:0009792	-	EC:1.2.4.1	IPR001017; G3DSA:3.40.50.970 (GENE3D), PTHR11516 (PANTHER), PTHR11516:SF3 (PANTHER), SignalP (SIGNALP), SSF52518 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	spermatogenesis associated 11	0		F:GO:0016491		G3DSA:2.60.120.590 (GENE3D), PTHR21052 (PANTHER), SSF51197 (SUPERFAMILY)
Caenorhabditis elegans	sushi domain	0		F:GO:0030414; C:GO:0005576		IPR000436; IPR016060; PTHR19325 (PANTHER), PTHR19325:SF37 (PANTHER)
Haemonchus contortus	superoxide dismutase	5	F:GO:0046872; C:GO:0005615; P:GO:0055114; P:GO:0006801; F:GO:0004784	-	EC:1.15.1.1	IPR001424; IPR018152; PTHR10003:SF12 (PANTHER), SignalP (SIGNALP)
Brugia malayi	hypothetical protein Bm1_50915 [Brugia malayi]	0				SignalP (SIGNALP)
Haemonchus contortus	heat shock protein family member (hsp-)	0		P:GO:0006950; P:GO:0009408		IPR001436; IPR002068; IPR008978; G3DSA:2.60.40.790 (GENE3D), PTHR11527 (PANTHER), PTHR11527:SF28 (PANTHER)
Haemonchus contortus	heat shock protein family member (hsp-)	0		P:GO:0006950; P:GO:0009408		IPR001436; IPR002068; IPR008978; G3DSA:2.60.40.790 (GENE3D), PTHR11527 (PANTHER), PTHR11527:SF28 (PANTHER)
Caenorhabditis elegans	protein transport protein sec61 subunit gamma	5	C:GO:0005789; F:GO:0015450; P:GO:0045047; P:GO:0055085; C:GO:0016021	-		-
Caenorhabditis elegans	zinc finger fyve domain-containing protein 28	3	C:GO:0005737; F:GO:0008270; F:GO:0016740	-		PTHR22835 (PANTHER), PTHR22835:SF41 (PANTHER)

Brugia malayi	notch domain-containing protein	0		P:GO:0043065; P:GO:0008285; C:GO:0009986; P:GO:0050793; C:GO:0005634; P:GO:0030154; P:GO:0030326; C:GO:0016021; C:GO:0016020; P:GO:0007219; F:GO:0005509; P:GO:0046579; P:GO:0009887; F:GO:0004872; P:GO:0007275; P:GO:0007368; P:GO:0002011; F:GO:0003976; P:GO:0016049; F:GO:0016740; F:GO:0005515; C:GO:0005887; P:GO:0007050; P:GO:0042060		-
Caenorhabditis elegans	ap-1 complex subunit gamma-1	10	P:GO:0040010; P:GO:0009306; P:GO:0000003; P:GO:0002119; C:GO:0030117; F:GO:0005515; P:GO:0040011; C:GO:0044431; P:GO:0009792; P:GO:0001703	-		IPR002553; IPR011989; IPR016024; PTHR22780 (PANTHER), PTHR22780:SF5 (PANTHER)
Brugia malayi	tm2 domain containing protein	14	P:GO:0035314; P:GO:0035168; F:GO:0000166; F:GO:0004672; C:GO:0044464; F:GO:0003702; P:GO:0046672; F:GO:0043565; P:GO:0042675; P:GO:0035165; P:GO:0001709; P:GO:0045944; P:GO:0045467; P:GO:0042981	-		IPR007829; PTHR21016 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein Y92H12A.3 [Caenorhabditis elegans]	0				IPR001368
Caenorhabditis elegans	electron transfer flavoprotein subunit mitochondrial precursor	4	F:GO:0050660; P:GO:0009792; P:GO:0000003; F:GO:0009055	-		-
Caenorhabditis elegans	uncoordi-ted family member (unc-103)	4	F:GO:0005249; P:GO:0055085; P:GO:0006813; C:GO:0016021	-		IPR000595; IPR014710; IPR018490; PTHR10217 (PANTHER), PTHR10217:SF15 (PANTHER)

Caenorhabditis elegans	briggsae cbr-mup-4 protein	2	F:GO:0005509; F:GO:0005515	-		IPR002035; IPR006210; IPR013032; G3DSA:2.10.25.10 (GENE3D), G3DSA:3.40.50.410 (GENE3D), PTHR22992 (PANTHER), PTHR22992:SF12 (PANTHER), SSF53300 (SUPERFAMILY)
Caenorhabditis briggsae	ribosome biogenesis protein rlp24	9	P:GO:0040035; P:GO:0009792; P:GO:0010171; P:GO:0002119; C:GO:0005840; F:GO:0003735; P:GO:0040010; P:GO:0006898; P:GO:0006412	-	EC:3.6.5.3	IPR000988; IPR011017; PTHR10792:SF2 (PANTHER), SSF57716 (SUPERFAMILY)
Brugia malayi	rap ran-gap family protein	12	P:GO:0051234; P:GO:0035467; P:GO:0008104; P:GO:0051128; C:GO:0005737; P:GO:0031323; P:GO:0050790; F:GO:0005515; P:GO:0009968; P:GO:0007166; N:GO:0035556; P:GO:0050896	-		PTHR10063 (PANTHER), PF11864 (PFAM)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis briggsae	thump domain containing 1	0				PTHR13452 (PANTHER)
Caenorhabditis briggsae	large subunit ribosomal protein 9	5	C:GO:0005840; F:GO:0003735; F:GO:0005515; P:GO:0006412; F:GO:0019843	-	EC:3.6.5.3	IPR000702; IPR002359; IPR020040; PTHR11655:SF2 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-pad-1 protein	0		F:GO:0003674; P:GO:0007275; P:GO:0008150; C:GO:0005575; P:GO:0006810; P:GO:0015031		PTHR14042 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	9	P:GO:0040010; C:GO:0005743; P:GO:0055114; F:GO:0004350; P:GO:0006898; P:GO:0006561; F:GO:0004349; C:GO:0005811; F:GO:0017084	-	EC:1.2.1.41; EC:2.7.2.11	IPR016161; IPR016162; IPR016163; IPR020593; PTHR11063 (PANTHER), PTHR11063:SF2 (PANTHER)
	-	0				-
Angiostrongylus cantonensis	tnf receptor-associated protein 1	6	P:GO:0006457; P:GO:0034599; P:GO:0040010; F:GO:0005524; F:GO:0051082; C:GO:0005739	-		IPR001404; IPR003594; IPR020568; IPR020576; PTHR11528:SF24 (PANTHER)

Angiostrongylus cantonensis	tnf receptor-associated protein 1	7	P:GO:0006457; P:GO:0034599; P:GO:0040010; F:GO:0005524; F:GO:0051082; F:GO:0005164; C:GO:0005739	-		IPR001404; IPR020568; IPR020576; PTHR11528:SF24 (PANTHER)
Caenorhabditis elegans	cd36 antigen	16	F:GO:0030169; P:GO:0007155; C:GO:0043231; P:GO:0006869; P:GO:0010033; P:GO:0034381; P:GO:0019915; C:GO:0009986; C:GO:0044425; P:GO:0048522; P:GO:0051704; F:GO:0004872; C:GO:0005886; C:GO:0044444; P:GO:0040035; N:GO:0035556	-		IPR002159; PTHR11923:SF8 (PANTHER)
	-	0				-
Caenorhabditis briggsae	protein disulfide	1	C:GO:0044464	-		-
Caenorhabditis elegans	briggsae cbr-nlp-40 protein	1	P:GO:0000003	-		SignalP (SIGNALP)
	-	0				IPR011009; G3DSA:1.10.510.10 (GENE3D)
Macaca mulatta	40s ribosomal protein s2-like isoform 2	0				IPR000851
Caenorhabditis elegans	sterile alpha motif domain containing isoform cra_a	1	C:GO:0044464	-		IPR001660; IPR010993; IPR013761; IPR015327; IPR021129; PTHR12515 (PANTHER), PTHR12515:SF1 (PANTHER)
Caenorhabditis briggsae	potassium channel tetramerisation domain containing 2	3	F:GO:0042802; P:GO:0006811; C:GO:0016020	-		-
	-	0				-
Caenorhabditis elegans	dipeptidylpeptidase 3	3	C:GO:0005737; P:GO:0006508; F:GO:0008239	-		IPR005317; PTHR23422 (PANTHER), SignalP (SIGNALP)
Brugia malayi	leucine rich repeat family protein	6	P:GO:0040035; P:GO:0009792; P:GO:0016336; P:GO:0040011; P:GO:0006898; P:GO:0016334	-		IPR001611; PR00019 (PRINTS), G3DSA:3.80.10.10 (GENE3D), PTHR10588 (PANTHER), PTHR10588:SF23 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)
Caenorhabditis elegans	selenocysteine-specific elongation factor	1	F:GO:0005488	-		IPR000795; G3DSA:2.40.30.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF25 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-

Loa loa	myotubularin related protein 9	0		P:GO:0016311; F:GO:0016791; C:GO:0005737; F:GO:0030234; F:GO:0005515		PTHR10807 (PANTHER), PTHR10807:SF9 (PANTHER)
Caenorhabditis elegans	sh3-domain grb2-like 2	2	C:GO:0005737; F:GO:0005515	-		IPR001452; G3DSA:2.30.30.40 (GENE3D), PTHR10661 (PANTHER), PTHR10661:SF23 (PANTHER)
Loa loa	ring finger protein 126	1	F:GO:0005515	-		IPR001841; IPR013083; PTHR22763 (PANTHER), SSF57850 (SUPERFAMILY)
	-	0				-
Angiostrongylus cantonensis	general transcription factor 1-like	4	P:GO:0016192; P:GO:0006367; C:GO:0005672; F:GO:0003702	-		IPR004855; IPR009083; IPR009088; IPR013028; PTHR12694:SF7 (PANTHER)
Angiostrongylus cantonensis	general transcription factor 1-like	4	P:GO:0016192; P:GO:0006367; C:GO:0005672; F:GO:0003702	-		IPR004855; IPR009083; IPR009088; IPR013028; PTHR12694:SF7 (PANTHER)
	-	0				-
Caenorhabditis elegans	hypothetical protein C14C10.6 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	dystrophin-like protein	37	C:GO:0005856; P:GO:0060025; P:GO:0010552; F:GO:0005277; P:GO:0030010; P:GO:0007314; P:GO:0007411; C:GO:0009925; P:GO:0007474; C:GO:0031594; F:GO:0005200; P:GO:0015870; F:GO:0050699; C:GO:0030315; P:GO:0007427; P:GO:0007271; P:GO:0045214; P:GO:0007274; P:GO:0016334; F:GO:0008270; F:GO:0016563; C:GO:0016011; P:GO:0045197; P:GO:0046716; F:GO:0046982; P:GO:0035147; P:GO:0007016;	-		IPR000433; IPR015154; PTHR11915 (PANTHER), PTHR11915:SF57 (PANTHER), SSF47473 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	protection of telomeres 1	0		P:GO:0040010; P:GO:0000723; C:GO:0000784; F:GO:0003677		IPR011564; IPR012340; IPR016027
Caenorhabditis elegans	protection of telomeres 1	0		P:GO:0040010; P:GO:0000723; C:GO:0000784; F:GO:0003677		IPR011564; IPR012340; IPR016027

Caenorhabditis elegans	exocyst complex component 5	12	C:GO:0005737; P:GO:0040035; P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040018; P:GO:0048278; P:GO:0018991; P:GO:0006887; P:GO:0040010; P:GO:0040011; P:GO:0002009	-		-
Loa loa	round spermatid basic protein 1	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	F:GO:0005515; P:GO:0009792	-		PTHR15836 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	F:GO:0005515; P:GO:0009792	-		PTHR15836 (PANTHER)
Caenorhabditis elegans	related to yeast vacuolar protein sorting factor family member (vps-39)	9	P:GO:0009792; P:GO:0010171; F:GO:0005515; P:GO:0016192; P:GO:0000003; C:GO:0030897; P:GO:0008219; P:GO:0048066; P:GO:0002009	-		IPR019453; PTHR12894 (PANTHER), PTHR12894:SF10 (PANTHER)
Caenorhabditis elegans	high mobility group protein	7	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0003677; P:GO:0040010; P:GO:0040011; C:GO:0005634	-		PD936484 (PRODOM)
Caenorhabditis elegans	massive surface protein	2	F:GO:0005488; C:GO:0016020	-		IPR012315
Caenorhabditis elegans	viral a-type inclusion protein	0		C:GO:0016020; F:GO:0043565; F:GO:0008565; F:GO:0003700; C:GO:0000139; F:GO:0003677; C:GO:0005737; F:GO:0046983; P:GO:0006886; P:GO:0006355; P:GO:0048280; C:GO:0005622; F:GO:0005488; F:GO:0003899		PD968187 (PRODOM), SSF46966 (SUPERFAMILY)

Caenorhabditis elegans	tyrosyl-tr- synthetase	15	P:GO:0006915; C:GO:0005625; F:GO:0004871; P:GO:0000003; C:GO:0005615; F:GO:0004825; F:GO:0005524; P:GO:0006437; F:GO:0005153; F:GO:0000049; F:GO:0004831; P:GO:0009792; C:GO:0005737; C:GO:0005634; P:GO:0006431	-	EC:6.1.1.10; EC:6.1.1.1	IPR002305; IPR002307; IPR014729; IPR015624; PTHR11946 (PANTHER), SSF52374 (SUPERFAMILY)
Caenorhabditis elegans	tyrosyl-tr- synthetase	15	P:GO:0006915; C:GO:0005625; F:GO:0004871; P:GO:0000003; C:GO:0005615; F:GO:0004825; F:GO:0005524; P:GO:0006437; F:GO:0005153; F:GO:0000049; F:GO:0004831; P:GO:0009792; C:GO:0005737; C:GO:0005634; P:GO:0006431	-	EC:6.1.1.10; EC:6.1.1.1	IPR002305; IPR002307; IPR014729; IPR015624; PTHR11946 (PANTHER), SSF52374 (SUPERFAMILY)
Caenorhabditis elegans	tyrosyl-tr- synthetase	15	P:GO:0006915; C:GO:0005625; F:GO:0004871; P:GO:0000003; C:GO:0005615; F:GO:0004825; F:GO:0005524; P:GO:0006437; F:GO:0005153; F:GO:0000049; F:GO:0004831; P:GO:0009792; C:GO:0005737; C:GO:0005634; P:GO:0006431	-	EC:6.1.1.10; EC:6.1.1.1	IPR002305; IPR002307; IPR014729; IPR015624; PTHR11946 (PANTHER), SSF52374 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-pcp- protein	3	P:GO:0009792; P:GO:0008152; F:GO:0070011	-		IPR008758; G3DSA:3.40.50.1820 (GENE3D), PTHR11010:SF6 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
Brugia malayi	polymerase iii (d- directed) polypeptide 155kda	8	F:GO:0003899; F:GO:0008270; P:GO:0032728; P:GO:0045087; F:GO:0003677; F:GO:0032549; P:GO:0006351; C:GO:0005666	-	EC:2.7.7.6	IPR000722; IPR006592; IPR007066; IPR007080; IPR015700; PTHR19376 (PANTHER), SSF64484 (SUPERFAMILY)

Loa loa	transportin 3	1	F:GO:0005515	-		IPR016024; PTHR12363 (PANTHER), PTHR12363:SF5 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	methylthioribose-1-phosphate isomerase	2	F:GO:0042802; P:GO:0044249	-		IPR000649; G3DSA:3.40.50.10470 (GENE3D), PTHR10233:SF6 (PANTHER), SignalP (SIGNALP), SSF100950 (SUPERFAMILY)
Loa loa	d- damage-binding protein 1	10	P:GO:0043161; P:GO:0000718; P:GO:0000075; F:GO:0003684; C:GO:0031464; C:GO:0031465; P:GO:0042787; F:GO:0005515; C:GO:0005654; C:GO:0005737	-		IPR004871; IPR011046; PTHR10644 (PANTHER), PTHR10644:SF3 (PANTHER)
Brugia malayi	ttk protein ki-se	7	P:GO:0016321; F:GO:0005488; P:GO:0060249; F:GO:0004672; P:GO:0031101; P:GO:0007093; P:GO:0009790	-		IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22974 (PANTHER), PTHR22974:SF4 (PANTHER)
Caenorhabditis elegans	wasp (actin cytoskeleton modulator) homolog family member (wsp-1)	2	F:GO:0005515; P:GO:0043933	-		IPR003124; PTHR12779 (PANTHER)
Caenorhabditis elegans	lethal isoform k	6	F:GO:0000827; F:GO:0003993; F:GO:0000832; P:GO:0006020; F:GO:0033857; C:GO:0005829	-	EC:3.1.3.2; EC:2.7.4.24	PTHR12750 (PANTHER), PTHR12750:SF5 (PANTHER)
Necator americanus	elegans protein partially confirmed by transcript evidence	1	F:GO:0005488	-		IPR001304; IPR002035; IPR016186; IPR016187; IPR018378; PR00453 (PRINTS), G3DSA:3.40.50.410 (GENE3D), PTHR22992 (PANTHER), PTHR22992:SF10 (PANTHER), SignalP (SIGNALP), SSF53300 (SUPERFAMILY)
	-	0				-
Branchiostoma floridae	gastric mucin	0		F:GO:0016301; F:GO:0005524; P:GO:0015937; F:GO:0004594		-
Branchiostoma floridae	gastric mucin	0		F:GO:0016301; F:GO:0005524; P:GO:0015937; F:GO:0004594		-
Trichostrongylus vitrinus	serine protease inhibitor-like protein	3	F:GO:0005488; P:GO:0007275; C:GO:0005634	-		IPR000215; G3DSA:3.30.497.10 (GENE3D), PTHR11461:SF25 (PANTHER)

Homo sapiens	uncharacterized protein cxorf62-like	31	F:GO:0047058; P:GO:0001659; F:GO:0000166; P:GO:0046677; N:GO:0035553; P:GO:0010243; F:GO:0047057; C:GO:0005792; P:GO:0030193; P:GO:0042245; C:GO:0016021; C:GO:0005789; N:GO:0035516; N:GO:0035515; P:GO:0014070; P:GO:0044065; P:GO:0070350; F:GO:0016702; C:GO:0005829; F:GO:0043734; P:GO:0006307; N:GO:0035552; C:GO:0005856; P:GO:0050820; P:GO:0060612; F:GO:0008198;	-	EC:1.1.4.2; EC:1.1.4.1; EC:1.13.11.0	PTHR12138 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	tubulointerstitial nephritis antigen	6	P:GO:0007443; P:GO:0007155; F:GO:0004197; P:GO:0006508; C:GO:0005604; F:GO:0000166	-	EC:3.4.22.0	IPR013128; PTHR12411:SF15 (PANTHER)
Brugia malayi	protein ki-se c inhibitor aswz variant 5	4	C:GO:0005856; P:GO:0007165; F:GO:0003824; F:GO:0005080	-		IPR001310; IPR011146; IPR011151; SignalP (SIGNALP)
Harpegnathos saltator	d- damage-binding protein 1	10	P:GO:0043161; P:GO:0000718; P:GO:0000075; F:GO:0003684; C:GO:0031464; C:GO:0031465; P:GO:0042787; F:GO:0005515; C:GO:0005654; C:GO:0005737	-		IPR004871; PTHR10644 (PANTHER), PTHR10644:SF3 (PANTHER)
Loa loa	briggsae cbr-syn-1 protein	0		P:GO:0016192; F:GO:0005484; C:GO:0016020; P:GO:0006886; F:GO:0005515		IPR006011; IPR010989; G3DSA:1.20.58.70 (GENE3D), PTHR19957 (PANTHER)
	-	0				-
	-	0				-
Loa loa	hypothetical protein LOAG_04211 [Loa loa]	0		C:GO:0016021; C:GO:0016020		-

	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0005515		SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein H20J04.3 [Caenorhabditis elegans]	0		F:GO:0046872; F:GO:0008270; F:GO:0005515; F:GO:0003677		-
Caenorhabditis elegans	hypothetical protein H20J04.3 [Caenorhabditis elegans]	0		F:GO:0046872; F:GO:0008270; F:GO:0005515; F:GO:0003677		-
Brugia malayi	hyaluronidase family protein	0		F:GO:0004415; P:GO:0008152; F:GO:0016787; F:GO:0016798		PTHR13170 (PANTHER), PTHR13170:SF7 (PANTHER)
Loa loa	subtilase family protein	3	P:GO:0019915; P:GO:0006508; F:GO:0004252	-	EC:3.4.21.0	-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	alp enigma encoding family member (alp-1)	5	F:GO:0042802; F:GO:0051371; P:GO:0001952; F:GO:0008270; C:GO:0015629	-		IPR001781; PTHR18973 (PANTHER), PTHR18973:SF57 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis elegans	alp enigma encoding family member (alp-1)	5	F:GO:0042802; F:GO:0051371; P:GO:0001952; F:GO:0008270; C:GO:0015629	-		IPR001781; PTHR18973 (PANTHER), PTHR18973:SF57 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis elegans	prion-like-(q n-rich)-domain-bearing protein family member (pqn-22)	1	P:GO:0009792	-		PTHR18973 (PANTHER), PTHR18973:SF57 (PANTHER)
Caenorhabditis briggsae	ribosomal protein l37 variant 1	11	P:GO:0000022; P:GO:0006412; P:GO:0040010; F:GO:0046872; F:GO:0019843; F:GO:0003735; P:GO:0040035; P:GO:0002119; P:GO:0009792; P:GO:0040018; C:GO:0022625	-	EC:3.6.5.3	IPR001569; IPR011331; IPR011332; IPR018267
Caenorhabditis briggsae	wd repeat domain 12	7	P:GO:0040010; C:GO:0070545; P:GO:0040035; P:GO:0000463; P:GO:0002119; P:GO:0009792; P:GO:0040019	-		-
Caenorhabditis briggsae	wd repeat domain 12	7	P:GO:0040010; C:GO:0070545; P:GO:0040035; P:GO:0000463; P:GO:0002119; P:GO:0009792; P:GO:0040019	-		-

Caenorhabditis briggsae	wd repeat domain 12	7	P:GO:0040010; C:GO:0070545; P:GO:0040035; P:GO:0000463; P:GO:0002119; P:GO:0009792; P:GO:0040019	-		-
Caenorhabditis elegans	thiamine pyrophosphate central domain containing protein	5	F:GO:0030976; C:GO:0016021; P:GO:0009792; F:GO:0000287; F:GO:0016740	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein T19A5.1 [Caenorhabditis elegans]	2	P:GO:0040010; P:GO:0040017	-		-
Brugia malayi	tr--splicing endonuclease subunit sen34	0		P:GO:0008033; F:GO:0016787; P:GO:0000379; F:GO:0003676; C:GO:0000214; F:GO:0003674; F:GO:0000213; P:GO:0006388; C:GO:0005575; F:GO:0004519; F:GO:0004518		IPR006677; IPR011856
Caenorhabditis elegans	major allergen	0				IPR002499
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0000003; P:GO:0040011; P:GO:0019915		IPR013090; G3DSA:2.10.60.10 (GENE3D), SignalP (SIGNALP), SSF57302 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0000003; P:GO:0040011; P:GO:0019915		IPR013090; SignalP (SIGNALP), SSF57302 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0000003; P:GO:0040011; P:GO:0019915		IPR013090; SignalP (SIGNALP), SSF57302 (SUPERFAMILY)
Caenorhabditis briggsae	myh9 protein	21	C:GO:0030863; P:GO:0008360; C:GO:0031594; P:GO:0051295; P:GO:0006928; C:GO:0005913; P:GO:0016337; C:GO:0001772; P:GO:0007520; F:GO:0003779; C:GO:0005819; P:GO:0007132; F:GO:0032559; F:GO:0003774; P:GO:0000904; P:GO:0001768; C:GO:0001725; C:GO:0001931; P:GO:0001701; C:GO:0016459; P:GO:0000212	-		IPR002928; PTHR13140 (PANTHER), PTHR13140:SF23 (PANTHER)

Ailuropoda melanoleuca	fibrillarin	11	C:GO:0001651; C:GO:0001652; C:GO:0031428; C:GO:0015030; F:GO:0030515; F:GO:0005515; P:GO:0016074; P:GO:0006364; P:GO:0032259; F:GO:0008168; P:GO:0008033	-	EC:2.1.1.0	-
Caenorhabditis briggsae	dead (asp-glu-ala-asp) box polypeptide 47	11	P:GO:0040010; F:GO:0003723; C:GO:0005730; F:GO:0008026; P:GO:0006200; P:GO:0040035; F:GO:0005524; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0009792	-		IPR000629; IPR001650; IPR011545; IPR014001; IPR014014; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF11 (PANTHER), SSF52540 (SUPERFAMILY)
Brugia malayi	trehalase family protein	5	P:GO:0009792; P:GO:0002119; F:GO:0016798; P:GO:0008152; P:GO:0040007	-		IPR001661; IPR008928; PTHR23403:SF1 (PANTHER)
	-	0				-
Caenorhabditis elegans	illin homolo family member (pxl-1)	6	P:GO:0009792; P:GO:0002119; C:GO:0030054; P:GO:0040010; C:GO:0005634; F:GO:0008270	-		-
Caenorhabditis elegans	alg2 protein	8	P:GO:0040010; P:GO:0009058; P:GO:0002119; F:GO:0005515; F:GO:0004376; P:GO:0009792; P:GO:0040015; C:GO:0005634	-		IPR001296; PTHR12526 (PANTHER), PTHR12526:SF22 (PANTHER), SSF53756 (SUPERFAMILY)
Caenorhabditis elegans	alg2 protein	8	P:GO:0040010; P:GO:0009058; P:GO:0002119; F:GO:0005515; F:GO:0004376; P:GO:0009792; P:GO:0040015; C:GO:0005634	-		IPR001296; PTHR12526 (PANTHER), PTHR12526:SF22 (PANTHER), SSF53756 (SUPERFAMILY)
	-	0				-
Loa loa	ph domain containing protein	1	F:GO:0005515	-		IPR001849; IPR011993; PTHR21538 (PANTHER), PTHR21538:SF10 (PANTHER), SignalP (SIGNALP), SSF50729 (SUPERFAMILY)

Caenorhabditis elegans	cbp p300 homolog family member (cbp-1)	13	F:GO:0008270; F:GO:0004402; P:GO:0040010; F:GO:0003712; P:GO:0040026; P:GO:0007283; P:GO:0018996; C:GO:0005737; P:GO:0040039; P:GO:0009792; P:GO:0045944; C:GO:0005634; P:GO:0040035	-	EC:2.3.1.48	IPR000197; IPR000315; IPR000433; PTHR13808 (PANTHER)
Caenorhabditis elegans	protein phosphatase	4	P:GO:0006470; F:GO:0046872; F:GO:0004722; C:GO:0008287	-		IPR000222; IPR001932; IPR014045; IPR015655; PTHR13832:SF91 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-epc-1 protein	8	P:GO:0009792; P:GO:0040027; P:GO:0040018; P:GO:0040010; P:GO:0000003; P:GO:0008340; P:GO:0040011; P:GO:0006898	-		PTHR14898 (PANTHER)
	-	0				IPR020857
	-	0				-
Caenorhabditis briggsae	proline-serine-threonine phosphatase interacting	0		C:GO:0030131; P:GO:0016192; P:GO:0006886; F:GO:0005515		IPR018808
Caenorhabditis briggsae	proline-serine-threonine phosphatase interacting	0		C:GO:0030131; P:GO:0016192; P:GO:0006886; F:GO:0005515		IPR018808
Caenorhabditis briggsae	proline-serine-threonine phosphatase interacting	0		C:GO:0030131; P:GO:0016192; P:GO:0006886; F:GO:0005515		IPR018808
Caenorhabditis briggsae	proline-serine-threonine phosphatase interacting	0		C:GO:0030131; P:GO:0016192; P:GO:0006886; F:GO:0005515		IPR018808
Caenorhabditis elegans	n-acetylglucosamine-phosphate mutase	3	P:GO:0009792; F:GO:0004610; P:GO:0005996	-	EC:5.4.2.3	IPR005844; IPR005845; IPR016055; IPR016066; PTHR22573 (PANTHER), PTHR22573:SF3 (PANTHER)
Caenorhabditis elegans	atp synthase subunit mitochondrial precursor	0		C:GO:0045263; C:GO:0016020; C:GO:0005743; P:GO:0006811; C:GO:0005739; P:GO:0006810; F:GO:0015078; P:GO:0006754; P:GO:0015992		G3DSA:3.80.10.10 (GENE3D), PTHR13382 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	briggsae cbr-eat-2 protein	7	P:GO:0043050; P:GO:0007274; P:GO:0048609; P:GO:0008340; C:GO:0045203; F:GO:0004889; C:GO:0005892	-		SignalP (SIGNALP)
Caenorhabditis briggsae	major facilitator superfamily protein	0		C:GO:0016021; C:GO:0016020; P:GO:0055085; F:GO:0005215; P:GO:0006810		PTHR11600 (PANTHER), PTHR11600:SF28 (PANTHER)
Caenorhabditis briggsae	major facilitator superfamily protein	0		C:GO:0016021; C:GO:0016020; P:GO:0055085; F:GO:0005215; P:GO:0006810		PTHR11600 (PANTHER), PTHR11600:SF28 (PANTHER)
Caenorhabditis elegans	human krit 1 (krev interaction trapped cerebral cavernous malformation 1) homolog family member (kri-1)	0				PTHR13283 (PANTHER), PTHR13283:SF1 (PANTHER)
Caenorhabditis elegans	aspartyl-tr- synthetase	6	C:GO:0005737; F:GO:0003676; P:GO:0006422; F:GO:0005515; F:GO:0005524; F:GO:0004815	-	EC:6.1.1.12	-
	-	0				-
Caenorhabditis elegans	hiv tat specific factor 1	4	F:GO:0003676; F:GO:0000166; P:GO:0040011; P:GO:0010171	-		-
Caenorhabditis briggsae	lagen with endostatin domain family member (cle-1)	0		F:GO:0005488; C:GO:0005604; C:GO:0030054; F:GO:0005198; P:GO:0007155; P:GO:0040035; C:GO:0031012		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	retinol dehydroge-se 12	3	F:GO:0016491; P:GO:0055114; F:GO:0005488	-		IPR002198; IPR002347; IPR016040; PTHR19410:SF103 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	dihydrouridine synthase 4-like	4	F:GO:0050660; P:GO:0055114; F:GO:0017150; P:GO:0008033	-		IPR001269; IPR013785; IPR018517; PTHR11082:SF6 (PANTHER), SSF51395 (SUPERFAMILY)
Caenorhabditis briggsae	dual specificity catalytic domain containing protein	4	F:GO:0004725; P:GO:0006470; P:GO:0008340; F:GO:0008138	-	EC:3.1.3.48	PTHR10159 (PANTHER), PTHR10159:SF21 (PANTHER)
Caenorhabditis elegans	larp (r- binding la related protein) homolog protein isoform partially confirmed by transcript evidence	2	F:GO:0003676; F:GO:0005515	-		IPR006630; IPR011991; PTHR22792 (PANTHER), PTHR22792:SF6 (PANTHER), SSF46785 (SUPERFAMILY)
Caenorhabditis elegans	larp (r- binding la related protein) homolog protein isoform partially confirmed by transcript evidence	2	F:GO:0003676; F:GO:0005515	-		IPR006630; IPR011991; PTHR22792 (PANTHER), PTHR22792:SF6 (PANTHER), SSF46785 (SUPERFAMILY)

Caenorhabditis elegans	ubiquitin protein ligase e3b	0		F:GO:0016874; F:GO:0016881; C:GO:0005622; P:GO:0006464		IPR000048
Brugia malayi	pan domain containing protein	0				-
Caenorhabditis elegans	possible sd repeat-containing cell surface protein precursor	0				-
Caenorhabditis elegans	ly1 antibody reactive homolog	0				-
Caenorhabditis elegans	myosin-rhogap myr	6	F:GO:0046872; C:GO:0016459; F:GO:0005524; P:GO:0007165; F:GO:0003774; F:GO:0016740	-		IPR001609; PTHR13140 (PANTHER), PTHR13140:SF30 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydroge-se mitochondrial	3	C:GO:0045252; F:GO:0004149; P:GO:0006099	-	EC:2.3.1.61	IPR000089; IPR001078; IPR003016; IPR011053; G3DSA:2.40.50.100 (GENE3D), G3DSA:3.30.559.10 (GENE3D), PTHR23151 (PANTHER), PTHR23151:SF8 (PANTHER), SSF52777 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	transbilayer amphipath transporters (subfamily iv p-type atpase) family member (tat-2)	7	C:GO:0016021; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0015914; F:GO:0000287; F:GO:0004012	-	EC:3.6.3.1	IPR001757; PTHR11939:SF3 (PANTHER), SignalP (SIGNALP)
Brugia malayi	zinc c2h2 type family protein	0		F:GO:0008270; C:GO:0005622		IPR015880
Brugia malayi	zinc c2h2 type family protein	0		F:GO:0008270; C:GO:0005622		IPR015880
Brugia malayi	cysteine-rich protein 1	4	F:GO:0008270; F:GO:0005515; C:GO:0005737; P:GO:0008283	-		IPR001781; PTHR18973 (PANTHER), PTHR18973:SF74 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis briggsae	ubr4 protein	2	F:GO:0005488; P:GO:0008152	-		PTHR21725 (PANTHER)
	-	0				-
Caenorhabditis briggsae	fatty acid-binding protein homolog	4	P:GO:0006810; F:GO:0005515; F:GO:0008289; F:GO:0005215	-		IPR000463; IPR011038; IPR012674; PTHR22725 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-dct-6 protein	0				-
Caenorhabditis elegans	c family member (clr-1)	12	P:GO:0006470; P:GO:0040037; P:GO:0040010; P:GO:0018991; P:GO:0040002; F:GO:0004872; F:GO:0004725; P:GO:0010171; P:GO:0002119; P:GO:0040017; P:GO:0002009; C:GO:0005886	-	EC:3.1.3.48	IPR003599; IPR003961; IPR007110; IPR013783; PTHR19831 (PANTHER), PTHR19831:SF16 (PANTHER), SignalP (SIGNALP), SSF48726 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-

Angiostrongylus cantonensis	nuclear localized metal responsive family member (numr-1)	0		F:GO:0005515		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR001534; SignalP (SIGNALP)
Brugia malayi	plus-3 domain containing protein	13	P:GO:0040010; P:GO:0006898; P:GO:0040011; P:GO:0045747; P:GO:0051571; P:GO:0009792; F:GO:0003677; P:GO:0002119; F:GO:0042800; P:GO:0010171; P:GO:0006352; C:GO:0005634; P:GO:0040035	-		-
Brugia malayi	spry domain containing protein	8	P:GO:0040010; P:GO:0008380; P:GO:0019915; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0002009; P:GO:0009792	-		IPR001870; IPR003877; IPR008985; G3DSA:3.40.50.300 (GENE3D), PTHR12381 (PANTHER), PTHR12381:SF7 (PANTHER), SSF52540 (SUPERFAMILY)
Brugia malayi	hypothetical protein [Brugia malayi]	0		F:GO:0046872; F:GO:0004325; C:GO:0005737; P:GO:0006783; P:GO:0006779; F:GO:0016829		IPR001015; G3DSA:3.40.50.1400 (GENE3D), SSF53800 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-bam-2 protein	1	C:GO:0005887	-		IPR001791; IPR006210; IPR008985; IPR013320
Caenorhabditis elegans	uncoordi-ted family member (unc-22)	3	P:GO:0006468; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR015730; IPR017442; IPR020636; G3DSA:1.10.510.10 (GENE3D)
Paramecium tetraurelia strain d4-2	hypothetical protein [Paramecium tetraurelia strain d4-2]	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-gly-3 protein	5	F:GO:0004653; F:GO:0005529; C:GO:0005794; P:GO:0009312; C:GO:0016021	-	EC:2.4.1.41	IPR000772; IPR008997; G3DSA:2.80.10.50 (GENE3D), G3DSA:3.90.550.10 (GENE3D), PTHR11675 (PANTHER), SSF53448 (SUPERFAMILY)
Loa loa	kh domain containing protein	4	F:GO:0003723; P:GO:0044419; C:GO:0005737; C:GO:0005634	-		IPR002110; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER), PTHR18958:SF277 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	F:GO:0003723; P:GO:0044419; C:GO:0005737; C:GO:0005634	-		IPR002110; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER), PTHR18958:SF275 (PANTHER)
Loa loa	kh domain containing protein	4	F:GO:0003723; P:GO:0044419; C:GO:0005737; C:GO:0005634	-		IPR002110; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER), PTHR18958:SF277 (PANTHER)
Loa loa	kh domain containing protein	4	F:GO:0003723; P:GO:0044419; C:GO:0005737; C:GO:0005634	-		IPR002110; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER), PTHR18958:SF277 (PANTHER)

	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	regulator of g protein sig-ling	5	P:GO:0007186; F:GO:0005096; F:GO:0004871; C:GO:0005737; C:GO:0005834	-	EC:3.6.5.1	IPR000342; IPR016137; G3DSA:1.10.167.10 (GENE3D), G3DSA:1.10.196.10 (GENE3D), PTHR10845 (PANTHER), PTHR10845:SF22 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Heligmosomoides polygyrus	elegans protein confirmed by transcript evidence	2	F:GO:0005515; F:GO:0008289	-		IPR008632; SignalP (SIGNALP)
Caenorhabditis elegans	coiled-coil domain-containing	7	P:GO:0040035; P:GO:0002119; P:GO:0040011; P:GO:0006898; P:GO:0040007; P:GO:0045132; P:GO:0002009	-		-
Brugia malayi	at-rich interactive domain-containing protein 2	7	F:GO:0005488; P:GO:0040007; P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0006898; P:GO:0009792	-		-
Canis familiaris	protein nef1	1	C:GO:0016021	-		IPR007915; SignalP (SIGNALP)
Culex quinquefasciatus	wolf-hirschhorn syndrome candidate 1	11	P:GO:0000122; P:GO:0003289; P:GO:0003290; P:GO:0060348; F:GO:0018024; C:GO:0031965; C:GO:0005730; P:GO:0003149; P:GO:0032259; F:GO:0003682; P:GO:0016568	-	EC:2.1.1.43	IPR006560; G3DSA:2.170.270.10 (GENE3D), PTHR22884 (PANTHER), PTHR22884:SF33 (PANTHER), SSF82199 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Haemonchus contortus	collagen family member (col-166)	5	C:GO:0016021; F:GO:0042302; P:GO:0010171; P:GO:0040010; P:GO:0040011	-		IPR002486; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	breast carcinoma amplified sequence	0		F:GO:0005515		IPR022175; PTHR13268 (PANTHER)

Caenorhabditis elegans	hot_caeel ame: full=probable hydroxyacid-oxoacid mitochondrial short=hot flags: precursor	0		F:GO:0047988; F:GO:0046872; C:GO:0005739; P:GO:0055114; P:GO:0015993; P:GO:0009073; F:GO:0003856		-
Loa loa	mediator of r- polymerase ii transcription subunit 11	7	P:GO:0040010; P:GO:0045449; P:GO:0010171; P:GO:0002119; F:GO:0005515; C:GO:0016592; P:GO:0009792	-		IPR019404; PTHR22890 (PANTHER)
Brugia malayi	gyf domain containing protein	0		P:GO:0008219; F:GO:0005515		PTHR14445 (PANTHER), PTHR14445:SF4 (PANTHER)
Caenorhabditis elegans	complement regulator factor h	0		F:GO:0001848; C:GO:0016021; P:GO:0045916		-
Loa loa	yth domain containing 2	1	F:GO:0003824	-		IPR001650; IPR007502; IPR011709; G3DSA:3.40.50.300 (GENE3D), PTHR18934 (PANTHER), SSF52540 (SUPERFAMILY)
Loa loa	yth domain containing 2	1	F:GO:0003824	-		IPR001650; IPR007502; IPR011709; G3DSA:3.40.50.300 (GENE3D), PTHR18934 (PANTHER), SSF52540 (SUPERFAMILY)
Loa loa	yth domain containing 2	1	F:GO:0003824	-		IPR001650; IPR007502; IPR011709; G3DSA:3.40.50.300 (GENE3D), PTHR18934 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein Y37E11AM.3 [Caenorhabditis elegans]	0				-
	-	0				SignalP (SIGNALP)
Brugia malayi	pab-dependent poly -specific ribonuclease subunit	0		F:GO:0004221; P:GO:0006397; F:GO:0016787; F:GO:0004535; F:GO:0003676; C:GO:0005737; F:GO:0004527; P:GO:0006511; C:GO:0005622; F:GO:0004518		-
Brugia malayi	mrg family protein	0		F:GO:0005488; F:GO:0003682; C:GO:0000785; P:GO:0006333; C:GO:0005634		IPR000953; IPR008676; IPR016197; G3DSA:2.30.30.270 (GENE3D), PF11717 (PFAM)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	ufm1-conjugating enzyme 1	1	F:GO:0005515	-		IPR014806; IPR016135

Caenorhabditis elegans	mediator of r- polymerase ii transcription subunit 12-like	9	P:GO:0040010; P:GO:0018991; P:GO:0040035; P:GO:0010171; P:GO:0040026; P:GO:0040011; P:GO:0009792; P:GO:0040018; P:GO:0006350	-		PTHR12796 (PANTHER)
Brugia malayi	cdc37	10	P:GO:0023033; P:GO:0040035; P:GO:0010171; F:GO:0005515; P:GO:0040011; P:GO:0006898; P:GO:0002009; P:GO:0009792; C:GO:0005737; P:GO:0040015	-		IPR004918; IPR013855; IPR013873; IPR013874; SSF101391 (SUPERFAMILY)
Caenorhabditis elegans	dihydropyrimidi-se	12	C:GO:0005829; F:GO:0004157; F:GO:0008270; C:GO:0005625; P:GO:0006212; P:GO:0019482; P:GO:0006210; F:GO:0016597; P:GO:0051289; F:GO:0002058; C:GO:0005634; F:GO:0002059	-	EC:3.5.2.2	SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-skp-1 protein	7	P:GO:0001700; F:GO:0005515; C:GO:0071011; P:GO:0000398; P:GO:0035214; C:GO:0071013; C:GO:0000790	-		IPR004015; IPR017862
Caenorhabditis elegans	briggsae cbr-skp-1 protein	7	P:GO:0001700; F:GO:0005515; C:GO:0071011; P:GO:0000398; P:GO:0035214; C:GO:0071013; C:GO:0000790	-		IPR004015; IPR017862
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	smek homolog suppressor of mek1	2	C:GO:0043229; F:GO:0005515	-		IPR006887; IPR011989; IPR011993; IPR016024; PTHR23318 (PANTHER), SSF50729 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	hypothetical protein Y92H12A.5 [Caenorhabditis elegans]	0				-
	-	0				IPR014044
Caenorhabditis elegans	d- polymerase zeta catalytic subunit	2	P:GO:0006259; P:GO:0006974	-		IPR006133; IPR012337; G3DSA:3.30.420.10 (GENE3D), PTHR10322 (PANTHER), PTHR10322:SF5 (PANTHER)

Caenorhabditis briggsae	phosphoglycerate mutase family member 5	4	F:GO:0004721; P:GO:0006470; C:GO:0016020; C:GO:0005739	-	EC:3.1.3.16	SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	alpha 1	13	P:GO:0030155; P:GO:0060441; P:GO:0060445; P:GO:0045198; P:GO:0045995; C:GO:0005606; P:GO:0031175; P:GO:0002011; F:GO:0043208; P:GO:0030334; F:GO:0005102; F:GO:0005201; P:GO:0007166	-		IPR002049; IPR013032; G3DSA:2.10.25.10 (GENE3D), PTHR10574 (PANTHER), PTHR10574:SF54 (PANTHER), SSF57196 (SUPERFAMILY)
Caenorhabditis briggsae	leucine rich repeat family protein	0		F:GO:0005515		G3DSA:3.80.10.10 (GENE3D), PTHR23154 (PANTHER), SignalP (SIGNALP), SSF52058 (SUPERFAMILY)
Caenorhabditis elegans	eukaryotic translation initiation factor 5a	9	F:GO:0003743; F:GO:0003746; F:GO:0003723; P:GO:0006452; P:GO:0008612; P:GO:0045905; F:GO:0043022; F:GO:0005515; P:GO:0045901	-		IPR001884; IPR005824; IPR008991; IPR012340; IPR014722; IPR016027; IPR019769; IPR020189; PTHR11673:SF2 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				PTHR19282 (PANTHER), PTHR19282:SF33 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				PTHR19282 (PANTHER), PTHR19282:SF33 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	ubiquitin specific peptidase 47	1	F:GO:0016787	-		IPR001394; IPR018200; PTHR10420 (PANTHER), PTHR10420:SF44 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		F:GO:0008270; F:GO:0005515		SignalP (SIGNALP)
Caenorhabditis briggsae	abnormal dauer formation family member (daf-36)	5	F:GO:0046872; F:GO:0016491; P:GO:0002165; P:GO:0055114; F:GO:0051537	-		-
Caenorhabditis elegans	beige beach domain containing protein	1	F:GO:0005488	-		SignalP (SIGNALP)
Loa loa	briggsae cbr-spe-10 protein	0		F:GO:0046872; F:GO:0016740; F:GO:0008270; C:GO:0005575		IPR001594; PTHR22883 (PANTHER), SignalP (SIGNALP)

Brugia malayi	transcription elongation factor b polypeptide 2	11	C:GO:0005829; P:GO:0018991; P:GO:0045944; P:GO:0040007; C:GO:0005667; P:GO:0040035; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0040011; C:GO:0030891	-		G3DSA:3.10.20.90 (GENE3D), PTHR13248 (PANTHER), SSF54236 (SUPERFAMILY)
Caenorhabditis briggsae	rab6	15	P:GO:0007293; P:GO:0007264; P:GO:0001745; P:GO:0006887; P:GO:0006913; F:GO:0004767; P:GO:0045451; P:GO:0008103; F:GO:0005515; F:GO:0003924; P:GO:0006886; P:GO:0009792; C:GO:0005737; C:GO:0005634; F:GO:0005525	-	EC:3.1.4.12; EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-cyp-36a1 protein	0		F:GO:0020037; F:GO:0005506; C:GO:0016021; F:GO:0009055; P:GO:0055114; F:GO:0016491; F:GO:0005515; F:GO:0046872; F:GO:0004497		IPR001128; PTHR19383:SF66 (PANTHER)
Caenorhabditis elegans	briggsae cbr-eel-1 protein	5	C:GO:0005622; F:GO:0016881; F:GO:0005488; P:GO:0006464; P:GO:0033227	-	EC:6.3.2.0	IPR000569; PTHR11254 (PANTHER), PTHR11254:SF67 (PANTHER)
Caenorhabditis elegans	briggsae cbr-npp-15 protein	1	P:GO:0040010	-		IPR015943; PTHR13405 (PANTHER), PTHR13405:SF6 (PANTHER), SSF117289 (SUPERFAMILY)
Caenorhabditis briggsae	gtp-binding protein guf1 homolog	4	F:GO:0003746; F:GO:0005525; C:GO:0005739; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000795; IPR005225; G3DSA:3.40.50.300 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF40 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	importin (ran-binding protein)	10	F:GO:0008565; P:GO:0040010; P:GO:0040035; P:GO:0002119; F:GO:0005515; P:GO:0040039; P:GO:0006898; P:GO:0009792; C:GO:0044424; P:GO:0016246	-		IPR005043; IPR011989; IPR013713; IPR016024; PTHR10997 (PANTHER), PTHR10997:SF8 (PANTHER)
Caenorhabditis elegans	importin (ran-binding protein)	10	F:GO:0008565; P:GO:0040010; P:GO:0040035; P:GO:0002119; F:GO:0005515; P:GO:0040039; P:GO:0006898; P:GO:0009792; C:GO:0044424; P:GO:0016246	-		IPR005043; IPR011989; IPR013713; IPR016024; PTHR10997 (PANTHER), PTHR10997:SF8 (PANTHER)
Loa loa	protein vprbp-like	2	C:GO:0005634; F:GO:0005515	-		PTHR13129 (PANTHER)
Caenorhabditis elegans	sig-l peptide peptidase-like 2b	1	F:GO:0005515	-		IPR007369; PTHR12174:SF21 (PANTHER)
Caenorhabditis briggsae	spaghetti squash	19	C:GO:0016461; P:GO:0035159; P:GO:0007349; F:GO:0005509; P:GO:0060288; C:GO:0005737; F:GO:0032036; P:GO:0001736; P:GO:0090254; P:GO:0032956; C:GO:0051233; C:GO:0032154; C:GO:0030496; P:GO:0035317; F:GO:0042623; P:GO:0007300; P:GO:0035191; P:GO:0007298; P:GO:0000910	-		IPR002048; IPR011992; IPR018247; IPR018248; IPR018249; PTHR23049 (PANTHER), PTHR23049:SF6 (PANTHER), SignalP (SIGNALP), SSF47473 (SUPERFAMILY)
Caenorhabditis elegans	tbc (tre-2 bub2 cdc16) domain family member (tbc-7)	2	P:GO:0008340; P:GO:0000003	-		IPR000195; IPR006571; PTHR23353 (PANTHER), PF07534 (PFAM)
Ailuropoda melanoleuca	polyadenylate-binding protein 1-like	9	P:GO:0006378; P:GO:0008380; P:GO:0048255; C:GO:0005681; F:GO:0008494; F:GO:0008022; C:GO:0005829; F:GO:0000166; F:GO:0008143	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF69 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
	-	0				-

Caenorhabditis elegans	briggsae cbr-lea-1 protein	0		C:GO:0005811; F:GO:0005488; C:GO:0005737; F:GO:0004871; C:GO:0016020; P:GO:0007165; F:GO:0005515; C:GO:0005886		IPR008611; PTHR23241 (PANTHER)
Caenorhabditis elegans	briggsae cbr-lea-1 protein	0		C:GO:0005811; F:GO:0005488; C:GO:0005737; F:GO:0005515; C:GO:0005886		IPR008611; PTHR23241 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-cku-80 protein	3	P:GO:0009628; F:GO:0005488; P:GO:0006281	-		IPR005160; IPR006164; IPR016194; G3DSA:2.40.290.10 (GENE3D), PTHR12604 (PANTHER), PTHR12604:SF3 (PANTHER)
Loa loa	centromere protein f	0				-
Caenorhabditis elegans	te-scin r	8	P:GO:0008340; P:GO:0000003; P:GO:0018996; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0006898; P:GO:0009792	-		IPR003961; IPR008957; IPR013783; PTHR10489 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	meiotic checkpoint regulator cut4	1	F:GO:0005515	-		-
Brugia malayi	chloride channel protein 3	5	F:GO:0005247; P:GO:0055085; P:GO:0000003; C:GO:0016021; P:GO:0006821	-		IPR001807; IPR014743; PTHR11689:SF21 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		IPR009771; PTHR22746 (PANTHER), PTHR22746:SF6 (PANTHER)
Caenorhabditis briggsae	mechanosensory abnormality family member (mec-1)	4	P:GO:0040010; F:GO:0005488; C:GO:0005578; P:GO:0030326	-		IPR000152; IPR000742; IPR001881; IPR013032; IPR013091; IPR018097; G3DSA:2.10.25.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF84 (PANTHER), SSF57196 (SUPERFAMILY)
Brugia malayi	leucine zipper transcription regulator 2	0		P:GO:0015031; C:GO:0016020; C:GO:0000139; P:GO:0006810; F:GO:0003674; C:GO:0005794; C:GO:0005789; C:GO:0005575; F:GO:0005515; C:GO:0005783; P:GO:0016192; P:GO:0008150		PTHR13402 (PANTHER)
	-	0				PTHR23194 (PANTHER), PTHR23194:SF1 (PANTHER)

	-	0				-
Caenorhabditis briggsae	polyribonucleotide nucleotidyltransferase 1	3	C:GO:0005758; F:GO:0016779; P:GO:0016070	-	EC:2.7.7.0	IPR001247; IPR012162; IPR015848; IPR020568
Caenorhabditis elegans	hypothetical protein Y50D4A.1 [Caenorhabditis elegans]	0		P:GO:0006412; C:GO:0005840; C:GO:0005622		-
Loa loa	dedicator of cytokinesis family protein	0		F:GO:0005525; F:GO:0051020; F:GO:0005085		IPR001849
Brugia malayi	cg9915-pa	1	P:GO:0000003	-		-
Caenorhabditis elegans	methionine synthase	9	P:GO:0042558; F:GO:0008705; C:GO:0005622; F:GO:0031419; F:GO:0005515; P:GO:0032940; F:GO:0008898; P:GO:0009086; F:GO:0008270	-	EC:2.1.1.13; EC:2.1.1.10	IPR004223; PTHR21091 (PANTHER), PTHR21091:SF18 (PANTHER)
	-	0				-
Loa loa	ubx domain containing 8	0		C:GO:0005811; F:GO:0003674; P:GO:0006986; C:GO:0005737; C:GO:0005783; P:GO:0008150; F:GO:0005515; C:GO:0005575		-
Loa loa	ubx domain containing 8	0		C:GO:0005811; F:GO:0003674; P:GO:0006986; C:GO:0005737; C:GO:0005783; P:GO:0008150; F:GO:0005515; C:GO:0005575		-
Caenorhabditis briggsae	variable abnormal morphology family member (vab-10)	0		F:GO:0005509; P:GO:0007050; F:GO:0003779		G3DSA:3.90.1290.10 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF49 (PANTHER), SSF75399 (SUPERFAMILY)
Brugia malayi	uncoordi-ted family member (unc-44)	11	F:GO:0008092; P:GO:0048675; P:GO:0007016; P:GO:0007528; C:GO:0043195; P:GO:0000226; C:GO:0042734; C:GO:0031594; P:GO:0007165; F:GO:0005200; C:GO:0005886	-		-

Caenorhabditis brenneri	calsyntenin 1	9	P:GO:0009792; C:GO:0005615; P:GO:0007156; F:GO:0005515; C:GO:0032809; P:GO:0008355; C:GO:0043231; F:GO:0005509; C:GO:0016021	-		SignalP (SIGNALP)
	-	0				-
Loa loa	fumarylacetoacetate hydrolase domain-containing protein 1	6	P:GO:0009792; P:GO:0008152; F:GO:0016787; P:GO:0040007; F:GO:0016853; P:GO:0002119	-		IPR002529; IPR011234; PTHR11820 (PANTHER), PTHR11820:SF7 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Strongylocentrotus purpuratus	d- damage-binding protein 1	10	P:GO:0043161; P:GO:0000718; P:GO:0000075; F:GO:0003684; C:GO:0031464; C:GO:0031465; P:GO:0042787; F:GO:0005515; C:GO:0005654; C:GO:0005737	-		PTHR10644 (PANTHER), PTHR10644:SF3 (PANTHER)
	-	0				-
Caenorhabditis elegans	uncoordi-ted family member (unc-79)	0				-
	-	0				-
	-	0				-
	-	0				-
Cooperia oncophora	latrophilin-like protein 2	6	P:GO:0007218; C:GO:0016021; P:GO:0007165; C:GO:0005886; F:GO:0005529; F:GO:0004930	-		IPR016186; IPR016187; PTHR22802 (PANTHER), PTHR22802:SF16 (PANTHER)
Dictyocaulus viviparus	acetylcholinesterase 2	6	F:GO:0004104; P:GO:0001507; F:GO:0003990; C:GO:0005623; P:GO:0040012; F:GO:0042803	-	EC:3.1.1.8; EC:3.1.1.7	IPR000997; IPR002018; G3DSA:3.40.50.1820 (GENE3D), PTHR11559:SF33 (PANTHER), SSF53474 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Angiostrongylus cantonensis	cell wall protein awa1p	0				-
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
	-	0				-
Caenorhabditis elegans	transmembrane protein 161b	0		F:GO:0008270; F:GO:0005515		IPR019395; PTHR13624 (PANTHER), PTHR13624:SF1 (PANTHER), SignalP (SIGNALP)

Brugia malayi	domain containing protein	3	P:GO:0018991; P:GO:0040011; P:GO:0006898	-		SignalP (SIGNALP)
Osmerus mordax	acidic leucine-rich nuclear phosphoprotein 32 family member a	4	C:GO:0005737; F:GO:0005515; C:GO:0016363; P:GO:0009987	-		IPR003603; G3DSA:3.80.10.10 (GENE3D), PTHR11375 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)
Caenorhabditis elegans	human a1 homolog family member (hrp-1)	6	F:GO:0003676; F:GO:0005515; C:GO:0030529; C:GO:0031981; F:GO:0000166; P:GO:0006396	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF13 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	human a1 homolog family member (hrp-1)	6	F:GO:0003676; F:GO:0005515; C:GO:0030529; C:GO:0031981; F:GO:0000166; P:GO:0006396	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF13 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	human a1 homolog family member (hrp-1)	5	F:GO:0003676; C:GO:0030529; C:GO:0031981; F:GO:0000166; P:GO:0006396	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF13 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	human a1 homolog family member (hrp-1)	6	F:GO:0003676; F:GO:0005515; C:GO:0030529; C:GO:0031981; F:GO:0000166; P:GO:0006396	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF13 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	t-complex protein 11	0		P:GO:0030154; C:GO:0016021; P:GO:0007275; P:GO:0007283		IPR008862; PTHR12832:SF6 (PANTHER)
Caenorhabditis elegans	ubiquitin-conjugating enzyme e2 j1	6	C:GO:0005789; P:GO:0016567; F:GO:0005524; F:GO:0004842; C:GO:0016021; P:GO:0051246	-	EC:6.3.2.19	IPR000608; IPR016135; PTHR11621 (PANTHER), PTHR11621:SF15 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis brenneri	nuclear and cytoplasmic polyadenylated r--binding protein	5	C:GO:0005730; C:GO:0005794; F:GO:0003676; F:GO:0005515; F:GO:0000166	-		IPR000504; IPR012677; PTHR23003 (PANTHER), PTHR23003:SF2 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
	-	0				-
Dictyocaulus viviparus	acetylcholinesterase 2	5	P:GO:0001507; F:GO:0003990; C:GO:0005623; P:GO:0040012; F:GO:0042803	-	EC:3.1.1.7	IPR000997; IPR002018; IPR019826; G3DSA:3.40.50.1820 (GENE3D), PTHR11559:SF33 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)

Homo sapiens	ribosomal protein s28	6	F:GO:0003735; F:GO:0005515; P:GO:0006364; C:GO:0022627; P:GO:0042274; P:GO:0006414	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	helix-loop-helix d--binding domain containing protein	8	F:GO:0030528; P:GO:0045941; F:GO:0005515; P:GO:0006355; F:GO:0044212; P:GO:0051726; F:GO:0043565; P:GO:0016481	-		IPR001092; IPR011598; PTHR15741 (PANTHER), PTHR15741:SF4 (PANTHER)
Brugia malayi	protein phosphatase regulatory subunit	4	C:GO:0000159; P:GO:0007165; F:GO:0005515; F:GO:0008601	-		IPR002554; IPR016024
	-	0				-
	-	0				-
	-	0				-
Loa loa	ferm domain containing 4a	0		F:GO:0003674; F:GO:0005488; C:GO:0005737; C:GO:0005856; P:GO:0008150; C:GO:0005575		IPR000299; IPR011993; IPR014352; IPR018979; IPR018980; IPR019748; IPR019749; IPR021774; G3DSA:3.10.20.90 (GENE3D), PTHR23280 (PANTHER), SSF50729 (SUPERFAMILY), SSF54236 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	9	P:GO:0009792; F:GO:0016491; P:GO:0040018; P:GO:0019373; F:GO:0005506; P:GO:0040017; P:GO:0040010; P:GO:0000003; P:GO:0008340	-		IPR001128; IPR002401; IPR017972; PTHR19383:SF176 (PANTHER)
	-	0				-
Caenorhabditis elegans	adenylate cyclase type ix	11	P:GO:0006952; P:GO:0008219; C:GO:0016021; F:GO:0004016; P:GO:0007188; P:GO:0042221; P:GO:0002119; P:GO:0040017; P:GO:0006171; C:GO:0005886; P:GO:0030431	-	EC:4.6.1.1	IPR001054; PTHR11920 (PANTHER), PTHR11920:SF10 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	phd finger protein 10-like	2	F:GO:0046872; C:GO:0005634	-		PTHR10615 (PANTHER), PTHR10615:SF18 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	protein unc-79 homolog	0		C:GO:0016021; C:GO:0016020		PTHR21696 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-

	-	0				-
Heliconius melpomene	endonuclease-reverse transcriptase	1	F:GO:0016787	-		IPR005135; G3DSA:3.60.10.10 (GENE3D), PTHR23227 (PANTHER), PTHR23227:SF14 (PANTHER)
Heliconius melpomene	endonuclease-reverse transcriptase	1	F:GO:0003824	-		-
Heliconius melpomene	endonuclease-reverse transcriptase	1	F:GO:0016787	-		IPR005135; G3DSA:3.60.10.10 (GENE3D), PTHR23227 (PANTHER), PTHR23227:SF14 (PANTHER)
Caenorhabditis elegans	phosphorylase beta	4	P:GO:0005976; P:GO:0044237; C:GO:0044464; F:GO:0003824	-		IPR008734; PTHR10749:SF1 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-unc-97 protein	4	C:GO:0005829; C:GO:0030054; F:GO:0017022; F:GO:0008270	-		IPR001781; PTHR18973 (PANTHER), PTHR18973:SF93 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	5	P:GO:0048856; F:GO:0005515; P:GO:0007275; P:GO:0000003; P:GO:0040007	-		-
Laccaria bicolor S238N-H82	set domain-containing protein	5	C:GO:0043229; P:GO:0044238; P:GO:0044260; P:GO:0006325; F:GO:0003824	-		IPR001214; IPR001917; IPR007728; G3DSA:2.170.270.10 (GENE3D), PTHR22884 (PANTHER), PTHR22884:SF25 (PANTHER), SSF82199 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR015915; SSF117281 (SUPERFAMILY)
Caenorhabditis elegans	down syndrome critical region gene 1-like 2	3	F:GO:0031013; P:GO:0019722; F:GO:0000166	-		IPR006931; PTHR10300:SF2 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	propionyl coenzyme a beta polypeptide	4	F:GO:0005515; C:GO:0005759; F:GO:0005524; F:GO:0004658	-	EC:6.4.1.3	IPR000022; IPR011762; IPR011763; G3DSA:3.90.226.10 (GENE3D), PTHR22855 (PANTHER), PTHR22855:SF14 (PANTHER), SSF52096 (SUPERFAMILY)
	-	0				-

Caenorhabditis briggsae	huntingtin interacting protein 1	21	F:GO:0035091; P:GO:0030324; P:GO:0006919; P:GO:0048268; C:GO:0005624; P:GO:0007405; C:GO:0005794; C:GO:0009986; F:GO:0003779; F:GO:0030276; P:GO:0006917; P:GO:0048260; C:GO:0005856; P:GO:0007165; P:GO:0040036; P:GO:0009887; P:GO:0009953; C:GO:0030136; C:GO:0005887; F:GO:0005200; P:GO:0045879	-		IPR008942; IPR011417; IPR013809; PTHR10407 (PANTHER), PTHR10407:SF4 (PANTHER)
Loa loa	elegans protein confirmed by transcript evidence	2	P:GO:0009987; P:GO:0043170	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	rhomboid family protein	0		F:GO:0004252; F:GO:0005509; F:GO:0008236; C:GO:0016021; P:GO:0007165; C:GO:0005886		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG21915 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	briggsae cbr-fli-1 protein	7	C:GO:0005730; P:GO:0051014; C:GO:0005813; P:GO:0030036; F:GO:0003779; P:GO:0007275; P:GO:0006936	-		IPR007122; G3DSA:3.40.20.10 (GENE3D), PTHR11977:SF6 (PANTHER)
Caenorhabditis elegans	zinc finger protein 236	3	P:GO:0016070; F:GO:0003676; C:GO:0005622	-		-
Caenorhabditis briggsae	dimethylglycine mitochondrial	7	P:GO:0055085; F:GO:0004047; F:GO:0005488; C:GO:0005739; P:GO:0006546; F:GO:0016491; C:GO:0016020	-	EC:2.1.2.10	IPR006076; G3DSA:3.50.50.60 (GENE3D), PTHR13847 (PANTHER), PTHR13847:SF15 (PANTHER), SSF51905 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	transformation transcription domain-associated protein	3	C:GO:0070461; F:GO:0005515; P:GO:0016573	-		IPR003151; IPR014009

Caenorhabditis elegans	transformation transcription domain-associated protein	6	F:GO:0003712; C:GO:0070461; C:GO:0005667; P:GO:0050794; P:GO:0016573; P:GO:0006350	-		IPR003151
Caenorhabditis elegans	transformation transcription domain-associated protein	3	C:GO:0070461; F:GO:0005515; P:GO:0016573	-		IPR003151; IPR014009
Caenorhabditis elegans	transformation transcription domain-associated protein	3	C:GO:0070461; F:GO:0005515; P:GO:0016573	-		IPR003151; IPR014009
Caenorhabditis elegans	g patch domain containing 3	3	F:GO:0003676; C:GO:0005622; F:GO:0000166	-		SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-rnt-1 protein	11	F:GO:0005509; P:GO:0045944; P:GO:0030853; F:GO:0003677; P:GO:0030854; F:GO:0016563; F:GO:0003700; F:GO:0008134; F:GO:0046982; F:GO:0042803; C:GO:0005634	-		-
						IPR002017; IPR018159; G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF48 (PANTHER), SSF46966 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-npp-17 protein	6	P:GO:0040035; P:GO:0009792; P:GO:0040010; P:GO:0040011; P:GO:0006898; P:GO:0002009	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR10971 (PANTHER), PTHR10971:SF11 (PANTHER)
Caenorhabditis elegans	kiaa1699 protein	5	P:GO:0016192; F:GO:0047485; C:GO:0044444; P:GO:0015031; P:GO:0051649	-		PTHR14146 (PANTHER)
	-	0				PTHR22576 (PANTHER), PTHR22576:SF1 (PANTHER)
Caenorhabditis briggsae	6-phosphofructo-2- isoform a	4	F:GO:0004331; F:GO:0003873; P:GO:0006003; F:GO:0005524	-	EC:3.1.3.46; EC:2.7.1.105	IPR003094; IPR013079; G3DSA:3.40.50.300 (GENE3D), PTHR10606:SF11 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	u3 small nucleolar r--interacting protein 2	0				IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR19865 (PANTHER)
Brugia malayi	elegans protein partially confirmed by transcript evidence	0				IPR001680; IPR011046; IPR015943; IPR019775

Caenorhabditis briggsae	patatin-like phospholipase family protein	1	P:GO:0008152	-		IPR002641; IPR016035; PTHR12406 (PANTHER), PTHR12406:SF3 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	spectrin alpha	28	P:GO:0007026; P:GO:0008360; C:GO:0031594; P:GO:0030721; P:GO:0007417; P:GO:0007009; P:GO:0016337; C:GO:0016323; F:GO:0005509; P:GO:0008302; C:GO:0008091; C:GO:0005794; C:GO:0045170; P:GO:0002168; F:GO:0003779; F:GO:0008017; P:GO:0030707; C:GO:0045169; P:GO:0007308; P:GO:0045478; P:GO:0042062; P:GO:0007274; C:GO:0005811; P:GO:0030727; P:GO:0048790; F:GO:0005516; P:GO:0007294	-		IPR002017; IPR018159; G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF6 (PANTHER), SSF46966 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	d330012f22rik protein	0		F:GO:0003674; P:GO:0008150		PTHR20884 (PANTHER), PTHR20884:SF5 (PANTHER)
Caenorhabditis briggsae	d330012f22rik protein	0		F:GO:0003674; P:GO:0008150; C:GO:0005575		PTHR20884 (PANTHER), PTHR20884:SF5 (PANTHER)
	-	0				-
Loa loa	protein ki-se domain containing protein	1	P:GO:0040010	-		IPR000719; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0006355; F:GO:0005509; F:GO:0004871; P:GO:0045449; P:GO:0007165; F:GO:0005515; F:GO:0003700; C:GO:0005634		IPR011992
Caenorhabditis briggsae	patterned expression site family member (pes-22)	0		C:GO:0016021; P:GO:0055085		-

Caenorhabditis elegans	r- binding motif protein 34	7	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0040011; P:GO:0040007; P:GO:0006898; P:GO:0002009	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF57 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	otu ubiquitin aldehyde binding 1	4	F:GO:0004843; P:GO:0071108; F:GO:0019784; F:GO:0043130	-		IPR003323; IPR019400; PTHR12931 (PANTHER), PTHR12931:SF2 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	P:GO:0000003; F:GO:0005488; P:GO:0040010	-		IPR001965; IPR011011; IPR013083; IPR019786; IPR019787; PTHR22880 (PANTHER), PTHR22880:SF1 (PANTHER)
Loa loa	polo-like ki-se 1	16	P:GO:0031572; P:GO:0040038; C:GO:0005654; P:GO:0051437; F:GO:0042801; P:GO:0046677; P:GO:0000236; F:GO:0019901; C:GO:0000942; C:GO:0005829; P:GO:0032436; C:GO:0051233; C:GO:0005813; F:GO:0010997; P:GO:0007346; C:GO:0000922	-		IPR000719; IPR002290; IPR008271; IPR011009; IPR015728; IPR017441; IPR017442; IPR020636; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
	-	0				-
Loa loa	hypothetical protein LOAG_05084 [Loa loa]	0				-
Pongo abelii	hsp90aa1 protein	14	C:GO:0005829; P:GO:0042026; P:GO:0006839; F:GO:0030235; P:GO:0070096; C:GO:0042470; F:GO:0005524; F:GO:0030911; P:GO:0007165; F:GO:0051082; P:GO:0006986; P:GO:0045429; F:GO:0042803; P:GO:0034619	-		IPR001404
	-	0				-
Caenorhabditis elegans	briggsae cbr-gei-13 protein	0		F:GO:0005515; F:GO:0003677; C:GO:0005575		-
Loa loa	zinc dhhc-type containing 14	5	F:GO:0015450; P:GO:0006886; C:GO:0005744; F:GO:0016740; F:GO:0008270	-		-
	-	0				-

Caenorhabditis elegans	eukaryotic peptide chain release factor subunit	15	C:GO:0005829; P:GO:0007224; C:GO:0016021; F:GO:0016149; P:GO:0035071; P:GO:0040007; F:GO:0008236; P:GO:0000003; P:GO:0006605; P:GO:0002119; P:GO:0040011; C:GO:0018444; P:GO:0006415; P:GO:0006898; P:GO:0009792	-		IPR004403; IPR005140; IPR005141; IPR005142; G3DSA:3.30.1330.30 (GENE3D), G3DSA:3.30.420.60 (GENE3D), G3DSA:3.30.960.10 (GENE3D), PTHR10113:SF1 (PANTHER), TIGR00108 (TIGRFAMs), SSF53137 (SUPERFAMILY), SSF55315 (SUPERFAMILY), SSF55481 (SUPERFAMILY)
Homo sapiens	fibronectin 1 protein	13	P:GO:0018149; P:GO:0016477; P:GO:0001525; P:GO:0008360; C:GO:0005793; C:GO:0031093; P:GO:0034446; F:GO:0005518; C:GO:0005577; F:GO:0008201; C:GO:0005578; F:GO:0005201; P:GO:0006953	-		IPR000083; IPR013032; IPR016060; PTHR19143 (PANTHER), PTHR19143:SF6 (PANTHER), SSF57603 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein T12C9.7 [Caenorhabditis elegans]	0		P:GO:0000003; C:GO:0005634; P:GO:0040018		IPR004367; IPR011028; IPR013763; PTHR10177 (PANTHER)
Caenorhabditis elegans	(d- helicase q1-like) isoform cra_a	4	P:GO:0000733; F:GO:0005515; F:GO:0004003; F:GO:0000739	-		IPR004589; IPR011545; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR13710:SF12 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-vps-54 protein	3	C:GO:0005622; P:GO:0006810; P:GO:0007291	-		IPR015880
Caenorhabditis elegans	patched family protein	8	P:GO:0040025; P:GO:0040018; P:GO:0018996; P:GO:0040002; P:GO:0000003; P:GO:0008340; P:GO:0040011; P:GO:0019915	-		IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER), SignalP (SIGNALP), SSF82866 (SUPERFAMILY)
Caenorhabditis elegans	cytosolic fe-s cluster assembly factor -rfl	5	F:GO:0005488; P:GO:0032364; P:GO:0016226; P:GO:0045449; P:GO:0001666	-		IPR004108; IPR009016; G3DSA:3.40.50.1780 (GENE3D), PTHR11615 (PANTHER), PTHR11615:SF31 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-npp-14 protein	0				PTHR23193 (PANTHER), PTHR23193:SF1 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-

Caenorhabditis elegans	dynein heavy chain	5	P:GO:0007018; C:GO:0030286; F:GO:0016887; F:GO:0005524; F:GO:0003777	-		G3DSA:3.40.50.300 (GENE3D), PTHR10676 (PANTHER), PTHR10676:SF28 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	fk506 binding protein 4	14	P:GO:0048731; F:GO:0005528; P:GO:0040011; F:GO:0016853; C:GO:0005737; C:GO:0005730; F:GO:0030674; F:GO:0031072; N:GO:0071842; P:GO:0009792; P:GO:0002009; P:GO:0048523; P:GO:0022414; P:GO:0051129	-		IPR001179; IPR001440; IPR011990; IPR013026; IPR019734; IPR023114; G3DSA:3.10.50.40 (GENE3D), PTHR10516:SF23 (PANTHER), SSF48452 (SUPERFAMILY), SSF54534 (SUPERFAMILY)
Caenorhabditis elegans	exocyst complex component 7	0		C:GO:0000145; P:GO:0006887; C:GO:0016020; P:GO:0006886; C:GO:0005801		IPR004140; IPR016159; PTHR12542:SF7 (PANTHER)
Caenorhabditis elegans	sec13-like 1	13	P:GO:0040007; P:GO:0000003; P:GO:0032940; P:GO:0010171; C:GO:0000776; P:GO:0002119; F:GO:0005515; P:GO:0006888; P:GO:0040011; P:GO:0006997; P:GO:0006898; P:GO:0009792; C:GO:0031080	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; PTHR11024 (PANTHER), PTHR11024:SF2 (PANTHER)
Caenorhabditis elegans	protein sec13 homolog	13	P:GO:0040007; P:GO:0000003; P:GO:0032940; P:GO:0010171; C:GO:0000776; P:GO:0002119; F:GO:0005515; P:GO:0006888; P:GO:0040011; P:GO:0006997; P:GO:0006898; P:GO:0009792; C:GO:0031080	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; PTHR11024 (PANTHER), PTHR11024:SF2 (PANTHER)

Caenorhabditis elegans	sec13-like 1	13	P:GO:0040007; P:GO:0000003; P:GO:0032940; P:GO:0010171; C:GO:0000776; P:GO:0002119; F:GO:0005515; P:GO:0006888; P:GO:0040011; P:GO:0006997; P:GO:0006898; P:GO:0009792; C:GO:0031080	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; PTHR11024 (PANTHER), PTHR11024:SF2 (PANTHER)
	-	0				-
Caenorhabditis briggsae	metallo-beta-lactamase superfamily protein	2	F:GO:0005515; F:GO:0016787	-		G3DSA:3.60.15.10 (GENE3D), PTHR12553 (PANTHER), PTHR12553:SF3 (PANTHER), SSF56281 (SUPERFAMILY)
Caenorhabditis briggsae	metallo-beta-lactamase superfamily protein	2	F:GO:0005515; F:GO:0016787	-		G3DSA:3.60.15.10 (GENE3D), PTHR12553 (PANTHER), PTHR12553:SF3 (PANTHER), SSF56281 (SUPERFAMILY)
Loa loa	elegans protein confirmed by transcript evidence	0				IPR011989
Loa loa	elegans protein confirmed by transcript evidence	0		F:GO:0005488		IPR011989
Caenorhabditis briggsae	nedd8-activating enzyme e1 regulatory subunit	0		F:GO:0005488; P:GO:0008152; F:GO:0003824		IPR009036; IPR016040; PTHR10953 (PANTHER), PTHR10953:SF4 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis sp. PS1010	transmembrane protein 120a	1	C:GO:0016020	-		IPR012926
Caenorhabditis briggsae	briggsae cbr-dnj-9 protein	0		F:GO:0031072		IPR015609; PTHR11821:SF15 (PANTHER), PF11875 (PFAM)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	tsa family protein	5	P:GO:0045454; F:GO:0051920; C:GO:0005737; P:GO:0055114; F:GO:0004601	-	EC:1.11.1.15; EC:1.11.1.7	IPR000866; IPR012335; IPR012336; IPR017936; PTHR10681 (PANTHER), PTHR10681:SF8 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	phenylalanyl-tr- alpha subunit	5	C:GO:0005737; F:GO:0004826; F:GO:0005524; P:GO:0006432; F:GO:0000049	-	EC:6.1.1.20	IPR002319; IPR006195; IPR011991; G3DSA:3.30.930.10 (GENE3D), PTHR11538:SF15 (PANTHER), SSF55681 (SUPERFAMILY)
Loa loa	nf-yc3 (nuclear factor subunit c3) d- binding transcription factor	11	P:GO:0040007; P:GO:0040035; F:GO:0003677; P:GO:0002119; F:GO:0016563; C:GO:0016602; F:GO:0005515; P:GO:0043193; F:GO:0003700; P:GO:0006898; C:GO:0005737	-		-

Loa loa	nf-yc3 (nuclear factor subunit c3) d- binding transcription factor	11	P:GO:0040007; P:GO:0040035; F:GO:0003677; P:GO:0002119; F:GO:0016563; C:GO:0016602; F:GO:0005515; P:GO:0043193; F:GO:0003700; P:GO:0006898; C:GO:0005737	-		IPR003958; IPR009072; PTHR10252 (PANTHER), PTHR10252:SF6 (PANTHER)
Caenorhabditis elegans	hypothetical protein C33A11.1 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	briggsae cbr-acl-6 protein	0		F:GO:0008415; P:GO:0008152		PTHR12563 (PANTHER), PTHR12563:SF3 (PANTHER)
Caenorhabditis elegans	s-re-associated protein s-pin	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F26F12.3 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	methionyl-tr- synthetase	5	F:GO:0005515; P:GO:0006418; F:GO:0004825; C:GO:0005829; F:GO:0000166	-	EC:6.1.1.10	IPR001412; IPR002547; IPR009080; IPR012340; IPR014729; IPR014758; IPR015413; IPR016027; G3DSA:1.10.730.10 (GENE3D), G3DSA:2.20.28.20 (GENE3D), PTHR11946 (PANTHER), PTHR11946:SF1 (PANTHER), SSF52374 (SUPERFAMILY), SSF57770 (SUPERFAMILY)
Pan troglodytes	ribosomal protein l28	5	F:GO:0003735; F:GO:0003723; F:GO:0005515; C:GO:0022625; P:GO:0006414	-		-
Caenorhabditis briggsae	briggsae cbr-tag-250 protein	1	F:GO:0003676	-		IPR008191; G3DSA:2.30.30.140 (GENE3D), SSF63748 (SUPERFAMILY)
	-	0				IPR013585
Heterorhabditis bacteriophora	sparc	6	P:GO:0009792; P:GO:0040018; P:GO:0000003; P:GO:0040010; F:GO:0005509; P:GO:0002119	-		IPR001999; IPR002350; IPR003645; IPR011497; IPR011992; IPR018247; IPR019577; G3DSA:3.30.60.30 (GENE3D), PTHR13866 (PANTHER), PTHR13866:SF5 (PANTHER), SSF100895 (SUPERFAMILY), SSF47473 (SUPERFAMILY)
Caenorhabditis briggsae	peroxin 2	1	F:GO:0046872	-		IPR006845; PTHR12590 (PANTHER)
	-	0				-
Loa loa	briggsae cbr-taf- protein	2	P:GO:0006350; C:GO:0005634	-		SignalP (SIGNALP)
Loa loa	briggsae cbr-taf- protein	2	P:GO:0006350; C:GO:0005634	-		SignalP (SIGNALP)
Loa loa	briggsae cbr-taf- protein	2	P:GO:0006350; C:GO:0005634	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Brugia malayi	hypothetical protein [Brugia malayi]	0				IPR012816; SSF143990 (SUPERFAMILY)

Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	10	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040002; P:GO:0040011; C:GO:0005576; P:GO:0019915; P:GO:0040007; P:GO:0006898; F:GO:0042302	-		SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0042773; P:GO:0006120; F:GO:0008137; F:GO:0003954; C:GO:0005743		IPR009947
Caenorhabditis briggsae	multidrug resistance protein family member (mrp-1)	6	F:GO:0042626; P:GO:0055085; P:GO:0055114; F:GO:0005524; C:GO:0016021; F:GO:0032440	-	EC:1.3.1.74	IPR003439; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF35 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	fatty acid amide hydrolase 2	0		F:GO:0016884; F:GO:0016787; C:GO:0016021; C:GO:0016020		IPR000120; IPR020556; PTHR11895:SF5 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	patched family protein	6	P:GO:0048856; P:GO:0040018; P:GO:0018996; P:GO:0007275; P:GO:0040011; P:GO:0051179	-		IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER)
	-	0				-
Caenorhabditis elegans	g in family member (glb-8)	4	F:GO:0020037; F:GO:0005344; P:GO:0015671; F:GO:0019825	-		-
	-	0				PR00021 (PRINTS), PR01217 (PRINTS)
Caenorhabditis elegans	hypothetical protein F40A3.6 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	hypothetical protein F40A3.6 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	atp-dependent r- helicase ddx54	5	F:GO:0004386; F:GO:0003676; P:GO:0040010; C:GO:0044464; F:GO:0000166	-		IPR012541; PTHR10967 (PANTHER), PTHR10967:SF17 (PANTHER)
Caenorhabditis briggsae	transmembrane protein 30a	3	C:GO:0016020; P:GO:0000003; P:GO:0040010	-		-
Caenorhabditis briggsae	briggsae cbr-sun-1 protein	0		P:GO:0006355; C:GO:0005783; P:GO:0007165; P:GO:0008150; C:GO:0005635; F:GO:0005515		IPR012919; PTHR12911 (PANTHER), PS51469 (PROFILE)
Caenorhabditis elegans	yo25_caeel ame: full=uncharacterized protein	0		P:GO:0000003; P:GO:0007165		IPR021925
Caenorhabditis briggsae	briggsae cbr-cua-1 protein	3	F:GO:0005488; F:GO:0022857; F:GO:0016787	-		-

Caenorhabditis briggsae	copper-transporting atpase 1	6	P:GO:0006825; F:GO:0004008; C:GO:0016021; F:GO:0046872; P:GO:0006754; F:GO:0005524	-	EC:3.6.3.4	IPR000695; IPR001757; IPR005834; G3DSA:3.40.1110.10 (GENE3D), G3DSA:3.40.50.1000 (GENE3D), PTHR11939:SF38 (PANTHER), SSF56784 (SUPERFAMILY)
Loa loa	elongation factor tu c-termi-l domain containing protein	5	F:GO:0003746; F:GO:0005525; F:GO:0004781; F:GO:0005515; F:GO:0003924	-	EC:2.7.7.4; EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR004160; IPR009001; G3DSA:2.40.30.10 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF36 (PANTHER)
Loa loa	calpain d	2	F:GO:0008233; P:GO:0007399	-		IPR001300; IPR022684; G3DSA:3.90.70.10 (GENE3D), PTHR10183 (PANTHER), PTHR10183:SF26 (PANTHER), SSF54001 (SUPERFAMILY)
Loa loa	calpain d	2	P:GO:0007399; F:GO:0008234	-		IPR001300; IPR022684; G3DSA:3.90.70.10 (GENE3D), PTHR10183 (PANTHER), PTHR10183:SF26 (PANTHER), SSF54001 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-rsks-1 protein	5	P:GO:0006468; C:GO:0005840; F:GO:0005524; P:GO:0007165; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR000961; IPR008271; IPR011009; IPR017442; IPR017892; G3DSA:1.10.510.10 (GENE3D), PTHR22985 (PANTHER), PTHR22985:SF83 (PANTHER)
Caenorhabditis elegans	briggsae cbr-rsks-1 protein	5	P:GO:0006468; C:GO:0005840; F:GO:0005524; P:GO:0007165; F:GO:0004674	-	EC:2.7.11.0	-
	-	0				-
	-	0				-
Caenorhabditis elegans	trafficking protein particle complex 9	0		P:GO:0030154; C:GO:0005783; C:GO:0005794		PTHR21512 (PANTHER), PTHR21512:SF6 (PANTHER)
Caenorhabditis elegans	trafficking protein particle complex 9	0		P:GO:0030154; C:GO:0005783; C:GO:0005794		PTHR21512 (PANTHER), PTHR21512:SF6 (PANTHER)
Caenorhabditis elegans	nik- and ikbkb-binding protein	0				PTHR21512 (PANTHER), PTHR21512:SF6 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	splicing factor	1	F:GO:0019899	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	yso2_caeel ame: full=uncharacterized protein flags: precursor	1	P:GO:0000003	-		-

Loa loa	activating sig-l cointegrator 1 complex subunit 3-like 1	12	P:GO:0018991; C:GO:0005681; F:GO:0008026; P:GO:0040007; F:GO:0003677; F:GO:0005524; P:GO:0007601; P:GO:0002119; F:GO:0005515; P:GO:0000354; C:GO:0005682; P:GO:0009792	-		IPR004179; IPR011545; IPR014001; IPR014021; G3DSA:1.10.3380.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR11752 (PANTHER), PTHR11752:SF7 (PANTHER), SSF52540 (SUPERFAMILY)
Loa loa	activating sig-l cointegrator 1 complex subunit 3-like 1 isoform 1	9	P:GO:0018991; C:GO:0005681; F:GO:0008026; P:GO:0040007; P:GO:0008380; F:GO:0003677; F:GO:0005524; P:GO:0002119; P:GO:0009792	-		IPR011545; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR11752 (PANTHER), PTHR11752:SF7 (PANTHER), SSF52540 (SUPERFAMILY)
Loa loa	heterotrimeric g protein alpha subunit	5	P:GO:0007186; F:GO:0004871; P:GO:0007165; F:GO:0005515; F:GO:0005525	-		IPR001019; IPR001408; G3DSA:3.40.50.300 (GENE3D), PTHR10218:SF76 (PANTHER), SSF52540 (SUPERFAMILY)
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0		F:GO:0003725; C:GO:0005622		-
Pan troglodytes	fxyd domain containing ion transport regulator 3	5	C:GO:0005887; P:GO:0034220; F:GO:0005254; P:GO:0006821; C:GO:0034707	-		-
	-	0				-
Caenorhabditis elegans	transcription initiation factor iif alpha subunit	8	F:GO:0030528; P:GO:0008340; F:GO:0003676; P:GO:0040035; P:GO:0050794; P:GO:0006898; P:GO:0009792; P:GO:0006350	-		IPR008851; IPR011991; SSF46785 (SUPERFAMILY)
Caenorhabditis elegans	lipid phosphate phosphohydrolase 1	2	F:GO:0016787; C:GO:0016020	-		IPR000326; IPR016118; PTHR10165 (PANTHER), PTHR10165:SF20 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	crossover junction endonuclease mus81	6	P:GO:0006259; F:GO:0005488; P:GO:0040010; F:GO:0016787; F:GO:0016740; P:GO:0019725	-		IPR006166; IPR011335; IPR020819; PTHR13451 (PANTHER)
Caenorhabditis briggsae	crossover junction endonuclease mus81	3	P:GO:0040010; F:GO:0016740; P:GO:0019725	-		IPR006166; IPR011335; IPR020819; PTHR13451 (PANTHER)
Caenorhabditis briggsae	crossover junction endonuclease mus81	3	P:GO:0040010; P:GO:0019725; F:GO:0003824	-		IPR006166; IPR010996; IPR011335; IPR020819; PTHR13451 (PANTHER)

Loa loa	mitochondrial trans-2-enoyl- reductase	6	P:GO:0006631; P:GO:0008340; C:GO:0005739; N:GO:0039020; F:GO:0016491; F:GO:0005102	-		IPR002085; IPR013149; IPR016040; PTHR11695:SF15 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis briggsae	crooked neck-like protein 1	9	P:GO:0009792; P:GO:0002119; C:GO:0005681; F:GO:0003723; P:GO:0018996; P:GO:0000003; P:GO:0040011; P:GO:0040007; P:GO:0000245	-		-
Caenorhabditis elegans	briggsae cbr-csn-3 protein	0				-
	-	0				IPR007087; IPR015880
	-	0				IPR007087; IPR015880
Caenorhabditis briggsae	origin recognition complex subunit 3	0		P:GO:0006260; C:GO:0005664; F:GO:0003677		IPR010748; IPR020795; IPR022357; SignalP (SIGNALP)
Brugia malayi	initiation factor 4g family member (ifg-1)	0		F:GO:0005488; P:GO:0016070; F:GO:0005515		IPR018271; SignalP (SIGNALP)
Caenorhabditis briggsae	calmodulin binding protein 3	17	P:GO:0033147; F:GO:0051721; C:GO:0005654; P:GO:0000122; C:GO:0000159; F:GO:0016740; C:GO:0005794; F:GO:0070016; C:GO:0030425; C:GO:0043025; F:GO:0003700; P:GO:0045944; F:GO:0032403; C:GO:0005886; F:GO:0005516; P:GO:0032355; F:GO:0016564	-		IPR001680; IPR011046; IPR013258; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR15653 (PANTHER)
Caenorhabditis elegans	pyruvate dehydroge-se	6	P:GO:0009792; F:GO:0005515; F:GO:0004739; P:GO:0040010; P:GO:0055114; C:GO:0005739	-	EC:1.2.4.1	IPR005475; IPR005476; IPR009014; IPR015941; G3DSA:3.40.50.970 (GENE3D), PTHR11624 (PANTHER), PTHR11624:SF11 (PANTHER), SignalP (SIGNALP), SSF52518 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	wd repeat-containing protein 37	0		F:GO:0003674; F:GO:0016740; F:GO:0016905; P:GO:0008150		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR19855 (PANTHER), PTHR19855:SF12 (PANTHER)
	-	0				SignalP (SIGNALP)

Haemonchus contortus	ilin (drosophila ecm protein) homolog family member (ppn-1)	8	F:GO:0004867; F:GO:0004222; F:GO:0005201; F:GO:0005515; C:GO:0005634; F:GO:0008270; P:GO:0030198; C:GO:0005604	-	EC:3.4.24.0	IPR000884; G3DSA:2.20.100.10 (GENE3D), PTHR13723 (PANTHER), PTHR13723:SF18 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-age-1 protein	8	P:GO:0008340; P:GO:0007611; P:GO:0000003; P:GO:0050920; F:GO:0016773; P:GO:0043053; F:GO:0004428; P:GO:0009792	-	EC:2.7.1.0	IPR000341; IPR003113; G3DSA:3.10.20.90 (GENE3D), SSF54236 (SUPERFAMILY)
Caenorhabditis elegans	charged multivesicular body protein 6	8	P:GO:0010171; P:GO:0002119; P:GO:0032940; P:GO:0040010; C:GO:0044464; P:GO:0008340; P:GO:0040011; P:GO:0015031	-		IPR005024; PTHR22761 (PANTHER)
Caenorhabditis elegans	mitotic spindle assembly checkpoint protein mad2a	11	P:GO:0007094; P:GO:0051436; C:GO:0000777; P:GO:0051301; C:GO:0005829; C:GO:0005643; P:GO:0000070; C:GO:0005816; C:GO:0048471; P:GO:0031145; F:GO:0042803	-		IPR003511; G3DSA:3.30.900.10 (GENE3D), PTHR11842 (PANTHER), PTHR11842:SF11 (PANTHER)
Caenorhabditis elegans	abnormal go-d development family member (gon-2)	3	P:GO:0007067; P:GO:0006810; P:GO:0008406	-		IPR005821; PTHR13800 (PANTHER)
Caenorhabditis elegans	abnormal go-d development family member (gon-2)	4	P:GO:0007067; P:GO:0006810; C:GO:0016020; P:GO:0008406	-		IPR005821; PTHR13800 (PANTHER)
Brugia malayi	ubiquitin-protein ligase e3c	2	P:GO:0000003; F:GO:0016881	-	EC:6.3.2.0	IPR000569; PTHR11254 (PANTHER), PTHR11254:SF31 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-clc-1 protein	1	C:GO:0016020	-		-
Caenorhabditis elegans	eukaryotic translation initiation factor 1b	10	F:GO:0003743; P:GO:0040010; P:GO:0008340; P:GO:0045948; P:GO:0000003; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0009792	-		IPR001950; G3DSA:3.30.780.10 (GENE3D), PTHR10388 (PANTHER)

Caenorhabditis brenneri	plasmid mainte-nce protein containing protein	12	F:GO:0003743; P:GO:0006413; P:GO:0040010; P:GO:0008340; P:GO:0006506; C:GO:0031227; P:GO:0000003; P:GO:0010171; P:GO:0002119; P:GO:0040011; P:GO:0009792; F:GO:0016757	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	P:GO:0007160	-		-
Caenorhabditis briggsae	microtubule associated serine threonine ki-se 2	11	F:GO:0008017; C:GO:0015630; F:GO:0004674; P:GO:0048515; F:GO:0019902; F:GO:0005524; F:GO:0000287; P:GO:0009792; P:GO:0045075; C:GO:0005886; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR000961; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22985 (PANTHER), PTHR22985:SF42 (PANTHER)
Brugia malayi	related to oncogene abl family member (abl-1)	2	F:GO:0005488; F:GO:0016301	-		G3DSA:1.20.120.330 (GENE3D)
	-	0				-
Brugia malayi	protein arginine n-methyltransferase 5	3	P:GO:0044238; P:GO:0044260; F:GO:0008168	-	EC:2.1.1.0	IPR007857
Caenorhabditis elegans	leucine-zipper-containing transcription factor lzf	2	P:GO:0040010; P:GO:0006974	-		IPR019386; PF10259 (PFAM)
	-	0				-
Caenorhabditis elegans	leucine-rich transmembrane protein	0		F:GO:0004623; F:GO:0016787; C:GO:0016021; P:GO:0008150; P:GO:0016042; F:GO:0005515; P:GO:0006644; F:GO:0004721		IPR000483; IPR001611; IPR003591; G3DSA:3.80.10.10 (GENE3D), PTHR23154 (PANTHER), PTHR23154:SF47 (PANTHER), SSF52058 (SUPERFAMILY)
Loa loa	cytochrome p450	2	F:GO:0046872; F:GO:0016491	-		IPR001128; IPR002401
	-	0				-
Caenorhabditis elegans	reti-l degeneration isoform h	12	F:GO:0008526; F:GO:0005388; P:GO:0006810; F:GO:0005509; P:GO:0030384; P:GO:0045494; P:GO:0007608; F:GO:0008525; C:GO:0016029; F:GO:0035091; P:GO:0016059; C:GO:0005887	-	EC:3.6.3.8	IPR001666; G3DSA:3.30.530.20 (GENE3D), PTHR10658:SF6 (PANTHER), SSF55961 (SUPERFAMILY)

Caenorhabditis elegans	sec14-like 1 (cerevisiae)	1	C:GO:0005622	-		PTHR23324 (PANTHER), PTHR23324:SF8 (PANTHER), SSF101576 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	ww domain-binding protein 2	3	P:GO:0000003; F:GO:0005515; P:GO:0006898	-		IPR004182; IPR018826; SSF50729 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	basic helix-loop-helix zip transcription factor	7	P:GO:0040010; P:GO:0044260; P:GO:0090304; P:GO:0002119; P:GO:0050794; P:GO:0006898; P:GO:0009792	-		IPR001092; IPR011598; PTHR15741 (PANTHER), PTHR15741:SF13 (PANTHER)
Caenorhabditis elegans	briggsae cbr-rbc-1 protein	0				PTHR13950 (PANTHER), PTHR13950:SF1 (PANTHER)
	-	0				-
Caenorhabditis elegans	immunoglobulin i-set domain containing protein	0				IPR013783; PTHR10489 (PANTHER), PTHR10489:SF39 (PANTHER), SSF48726 (SUPERFAMILY)
Brugia malayi	myb-like d--binding domain containing protein	5	P:GO:0009792; P:GO:0002119; P:GO:0040010; P:GO:0000003; P:GO:0006898	-		IPR001005; IPR009057; PTHR22929 (PANTHER)
Caenorhabditis elegans	beta-lactamase family protein	0				IPR001466; IPR012338; G3DSA:3.40.710.10 (GENE3D), PTHR10566 (PANTHER), PTHR10566:SF6 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-apd-3 protein	8	P:GO:0009792; P:GO:0010171; P:GO:0002119; F:GO:0005488; C:GO:0044444; P:GO:0009987; P:GO:0040007; P:GO:0015031	-		-
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
Caenorhabditis elegans	phosphorylase b ki-se kpbb	2	F:GO:0004339; P:GO:0005976	-	EC:3.2.1.3	IPR008734; IPR011613; PTHR10749:SF1 (PANTHER)
	-	0				-
Caenorhabditis elegans	ferm domain (-ezrin-radixin-moesin) family member (frm-1)	1	F:GO:0005488	-		-
Caenorhabditis briggsae	briggsae cbr-nep-1 protein	2	F:GO:0004222; P:GO:0006508	-	EC:3.4.24.0	IPR000718; IPR018497; G3DSA:3.40.390.10 (GENE3D), PTHR11733:SF24 (PANTHER), SSF55486 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	zinc finger protein 277	3	C:GO:0005622; F:GO:0005515; F:GO:0008270	-		-
Caenorhabditis briggsae	zinc finger protein 277	3	C:GO:0005622; F:GO:0005515; F:GO:0008270	-		-

Caenorhabditis briggsae	zinc finger protein 277	3	C:GO:0005622; F:GO:0005515; F:GO:0008270	-		-
Caenorhabditis briggsae	zinc finger protein 277	3	C:GO:0005622; F:GO:0005515; F:GO:0008270	-		-
Caenorhabditis elegans	methyltransferase type 11	2	P:GO:0008152; F:GO:0008168	-	EC:2.1.1.0	IPR013216; G3DSA:3.40.50.150 (GENE3D), PTHR10108 (PANTHER), PTHR10108:SF17 (PANTHER), SSF53335 (SUPERFAMILY)
Ostertagia ostertagi	secreted protein asp-2	1	P:GO:0040011	-		IPR001283; IPR002413; IPR014044; IPR018244; PTHR10334:SF11 (PANTHER), SignalP (SIGNALP)
Danio rerio	morc family cw-type zinc finger 2	0		F:GO:0046872; F:GO:0005524; F:GO:0003674; P:GO:0008150; F:GO:0008270; C:GO:0005575		IPR003594; IPR011124; PTHR23337 (PANTHER)
Brugia malayi	d- primase large subunit	7	F:GO:0003899; P:GO:0000910; P:GO:0006260; P:GO:0040035; P:GO:0006997; P:GO:0006898; P:GO:0009792	-	EC:2.7.7.6	IPR007238
Caenorhabditis elegans	sorting nexin	4	F:GO:0005488; P:GO:0040010; P:GO:0009987; F:GO:0016740	-		-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0003674; P:GO:0045449; P:GO:0008150; C:GO:0005576; F:GO:0003700		PTHR13029 (PANTHER), PTHR13029:SF7 (PANTHER)
	-	0				-
Brugia malayi	myc associated factor x	8	P:GO:0006351; P:GO:0051716; F:GO:0003712; C:GO:0005737; F:GO:0003677; P:GO:0045449; P:GO:0006950; C:GO:0071339	-		SignalP (SIGNALP)
Monodelphis domestica	myc associated factor x	6	F:GO:0030528; F:GO:0005515; P:GO:0050896; F:GO:0003677; P:GO:0045449; C:GO:0044451	-		-
Caenorhabditis briggsae	lmbr1 domain containing 2	1	C:GO:0016020	-		PTHR21355 (PANTHER)
Canis familiaris	haloacid dehaloge-se-like hydrolase domain containing 2	2	F:GO:0003824; C:GO:0044425	-		G3DSA:3.40.50.1000 (GENE3D), G3DSA:3.40.50.10410 (GENE3D), PTHR19288 (PANTHER), PTHR19288:SF1 (PANTHER), SSF56784 (SUPERFAMILY)

Caenorhabditis elegans	voltage-dependent anion channel 2	6	P:GO:0006820; F:GO:0008308; P:GO:0055085; P:GO:0000003; C:GO:0016021; C:GO:0005741	-		IPR001925; PTHR11743 (PANTHER), PTHR11743:SF8 (PANTHER)
Caenorhabditis elegans	hypothetical protein C06A6.2 [Caenorhabditis elegans]	2	F:GO:0005515; P:GO:0009792	-		-
Caenorhabditis briggsae	mammalian fe65 homolog family member (feh-1)	11	P:GO:0007411; P:GO:0001764; P:GO:0007050; P:GO:0043065; P:GO:0030308; P:GO:0045749; F:GO:0008134; P:GO:0043066; C:GO:0005737; P:GO:0030198; C:GO:0005634	-		IPR003006; IPR006020; IPR011993; PTHR14058 (PANTHER), PTHR14058:SF9 (PANTHER), SSF50729 (SUPERFAMILY)
Caenorhabditis elegans	isoform a	0				IPR002172; PTHR20967 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0003677; C:GO:0005634		-
Caenorhabditis elegans	dual specificity tyrosine-phosphorylation-regulated ki-se	4	F:GO:0016301; F:GO:0005515; P:GO:0040010; P:GO:0040011	-		PTHR11295 (PANTHER), PTHR11295:SF116 (PANTHER)
Caenorhabditis briggsae	importin alpha	0		P:GO:0006606; C:GO:0005643; P:GO:0015031; F:GO:0008565; C:GO:0005634; P:GO:0006810; C:GO:0005737; P:GO:0006886; F:GO:0005488		IPR002652; IPR011989; IPR016024; PTHR23316 (PANTHER)
Caenorhabditis briggsae	set domain protein	3	F:GO:0046872; F:GO:0016740; P:GO:0006911	-		IPR001965; IPR011011; IPR013083; IPR019786; IPR019787; PTHR10615 (PANTHER), PTHR10615:SF7 (PANTHER)
Caenorhabditis briggsae	g protein-coupled receptor	2	P:GO:0007186; C:GO:0016021	-		IPR000276; IPR017452; G3DSA:1.20.1070.10 (GENE3D), PTHR22751 (PANTHER), PTHR22751:SF8 (PANTHER), SignalP (SIGNALP), SSF81321 (SUPERFAMILY)
Loa loa	i lweq domain containing protein	4	F:GO:0003779; P:GO:0007155; C:GO:0015629; F:GO:0005198	-		IPR015710; IPR015711; G3DSA:1.20.1410.10 (GENE3D)

Patiria pectinifera	aurora ki-se a	20	P:GO:0031991; F:GO:0000166; P:GO:0007052; F:GO:0004713; P:GO:0040011; F:GO:0019894; P:GO:0030261; C:GO:0005737; F:GO:0051117; P:GO:0009792; F:GO:0004674; C:GO:0051233; P:GO:0007059; P:GO:0007126; P:GO:0045184; P:GO:0018108; C:GO:0000794; P:GO:0007109; P:GO:0051256; P:GO:0040035	-	EC:2.7.10.0; EC:2.7.11.0	IPR000719; IPR011009; IPR017442; IPR020636; IPR020663; G3DSA:1.10.510.10 (GENE3D)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR021010; SSF141739 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR021010; SSF141739 (SUPERFAMILY)
Nippostrongylus brasiliensis	globin	6	F:GO:0020037; C:GO:0005615; C:GO:0005737; F:GO:0005344; P:GO:0015671; F:GO:0019825	-		
Caenorhabditis briggsae	vit-2	0		F:GO:0045735; F:GO:0005319; F:GO:0008565; P:GO:0006869; P:GO:0009792; C:GO:0005576; P:GO:0006886; P:GO:0008340; P:GO:0040010		-
Caenorhabditis elegans	coatomer subunit gamma-2	12	C:GO:0030126; P:GO:0040010; P:GO:0006890; P:GO:0000003; P:GO:0032940; P:GO:0006891; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0006898; P:GO:0006886; F:GO:0005198	-		IPR002553; IPR009028; IPR011989; IPR013040; IPR013041; IPR014863; IPR015873; IPR016024; PTHR10261 (PANTHER)

Caenorhabditis elegans	paraplegin	13	F:GO:0017111; P:GO:0030155; F:GO:0008270; C:GO:0005739; C:GO:0016021; F:GO:0004222; P:GO:0006508; F:GO:0005524; P:GO:0007399; P:GO:0007005; P:GO:0008089; F:GO:0051082; P:GO:0030163	-	EC:3.6.1.15; EC:3.4.24.0	IPR000642; IPR003959; G3DSA:1.10.8.60 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23076 (PANTHER), PTHR23076:SF7 (PANTHER), SSF140990 (SUPERFAMILY), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	paraplegin	13	F:GO:0017111; P:GO:0030155; F:GO:0008270; C:GO:0005739; C:GO:0016021; F:GO:0004222; P:GO:0006508; F:GO:0005524; P:GO:0007399; P:GO:0007005; P:GO:0008089; F:GO:0051082; P:GO:0030163	-	EC:3.6.1.15; EC:3.4.24.0	IPR000642; IPR001315; IPR003959; G3DSA:1.10.8.60 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23076 (PANTHER), PTHR23076:SF7 (PANTHER), SSF140990 (SUPERFAMILY), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	paraplegin	13	F:GO:0017111; P:GO:0030155; F:GO:0008270; C:GO:0005739; C:GO:0016021; F:GO:0004222; P:GO:0006508; F:GO:0005524; P:GO:0007399; P:GO:0007005; P:GO:0008089; F:GO:0051082; P:GO:0030163	-	EC:3.6.1.15; EC:3.4.24.0	IPR000642; IPR001315; IPR003959; G3DSA:1.10.8.60 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23076 (PANTHER), PTHR23076:SF7 (PANTHER), SSF140990 (SUPERFAMILY), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	apical junction molecule family member (ajm-1)	9	P:GO:0009792; C:GO:0043296; P:GO:0045216; F:GO:0008092; C:GO:0005913; P:GO:0040010; P:GO:0040011; C:GO:0016021; F:GO:0008270	-		-
Caenorhabditis briggsae	low-density lipoprotein receptor-related protein 2	2	C:GO:0016021; F:GO:0005509	-		IPR000033; IPR000742; IPR006210; IPR011042; IPR013032; G3DSA:2.170.300.10 (GENE3D), PTHR10529 (PANTHER), SSF63825 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	3	P:GO:0006952; P:GO:0008152; F:GO:0003824	-		IPR002198; IPR002347; IPR016040; PTHR19410:SF18 (PANTHER), SSF51735 (SUPERFAMILY)

Caenorhabditis elegans	hypothetical protein Y67D8A.2 [Caenorhabditis elegans]	0		P:GO:0006418; C:GO:0016021; C:GO:0005737; P:GO:0006412; P:GO:0005977; F:GO:0005524; P:GO:0005976; F:GO:0003824; F:GO:0005516; F:GO:0004339; F:GO:0004812		-
Caenorhabditis briggsae	sentrin-specific protease 1	7	C:GO:0005737; F:GO:0004175; P:GO:0006919; P:GO:0008624; P:GO:0016926; F:GO:0016929; C:GO:0005634	-		IPR003653; PTHR12606 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis elegans	specifically rac-associated	12	P:GO:0016477; P:GO:0007411; P:GO:0050807; P:GO:0008360; C:GO:0045202; P:GO:0006911; P:GO:0022416; C:GO:0031209; P:GO:0030866; F:GO:0005515; P:GO:0010172; P:GO:0030031	-		IPR008081; PF07159 (PFAM)
Caenorhabditis elegans	casein ki-se beta polypeptide	35	P:GO:0031101; P:GO:0016246; C:GO:0005929; F:GO:0005102; F:GO:0004252; P:GO:0033211; P:GO:0040010; C:GO:0005956; P:GO:0040011; C:GO:0005576; P:GO:0034606; C:GO:0005737; P:GO:0008285; C:GO:0030425; F:GO:0019904; C:GO:0043025; P:GO:0009792; P:GO:0002009; P:GO:0007249; F:GO:0004674; F:GO:0042802; P:GO:0042325; C:GO:0030424; P:GO:0006956; P:GO:0002119; P:GO:0050790; F:GO:0019887; P:GO:0043623;	-	EC:3.4.21.0; EC:2.7.11.0	-

	-	0				IPR000215; G3DSA:2.30.39.10 (GENE3D)
Drosophila yakuba	GE11922 [Drosophila yakuba]	0		F:GO:0004867		IPR000215; G3DSA:2.30.39.10 (GENE3D)
Caenorhabditis briggsae	serine or cysteine protease inhibitor	2	F:GO:0005488; P:GO:0010955	-		IPR000215; G3DSA:2.30.39.10 (GENE3D), G3DSA:3.30.497.10 (GENE3D)
Caenorhabditis elegans	isoform cra_a	2	P:GO:0040015; F:GO:0005515	-		IPR007087; IPR013087; IPR015880; PTHR23229 (PANTHER), PTHR23229:SF13 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis elegans	fumarate hydratase	12	P:GO:0040010; P:GO:0048873; P:GO:0000003; P:GO:0006108; P:GO:0006099; F:GO:0004333; F:GO:0005515; C:GO:0045239; C:GO:0005759; P:GO:0006898; P:GO:0009792; P:GO:0006106	-	EC:4.2.1.2	IPR000362; IPR008948; IPR022761; G3DSA:1.10.275.10 (GENE3D), G3DSA:1.20.200.10 (GENE3D), PTHR11444 (PANTHER), PTHR11444:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	fumarate hydratase	12	P:GO:0040010; P:GO:0048873; P:GO:0000003; P:GO:0006108; P:GO:0006099; F:GO:0004333; F:GO:0005515; C:GO:0045239; C:GO:0005759; P:GO:0006898; P:GO:0009792; P:GO:0006106	-	EC:4.2.1.2	IPR000362; IPR008948; IPR022761; G3DSA:1.10.275.10 (GENE3D), G3DSA:1.20.200.10 (GENE3D), PTHR11444 (PANTHER), PTHR11444:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	fumarate hydratase	12	P:GO:0040010; P:GO:0048873; P:GO:0000003; P:GO:0006108; P:GO:0006099; F:GO:0004333; F:GO:0005515; C:GO:0045239; C:GO:0005759; P:GO:0006898; P:GO:0009792; P:GO:0006106	-	EC:4.2.1.2	IPR000362; IPR008948; IPR022761; G3DSA:1.10.275.10 (GENE3D), G3DSA:1.20.200.10 (GENE3D), PTHR11444 (PANTHER), PTHR11444:SF1 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	28s ribosomal protein s5	9	P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; F:GO:0003723; P:GO:0040010; P:GO:0006898; P:GO:0006412; C:GO:0005739	-	EC:3.6.5.3	IPR000851; PTHR13718:SF3 (PANTHER)

Brugia malayi	(d- helicase q1-like) isoform cra_a	5	P:GO:0000733; F:GO:0005515; F:GO:0004003; F:GO:0000739; F:GO:0000166	-		IPR001650; IPR004589; G3DSA:3.40.50.300 (GENE3D), PTHR13710:SF12 (PANTHER), SSF52540 (SUPERFAMILY)
Heligmosomoides polygyrus	transforming growth protein 2-like protein	2	P:GO:0040007; F:GO:0008083	-		IPR001839; IPR015615; IPR017948; G3DSA:2.10.90.10 (GENE3D), PTHR11848:SF3 (PANTHER), SignalP (SIGNALP), SSF57501 (SUPERFAMILY)
Loa loa	nipped-b homolog	5	F:GO:0005488; P:GO:0034088; P:GO:0051240; P:GO:0048701; C:GO:0032116	-		PTHR21704 (PANTHER), PTHR21704:SF5 (PANTHER)
	-	0				-
	-	0				-
synthetic construct	ribosomal protein l30	4	F:GO:0003735; F:GO:0003723; C:GO:0022625; P:GO:0006414	-		IPR000231; IPR004038; IPR022991; G3DSA:3.30.1330.30 (GENE3D), PTHR11449:SF1 (PANTHER), SSF55315 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	protein ki-se theta	16	P:GO:0090066; F:GO:0046872; F:GO:0004697; P:GO:0008340; P:GO:0051128; P:GO:0040007; P:GO:0010033; P:GO:0009792; P:GO:0000003; F:GO:0005515; P:GO:0006468; F:GO:0005524; P:GO:0048522; P:GO:0033554; P:GO:0023034; C:GO:0005622	-	EC:2.7.11.13	IPR002219; IPR008973; IPR015727; IPR020454; G3DSA:2.60.40.150 (GENE3D), G3DSA:3.30.60.20 (GENE3D), SSF57889 (SUPERFAMILY)
Loa loa	taf3 protein	3	P:GO:0051457; F:GO:0005515; C:GO:0005669	-		IPR006565; IPR009072
Haemonchus contortus	astacin metalloprotease b	4	F:GO:0004222; P:GO:0009792; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	IPR000859; IPR001506; IPR006026; IPR006210; IPR013032; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-pfd-1 protein	7	P:GO:0040035; P:GO:0009792; P:GO:0010171; P:GO:0040018; P:GO:0040010; P:GO:0040011; P:GO:0007020	-		-

Loa loa	domain containing protein	0		P:GO:0007165; C:GO:0005622		-
Caenorhabditis briggsae	ribosomal r-	10	F:GO:0008649; P:GO:0040010; P:GO:0031167; F:GO:0003676; C:GO:0005730; P:GO:0000003; P:GO:0002119; P:GO:0040039; P:GO:0006898; P:GO:0009792	-		IPR002877; IPR015507; G3DSA:3.40.50.150 (GENE3D), PF11861 (PFAM), SSF53335 (SUPERFAMILY)
Loa loa	mr- cleavage factor complex component	2	P:GO:0009987; P:GO:0007275	-		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR001810
Caenorhabditis elegans	tripartite motif-containing 71	3	P:GO:0045138; C:GO:0005737; P:GO:0009957	-		IPR000315; IPR001841; PTHR13712 (PANTHER), PTHR13712:SF59 (PANTHER)
Caenorhabditis elegans	tripartite motif-containing 71	3	P:GO:0045138; C:GO:0005737; P:GO:0009957	-		IPR000315; IPR001258; IPR001298; IPR001841; IPR011042; IPR013017; IPR013783; IPR014756; IPR017868; PTHR13712 (PANTHER), PTHR13712:SF5 (PANTHER), SSF101898 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-emb-30 protein	0		F:GO:0020037; F:GO:0005506; F:GO:0004725; P:GO:0016311; F:GO:0009055; F:GO:0016791; F:GO:0008138; F:GO:0016787; P:GO:0006470; F:GO:0005515		IPR015943
Caenorhabditis briggsae	briggsae cbr-emb-30 protein	1	F:GO:0005515	-		-
	-	0				IPR003582; SignalP (SIGNALP)
Caenorhabditis elegans	pqq enzyme repeat family protein	2	F:GO:0005515; P:GO:0006898	-		IPR011678; PTHR21573 (PANTHER)
Caenorhabditis elegans	protein	4	F:GO:0003676; P:GO:0009792; C:GO:0030529; P:GO:0040010	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	adaptor-related protein complex mu 2 subunit	9	F:GO:0009982; F:GO:0030515; C:GO:0005794; F:GO:0005515; C:GO:0031429; P:GO:0016192; P:GO:0006886; C:GO:0031410; C:GO:0030131	-	EC:5.4.99.12	IPR008968; PTHR11998 (PANTHER), PTHR11998:SF4 (PANTHER)

Caenorhabditis elegans	actin-related protein 2 3 complex subunit 3	12	P:GO:0030833; C:GO:0005885; P:GO:0040010; P:GO:0018991; P:GO:0045132; P:GO:0016331; P:GO:0010631; P:GO:0040027; F:GO:0005515; F:GO:0005200; P:GO:0009792; C:GO:0030027	-		IPR007204
Loa loa	tk fer protein ki-se	0				-
Caenorhabditis briggsae	xeroderma complementation group a	6	P:GO:0009411; P:GO:0006979; P:GO:0006289; F:GO:0005488; P:GO:0009636; P:GO:0008630	-		IPR000465; IPR009061; IPR022652; IPR022656; G3DSA:3.90.530.10 (GENE3D), SSF57716 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein Y55D5A.3 [Caenorhabditis elegans]	0		P:GO:0006629; C:GO:0005764		-
	-	0				-
Brugia malayi	hypothetical protein Bm1_39710 [Brugia malayi]	0				-
	-	0				-
Caenorhabditis briggsae	initiation factor 2 subunit family protein	1	P:GO:0044237	-		IPR000649; G3DSA:3.40.50.10470 (GENE3D), PTHR10233:SF5 (PANTHER), SignalP (SIGNALP), SSF100950 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-eel-1 protein	0		P:GO:0033227; F:GO:0005488; F:GO:0016881; C:GO:0005622; P:GO:0006464		-
Caenorhabditis elegans	briggsae cbr-eel-1 protein	0		P:GO:0033227; F:GO:0005488; F:GO:0016881; C:GO:0005622; P:GO:0006464		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	n-acetyltransferase 15	1	F:GO:0016740	-		IPR000182; IPR016181; PTHR14744 (PANTHER), PTHR14744:SF2 (PANTHER)
Caenorhabditis elegans	mitochondrial ribosomal protein l45	3	P:GO:0009987; C:GO:0005739; C:GO:0030529	-		IPR007379; SSF54427 (SUPERFAMILY)
Caenorhabditis briggsae	potassium channel modulatory factor 1	1	F:GO:0005515	-		IPR000433; IPR008598; IPR015880; PTHR12268 (PANTHER), PTHR12268:SF3 (PANTHER)
	-	0				-
Caenorhabditis elegans	hed family member (ptc-3)	8	P:GO:0009792; P:GO:0002119; F:GO:0008158; P:GO:0040018; P:GO:0018996; P:GO:0000003; P:GO:0040011; C:GO:0016021	-		PTHR10796 (PANTHER), PTHR10796:SF34 (PANTHER)

Caenorhabditis elegans	hed family member (ptc-3)	8	P:GO:0009792; P:GO:0002119; F:GO:0008158; P:GO:0040018; P:GO:0018996; P:GO:0000003; P:GO:0040011; C:GO:0016021	-		PTHR10796 (PANTHER), PTHR10796:SF34 (PANTHER)
	-	0				-
Loa loa	dedicator of cytokinesis 7	7	P:GO:0000226; C:GO:0043005; P:GO:0045200; P:GO:0032863; P:GO:0033138; P:GO:0007409; F:GO:0048365	-		PTHR23317 (PANTHER), PTHR23317:SF27 (PANTHER)
Polysphondylium pallidum PN500	transmembrane protein	0		C:GO:0016021		-
Caenorhabditis elegans	yl54_caeel ame: full=uncharacterized protein	0				-
Caenorhabditis elegans	yl54_caeel ame: full=uncharacterized protein	0				-
Caenorhabditis elegans	hypothetical protein Y71G12A.2 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	tomosyn sy-ptic protein family member (tom-1)	1	P:GO:0006810	-		IPR000664; IPR001680; IPR011046; IPR013577; IPR015943; IPR019781; PTHR10241 (PANTHER), PTHR10241:SF7 (PANTHER)
Caenorhabditis elegans	briggsae cbr-gei-13 protein	1	F:GO:0005515	-		IPR003656; SSF57667 (SUPERFAMILY)
Caenorhabditis briggsae	dipeptidyl anminopeptidase	1	F:GO:0008236	-		G3DSA:3.40.50.1820 (GENE3D), PTHR11731 (PANTHER), PTHR11731:SF7 (PANTHER), SSF53474 (SUPERFAMILY)
Brugia malayi	mothers against decapentaplegic homolog 2 isoform 2	74	F:GO:0034713; P:GO:0030878; P:GO:0016202; F:GO:0042803; P:GO:0031016; P:GO:0035265; P:GO:0032909; P:GO:0060039; P:GO:0070306; P:GO:0001701; F:GO:0070411; P:GO:0050678; P:GO:0050776; F:GO:0003690; F:GO:0031625; P:GO:0009749; P:GO:0002520; P:GO:0070723; P:GO:0042993; P:GO:0007182; C:GO:0005829; P:GO:0001707; P:GO:0045930; P:GO:0048701; P:GO:0009791; F:GO:0008134; P:GO:0001889;	-		IPR001132; IPR008984; IPR013790; IPR017855; PTHR13703:SF19 (PANTHER)

Caenorhabditis briggsae	briggsae cbr-rga-2 protein	6	P:GO:0009792; F:GO:0005096; C:GO:0005622; P:GO:0040010; P:GO:0000003; P:GO:0007165	-		IPR001849; IPR011993; PTHR23179 (PANTHER), PTHR23179:SF2 (PANTHER), SSF50729 (SUPERFAMILY)
Caenorhabditis elegans	integrin beta pat-3	6	C:GO:0008305; P:GO:0007160; F:GO:0004872; P:GO:0007275; F:GO:0005488; P:GO:0007229	-		IPR001169; IPR002369; IPR013032; IPR015812; PTHR10082:SF12 (PANTHER), SSF53300 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	decapping protein 1	0				IPR010334; SSF50729 (SUPERFAMILY)
Caenorhabditis elegans	abnormal cell migration family member (mig-10)	2	F:GO:0005515; P:GO:0007165	-		IPR000159; IPR001849; IPR011993; PTHR11243 (PANTHER), PTHR11243:SF11 (PANTHER), SSF50729 (SUPERFAMILY), SSF54236 (SUPERFAMILY)
Caenorhabditis elegans	abnormal cell migration family member (mig-10)	2	F:GO:0005515; P:GO:0007165	-		IPR000159; IPR001849; IPR011993; PTHR11243 (PANTHER), PTHR11243:SF11 (PANTHER), SSF50729 (SUPERFAMILY), SSF54236 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	2	F:GO:0005515; P:GO:0009792	-		G3DSA:2.30.42.10 (GENE3D), PTHR15963 (PANTHER), PTHR15963:SF4 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	F:GO:0005515; P:GO:0009792	-		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR15963 (PANTHER), PTHR15963:SF4 (PANTHER)
Caenorhabditis elegans	endothelial differentiation-related factor 1	11	P:GO:0019216; P:GO:0043388; P:GO:0006355; F:GO:0043565; F:GO:0003700; P:GO:0045446; F:GO:0004402; F:GO:0003713; C:GO:0005669; C:GO:0005737; F:GO:0008168	-	EC:2.3.1.48; EC:2.1.1.0	-
	-	0				-
Caenorhabditis elegans	briggsae cbr-tac-1 protein	1	F:GO:0005515	-		-
Caenorhabditis briggsae	adp-ribosylation factor gtpase activating protein 3	3	C:GO:0044444; P:GO:0015031; P:GO:0051649	-		-
Caenorhabditis briggsae	adp-ribosylation factor gtpase activating protein 3	3	C:GO:0044444; P:GO:0015031; P:GO:0051649	-		IPR001164; PTHR23180 (PANTHER), PTHR23180:SF16 (PANTHER)

Loa loa	elegans protein partially confirmed by transcript evidence	12	F:GO:0030528; P:GO:0007420; P:GO:0007492; P:GO:0000122; F:GO:0043565; P:GO:0001892; P:GO:0043193; F:GO:0008134; F:GO:0008094; P:GO:0009952; P:GO:0006338; C:GO:0005634	-		PTHR22880 (PANTHER), PTHR22880:SF1 (PANTHER)
Ixodes scapularis	pab-dependent poly -specific ribonuclease subunit 2	4	F:GO:0004527; P:GO:0044260; C:GO:0005622; P:GO:0044238	-		-
Trypanosoma brucei gambiense DAL972	pab-dependent poly -specific ribonuclease subunit 2	1	F:GO:0004527	-		-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG06657 [Caenorhabditis briggsae]	0		F:GO:0005515		-
	-	0				SignalP (SIGNALP)
Homo sapiens	macrophage migration inhibitory factor	44	P:GO:0006954; P:GO:0033138; P:GO:0048146; P:GO:0007506; P:GO:0007530; P:GO:0090238; P:GO:0070374; P:GO:0001546; P:GO:0031666; P:GO:0043030; P:GO:0043406; F:GO:0008083; C:GO:0005615; P:GO:0007569; P:GO:0061081; F:GO:0005160; P:GO:0071157; P:GO:0043518; P:GO:0050731; P:GO:0030890; P:GO:0045087; P:GO:0001516; F:GO:0005125; P:GO:0032269; C:GO:0005737; P:GO:0010629; P:GO:0051092;	-	EC:5.3.3.12; EC:5.3.2.1	IPR001398; IPR014347; PTHR11954:SF4 (PANTHER), SSF55331 (SUPERFAMILY)
Caenorhabditis elegans	sodium-coupled neutral amino acid transporter 9	2	C:GO:0016021; P:GO:0006810	-		IPR013057; PTHR22950 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	vps53- n-termi-l family protein	0		C:GO:0010008; C:GO:0016020; C:GO:0005794; C:GO:0005768; P:GO:0015031		IPR007234; PTHR12820 (PANTHER)
Brugia malayi	lmbr1 domain containing 2	1	C:GO:0016020	-		IPR006876; PTHR21355 (PANTHER), SignalP (SIGNALP)
Brugia malayi	transmembrane 9 superfamily member 2	2	C:GO:0016021; C:GO:0005768	-		IPR004240; PTHR10766:SF13 (PANTHER)

Caenorhabditis briggsae	beta chain spectrin	3	F:GO:0005200; C:GO:0008091; F:GO:0003779	-		IPR002017; IPR018159; G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF48 (PANTHER), SSF46966 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	major facilitator superfamily	0		C:GO:0016021; F:GO:0022891; C:GO:0016020; P:GO:0055085; F:GO:0005215; P:GO:0006810		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	potassium channel tetramerisation domain containing 3	0		F:GO:0005249; C:GO:0016020; P:GO:0006813; F:GO:0005515; C:GO:0008076		-
Caenorhabditis briggsae	branched chain aminotransferase cytosolic	6	C:GO:0005829; P:GO:0009083; C:GO:0005739; P:GO:0008652; F:GO:0004084; P:GO:0051716	-	EC:2.6.1.42	IPR001544; IPR005786; IPR018300; G3DSA:3.20.10.10 (GENE3D), G3DSA:3.30.470.10 (GENE3D)
Caenorhabditis elegans	transmembrane protein 104	1	C:GO:0016020	-		PTHR16189 (PANTHER)
Caenorhabditis elegans	lethal 07882	3	P:GO:0009792; P:GO:0006898; P:GO:0002119	-		IPR007276
Caenorhabditis briggsae	rap ran-gap family protein	0		F:GO:0005096; P:GO:0051056; C:GO:0005622		-
Caenorhabditis briggsae	rap ran-gap family protein	0		F:GO:0005096; P:GO:0051056; C:GO:0005622		IPR000331; PTHR10063 (PANTHER), SSF111347 (SUPERFAMILY)
Caenorhabditis elegans	loc553384 protein	4	P:GO:0048034; F:GO:0008495; C:GO:0016021; C:GO:0031966	-		IPR000537; IPR006369; PTHR11048 (PANTHER)
Caenorhabditis elegans	briggsae cbr-trm-1 protein	2	F:GO:0003676; F:GO:0008168	-	EC:2.1.1.0	-
Caenorhabditis elegans	asparaginyl-tr- cytoplasmic	7	C:GO:0005737; F:GO:0003676; P:GO:0006422; F:GO:0004816; F:GO:0005524; P:GO:0006421; F:GO:0004815	-	EC:6.1.1.22; EC:6.1.1.12	IPR004365; IPR012340; IPR016027
Loa loa	iesterase family member (pde-2)	3	F:GO:0046872; P:GO:0007165; F:GO:0004114	-	EC:3.1.4.17	IPR002073; IPR003607; IPR023088; IPR023174; PTHR11347 (PANTHER), PTHR11347:SF17 (PANTHER), SSF109604 (SUPERFAMILY)
	-	0				-
	-	0				-

Caenorhabditis elegans	28s ribosomal protein mitochondrial	9	P:GO:0006412; C:GO:0005840; C:GO:0005739; F:GO:0003735; P:GO:0040035; P:GO:0002119; P:GO:0040039; P:GO:0040018; P:GO:0006974	-	EC:3.6.5.3	IPR007087
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	ankyrin repeat domain 13c	1	C:GO:0005783	-		IPR002110; IPR020683; PTHR12447 (PANTHER)
Caenorhabditis elegans	wd repeat domain 68	6	C:GO:0005737; F:GO:0005515; P:GO:0016567; C:GO:0080008; C:GO:0005634; P:GO:0051216	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR19919 (PANTHER)
Caenorhabditis elegans	briggsae cbr-casy-1 protein	9	P:GO:0009792; C:GO:0005615; P:GO:0007156; F:GO:0005515; C:GO:0032809; P:GO:0008355; C:GO:0043231; F:GO:0005509; C:GO:0016021	-		-
Caenorhabditis sp. PS1010	hypothetical protein Csp3_JD07.006 [Caenorhabditis sp. PS1010]	0				-
Caenorhabditis elegans	uba and wwe domain containing 1	0		P:GO:0030154; F:GO:0016874; F:GO:0005488; F:GO:0016881; C:GO:0005634; F:GO:0003677; C:GO:0005622; P:GO:0006464		-
Caenorhabditis briggsae	uba and wwe domain containing 1	0		P:GO:0030154; F:GO:0016874; F:GO:0005488; F:GO:0016881; C:GO:0005634; F:GO:0003677; C:GO:0005622; P:GO:0006464		-
Caenorhabditis elegans	protein fat-free homolog	1	F:GO:0005515	-		IPR014812; PTHR15954 (PANTHER)
Caenorhabditis briggsae	ets homologous factor	4	P:GO:0006355; F:GO:0043565; F:GO:0003700; C:GO:0005634	-		IPR000418; IPR011991; PTHR11849 (PANTHER), PTHR11849:SF18 (PANTHER), SSF46785 (SUPERFAMILY)
	-	0				-
Loa loa	cerebral cavernous malformation 2	0		P:GO:0051403; P:GO:0007229; C:GO:0005737; P:GO:0001570; F:GO:0005515; P:GO:0007043		-
	-	0				-

Loa loa	vesicle transport-related protein	5	P:GO:0031101; P:GO:0018996; P:GO:0006904; P:GO:0000003; P:GO:0006898	-		-
Caenorhabditis elegans	suppressor of ypt1	5	P:GO:0031101; P:GO:0018996; P:GO:0006904; P:GO:0000003; P:GO:0006898	-		IPR001619; G3DSA:3.40.50.1910 (GENE3D), PTHR11679:SF2 (PANTHER)
Caenorhabditis elegans	s head family member (skn-1)	4	F:GO:0003700; F:GO:0005515; P:GO:0007275; C:GO:0005634	-		IPR004827; IPR008917; IPR013089; G3DSA:1.10.880.10 (GENE3D), PTHR23230:SF19 (PANTHER)
Caenorhabditis elegans	stromal cell-derived factor 2-like 1	2	C:GO:0044464; F:GO:0016740	-		IPR003608; IPR016093; G3DSA:2.80.10.50 (GENE3D), PTHR10050 (PANTHER), PTHR10050:SF6 (PANTHER), SignalP (SIGNALP)
Ancylostoma ceylanicum	tissue factor pathway inhibitor	1	F:GO:0030414	-		IPR002223; IPR020901; PTHR10083 (PANTHER), PTHR10083:SF39 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis brenneri	hypothetical protein Cbre_JD09.010 [Caenorhabditis brenneri]	0				-
Loa loa	hypothetical protein LOAG_05660 [Loa loa]	0				-
Loa loa	hypothetical protein LOAG_05660 [Loa loa]	0				-
Caenorhabditis elegans	briggsae cbr-edc-3 protein	0		F:GO:0005515		-
Caenorhabditis elegans	excretory ca-l abnormal family member (exc-5)	4	F:GO:0005089; C:GO:0005622; P:GO:0035023; F:GO:0008270	-		-
synthetic construct	fxyd domain containing ion transport regulator 5	7	P:GO:0030033; F:GO:0003779; P:GO:0046588; P:GO:0006811; C:GO:0016021; F:GO:0045296; F:GO:0005216	-		-
Macaca mulatta	40s ribosomal protein s2-like isoform 2	4	F:GO:0003735; F:GO:0003723; C:GO:0015935; P:GO:0006412	-	EC:3.6.5.3	IPR000851; IPR005324; IPR005711; IPR013810; IPR014720; IPR014721; IPR018192; IPR020568; PTHR13718:SF4 (PANTHER), SSF54768 (SUPERFAMILY)
Caenorhabditis briggsae	mgc68950 protein	5	C:GO:0000776; F:GO:0005515; P:GO:0009987; C:GO:0000922; C:GO:0005829	-		PTHR18916 (PANTHER), PTHR18916:SF2 (PANTHER)
Caenorhabditis briggsae	mgc68950 protein	5	C:GO:0000776; F:GO:0005515; P:GO:0009987; C:GO:0000922; C:GO:0005829	-		PTHR18916 (PANTHER), PTHR18916:SF2 (PANTHER)

Caenorhabditis briggsae	mgc68950 protein	5	C:GO:0000776; F:GO:0005515; P:GO:0009987; C:GO:0000922; C:GO:0005829	-		PTHR18916 (PANTHER), PTHR18916:SF2 (PANTHER)
	-	0				-
	-	0				IPR006578
Caenorhabditis elegans	calcineurin binding protein 1	0		F:GO:0030346; C:GO:0005634; P:GO:0006916; C:GO:0005737; P:GO:0016568; P:GO:0007166; P:GO:0007165; F:GO:0005515; F:GO:0005488; F:GO:0004864		-
Caenorhabditis elegans	tpr domain containing protein	0		F:GO:0008312; F:GO:0005488; P:GO:0006614; C:GO:0048500		PTHR14094 (PANTHER), PTHR14094:SF9 (PANTHER)
	-	0				-
Brugia malayi	r- polymerase ii:subunit=	2	F:GO:0005488; P:GO:0006350	-		IPR017923; PTHR15141 (PANTHER), PTHR15141:SF12 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0055114; F:GO:0005488; F:GO:0016491; P:GO:0008152; F:GO:0003824		IPR012877; G3DSA:3.90.1200.10 (GENE3D)
	-	0				-
Caenorhabditis briggsae	26s protease regulatory subunit 4	6	C:GO:0005737; F:GO:0008233; P:GO:0030163; F:GO:0005524; C:GO:0000502; F:GO:0017111	-	EC:3.6.1.15	IPR003959; G3DSA:3.40.50.300 (GENE3D), PTHR23073 (PANTHER), PTHR23073:SF9 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	yfe5_caeel ame: full=uncharacterized protein flags: precursor	0				-
Caenorhabditis elegans	high density lipoprotien binding protein vigilin	7	P:GO:0040010; P:GO:0018991; P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0040017; P:GO:0009792	-		IPR004087; IPR004088; IPR018111; G3DSA:3.30.1370.10 (GENE3D), PTHR10627 (PANTHER), PTHR10627:SF9 (PANTHER), SSF54791 (SUPERFAMILY)
Branchiostoma floridae	abc transporter c family protein	12	F:GO:0016772; F:GO:0015238; C:GO:0016021; F:GO:0042626; P:GO:0006855; C:GO:0031088; P:GO:0006811; C:GO:0005624; F:GO:0005524; C:GO:0016323; F:GO:0005254; P:GO:0048661	-		IPR003439; IPR003593; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF97 (PANTHER), SSF52540 (SUPERFAMILY)

Loa loa	mutator family member (mut-7)	0		F:GO:0003676; P:GO:0006139; F:GO:0004527; F:GO:0016787; F:GO:0004518; F:GO:0005515; C:GO:0005622; F:GO:0008408		-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	pole2 protein	3	P:GO:0006260; F:GO:0016779; C:GO:0005634	-	EC:2.7.7.0	IPR007185; PTHR12708 (PANTHER)
Caenorhabditis elegans	acylglycerol mitochondrial	2	F:GO:0016301; P:GO:0044237	-		-
Pongo abelii	collagen alpha-2 chain-like	17	P:GO:0042476; F:GO:0030674; P:GO:0070208; P:GO:0043589; P:GO:0008217; F:GO:0042802; C:GO:0005615; F:GO:0046332; P:GO:0001501; F:GO:0048407; C:GO:0005584; P:GO:0030199; P:GO:0007179; F:GO:0005201; P:GO:0001568; P:GO:0007266; C:GO:0005886	-		-
Caenorhabditis briggsae	sh2 domain containing 4b	1	F:GO:0005515	-		IPR000980; PTHR14388 (PANTHER), SSF55550 (SUPERFAMILY)
Loa loa	probable d- mismatch repair protein msh6	2	F:GO:0003677; P:GO:0000710	-		-
Caenorhabditis briggsae	testis expressed sequence 2 isoform 1	0		C:GO:0016020; P:GO:0008150; C:GO:0005575		IPR001849; PTHR13466 (PANTHER)
Caenorhabditis briggsae	testis expressed sequence 2 isoform 1	0		C:GO:0016020; P:GO:0008150; C:GO:0005575		IPR001849; PTHR13466 (PANTHER)
Caenorhabditis briggsae	ribosome biogenesis protein bms1 homolog	4	F:GO:0003924; C:GO:0005634; P:GO:0042254; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	PTHR12858 (PANTHER), PTHR12858:SF2 (PANTHER)
Caenorhabditis briggsae	tight junction protein	0		F:GO:0005515		IPR001478; G3DSA:2.30.42.10 (GENE3D), PTHR13865 (PANTHER), PTHR13865:SF7 (PANTHER)

Caenorhabditis elegans	u4 u6 small nuclear ribonucleoprotein	11	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0008380; F:GO:0003676; P:GO:0001703; F:GO:0005515; P:GO:0040010; P:GO:0040011; F:GO:0016740; C:GO:0030529	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR19846 (PANTHER)
Brugia malayi	rab3 gtpase-activating protein	4	F:GO:0005097; F:GO:0017137; C:GO:0005625; P:GO:0043087	-		PTHR21422 (PANTHER)
Caenorhabditis elegans	tubulointerstitial nephritis antigen-like	4	C:GO:0031012; P:GO:0016197; F:GO:0004197; P:GO:0006508	-	EC:3.4.22.0	-
Caenorhabditis briggsae	zinc finger protein	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		IPR007087; IPR015880
	-	0				-
Caenorhabditis elegans	hypothetical tyrosi-se-like protein in chromosome	4	F:GO:0005515; F:GO:0046872; P:GO:0008152; F:GO:0016491	-		IPR002227; IPR008922; PTHR11474 (PANTHER)
Caenorhabditis elegans	hypothetical protein Y73B6BL.1 [Caenorhabditis elegans]	0		F:GO:0046872; F:GO:0016491; P:GO:0008152		-
	-	0				-
Caenorhabditis elegans	abnormal cell lineage family member (lin-10)	1	F:GO:0005515	-		IPR001478; IPR006020; IPR011993; G3DSA:2.30.42.10 (GENE3D), PTHR12345 (PANTHER), PTHR12345:SF2 (PANTHER), SSF50729 (SUPERFAMILY)
Caenorhabditis briggsae	a-phase promoting complex subunit 1	3	P:GO:0051439; F:GO:0005515; C:GO:0044428	-		-
Brugia malayi	subfamily member 1	6	P:GO:0040035; F:GO:0005515; P:GO:0051085; P:GO:0006986; P:GO:0070389; C:GO:0044424	-		IPR001623; IPR002939; IPR003095; IPR008971; IPR015609; IPR018253; G3DSA:2.60.260.20 (GENE3D), PTHR11821:SF88 (PANTHER)
	-	0				-
Loa loa	heavy unconventio-l myosin family member (hum-2)	4	C:GO:0016459; F:GO:0005515; F:GO:0005524; F:GO:0003774	-		IPR002710; IPR018444; PTHR13140 (PANTHER), PTHR13140:SF15 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	F:GO:0003824	-		-
Loa loa	fizzy-related protein	6	P:GO:0007126; P:GO:0045449; P:GO:0051301; P:GO:0007067; F:GO:0004402; P:GO:0009792	-	EC:2.3.1.48	IPR001680; IPR015943; IPR017986; IPR019781; IPR019782; PTHR19918 (PANTHER), SSF117289 (SUPERFAMILY)

Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	11	C:GO:0005737; P:GO:0008272; C:GO:0005886; P:GO:0042391; P:GO:0055085; P:GO:0019532; C:GO:0016021; F:GO:0019531; F:GO:0015380; F:GO:0008271; P:GO:0006821	-		IPR011547; PTHR11814 (PANTHER), PTHR11814:SF25 (PANTHER)
Caenorhabditis elegans	proteasome (macropain) beta 2	10	P:GO:0008340; P:GO:0010243; P:GO:0051436; P:GO:0051437; P:GO:0000003; F:GO:0004298; P:GO:0031145; P:GO:0014070; P:GO:0009792; C:GO:0005839	-	EC:3.4.25.0	IPR001353; G3DSA:3.60.20.10 (GENE3D), PTHR11599 (PANTHER), PTHR11599:SF6 (PANTHER), PS51476 (PROFILE), SSF56235 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	F:GO:0051537; C:GO:0043231	-		IPR006622; IPR018967; SignalP (SIGNALP)
Coprinopsis cinerea okayama7#130	200 kda antigen p200	0		P:GO:0007018; C:GO:0005874; F:GO:0000166; F:GO:0005525; F:GO:0008270; F:GO:0005524; F:GO:0003777; C:GO:0016459; F:GO:0003774; F:GO:0046872; C:GO:0032982; F:GO:0005488; F:GO:0003950		-
Caenorhabditis elegans	nitrilase and fragile histidine triad fusion protein hit	4	F:GO:0016810; P:GO:0006139; F:GO:0047710; F:GO:0005515	-	EC:3.6.1.29	IPR001310; IPR003010; IPR011146; IPR011151; IPR019808; PTHR23088 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-prmt-5 protein	0		F:GO:0016740; P:GO:0030719; F:GO:0008276; F:GO:0008168; P:GO:0007067; C:GO:0005737; P:GO:0008298; F:GO:0016301; P:GO:0007318; P:GO:0007315		IPR007857
Caenorhabditis elegans	spingomyelin synthetase	3	F:GO:0047493; P:GO:0006686; C:GO:0030173	-	EC:2.7.8.3	IPR000326; PTHR21290 (PANTHER), PTHR21290:SF5 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG12154 [Caenorhabditis briggsae]	0				-

Loa loa	zinc finger in n-recognin family protein	5	P:GO:0042066; P:GO:0007291; F:GO:0005516; F:GO:0008270; F:GO:0004842	-	EC:6.3.2.19	IPR003126; PTHR21725 (PANTHER)
Caenorhabditis elegans	briggsae cbr-snx-1 protein	9	P:GO:0016192; C:GO:0043231; P:GO:0007126; P:GO:0018991; F:GO:0005515; C:GO:0044444; P:GO:0007154; F:GO:0035091; P:GO:0009792	-		IPR001683; IPR015404; PTHR10555 (PANTHER), PTHR10555:SF28 (PANTHER)
Caenorhabditis briggsae	choline dehydroge-se	4	P:GO:0006066; P:GO:0000003; F:GO:0016614; F:GO:0050660	-		-
	-	0				-
Loa loa	myosin xviiia	2	C:GO:0005856; F:GO:0005488	-		-
Loa loa	af153723_1novel immunogenic protein nip-2	0		F:GO:0003735; C:GO:0005739; P:GO:0006412; C:GO:0005840		-
	-	0				-
Brugia malayi	d- mismatch repair protein containing protein	21	P:GO:0051257; F:GO:0032407; P:GO:0045950; P:GO:0043060; P:GO:0007283; C:GO:0005712; P:GO:0000712; P:GO:0006303; P:GO:0008630; F:GO:0003697; P:GO:0007060; C:GO:0000795; P:GO:0016446; C:GO:0001673; P:GO:0000239; P:GO:0048477; F:GO:0032137; P:GO:0000289; C:GO:0032389; P:GO:0006298; P:GO:0045190	-		IPR002099; IPR011186
Caenorhabditis elegans	briggsae cbr-lpd-7 protein	2	P:GO:0042254; C:GO:0031981	-		-
	-	0				SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	d--directed r- polymerases and iii subunit rpabc4	10	F:GO:0003899; F:GO:0046872; P:GO:0040035; F:GO:0003677; P:GO:0002119; P:GO:0040017; P:GO:0009792; P:GO:0040015; P:GO:0006350; C:GO:0005634	-	EC:2.7.7.6	-
Caenorhabditis briggsae	glycyl-tr- synthetase	6	P:GO:0015966; F:GO:0046983; F:GO:0000166; P:GO:0006418; C:GO:0044464; F:GO:0004820	-	EC:6.1.1.14	-
Caenorhabditis briggsae	ring finger protein 14	0		F:GO:0046872; F:GO:0008270; F:GO:0005515		IPR001841; IPR002867; IPR006575; IPR016135; IPR017907; PTHR11685 (PANTHER), PTHR11685:SF7 (PANTHER), SSF57850 (SUPERFAMILY)
Drosophila sechellia	cg4299	4	F:GO:0004864; F:GO:0030332; P:GO:0035308; C:GO:0005634	-		IPR002164; PTHR11875:SF9 (PANTHER), SSF143113 (SUPERFAMILY)
Brugia malayi	enth domain containing protein	0		F:GO:0003674; P:GO:0008283; P:GO:0048488; C:GO:0005794; P:GO:0007269		IPR001026; IPR008942; IPR013809; PTHR12276 (PANTHER), PTHR12276:SF12 (PANTHER)
Caenorhabditis elegans	atp-binding sub-family b (mdr tap) member 10	5	F:GO:0042626; P:GO:0055085; F:GO:0005524; C:GO:0016021; C:GO:0031966	-		IPR001140; IPR011527; IPR017940; G3DSA:1.20.1560.10 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF76 (PANTHER), SignalP (SIGNALP)
Loa loa	si:busm1- protein	0				-
Danio rerio	si:busm1- protein	0		F:GO:0003677		-
	-	0				-
Caenorhabditis briggsae	d- repair transcription protein met18 mms19	0		F:GO:0005488		PTHR12891 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	ribosome recycling factor family protein	3	P:GO:0034645; P:GO:0010467; P:GO:0044238	-		IPR002661; IPR016001; G3DSA:1.10.132.20 (GENE3D)
Loa loa	suppression of tumorigenicity	6	C:GO:0016020; P:GO:0040018; P:GO:0000003; F:GO:0005488; P:GO:0010171; P:GO:0002119	-		IPR007311
	-	0				-
Caenorhabditis elegans	e1a binding protein p400	5	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0040010; P:GO:0040011	-		-

Loa loa	suppressor of t-cell receptor sig-ling 1	0		F:GO:0004619; F:GO:0004872; P:GO:0016070; F:GO:0003824; C:GO:0005622; F:GO:0016853		IPR013078; G3DSA:3.40.50.1240 (GENE3D), PTHR16469 (PANTHER), SSF53254 (SUPERFAMILY)
Caenorhabditis briggsae	upf0487 protein c17orf71-like protein	1	P:GO:0000184	-		IPR019354; PTHR13091 (PANTHER)
Caenorhabditis briggsae	cg6729 cg6729-pa	1	P:GO:0000184	-		IPR019354; PTHR13091 (PANTHER)
Drosophila sechellia	middle molecular weight neurofilament protein nf-m	0		F:GO:0003676; F:GO:0005524; C:GO:0005882; F:GO:0000166; F:GO:0005198; F:GO:0008270; P:GO:0006298; F:GO:0030983		-
Caenorhabditis briggsae	eukaryotic initiation factor 4a-iii	22	P:GO:0000184; P:GO:0017148; P:GO:0051028; F:GO:0005515; C:GO:0016607; P:GO:0040010; F:GO:0008143; P:GO:0006397; F:GO:0003743; P:GO:0045727; C:GO:0005737; P:GO:0018996; C:GO:0005681; P:GO:0009792; P:GO:0008380; P:GO:0002119; P:GO:0001703; F:GO:0004004; P:GO:0006364; F:GO:0005524; P:GO:0040035; P:GO:0000910	-		IPR000629; IPR001650; IPR011545; IPR014001; IPR014014; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF2 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	protein phosphatase regulatory subunit 3c	5	P:GO:0070873; F:GO:0005515; C:GO:0000267; F:GO:0004721; P:GO:0005978	-	EC:3.1.3.16	IPR005036; PTHR12307 (PANTHER)

Loa loa	d- mismatch repair protein msh6	23	F:GO:0032357; P:GO:0045910; P:GO:0008340; F:GO:0032405; F:GO:0000400; F:GO:0043531; P:GO:0008630; P:GO:0009411; F:GO:0032142; F:GO:0032143; P:GO:0016446; F:GO:0000287; P:GO:0051096; C:GO:0000790; F:GO:0016887; F:GO:0042803; F:GO:0003682; F:GO:0032137; P:GO:0006298; F:GO:0005524; C:GO:0032301; P:GO:0043570; P:GO:0045190	-		IPR000432; IPR007695; IPR007696; IPR007860; IPR007861; IPR015536; IPR016151; G3DSA:1.10.1420.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), SSF52540 (SUPERFAMILY)
Loa loa	phd finger protein 14	1	F:GO:0046872	-		IPR001965; IPR011011; IPR013083; IPR019786; PTHR13793 (PANTHER), PTHR13793:SF9 (PANTHER)
Caenorhabditis elegans	member ras oncogene family	23	C:GO:0001750; C:GO:0070382; P:GO:0032402; P:GO:0043320; P:GO:0040007; P:GO:0006913; P:GO:0006605; C:GO:0042470; F:GO:0005525; C:GO:0005764; C:GO:0005794; C:GO:0005770; P:GO:0030318; C:GO:0030425; P:GO:0007264; P:GO:0007596; C:GO:0030667; P:GO:0002119; F:GO:0003924; F:GO:0031489; P:GO:0043316; P:GO:0040035; C:GO:0016324	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
Caenorhabditis briggsae	methionine-r-sulfoxide reductase	2	P:GO:0055114; F:GO:0008113	-	EC:1.8.4.11	IPR002579; IPR011057; PTHR10173 (PANTHER)
	-	0				SignalP (SIGNALP)

Loa loa	zygote defective: embryonic lethal family member (zyg-12)	10	P:GO:0006810; P:GO:0006996; C:GO:0043231; C:GO:0043234; C:GO:0005856; C:GO:0044446; F:GO:0005515; C:GO:0044444; P:GO:0051641; C:GO:0016020	-		IPR008636; PTHR18947 (PANTHER), PTHR18947:SF5 (PANTHER)
Loa loa	zygote defective: embryonic lethal family member (zyg-12)	10	C:GO:0043234; C:GO:0015630; P:GO:0051640; P:GO:0000226; C:GO:0044425; F:GO:0005515; C:GO:0031090; P:GO:0016197; C:GO:0044430; C:GO:0005794	-		IPR008636
Caenorhabditis elegans	gamma-glutamyltranspeptidase 1	1	F:GO:0003840	-	EC:2.3.2.2	IPR000101; SSF56235 (SUPERFAMILY)
Caenorhabditis elegans	p-type had subfamily ic	5	C:GO:0016021; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0006812	-		IPR001757; IPR006068; G3DSA:1.20.1110.10 (GENE3D), PTHR11939:SF63 (PANTHER), SignalP (SIGNALP), SSF81665 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Rattus norvegicus	ribosomal protein s10	4	C:GO:0005730; F:GO:0005515; C:GO:0022627; P:GO:0006414	-		IPR005326; PTHR12146 (PANTHER)
Brugia malayi	methylenetetrahydrofolate reductase	7	P:GO:0008015; F:GO:0005515; P:GO:0040010; P:GO:0055114; C:GO:0005829; F:GO:0004489; P:GO:0006555	-	EC:1.5.1.20	IPR003171; G3DSA:3.20.20.220 (GENE3D), PTHR21091 (PANTHER), PTHR21091:SF1 (PANTHER), SSF51730 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	hatching enzyme	3	F:GO:0008233; P:GO:0000003; P:GO:0007413	-		IPR001506; IPR006026; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF73 (PANTHER), SignalP (SIGNALP), SSF55486 (SUPERFAMILY)
Haemonchus contortus	peptidyl-prolyl cis-trans isomerase e	9	P:GO:0006457; P:GO:0045449; F:GO:0003723; F:GO:0005515; F:GO:0016018; C:GO:0005634; F:GO:0003755; F:GO:0000166; P:GO:0006396	-	EC:5.2.1.8	IPR000504; IPR002130; IPR012677; IPR015891; IPR020892; PTHR11071 (PANTHER), PTHR11071:SF68 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG03410 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)

Caenorhabditis briggsae	integrin alpha-5	17	C:GO:0005925; C:GO:0005911; P:GO:0018991; C:GO:0032587; P:GO:0007155; P:GO:0040007; P:GO:0006898; P:GO:0007229; P:GO:0040039; C:GO:0008305; P:GO:0009792; F:GO:0070851; P:GO:0050731; P:GO:0002119; P:GO:0035313; F:GO:0004872; P:GO:0032940	-		IPR000413; IPR013517; IPR013519; G3DSA:2.130.10.130 (GENE3D), PTHR23220 (PANTHER), PTHR23220:SF11 (PANTHER), PS51470 (PROFILE), SSF69318 (SUPERFAMILY)
Caenorhabditis elegans	jmjc domain containing protein	5	F:GO:0046872; P:GO:0000003; F:GO:0016491; P:GO:0008152; P:GO:0006974	-		IPR003347; PTHR23123 (PANTHER), SSF51197 (SUPERFAMILY)
Caenorhabditis remanei	ubiquitin-conjugating enzyme e2i	16	F:GO:0016566; P:GO:0007275; C:GO:0016605; F:GO:0019789; P:GO:0051246; P:GO:0051301; P:GO:0045892; P:GO:0006511; P:GO:0007088; C:GO:0000795; P:GO:0007059; P:GO:0016925; F:GO:0019899; F:GO:0008134; F:GO:0005524; P:GO:0044419	-		-
	-	0				-
Caenorhabditis briggsae	endoplasmic reticulum multispan transmembrane protein	3	P:GO:0040015; P:GO:0040017; P:GO:0040010	-		IPR007594; SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis briggsae	alpha gamma epsilon	15	F:GO:0008565; P:GO:0040010; P:GO:0009306; P:GO:0016183; C:GO:0008021; P:GO:0000003; C:GO:0030131; P:GO:0002119; P:GO:0007269; F:GO:0005515; P:GO:0040011; P:GO:0006886; C:GO:0044431; P:GO:0009792; P:GO:0001703	-		IPR002553; IPR011989; IPR016024; PTHR22780 (PANTHER), PTHR22780:SF5 (PANTHER)
Caenorhabditis elegans	4-hydroxyphenylpyruvate dioxyge-se	7	F:GO:0046872; P:GO:0006572; P:GO:0040010; P:GO:0055114; F:GO:0003868; P:GO:0006559; F:GO:0004462	-	EC:1.13.11.27; EC:4.4.1.5	IPR004360; IPR005956; G3DSA:3.10.180.10 (GENE3D), SSF54593 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				PTHR22739 (PANTHER)
Caenorhabditis briggsae	hypothetical kda protein in chromosome	0				-
Ectocarpus siliculosus	conserved unknown protein [Ectocarpus siliculosus]	0		F:GO:0016810; F:GO:0016787; F:GO:0003824; F:GO:0008270		IPR015517
Adineta vaga	transposase	0				-
	-	0				-
	-	0				IPR001202; PR01217 (PRINTS), G3DSA:2.20.70.10 (GENE3D)
Caenorhabditis elegans	camp-dependent protein ki-se catalytic	11	F:GO:0004872; P:GO:0006468; F:GO:0047696; C:GO:0043197; C:GO:0043198; C:GO:0030424; F:GO:0005524; P:GO:0007165; F:GO:0004703; C:GO:0005634; C:GO:0045202	-	EC:2.7.11.15; EC:2.7.11.16	IPR000239; IPR000342; IPR000719; IPR011009; IPR015743; IPR016137; IPR017441; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR22985 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	dihydrolipoamide branched chain transacylase e2	4	P:GO:0009792; F:GO:0005515; F:GO:0016740; C:GO:0042645	-		IPR000089; IPR003016; IPR004167; IPR011053; IPR015761; G3DSA:2.40.50.100 (GENE3D), G3DSA:3.30.559.10 (GENE3D), PTHR23151 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Brugia malayi	telomere length regulation protein tel2 homolog isoform 1	4	P:GO:0009314; P:GO:0065007; C:GO:0044424; P:GO:0006974	-		PTHR15830 (PANTHER), PTHR15830:SF7 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	immunoglobulin i-set domain containing protein	0				IPR007110; IPR013783; PTHR10075 (PANTHER), PTHR10075:SF2 (PANTHER), SignalP (SIGNALP)

Caenorhabditis briggsae	coatomer subunit beta	11	C:GO:0030126; C:GO:0005829; P:GO:0008340; P:GO:0006890; P:GO:0000003; P:GO:0032940; P:GO:0006891; F:GO:0005515; P:GO:0048205; P:GO:0006886; F:GO:0005198	-		IPR002553; IPR011989; IPR016024; PTHR10635 (PANTHER)
Caenorhabditis briggsae	sinc finger protein ci-zf -148	0		F:GO:0008270; F:GO:0005515; C:GO:0005622		IPR007087; IPR015880
Caenorhabditis briggsae	temporarily assigned gene -me family member (tag-333)	2	F:GO:0005488; P:GO:0007165	-		PTHR23101 (PANTHER), PTHR23101:SF1 (PANTHER)
	-	0				-
Caenorhabditis briggsae	exocyst complex component 6	2	C:GO:0000145; P:GO:0006904	-		IPR007225
Brugia malayi	protein ki-se domain containing protein	22	P:GO:0001501; P:GO:0009888; P:GO:0006984; P:GO:0031016; F:GO:0005515; P:GO:0065008; P:GO:0046777; P:GO:0010646; P:GO:0071216; P:GO:0032057; P:GO:0001503; F:GO:0004694; P:GO:0034976; C:GO:0044425; P:GO:0006915; P:GO:0007165; P:GO:0044093; P:GO:0016043; P:GO:0030154; C:GO:0005783; P:GO:0046903; P:GO:0006986	-		IPR000719; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11042 (PANTHER), PTHR11042:SF12 (PANTHER)
Homo sapiens	immunoglobulin lambda 3 light chain	1	F:GO:0003823	-		IPR003006; IPR003597; IPR007110; IPR013106; IPR013783; PTHR23267 (PANTHER), PTHR23267:SF1 (PANTHER), SSF48726 (SUPERFAMILY)
Homo sapiens	immunoglobulin lambda light chain	0				IPR003006; IPR003597; IPR007110; IPR013106; IPR013783; PTHR23267 (PANTHER), PTHR23267:SF1 (PANTHER), SSF48726 (SUPERFAMILY)
Brugia malayi	abhydrolase domain containing 2	4	P:GO:0006629; P:GO:0009611; F:GO:0016298; C:GO:0016020	-		IPR000073; G3DSA:3.40.50.1820 (GENE3D), PTHR10794 (PANTHER), PTHR10794:SF9 (PANTHER), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	o-sialoglycoprotein endopeptidase-like 1	2	C:GO:0005739; F:GO:0070011	-		IPR000905; IPR017861; SSF53067 (SUPERFAMILY)
Caenorhabditis elegans	sjchgc00146 partial	0				-
	-	0				-

Caenorhabditis briggsae	dead (asp-glu-ala-asp) box polypeptide 20	11	C:GO:0032991; P:GO:0000003; F:GO:0005515; P:GO:0040010; P:GO:0006898; P:GO:0006397; F:GO:0004386; P:GO:0008380; P:GO:0016481; C:GO:0044451; P:GO:0043065	-		IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF13 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	dead (asp-glu-ala-asp) box polypeptide 20	8	C:GO:0032991; F:GO:0005515; C:GO:0005737; F:GO:0004386; P:GO:0016481; C:GO:0044451; P:GO:0043065; P:GO:0000387	-		IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF13 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	dead (asp-glu-ala-asp) box polypeptide 20	8	C:GO:0032991; F:GO:0005515; C:GO:0005737; F:GO:0004386; P:GO:0016481; C:GO:0044451; P:GO:0043065; P:GO:0000387	-		IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF13 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	subfamily member 13	1	F:GO:0031072	-		-
Caenorhabditis briggsae	temporarily assigned gene -me family member (tag-163)	1	F:GO:0005515	-		PTHR12583 (PANTHER), PTHR12583:SF1 (PANTHER)
Caenorhabditis elegans	coenzyme q6 homolog	3	F:GO:0016491; P:GO:0008152; C:GO:0005739	-		IPR002938; IPR003042; IPR010971; IPR018168; G3DSA:3.50.50.60 (GENE3D), PTHR13789 (PANTHER), PTHR13789:SF5 (PANTHER), SSF51905 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	d--directed r- polymerase ii largest subunit	10	F:GO:0003899; F:GO:0004672; P:GO:0006367; C:GO:0005730; F:GO:0046872; F:GO:0031625; P:GO:0008380; C:GO:0005665; F:GO:0003677; P:GO:0006368	-	EC:2.7.7.6	IPR000722; IPR006592; IPR007066; IPR007080; IPR007081; IPR007083; PTHR19376 (PANTHER), PTHR19376:SF14 (PANTHER), SSF64484 (SUPERFAMILY)
Caenorhabditis briggsae	d--directed r- polymerase ii largest subunit	10	F:GO:0003899; F:GO:0004672; P:GO:0006367; C:GO:0005730; F:GO:0046872; F:GO:0031625; P:GO:0008380; C:GO:0005665; F:GO:0003677; P:GO:0006368	-	EC:2.7.7.6	IPR000722; IPR006592; IPR007066; IPR007080; IPR007081; IPR007083; PTHR19376 (PANTHER), PTHR19376:SF14 (PANTHER), SSF64484 (SUPERFAMILY)

Caenorhabditis briggsae	d--directed r- polymerase ii largest	10	F:GO:0003899; F:GO:0004672; P:GO:0006367; C:GO:0005730; F:GO:0046872; F:GO:0031625; P:GO:0008380; C:GO:0005665; F:GO:0003677; P:GO:0006368	-	EC:2.7.7.6	IPR000722; IPR006592; IPR007066; IPR007080; IPR007083; PTHR19376 (PANTHER), PTHR19376:SF14 (PANTHER), SSF64484 (SUPERFAMILY)
Caenorhabditis briggsae	d--directed r- polymerase ii largest	10	F:GO:0003899; F:GO:0004672; P:GO:0006367; C:GO:0005730; F:GO:0046872; F:GO:0031625; P:GO:0008380; C:GO:0005665; F:GO:0003677; P:GO:0006368	-	EC:2.7.7.6	IPR000722; IPR006592; IPR007066; IPR007080; IPR007081; IPR007083; PTHR19376 (PANTHER), PTHR19376:SF14 (PANTHER), SSF64484 (SUPERFAMILY)
Caenorhabditis briggsae	zinc finger protein 183	6	F:GO:0003676; P:GO:0009792; P:GO:0040007; F:GO:0008270; F:GO:0005515; P:GO:0002119	-		SignalP (SIGNALP)
Caenorhabditis briggsae	zinc finger protein 183	6	F:GO:0003676; P:GO:0009792; P:GO:0040007; F:GO:0008270; F:GO:0005515; P:GO:0002119	-		SignalP (SIGNALP)
Caenorhabditis briggsae	zinc finger protein 183	6	F:GO:0003676; P:GO:0009792; P:GO:0040007; F:GO:0008270; F:GO:0005515; P:GO:0002119	-		IPR000571; IPR001841; IPR013083; IPR017907; IPR018957; G3DSA:4.10.1000.10 (GENE3D), PTHR12930 (PANTHER), SSF57850 (SUPERFAMILY), SSF90229 (SUPERFAMILY)
Caenorhabditis elegans	zinc finger protein 183	5	F:GO:0046872; P:GO:0009792; P:GO:0040007; F:GO:0005515; P:GO:0002119	-		SignalP (SIGNALP)
Caenorhabditis briggsae	zinc finger protein 183	6	F:GO:0003676; P:GO:0009792; P:GO:0040007; F:GO:0008270; F:GO:0005515; P:GO:0002119	-		SignalP (SIGNALP)
Caenorhabditis elegans	probable inner membrane protein oxa1l2	1	C:GO:0016020	-		SignalP (SIGNALP)

Brugia malayi	amine oxidase (flavin containing) domain 1	10	F:GO:0034649; P:GO:0034720; F:GO:0008270; F:GO:0034647; P:GO:0006349; P:GO:0044030; F:GO:0034648; P:GO:0043046; F:GO:0050660; C:GO:0005634	-		IPR002937; IPR007526; IPR009057; IPR011991; G3DSA:3.50.50.60 (GENE3D), PTHR10742 (PANTHER), PTHR10742:SF33 (PANTHER), SSF51905 (SUPERFAMILY)
Brugia malayi	loc494846 protein	1	C:GO:0044464	-		PD968187 (PRODOM), PTHR23161 (PANTHER), PTHR23161:SF2 (PANTHER)
Brugia malayi	protein cip2a	1	C:GO:0044464	-		PD968187 (PRODOM), PTHR23161 (PANTHER), PTHR23161:SF2 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-cyp-33c9 protein	5	F:GO:0020037; P:GO:0055114; F:GO:0016491; F:GO:0009055; P:GO:0040010	-		-
Caenorhabditis elegans	gtp-binding protein ard-1	5	C:GO:0043231; F:GO:0046872; P:GO:0043687; C:GO:0044444; F:GO:0005525	-		IPR000315; IPR001841; IPR007087; IPR013083; IPR017907; PTHR13712 (PANTHER), PTHR13712:SF58 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis briggsae	prefoldin subunit 3	8	P:GO:0040035; P:GO:0009792; P:GO:0006457; P:GO:0035046; F:GO:0051082; P:GO:0006898; C:GO:0016272; P:GO:0002009	-		IPR004127; IPR009053; PTHR12409 (PANTHER)
Caenorhabditis elegans	ain family member (clp-1)	3	C:GO:0044464; P:GO:0008219; F:GO:0004197	-	EC:3.4.22.0	-
Caenorhabditis briggsae	mitochondrial import inner membrane translocase subunit	8	C:GO:0005743; F:GO:0046872; P:GO:0045039; P:GO:0040035; C:GO:0042719; P:GO:0040011; P:GO:0009792; P:GO:0040018	-		IPR004217; PTHR11038 (PANTHER), PTHR11038:SF8 (PANTHER), SSF144122 (SUPERFAMILY)

Brugia malayi	myh9 protein	41	C:GO:0030863; P:GO:0008360; C:GO:0031594; P:GO:0030048; F:GO:0030898; P:GO:0051295; C:GO:0005913; P:GO:0016337; F:GO:0043531; P:GO:0032796; P:GO:0015031; C:GO:0001772; C:GO:0005829; P:GO:0007520; F:GO:0000146; P:GO:0006509; P:GO:0043534; C:GO:0008305; C:GO:0005819; C:GO:0001726; P:GO:0007132; F:GO:0005391; C:GO:0032154; P:GO:0000904; P:GO:0001768; F:GO:0043495; F:GO:0051015;	-	EC:3.6.3.9	-
Brugia malayi	myh9 protein	41	C:GO:0030863; P:GO:0008360; C:GO:0031594; P:GO:0030048; F:GO:0030898; P:GO:0051295; C:GO:0005913; P:GO:0016337; F:GO:0043531; P:GO:0032796; P:GO:0015031; C:GO:0001772; C:GO:0005829; P:GO:0007520; F:GO:0000146; P:GO:0006509; P:GO:0043534; C:GO:0008305; C:GO:0005819; C:GO:0001726; P:GO:0007132; F:GO:0005391; C:GO:0032154; P:GO:0000904; P:GO:0001768; F:GO:0043495; F:GO:0051015;	-	EC:3.6.3.9	-
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-

Caenorhabditis elegans	tbc (tre-2 bub2 cdc16) domain family member (tbc-9)	0		P:GO:0032313; F:GO:0005509; P:GO:0008150; C:GO:0005575; F:GO:0005097; C:GO:0005622		PTHR22957 (PANTHER), PTHR22957:SF48 (PANTHER)
Caenorhabditis elegans	pseudouridylate synthase 7 homolog	1	P:GO:0009451	-		IPR001656; IPR011760; IPR020103; IPR020119
Caenorhabditis elegans	pseudouridylate synthase 7 homolog	1	P:GO:0009451	-		IPR001656; IPR011760; IPR020103; IPR020119
Caenorhabditis elegans	pseudouridylate synthase 7 homolog	1	P:GO:0009451	-		IPR001656; IPR011760; IPR020103; IPR020119
	-	0				-
	-	0				-
Caenorhabditis briggsae	r--binding protein	5	P:GO:0008340; P:GO:0040007; P:GO:0040035; P:GO:0006898; P:GO:0002119	-		-
Caenorhabditis elegans	suppressor of g2 allele of skp1 homolog	3	P:GO:0040035; C:GO:0043234; C:GO:0044424	-		SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				IPR010800; SignalP (SIGNALP)
Caenorhabditis elegans	dual specificity phosphatase 11 (r- rnp complex 1-interacting)	7	F:GO:0004725; P:GO:0009792; F:GO:0008138; P:GO:0006470; P:GO:0000003; P:GO:0002009; P:GO:0006396	-	EC:3.1.3.48	IPR000340; IPR000387; IPR016130; IPR020422; G3DSA:3.90.190.10 (GENE3D), PTHR10367 (PANTHER), SSF52799 (SUPERFAMILY)
Ostertagia ostertagi	metalloprotease 1 precursor	3	F:GO:0046872; P:GO:0000003; F:GO:0008237	-		IPR000859; IPR001506; IPR006026; IPR013032; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	spindle and kinetochore-associated protein 1	5	F:GO:0005515; P:GO:0007067; C:GO:0005819; C:GO:0000777; C:GO:0005874	-		IPR009829
Caenorhabditis briggsae	gamma-inducible protein 30	0				IPR004911; PTHR13234:SF5 (PANTHER)
Caenorhabditis briggsae	g elongation mitochondrial 1	10	F:GO:0003746; P:GO:0040010; P:GO:0070125; C:GO:0005739; P:GO:0000003; P:GO:0002119; F:GO:0003924; P:GO:0006898; P:GO:0009792; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000795; IPR005225; IPR009000; G3DSA:2.40.30.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF13 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	briggsae cbr-brd-1 protein	0		F:GO:0008270; F:GO:0005515; C:GO:0005622		IPR001357; G3DSA:3.40.50.10190 (GENE3D)

Cooperia oncophora	calcium-activated potassium channel alpha chain	10	P:GO:0009790; P:GO:0000278; C:GO:0008076; F:GO:0005488; F:GO:0005249; F:GO:0015269; P:GO:0055085; P:GO:0006813; P:GO:0008152; F:GO:0003824	-		PTHR10027 (PANTHER), PTHR10027:SF3 (PANTHER)
Caenorhabditis briggsae	transmembrane protein 49	2	C:GO:0016020; C:GO:0005783	-		PTHR10281 (PANTHER), PTHR10281:SF1 (PANTHER)
Caenorhabditis briggsae	-dh dehydroge-se 1 beta subcomplex subunit mitochondrial precursor	4	P:GO:0009792; F:GO:0008137; P:GO:0018996; C:GO:0005739	-	EC:1.6.5.3	IPR008699; PF05821 (PFAM)
Caenorhabditis briggsae	-dh dehydroge-se 1 beta subcomplex subunit mitochondrial precursor	4	P:GO:0009792; F:GO:0008137; P:GO:0018996; C:GO:0005739	-	EC:1.6.5.3	IPR008699; PF05821 (PFAM)
Caenorhabditis elegans	protein	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	coiled-coil-helix-coiled-coil-helix domain-containing protein 8	0		P:GO:0006412; F:GO:0004045		IPR011990
Caenorhabditis briggsae	prion-like-(q n-rich)-domain-bearing protein family member (pqn-52)	0				SignalP (SIGNALP)
Caenorhabditis elegans	peptidase c19 family protein	1	F:GO:0016787	-		IPR006615; SSF143791 (SUPERFAMILY)
Caenorhabditis elegans	gtp-ase activating protein for arf containing protein	4	P:GO:0040010; F:GO:0046872; P:GO:0019915; P:GO:0002119	-		IPR001164; PTHR23180 (PANTHER), PTHR23180:SF30 (PANTHER)
	-	0				IPR000408
	-	0				IPR003582
Caenorhabditis elegans	ankyrin repeat and sam domain-containing protein 3	3	P:GO:0040007; P:GO:0008340; P:GO:0040011	-		IPR002110; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER), PTHR18958:SF183 (PANTHER)
Caenorhabditis briggsae	a-phase-promoting complex subunit 2	4	P:GO:0051239; P:GO:0007268; F:GO:0005515; P:GO:0050794	-		PTHR11932 (PANTHER), PTHR11932:SF5 (PANTHER)
Caenorhabditis briggsae	a-phase-promoting complex subunit 2	4	P:GO:0051239; P:GO:0007268; F:GO:0005515; P:GO:0050794	-		PTHR11932 (PANTHER), PTHR11932:SF5 (PANTHER)
Caenorhabditis briggsae	tuftelin-interacting protein 11	7	C:GO:0005681; P:GO:0040007; P:GO:0040035; P:GO:0002119; F:GO:0005515; P:GO:0040011; P:GO:0009792	-		IPR022783; PTHR23329 (PANTHER), PTHR23329:SF1 (PANTHER)
Caenorhabditis elegans	tetratricopeptide repeat protein 15	0		F:GO:0003674; F:GO:0005488; P:GO:0008150; C:GO:0005575		IPR011990; SignalP (SIGNALP)

Loa loa	adaptor-related protein complex beta 1 subunit	9	P:GO:0009792; P:GO:0002119; F:GO:0005515; F:GO:0008565; P:GO:0000003; P:GO:0006886; P:GO:0040007; P:GO:0006898; C:GO:0030131	-		IPR009028; IPR012295; IPR015151; PTHR11134 (PANTHER), PTHR11134:SF2 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	dynein light chain	8	F:GO:0003777; C:GO:0005829; C:GO:0030286; F:GO:0005515; P:GO:0007017; C:GO:0043186; C:GO:0005634; C:GO:0005886	-		IPR001372; IPR019763
Caenorhabditis briggsae	protein disulfide-isomerase 1	4	F:GO:0016491; P:GO:0040017; P:GO:0040010; C:GO:0016020	-		IPR006863; IPR017905; PTHR22897 (PANTHER), PTHR22897:SF4 (PANTHER)
Caenorhabditis briggsae	protein disulfide-isomerase 1	4	F:GO:0016491; P:GO:0040017; P:GO:0040010; C:GO:0016020	-		IPR006863; IPR017905; PTHR22897 (PANTHER), PTHR22897:SF4 (PANTHER)
Caenorhabditis briggsae	type xxviii	0		F:GO:0004867; C:GO:0019031; C:GO:0005604; P:GO:0007267; F:GO:0003674; P:GO:0007156; C:GO:0016021; P:GO:0007155; C:GO:0016020; P:GO:0010951; F:GO:0005509; F:GO:0030414; P:GO:0007275; P:GO:0008150; P:GO:0016032; P:GO:0006952; C:GO:0005578; P:GO:0010466; F:GO:0005515; C:GO:0005886; C:GO:0005576		IPR002035; G3DSA:3.40.50.410 (GENE3D), SignalP (SIGNALP), SSF53300 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG02513 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	c2 domain containing protein	1	F:GO:0005515	-		IPR000008; IPR008973; IPR018029; G3DSA:2.60.40.150 (GENE3D), PTHR10024 (PANTHER), PTHR10024:SF27 (PANTHER)

Caenorhabditis elegans	sphingosine-1-phosphate lyase 1	9	P:GO:0009653; P:GO:0008340; P:GO:0006672; P:GO:0040010; P:GO:0008406; C:GO:0044425; P:GO:0006915; F:GO:0016829; C:GO:0005783	-		IPR002129; IPR015421; IPR015424; PTHR11999:SF5 (PANTHER)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG11506 [Caenorhabditis briggsae]	3	F:GO:0005509; C:GO:0016020; P:GO:0007156	-		SignalP (SIGNALP)
Caenorhabditis elegans	protein fam113b-like	0		F:GO:0016787; P:GO:0008150		IPR013830; IPR013831; PTHR14469 (PANTHER)
Caenorhabditis briggsae	d- helicase hel308	2	F:GO:0005488; F:GO:0004386	-		G3DSA:3.40.50.300 (GENE3D), PTHR11752 (PANTHER), PTHR11752:SF3 (PANTHER)
Brugia malayi	hypothetical protein Bm1_51405 [Brugia malayi]	0				-
Caenorhabditis elegans	syntaxin 12	7	C:GO:0045335; F:GO:0005515; P:GO:0033344; C:GO:0045121; P:GO:0050821; P:GO:0009987; P:GO:0015031	-		-
	-	0				-
Caenorhabditis elegans	glucoki-se	30	P:GO:0032024; P:GO:0046835; P:GO:0032811; P:GO:0051156; P:GO:0007204; F:GO:0004674; P:GO:0019932; C:GO:0005884; C:GO:0030141; P:GO:0007243; C:GO:0005829; P:GO:0001678; P:GO:0045725; C:GO:0005654; F:GO:0000287; P:GO:0051594; P:GO:0045821; F:GO:0004340; P:GO:0045721; C:GO:0005739; P:GO:0042149; P:GO:0060361; F:GO:0005536; P:GO:0006468; F:GO:0005524; F:GO:0019903; C:GO:0044448; P:GO:0006003;	-	EC:2.7.11.0; EC:2.7.1.2	IPR001312; IPR022672; IPR022673; G3DSA:3.40.367.20 (GENE3D), SSF53067 (SUPERFAMILY)

Loa loa	variant sh3 domain containing protein	19	C:GO:0045121; P:GO:0045725; P:GO:0008286; F:GO:0019901; C:GO:0005913; P:GO:0006936; P:GO:0048041; C:GO:0005829; F:GO:0008092; C:GO:0005924; C:GO:0005899; P:GO:0090004; P:GO:0043149; C:GO:0001725; F:GO:0005070; C:GO:0005634; P:GO:0046889; F:GO:0005158; P:GO:0046326	-		IPR000108; IPR001452; IPR011511; G3DSA:2.30.30.40 (GENE3D), PTHR10661 (PANTHER), PTHR10661:SF5 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	zinc finger cchc domain-containing protein 4	1	F:GO:0005488	-		IPR001594; PTHR13493 (PANTHER)
	-	0				-
Drosophila ananassae	transmembrane protein 167 precursor	2	C:GO:0000139; C:GO:0016021	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	dihydrolipoamide branched chain transacylase e2	12	F:GO:0008415; F:GO:0004672; C:GO:0042645; F:GO:0043754; F:GO:0000166; P:GO:0032436; C:GO:0005576; F:GO:0005179; P:GO:0009792; P:GO:0046949; F:GO:0048037; P:GO:0006468	-	EC:2.3.1.168	IPR001078; IPR015761; G3DSA:3.30.559.10 (GENE3D), PTHR23151 (PANTHER), SignalP (SIGNALP), SSF52777 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-ril-1 protein	5	P:GO:0009792; P:GO:0008340; P:GO:0000003; P:GO:0040010; P:GO:0002119	-		-
Caenorhabditis briggsae	alpha-amylase	1	F:GO:0003824	-		IPR006048; IPR013780; IPR017853; PTHR10357 (PANTHER), PTHR10357:SF26 (PANTHER), SSF51011 (SUPERFAMILY)
Loa loa	beta-lactamase-like protein 2	0		F:GO:0046872; C:GO:0005739; F:GO:0016787; C:GO:0005575		IPR001279; G3DSA:3.60.15.10 (GENE3D), PTHR23131 (PANTHER), SignalP (SIGNALP), SSF56281 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-chs-1 protein	5	P:GO:0009792; P:GO:0000003; C:GO:0005887; P:GO:0040010; F:GO:0016740	-		-
	-	0				SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	tr- guanosine-2 -o-methyltransferase trm11 homolog	0		F:GO:0003676; F:GO:0008168; F:GO:0003674; P:GO:0008033; F:GO:0016740; P:GO:0008150; P:GO:0032259; C:GO:0005575		IPR000241; IPR002052; G3DSA:3.40.50.150 (GENE3D), PTHR13370 (PANTHER), SSF53335 (SUPERFAMILY)
Loa loa	zinc c2h2 type family protein	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		IPR007087; IPR015880; PTHR14596 (PANTHER)
Caenorhabditis elegans	patched family protein	8	P:GO:0040025; F:GO:0008158; P:GO:0040018; P:GO:0018996; P:GO:0000003; P:GO:0008340; P:GO:0040011; C:GO:0016021	-		-
Caenorhabditis elegans	immunoglobulin i-set domain containing protein	0				IPR002602; IPR003599; IPR003961; IPR007110; IPR008957; IPR013098; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)
Xenopus (Silurana) tropicalis	lyr motif-containing protein 5	1	C:GO:0005739	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	nucleolar protein 14-like	3	P:GO:0009792; P:GO:0006898; P:GO:0002119	-		IPR007276
Caenorhabditis elegans	mitotic checkpoint protein bub3	10	C:GO:0005829; P:GO:0008608; P:GO:0000070; C:GO:0005730; P:GO:0051436; P:GO:0031145; P:GO:0071173; C:GO:0000776; F:GO:0005515; P:GO:0051983	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR10971 (PANTHER), PTHR10971:SF5 (PANTHER)

Haemonchus contortus	catalase	20	P:GO:0007411; P:GO:0008340; P:GO:0009650; P:GO:0042744; F:GO:0020037; F:GO:0050661; F:GO:0004096; P:GO:0006629; P:GO:0006637; P:GO:0048522; F:GO:0008415; P:GO:0051090; P:GO:0044281; P:GO:0009636; P:GO:0055114; F:GO:0042803; P:GO:0051262; C:GO:0005778; P:GO:0043066; C:GO:0005739	-	EC:1.11.1.6	IPR002226; IPR010582; IPR011614; IPR018028; IPR020835
Caenorhabditis elegans	ribosomal protein l15	11	P:GO:0009792; P:GO:0002119; C:GO:0005840; P:GO:0040018; F:GO:0003735; F:GO:0003723; P:GO:0018996; P:GO:0040010; P:GO:0000003; C:GO:0005829; P:GO:0006414	-		IPR000439; IPR012678
Homo sapiens	poly	5	C:GO:0005730; P:GO:0006284; C:GO:0005654; F:GO:0005515; F:GO:0003950	-	EC:2.4.2.30	IPR004102; IPR008893; IPR012317; IPR016129; G3DSA:3.90.228.10 (GENE3D), PTHR15447 (PANTHER), SSF142921 (SUPERFAMILY)
Caenorhabditis elegans	short chain dehydroge-se reductase family protein	0		P:GO:0055114; F:GO:0005488; F:GO:0016491; P:GO:0008152; F:GO:0003824		-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG04540 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	briggsae cbr-spe-39 protein	1	F:GO:0005515	-		IPR019177
Caenorhabditis elegans	protein ki-se c	7	P:GO:0006468; F:GO:0046872; P:GO:0023034; F:GO:0019992; F:GO:0004698; F:GO:0005524; C:GO:0016020	-		IPR000719; IPR011009; IPR015745; IPR017441; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR22985 (PANTHER)
Caenorhabditis elegans	phosphatidylcholine:ceramide cholinephosphotransferase	3	F:GO:0047493; C:GO:0016021; P:GO:0006686	-	EC:2.7.8.3	PTHR21290 (PANTHER), PTHR21290:SF3 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis briggsae	sorting nexin-13	2	F:GO:0005515; P:GO:0007154	-		IPR001683; PTHR22775 (PANTHER), PTHR22775:SF8 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	6	P:GO:0009792; P:GO:0002119; P:GO:0040010; P:GO:0000003; P:GO:0006898; P:GO:0002009	-		IPR013870
Loa loa	transmembrane protein 185b	0		F:GO:0003676		-
Caenorhabditis elegans	mitochondrial import inner membrane translocase subunit tim16	7	P:GO:0040035; P:GO:0002119; C:GO:0005743; F:GO:0031072; P:GO:0055085; P:GO:0040007; P:GO:0015031	-		IPR005341
Caenorhabditis briggsae	cell division protein ftsj	11	P:GO:0055085; F:GO:0005488; C:GO:0005730; C:GO:0005743; P:GO:0006364; P:GO:0040007; P:GO:0040035; P:GO:0032259; P:GO:0002119; F:GO:0008168; P:GO:0015031	-	EC:2.1.1.0	IPR002877; IPR015507; G3DSA:3.40.50.150 (GENE3D), SSF53335 (SUPERFAMILY)
Caenorhabditis elegans	glutaminyl-tr- synthetase	4	F:GO:0004819; C:GO:0005875; P:GO:0006425; F:GO:0005524	-	EC:6.1.1.18	IPR000924; IPR001412; IPR004514; IPR007638; IPR007639; IPR014729; IPR020058; G3DSA:3.90.800.10 (GENE3D), SSF52374 (SUPERFAMILY)
Brugia malayi	serine threonine-protein ki-se 16	0		F:GO:0016301; F:GO:0004672; F:GO:0005524; P:GO:0006468; F:GO:0004674		-
Brugia malayi	integrator complex subunit 12	0		C:GO:0005634; P:GO:0016180; C:GO:0032039; F:GO:0008270; F:GO:0003674; C:GO:0005575; F:GO:0005515; F:GO:0046872; P:GO:0008150		IPR001965; IPR011011; IPR013083; IPR019786; IPR019787; PTHR12628 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	dicer-1	1	F:GO:0005515	-		PTHR14950 (PANTHER), PTHR14950:SF3 (PANTHER)
Caenorhabditis elegans	elongation factor tu gtp-binding domain-containing protein 1	1	F:GO:0000166	-		IPR000795; IPR009000; G3DSA:2.40.30.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), G3DSA:3.90.1430.10 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF15 (PANTHER), SSF52540 (SUPERFAMILY)

Caenorhabditis elegans	ras-related protein m-ras	9	P:GO:0007264; C:GO:0005622; P:GO:0006913; P:GO:0006184; F:GO:0030742; F:GO:0003924; P:GO:0006886; F:GO:0005525; C:GO:0005886	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001806; IPR003577; IPR005225; IPR013753; IPR020849; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF273 (PANTHER), SSF52540 (SUPERFAMILY)
Brugia malayi	rho gtpase-activating protein 26	7	F:GO:0005096; C:GO:0005622; P:GO:0046847; P:GO:0007165; P:GO:0019915; F:GO:0017124; F:GO:0008093	-		IPR013606; PTHR12552 (PANTHER), PTHR12552:SF1 (PANTHER), SSF103657 (SUPERFAMILY)
Caenorhabditis elegans	transketolase	2	F:GO:0004802; P:GO:0008152	-	EC:2.2.1.1	IPR005474; IPR005475; IPR005476; IPR009014; IPR015941; IPR020826; G3DSA:3.40.50.970 (GENE3D), PTHR11624 (PANTHER), PTHR11624:SF2 (PANTHER), SSF52518 (SUPERFAMILY)
Caenorhabditis elegans	transketolase	2	F:GO:0004802; P:GO:0008152	-	EC:2.2.1.1	IPR005474; IPR005475; IPR005476; IPR009014; IPR015941; IPR020826; G3DSA:3.40.50.970 (GENE3D), PTHR11624 (PANTHER), PTHR11624:SF2 (PANTHER), SSF52518 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	briggsae cbr-lir-3 protein	0		F:GO:0008270; C:GO:0005622		-
Caenorhabditis briggsae	taxilin alpha	0		F:GO:0003674; C:GO:0005737; C:GO:0005575		IPR019132; PTHR16127 (PANTHER), PTHR16127:SF8 (PANTHER)
Brugia malayi	bromodomain containing protein	6	P:GO:0016570; P:GO:0040011; P:GO:0007399; F:GO:0005488; C:GO:0005634; F:GO:0008080	-		IPR001487; IPR018359; PTHR22880 (PANTHER), PTHR22880:SF31 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis briggsae	proteasome (macropain) 26s non- 1	5	P:GO:0051436; P:GO:0051437; C:GO:0005838; P:GO:0031145; F:GO:0005515	-		IPR002015; IPR011989; IPR016024; IPR016642; PTHR10943 (PANTHER), PTHR10943:SF2 (PANTHER)
Caenorhabditis briggsae	proteasome (macropain) 26s non- 1	5	P:GO:0051436; P:GO:0051437; C:GO:0005838; P:GO:0031145; F:GO:0005515	-		IPR002015; IPR011989; IPR016024; IPR016642; PTHR10943 (PANTHER), PTHR10943:SF2 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-ida-1 protein	2	P:GO:0016311; F:GO:0004721	-	EC:3.1.3.16	SignalP (SIGNALP)

Caenorhabditis elegans	variable abnormal morphology family member (vab-10)	11	P:GO:0000226; P:GO:0007424; P:GO:0065008; P:GO:0007409; P:GO:0007517; C:GO:0005874; F:GO:0008092; P:GO:0035239; P:GO:0051128; P:GO:0048523; C:GO:0044444	-		IPR002017; IPR018159; G3DSA:1.20.58.60 (GENE3D), SSF46966 (SUPERFAMILY)
	-	0				-
Branchiostoma floridae	serine arginine repetitive matrix protein 1	2	F:GO:0005488; C:GO:0044428	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	5	F:GO:0004222; P:GO:0000003; P:GO:0006508; F:GO:0008270; P:GO:0007413	-	EC:3.4.24.0	IPR001506; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF80 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr--s-1 protein	5	F:GO:0004222; P:GO:0000003; P:GO:0006508; F:GO:0008270; P:GO:0007413	-	EC:3.4.24.0	IPR001506; IPR006026; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF80 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	5	F:GO:0004222; P:GO:0000003; P:GO:0006508; F:GO:0008270; P:GO:0007413	-	EC:3.4.24.0	IPR001506; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF80 (PANTHER), SSF55486 (SUPERFAMILY)
Homo sapiens	glucose phosphate isomerase	10	P:GO:0001525; F:GO:0005125; C:GO:0005615; F:GO:0004347; P:GO:0006959; P:GO:0006096; P:GO:0007599; P:GO:0006094; C:GO:0005737; F:GO:0008083	-	EC:5.3.1.9	IPR001672; IPR018189; G3DSA:3.40.50.10490 (GENE3D), PS51463 (PROFILE), SSF53697 (SUPERFAMILY)
Brugia malayi	sap domain containing protein	0		F:GO:0003676; F:GO:0000166		IPR003034
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
Loa loa	actin	4	C:GO:0005856; C:GO:0005737; F:GO:0005524; F:GO:0005515	-		SignalP (SIGNALP)
Loa loa	cytoplasmic 2-like isoform 1	4	C:GO:0005856; C:GO:0005737; F:GO:0005524; F:GO:0005515	-		-
Caenorhabditis elegans	transmembrane protein 50b	2	C:GO:0005783; C:GO:0005886	-		IPR007919; SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	hypothetical protein C10B5.3 [Caenorhabditis elegans]	0				-

Caenorhabditis elegans	pdf receptor homolog family member (pdfr-1)	6	F:GO:0004930; F:GO:0005488; P:GO:0007186; C:GO:0016020; P:GO:0042745; P:GO:0050789	-		IPR000832; IPR001879; IPR017981; IPR017983; PTHR12011 (PANTHER), PTHR12011:SF14 (PANTHER), SSF111418 (SUPERFAMILY)
Loa loa	zinc finger protein zfat isoform 2	0		C:GO:0005634; F:GO:0003677; F:GO:0003676; C:GO:0005737; F:GO:0008270; F:GO:0003674; C:GO:0005575; C:GO:0005622; F:GO:0046872; C:GO:0005829; P:GO:0006350; P:GO:0008150; P:GO:0045449		IPR015880
Loa loa	zinc finger protein	0		C:GO:0005634; F:GO:0003677; F:GO:0003676; C:GO:0005737; F:GO:0003674; F:GO:0008270; C:GO:0005575; C:GO:0005622; F:GO:0046872; P:GO:0006350; C:GO:0005829; P:GO:0008150; P:GO:0045449		IPR015880
Caenorhabditis briggsae	pescadillo homolog	10	P:GO:0051726; P:GO:0042273; C:GO:0070545; P:GO:0000463; F:GO:0005515; C:GO:0030687; C:GO:0005694; C:GO:0005654; P:GO:0008283; P:GO:0000466	-		IPR001357; IPR010613; G3DSA:3.40.50.10190 (GENE3D), PTHR12221 (PANTHER)
Ancylostoma caninum	metalloprotease 1 precursor	2	F:GO:0046872; F:GO:0008237	-		IPR001506; IPR006026; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				IPR014893
	-	0				-
Loa loa	28s ribosomal protein mitochondrial precursor	5	P:GO:0009792; C:GO:0005763; F:GO:0003735; F:GO:0005515; P:GO:0006412	-	EC:3.6.5.3	-

Caenorhabditis elegans	myotubularin-related family protein	0		P:GO:0016311; F:GO:0016791		-
	-	0				-
Caenorhabditis elegans	uncoordi-ted family member (unc-22)	6	C:GO:0030018; P:GO:0006468; F:GO:0008307; P:GO:0007498; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	-
Chromobacterium violaceum ATCC 12472	hydroxymethylglutaryl- lyase	3	F:GO:0004419; F:GO:0016740; P:GO:0006629	-	EC:4.1.3.4	PTHR10277 (PANTHER), PTHR10277:SF1 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG19140 [Caenorhabditis briggsae]	0		P:GO:0040017; F:GO:0005488; P:GO:0040010		IPR011990
Caenorhabditis elegans	translocase of inner mitochondrial membrane 44 homolog	11	P:GO:0040010; F:GO:0008270; F:GO:0015450; C:GO:0005744; P:GO:0000003; P:GO:0006626; P:GO:0002119; F:GO:0005515; C:GO:0005759; P:GO:0006898; P:GO:0009792	-		PTHR10721 (PANTHER), PTHR10721:SF1 (PANTHER)
	-	0				-
	-	0				-
Homo sapiens	cytochrome c oxidase subunit viii liver form	4	C:GO:0005743; C:GO:0016021; F:GO:0004129; P:GO:0006091	-	EC:1.9.3.1	-
	-	0				-
Caenorhabditis briggsae	d- mismatch repair protein msh-2	3	F:GO:0003677; C:GO:0044428; C:GO:0032300	-		IPR000432; G3DSA:3.40.50.300 (GENE3D), PTHR11361:SF28 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	fmrfamide receptor	3	P:GO:0007186; C:GO:0016021; F:GO:0001653	-		IPR000276; IPR017452; G3DSA:1.20.1070.10 (GENE3D), PTHR22751 (PANTHER), PTHR22751:SF8 (PANTHER), SignalP (SIGNALP), SSF81321 (SUPERFAMILY)
Caenorhabditis briggsae	carboxypeptidase d	12	F:GO:0004181; F:GO:0035256; F:GO:0008270; P:GO:0071352; C:GO:0016021; P:GO:0006508; C:GO:0005792; F:GO:0003779; P:GO:0007216; C:GO:0005802; F:GO:0030160; C:GO:0005634	-	EC:3.4.17.0	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11532 (PANTHER), PTHR11532:SF2 (PANTHER), SSF53187 (SUPERFAMILY)

Caenorhabditis briggsae	briggsae cbr-chs-1 protein	5	P:GO:0009792; P:GO:0000003; C:GO:0005887; F:GO:0016758; P:GO:0040010	-	EC:2.4.1.0	PTHR22914 (PANTHER)
Caenorhabditis briggsae	protein fat-free homolog	4	C:GO:0016021; C:GO:0005737; F:GO:0005515; C:GO:0043231	-		PTHR15954 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-sgo-1 protein	0		C:GO:0005694; P:GO:0045132; P:GO:0007049; P:GO:0007059; C:GO:0000775; P:GO:0051301; C:GO:0005634		IPR011515
Caenorhabditis elegans	die-1	0		F:GO:0008270; C:GO:0005622		IPR007087; IPR015880; IPR017900
	-	0				-
	-	0				-
Caenorhabditis elegans	programmed cell death	1	F:GO:0005515	-		IPR009652
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	adp atp translocase	15	P:GO:0055085; P:GO:0040010; P:GO:0008340; C:GO:0016021; C:GO:0005743; P:GO:0040002; P:GO:0040035; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0040017; F:GO:0005215; P:GO:0006898; P:GO:0002009; P:GO:0009792	-		IPR001993; IPR002113; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF35 (PANTHER)
	-	0				-
Loa loa	autophagy protein apg5 containing protein	11	C:GO:0034045; P:GO:0000045; P:GO:0055015; F:GO:0005515; P:GO:0001974; P:GO:0060047; C:GO:0005776; P:GO:0031397; P:GO:0042493; P:GO:0043066; P:GO:0042311	-		-
Loa loa	class member 2	4	C:GO:0016020; P:GO:0008340; F:GO:0004571; F:GO:0005509	-	EC:3.2.1.113	IPR001382; PTHR11742:SF6 (PANTHER)

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	mitochondrial import inner membrane translocase subunit tim8 a	4	F:GO:0046872; P:GO:0045039; C:GO:0005743; C:GO:0042719	-		-
Brugia malayi	elegans protein confirmed by transcript evidence	9	P:GO:0010171; P:GO:0002119; P:GO:0040002; P:GO:0040011; C:GO:0016021; C:GO:0005576; P:GO:0019915; P:GO:0006898; F:GO:0042302	-		-
	-	0				-
Caenorhabditis elegans	zinc finger cchc domain-containing protein 9	4	P:GO:0040035; P:GO:0040010; P:GO:0040011; P:GO:0006898	-		-
Brugia malayi	leucine rich repeat family protein	0		F:GO:0005515		IPR001611; IPR003591; PR00019 (PRINTS), G3DSA:3.80.10.10 (GENE3D), PTHR23155 (PANTHER), PTHR23155:SF26 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)
Caenorhabditis elegans	gpi-anchor transamidase	6	F:GO:0003923; F:GO:0005515; C:GO:0042765; F:GO:0004197; P:GO:0006508; P:GO:0050976	-	EC:3.4.22.0	-
Caenorhabditis briggsae	gpi-anchor transamidase	7	F:GO:0003676; F:GO:0003923; F:GO:0005515; C:GO:0042765; F:GO:0004197; P:GO:0006508; F:GO:0008270	-	EC:3.4.22.0	IPR001096; PTHR12000:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein F55F10.1 [Caenorhabditis elegans]	4	F:GO:0017111; P:GO:0050789; C:GO:0005622; F:GO:0000166	-	EC:3.6.1.15	PTHR22908 (PANTHER), PTHR22908:SF13 (PANTHER)
Brugia malayi	zinc finger	0		F:GO:0046872; P:GO:0055114; F:GO:0016491; C:GO:0016021; F:GO:0032440; F:GO:0008270; C:GO:0005575		IPR001594; PTHR22883 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	gns1 sur4 family protein	2	C:GO:0016021; P:GO:0007283	-		IPR002076
Caenorhabditis briggsae	sjchgc05781 protein	0				-
Caenorhabditis briggsae	sjchgc05781 protein	0				IPR013869
Caenorhabditis briggsae	sjchgc05781 protein	0				IPR013869
Caenorhabditis elegans	cation efflux protein zinc transporter	4	C:GO:0016020; P:GO:0040010; F:GO:0005515; P:GO:0006810	-		-

	-	0				-
Caenorhabditis elegans	translatio-l activator gcn1	4	P:GO:0009987; P:GO:0000003; F:GO:0005488; P:GO:0006810	-		IPR011989
Ascaris suum	elegans protein partially confirmed by transcript evidence	3	P:GO:0006032; P:GO:0016998; F:GO:0004568	-	EC:3.2.1.14	IPR000726; G3DSA:1.10.530.10 (GENE3D), SignalP (SIGNALP), SSF53955 (SUPERFAMILY)
Ascaris suum	elegans protein partially confirmed by transcript evidence	3	P:GO:0006032; P:GO:0016998; F:GO:0004568	-	EC:3.2.1.14	IPR000726; G3DSA:1.10.530.10 (GENE3D), SignalP (SIGNALP), SSF53955 (SUPERFAMILY)
	-	0				-
Brugia malayi	ring finger-h2 protein	4	F:GO:0046872; F:GO:0004842; F:GO:0005515; P:GO:0045941	-	EC:6.3.2.19	IPR001841; IPR002350; IPR013083; IPR018957; PTHR13644 (PANTHER), SSF57850 (SUPERFAMILY)
Brugia malayi	ring finger-h2 protein	4	F:GO:0046872; F:GO:0004842; F:GO:0005515; P:GO:0045941	-	EC:6.3.2.19	IPR001841; IPR002350; IPR013083; IPR018957; PTHR13644 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis elegans	aldehyde dehydroge-se 2 family	17	F:GO:0004030; P:GO:0033574; P:GO:0006066; P:GO:0001889; P:GO:0055114; P:GO:0071398; P:GO:0005975; F:GO:0042802; F:GO:0009055; F:GO:0001758; P:GO:0035094; P:GO:0032870; C:GO:0005759; P:GO:0032496; P:GO:0032570; F:GO:0004029; P:GO:0055093	-	EC:1.2.1.5; EC:1.2.1.36; EC:1.2.1.3	IPR015590; IPR016160; IPR016161; IPR016162; PTHR11699:SF46 (PANTHER)
Caenorhabditis elegans	aldehyde dehydroge-se 2 family	17	F:GO:0004030; P:GO:0033574; P:GO:0006066; P:GO:0001889; P:GO:0055114; P:GO:0071398; P:GO:0005975; F:GO:0042802; F:GO:0009055; F:GO:0001758; P:GO:0035094; P:GO:0032870; C:GO:0005759; P:GO:0032496; P:GO:0032570; F:GO:0004029; P:GO:0055093	-	EC:1.2.1.5; EC:1.2.1.36; EC:1.2.1.3	IPR015590; IPR016160; IPR016161; IPR016162; PTHR11699:SF46 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-mat-2 protein	0		P:GO:0000003; P:GO:0040039; P:GO:0040035; P:GO:0006898		-

Caenorhabditis briggsae	a-phase promoting complex subunit 1	0		P:GO:0070979; P:GO:0006898; C:GO:0005634; P:GO:0007067; P:GO:0051437; P:GO:0051436; P:GO:0000003; P:GO:0051301; C:GO:0005654; P:GO:0031145; F:GO:0005515; C:GO:0005680; P:GO:0040039; C:GO:0005829; P:GO:0007049; P:GO:0040035		-
	-	0				-
Caenorhabditis briggsae	receptor expression-enhancing protein 4	0		C:GO:0016021; C:GO:0016020		IPR004345; SignalP (SIGNALP)
Saccoglossus kowalevskii	d--directed r- polymerases and iii subunit rpabc5	9	F:GO:0003899; F:GO:0008270; P:GO:0006356; F:GO:0004672; P:GO:0006367; P:GO:0008380; C:GO:0005665; F:GO:0003677; P:GO:0006368	-	EC:2.7.7.6	-
Brugia malayi	atp-binding sub-family c (cftr mrp) member isoform cra_a	2	C:GO:0016020; P:GO:0010033	-		G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF14 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				IPR001005; IPR009057; IPR012287; IPR017930
Branchiostoma floridae	nicoti-mide nucleotide transhydroge-se	4	F:GO:0005488; P:GO:0010467; F:GO:0008746; C:GO:0016020	-		IPR007886; G3DSA:3.40.50.1770 (GENE3D), PTHR10160 (PANTHER), PTHR10160:SF2 (PANTHER), SSF52283 (SUPERFAMILY)
Caenorhabditis briggsae	inositol polyphosphate-5-phosphatase b	6	P:GO:0040013; P:GO:0007283; F:GO:0016788; C:GO:0016021; C:GO:0005829; P:GO:0030317	-		IPR000300; IPR005135; G3DSA:3.60.10.10 (GENE3D), PTHR11200 (PANTHER), PTHR11200:SF26 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0051301; P:GO:0009792; P:GO:0007126		IPR008574
Loa loa	wd-repeat protein	0		P:GO:0009725; P:GO:0045449; F:GO:0003677; C:GO:0005634		IPR001487; PTHR16266 (PANTHER), PTHR16266:SF3 (PANTHER)
Brugia malayi	pleckstrin homology domain interacting protein	4	P:GO:0080090; P:GO:0031323; P:GO:0006350; P:GO:0060255	-		IPR001487; PTHR16266 (PANTHER), PTHR16266:SF4 (PANTHER)
Caenorhabditis briggsae	leucine rich repeat family protein	1	P:GO:0009792	-		-

Caenorhabditis briggsae	leucine rich repeat family protein	2	C:GO:0044464; P:GO:0009792	-		IPR000483; IPR001611; IPR003591; PR00019 (PRINTS), G3DSA:3.80.10.10 (GENE3D), PTHR23154 (PANTHER), PTHR23154:SF51 (PANTHER), PS51450 (PROFILE), SignalP (SIGNALP), SSF52058 (SUPERFAMILY)
Caenorhabditis briggsae	leucine-rich repeats and immunoglobulin-like domains 2	2	P:GO:0009792; C:GO:0016020	-		IPR000483; IPR001611; IPR003591; G3DSA:3.80.10.10 (GENE3D), PTHR23154 (PANTHER), PTHR23154:SF51 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)
Caenorhabditis elegans	eukaryotic translation initiation factor 3 subunit i	5	C:GO:0005852; P:GO:0006413; F:GO:0005515; F:GO:0003743; C:GO:0005829	-		-
	-	0				-
Brugia malayi	Conserved hypothetical protein [Brugia malayi]	0				IPR019481
Caenorhabditis elegans	myotubularin-related family protein	0		P:GO:0016311; F:GO:0016791		IPR010569; IPR017906; PTHR10807 (PANTHER), PTHR10807:SF3 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis briggsae	rad25 xp-b d- repair helicase	10	P:GO:0009411; P:GO:0006289; P:GO:0006367; F:GO:0004003; P:GO:0000381; F:GO:0016251; F:GO:0003677; F:GO:0005524; C:GO:0005675; P:GO:0009792	-		PTHR11274 (PANTHER)
Caenorhabditis elegans	cyclin e	5	P:GO:0000082; F:GO:0016301; P:GO:0007088; F:GO:0016538; C:GO:0005634	-		IPR004367; IPR013763; PTHR10177 (PANTHER), PTHR10177:SF15 (PANTHER), SignalP (SIGNALP)
Brugia malayi	isoform c	1	C:GO:0016020	-		-
Caenorhabditis elegans	oligopeptidase a	6	F:GO:0004222; P:GO:0045449; F:GO:0003702; P:GO:0006367; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	IPR001567; G3DSA:1.10.1370.10 (GENE3D), G3DSA:3.40.390.10 (GENE3D), PTHR11804 (PANTHER), PTHR11804:SF4 (PANTHER), SSF55486 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	bhlhzip transcription factor bigmax	2	P:GO:0040010; P:GO:0008340	-		-

Caenorhabditis briggsae	homeobox protein abdomi-l-b	22	P:GO:0035225; F:GO:0030528; F:GO:0005515; P:GO:0008354; F:GO:0004000; P:GO:0035263; P:GO:0006355; P:GO:0008584; P:GO:0007506; F:GO:0043565; P:GO:0007486; P:GO:0035261; P:GO:0007385; F:GO:0003700; P:GO:0030539; P:GO:0007431; P:GO:0009997; P:GO:0035224; C:GO:0005634; P:GO:0035277; P:GO:0045843; P:GO:0048066	-	EC:3.5.4.4	-
Caenorhabditis briggsae	isoform b	3	C:GO:0043231; C:GO:0031410; C:GO:0044446	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019782; PTHR13923 (PANTHER), PTHR13923:SF1 (PANTHER)
Caenorhabditis briggsae	isoform b	3	C:GO:0043231; C:GO:0031410; C:GO:0044446	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019782; PTHR13923 (PANTHER), PTHR13923:SF1 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	pre-mr--processing-splicing factor 8	17	P:GO:0050896; F:GO:0003723; C:GO:0005681; P:GO:0045132; P:GO:0040007; C:GO:0016607; P:GO:0040027; P:GO:0040035; P:GO:0018996; P:GO:0007601; F:GO:0005515; P:GO:0040011; P:GO:0000398; C:GO:0005682; P:GO:0006898; P:GO:0002009; P:GO:0009792	-		IPR012592; IPR019580; IPR019581; IPR019582; PTHR11140 (PANTHER)

synthetic construct	filamin a	28	F:GO:0004871; C:GO:0005802; P:GO:0043433; P:GO:0034394; C:GO:0015629; P:GO:0050821; P:GO:0051220; C:GO:0005576; C:GO:0005829; F:GO:0001948; P:GO:0051764; P:GO:0043123; F:GO:0051015; F:GO:0048365; P:GO:0045022; P:GO:0007195; F:GO:0042803; F:GO:0034989; P:GO:0031532; F:GO:0034988; C:GO:0005886; F:GO:0008134; P:GO:0042177; C:GO:0005634; P:GO:0042993; C:GO:0005938; P:GO:0043113	-		IPR001298; IPR013783; IPR014756; IPR017868; PTHR11915 (PANTHER), PTHR11915:SF24 (PANTHER)
Caenorhabditis briggsae	phosphatidylserine decarboxylase	4	F:GO:0004609; P:GO:0040010; P:GO:0008654; C:GO:0005739	-	EC:4.1.1.65	IPR003817; IPR005221
Caenorhabditis sp. PS1010	betaine aldehyde dehydroge-se	3	C:GO:0005737; P:GO:0055114; F:GO:0008802	-	EC:1.2.1.8	IPR015590; IPR016160; IPR016161; IPR016162; IPR016163; PTHR11699:SF47 (PANTHER)
Caenorhabditis briggsae	d ki-se family family member (dkf-2)	7	C:GO:0005737; P:GO:0006468; F:GO:0046872; P:GO:0045087; F:GO:0004697; F:GO:0005524; C:GO:0016020	-	EC:2.7.11.13	-
Caenorhabditis elegans	glutathione reductase	13	C:GO:0005829; C:GO:0009897; C:GO:0005625; C:GO:0005739; P:GO:0045454; P:GO:0055114; P:GO:0007283; P:GO:0006749; F:GO:0004362; F:GO:0043295; F:GO:0042803; F:GO:0050660; F:GO:0050661	-	EC:1.8.1.7	IPR000815; IPR001327; IPR004099; IPR013027; IPR016156; PR00411 (PRINTS), G3DSA:3.50.50.60 (GENE3D), PTHR22912 (PANTHER), PTHR22912:SF27 (PANTHER), SSF51905 (SUPERFAMILY)
Caenorhabditis briggsae	trehalase family protein	4	P:GO:0009792; F:GO:0003824; P:GO:0040007; P:GO:0002119	-		IPR001661; PTHR23403:SF1 (PANTHER)

	-	0				-
Caenorhabditis briggsae	msp-domain protein 1 variant	7	C:GO:0044297; P:GO:0019915; C:GO:0005856; P:GO:0040018; P:GO:0000003; F:GO:0005198; C:GO:0031143	-		IPR000535; IPR008962; PTHR22947 (PANTHER)
Caenorhabditis elegans	saposin-like type region 1 family protein	3	C:GO:0005764; F:GO:0005488; P:GO:0006665	-		IPR007856; IPR008138; IPR008139; IPR011001; PTHR11480 (PANTHER), PTHR11480:SF2 (PANTHER)
Caenorhabditis elegans	saposin-like type region 1 family protein	3	C:GO:0005764; F:GO:0005488; P:GO:0006665	-		IPR007856; IPR008138; IPR008139; IPR011001; PTHR11480 (PANTHER), PTHR11480:SF2 (PANTHER)
Caenorhabditis elegans	saposin-like type region 1 family protein	3	C:GO:0005764; F:GO:0005488; P:GO:0006665	-		IPR007856; IPR008138; IPR008139; IPR011001; PTHR11480 (PANTHER), PTHR11480:SF2 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	lysocardiolipin acyltransferase 1	3	F:GO:0005515; C:GO:0044464; F:GO:0016740	-		PTHR10983 (PANTHER), PTHR10983:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	smad anchor for receptor activation	1	F:GO:0046872	-		IPR000306; IPR011011; IPR013083; PTHR22835 (PANTHER), PTHR22835:SF12 (PANTHER)
Brugia malayi	structural mainte-nce of chromosomes 2	10	C:GO:0005737; P:GO:0044403; C:GO:0000796; P:GO:0007076; P:GO:0055114; F:GO:0005524; C:GO:0005634; F:GO:0046982; P:GO:0051301; F:GO:0032440	-	EC:1.3.1.74	IPR003395; G3DSA:3.40.50.300 (GENE3D), PTHR18937 (PANTHER), PTHR18937:SF9 (PANTHER), SSF52540 (SUPERFAMILY)
Macaca mulatta	loc400590 protein	0				-
Brugia malayi	nucleotide-binding head-stalk	0		P:GO:0007018; F:GO:0030246; C:GO:0016020; F:GO:0008565; C:GO:0000139; C:GO:0005874; F:GO:0000166; C:GO:0005737; F:GO:0005524; F:GO:0003777; P:GO:0005975; F:GO:0003824; F:GO:0003774; P:GO:0006886; P:GO:0048280; F:GO:0005488		PD936484 (PRODOM)

Loa loa	dicer-1	15	P:GO:0007279; F:GO:0005515; C:GO:0016442; P:GO:0033227; P:GO:0042078; P:GO:0048813; P:GO:0035087; P:GO:0030422; C:GO:0005737; P:GO:0007367; F:GO:0003723; P:GO:0045448; F:GO:0016443; P:GO:0031054; C:GO:0005634	-		IPR000999; IPR001159; PTHR14950 (PANTHER), PTHR14950:SF3 (PANTHER), SSF54768 (SUPERFAMILY)
Caenorhabditis elegans	protein	0				IPR012936; PTHR10984 (PANTHER), PTHR10984:SF1 (PANTHER)
	-	0				-
Caenorhabditis elegans	rhodanese domain protein	0		C:GO:0005739; F:GO:0004792; C:GO:0009507; F:GO:0016740; P:GO:0008272; F:GO:0016784; F:GO:0016783; P:GO:0007568		IPR001763; PTHR11364 (PANTHER)
Caenorhabditis briggsae	protein sidekick	3	C:GO:0016021; P:GO:0007155; F:GO:0016740	-		-
	-	0				-
Drosophila willistoni	zinc finger protein	0		F:GO:0003676; P:GO:0045449; F:GO:0008270; F:GO:0030528; C:GO:0005634; C:GO:0005622		IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)
Drosophila willistoni	zinc finger protein	0		F:GO:0003676; P:GO:0045449; F:GO:0008270; F:GO:0030528; C:GO:0005634; C:GO:0005622		IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Nippostrongylus brasiliensis	elegans protein confirmed by transcript evidence	1	P:GO:0009792	-		IPR003677; PTHR21593 (PANTHER)
	-	0				-

Caenorhabditis elegans	iator family member (mdt-15)	16	P:GO:0030730; P:GO:0040010; P:GO:0008340; P:GO:0006357; P:GO:0000003; F:GO:0016455; P:GO:0002119; P:GO:0019217; P:GO:0040011; P:GO:0006898; C:GO:0016592; F:GO:0035257; F:GO:0003713; P:GO:0045893; P:GO:0009792; P:GO:0040014	-		IPR019087; PTHR23189 (PANTHER), PTHR23189:SF1 (PANTHER)
Caenorhabditis elegans	iator family member (mdt-15)	16	P:GO:0030730; P:GO:0040010; P:GO:0008340; P:GO:0006357; P:GO:0000003; F:GO:0016455; P:GO:0002119; P:GO:0019217; P:GO:0040011; P:GO:0006898; C:GO:0016592; F:GO:0035257; F:GO:0003713; P:GO:0045893; P:GO:0009792; P:GO:0040014	-		IPR019087; PTHR23189 (PANTHER), PTHR23189:SF1 (PANTHER)
Haemonchus contortus	metalloprotease 1 precursor	2	F:GO:0046872; F:GO:0008237	-		IPR001506; IPR006026; IPR013032; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG07208 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	klraq motif-containing protein 1	0		F:GO:0003674; C:GO:0005575		IPR019343; PTHR21448 (PANTHER)
Loa loa	mgc81609 protein	3	P:GO:0050873; C:GO:0016020; C:GO:0005737	-		IPR019144; PTHR21650 (PANTHER), PTHR21650:SF3 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	carbonic anhydrase 2	4	P:GO:0006950; P:GO:0000003; P:GO:0040011; F:GO:0016829	-		IPR001148; IPR018425

Caenorhabditis elegans	hydroxysteroid (17-beta) dehydroge-se 10	19	F:GO:0008667; C:GO:0005743; P:GO:0033327; P:GO:0055114; P:GO:0040007; F:GO:0018454; P:GO:0040035; F:GO:0042802; F:GO:0001540; F:GO:0005496; P:GO:0006508; P:GO:0007569; F:GO:0051287; P:GO:0002119; P:GO:0040017; F:GO:0004303; P:GO:0009239; P:GO:0051289; C:GO:0005783	-	EC:1.3.1.28; EC:1.1.1.36; EC:1.1.1.62	IPR000169; IPR002198; IPR002347; IPR016040; IPR020904; PTHR19410:SF78 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	hydroxysteroid (17-beta) dehydroge-se 10	19	F:GO:0008667; C:GO:0005743; P:GO:0033327; P:GO:0055114; P:GO:0040007; F:GO:0018454; P:GO:0040035; F:GO:0042802; F:GO:0001540; F:GO:0005496; P:GO:0006508; P:GO:0007569; F:GO:0051287; P:GO:0002119; P:GO:0040017; F:GO:0004303; P:GO:0009239; P:GO:0051289; C:GO:0005783	-	EC:1.3.1.28; EC:1.1.1.36; EC:1.1.1.62	IPR000169; IPR002198; IPR002347; IPR016040; IPR020904; PTHR19410:SF78 (PANTHER), SSF51735 (SUPERFAMILY)
Trichomonas vaginalis G3	hypothetical protein [Trichomo-s vagi-lis G3]	0				-
synthetic construct	histone-lysine n-methyltransferase setmar	10	P:GO:0016568; F:GO:0004519; P:GO:0006313; F:GO:0003677; F:GO:0018024; C:GO:0005634; F:GO:0008270; F:GO:0004803; P:GO:0015074; P:GO:0006281	-	EC:2.1.1.43	IPR001888; IPR002622; IPR012287; PTHR23016 (PANTHER)
synthetic construct	histone-lysine n-methyltransferase setmar	5	F:GO:0046872; P:GO:0006313; F:GO:0016787; F:GO:0008168; F:GO:0004803	-	EC:2.1.1.0	-

Ascaris lumbricoides	cytoplasmic intermediate filament protein	13	C:GO:0005737; P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0018996; F:GO:0005515; P:GO:0040002; C:GO:0005882; P:GO:0008340; P:GO:0040011; P:GO:0040007; P:GO:0006898; F:GO:0005198	-		-
Caenorhabditis elegans	tyrosine-protein ki-se csk	6	F:GO:0035014; P:GO:0006468; F:GO:0004715; C:GO:0005942; F:GO:0005515; F:GO:0005524	-	EC:2.7.10.2	IPR000719; IPR000980; IPR001245; IPR001720; IPR008266; IPR011009; IPR015778; IPR017441; IPR020635; IPR020685; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), SSF55550 (SUPERFAMILY)
Caenorhabditis elegans	small subunit ribosomal protein 20	4	F:GO:0003735; F:GO:0003723; C:GO:0015935; P:GO:0006412	-	EC:3.6.5.3	-
	-	0				-
Caenorhabditis briggsae	b-box zinc finger family protein	3	F:GO:0046872; P:GO:0050794; C:GO:0005634	-		IPR000408; IPR009091; PTHR12846 (PANTHER), PTHR12846:SF2 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-ctns-1 protein	4	P:GO:0006810; C:GO:0043231; C:GO:0044444; C:GO:0016020	-		IPR006603; PTHR13131 (PANTHER), PF04193 (PFAM), SignalP (SIGNALP)
Caenorhabditis elegans	me-ge a trois 1	19	P:GO:0006367; P:GO:0000718; P:GO:0044236; F:GO:0008094; P:GO:0051592; F:GO:0047485; C:GO:0005737; F:GO:0046872; P:GO:0021591; C:GO:0005675; P:GO:0048661; P:GO:0006368; P:GO:0050790; P:GO:0045944; F:GO:0008353; F:GO:0008080; P:GO:0043066; P:GO:0007049; P:GO:0007512	-	EC:2.7.11.23	SignalP (SIGNALP)

Caenorhabditis elegans	me-ge a trois 1	17	P:GO:0006367; P:GO:0000718; P:GO:0044236; F:GO:0008094; P:GO:0051592; F:GO:0047485; C:GO:0005737; P:GO:0000079; P:GO:0021591; C:GO:0005675; P:GO:0048661; P:GO:0006368; P:GO:0045944; F:GO:0008353; F:GO:0008080; P:GO:0043066; P:GO:0007512	-	EC:2.7.11.23	IPR001841; IPR004575; IPR013083; IPR015877; IPR017907; PTHR12683:SF5 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis elegans	me-ge a trois 1	19	P:GO:0006367; P:GO:0000718; P:GO:0044236; F:GO:0008094; P:GO:0051592; F:GO:0047485; C:GO:0005737; F:GO:0046872; P:GO:0021591; C:GO:0005675; P:GO:0048661; P:GO:0006368; P:GO:0050790; P:GO:0045944; F:GO:0008353; F:GO:0008080; P:GO:0043066; P:GO:0007049; P:GO:0007512	-	EC:2.7.11.23	SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein Y37E11AL.3 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	hypothetical protein Y37E11AL.3 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	briggsae cbr-pqn-85 protein	2	C:GO:0032116; P:GO:0034088	-		IPR011989; IPR016024; PTHR21704 (PANTHER), PTHR21704:SF5 (PANTHER)
Caenorhabditis elegans	briggsae cbr-nsy-1 protein	4	P:GO:0006468; F:GO:0005515; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	-
Ostertagia ostertagi	secreted protein 5 precursor	0		P:GO:0040011; P:GO:0006898; C:GO:0005576		IPR001283; IPR014044; PTHR10334:SF5 (PANTHER), SignalP (SIGNALP)
	-	0				-
Loa loa	briggsae cbr-tre-2 protein	3	P:GO:0005991; C:GO:0005886; F:GO:0004555	-	EC:3.2.1.28	IPR001661; IPR008928; IPR018232; PTHR23403:SF1 (PANTHER)
Pongo abelii	interferon regulatory factor 2 binding protein 2	0		P:GO:0000122; P:GO:0045449; F:GO:0003714; C:GO:0005634		IPR022750
Loa loa	gyf domain containing protein	0				PTHR14445 (PANTHER), PTHR14445:SF9 (PANTHER)

Loa loa	gyf domain containing protein	0				PTHR14445 (PANTHER), PTHR14445:SF9 (PANTHER)
Caenorhabditis elegans	adenine phosphoribosyltransferase	4	C:GO:0005737; F:GO:0003999; P:GO:0009116; P:GO:0006168	-	EC:2.4.2.7	IPR000836; G3DSA:3.40.50.2020 (GENE3D), SignalP (SIGNALP), SSF53271 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Mus musculus	ribosomal protein l15	5	C:GO:0005840; F:GO:0003735; F:GO:0003723; C:GO:0005829; P:GO:0006414	-		IPR000439; IPR012678; IPR020925
Caenorhabditis elegans	beta-lactamase family protein	0				IPR001466; IPR012338; G3DSA:3.40.710.10 (GENE3D), PTHR10566 (PANTHER), PTHR10566:SF6 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-gly-10 protein	0		F:GO:0016740; C:GO:0016021; C:GO:0016020; F:GO:0005529; C:GO:0000139; F:GO:0016757; F:GO:0003674; C:GO:0005794; C:GO:0005575; F:GO:0046872; P:GO:0008150; F:GO:0004653		SignalP (SIGNALP)
Angiostrongylus cantonensis	briggsae cbr-npp-4 protein	0		C:GO:0005643; F:GO:0003735; P:GO:0015031; P:GO:0006810; F:GO:0003676; P:GO:0006412; F:GO:0008270; C:GO:0005840; F:GO:0017056; C:GO:0005622; F:GO:0005515; P:GO:0008150		PTHR13437 (PANTHER)
Caenorhabditis elegans	heterotrimeric guanine nucleotide-binding protein beta subunit	3	F:GO:0004871; P:GO:0007165; F:GO:0004402	-	EC:2.3.1.48	IPR001632; IPR001680; IPR011046; IPR015943; IPR016346; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR19850 (PANTHER)
Caenorhabditis elegans	udp-galactose transporter family protein	5	C:GO:0000139; P:GO:0015780; F:GO:0005338; F:GO:0005351; C:GO:0016021	-		IPR007271; PTHR10231:SF13 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	dehydroge-se reductase sdr family member 1	4	P:GO:0055114; P:GO:0040010; F:GO:0016491; F:GO:0005488	-		IPR002198; IPR002347; IPR016040; IPR020904; PTHR19410:SF32 (PANTHER), SSF51735 (SUPERFAMILY)

Caenorhabditis elegans	short-chain dehydroge-se reductase sdr	4	P:GO:0055114; F:GO:0016491; F:GO:0005488; P:GO:0040010	-		IPR002198; IPR002347; IPR016040; PTHR19410:SF32 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	dehydroge-se reductase sdr family member 1	3	P:GO:0040010; P:GO:0008152; F:GO:0003824	-		IPR002198; IPR002347; IPR016040; IPR020904; PTHR19410:SF32 (PANTHER), SSF51735 (SUPERFAMILY)
Loa loa	notch sig-ling pathway homolog protein 1	1	F:GO:0005488	-		IPR001650; PTHR12706 (PANTHER), SSF52540 (SUPERFAMILY)
Loa loa	notch sig-ling pathway homolog protein 1	1	F:GO:0005488	-		IPR001650; PTHR12706 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein F25F8.1 [Caenorhabditis elegans]	0				IPR011042; SSF101898 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein E04F6.6 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	zip zinc transporter family protein	3	P:GO:0009792; C:GO:0016020; P:GO:0030001	-		IPR003689; PTHR11040 (PANTHER), PTHR11040:SF8 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	protein ki-se c alpha binding protein	1	F:GO:0005515	-		IPR010504; PTHR12141 (PANTHER), PTHR12141:SF2 (PANTHER), SSF103657 (SUPERFAMILY)
Caenorhabditis briggsae	nedd8 activating enzyme e1 subunit 1	6	C:GO:0005626; P:GO:0006917; P:GO:0031574; F:GO:0019781; P:GO:0045116; F:GO:0046982	-		IPR009036; IPR016040; PTHR10953 (PANTHER), PTHR10953:SF29 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	motor axon guidance family member (max-1)	2	P:GO:0008340; P:GO:0040010	-		IPR001849; IPR011993; PTHR22903 (PANTHER), PTHR22903:SF2 (PANTHER), SSF50729 (SUPERFAMILY)
Macaca mulatta	ribosomal protein l37	6	F:GO:0046872; F:GO:0003735; F:GO:0005515; C:GO:0022625; F:GO:0019843; P:GO:0006414	-		IPR001569; IPR011331; IPR011332; IPR018267
Caenorhabditis briggsae	serine threonine-protein ki-se chk1	14	P:GO:0040010; P:GO:0006281; F:GO:0004672; P:GO:0000086; P:GO:0006975; P:GO:0000003; P:GO:0010171; P:GO:0002119; F:GO:0005515; C:GO:0005657; P:GO:0040011; C:GO:0005654; P:GO:0009792; P:GO:0031572	-		IPR000719; IPR008271; IPR011009; IPR015729; IPR017441; IPR017442; IPR020636; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D)
Caenorhabditis briggsae	briggsae cbr-him-17 protein	0				-
	-	0				-

Caenorhabditis elegans	cysteinyl-tr- cytoplasmic	6	P:GO:0006423; F:GO:0005524; C:GO:0005829; F:GO:0000049; F:GO:0042803; F:GO:0004817	-	EC:6.1.1.16	IPR009080; IPR014729; IPR015803; SSF52374 (SUPERFAMILY)
Brugia malayi	cysteinyl-tr- synthetase	3	F:GO:0004812; P:GO:0006418; F:GO:0000166	-		IPR009080; IPR015803
Caenorhabditis elegans	cysteinyl-tr- synthetase	5	C:GO:0005737; P:GO:0006423; F:GO:0005524; F:GO:0000049; F:GO:0004817	-	EC:6.1.1.16	IPR009080; IPR014729; IPR015803; SSF52374 (SUPERFAMILY)
Caenorhabditis briggsae	nuclear prelamin a recognition factor-like	5	F:GO:0005488; P:GO:0032364; P:GO:0016226; P:GO:0045449; P:GO:0001666	-		IPR004108; IPR009016; G3DSA:3.40.50.1780 (GENE3D), PTHR11615 (PANTHER), PTHR11615:SF31 (PANTHER)
Ixodes scapularis	fun14 domain containing 1	1	P:GO:0009792	-		IPR007014; PTHR21346 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	adp-ribosylation factor gtpase activating protein 1	5	F:GO:0046872; P:GO:0016044; P:GO:0048193; F:GO:0005096; C:GO:0005794	-		IPR001164; PTHR23180 (PANTHER), PTHR23180:SF16 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	adp-ribosylation factor gtpase activating protein 1	4	P:GO:0016044; P:GO:0048193; F:GO:0005096; C:GO:0005794	-		-
Caenorhabditis elegans	hypothetical kda protein in chromosome	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	gpn-loop gtpase 3	4	P:GO:0009792; C:GO:0043234; F:GO:0032555; F:GO:0005515	-		IPR004130; G3DSA:3.40.50.300 (GENE3D), PTHR21231 (PANTHER), PTHR21231:SF4 (PANTHER), SSF52540 (SUPERFAMILY)
Brugia malayi	protein ki-se domain containing protein	3	F:GO:0005488; F:GO:0004672; P:GO:0000003	-		-
Brugia malayi	protein ki-se domain containing protein	8	C:GO:0005929; C:GO:0030425; F:GO:0005515; P:GO:0034606; F:GO:0004672; C:GO:0030424; P:GO:0034608; C:GO:0043025	-		-
Caenorhabditis elegans	udp-glucuronic acid decarboxylase	6	C:GO:0032580; F:GO:0048040; P:GO:0044237; C:GO:0016021; F:GO:0050662; C:GO:0005739	-	EC:4.1.1.35	IPR001509; IPR016040; G3DSA:3.90.25.10 (GENE3D), PTHR10366 (PANTHER), PTHR10366:SF35 (PANTHER), SSF51735 (SUPERFAMILY)

Caenorhabditis elegans	briggsae cbr-tol-1 protein	5	C:GO:0016021; P:GO:0007165; P:GO:0045087; F:GO:0005515; F:GO:0004888	-		-
Caenorhabditis elegans	proteasome (macropain) activator subunit 3 (pa28 gamma ki)	12	F:GO:0002039; N:GO:0061136; P:GO:0051436; P:GO:0042981; P:GO:0051437; F:GO:0070215; C:GO:0008537; F:GO:0042802; P:GO:0031145; F:GO:0003824; N:GO:0061133; C:GO:0016020	-		SignalP (SIGNALP)
Caenorhabditis elegans	proteasome (macropain) activator subunit 3 (pa28 gamma ki)	12	F:GO:0002039; N:GO:0061136; P:GO:0051436; P:GO:0042981; P:GO:0051437; F:GO:0070215; C:GO:0008537; F:GO:0042802; P:GO:0031145; F:GO:0003824; N:GO:0061133; C:GO:0016020	-		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Ancylostoma Ceylanicum	macrophage migration inhibitory factor	1	F:GO:0003824	-		-
Caenorhabditis elegans	amidinotransferase	2	C:GO:0005737; F:GO:0016813	-	EC:3.5.3.0	G3DSA:3.75.10.10 (GENE3D), PTHR12737 (PANTHER), PTHR12737:SF1 (PANTHER), SSF55909 (SUPERFAMILY)
Caenorhabditis elegans	amidinotransferase	2	C:GO:0005737; F:GO:0016813	-	EC:3.5.3.0	IPR003198; G3DSA:3.75.10.10 (GENE3D), PTHR12737 (PANTHER), PTHR12737:SF1 (PANTHER), SSF55909 (SUPERFAMILY)
Caenorhabditis elegans	lor sdh bifunctio-l protein conserved domain protein	2	C:GO:0005737; F:GO:0016813	-	EC:3.5.3.0	IPR003198; G3DSA:3.75.10.10 (GENE3D), PTHR12737 (PANTHER), PTHR12737:SF1 (PANTHER), SSF55909 (SUPERFAMILY)
Caenorhabditis briggsae	gtp binding protein 1	5	F:GO:0005525; P:GO:0007165; C:GO:0030529; P:GO:0006955; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000795; IPR004160; IPR004161; IPR009000; IPR009001; G3DSA:2.40.30.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF6 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	gtp binding protein 1	5	F:GO:0005525; P:GO:0007165; C:GO:0030529; P:GO:0006955; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000795; IPR004160; IPR004161; IPR009000; IPR009001; G3DSA:2.40.30.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF6 (PANTHER), SSF52540 (SUPERFAMILY)

Caenorhabditis briggsae	protein couch potato	3	F:GO:0005515; F:GO:0003676; F:GO:0000166	-		IPR000504; IPR012677; PTHR12742 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	protein couch potato	3	F:GO:0005515; F:GO:0003676; F:GO:0000166	-		IPR000504; IPR012677; PTHR12742 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	protein ki-se domain containing protein	4	P:GO:0001700; P:GO:0007283; F:GO:0005488; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR008266; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR23257 (PANTHER)
Caenorhabditis elegans	protein ki-se family member (kin-32)	23	F:GO:0004713; P:GO:0032879; P:GO:0051234; P:GO:0050767; P:GO:0007268; P:GO:0043062; C:GO:0043232; C:GO:0016323; P:GO:0051129; C:GO:0030054; P:GO:0016477; P:GO:0007409; F:GO:0000166; P:GO:0040008; F:GO:0005515; P:GO:0006468; P:GO:0048523; N:GO:0071844; P:GO:0048522; P:GO:0065008; P:GO:0007166; P:GO:0048514; P:GO:0051093	-	EC:2.7.10.0	IPR000299; IPR019748; IPR019749; IPR020685; IPR020773; SSF50729 (SUPERFAMILY), SSF54236 (SUPERFAMILY)
Brugia malayi	transformation transcription domain-associated protein	3	C:GO:0005700; P:GO:0050794; C:GO:0000123	-		IPR010916
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	superkiller viralicidic activity 2-like	3	F:GO:0003676; F:GO:0005524; F:GO:0008026	-		IPR001650; IPR011545; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR11752 (PANTHER), PTHR11752:SF2 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	superkiller viralicidic activity 2-like	3	F:GO:0003676; F:GO:0005524; F:GO:0008026	-		IPR001650; IPR011545; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR11752 (PANTHER), PTHR11752:SF2 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	adipor-like receptor	6	F:GO:0042562; C:GO:0016021; P:GO:0006355; P:GO:0009755; P:GO:0007165; P:GO:0019395	-		IPR004254; PTHR20855:SF13 (PANTHER)

Caenorhabditis elegans	d-k protein	2	C:GO:0044464; F:GO:0000166	-		IPR001023; IPR013126; G3DSA:3.30.420.40 (GENE3D), PTHR19375:SF7 (PANTHER), SSF53067 (SUPERFAMILY)
Caenorhabditis elegans	d-k protein	2	C:GO:0044464; F:GO:0000166	-		IPR001023; IPR013126; G3DSA:3.30.420.40 (GENE3D), PTHR19375:SF7 (PANTHER), SSF53067 (SUPERFAMILY)
Caenorhabditis elegans	d-k protein	2	C:GO:0044464; F:GO:0000166	-		IPR001023; IPR013126; G3DSA:3.30.420.40 (GENE3D), PTHR19375:SF7 (PANTHER), SSF53067 (SUPERFAMILY)
Homo sapiens	ribosomal protein l4	5	F:GO:0003735; F:GO:0003723; F:GO:0005515; C:GO:0022625; P:GO:0006414	-		PTHR19431 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	nucleoporin 210kda-like	0		C:GO:0016021; C:GO:0016020		PTHR23019 (PANTHER)
Ancylostoma duodenale	manganese superoxide dismutase	6	P:GO:0046686; F:GO:0046872; P:GO:0055114; P:GO:0006801; F:GO:0004784; P:GO:0051597	-	EC:1.15.1.1	IPR001189; IPR019831; IPR019832; IPR019833; PTHR11404:SF5 (PANTHER)
Caenorhabditis briggsae	cell division control protein	11	P:GO:0000910; P:GO:0040007; P:GO:0045449; P:GO:0000003; P:GO:0018996; F:GO:0003677; P:GO:0002119; P:GO:0009792; P:GO:0001703; C:GO:0005634; P:GO:0006974	-		IPR001005; IPR009057; IPR012287; IPR014778; IPR015495; IPR017930; PTHR10641:SF17 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG14950 [Caenorhabditis briggsae]	0		P:GO:0040035; P:GO:0002119; P:GO:0040007; P:GO:0040018		-
Caenorhabditis elegans	Hypothetical protein W05F2.4a [Caenorhabditis elegans]	1	P:GO:0032501	-		-
Caenorhabditis brenneri	calsyntenin 1	9	C:GO:0043231; C:GO:0032809; C:GO:0016021; C:GO:0005615; P:GO:0007155; F:GO:0005515; C:GO:0045211; P:GO:0008355; P:GO:0009792	-		PTHR14139 (PANTHER)
Caenorhabditis elegans	rt15_caeel ame: full=28s ribosomal protein mitochondrial short=mrp-s15 short=s15mt flags: precursor	0				-

Caenorhabditis elegans	fbxo11 protein	5	P:GO:0007605; F:GO:0005515; P:GO:0016567; F:GO:0004842; F:GO:0008270	-	EC:6.3.2.19	IPR006626; IPR011050; IPR012334; IPR022441; PTHR22990 (PANTHER), PTHR22990:SF6 (PANTHER)
Loa loa	amp-activated protein gamma regulatory subunit	2	P:GO:0040035; P:GO:0040011	-		IPR000644; IPR013785; PTHR13780 (PANTHER), SSF54631 (SUPERFAMILY)
Brugia malayi	ph domain containing protein	0				-
Caenorhabditis elegans	mitochondrial 28s ribosomal protein s33	5	P:GO:0009792; P:GO:0002119; C:GO:0005840; P:GO:0008340; P:GO:0040007	-		-
Caenorhabditis briggsae	briggsae cbr-elpc-2 protein	1	C:GO:0031981	-		IPR001680; IPR007087; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR13729 (PANTHER)
	-	0				-
Loa loa	zinc c2h2 type family protein	1	F:GO:0005488	-		IPR000210; IPR007087; IPR011333; IPR013069; IPR013087; IPR015880; PTHR23229 (PANTHER), PTHR23229:SF13 (PANTHER), SSF57667 (SUPERFAMILY)
Loa loa	zinc c2h2 type family protein	1	F:GO:0005488	-		IPR000210; IPR007087; IPR011333; IPR013069; IPR013087; IPR015880; PTHR23229 (PANTHER), PTHR23229:SF13 (PANTHER), SSF57667 (SUPERFAMILY)
Brugia malayi	fragile site-associated protein	0				IPR018863
Caenorhabditis briggsae	hypothetical tyrosi-se-like protein in chromosome	4	F:GO:0005515; F:GO:0046872; P:GO:0008152; F:GO:0016491	-		IPR002227; IPR008922; PTHR11474 (PANTHER)
Caenorhabditis briggsae	mitochondrial glutamate	4	F:GO:0005488; P:GO:0055085; P:GO:0008340; C:GO:0016021	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF23 (PANTHER)
	-	0				-
	-	0				-
Trypanosoma cruzi strain CL Brener	abc permease atp-binding protein	0		F:GO:0005524; P:GO:0006397		-
Nematostella vectensis	abc permease atp-binding protein	0		F:GO:0005524		-
	-	0				-
Caenorhabditis briggsae	catechol-o-methyltransferase domain-containing protein 1	1	F:GO:0008171	-		IPR002935; G3DSA:3.40.50.150 (GENE3D), SSF53335 (SUPERFAMILY)
Brugia malayi	disorganized muscle protein 1	5	C:GO:0030018; F:GO:0008307; P:GO:0007498; F:GO:0005515; F:GO:0004672	-		IPR003598; IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF7 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
Loa loa	serine threonine-protein phosphatase dullard-a	5	C:GO:0005789; P:GO:0006998; F:GO:0004722; C:GO:0005635; C:GO:0016021	-		-

Ixodes scapularis	nuclear hormone receptor	0		F:GO:0043565; F:GO:0003700; F:GO:0003677; C:GO:0005634; F:GO:0004879; F:GO:0008270; P:GO:0006355; F:GO:0004872; F:GO:0046872; P:GO:0006350; F:GO:0003707; P:GO:0045449		SignalP (SIGNALP)
Caenorhabditis elegans	family with sequence similarity member a	0		C:GO:0005789; F:GO:0003674; C:GO:0033116; C:GO:0016021; C:GO:0016020; P:GO:0008150		PTHR13167 (PANTHER)
Caenorhabditis elegans	alpha-glucosidase ii	7	F:GO:0004553; P:GO:0005975; P:GO:0009792; F:GO:0030246; P:GO:0040007; F:GO:0005515; P:GO:0002119	-	EC:3.2.1.0	IPR000322; IPR017853; PTHR22762:SF7 (PANTHER), SSF51011 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-apt-10 protein	0		C:GO:0030131; F:GO:0008060; P:GO:0032312; P:GO:0016192; F:GO:0008270; P:GO:0006886; P:GO:0006897; F:GO:0005515		-
Caenorhabditis elegans	sel1l protein	2	C:GO:0016020; F:GO:0005515	-		IPR006597; IPR011990; PTHR11102 (PANTHER), PTHR11102:SF11 (PANTHER), SignalP (SIGNALP), SSF81901 (SUPERFAMILY)
Caenorhabditis elegans	endou_caeel ame: full=poly -specific endoribonuclease homolog ame: full=protein endou ame: full=uridylate-specific endoribonuclease homolog flags: precursor	2	F:GO:0004521; F:GO:0003723	-		IPR018998; SSF142877 (SUPERFAMILY)
Caenorhabditis elegans	methylmalonic aciduria (cobalamin deficiency) cblc with homocystinuria	0		C:GO:0005739; F:GO:0031419; P:GO:0008150		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	r- binding homolog 1	2	P:GO:0007126; P:GO:0009792	-		IPR001159; IPR014720; PTHR10910 (PANTHER), PTHR10910:SF2 (PANTHER), SSF54768 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-

	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR011680; PTHR12394:SF1 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR011680; PTHR12394:SF1 (PANTHER)
Caenorhabditis elegans	metal-dependent phosphohydrolase hd domain-containing protein	1	F:GO:0003824	-		IPR003607; IPR006674; G3DSA:1.10.3210.10 (GENE3D), PTHR11845 (PANTHER), SSF109604 (SUPERFAMILY)
Caenorhabditis elegans	cgmp-dependent protein ki-se	4	P:GO:0006468; F:GO:0005524; P:GO:0000003; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR22985 (PANTHER), PTHR22985:SF90 (PANTHER)
Caenorhabditis elegans	cgmp-dependent protein ki-se	4	P:GO:0006468; F:GO:0005524; P:GO:0000003; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22985 (PANTHER), PTHR22985:SF90 (PANTHER)
Caenorhabditis elegans	formin homology 2 domain containing 3	2	P:GO:0030036; F:GO:0003779	-		IPR010472; IPR014768; IPR016024; PTHR23213 (PANTHER), PTHR23213:SF3 (PANTHER)
Caenorhabditis elegans	formin homology 2 domain containing 3	3	P:GO:0030036; C:GO:0044424; F:GO:0003779	-		IPR014768; IPR016024; PTHR23213 (PANTHER), PTHR23213:SF3 (PANTHER)
	-	0				-
Ancylostoma ceylanicum	glutamate cysteine ligase	19	F:GO:0005515; F:GO:0043531; P:GO:0006916; P:GO:0006534; P:GO:0045454; F:GO:0016595; F:GO:0050662; F:GO:0000287; P:GO:0009408; P:GO:0016481; P:GO:0006536; P:GO:0032268; P:GO:0006750; P:GO:0009725; P:GO:0050880; C:GO:0044444; F:GO:0005524; P:GO:0006979; F:GO:0004357	-	EC:6.3.2.2	IPR004308; SSF55931 (SUPERFAMILY)
Caenorhabditis elegans	mitochondrial aminomethyltransferase	5	P:GO:0006546; F:GO:0004047; C:GO:0005811; F:GO:0008483; C:GO:0005960	-	EC:2.1.2.10; EC:2.6.1.0	IPR006222; PTHR13847 (PANTHER), PTHR13847:SF5 (PANTHER), SSF103025 (SUPERFAMILY)
	-	0				-
	-	0				-

Harpegnathos saltator	dehydroge-se reductase (sdr family) member 7	0		P:GO:0055114; F:GO:0005488; F:GO:0016491; P:GO:0008152; F:GO:0003824; C:GO:0005575		IPR002198; IPR002347; IPR016040; IPR020904; PTHR19410:SF44 (PANTHER), SSF51735 (SUPERFAMILY)
Xenopus laevis	dehydroge-se reductase (sdr family) member 7	0		P:GO:0055114; F:GO:0005488; F:GO:0016491; P:GO:0008152; F:GO:0003824; C:GO:0005575		IPR002198; IPR002347; IPR016040; IPR020904; PTHR19410:SF44 (PANTHER), SSF51735 (SUPERFAMILY)
Loa loa	nuclear factor i	3	P:GO:0010552; P:GO:0010553; F:GO:0003700	-		IPR000647; IPR020604
Brugia malayi	nuclear factor i	3	P:GO:0010552; P:GO:0010553; F:GO:0003700	-		IPR000647; IPR020604
Caenorhabditis elegans	briggsae cbr-tag-264 protein	7	C:GO:0043229; P:GO:0040035; P:GO:0002119; C:GO:0044444; P:GO:0040039; P:GO:0040018; P:GO:0006974	-		IPR010793
	-	0				-
Caenorhabditis elegans	Hypothetical protein D1014.2 [Caenorhabditis elegans]	2	P:GO:0007186; C:GO:0016021	-		-
Caenorhabditis elegans	variant sh3 domain containing protein	10	P:GO:0051239; P:GO:0048514; F:GO:0004435; F:GO:0004871; P:GO:0009395; P:GO:0048646; P:GO:0030154; F:GO:0005515; P:GO:0007165; P:GO:0007275	-	EC:3.1.4.11	IPR011993; PTHR10336 (PANTHER), PTHR10336:SF22 (PANTHER)
Loa loa	dead (asp-glu-ala-asp) box polypeptide 52	4	F:GO:0004386; F:GO:0003676; P:GO:0006364; F:GO:0000166	-		IPR001650; IPR011545; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF21 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	calponin transgelin	4	F:GO:0003779; P:GO:0040007; P:GO:0006939; P:GO:0002119	-		-
Caenorhabditis briggsae	diphthamide biosynthesis protein 2	1	P:GO:0040002	-		IPR002728; IPR010014
Caenorhabditis elegans	diphthamide biosynthesis protein 2	1	P:GO:0040002	-		IPR002728; IPR010014
	-	0				SignalP (SIGNALP)
	-	0				-

Loa loa	protein jade-1	0		F:GO:0016740; F:GO:0008168; C:GO:0005634; P:GO:0006915; C:GO:0005737; P:GO:0000003; F:GO:0003674; F:GO:0008270; F:GO:0018024; C:GO:0005575; F:GO:0005515; F:GO:0046872; P:GO:0006350; P:GO:0008150; P:GO:0045449		IPR001965; IPR011011; IPR013083; IPR017956; IPR019786; IPR019787; PTHR13793 (PANTHER), PTHR13793:SF24 (PANTHER)
Loa loa	protein jade-1	0		F:GO:0016740; F:GO:0008168; C:GO:0005634; P:GO:0006915; C:GO:0005737; P:GO:0000003; F:GO:0003674; F:GO:0008270; F:GO:0018024; C:GO:0005575; F:GO:0005515; F:GO:0046872; P:GO:0006350; P:GO:0008150; P:GO:0045449		IPR001965; IPR011011; IPR013083; IPR017956; IPR019786; IPR019787; PTHR13793 (PANTHER), PTHR13793:SF24 (PANTHER)
Brugia malayi	immunosuppressive ovarian message protein	0		P:GO:0000281; F:GO:0008061; P:GO:0051301; P:GO:0009792; P:GO:0007275; P:GO:0009790; C:GO:0005576; P:GO:0030703; F:GO:0005515; P:GO:0007049; P:GO:0006030		IPR002557; G3DSA:2.170.140.10 (GENE3D), PTHR23301 (PANTHER)
Brugia malayi	immunosuppressive ovarian message protein	0		P:GO:0000281; F:GO:0008061; P:GO:0051301; P:GO:0009792; P:GO:0007275; P:GO:0009790; C:GO:0005576; P:GO:0030703; F:GO:0005515; P:GO:0007049; P:GO:0006030		-

Brugia malayi	immunosuppressive ovarian message protein	0		P:GO:0000281; F:GO:0008061; P:GO:0051301; P:GO:0009792; P:GO:0007275; P:GO:0009790; C:GO:0005576; P:GO:0030703; F:GO:0005515; P:GO:0007049; P:GO:0006030		IPR002557; G3DSA:2.170.140.10 (GENE3D), PTHR23301 (PANTHER)
Caenorhabditis briggsae	uncoordi-ted family member (unc-11)	4	F:GO:0005545; C:GO:0005905; F:GO:0005515; P:GO:0006898	-		PTHR22951 (PANTHER), PTHR22951:SF3 (PANTHER)
Caenorhabditis elegans	zygote defective: embryonic lethal family member (zyg-11)	0		F:GO:0005515		G3DSA:3.80.10.10 (GENE3D), SSF52047 (SUPERFAMILY)
Caenorhabditis elegans	40s ribosomal protein s3a	3	P:GO:0044267; C:GO:0005622; F:GO:0016787	-		IPR000938; IPR001394; IPR001593; SSF54001 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Loa loa	isoform b	5	P:GO:0007274; P:GO:0046785; P:GO:0007021; P:GO:0008582; C:GO:0005737	-		IPR000938; PTHR18916 (PANTHER), PTHR18916:SF6 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	d- polymerase eta	8	F:GO:0003887; P:GO:0006468; P:GO:0010224; F:GO:0005515; F:GO:0004672; F:GO:0005524; F:GO:0003684; P:GO:0042276	-	EC:2.7.7.7	IPR001126; IPR017963; PTHR11076:SF11 (PANTHER), SSF56672 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	udp-n-acetylglucosamine transferase subunit alg14 homolog	1	C:GO:0016020	-		IPR013969; G3DSA:3.40.50.2000 (GENE3D), SignalP (SIGNALP)
Caenorhabditis elegans	udp-n-acetylglucosamine transferase subunit alg14 homolog	1	C:GO:0016020	-		IPR013969; G3DSA:3.40.50.2000 (GENE3D), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	probable o-sialoglycoprotein endopeptidase	4	F:GO:0004222; P:GO:0006508; F:GO:0008270; F:GO:0005515	-	EC:3.4.24.0	IPR000905; IPR017861; SSF53067 (SUPERFAMILY)
Caenorhabditis briggsae	abhydrolase domain-containing protein fam108b1	1	F:GO:0016787	-		G3DSA:3.40.50.1820 (GENE3D), PTHR12277 (PANTHER), PTHR12277:SF8 (PANTHER), SSF53474 (SUPERFAMILY)
	-	0				-
Ancylostoma caninum	secreted protein 5 precursor	0		P:GO:0040011; P:GO:0006898; C:GO:0005576		IPR001283; IPR014044; IPR022407; PTHR10334:SF11 (PANTHER)
	-	0				-

Caenorhabditis briggsae	leucine zipper-ef-hand containing transmembrane protein 1	7	P:GO:0009792; P:GO:0042407; C:GO:0005743; P:GO:0040018; F:GO:0005515; P:GO:0000003; P:GO:0006898	-		IPR011685; PTHR14009 (PANTHER), PTHR14009:SF1 (PANTHER)
Caenorhabditis elegans	leucine zipper-ef-hand containing transmembrane protein 1	7	P:GO:0009792; P:GO:0042407; C:GO:0005743; P:GO:0040018; F:GO:0005515; P:GO:0000003; P:GO:0006898	-		IPR011685; PTHR14009 (PANTHER), PTHR14009:SF1 (PANTHER)
Caenorhabditis briggsae	group ii plp decarboxylase	3	F:GO:0030170; P:GO:0019752; F:GO:0016831	-	EC:4.1.1.0	IPR002129; IPR015421; IPR015424; PTHR11999:SF15 (PANTHER)
Caenorhabditis briggsae	mgc84609 protein	3	F:GO:0030170; P:GO:0019752; F:GO:0016831	-	EC:4.1.1.0	IPR002129; IPR015421; IPR015424; PTHR11999:SF15 (PANTHER)
Loa loa	elegans protein partially confirmed by transcript evidence	0		F:GO:0005515		-
Caenorhabditis briggsae	beta chain spectrin	5	F:GO:0008017; C:GO:0016324; F:GO:0003779; P:GO:0000910; P:GO:0006897	-		IPR002017; G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF48 (PANTHER), SSF46966 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	briggsae cbr-scp-1 protein	0		C:GO:0016021; C:GO:0016020; P:GO:0009792		SignalP (SIGNALP)
Loa loa	guanine nucleotide-binding protein g alpha subunit	7	F:GO:0005525; F:GO:0004871; C:GO:0005794; F:GO:0005515; F:GO:0016787; P:GO:0007165; P:GO:0007186	-		-
Loa loa	ser thr protein phosphatase family protein	2	F:GO:0016787; P:GO:0000003	-		IPR004843; IPR006186; G3DSA:3.60.21.10 (GENE3D), PTHR11668:SF16 (PANTHER), SSF56300 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	hypothetical protein F10G8.8 [Caenorhabditis elegans]	1	F:GO:0005515	-		-
Caenorhabditis elegans	briggsae cbr-pgp-9 protein	5	P:GO:0009792; F:GO:0016887; P:GO:0006810; C:GO:0016020; F:GO:0000166	-		IPR001140; IPR011527; IPR017940; G3DSA:1.20.1560.10 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF96 (PANTHER)
Caenorhabditis elegans	multidrug resistance p-glycoprotein	5	P:GO:0009792; F:GO:0042626; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		IPR001140; IPR011527; IPR017940; G3DSA:1.20.1560.10 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF96 (PANTHER)

Caenorhabditis briggsae	carboxypeptidase polypeptide 1	11	P:GO:0006629; C:GO:0005615; F:GO:0004181; F:GO:0005515; F:GO:0001786; P:GO:0051384; P:GO:0016192; P:GO:0006508; F:GO:0008270; F:GO:0005544; F:GO:0005215	-	EC:3.4.17.0	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11532 (PANTHER), PTHR11532:SF5 (PANTHER), SignalP (SIGNALP), SSF53187 (SUPERFAMILY)
Caenorhabditis briggsae	troponin t	3	P:GO:0043050; P:GO:0006952; P:GO:0040017	-		IPR001978; G3DSA:1.20.5.350 (GENE3D), PTHR11521 (PANTHER), PTHR11521:SF1 (PANTHER)
Caenorhabditis elegans	mevalo-te ki-se	10	P:GO:0008340; P:GO:0040007; F:GO:0005524; P:GO:0002119; P:GO:0016310; P:GO:0040011; P:GO:0009792; C:GO:0005737; F:GO:0004496; P:GO:0008299	-	EC:2.7.1.36	IPR006205; IPR013750; G3DSA:3.30.70.890 (GENE3D), PTHR10457 (PANTHER), SSF55060 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	sodium:neurotransmitter symporter family protein	13	P:GO:0055085; P:GO:0007274; F:GO:0005277; F:GO:0005328; F:GO:0015187; P:GO:0001504; P:GO:0015870; P:GO:0015871; F:GO:0030165; P:GO:0040017; C:GO:0045211; P:GO:0015816; C:GO:0005887	-		IPR000175; PTHR11616:SF17 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	atp-binding cassette sub-family f member 2	4	F:GO:0005524; F:GO:0015417; F:GO:0015439; C:GO:0043190	-	EC:3.6.3.31; EC:3.6.3.41	IPR003439; IPR007406; PTHR19211 (PANTHER), PTHR19211:SF15 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	atp-binding cassette sub-family f member 2	4	F:GO:0005524; F:GO:0015417; F:GO:0015439; C:GO:0043190	-	EC:3.6.3.31; EC:3.6.3.41	IPR003439; G3DSA:3.40.50.300 (GENE3D), PTHR19211 (PANTHER), PTHR19211:SF15 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	atp-binding cassette sub-family f member 2	3	F:GO:0005524; F:GO:0015417; F:GO:0015439	-	EC:3.6.3.31; EC:3.6.3.41	IPR003439; IPR003593; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR19211 (PANTHER), PTHR19211:SF15 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	atp-binding cassette sub-family f member 2	3	F:GO:0005524; F:GO:0015417; F:GO:0015439	-	EC:3.6.3.31; EC:3.6.3.41	IPR003439; IPR003593; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR19211 (PANTHER), PTHR19211:SF15 (PANTHER), SSF52540 (SUPERFAMILY)

Caenorhabditis briggsae	ras-related gtp-binding protein d	5	F:GO:0046982; P:GO:0009792; C:GO:0005737; C:GO:0005634; F:GO:0005525	-		IPR006762; G3DSA:3.40.50.300 (GENE3D), PTHR11259:SF2 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	lor sdh bifunctio-l protein conserved domain protein	2	C:GO:0005737; F:GO:0016813	-	EC:3.5.3.0	IPR003198; G3DSA:3.75.10.10 (GENE3D), PTHR12737 (PANTHER), PTHR12737:SF1 (PANTHER), SSF55909 (SUPERFAMILY)
Loa loa	dead (asp-glu-ala-asp) box polypeptide 28	1	C:GO:0043231	-		IPR001650; IPR011545; IPR014001; IPR014014; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF44 (PANTHER), SSF52540 (SUPERFAMILY)
Uncinaria stenocephala	cathepsin d-like aspartic protease	4	P:GO:0012502; C:GO:0005764; F:GO:0004190; P:GO:0006508	-	EC:3.4.23.0	IPR001461; IPR001969; IPR009007; IPR021109; PTHR13683:SF84 (PANTHER)
Brugia malayi	dedicator of cytokinesis protein 6	0		F:GO:0005525; P:GO:0050790; F:GO:0051020; F:GO:0004872; P:GO:0008150; C:GO:0005575; F:GO:0005085		PTHR23317 (PANTHER), PTHR23317:SF27 (PANTHER)
Pongo abelii	histone	16	P:GO:0040010; C:GO:0000786; P:GO:0008340; P:GO:0009725; P:GO:0008360; P:GO:0007420; F:GO:0003677; C:GO:0005700; P:GO:0010171; P:GO:0007155; P:GO:0002119; P:GO:0006334; P:GO:0009792; P:GO:0007140; C:GO:0005634; P:GO:0006974	-		IPR000164; IPR007125; IPR009072

Caenorhabditis sp. PS1010	secretory carrier membrane protein 5	13	P:GO:0051047; C:GO:0016021; P:GO:0055114; P:GO:0006887; F:GO:0016491; P:GO:0048522; P:GO:0060341; C:GO:0044446; C:GO:0031090; C:GO:0012505; P:GO:0015031; C:GO:0005794; C:GO:0005886	-		IPR007273; PTHR10687:SF3 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	kinesin heavy chain	18	P:GO:0007411; F:GO:0008574; P:GO:0008103; P:GO:0007317; P:GO:0007310; C:GO:0005874; P:GO:0048311; P:GO:0007303; F:GO:0008017; P:GO:0008088; P:GO:0019226; P:GO:0047497; F:GO:0032403; C:GO:0033267; C:GO:0005871; F:GO:0005524; P:GO:0001754; C:GO:0005739	-	EC:3.6.4.4	IPR001752; IPR019821; PD936484 (PRODOM), PTHR16012 (PANTHER), PTHR16012:SF131 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	kinesin heavy chain	18	P:GO:0007411; F:GO:0008574; P:GO:0008103; P:GO:0007317; P:GO:0007310; C:GO:0005874; P:GO:0048311; P:GO:0007303; F:GO:0008017; P:GO:0008088; P:GO:0019226; P:GO:0047497; F:GO:0032403; C:GO:0033267; C:GO:0005871; F:GO:0005524; P:GO:0001754; C:GO:0005739	-	EC:3.6.4.4	IPR001752; IPR019821; PD936484 (PRODOM), PTHR16012 (PANTHER), PTHR16012:SF131 (PANTHER), SSF52540 (SUPERFAMILY)

Caenorhabditis briggsae	kinesin heavy chain	18	P:GO:0007411; F:GO:0008574; P:GO:0008103; P:GO:0007317; P:GO:0007310; C:GO:0005874; P:GO:0048311; P:GO:0007303; F:GO:0008017; P:GO:0008088; P:GO:0019226; P:GO:0047497; F:GO:0032403; C:GO:0033267; C:GO:0005871; F:GO:0005524; P:GO:0001754; C:GO:0005739	-	EC:3.6.4.4	IPR001752; IPR019821; PD936484 (PRODOM), PTHR16012 (PANTHER), PTHR16012:SF131 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	transcriptio-l regulator	0				IPR002634; PTHR12735:SF3 (PANTHER)
Caenorhabditis elegans	briggsae cbr-unc-59 protein	11	P:GO:0051291; P:GO:0000910; P:GO:0007049; C:GO:0031105; C:GO:0001725; F:GO:0005515; C:GO:0019717; C:GO:0005694; F:GO:0005198; C:GO:0005634; F:GO:0005525	-		IPR000038; IPR016491; G3DSA:3.40.50.300 (GENE3D), PTHR18884:SF29 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Loa loa	briggsae cbr-taf-9 protein	3	C:GO:0043234; F:GO:0005515; C:GO:0044451	-		-
	-	0				-
Caenorhabditis elegans	coiled-coil domain-containing protein 101	0				-
Brugia malayi	cre-	2	F:GO:0016787; P:GO:0006629	-		IPR002641; IPR016035; G3DSA:3.40.1090.10 (GENE3D), PTHR18958 (PANTHER), PTHR18958:SF81 (PANTHER)
	-	0				-
Brugia malayi	dj-1 family protein	2	P:GO:0008344; P:GO:0006979	-		IPR002818; IPR006287; G3DSA:3.40.50.880 (GENE3D), PTHR11019 (PANTHER), PTHR11019:SF5 (PANTHER), SSF52317 (SUPERFAMILY)
Caenorhabditis elegans	mitochondrial ribosomal protein l41	7	P:GO:0009792; P:GO:0002119; C:GO:0005762; F:GO:0003735; P:GO:0040010; P:GO:0000003; P:GO:0006412	-	EC:3.6.5.3	IPR019189; PTHR21338 (PANTHER)

Caenorhabditis briggsae	briggsae cbr-syn-1 protein	6	F:GO:0005515; P:GO:0050796; P:GO:0016081; C:GO:0044425; C:GO:0043229; C:GO:0005886	-		IPR000727; IPR006012; IPR010989; G3DSA:1.20.58.70 (GENE3D), PTHR19957 (PANTHER), PTHR19957:SF25 (PANTHER)
Loa loa	symplekin	2	F:GO:0005488; C:GO:0005634	-		PTHR15245 (PANTHER), PTHR15245:SF2 (PANTHER)
Caenorhabditis elegans	wd40 repeat domain 11 partial	0		F:GO:0003674; P:GO:0008286; C:GO:0016021; C:GO:0016020; P:GO:0008150; C:GO:0005575; C:GO:0005634		IPR011046; IPR015943
Caenorhabditis elegans	hypothetical protein T19D12.9 [Caenorhabditis elegans]	1	P:GO:0019915	-		PTHR11662 (PANTHER), PTHR11662:SF17 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	muts homolog 5 (coli)	4	F:GO:0005515; P:GO:0007131; P:GO:0007136; C:GO:0005634	-		IPR000432; G3DSA:3.40.50.300 (GENE3D), PTHR11361:SF20 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	complement factor h-related 5	0		P:GO:0006957; C:GO:0005576		IPR000436; IPR016060; PTHR19325 (PANTHER), PTHR19325:SF25 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	complement factor h-like	0				IPR000436; IPR016060; PTHR19325 (PANTHER), PTHR19325:SF25 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	complement binding protein	0				IPR000436; IPR016060; PTHR19325 (PANTHER), PTHR19325:SF25 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	udp-glucuronosyltransferase 2a1 precursor	1	F:GO:0016758	-	EC:2.4.1.0	IPR002213; SignalP (SIGNALP), SSF53756 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-nlp-11 protein	0				SignalP (SIGNALP)
Pristionchus pacificus	phosphopantetheine attachment site family protein	6	P:GO:0006120; P:GO:0006633; F:GO:0000036; F:GO:0048037; F:GO:0031177; C:GO:0005739	-		IPR006163; IPR009081; PD000887 (PRODOM), PTHR20863 (PANTHER), PTHR20863:SF5 (PANTHER)
	-	0				-
Caenorhabditis briggsae	probable ribosome biogenesis protein rlp24-like	9	P:GO:0006412; P:GO:0040010; C:GO:0005840; F:GO:0003735; P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0006898; P:GO:0009792	-	EC:3.6.5.3	PS51257 (PROFILE)
	-	0				-

Caenorhabditis elegans	proteasome activator complex subunit 4	0		P:GO:0030154; F:GO:0005488; C:GO:0000502; C:GO:0016607; P:GO:0007275; P:GO:0007283; C:GO:0005634		IPR011989; IPR016024; IPR021843
	-	0				-
Caenorhabditis elegans	r- and export factor binding protein	5	P:GO:0016070; F:GO:0005515; P:GO:0040011; C:GO:0044428; P:GO:0010467	-		-
Caenorhabditis elegans	r- and export factor binding protein	4	P:GO:0009987; F:GO:0005515; P:GO:0040011; C:GO:0044428	-		IPR000504; IPR012677; PTHR19965 (PANTHER), PTHR19965:SF8 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein F26F12.3 [Caenorhabditis elegans]	0		F:GO:0005515		-
Caenorhabditis briggsae	chromosome 9 open reading frame 64	0		F:GO:0003723; F:GO:0003674; P:GO:0008150; C:GO:0005575		IPR000834; IPR019438; PTHR21314 (PANTHER)
	-	0				-
Caenorhabditis briggsae	casein ki-se gamma 2	10	P:GO:0040010; P:GO:0018991; F:GO:0004672; P:GO:0040035; P:GO:0010171; P:GO:0002119; F:GO:0000166; P:GO:0040011; P:GO:0009792; P:GO:0040018	-		-
Brugia malayi	nsfl1 cofactor p47	2	F:GO:0005515; C:GO:0043229	-		IPR001012; IPR012989; G3DSA:3.10.20.90 (GENE3D), PTHR23333 (PANTHER), SSF54236 (SUPERFAMILY)
Loa loa	nsfl1 cofactor p47	2	F:GO:0005515; C:GO:0043229	-		IPR001012; IPR012989; G3DSA:3.10.20.90 (GENE3D), PTHR23333 (PANTHER), SSF54236 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-sep-1 protein	0		P:GO:0006508; P:GO:0045143; P:GO:0000212; F:GO:0008233; P:GO:0007127; F:GO:0005515; C:GO:0005813; C:GO:0005634		IPR005314
Caenorhabditis elegans	alg6_caeel ame: full=probable dolichyl pyrophosphate man9 c2 alpha- -glucosyltransferase ame: full=asparagine-linked glycosylation protein 6 homolog ame: full=dolichyl-p-glc:man9 c2-pp-dolichyl glucosyltransferase	1	P:GO:0000003	-		IPR004856; SignalP (SIGNALP)

Caenorhabditis elegans	cytochrome c-type heme	12	P:GO:0040010; P:GO:0008340; C:GO:0005743; P:GO:0055114; P:GO:0000003; P:GO:0018996; F:GO:0016491; P:GO:0002119; F:GO:0004408; P:GO:0006898; P:GO:0009792; P:GO:0018063	-	EC:4.4.1.17	-
	-	0				-
Brugia malayi	heterogeneous nuclear ribonucleoprotein r	4	P:GO:0008380; C:GO:0030530; F:GO:0003676; F:GO:0005515	-		IPR000504; IPR006535; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF42 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	cathepsin a	3	P:GO:0019915; F:GO:0004185; P:GO:0006508	-	EC:3.4.16.0	IPR001563; G3DSA:3.40.50.1820 (GENE3D), PTHR11802:SF9 (PANTHER), SSF53474 (SUPERFAMILY)
	-	0				-
Brugia malayi	ymf7_caeel ame: full=uncharacterized protein	0		F:GO:0046872; F:GO:0003676; P:GO:0007049; F:GO:0008270; F:GO:0003677; C:GO:0005634		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	usp4 protein	2	F:GO:0005515; F:GO:0016787	-		IPR001394; IPR003006; IPR018200; PTHR10420 (PANTHER), PTHR10420:SF72 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis briggsae	loc398480 protein	4	F:GO:0046872; P:GO:0006511; F:GO:0004221; F:GO:0008234	-	EC:3.1.2.15	IPR001394; IPR018200; PTHR10420 (PANTHER), PTHR10420:SF72 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis briggsae	usp4 protein	2	F:GO:0005515; F:GO:0016787	-		IPR001394; IPR003006; IPR018200; PTHR10420 (PANTHER), PTHR10420:SF72 (PANTHER), SSF54001 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein Y23H5A.3 [Caenorhabditis elegans]	1	P:GO:0007369	-		SSF54928 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	nuclear pore complex protein family member (npp-7)	0		C:GO:0005643; F:GO:0017056; P:GO:0006997; F:GO:0008270; P:GO:0009792; P:GO:0002119; P:GO:0040007		IPR001876; SSF90209 (SUPERFAMILY)

Angiostrongylus cantonensis	ef hand family protein	4	F:GO:0005515; F:GO:0005509; C:GO:0005625; C:GO:0005626	-		IPR002048; IPR011992; IPR018247; IPR018248; IPR018249; PTHR23050 (PANTHER), PTHR23050:SF9 (PANTHER), SSF47473 (SUPERFAMILY)
Caenorhabditis briggsae	dihydrofolate reductase	6	P:GO:0044238; P:GO:0000003; F:GO:0016491; P:GO:0044271; P:GO:0009792; P:GO:0044283	-		IPR001796; IPR012259; IPR017925; G3DSA:3.40.430.10 (GENE3D), PTHR11549 (PANTHER), SSF53597 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	protein regulator of cytokinesis 1	1	C:GO:0005856	-		IPR007145
Caenorhabditis elegans	protein regulator of cytokinesis 1	1	C:GO:0005856	-		IPR007145
Caenorhabditis elegans	protein regulator of cytokinesis 1	1	C:GO:0005856	-		IPR007145
Caenorhabditis briggsae	Hypothetical protein CBG22064 [Caenorhabditis briggsae]	3	P:GO:0009792; P:GO:0006898; P:GO:0002119	-		-
Caenorhabditis briggsae	briggsae cbr-pld-1 protein	3	P:GO:0009987; F:GO:0005488; F:GO:0003824	-		IPR001683; IPR015679; PTHR18896:SF6 (PANTHER)
Loa loa	subfamily member 4	6	P:GO:0008340; P:GO:0007052; F:GO:0005515; C:GO:0044464; P:GO:0009792; P:GO:0006950	-		-
Loa loa	subfamily member 4	6	P:GO:0008340; P:GO:0007052; F:GO:0005515; C:GO:0044464; P:GO:0009792; P:GO:0006950	-		-
Loa loa	subfamily member 4	6	P:GO:0008340; P:GO:0007052; F:GO:0005515; C:GO:0044464; P:GO:0009792; P:GO:0006950	-		-
Loa loa	subfamily member 4	6	P:GO:0008340; P:GO:0007052; F:GO:0005515; C:GO:0044464; P:GO:0009792; P:GO:0006950	-		-
Loa loa	subfamily member 4	6	P:GO:0008340; P:GO:0007052; F:GO:0005515; C:GO:0044464; P:GO:0009792; P:GO:0006950	-		-
Loa loa	subfamily member 4	6	P:GO:0008340; P:GO:0007052; F:GO:0005515; C:GO:0044464; P:GO:0009792; P:GO:0006950	-		-
	-	0				-

Caenorhabditis elegans	wd repeat-containing protein 81	0		F:GO:0003674; P:GO:0008150		IPR000409
	-	0				-
	-	0				-
	-	0				-
Loa loa	protein smg9	0		P:GO:0000184; F:GO:0003674; P:GO:0008150; F:GO:0005515; C:GO:0005575; C:GO:0005622		G3DSA:3.40.50.300 (GENE3D), PTHR14270 (PANTHER)
Angiostrongylus cantonensis	temporarily assigned gene -me family member	4	F:GO:0017089; C:GO:0005737; F:GO:0051861; P:GO:0046836	-		IPR014830; PTHR10219 (PANTHER), PTHR10219:SF1 (PANTHER)
	-	0				-
Pongo abelii	heterogeneous nuclear ribonucleoprotein u (scaffold attachment factor a)	12	F:GO:0003723; C:GO:0005681; C:GO:0070937; P:GO:0070934; P:GO:0001906; P:GO:0008380; C:GO:0009986; F:GO:0003677; F:GO:0005524; C:GO:0030530; F:GO:0005515; P:GO:0006397	-		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		C:GO:0005777; P:GO:0055114; F:GO:0005488; C:GO:0005737; F:GO:0016491; F:GO:0046592; P:GO:0008152; P:GO:0006598		IPR002937; G3DSA:3.50.50.60 (GENE3D), PTHR10742 (PANTHER), PTHR10742:SF23 (PANTHER), SSF54373 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	dr1-associated corepressor	5	F:GO:0003677; P:GO:0000122; F:GO:0003714; F:GO:0003700; C:GO:0005634	-		IPR003958; IPR009072; PTHR10252 (PANTHER), PTHR10252:SF1 (PANTHER)
Loa loa	er degradation mannosidase alpha-like 2	9	F:GO:0046873; C:GO:0005788; F:GO:0004571; P:GO:0055085; F:GO:0005509; P:GO:0006986; C:GO:0005576; C:GO:0016020; P:GO:0030001	-	EC:3.2.1.113	IPR001382; PTHR11742:SF10 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	suppressor with morphological effect on genitalia family member (smg-3)	0				IPR007193

Caenorhabditis briggsae	atp-dependent r- helicase ddx51-like	7	P:GO:0040010; P:GO:0008340; F:GO:0003676; C:GO:0005622; P:GO:0002119; P:GO:0006898; F:GO:0016787	-		IPR000629; IPR011545; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF34 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	spectrin beta chain	4	F:GO:0005200; C:GO:0008091; F:GO:0003779; F:GO:0016787	-		IPR002017; IPR018159; G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF48 (PANTHER), SSF46966 (SUPERFAMILY)
Caenorhabditis briggsae	acyl carrier protein	10	P:GO:0040010; F:GO:0031177; P:GO:0006633; P:GO:0008340; C:GO:0005739; F:GO:0000036; P:GO:0006120; P:GO:0002119; P:GO:0006898; F:GO:0048037	-		-
	-	0				-
	-	0				-
Trichomonas vaginalis G3	viral a-type inclusion protein	0		F:GO:0043565; C:GO:0016020; F:GO:0008565; F:GO:0003700; C:GO:0000139; C:GO:0005737; F:GO:0046983; P:GO:0006355; P:GO:0006886; F:GO:0005515; P:GO:0048280; F:GO:0005488		IPR009053; PD936484 (PRODOM)
	-	0				-
Brugia malayi	briggsae cbr-evl-14 protein	2	F:GO:0005488; P:GO:0007049	-		IPR011989; IPR016024; PTHR12663 (PANTHER)

Brugia malayi	rnp (rrm r- binding domain) containing family member (rnp-6)	21	P:GO:0007411; P:GO:0000381; P:GO:0018991; F:GO:0005515; F:GO:0000166; P:GO:0040010; P:GO:0006898; P:GO:0006376; C:GO:0071011; P:GO:0040011; C:GO:0071013; P:GO:0007282; P:GO:0009792; P:GO:0002009; P:GO:0051726; C:GO:0043234; P:GO:0002119; P:GO:0007413; F:GO:0008266; P:GO:0040035; F:GO:0003729	-		IPR000504; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF70 (PANTHER), SSF54928 (SUPERFAMILY)
Brugia malayi	rnp (rrm r- binding domain) containing family member (rnp-6)	21	P:GO:0007411; P:GO:0000381; P:GO:0018991; F:GO:0005515; F:GO:0000166; P:GO:0040010; P:GO:0006898; P:GO:0006376; C:GO:0071011; P:GO:0040011; C:GO:0071013; P:GO:0007282; P:GO:0009792; P:GO:0002009; P:GO:0051726; C:GO:0043234; P:GO:0002119; P:GO:0007413; F:GO:0008266; P:GO:0040035; F:GO:0003729	-		IPR000504; IPR006532; IPR012677; PTHR10432 (PANTHER), PTHR10432:SF70 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG15698 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	tar-binding protein	1	F:GO:0042802	-		PTHR10432 (PANTHER), PTHR10432:SF6 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	pctp-like protein	0				IPR002913; G3DSA:3.30.530.20 (GENE3D), PTHR19308 (PANTHER), SSF55961 (SUPERFAMILY)

Homo sapiens	antigen cd18	14	C:GO:0008305; P:GO:0006915; P:GO:0007267; P:GO:0006954; P:GO:0008360; P:GO:0007229; F:GO:0001948; F:GO:0004872; P:GO:0007160; P:GO:0050730; F:GO:0019901; P:GO:0007159; P:GO:0007275; P:GO:0030593	-		-
	-	0				-
Caenorhabditis elegans	d- polymerase i	2	F:GO:0004518; P:GO:0009987	-		-
Caenorhabditis sp. PS1010	transmembrane protein 120b	1	C:GO:0016021	-		IPR012926
Caenorhabditis elegans	iesterase family member (pde-4)	8	F:GO:0004115; C:GO:0005625; F:GO:0046872; C:GO:0005815; P:GO:0007165; C:GO:0005626; C:GO:0016020; C:GO:0005829	-		IPR002073; IPR023088; PTHR11347 (PANTHER), PTHR11347:SF37 (PANTHER), SSF109604 (SUPERFAMILY)
Haemonchus contortus	elegans protein confirmed by transcript evidence	4	P:GO:0040019; P:GO:0009792; P:GO:0040010; P:GO:0002119	-		-
Callithrix jacchus	ribosomal protein l3	6	C:GO:0005730; F:GO:0003735; F:GO:0003723; F:GO:0005515; C:GO:0022625; P:GO:0006414	-		IPR000597; IPR009000; G3DSA:2.40.30.10 (GENE3D), PTHR11363 (PANTHER)
Trichomonas vaginalis G3	small gtp-binding protein	0		C:GO:0016020; F:GO:0000166; F:GO:0005525; F:GO:0008270; P:GO:0007165; F:GO:0005515; C:GO:0005622; F:GO:0003924; F:GO:0046872; P:GO:0007264		SignalP (SIGNALP)
Caenorhabditis elegans	iesterase family member (pde-6)	5	P:GO:0007411; F:GO:0004871; F:GO:0046872; F:GO:0004114; P:GO:0007165	-	EC:3.1.4.17	IPR000014; IPR002073; IPR013767; IPR023088; G3DSA:3.30.450.20 (GENE3D), PTHR11347 (PANTHER), PTHR11347:SF38 (PANTHER), SSF109604 (SUPERFAMILY), SSF55785 (SUPERFAMILY)

Caenorhabditis elegans	werner syndrome atp-dependent helicase homolog	25	F:GO:0030145; C:GO:0005654; F:GO:0000403; P:GO:0000731; P:GO:0007569; P:GO:0010259; P:GO:0031297; C:GO:0005730; P:GO:0051345; P:GO:0010225; C:GO:0005813; P:GO:0006284; F:GO:0000287; F:GO:0051880; P:GO:0000723; F:GO:0032403; F:GO:0042803; F:GO:0004003; P:GO:0042981; C:GO:0032389; F:GO:0000405; F:GO:0009378; P:GO:0006979; F:GO:0008408; F:GO:0043138	-		IPR001650; IPR004589; G3DSA:3.40.50.300 (GENE3D), PTHR13710:SF16 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	dead (asp-glu-ala-asp) box polypeptide 27	5	P:GO:0040010; P:GO:0002119; F:GO:0005515; F:GO:0000166; F:GO:0004386	-		IPR000629; IPR011545; IPR014001; IPR014014; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF19 (PANTHER), SSF52540 (SUPERFAMILY)
Brugia malayi	rr- promoter binding protein	0				-
Brugia malayi	rr- promoter binding protein	0				-
Caenorhabditis elegans	hypothetical wd-repeat protein in chromosome	0		P:GO:0016567; C:GO:0080008		-
Caenorhabditis elegans	hypothetical wd-repeat protein in chromosome	0		P:GO:0016567; C:GO:0080008		IPR011046; IPR015943
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	r- polymerase rpb3 rpb11 dimerisation domain containing protein	9	C:GO:0005666; P:GO:0006383; F:GO:0003899; C:GO:0005875; F:GO:0016757; F:GO:0003677; C:GO:0005736; F:GO:0046983; P:GO:0006360	-	EC:2.7.7.6	IPR009025; IPR011261; G3DSA:3.30.1360.10 (GENE3D), PTHR11800 (PANTHER), PTHR11800:SF13 (PANTHER)
Caenorhabditis briggsae	chloride channel protein 7	5	F:GO:0005488; F:GO:0005247; P:GO:0055085; C:GO:0016021; P:GO:0006821	-		IPR000644; IPR001807; IPR014743; G3DSA:3.10.580.10 (GENE3D), PTHR11689:SF15 (PANTHER), SignalP (SIGNALP), SSF54631 (SUPERFAMILY)

Caenorhabditis elegans	nucleoporin 98-96	0		C:GO:0005643; P:GO:0006810		IPR021967; PTHR23198 (PANTHER)
Caenorhabditis elegans	pyrroline-5-carboxylate reductase	1	P:GO:0008152	-		IPR000304; IPR016040; SSF51735 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	lycerol ki-se family member (dgk-1)	8	F:GO:0003676; P:GO:0007205; F:GO:0019992; F:GO:0005515; P:GO:0007165; F:GO:0008270; F:GO:0004143; F:GO:0000166	-	EC:2.7.1.107	IPR001965; IPR002219; IPR020454; G3DSA:3.30.60.20 (GENE3D), PTHR11255 (PANTHER), PTHR11255:SF8 (PANTHER), SSF57889 (SUPERFAMILY)
Brugia malayi	hypothetical protein Bm1_08910 [Brugia malayi]	0				SignalP (SIGNALP)
Caenorhabditis briggsae	subfamily member 10	0		F:GO:0051082; C:GO:0005788; P:GO:0045454; P:GO:0006457; C:GO:0005783; F:GO:0031072; C:GO:0005576		IPR015609; PTHR11821:SF16 (PANTHER)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				PTHR13243 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR019002; PTHR13243 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	fatty acid binding protein 4	16	P:GO:0050872; P:GO:0008340; F:GO:0005515; P:GO:0006469; P:GO:0050873; C:GO:0005829; P:GO:0051384; P:GO:0001816; P:GO:0008284; P:GO:0006631; P:GO:0071285; P:GO:0042493; F:GO:0008289; P:GO:0016481; P:GO:0050729; P:GO:0042632	-		-

Caenorhabditis brenneri	ubiquitin protein ligase e3 component n-recognin 4	0		F:GO:0016874; C:GO:0016021; C:GO:0016020; C:GO:0005634; P:GO:0006260; F:GO:0008270; P:GO:0016567; F:GO:0005516; F:GO:0004842; F:GO:0046872; P:GO:0008152; C:GO:0005856; F:GO:0005488		PTHR21725 (PANTHER), SignalP (SIGNALP)
Caenorhabditis brenneri	ubiquitin protein ligase e3 component n-recognin 4	1	F:GO:0005488	-		PTHR21725 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	histone h4 transcription factor	12	P:GO:0051234; C:GO:0031981; P:GO:0000003; F:GO:0030528; P:GO:0010628; F:GO:0005515; P:GO:0048519; F:GO:0003676; P:GO:0009792; P:GO:0048856; P:GO:0022402; P:GO:0045449	-		IPR007087; IPR013087; IPR015880; PTHR23224 (PANTHER), PTHR23224:SF469 (PANTHER), SSF57667 (SUPERFAMILY)
	-	0				-
	-	0				-
Loa loa	udp-galactopyranose mutase	0		F:GO:0008767; F:GO:0016491; P:GO:0008152; F:GO:0016853		IPR002937; G3DSA:3.50.50.60 (GENE3D), SSF51971 (SUPERFAMILY)
	-	0				-
						IPR003598; IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	ribosomal protein s18	9	P:GO:0006417; P:GO:0051726; F:GO:0019843; F:GO:0003735; P:GO:0000003; P:GO:0006414; C:GO:0022627; P:GO:0006898; P:GO:0007275	-		IPR001892; IPR010979; IPR018269; G3DSA:1.10.8.50 (GENE3D), G3DSA:4.10.910.10 (GENE3D), PTHR10871 (PANTHER), PTHR10871:SF2 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG14752 [Caenorhabditis briggsae]	0				-
	-	0				-
Caenorhabditis briggsae	nuclear transport factor 2-like export factor 2	7	P:GO:0040035; P:GO:0009792; P:GO:0002119; C:GO:0005622; P:GO:0040011; P:GO:0040007; P:GO:0006898	-		IPR002075; IPR018222; G3DSA:3.10.450.50 (GENE3D), PTHR12612 (PANTHER), SSF54427 (SUPERFAMILY)

Caenorhabditis briggsae	briggsae cbr-elt-3 protein	13	P:GO:0030097; F:GO:0030528; P:GO:0045941; F:GO:0008270; P:GO:0048729; P:GO:0048542; P:GO:0006355; P:GO:0045165; P:GO:0051179; P:GO:0001700; F:GO:0043565; P:GO:0042386; P:GO:0001704	-		IPR000679; IPR013088; PTHR10071 (PANTHER), PTHR10071:SF15 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-calu-1 protein	8	P:GO:0002009; P:GO:0018996; P:GO:0008340; P:GO:0000003; P:GO:0040007; P:GO:0010171; P:GO:0002119; P:GO:0040011	-		SignalP (SIGNALP)
Caenorhabditis elegans	transmembrane protein 55b	0				IPR019178
Caenorhabditis briggsae	immature colon carcinoma transcript 1 protein	1	P:GO:0006415	-		IPR000352; G3DSA:3.30.160.200 (GENE3D), PTHR11075 (PANTHER), PTHR11075:SF12 (PANTHER), SSF110916 (SUPERFAMILY)
Caenorhabditis elegans	transcription factor tfb2 family protein	2	P:GO:0006351; C:GO:0005634	-		IPR004598; SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	endoplasmic reticulum-golgi intermediate compartment protein 3	4	C:GO:0043227; F:GO:0005515; C:GO:0044444; C:GO:0016020	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	kh domain containing protein	7	C:GO:0005730; C:GO:0030530; P:GO:0008380; F:GO:0003723; F:GO:0005515; F:GO:0003697; P:GO:0007165	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	kh domain containing protein	6	C:GO:0005730; C:GO:0030530; P:GO:0008380; F:GO:0003723; F:GO:0005515; P:GO:0007165	-		SignalP (SIGNALP)
Nematostella vectensis	hydroxyacyl glutathione hydrolase	4	P:GO:0005975; C:GO:0005759; F:GO:0004416; P:GO:0006750	-	EC:3.1.2.6	IPR001279; IPR017782; G3DSA:3.60.15.10 (GENE3D), PTHR11935 (PANTHER), PTHR11935:SF7 (PANTHER), SSF56281 (SUPERFAMILY)

Xenopus (Silurana) tropicalis	hydroxyacylglutathione hydrolase	5	P:GO:0006750; C:GO:0005739; P:GO:0005975; P:GO:0019853; F:GO:0004416	-	EC:3.1.2.6	IPR001279; G3DSA:3.60.15.10 (GENE3D), PTHR11935 (PANTHER), PTHR11935:SF7 (PANTHER), SSF56281 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	serine threonine protein ki-se braf	5	F:GO:0005515; F:GO:0004672; P:GO:0009987; P:GO:0023052; F:GO:0000166	-		-
Caenorhabditis elegans	o ant response abnormal family member (odr-4)	0		P:GO:0055114; F:GO:0016491; F:GO:0008270		IPR002085; PTHR11695:SF3 (PANTHER)
Caenorhabditis briggsae	wd repeat and hmg-box d- binding protein 1	1	C:GO:0005634	-		IPR001680; IPR011044; IPR011046; IPR015943; IPR019781; PTHR19932 (PANTHER), PTHR19932:SF2 (PANTHER)
Caenorhabditis briggsae	uncoordi-ted family member (unc-43)	21	P:GO:0006468; F:GO:0004683; P:GO:0040018; P:GO:0040017; C:GO:0048786; P:GO:0008049; P:GO:0007616; C:GO:0005737; C:GO:0045211; F:GO:0046872; C:GO:0030425; P:GO:0007528; P:GO:0007067; C:GO:0030424; P:GO:0051932; C:GO:0005886; P:GO:0006952; F:GO:0005516; F:GO:0005524; P:GO:0051489; C:GO:0005954	-	EC:2.7.11.17	IPR013543; IPR015742; IPR020636; G3DSA:3.10.450.50 (GENE3D), SSF54427 (SUPERFAMILY)
Caenorhabditis briggsae	uncoordi-ted family member (unc-43)	18	P:GO:0006468; C:GO:0005654; P:GO:0000003; C:GO:0030666; F:GO:0004683; P:GO:0040018; P:GO:0040017; C:GO:0005829; F:GO:0046872; P:GO:0007067; P:GO:0051932; P:GO:0051092; C:GO:0005886; P:GO:0006952; F:GO:0005516; F:GO:0005524; C:GO:0045202; C:GO:0005954	-	EC:2.7.11.17	IPR013543; IPR015742; IPR020636; G3DSA:3.10.450.50 (GENE3D), SSF54427 (SUPERFAMILY)

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	P:GO:0000003; P:GO:0040010	-		PTHR22880 (PANTHER), PTHR22880:SF1 (PANTHER)
Trypanosoma brucei gambiense DAL972	hypothetical protein, conserved, (fragment) [Trypanosoma brucei gambiense DAL972]	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	guanine nucleotide exchange factor for ras-like gtpases n-termi-l motif family protein	0		P:GO:0051056; P:GO:0007264; F:GO:0005085; C:GO:0005622		-
Caenorhabditis elegans	inositol-1(or 4)-monophosphatase	4	F:GO:0004437; F:GO:0005488; P:GO:0016311; P:GO:0006020	-		IPR000760; IPR020550; IPR020552; IPR020583; G3DSA:3.30.540.10 (GENE3D), G3DSA:3.40.190.80 (GENE3D), PTHR20854:SF4 (PANTHER), SSF56655 (SUPERFAMILY)
Caenorhabditis elegans	inositol-1(or 4)-monophosphatase	4	F:GO:0004437; F:GO:0005488; P:GO:0016311; P:GO:0006020	-		IPR000760; IPR020552; IPR020583; G3DSA:3.30.540.10 (GENE3D), PTHR20854:SF4 (PANTHER), SSF56655 (SUPERFAMILY)
Caenorhabditis elegans	josephin-like protein	0				IPR006155; PTHR13291 (PANTHER)
	-	0				-
Caenorhabditis elegans	uncoordi-ted family member (unc-16)	6	C:GO:0005737; F:GO:0005078; F:GO:0019894; P:GO:0046328; P:GO:0016192; F:GO:0019901	-		IPR019143; PTHR13886 (PANTHER)
Caenorhabditis elegans	uncoordi-ted family member (unc-16)	6	C:GO:0005737; F:GO:0005078; F:GO:0019894; P:GO:0046328; P:GO:0016192; F:GO:0019901	-		IPR019143; PTHR13886 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-exoc-8 protein	9	P:GO:0006810; P:GO:0000003; P:GO:0010171; P:GO:0002119; P:GO:0040011; P:GO:0009792; P:GO:0033206; P:GO:0040018; P:GO:0051649	-		IPR016159; PTHR21426 (PANTHER), PTHR21426:SF9 (PANTHER)
Caenorhabditis elegans	briggsae cbr-exoc-8 protein	9	P:GO:0006810; P:GO:0000003; P:GO:0010171; P:GO:0002119; P:GO:0040011; P:GO:0009792; P:GO:0033206; P:GO:0040018; P:GO:0051649	-		IPR016159; PTHR21426 (PANTHER), PTHR21426:SF9 (PANTHER)
	-	0				-
Caenorhabditis elegans	hypothetical protein W05F2.4 [Caenorhabditis elegans]	3	P:GO:0040018; P:GO:0040035; P:GO:0002119	-		-
	-	0				IPR007087; IPR015880

Anisakis simplex	nucleosome assembly protein 1-like 1	11	P:GO:0040010; P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0040011; P:GO:0006334; P:GO:0002009; P:GO:0009792; P:GO:0040018; C:GO:0005634; P:GO:0016246	-		IPR002164; PTHR11875:SF7 (PANTHER), SSF143113 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; C:GO:0016020; F:GO:0008375		SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	chloride channel protein 3	8	F:GO:0005247; C:GO:0016021; P:GO:0000003; P:GO:0006821; F:GO:0000166; C:GO:0010008; P:GO:0034220; P:GO:0043269	-		IPR000644; IPR001807; IPR014743; G3DSA:3.10.580.10 (GENE3D), PTHR11689:SF21 (PANTHER), SignalP (SIGNALP), SSF54631 (SUPERFAMILY)
Loa loa	myotubularin-related protein 13	0		F:GO:0046872; P:GO:0006508; F:GO:0008239; P:GO:0016311; F:GO:0016791; F:GO:0008235; F:GO:0016805		IPR001849; IPR002219; IPR011993; G3DSA:3.30.60.20 (GENE3D), PTHR10807 (PANTHER), PTHR10807:SF4 (PANTHER), SSF50729 (SUPERFAMILY), SSF57889 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-lin-59 protein	0				-
Caenorhabditis elegans	briggsae cbr-dis-3 protein	4	C:GO:0000176; F:GO:0003723; F:GO:0004540; C:GO:0005652	-		PTHR23355 (PANTHER), PTHR23355:SF13 (PANTHER)
Caenorhabditis elegans	nuclear hormone receptor family member (nhr-11)	3	F:GO:0004872; F:GO:0005515; P:GO:0006350	-		PTHR11865 (PANTHER), PTHR11865:SF235 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG00701 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	tbc (tre-2 bub2 cdc16) domain family member (tbc-11)	5	F:GO:0005097; C:GO:0015630; P:GO:0032313; C:GO:0044444; C:GO:0044430	-		-
Caenorhabditis briggsae	pyruvate ki-se	9	P:GO:0009792; F:GO:0004743; F:GO:0016830; P:GO:0006725; F:GO:0005515; F:GO:0030955; F:GO:0000287; P:GO:0006096; F:GO:0000166	-	EC:2.7.1.40	IPR001697; IPR011037; IPR015793; IPR015806; IPR015813
Ktedonobacter racemifer DSM 44963	penicillin-binding 1a	1	F:GO:0005488	-		-

Ktedonobacter racemifer DSM 44963	penicillin-binding 1a	0		F:GO:0004871; P:GO:0006869; P:GO:0007047; P:GO:0008152; C:GO:0016021; C:GO:0016020; F:GO:0016820; F:GO:0003824; P:GO:0009190; F:GO:0016787; F:GO:0003723; P:GO:0007165; F:GO:0008270; F:GO:0005524; P:GO:0009252; F:GO:0016301; F:GO:0016818; F:GO:0005261; F:GO:0000166; F:GO:0016849; F:GO:0008658; P:GO:0000160; P:GO:0006754; P:GO:0008360; C:GO:0005643; F:GO:0008233; F:GO:0016740;		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0009792		IPR003677; PTHR21593 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				IPR009281; PTHR15756:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	gram domain-containing protein 1b	1	P:GO:0009792	-		-
Caenorhabditis briggsae	tubulin-specific chaperone d	5	P:GO:0006457; P:GO:0000003; P:GO:0007275; P:GO:0009653; C:GO:0044424	-		IPR011989; IPR016024; PTHR12658 (PANTHER)
Caenorhabditis elegans	malate dehydroge-se	4	P:GO:0018991; P:GO:0055114; F:GO:0016491; P:GO:0040011	-		SignalP (SIGNALP)
Caenorhabditis briggsae	pre-mr--splicing factor 38a	10	P:GO:0009792; P:GO:0002119; P:GO:0008380; C:GO:0005681; P:GO:0006397; P:GO:0000003; P:GO:0008340; P:GO:0040007; P:GO:0006898; P:GO:0045132	-		IPR005037
Trichoplax adhaerens	zinc finger protein 330	4	F:GO:0046872; C:GO:0005634; C:GO:0044446; C:GO:0043232	-		-

Caenorhabditis briggsae	malig-nt t cell amplified sequence 1	8	C:GO:0005737; P:GO:0008284; P:GO:0045449; F:GO:0003723; P:GO:0007049; P:GO:0000003; P:GO:0006974; P:GO:0040008	-		IPR002478; IPR004521; IPR015947; G3DSA:2.30.130.10 (GENE3D), PTHR22798 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	6	P:GO:0002009; P:GO:0018996; P:GO:0008340; P:GO:0000003; P:GO:0040010; P:GO:0002119	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	trp channel protein -nchung	1	P:GO:0006810	-		PTHR10582 (PANTHER), PTHR10582:SF2 (PANTHER)
Brugia malayi	selenocysteine-specific elongation factor	1	F:GO:0005488	-		-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0006685; C:GO:0005783; C:GO:0005794; C:GO:0005802; F:GO:0050290		-
	-	0				-
Caenorhabditis elegans	bladder cancer-associated protein	0				-
Angiostrongylus cantonensis	major allergen	0				-
Homo sapiens	major facilitator superfamily domain-containing protein 10	4	P:GO:0006915; C:GO:0016021; F:GO:0008493; P:GO:0055085	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis briggsae	tpa: contactin-associated protein 5	2	C:GO:0016021; P:GO:0048666	-		IPR000152; IPR000742; IPR006210; G3DSA:2.10.25.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF2 (PANTHER), SSF57196 (SUPERFAMILY)
Caenorhabditis elegans	small family member (sma-1)	18	P:GO:0016199; P:GO:0007026; C:GO:0031594; P:GO:0007417; C:GO:0016323; C:GO:0005794; C:GO:0045170; F:GO:0003779; F:GO:0008017; C:GO:0045169; P:GO:0007308; P:GO:0042062; P:GO:0007274; C:GO:0005811; P:GO:0030727; P:GO:0048790; P:GO:0007294; C:GO:0005938	-		IPR002017; IPR018159; G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF6 (PANTHER), SSF46966 (SUPERFAMILY)
	-	0				-

	-	0				-
						IPR003961; IPR008957; IPR013783; PR00014 (PRINTS), PTHR19900 (PANTHER), PTHR19900:SF7 (PANTHER)
Caenorhabditis briggsae	uncharacterized protein c2orf34-like	0		F:GO:0003677		IPR019410; G3DSA:3.40.50.150 (GENE3D), PTHR13539 (PANTHER), SSF53335 (SUPERFAMILY)
Caenorhabditis elegans	sig-l recognition particle	6	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0040018; P:GO:0040002; P:GO:0006898	-		IPR004328; G3DSA:1.25.40.280 (GENE3D), PTHR12860 (PANTHER)
Pongo abelii	fau	5	F:GO:0003735; F:GO:0003723; F:GO:0005515; C:GO:0022627; P:GO:0006414	-		IPR000626; IPR006846; IPR019954; IPR019955; G3DSA:3.10.20.90 (GENE3D), PTHR12650:SF5 (PANTHER), SSF54236 (SUPERFAMILY)
Caenorhabditis briggsae	cytochrome b561	0		F:GO:0009055; C:GO:0016021		IPR004877; IPR006593; PTHR10106 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	polymerase (d- directed) alpha 2 (70kd subunit)	1	P:GO:0007275	-		IPR007185; IPR013627; PTHR23061 (PANTHER), PTHR23061:SF2 (PANTHER)
Caenorhabditis elegans	sodium hydrogen exchanger 9 (nhe9)	5	F:GO:0015385; P:GO:0055085; P:GO:0006885; C:GO:0016021; P:GO:0006814	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	C:GO:0016021	-		IPR005578
Schistosoma mansoni	hypothetical protein [Schistosoma mansoni]	0				-
Brugia malayi	ferm domain (-ezrin-radixin-moesin) family member (frm-1)	0		F:GO:0005488; C:GO:0019898; F:GO:0008092; F:GO:0005515		-
Brugia malayi	ferm domain (-ezrin-radixin-moesin) family member (frm-1)	0		F:GO:0005488; C:GO:0019898; F:GO:0008092; F:GO:0005515		-
Schistosoma mansoni	ferm domain (-ezrin-radixin-moesin) family member (frm-1)	0		F:GO:0005488; C:GO:0019898; F:GO:0008092; F:GO:0005515		-
Caenorhabditis elegans	vps20-associated 1 like 1	1	C:GO:0005622	-		IPR006745; IPR009003; IPR023175; G3DSA:1.20.5.420 (GENE3D), PTHR12741 (PANTHER)
Caenorhabditis elegans	vps20-associated 1 like 1	2	C:GO:0005622; F:GO:0005515	-		IPR006745; IPR009003; IPR023175; G3DSA:1.20.5.420 (GENE3D), PTHR12741 (PANTHER)
	-	0				IPR021917
synthetic construct	histone-lysine n-methyltransferase setmar	5	F:GO:0046872; P:GO:0006313; F:GO:0016787; F:GO:0008168; F:GO:0004803	-	EC:2.1.1.0	IPR002622; PTHR23016 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	C:GO:0016021	-		IPR013057; PTHR22950 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	C:GO:0016021	-		IPR013057; PTHR22950 (PANTHER)

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	5	P:GO:0009792; F:GO:0046872; F:GO:0016301; F:GO:0005515; P:GO:0044237	-		-
Caenorhabditis briggsae	sluggish isoform c	5	F:GO:0004657; P:GO:0006537; P:GO:0042331; C:GO:0005759; P:GO:0006562	-	EC:1.5.99.8	IPR002872; IPR015659; G3DSA:3.20.20.220 (GENE3D), SSF51730 (SUPERFAMILY)
Caenorhabditis elegans	peptidylglycine alpha-amidating isoform cra_c	9	P:GO:0009987; P:GO:0048545; F:GO:0016829; F:GO:0046872; F:GO:0004497; C:GO:0016023; P:GO:0048513; P:GO:0008152; C:GO:0016020	-		IPR000323; IPR000720; IPR008977; IPR014783; IPR014784; PTHR10680 (PANTHER), PF03712 (PFAM), SignalP (SIGNALP)
Ancylostoma caninum	metalloprotease 1 precursor	1	F:GO:0008233	-		IPR001506; IPR006026; IPR013032; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
Ancylostoma ceylanicum	metalloprotease 1 precursor	1	F:GO:0008233	-		IPR001506; IPR003582; IPR006026; IPR013032; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
Ancylostoma caninum	metalloprotease 1 precursor	1	F:GO:0008233	-		IPR001506; IPR006026; IPR013032; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	briggsae cbr-him-10 protein	1	F:GO:0005515	-		IPR005549; PD968187 (PRODOM), PTHR21650 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG05378 [Caenorhabditis briggsae]	0		P:GO:0008152; F:GO:0008080		-
Caenorhabditis elegans	isoform c	0				IPR001849; IPR011993; PTHR22902 (PANTHER), PTHR22902:SF8 (PANTHER), SSF50729 (SUPERFAMILY)
Loa loa	elegans protein partially confirmed by transcript evidence	0				-
Loa loa	elegans protein partially confirmed by transcript evidence	0		F:GO:0005515		-
	-	0				-
Caenorhabditis elegans	d- replication complex gins protein sld5	4	C:GO:0005737; F:GO:0005515; P:GO:0009987; C:GO:0005634	-		IPR008591
Mus musculus	yippee-like 5	0		P:GO:0055114; F:GO:0003674; F:GO:0008113; C:GO:0005575		-
Caenorhabditis elegans	chromosome partition protein smc	0		C:GO:0005694; F:GO:0005524; P:GO:0051276; F:GO:0005515		PD936484 (PRODOM)

Haemaphysalis longicornis	protein disulfide isomerase	2	C:GO:0005783; C:GO:0044446	-		IPR012335; IPR012336; PTHR18929 (PANTHER)
Caenorhabditis elegans	ras-related protein 2	8	P:GO:0032486; F:GO:0019904; F:GO:0003924; C:GO:0055038; F:GO:0005525; P:GO:0061097; C:GO:0005886; P:GO:0030718	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR001466; IPR012338; G3DSA:3.40.710.10 (GENE3D), PTHR10566 (PANTHER), PTHR10566:SF6 (PANTHER)
Caenorhabditis elegans	thymidine ki-se	6	F:GO:0004797; P:GO:0006260; F:GO:0003677; F:GO:0005524; F:GO:0016853; P:GO:0009792	-	EC:2.7.1.21	IPR001267; IPR020633; SSF52540 (SUPERFAMILY), SSF57716 (SUPERFAMILY)
Ancylostoma ceylanicum	tissue factor pathway inhibitor isoform b precursor	2	F:GO:0004867; F:GO:0008233	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	acetyl- carboxylase partial	2	F:GO:0005488; F:GO:0003824	-		IPR013537; IPR022398
Caenorhabditis briggsae	briggsae cbr-ttr-5 protein	0				IPR001534; SignalP (SIGNALP)
Ancylostoma caninum	c-type lectin family member (clec-266)	0		C:GO:0016021; F:GO:0005529; P:GO:0006897; F:GO:0003674; C:GO:0005575; P:GO:0045087; C:GO:0005886; P:GO:0008150; F:GO:0005488		IPR001304; IPR016186; IPR016187; PTHR22802 (PANTHER), PTHR22802:SF15 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	alcohol dehydroge-se class-3	17	P:GO:0003016; F:GO:0008270; P:GO:0006069; F:GO:0018467; P:GO:0001523; C:GO:0005739; F:GO:0051903; P:GO:0055114; P:GO:0051409; P:GO:0051775; P:GO:0046294; P:GO:0045777; F:GO:0004024; F:GO:0042803; P:GO:0032496; P:GO:0018119; F:GO:0005504	-	EC:1.2.1.46; EC:1.1.1.284	IPR002085; IPR002328; IPR011032; IPR013149; IPR013154; IPR016040; G3DSA:3.90.180.10 (GENE3D), PTHR11695:SF4 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG16801 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	briggsae cbr-ugt-49 protein	2	F:GO:0016758; P:GO:0008152	-	EC:2.4.1.0	-

	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-pme-5 protein	0		F:GO:0003676; F:GO:0003950; P:GO:0006471		IPR008893; IPR012317; G3DSA:3.90.228.10 (GENE3D), PTHR15447 (PANTHER)
Caenorhabditis briggsae	ubiquitin carboxyl-termi-l hydrolase isozyme l5	6	F:GO:0004175; P:GO:0016579; F:GO:0005515; C:GO:0005838; F:GO:0004221; P:GO:0006508	-	EC:3.1.2.15	IPR001578; PTHR10589:SF16 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis briggsae	ubiquitin c-termi-l hydrolase	7	C:GO:0005737; F:GO:0004175; P:GO:0016579; F:GO:0005515; C:GO:0005838; F:GO:0004221; P:GO:0006508	-	EC:3.1.2.15	IPR001578; PTHR10589:SF16 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis briggsae	ubiquitin carboxyl-termi-l hydrolase isozyme l5	6	F:GO:0004175; P:GO:0016579; F:GO:0005515; C:GO:0005838; F:GO:0004221; P:GO:0006508	-	EC:3.1.2.15	IPR001578; PTHR10589:SF16 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis briggsae	ubiquitin carboxyl-termi-l hydrolase isozyme l5	7	C:GO:0005737; F:GO:0004175; P:GO:0016579; F:GO:0005515; C:GO:0005838; F:GO:0004221; P:GO:0006508	-	EC:3.1.2.15	IPR001578; PTHR10589:SF16 (PANTHER), SSF54001 (SUPERFAMILY)
	-	0				IPR004987; PTHR21516 (PANTHER)
Mus musculus	eukaryotic translation initiation factor isoform cra_i	0		F:GO:0003723; P:GO:0051149; C:GO:0005634; F:GO:0003674; P:GO:0045905; P:GO:0006915; P:GO:0045901; C:GO:0016020; C:GO:0005783; P:GO:0015031; C:GO:0005643; P:GO:0006412; P:GO:0055085; C:GO:0043025; C:GO:0005737; F:GO:0003746; F:GO:0043022; C:GO:0030425; P:GO:0051028; P:GO:0006452; P:GO:0008612; P:GO:0043066		-
Caenorhabditis elegans	serine threonine-protein ki-se smg1	2	F:GO:0005488; F:GO:0016772	-		IPR011989; IPR014009; PTHR11139 (PANTHER), PTHR11139:SF9 (PANTHER)
	-	0				-

Haemonchus contortus	zinc metallopeptidase	1	F:GO:0003824	-		IPR000718; IPR008753; G3DSA:1.10.1380.10 (GENE3D), PTHR11733:SF15 (PANTHER), SignalP (SIGNALP), SSF55486 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	mitochondrial ribosomal l23	11	P:GO:0006412; P:GO:0040010; C:GO:0005840; C:GO:0005739; F:GO:0003735; P:GO:0040035; P:GO:0002119; F:GO:0000166; P:GO:0006898; P:GO:0002009; P:GO:0009792	-	EC:3.6.5.3	IPR012677; IPR012678; IPR013025
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0046872; F:GO:0008236; C:GO:0016021; F:GO:0008270; F:GO:0005515		-
Loa loa	short-chain dehydroge-se	2	P:GO:0008152; F:GO:0016491	-		IPR002198; IPR002347; IPR016040; PTHR19410:SF36 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Ancylostoma ceylanicum	metalloprotease 1 precursor	2	F:GO:0046872; F:GO:0008237	-		IPR000859; IPR001506; IPR013032; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
Ancylostoma ceylanicum	metalloprotease 1 precursor	2	F:GO:0046872; F:GO:0008237	-		IPR000859; IPR001506; IPR003582; IPR013032; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
Ancylostoma ceylanicum	metalloprotease 1 precursor	2	F:GO:0046872; F:GO:0008237	-		IPR000859; IPR001506; IPR003582; IPR013032; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF65 (PANTHER), SSF55486 (SUPERFAMILY)
Loa loa	protein ki-se domain containing protein	4	P:GO:0006468; F:GO:0005524; P:GO:0040011; F:GO:0004674	-	EC:2.7.11.0	IPR011009; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
Caenorhabditis briggsae	protein ki-se domain containing protein	4	P:GO:0006468; F:GO:0005524; P:GO:0040011; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	3	P:GO:0044238; P:GO:0019915; F:GO:0016757	-		IPR002213; G3DSA:3.40.50.2000 (GENE3D), PTHR11926:SF3 (PANTHER), SSF53756 (SUPERFAMILY)

Brugia malayi	mitochondrial ribosomal protein l30	4	P:GO:0002119; P:GO:0009792; P:GO:0000003; P:GO:0040007	-		PTHR15892 (PANTHER)
	-	0				-
Loa loa	hypothetical protein LOAG_00426 [Loa loa]	0				-
Caenorhabditis briggsae	briggsae cbr-cst-1 protein	5	F:GO:0004674; F:GO:0005524; F:GO:0005515; P:GO:0035329; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR002290; IPR011009; IPR011524; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF89 (PANTHER), PF11629 (PFAM)
Caenorhabditis briggsae	serine threonine ki-se 4	13	P:GO:0018105; P:GO:0043065; P:GO:0007243; F:GO:0004674; P:GO:0000902; F:GO:0005524; F:GO:0000287; P:GO:0035329; F:GO:0008134; F:GO:0042803; P:GO:0046777; C:GO:0005737; C:GO:0005634	-	EC:2.7.11.0	IPR000719; IPR002290; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF89 (PANTHER)
Caenorhabditis elegans	ran binding protein 17	5	C:GO:0005737; C:GO:0005643; F:GO:0005049; F:GO:0008536; P:GO:0006611	-		PTHR12596 (PANTHER), PTHR12596:SF2 (PANTHER)
Caenorhabditis elegans	growth hormone inducible transmembrane protein	1	C:GO:0016020	-		-
Loa loa	vcell division cycle paf1 r- polymerase ii complex homolog (cerevisiae)	0				IPR007852; PTHR12466:SF7 (PANTHER)
Loa loa	vcell division cycle paf1 r- polymerase ii complex homolog (cerevisiae)	0				IPR007852; PTHR12466:SF7 (PANTHER)
Loa loa	vcell division cycle paf1 r- polymerase ii complex homolog (cerevisiae)	0				IPR007852; PTHR12466:SF7 (PANTHER)
Caenorhabditis elegans	briggsae cbr-vab-2 protein	2	P:GO:0048856; C:GO:0016020	-		IPR001799; IPR008972; PTHR11304:SF23 (PANTHER)
Caenorhabditis elegans	ephrin-b2	2	P:GO:0048856; C:GO:0016020	-		IPR001799; IPR008972; PTHR11304:SF23 (PANTHER)
Caenorhabditis briggsae	amop domain containing protein	1	P:GO:0007160	-		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	9	P:GO:0002009; P:GO:0019915; C:GO:0016021; P:GO:0008340; P:GO:0040007; P:GO:0010171; F:GO:0042302; P:GO:0002119; P:GO:0040011	-		-
Loa loa	major facilitator superfamily protein	1	C:GO:0016020	-		-
Caenorhabditis briggsae	Hypothetical protein CBG14951 [Caenorhabditis briggsae]	3	P:GO:0040018; P:GO:0040035; P:GO:0002119	-		-

Brugia malayi	protein ki-se domain containing protein	5	P:GO:0006468; P:GO:0040022; F:GO:0005524; P:GO:0051729; F:GO:0004674	-	EC:2.7.11.0	-
Caenorhabditis elegans	yqc2_caeel ame: full=uncharacterized protein	0				-
Caenorhabditis briggsae	briggsae cbr-clc-1 protein	2	P:GO:0018996; C:GO:0005911	-		IPR004031; SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	glutamine synthetase 2 (glutamate-amonia ligase)	5	P:GO:0009792; F:GO:0004356; F:GO:0005515; F:GO:0005524; P:GO:0006542	-	EC:6.3.1.2	-
Caenorhabditis briggsae	glutamine synthetase 2 (glutamate-amonia ligase)	5	P:GO:0009792; F:GO:0004356; F:GO:0005515; F:GO:0005524; P:GO:0006542	-	EC:6.3.1.2	-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)
	-	0				-
Ciona intestinalis	coiled-coil domain containing 53	0		F:GO:0003674; P:GO:0008150; F:GO:0005515; C:GO:0071203		-
	-	0				-
	-	0				-
Angiostrongylus cantonensis	myosin vi	27	C:GO:0012506; P:GO:0051046; C:GO:0016461; C:GO:0031941; P:GO:0030048; C:GO:0031965; F:GO:0060001; F:GO:0043531; C:GO:0005794; P:GO:0006886; C:GO:0005829; C:GO:0001726; P:GO:0048839; C:GO:0044425; P:GO:0006897; P:GO:0007268; F:GO:0051015; P:GO:0030330; C:GO:0016591; P:GO:0045944; C:GO:0048471; C:GO:0005886; F:GO:0005516; F:GO:0005524; C:GO:0005938; P:GO:0030182; C:GO:0045334	-		PTHR13140 (PANTHER), PTHR13140:SF26 (PANTHER)
	-	0				-
	-	0				-

Caenorhabditis elegans	nedd8-conjugating enzyme ube2f	13	P:GO:0040010; P:GO:0008340; P:GO:0000910; P:GO:0051246; P:GO:0040035; P:GO:0045116; F:GO:0019788; P:GO:0040025; F:GO:0000166; P:GO:0040011; P:GO:0002009; P:GO:0009792; P:GO:0016246	-		IPR000608; IPR016135; PTHR11621 (PANTHER), PTHR11621:SF18 (PANTHER)
Caenorhabditis elegans	nedd8-conjugating enzyme ube2f	13	P:GO:0040010; P:GO:0008340; P:GO:0000910; P:GO:0051246; P:GO:0040035; P:GO:0045116; F:GO:0019788; P:GO:0040025; F:GO:0000166; P:GO:0040011; P:GO:0002009; P:GO:0009792; P:GO:0016246	-		IPR000608; IPR016135; PTHR11621 (PANTHER), PTHR11621:SF18 (PANTHER)
Caenorhabditis elegans	nedd8-conjugating enzyme ube2f	13	P:GO:0040010; P:GO:0008340; P:GO:0000910; P:GO:0051246; P:GO:0040035; P:GO:0045116; F:GO:0019788; P:GO:0040025; F:GO:0000166; P:GO:0040011; P:GO:0002009; P:GO:0009792; P:GO:0016246	-		IPR000608; IPR016135; PTHR11621 (PANTHER), PTHR11621:SF18 (PANTHER)
Caenorhabditis elegans	transmembrane 9 superfamily member 3	2	C:GO:0016021; F:GO:0005488	-		-
Drosophila melanogaster	isoform a	0		F:GO:0004674; F:GO:0004672; P:GO:0006468; F:GO:0000166; P:GO:0006412; F:GO:0005524; F:GO:0016301; C:GO:0005730; F:GO:0003743; F:GO:0004812; P:GO:0008152		-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-scd-1 protein	1	P:GO:0040010	-		-
Caenorhabditis elegans	beta	3	C:GO:0005886; F:GO:0005515; C:GO:0005829	-		IPR001715; PTHR12114 (PANTHER), PTHR12114:SF4 (PANTHER)
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	briggsae cbr-cpg-3 protein	0		F:GO:0016740; F:GO:0004714; F:GO:0016787; F:GO:0003944		SignalP (SIGNALP)
Caenorhabditis briggsae	loc443608 protein	3	C:GO:0005737; C:GO:0043231; F:GO:0005102	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	6	P:GO:0050789; P:GO:0040007; F:GO:0004872; P:GO:0032501; F:GO:0005515; P:GO:0006350	-		IPR000536; IPR001723; IPR008946; PTHR11865 (PANTHER), PTHR11865:SF238 (PANTHER)
Caenorhabditis elegans	ylpd_caeel ame: full=uncharacterized protein	0		F:GO:0003723; F:GO:0004525; P:GO:0006396		-
Caenorhabditis briggsae	methylcrotonoyl-coenzyme a carboxylase 2	10	P:GO:0015936; P:GO:0040010; F:GO:0004525; F:GO:0003723; P:GO:0006396; C:GO:0005739; P:GO:0002119; F:GO:0000166; F:GO:0004485; P:GO:0009792	-	EC:3.1.26.3; EC:6.4.1.4	IPR000022; IPR011762; G3DSA:3.90.226.10 (GENE3D), PTHR22855 (PANTHER), PTHR22855:SF13 (PANTHER), SSF52096 (SUPERFAMILY)
Caenorhabditis elegans	39s ribosomal protein	0		F:GO:0003735; F:GO:0003723; F:GO:0004525; F:GO:0016787; P:GO:0006396; C:GO:0005840; F:GO:0003725; C:GO:0005622		IPR000999
Caenorhabditis briggsae	tubulin tyrosine ligase-like member 4	1	F:GO:0016874	-		-
	-	0				SignalP (SIGNALP)
Brugia malayi	splicing factor	11	P:GO:0040010; F:GO:0003729; P:GO:0008340; C:GO:0071011; P:GO:0000381; P:GO:0040035; P:GO:0002119; P:GO:0040011; C:GO:0071013; P:GO:0002009; P:GO:0009792	-		IPR000504; IPR006509; IPR012677; PTHR10432 (PANTHER), SSF54928 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG03790 [Caenorhabditis briggsae]	0		F:GO:0005515		-
Caenorhabditis briggsae	Hypothetical protein CBG03790 [Caenorhabditis briggsae]	0		F:GO:0005515		-

Brugia malayi	splicing factor	11	P:GO:0040010; F:GO:0003729; P:GO:0008340; C:GO:0071011; P:GO:0000381; P:GO:0040035; P:GO:0002119; P:GO:0040011; C:GO:0071013; P:GO:0002009; P:GO:0009792	-		IPR000504; IPR006509; IPR012677; PTHR10432 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-nsf-1 protein	14	F:GO:0017111; P:GO:0007274; P:GO:0000003; P:GO:0006891; F:GO:0005524; P:GO:0002119; F:GO:0005515; P:GO:0016082; P:GO:0006888; P:GO:0040011; P:GO:0006898; P:GO:0008582; P:GO:0009792; C:GO:0005737	-	EC:3.6.1.15	IPR003959; G3DSA:3.40.50.300 (GENE3D), PTHR23078 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	pik3r4 protein	3	F:GO:0004672; P:GO:0019915; F:GO:0000166	-		IPR000719; IPR011009; IPR011989; IPR016024; IPR017442; IPR020636; IPR021133; G3DSA:1.10.510.10 (GENE3D)
Caenorhabditis elegans	isoform cra_a	9	P:GO:0016044; C:GO:0005737; P:GO:0048513; P:GO:0031401; F:GO:0008641; P:GO:0006914; P:GO:0007399; F:GO:0042803; P:GO:0006497	-		IPR000594; IPR006285; IPR009036; IPR016040; PTHR10953 (PANTHER), PTHR10953:SF3 (PANTHER)
Caenorhabditis elegans	prion-like-(q n-rich)-domain-bearing protein protein partially confirmed by transcript evidence	1	F:GO:0005515	-		-
	-	0				-
	-	0				IPR002544
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-pink-1 protein	1	F:GO:0005488	-		IPR011422
	-	0				-
	-	0				-
Brugia malayi	alter-tive splicing defective family member (asd-2)	1	F:GO:0005515	-		-

Brugia malayi	structural mainte-nce of chromosomes protein 3	17	C:GO:0000785; F:GO:0045502; C:GO:0005604; F:GO:0000166; P:GO:0007052; F:GO:0005201; C:GO:0005737; F:GO:0046982; P:GO:0009294; F:GO:0042802; P:GO:0007126; P:GO:0007165; C:GO:0000800; C:GO:0016363; P:GO:0007062; P:GO:0032876; C:GO:0000922	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	tr--splicing endonuclease subunit	1	F:GO:0016787	-		IPR006677; IPR006678; IPR011856; PTHR21227 (PANTHER)
	-	0				-
Loa loa	acidic repeat-containing protein	1	P:GO:0045132	-		IPR006640; PTHR23099 (PANTHER)
Caenorhabditis elegans	temporarily assigned gene -me protein isoform confirmed by transcript evidence	0		F:GO:0003676		IPR008191; IPR018247; G3DSA:2.30.30.140 (GENE3D), SSF63748 (SUPERFAMILY)
Caenorhabditis elegans	temporarily assigned gene -me protein isoform confirmed by transcript evidence	0		F:GO:0003676		IPR008191; IPR018247; G3DSA:2.30.30.140 (GENE3D), SSF63748 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0005488; F:GO:0005044; C:GO:0016020		-
Caenorhabditis elegans	ribosome biogenesis protein bms1	4	F:GO:0005525; P:GO:0042254; C:GO:0005634; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	G3DSA:3.40.50.300 (GENE3D), PTHR12858 (PANTHER), PTHR12858:SF2 (PANTHER), PF03205 (PFAM), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	adenylosucci-te synthetase	11	P:GO:0040010; F:GO:0004019; P:GO:0006164; P:GO:0040027; P:GO:0040035; F:GO:0000287; P:GO:0040011; P:GO:0006898; P:GO:0009792; C:GO:0005737; F:GO:0005525	-	EC:6.3.4.4	IPR001114; G3DSA:3.90.170.10 (GENE3D), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005488	-		IPR000536; IPR001723; IPR008946; PTHR11865 (PANTHER), PTHR11865:SF35 (PANTHER)
Loa loa	elegans protein partially confirmed by transcript evidence	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-

Brugia malayi	pdz domain containing protein	5	P:GO:0009792; P:GO:0040007; P:GO:0040035; F:GO:0005515; P:GO:0002119	-		-
Caenorhabditis briggsae	pdz domain containing protein	5	P:GO:0009792; P:GO:0040007; P:GO:0040035; F:GO:0005515; P:GO:0002119	-		-
	-	0				-
Caenorhabditis elegans	ercc4 domain containing protein	6	P:GO:0006310; P:GO:0006281; F:GO:0003677; P:GO:0007127; F:GO:0004518; P:GO:0009792	-		-
Loa loa	uncoordi-ted family member (unc-13)	3	F:GO:0001566; P:GO:0016082; C:GO:0016020	-		-
Caenorhabditis elegans	amino acid transporter	1	C:GO:0016021	-		IPR013057; PTHR22950 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG22147 [Caenorhabditis briggsae]	0				IPR009496
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein C39H7.4 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
Caenorhabditis brenneri	elegans protein confirmed by transcript evidence	0				IPR021010; SSF141739 (SUPERFAMILY)
Caenorhabditis brenneri	elegans protein confirmed by transcript evidence	0				IPR021010; SSF141739 (SUPERFAMILY)
Loa loa	d- repair protein	2	P:GO:0050789; P:GO:0007126	-		PD936484 (PRODOM), PTHR18867 (PANTHER), PTHR18867:SF11 (PANTHER)
Loa loa	cyclin m4	2	P:GO:0032501; C:GO:0016020	-		IPR002550; PTHR12064 (PANTHER), PTHR12064:SF6 (PANTHER)
Brugia malayi	autophagy protein apg6 containing protein	15	P:GO:0035121; P:GO:0040010; P:GO:0008340; P:GO:0009267; P:GO:0035071; P:GO:0040024; P:GO:0040027; P:GO:0040035; C:GO:0031410; P:GO:0040011; P:GO:0030163; P:GO:0009792; P:GO:0040018; P:GO:0006914; C:GO:0005634	-		IPR007243; PTHR12768:SF2 (PANTHER)

Caenorhabditis elegans	nonmuscle myosin-ii heavy chain	27	P:GO:0046664; P:GO:0045200; P:GO:0035159; P:GO:0031036; C:GO:0016460; P:GO:0007443; P:GO:0007395; P:GO:0045214; P:GO:0035017; P:GO:0006936; P:GO:0007297; P:GO:0046663; F:GO:0003779; F:GO:0032027; P:GO:0008258; P:GO:0051259; P:GO:0016203; C:GO:0032154; C:GO:0045179; F:GO:0003774; P:GO:0045184; P:GO:0035317; C:GO:0030018; C:GO:0005886; F:GO:0005524; P:GO:0007435; P:GO:0000910	-			IPR002928; PTHR13140 (PANTHER), PTHR13140:SF23 (PANTHER)
Caenorhabditis briggsae	zinc c2h2 type family protein	4	F:GO:0005488; P:GO:0040010; P:GO:0040011; P:GO:0001703	-			IPR007087; IPR013087; IPR015880; PTHR23233 (PANTHER), PTHR23233:SF1 (PANTHER), SSF57667 (SUPERFAMILY)
Harpegnathos saltator	heterochromatin protein 1-beta-like	3	C:GO:0000785; F:GO:0005515; C:GO:0005634	-			IPR000953; IPR016197; G3DSA:2.40.50.40 (GENE3D), PTHR22812 (PANTHER), PTHR22812:SF4 (PANTHER)
Heligmosomoides polygyrus	mannose c type 1	3	C:GO:0009986; F:GO:0005537; F:GO:0004888	-			IPR001304; IPR016186; IPR016187; PTHR22801 (PANTHER), PTHR22801:SF9 (PANTHER), SignalP (SIGNALP)
Heligmosomoides polygyrus	venom c-type lectin mannose binding isoform 3	1	F:GO:0005529	-			IPR001304; IPR016186; IPR016187; PTHR22801 (PANTHER), PTHR22801:SF9 (PANTHER), SignalP (SIGNALP)
Heligmosomoides polygyrus	c-type lectin-1	1	F:GO:0005529	-			IPR001304; IPR016186; IPR016187; PTHR22801 (PANTHER), PTHR22801:SF9 (PANTHER), SignalP (SIGNALP)
	-	0					-
	-	0					-
Caenorhabditis elegans	subtilisin-like serine protease	8	P:GO:0018996; P:GO:0009792; P:GO:0008340; P:GO:0000003; F:GO:0005515; P:GO:0006898; P:GO:0002119; P:GO:0040011	-			-

Caenorhabditis briggsae	Hypothetical protein CBG14981 [Caenorhabditis briggsae]	2	P:GO:0040039; P:GO:0000003	-		-
Caenorhabditis briggsae	zyg-9 protein	0		F:GO:0005488; F:GO:0005515		-
Caenorhabditis briggsae	zyg-9 protein	0		F:GO:0005488; F:GO:0005515		-
Caenorhabditis elegans	laminin sub domain 2	0		P:GO:0006606; C:GO:0000786; F:GO:0016740; C:GO:0005643; C:GO:0016020; C:GO:0005694; C:GO:0005634; F:GO:0003677; P:GO:0006334; C:GO:0019861		PTHR12609 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	laminin sub domain 2	0		P:GO:0006606; C:GO:0005643; C:GO:0000786; F:GO:0016740; C:GO:0016020; C:GO:0005694; C:GO:0005634; F:GO:0003677; P:GO:0016998; P:GO:0006334		PTHR12609 (PANTHER), SignalP (SIGNALP)
Loa loa	briggsae cbr-set-16 protein	1	F:GO:0005515	-		-
	-	0				PTHR10721 (PANTHER), PTHR10721:SF2 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	oxidative stress induced growth inhibitor 1	0		P:GO:0030308; F:GO:0003674; F:GO:0005488; F:GO:0008083; P:GO:0008152; F:GO:0003824; P:GO:0008150		SSF51971 (SUPERFAMILY)
Caenorhabditis elegans	electron transfer flavoprotein-ubiquinone oxidoreductase	9	P:GO:0006979; F:GO:0004174; P:GO:0022900; F:GO:0048039; C:GO:0005743; F:GO:0009055; F:GO:0051539; F:GO:0043783; F:GO:0050660	-	EC:1.5.5.1; EC:1.16.8.0	IPR007859; IPR017896; PTHR10617 (PANTHER), PTHR10617:SF1 (PANTHER), SSF51905 (SUPERFAMILY), SSF54862 (SUPERFAMILY)
Caenorhabditis briggsae	electron transfer flavoprotein-ubiquinone mitochondrial	9	F:GO:0004174; F:GO:0046872; P:GO:0006979; C:GO:0005743; C:GO:0017133; F:GO:0009055; P:GO:0006810; F:GO:0051539; P:GO:0022900	-	EC:1.5.5.1	IPR003953; IPR007859; IPR017896; G3DSA:3.50.50.60 (GENE3D), PTHR10617 (PANTHER), PTHR10617:SF1 (PANTHER), SSF51905 (SUPERFAMILY), SSF54373 (SUPERFAMILY), SSF54862 (SUPERFAMILY)

Caenorhabditis elegans	electron transfer flavoprotein-ubiquinone oxidoreductase	9	P:GO:0006979; F:GO:0004174; P:GO:0022900; F:GO:0048039; C:GO:0005743; F:GO:0009055; F:GO:0051539; F:GO:0043783; F:GO:0050660	-	EC:1.5.5.1; EC:1.16.8.0	IPR007859; IPR017896; PTHR10617 (PANTHER), PTHR10617:SF1 (PANTHER), SSF51905 (SUPERFAMILY), SSF54862 (SUPERFAMILY)
Caenorhabditis elegans	low-density lipoprotein receptor-related protein 2	3	C:GO:0016021; F:GO:0004872; F:GO:0005509	-		-
Caenorhabditis elegans	branched-chain-amino-acid cytosolic	3	P:GO:0008652; P:GO:0009081; F:GO:0008483	-	EC:2.6.1.0	IPR001544; IPR005786; IPR018300; G3DSA:3.20.10.10 (GENE3D), G3DSA:3.30.470.10 (GENE3D)
Caenorhabditis elegans	vang (van gogh strabismus pla-r polarity protein) homolog family member (vang-1)	1	P:GO:0009792	-		IPR009539; PTHR20886:SF1 (PANTHER)
Loa loa	protein vprbp-like	0		F:GO:0005488; F:GO:0005515; C:GO:0005634		IPR006594; IPR011046; IPR013720; IPR015943; PTHR13129 (PANTHER)
Caenorhabditis elegans	protein vprbp-like	0		F:GO:0005488; F:GO:0005515; C:GO:0005634		IPR006594; IPR011046; IPR013720; IPR015943; PTHR13129 (PANTHER)
Caenorhabditis elegans	disulfide oxidoreductase	7	P:GO:0006917; F:GO:0051536; C:GO:0005743; F:GO:0008656; P:GO:0008635; P:GO:0051882; C:GO:0005783	-		IPR017941
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	dual specificity catalytic domain containing protein	5	F:GO:0004725; P:GO:0006470; P:GO:0000003; F:GO:0008138; P:GO:0040010	-	EC:3.1.3.48	IPR000340; IPR000387; IPR016130; IPR020422; G3DSA:3.90.190.10 (GENE3D), PTHR10159 (PANTHER), PTHR10159:SF5 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis briggsae	dual specificity catalytic domain containing protein	5	F:GO:0004725; F:GO:0008138; P:GO:0006470; P:GO:0040010; P:GO:0000003	-	EC:3.1.3.48	-
Loa loa	variable abnormal morphology family member (vab-10)	0				G3DSA:3.90.1290.10 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF49 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-dnj-4 protein	0		F:GO:0051082; C:GO:0016021; P:GO:0006457; F:GO:0031072		-

Loa loa	protein tyrosine non-receptor type 2	9	P:GO:0006470; C:GO:0005626; C:GO:0005829; F:GO:0005158; F:GO:0008270; C:GO:0031410; F:GO:0004725; P:GO:0046626; C:GO:0005783	-	EC:3.1.3.48	-
	-	0				-
Caenorhabditis briggsae	patched family protein	8	P:GO:0040025; F:GO:0008158; P:GO:0040018; P:GO:0018996; P:GO:0000003; P:GO:0008340; P:GO:0040011; C:GO:0016021	-		-
Caenorhabditis briggsae	hed family member (ptc-3)	8	P:GO:0009792; P:GO:0002119; F:GO:0008158; P:GO:0040018; P:GO:0018996; P:GO:0000003; P:GO:0040011; C:GO:0016021	-		SignalP (SIGNALP)
Ratus norvegicus	muc2_rat ame: full=mucin-2 short=muc-2 ame: full=intesti-l mucin-2 flags: precursor	0		P:GO:0032496; P:GO:0006917; C:GO:0005634; C:GO:0070703; P:GO:0071356; C:GO:0070702; P:GO:0006915; C:GO:0005737; C:GO:0005578; P:GO:0033189; C:GO:0005576; P:GO:0030336; P:GO:0071559; F:GO:0046983; P:GO:0009725; P:GO:0008285		-
Caenorhabditis elegans	protein phosphatase type 1	1	F:GO:0004721	-	EC:3.1.3.16	-
Caenorhabditis elegans	variable abnormal morphology family member (vab-10)	1	F:GO:0003779	-		PTHR11915 (PANTHER), PTHR11915:SF49 (PANTHER)
Caenorhabditis briggsae	variable abnormal morphology family member (vab-10)	1	F:GO:0003779	-		IPR001715; PTHR11915 (PANTHER), PTHR11915:SF49 (PANTHER)
Caenorhabditis elegans	variable abnormal morphology family member (vab-10)	1	F:GO:0003779	-		IPR001715; PTHR11915 (PANTHER), PTHR11915:SF49 (PANTHER)
Caenorhabditis briggsae	fibrillarin	6	C:GO:0005730; F:GO:0003723; P:GO:0006364; C:GO:0030529; F:GO:0008168; P:GO:0008033	-	EC:2.1.1.0	IPR000692; IPR020813; G3DSA:3.30.200.20 (GENE3D), G3DSA:3.40.50.150 (GENE3D), SSF53335 (SUPERFAMILY)

Caenorhabditis briggsae	fibrillarin	6	C:GO:0005730; F:GO:0003723; P:GO:0006364; C:GO:0030529; F:GO:0008168; P:GO:0008033	-	EC:2.1.1.0	IPR000692; IPR020813; G3DSA:3.30.200.20 (GENE3D), G3DSA:3.40.50.150 (GENE3D), SSF53335 (SUPERFAMILY)
Homo sapiens	tryptophanyl-tr- isoform cra_a	8	C:GO:0005625; F:GO:0004830; P:GO:0008285; P:GO:0006436; F:GO:0005524; F:GO:0005515; P:GO:0045765; C:GO:0005737	-	EC:6.1.1.2	-
	-	0				-
Caenorhabditis elegans	sphingosine-1-phosphate lyase 1	15	P:GO:0009653; P:GO:0008340; P:GO:0008202; P:GO:0040010; P:GO:0008585; C:GO:0016021; P:GO:0009058; F:GO:0016769; P:GO:0048609; F:GO:0030170; P:GO:0034754; P:GO:0030154; C:GO:0005783; F:GO:0016831; P:GO:0019752	-	EC:4.1.1.0	-
Caenorhabditis briggsae	glutamic acid-rich protein precursor	4	P:GO:0002119; F:GO:0005515; P:GO:0009792; P:GO:0040007	-		SignalP (SIGNALP)
Caenorhabditis briggsae	glutamic acid-rich protein precursor	4	P:GO:0002119; F:GO:0005515; P:GO:0009792; P:GO:0040007	-		-
Caenorhabditis briggsae	glutamic acid-rich protein precursor	4	P:GO:0002119; F:GO:0005515; P:GO:0009792; P:GO:0040007	-		-
Caenorhabditis briggsae	glutamic acid-rich protein precursor	4	P:GO:0002119; F:GO:0005515; P:GO:0009792; P:GO:0040007	-		-
Caenorhabditis elegans	rab-related protein 3	8	C:GO:0005737; F:GO:0005525; F:GO:0005515; P:GO:0006913; P:GO:0006886; C:GO:0005634; P:GO:0007264; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001806; IPR013753; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF242 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		PTHR23290 (PANTHER)

Homo sapiens	serpin peptidase clade a (alpha-1 antitrypsin) member 3	8	F:GO:0004867; F:GO:0003677; P:GO:0030277; P:GO:0006953; F:GO:0005515; C:GO:0005576; C:GO:0005634; P:GO:0019216	-		IPR000215; G3DSA:2.30.39.10 (GENE3D), G3DSA:3.30.497.10 (GENE3D), PTHR11461:SF44 (PANTHER)
Caenorhabditis briggsae	e3 ubiquitin-protein ligase rnf19a	7	P:GO:0006464; F:GO:0003676; P:GO:0000226; C:GO:0005813; F:GO:0008134; C:GO:0016020; F:GO:0008270	-		IPR001878; IPR002867; PTHR11685 (PANTHER), PTHR11685:SF5 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis elegans	e3 ubiquitin-protein ligase rnf19a	5	C:GO:0005856; C:GO:0016020; F:GO:0046872; C:GO:0005737; F:GO:0005515	-		IPR001878; IPR002867; PTHR11685 (PANTHER), PTHR11685:SF5 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-reps-1 protein	0		F:GO:0005509		-
Ailuropoda melanoleuca	tubulin beta-2c chain	6	P:GO:0007018; F:GO:0005525; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000217; IPR002453; IPR003008; IPR010916; IPR017975
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	spc97 spc98 family protein	2	P:GO:0007275; P:GO:0000003	-		IPR007259; IPR018483
Acyrthosiphon pisum	splicing arginine serine-rich 16	0		F:GO:0003676; F:GO:0000166; F:GO:0008270; P:GO:0008150; C:GO:0005575		-
Teladorsagia circumcincta	calcium activated nucleotidase isoform cra_b	8	P:GO:0040010; P:GO:0008340; F:GO:0004871; P:GO:0043123; F:GO:0017110; F:GO:0005515; P:GO:0008152; C:GO:0005789	-	EC:3.6.1.6	IPR009283
Teladorsagia circumcincta	calcium-activated apyrase	0		F:GO:0005509; F:GO:0016787; F:GO:0016462		-
Sorghum bicolor	10 kda secreted protein	0				-
Caenorhabditis elegans	metastasis suppressor protein 1	3	N:GO:0071842; F:GO:0005515; C:GO:0044424	-		-
Caenorhabditis elegans	metastasis suppressor protein 1	3	N:GO:0071842; F:GO:0005515; C:GO:0044424	-		-

Pongo abelii	cuta divalent cation tolerance homolog (coli)	3	P:GO:0008104; F:GO:0019899; C:GO:0016020	-		IPR004323; IPR011322
	-	0				-
Caenorhabditis elegans	eukaryotic translation initiation factor subunit 1 alpha	13	F:GO:0003743; C:GO:0005829; C:GO:0005850; F:GO:0003723; P:GO:0045948; C:GO:0005851; P:GO:0040007; P:GO:0043558; P:GO:0002119; F:GO:0005515; P:GO:0046777; P:GO:0009792; C:GO:0005634	-		IPR006186; SignalP (SIGNALP)
Caenorhabditis elegans	phospholipase d3	3	F:GO:0016787; P:GO:0008152; C:GO:0044425	-		IPR013582; G3DSA:3.30.870.10 (GENE3D), PTHR10185 (PANTHER), SSF56024 (SUPERFAMILY)
Caenorhabditis briggsae	rhomboid family protein	0		F:GO:0003676; F:GO:0016787; C:GO:0016021; F:GO:0008270		-
Caenorhabditis briggsae	mercaptopyruvate sulfurtransferase	0		F:GO:0016740; C:GO:0016021; C:GO:0005743; P:GO:0008272; C:GO:0005737; F:GO:0016784; F:GO:0003674; F:GO:0004792; P:GO:0008152; P:GO:0008150		IPR001763; PTHR11364 (PANTHER)
Caenorhabditis briggsae	mercaptopyruvate sulfurtransferase	0		F:GO:0016740; C:GO:0016021; C:GO:0005743; P:GO:0008272; C:GO:0005737; F:GO:0016784; F:GO:0003674; F:GO:0004792; P:GO:0008152; P:GO:0008150		IPR001763; PTHR11364 (PANTHER)
						IPR010939; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF14 (PANTHER), SSF48726 (SUPERFAMILY)
Angiostrongylus cantonensis	transmembrane protein 161b	0		P:GO:0043066; C:GO:0016021; C:GO:0016020; F:GO:0003674; C:GO:0005575; P:GO:0034599; P:GO:0032526; P:GO:0008150; P:GO:0045739; P:GO:0034644		IPR019395; PTHR13624 (PANTHER), PTHR13624:SF1 (PANTHER), SignalP (SIGNALP)

Caenorhabditis elegans	a in (actin filament binding protein) homolog family member (afd-1)	6	C:GO:0005911; P:GO:0040010; P:GO:0007267; P:GO:0007165; F:GO:0008022; C:GO:0005829	-		IPR000159; PTHR10398 (PANTHER), SSF54236 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	transcription factor btf3 homolog 4	1	F:GO:0005515	-		IPR002715; PTHR10351 (PANTHER)
Caenorhabditis elegans	rad54 homolog b	2	F:GO:0003676; F:GO:0003824	-		IPR000330; PTHR10799 (PANTHER), PTHR10799:SF66 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	kiaa1520 splice	16	P:GO:0001916; F:GO:0046979; C:GO:0042825; C:GO:0005764; C:GO:0005743; P:GO:0015031; F:GO:0042288; F:GO:0046978; P:GO:0015833; F:GO:0015421; P:GO:0055085; F:GO:0042605; P:GO:0006200; C:GO:0005886; F:GO:0005524; F:GO:0046980	-	EC:3.6.3.23	IPR011527; IPR017940; G3DSA:1.20.1560.10 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF82 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	actin-related protein 3	21	P:GO:0050775; C:GO:0030056; C:GO:0030027; C:GO:0000139; P:GO:0043519; C:GO:0005884; P:GO:0010631; P:GO:0046677; P:GO:0034314; F:GO:0003779; P:GO:0009792; C:GO:0060076; P:GO:0051789; C:GO:0005885; P:GO:0045666; P:GO:0016331; P:GO:0010592; P:GO:0009743; F:GO:0005524; C:GO:0002102; P:GO:0051491	-		IPR004000; IPR015623; IPR020902; G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), SSF53067 (SUPERFAMILY)
Caenorhabditis elegans	small conductance calcium-activated potassium isoform m	4	F:GO:0015269; P:GO:0006813; C:GO:0016021; F:GO:0005516	-		IPR004178; IPR011996; IPR013099; IPR015449; G3DSA:1.10.287.70 (GENE3D), PTHR10153:SF5 (PANTHER), SignalP (SIGNALP), SSF81324 (SUPERFAMILY)
	-	0				PD015172 (PRODOM)
	-	0				-

Loa loa	eukaryotic translation initiation factor 2 alpha ki-se pek	16	C:GO:0016020; P:GO:0065008; P:GO:0046777; P:GO:0031018; P:GO:0001503; P:GO:0006983; P:GO:0032055; P:GO:0007154; F:GO:0004694; P:GO:0023060; F:GO:0042802; P:GO:0006446; P:GO:0006915; P:GO:0051260; C:GO:0005783; P:GO:0030968	-		IPR011047; IPR018391; SignalP (SIGNALP)
Caenorhabditis elegans	choline-phosphate cytidylyltransferase b	15	P:GO:0042067; P:GO:0008340; P:GO:0040007; P:GO:0007052; P:GO:0040017; F:GO:0004105; P:GO:0006911; P:GO:0002119; C:GO:0005875; P:GO:0048477; P:GO:0006656; F:GO:0005488; C:GO:0044444; C:GO:0005634; P:GO:0007476	-	EC:2.7.7.15	IPR004820; IPR004821; IPR014729; PTHR10739 (PANTHER), PTHR10739:SF13 (PANTHER), SSF52374 (SUPERFAMILY)
Caenorhabditis briggsae	protein tbrg4	0				-
Caenorhabditis elegans	inhibitor of nf ki-se epsilon subunit homolog family member (ikke-1)	0		F:GO:0004672; F:GO:0005524; F:GO:0000166; P:GO:0006468; P:GO:0019915; F:GO:0005515; F:GO:0004674		-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	slit homolog 3	0		P:GO:0035385; P:GO:0070100; P:GO:0008285; P:GO:0007420; P:GO:0032870; P:GO:0030154; F:GO:0003674; P:GO:0050919; F:GO:0005102; C:GO:0005615; P:GO:0048846; F:GO:0005509; P:GO:0030308; P:GO:0009887; P:GO:0010629; P:GO:0007275; C:GO:0005739; P:GO:0021510; P:GO:0001554; P:GO:0007399; P:GO:0007411; C:GO:0005624; P:GO:0051414; P:GO:0021834; F:GO:0005515; C:GO:0005576; F:GO:0048495		IPR000483; IPR001611; IPR003591; PR00019 (PRINTS), G3DSA:3.80.10.10 (GENE3D), PTHR23154 (PANTHER), PTHR23154:SF44 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)
Caenorhabditis briggsae	vacuolar protein sorting 33a	3	F:GO:0005515; P:GO:0006810; P:GO:0009987	-		IPR001619; PTHR11679:SF1 (PANTHER)
Caenorhabditis elegans	attractin-like 1	5	P:GO:0018991; F:GO:0005515; P:GO:0040010; P:GO:0040011; C:GO:0016021	-		IPR000859; IPR006210; IPR013032; PTHR10574 (PANTHER), PTHR10574:SF3 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	die-1	0		F:GO:0008270; C:GO:0005622		IPR007087; IPR015880; PTHR21190 (PANTHER), SSF57667 (SUPERFAMILY)
Caenorhabditis briggsae	kinesin-like protein family member (klp-12)	5	P:GO:0009792; F:GO:0005515; P:GO:0007067; F:GO:0003824; F:GO:0000166	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR22844 (PANTHER)
	-	0				-
Caenorhabditis elegans	prolyl carboxy peptidase like family member (pcp-3)	0		P:GO:0006508; F:GO:0004180; F:GO:0008236; C:GO:0016021; P:GO:0008150; F:GO:0005515; C:GO:0005575		IPR008758; PTHR11010:SF4 (PANTHER)
Caenorhabditis elegans	prolyl carboxy peptidase like family member (pcp-3)	0		P:GO:0006508; F:GO:0004180; F:GO:0008236; C:GO:0016021; P:GO:0008150; F:GO:0005515; C:GO:0005575		IPR008758; PTHR11010:SF4 (PANTHER)

	-	0				-
Caenorhabditis elegans	ras family protein	0		F:GO:0005525; P:GO:0007264; F:GO:0000166; P:GO:0015031		G3DSA:3.40.50.300 (GENE3D)
	-	0				-
Caenorhabditis briggsae	variable abnormal morphology family member (vab-10)	0		F:GO:0005509; P:GO:0007050; F:GO:0003779		IPR001101; G3DSA:3.90.1290.10 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF49 (PANTHER), SSF75399 (SUPERFAMILY)
	-	0				-
	-	0				-
Loa loa	origin recognition subunit 1-like	6	C:GO:0043229; F:GO:0005488; P:GO:0040007; P:GO:0040035; P:GO:0002119; P:GO:0009792	-		IPR020793; G3DSA:3.40.50.300 (GENE3D), PTHR10763 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	nuclear receptor nhr-6	1	F:GO:0005515	-		IPR000536; IPR008946; PTHR11865 (PANTHER), PTHR11865:SF168 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-kcc-3 protein	4	P:GO:0055085; P:GO:0006811; C:GO:0016020; F:GO:0005215	-		IPR004841; PTHR11827 (PANTHER), PTHR11827:SF5 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	major allergen	0				-
Ovis aries	myl6 protein	7	C:GO:0016461; F:GO:0008307; P:GO:0007519; P:GO:0030049; F:GO:0030898; F:GO:0005509; F:GO:0003774	-		SignalP (SIGNALP)
Caenorhabditis elegans	2-oxoglutarate dehydroge-se e1 component	3	F:GO:0004591; F:GO:0030976; P:GO:0006096	-	EC:1.2.4.2	IPR011603
Caenorhabditis elegans	hypothetical protein R12C12.9 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein R12C12.9 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein R12C12.9 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	temporarily assigned gene -me family member (tag-233)	5	P:GO:0007268; C:GO:0043231; C:GO:0044444; P:GO:0019915; C:GO:0045202	-		IPR001594; PTHR22883 (PANTHER), SignalP (SIGNALP)

Caenorhabditis briggsae	lysocardiolipin acyltransferase 1	0		F:GO:0016740; F:GO:0003841; C:GO:0016021; C:GO:0016020; P:GO:0007275; C:GO:0005789; F:GO:0005515; F:GO:0008415; C:GO:0005783; P:GO:0008654; P:GO:0008152		PTHR10983 (PANTHER), PTHR10983:SF1 (PANTHER)
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	0				-
Caenorhabditis elegans	solute carrier family 30 (zinc transporter) member 6	8	F:GO:0005385; P:GO:0055085; P:GO:0040010; F:GO:0005488; P:GO:0018991; P:GO:0006829; C:GO:0016021; C:GO:0000139	-		-
	-	0				-
Caenorhabditis elegans	zinc carboxypeptidase family protein	3	P:GO:0006508; F:GO:0004181; F:GO:0008270	-	EC:3.4.17.0	IPR000834; IPR003146; IPR009020; G3DSA:3.30.70.340 (GENE3D), G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), PTHR11705:SF12 (PANTHER), SSF53187 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	nuc173 domain-containing protein	0		F:GO:0005488		PTHR21576 (PANTHER), PTHR21576:SF2 (PANTHER), SignalP (SIGNALP)
Saccoglossus kowalevskii	f-box-like wd repeat-containing protein tbl1y	9	F:GO:0030528; P:GO:0006357; P:GO:0048545; P:GO:0045892; C:GO:0043234; F:GO:0003677; P:GO:0006508; C:GO:0044451; F:GO:0008134	-		IPR006594; IPR013720
Caenorhabditis elegans	dph3 homolog	7	P:GO:0017183; P:GO:0051099; F:GO:0005515; P:GO:0050709; P:GO:0009792; C:GO:0005737; C:GO:0005634	-		IPR007872; PTHR21454 (PANTHER), PTHR21454:SF2 (PANTHER), SSF144217 (SUPERFAMILY)
Caenorhabditis briggsae	moving junction protein	0		C:GO:0005618; P:GO:0006950; P:GO:0007155; C:GO:0009986; C:GO:0016020; P:GO:0016998; F:GO:0005515		-
Hydra magnipapillata	nuclease harbi1-like	0				PTHR22930 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)

	-	0				-
Caenorhabditis briggsae	phosphoribosyl pyrophosphate synthetase 1	8	P:GO:0009792; F:GO:0016301; P:GO:0009156; F:GO:0004749; F:GO:0005524; F:GO:0000287; P:GO:0009116; F:GO:0042803	-	EC:2.7.6.1	IPR000836; IPR000842; IPR005946; G3DSA:3.40.50.2020 (GENE3D), PTHR10210 (PANTHER), PTHR10210:SF14 (PANTHER), SSF53271 (SUPERFAMILY)
Caenorhabditis elegans	Hypothetical protein ZK355.2a [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	briggsae cbr-dys-1 protein	7	P:GO:0007271; F:GO:0005515; P:GO:0040017; C:GO:0016010; F:GO:0005277; P:GO:0015870; P:GO:0046716	-		-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Loa loa	histone deacetylase 3	3	P:GO:0016575; P:GO:0006350; F:GO:0004407	-		-
Brugia malayi	mbt repeat family protein	0		P:GO:0045449; F:GO:0008270; C:GO:0005634		IPR004092; G3DSA:2.30.30.160 (GENE3D), SSF63748 (SUPERFAMILY)
Caenorhabditis elegans	jmjc domain containing protein	5	P:GO:0034720; F:GO:0034647; P:GO:0043970; F:GO:0043992; F:GO:0005515	-		IPR011011; IPR013083; PTHR10694 (PANTHER), PTHR10694:SF1 (PANTHER)
Brugia malayi	uncoordi-ted family member (unc-73)	5	P:GO:0023034; P:GO:0031175; P:GO:0050794; F:GO:0005488; C:GO:0044444	-		IPR018159; G3DSA:1.20.58.60 (GENE3D), PTHR22826 (PANTHER), PTHR22826:SF39 (PANTHER), SSF46966 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	6	P:GO:0018996; P:GO:0009792; P:GO:0040017; P:GO:0040007; F:GO:0005488; P:GO:0002119	-		IPR001611; IPR003591; G3DSA:3.80.10.10 (GENE3D), PTHR23154 (PANTHER), PTHR23154:SF116 (PANTHER), PS51450 (PROFILE), SSF52058 (SUPERFAMILY)
	-	0				-
Brugia malayi	sigma non-opioid intracellular receptor 1	6	F:GO:0005488; F:GO:0004872; C:GO:0044425; C:GO:0044444; C:GO:0005635; C:GO:0005886	-		IPR006716; SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	clathrin-associated protein	7	P:GO:0016183; C:GO:0008021; P:GO:0007269; C:GO:0030122; F:GO:0005515; P:GO:0006886; P:GO:0033227	-		IPR001392; IPR008968; IPR015629; IPR018240; G3DSA:2.60.40.1170 (GENE3D), PTHR11998 (PANTHER)
Caenorhabditis elegans	early endosome antigen 1	4	P:GO:0016192; F:GO:0005515; C:GO:0044444; C:GO:0016020	-		IPR007087; IPR015880; PD936484 (PRODOM), PTHR23164 (PANTHER)
Caenorhabditis elegans	mitochondrial carrier triple repeat 1	4	P:GO:0009792; F:GO:0005488; P:GO:0055085; C:GO:0016021	-		IPR001993; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF14 (PANTHER)
Caenorhabditis elegans	transcription termi-tion r- polymerase ii	5	F:GO:0005488; P:GO:0044260; P:GO:0090304; P:GO:0010467; F:GO:0016787	-		IPR000330; IPR001650; IPR002464; G3DSA:3.40.50.300 (GENE3D), PTHR10799 (PANTHER), PTHR10799:SF63 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	transaldolase	8	P:GO:0009052; F:GO:0004801; P:GO:0032231; P:GO:0035107; P:GO:0007424; P:GO:0009792; C:GO:0005737; P:GO:0002064	-	EC:2.2.1.2	-
Caenorhabditis elegans	denticleless homolog	4	P:GO:0050896; P:GO:0044238; P:GO:0044260; C:GO:0044424	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR22852 (PANTHER)
Caenorhabditis elegans	denticleless homolog	4	P:GO:0050896; P:GO:0044238; P:GO:0044260; C:GO:0044424	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR22852 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein W05H9.1 [Caenorhabditis elegans]	0				-
Ancylostoma caninum	af132291_1ancylostoma-secreted protein 1 precursor	0		C:GO:0005576		-

Homo sapiens	matrix metalloprotei-se 2	39	P:GO:0001957; P:GO:0035094; P:GO:0001541; P:GO:0001542; P:GO:0051602; P:GO:0060033; F:GO:0008270; P:GO:0071347; P:GO:0042542; P:GO:0048771; P:GO:0014823; P:GO:0009612; P:GO:0007568; P:GO:0060325; C:GO:0005615; P:GO:0060740; P:GO:0007162; P:GO:0001955; P:GO:0045906; P:GO:0007565; F:GO:0004222; C:GO:0005578; P:GO:0001666; P:GO:0060346; P:GO:0030574; P:GO:0042493; P:GO:0014012;	-	EC:3.4.24.0	IPR001818; G3DSA:3.40.390.10 (GENE3D), PTHR10201 (PANTHER), PTHR10201:SF29 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	ras family protein	6	P:GO:0007264; C:GO:0005622; P:GO:0006355; F:GO:0005524; F:GO:0008134; P:GO:0015031	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	C:GO:0016020	-		IPR000175; PTHR11616:SF16 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	hypotheticial protein	0				IPR018943
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG02063 [Caenorhabditis briggsae]	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	p21-activated ki-se family member (pak-1)	16	C:GO:0005925; P:GO:0007411; P:GO:0006468; F:GO:0004702; P:GO:0008360; F:GO:0005515; P:GO:0050803; P:GO:0007155; F:GO:0005525; C:GO:0016021; P:GO:0007391; P:GO:0007254; C:GO:0005856; P:GO:0016601; F:GO:0005524; P:GO:0050770	-		-
	-	0				-

Caenorhabditis briggsae	muscle glycogen phosphorylase	19	P:GO:0001666; F:GO:0008184; C:GO:0016529; F:GO:0008144; C:GO:0005829; C:GO:0030018; P:GO:0000910; P:GO:0005980; C:GO:0005625; F:GO:0005509; P:GO:0006874; F:GO:0005085; P:GO:0051056; F:GO:0042803; F:GO:0016208; P:GO:0009792; F:GO:0030170; P:GO:0051591; F:GO:0005529	-		IPR000811; IPR011833; G3DSA:3.40.50.2000 (GENE3D), SSF53756 (SUPERFAMILY)
Angiostrongylus cantonensis	-nos homolog 3	0		P:GO:0006417; P:GO:0007283; P:GO:0048477; F:GO:0008270; F:GO:0003674; F:GO:0003723; P:GO:0007275; P:GO:0009792; P:GO:0030154; C:GO:0005575; F:GO:0005515		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	enhancer of -1 mutant phenotype family member (eel-1)	0				-
Loa loa	adrenocortical alacrimia (triple-a)	0		C:GO:0005643; C:GO:0005635; F:GO:0003674; P:GO:0006913; P:GO:0007612; P:GO:0046822; C:GO:0005575; P:GO:0008150; P:GO:0009566		IPR001680; IPR015943; IPR019781; PTHR14494 (PANTHER), SSF101908 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	3-oxoacyl-acyl-carrier-protein reductase	5	F:GO:0008667; P:GO:0009239; P:GO:0055114; F:GO:0005488; F:GO:0004022	-	EC:1.3.1.28; EC:1.1.1.1	IPR002198; IPR002347; IPR016040; IPR020904; PTHR19410:SF76 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	hypothetical protein T25C12.3 [Caenorhabditis elegans]	0		F:GO:0005488; P:GO:0040010		-
	-	0				-
Caenorhabditis elegans	type iii restriction res subunit family protein	3	F:GO:0005524; F:GO:0003677; F:GO:0008026	-		IPR011545; G3DSA:3.40.50.300 (GENE3D), PTHR11752 (PANTHER), PTHR11752:SF8 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)

Loa loa	hypothetical protein LOAG_03273 [Loa loa]	0		F:GO:0008270; C:GO:0005622		IPR007087; IPR015880; PTHR23224 (PANTHER), PTHR23224:SF120 (PANTHER), SSF57667 (SUPERFAMILY)
Drosophila virilis	proteophosphoglycan 5	0		F:GO:0008061; P:GO:0006030; C:GO:0005576		-
	-	0				G3DSA:3.40.50.300 (GENE3D), PTHR10887 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	calcium calmodulin-dependent protein ki-se ki-se alpha	10	C:GO:0005829; F:GO:0005516; P:GO:0032147; C:GO:0005625; P:GO:0032793; F:GO:0005524; P:GO:0019722; F:GO:0004683; C:GO:0005634; P:GO:0006468	-	EC:2.7.11.17	IPR011009; IPR020636; IPR020657; G3DSA:1.10.510.10 (GENE3D)
Ixodes scapularis	multidrug resistance-associated protein 4-like	6	F:GO:0017111; P:GO:0006810; C:GO:0031088; C:GO:0005624; F:GO:0016491; C:GO:0005886	-	EC:3.6.1.15	PTHR19242 (PANTHER), PTHR19242:SF97 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	metaxin 1	5	P:GO:0006626; F:GO:0005515; P:GO:0000003; C:GO:0016021; C:GO:0005741	-		IPR010987; IPR017933; IPR019564; PTHR12289 (PANTHER), PTHR12289:SF16 (PANTHER)
Caenorhabditis elegans	aarf domain containing ki-se 1	1	F:GO:0016740	-		PTHR10566 (PANTHER), PTHR10566:SF7 (PANTHER)
	-	0				-
Brugia malayi	hypothetical protein Bm1_01005 [Brugia malayi]	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	gtp-binding protein parf	2	C:GO:0005622; F:GO:0000166	-		IPR001806; IPR013753; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR14932 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	kinesin family member 11	11	P:GO:0006915; C:GO:0000922; P:GO:0090307; C:GO:0005876; P:GO:0007100; C:GO:0016585; F:GO:0003774; F:GO:0000166; C:GO:0005871; F:GO:0019901; C:GO:0051233	-		IPR001752; IPR019821; PTHR16012 (PANTHER), PTHR16012:SF151 (PANTHER), SSF52540 (SUPERFAMILY)
Ancylostoma caninum	venom-allergen-like protein family member (vap-1)	2	P:GO:0040011; P:GO:0006898	-		-
Brugia malayi	fragile site-associated protein	0				-
	-	0				-

Callithrix jacchus	dead (asp-glu-ala-asp) box polypeptide 5 isoform 1	11	F:GO:0003723; F:GO:0003712; P:GO:0016049; C:GO:0005681; C:GO:0005730; F:GO:0008026; P:GO:0008380; F:GO:0005524; P:GO:0006397; F:GO:0003724; P:GO:0045941	-		-
Brugia malayi	hypothetical protein [Brugia malayi]	0		F:GO:0005096; P:GO:0051056; P:GO:0007165; C:GO:0005622		-
Caenorhabditis briggsae	wd repeat domain 3	1	P:GO:0006898	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; IPR020472; PTHR19853 (PANTHER)
Caenorhabditis briggsae	wd repeat domain 3	1	P:GO:0006898	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; IPR020472; PTHR19853 (PANTHER)
Loa loa	sp1070 cg9138-pa	2	F:GO:0005488; C:GO:0044425	-		IPR008985; IPR013032; IPR013320; PTHR19277 (PANTHER)
Caenorhabditis elegans	uncharacterized protein c10orf58-like	2	C:GO:0005739; F:GO:0005515	-		IPR012335; SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR011680; PTHR12394:SF1 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	programmed cell death 6 interacting protein	5	P:GO:0006915; F:GO:0046983; F:GO:0048306; C:GO:0005829; F:GO:0017124	-		IPR004328; G3DSA:1.25.40.280 (GENE3D), PTHR23030 (PANTHER), PTHR23030:SF11 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-gbf-1 protein	0		P:GO:0032012; F:GO:0005086; C:GO:0005622		-
Caenorhabditis elegans	briggsae cbr-gbf-1 protein	0		P:GO:0032012; F:GO:0005086; C:GO:0005622		-
Caenorhabditis elegans	briggsae cbr-gbf-1 protein	0		P:GO:0032012; F:GO:0005086; C:GO:0005622		-
	-	0				-
	-	0				-
	-	0				-
Danio rerio	si: (novel transposase)	0		C:GO:0009507		PTHR22930 (PANTHER)
Caenorhabditis elegans	u3 small nucleolar r--associated protein 18 homolog	4	P:GO:0009792; P:GO:0002119; P:GO:0040010; P:GO:0006898	-		IPR001680; IPR011046; IPR015943; PTHR18359 (PANTHER)
	-	0				-
Caenorhabditis elegans	cysteine protease atg4b	3	P:GO:0006508; F:GO:0005515; F:GO:0008234	-		IPR005078; PTHR22624:SF18 (PANTHER)

Caenorhabditis elegans	high-affinity copper uptake protein	5	P:GO:0010171; P:GO:0040018; P:GO:0040010; P:GO:0000003; C:GO:0016020	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	developmentally-regulated gtp-binding protein 2	5	F:GO:0005525; C:GO:0016021; P:GO:0015684; F:GO:0015093; C:GO:0005739	-		IPR002917; IPR006073; IPR006074; G3DSA:3.40.50.300 (GENE3D), PTHR11702 (PANTHER), PTHR11702:SF7 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR001534; SignalP (SIGNALP)
Caenorhabditis elegans	dihydropteridine reductase	3	F:GO:0016491; P:GO:0044237; F:GO:0050662	-		IPR002198; IPR016040; IPR020904; PTHR15104 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-phat-2 protein	1	F:GO:0005515	-		-
Caenorhabditis elegans	briggsae cbr-phat-2 protein	1	F:GO:0005515	-		IPR003582; PTHR21724 (PANTHER)
Caenorhabditis elegans	briggsae cbr-phat-2 protein	1	F:GO:0005515	-		-
Brugia malayi	briggsae cbr-sax-2 protein	11	F:GO:0005515; P:GO:0048601; P:GO:0016055; P:GO:0042052; P:GO:0008407; F:GO:0016563; P:GO:0045860; P:GO:0048800; P:GO:0035317; P:GO:0048814; C:GO:0005938	-		PTHR12295 (PANTHER), PTHR12295:SF6 (PANTHER)
	-	0				IPR007087; IPR015880
Caenorhabditis briggsae	non-specific lipid-transfer protein	6	F:GO:0016747; F:GO:0008289; C:GO:0005777; F:GO:0005515; P:GO:0019915; P:GO:0008152	-	EC:2.3.1.0	IPR002155; IPR016038; IPR016039; IPR020615; IPR020616; PTHR18919:SF9 (PANTHER)
Caenorhabditis briggsae	non-specific lipid-transfer protein	6	F:GO:0016747; F:GO:0008289; C:GO:0005777; F:GO:0005515; P:GO:0019915; P:GO:0008152	-	EC:2.3.1.0	IPR002155; IPR016038; IPR016039; IPR020615; IPR020616; PTHR18919:SF9 (PANTHER)
Caenorhabditis briggsae	ankyrin repeat domain protein	0		F:GO:0016740; F:GO:0008270; F:GO:0005515; C:GO:0005622		-
Caenorhabditis elegans	testis derived transcript	1	P:GO:0008340	-		IPR007087; IPR010442; PTHR18973 (PANTHER), PTHR18973:SF81 (PANTHER)
	-	0				-
Caenorhabditis elegans	hypothetical protein Y45F10B.13 [Caenorhabditis elegans]	1	P:GO:0009792	-		-
Caenorhabditis elegans	hypothetical protein Y45F10B.13 [Caenorhabditis elegans]	1	P:GO:0009792	-		-
Caenorhabditis elegans	briggsae cbr-vha-19 protein	4	P:GO:0000003; P:GO:0018996; P:GO:0002119; P:GO:0006898	-		IPR008388; PF05827 (PFAM)
	-	0				SignalP (SIGNALP)
Brugia malayi	synthetic lethal with mec family member (sym-4)	1	P:GO:0040011	-		-

Brugia malayi	synthetic lethal with mec family member (sym-4)	0		P:GO:0040011		-
Caenorhabditis briggsae	tumor protein d52	6	F:GO:0005509; F:GO:0046982; C:GO:0005783; F:GO:0042803; C:GO:0048471; P:GO:0030183	-		-
	-	0				-
Caenorhabditis briggsae	cg30118 cg30118-pb	0		C:GO:0031533; F:GO:0004651; F:GO:0005515; P:GO:0006370		IPR004206; SSF52540 (SUPERFAMILY)
Homo sapiens	t cell receptor beta chain	0				SignalP (SIGNALP)
Caenorhabditis elegans	g in family member (glb-8)	4	F:GO:0020037; F:GO:0005344; P:GO:0015671; F:GO:0019825	-		IPR000971; IPR009050; IPR012292
Loa loa	hypothetical protein LOAG_02232 [Loa loa]	0				-
	-	0				-
Pristionchus pacificus	armadillo beta-catenin-like repeat family protein	39	P:GO:0009887; P:GO:0016055; P:GO:0048754; P:GO:0060562; P:GO:0007154; N:GO:0061138; C:GO:0043234; P:GO:0001822; C:GO:0044463; P:GO:0030324; P:GO:0045944; P:GO:0030334; P:GO:0003002; C:GO:0005913; P:GO:0007399; P:GO:0048523; C:GO:0005634; P:GO:0048598; P:GO:0042659; P:GO:0048646; P:GO:0042127; P:GO:0040010; P:GO:0007155; P:GO:0030855; P:GO:0040026; F:GO:0003713; C:GO:0005624;	-		IPR000225; IPR011989; IPR016024; PTHR23315 (PANTHER), PTHR23315:SF3 (PANTHER)
Dictyocaulus viviparus	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis elegans	acid phosphatase	3	F:GO:0046872; C:GO:0016021; F:GO:0003993	-	EC:3.1.3.2	IPR003961; IPR004843; IPR008963; IPR015914; G3DSA:3.60.21.10 (GENE3D), PTHR22953 (PANTHER), SSF56300 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	zinc carboxypeptidase family protein	3	P:GO:0006508; F:GO:0004181; F:GO:0008270	-	EC:3.4.17.0	IPR000834; G3DSA:3.40.630.10 (GENE3D), PTHR11705 (PANTHER), PTHR11705:SF10 (PANTHER), SSF53187 (SUPERFAMILY)
	-	0				-

Caenorhabditis briggsae	glutamate-rich wd repeat containing 1	1	F:GO:0016740	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR22850 (PANTHER), PTHR22850:SF6 (PANTHER)
Caenorhabditis elegans	mitochondrial ribosomal protein s17	7	P:GO:0009792; P:GO:0002119; F:GO:0005515; C:GO:0044444; P:GO:0000003; C:GO:0043229; P:GO:0040007	-		IPR001993; IPR016027; PTHR11896:SF2 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	ke (drosophila actin-binding) homolog family member (ketn-1)	1	P:GO:0000003	-		SignalP (SIGNALP)
Loa loa	msp domain protein with glu-rich domain	2	C:GO:0005856; F:GO:0005198	-		IPR000535; IPR008962; PTHR21513 (PANTHER), PTHR21513:SF1 (PANTHER)
Caenorhabditis elegans	thioredoxin	3	C:GO:0005737; P:GO:0006516; F:GO:0003824	-		-
Caenorhabditis elegans	briggsae cbr-unc-71 protein	0		P:GO:0006508; F:GO:0008270; F:GO:0004222		SignalP (SIGNALP)
Pediculus humanus corporis	mitogen-activated protein ki-se ki-se 7	2	F:GO:0016301; F:GO:0005515	-		IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22986 (PANTHER), PTHR22986:SF34 (PANTHER)
Caenorhabditis elegans	mboat family protein	2	C:GO:0016020; F:GO:0016740	-		SignalP (SIGNALP)
Brugia malayi	elegans protein partially confirmed by transcript evidence	0		F:GO:0008270; C:GO:0005622		-
	-	0				-
Nematostella vectensis	ribosomal protein s5	14	P:GO:0006413; F:GO:0003729; P:GO:0008340; F:GO:0008270; P:GO:0006355; P:GO:0040007; F:GO:0003735; P:GO:0006450; P:GO:0000003; C:GO:0022627; P:GO:0002119; F:GO:0005515; P:GO:0009792; C:GO:0005634	-		IPR000235; IPR005716; IPR020606
Caenorhabditis elegans	abnormal cell lineage family member (lin-54)	1	C:GO:0070176	-		IPR005172; PTHR12446 (PANTHER), PTHR12446:SF6 (PANTHER)
	-	0				-
	-	0				-

Caenorhabditis elegans	aldehyde dehydroge-se	8	F:GO:0004029; F:GO:0003676; F:GO:0001758; P:GO:0055114; F:GO:0004028; C:GO:0005622; P:GO:0006081; F:GO:0008270	-	EC:1.2.1.3; EC:1.2.1.36	IPR015590; IPR016161; IPR016163; PTHR11699:SF46 (PANTHER)
Caenorhabditis elegans	aldehyde dehydroge-se	8	F:GO:0004029; F:GO:0003676; F:GO:0001758; P:GO:0055114; F:GO:0004028; C:GO:0005622; P:GO:0006081; F:GO:0008270	-	EC:1.2.1.3; EC:1.2.1.36	IPR015590; IPR016161; IPR016163; PTHR11699:SF46 (PANTHER)
Caenorhabditis elegans	aldehyde dehydroge-se	8	F:GO:0004029; F:GO:0003676; F:GO:0001758; P:GO:0055114; F:GO:0004028; C:GO:0005622; P:GO:0006081; F:GO:0008270	-	EC:1.2.1.3; EC:1.2.1.36	IPR015590; IPR016161; IPR016163; PTHR11699:SF46 (PANTHER)
	-	0				-
Caenorhabditis elegans	lactb protein	3	P:GO:0009792; P:GO:0040007; P:GO:0002119	-		SignalP (SIGNALP)
Caenorhabditis elegans	isoform a	0				SignalP (SIGNALP)
Caenorhabditis briggsae	progesterone receptor membrane component 1	8	P:GO:0007411; C:GO:0005730; F:GO:0008289; C:GO:0009986; F:GO:0005515; C:GO:0044425; F:GO:0020037; C:GO:0005783	-		IPR001199; PTHR10281 (PANTHER), PTHR10281:SF5 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	d- cross-link repair 1b (pso2 cerevisiae)	6	F:GO:0005488; P:GO:0006281; P:GO:0016233; C:GO:0044446; F:GO:0004527; C:GO:0005694	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	fragile site-associated protein	0		C:GO:0016021; C:GO:0016020		-
Angiostrongylus cantonensis	briggsae cbr-gbh-1 protein	5	F:GO:0005506; P:GO:0055114; F:GO:0016702; F:GO:0008336; P:GO:0045329	-	EC:1.13.11.0; EC:1.14.11.1	PTHR10696 (PANTHER), PTHR10696:SF3 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	plexin a	4	P:GO:0016199; F:GO:0005515; C:GO:0016020; F:GO:0004888	-		IPR000215; IPR002909; IPR008936; IPR013548; IPR013783; IPR014756; G3DSA:3.10.20.90 (GENE3D), PTHR22625 (PANTHER), PTHR22625:SF11 (PANTHER)

Caenorhabditis elegans	plexin a	4	P:GO:0016199; F:GO:0005515; C:GO:0016020; F:GO:0004888	-		IPR000215; IPR002909; IPR008936; IPR013548; IPR013783; IPR014756; G3DSA:3.10.20.90 (GENE3D), PTHR22625 (PANTHER), PTHR22625:SF11 (PANTHER)
Caenorhabditis elegans	plexin a	4	P:GO:0016199; F:GO:0005515; C:GO:0016020; F:GO:0004888	-		IPR000215; IPR002909; IPR008936; IPR013548; IPR013783; IPR014756; G3DSA:3.10.20.90 (GENE3D), PTHR22625 (PANTHER), PTHR22625:SF11 (PANTHER)
Caenorhabditis elegans	plexin a	4	P:GO:0016199; F:GO:0005515; C:GO:0016020; F:GO:0004888	-		IPR000215; IPR002909; IPR008936; IPR013548; IPR013783; IPR014756; G3DSA:3.10.20.90 (GENE3D), PTHR22625 (PANTHER), PTHR22625:SF11 (PANTHER)
Caenorhabditis elegans	plexin a	4	P:GO:0016199; F:GO:0005515; C:GO:0016020; F:GO:0004888	-		IPR000215; IPR002909; IPR008936; IPR013548; IPR013783; IPR014756; G3DSA:3.10.20.90 (GENE3D), PTHR22625 (PANTHER), PTHR22625:SF11 (PANTHER)
Caenorhabditis elegans	briggsae cbr-skr-18 protein	4	P:GO:0002009; P:GO:0040035; P:GO:0006898; P:GO:0040011	-		-
Caenorhabditis elegans	hypocretin receptor 2	3	F:GO:0042277; F:GO:0004930; P:GO:0023052	-		IPR000276; IPR017452; G3DSA:1.20.1070.10 (GENE3D), PTHR19264 (PANTHER), PTHR19264:SF105 (PANTHER), SSF81321 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-acy-1 protein	9	P:GO:0006952; P:GO:0008219; P:GO:0007188; F:GO:0016849; P:GO:0042221; P:GO:0002119; P:GO:0040017; C:GO:0005886; P:GO:0030431	-		-

Caenorhabditis elegans	3-hydroxyacyl- dehydroge-se type ii	25	P:GO:0051289; P:GO:0040007; P:GO:0008210; P:GO:0008209; P:GO:0040017; F:GO:0047035; C:GO:0005743; F:GO:0004303; P:GO:0007569; F:GO:0018454; P:GO:0008205; F:GO:0050327; P:GO:0006631; F:GO:0042802; P:GO:0006637; F:GO:0051287; F:GO:0005496; P:GO:0002119; F:GO:0047022; C:GO:0005875; P:GO:0043170; C:GO:0005783; C:GO:0005811; P:GO:0033327; P:GO:0040035	-	EC:1.1.1.239 ; EC:1.1.1.62; EC:1.1.1.36; EC:1.1.1.63; EC:1.1.1.201	IPR002198; IPR002347; IPR016040; IPR020904; PTHR19410:SF78 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	gmp synthase	6	F:GO:0016884; P:GO:0009168; P:GO:0006520; F:GO:0005515; F:GO:0000166; P:GO:0009113	-	EC:6.3.5.0	IPR000991; IPR001317; IPR001674; IPR001962; IPR004739; IPR006220; IPR011702; IPR014729; IPR017926; G3DSA:3.30.300.10 (GENE3D), G3DSA:3.40.50.880 (GENE3D), PTHR11922 (PANTHER), PTHR11922:SF2 (PANTHER), SSF52317 (SUPERFAMILY), SSF52402 (SUPERFAMILY), SSF54810 (SUPERFAMILY)
Caenorhabditis elegans	sy-ptotagmin xvi	1	F:GO:0005515	-		IPR000008; IPR008973; G3DSA:2.60.40.150 (GENE3D), PTHR10024 (PANTHER), PTHR10024:SF14 (PANTHER)
Caenorhabditis elegans	sy-ptotagmin xvi	1	F:GO:0005515	-		IPR000008; IPR008973; G3DSA:2.60.40.150 (GENE3D), PTHR10024 (PANTHER), PTHR10024:SF14 (PANTHER)
Caenorhabditis elegans	caseinolytic atp- proteolytic subunit homolog (coli)	14	P:GO:0040010; P:GO:0051260; P:GO:0040035; F:GO:0042802; F:GO:0005524; P:GO:0010171; P:GO:0002119; P:GO:0040017; C:GO:0005759; P:GO:0006898; F:GO:0004252; P:GO:0009792; P:GO:0040018; P:GO:0006515	-	EC:3.4.21.0	IPR001907; IPR018215; G3DSA:3.90.226.10 (GENE3D), SSF52096 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	ophagy (yeast atg homolog) family member (atg-9)	1	P:GO:0009792	-		IPR007241; PTHR13038:SF1 (PANTHER), SignalP (SIGNALP)
	-	0				-
Loa loa	hypothetical protein LOAG_05238 [Loa loa]	0				SignalP (SIGNALP)
Caenorhabditis briggsae	coiled-coil and c2 domain containing 1b	1	F:GO:0005515	-		IPR000008; IPR008973; G3DSA:2.60.40.150 (GENE3D), PTHR13076 (PANTHER)
Danio rerio	zinc finger	0		F:GO:0003676; F:GO:0004803; P:GO:0015074; P:GO:0006313; F:GO:0046983; F:GO:0003677		IPR012337
Caenorhabditis elegans	erv1 alr family protein	0		F:GO:0016972; P:GO:0055114; P:GO:0045454		-
Haemonchus contortus	nefa-interacting nuclear protein nip30	0		F:GO:0003674; P:GO:0008150; C:GO:0005634; C:GO:0005575		IPR019331; PTHR13495 (PANTHER)
Haemonchus contortus	nefa-interacting nuclear protein nip30	0		P:GO:0008150; C:GO:0005575		IPR019331; PTHR13495 (PANTHER)
	-	0				SignalP (SIGNALP)
Loa loa	hypothetical protein LOAG_03848 [Loa loa]	0				-
Loa loa	hypothetical protein LOAG_03848 [Loa loa]	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	nucleolar protein 9	0		P:GO:0000003; F:GO:0003674; P:GO:0006974; P:GO:0008150; C:GO:0005634; C:GO:0005730; C:GO:0005575		IPR010655
	-	0				-
Caenorhabditis elegans	hypothetical protein T14G10.7 [Caenorhabditis elegans]	1	P:GO:0006898	-		PTHR21072 (PANTHER), PTHR21072:SF1 (PANTHER)
Caenorhabditis elegans	abnormal cell migration family member (mig-5)	1	F:GO:0042802	-		IPR015506; PTHR10878:SF1 (PANTHER)
Caenorhabditis briggsae	loc398196 protein	0		P:GO:0006260; F:GO:0046872; C:GO:0005654; C:GO:0005634		IPR015408; IPR015411; PTHR13454 (PANTHER), PTHR13454:SF6 (PANTHER)
Caenorhabditis briggsae	phosphatidylinositol-5-phosphate 4- type alpha	7	P:GO:0046488; P:GO:0008360; P:GO:0007015; P:GO:0016310; F:GO:0016308; P:GO:0007155; F:GO:0000166	-	EC:2.7.1.68	IPR002498; G3DSA:3.30.800.10 (GENE3D), PTHR23086:SF3 (PANTHER), SSF56104 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG12578 [Caenorhabditis briggsae]	0				-
Caenorhabditis briggsae	initiation factor 2 subunit family protein	0		F:GO:0003743; P:GO:0044237; C:GO:0005575		IPR000649; PTHR10233:SF5 (PANTHER), SSF100950 (SUPERFAMILY)

Caenorhabditis briggsae	uncoordi-ted family member (unc-89)	0				PTHR19897 (PANTHER), PTHR19897:SF5 (PANTHER)
Caenorhabditis brenneri	mgc68650 protein	0		F:GO:0005524; C:GO:0005739; F:GO:0004658; F:GO:0016874; F:GO:0000166; C:GO:0005759		SignalP (SIGNALP)
Caenorhabditis brenneri	mgc68650 protein	0		F:GO:0005524; C:GO:0005739; F:GO:0004658; F:GO:0016874; F:GO:0000166; C:GO:0005759		SignalP (SIGNALP)
	-	0				-
	-	0				-
Sus scrofa	propionyl coenzyme a beta polypeptide	0		F:GO:0005524; C:GO:0005739; F:GO:0004658; F:GO:0016874; F:GO:0000166; C:GO:0005759; P:GO:0009063; P:GO:0009062		SignalP (SIGNALP)
Caenorhabditis briggsae	#NAME?	3	P:GO:0009086; F:GO:0016787; C:GO:0044424	-		-
Caenorhabditis briggsae	tyrosine-protein ki-se pr2	8	F:GO:0004674; P:GO:0042059; P:GO:0040027; F:GO:0004713; F:GO:0005524; F:GO:0005515; P:GO:0009792; P:GO:0006468	-	EC:2.7.11.0; EC:2.7.10.0	-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	mps one binder ki-se activator-like 3	7	C:GO:0032580; F:GO:0046872; C:GO:0005624; F:GO:0005515; P:GO:0006810; C:GO:0005813; C:GO:0048471	-		IPR005301; PTHR22599:SF1 (PANTHER)
	-	0				PS51257 (PROFILE), SignalP (SIGNALP)
Caenorhabditis briggsae	Hypothetical protein CBG09343 [Caenorhabditis briggsae]	0				IPR018627
Caenorhabditis briggsae	-dh oxidase	1	F:GO:0003824	-		IPR001155; IPR013785; PTHR22893 (PANTHER), PTHR22893:SF6 (PANTHER), SSF51395 (SUPERFAMILY)
Caenorhabditis elegans	eukaryotic translation initiation factor 3 subunit f-1	6	P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0040010; P:GO:0008340; P:GO:0006898	-		PTHR10540 (PANTHER), PTHR10540:SF6 (PANTHER)

Homo sapiens	type alpha 1	31	P:GO:0060351; P:GO:0001957; P:GO:0071363; P:GO:0007605; P:GO:0034505; P:GO:0042542; P:GO:0001649; P:GO:0009612; P:GO:0001568; P:GO:0060325; F:GO:0005201; C:GO:0005615; P:GO:0048706; P:GO:0015031; F:GO:0048407; C:GO:0005737; P:GO:0043434; P:GO:0071300; P:GO:0007601; P:GO:0010812; C:GO:0005584; F:GO:0042802; P:GO:0060346; P:GO:0032964; P:GO:0030199; P:GO:0051591; P:GO:0031960;	-		IPR000885; IPR008160; PTHR10499 (PANTHER), PTHR10499:SF71 (PANTHER), PS51461 (PROFILE)
Caenorhabditis briggsae	elegans fln-1 isoform partially confirmed by transcript evidence	5	P:GO:0051179; P:GO:0007293; P:GO:0048610; P:GO:0030725; P:GO:0030154	-		IPR001298; IPR013783; IPR014756; IPR017868; PTHR11915 (PANTHER), PTHR11915:SF24 (PANTHER)
Caenorhabditis briggsae	elegans fln-1 isoform partially confirmed by transcript evidence	4	P:GO:0051179; P:GO:0007293; P:GO:0048610; P:GO:0030725	-		IPR001298; IPR013783; IPR014756; IPR017868
Caenorhabditis briggsae	filamin gamma	1	C:GO:0044464	-		IPR001298; IPR013783; IPR014756; IPR017868; PTHR11915 (PANTHER), PTHR11915:SF24 (PANTHER)
Caenorhabditis briggsae	elegans fln-1 isoform partially confirmed by transcript evidence	5	P:GO:0051179; P:GO:0007293; P:GO:0048610; P:GO:0030725; P:GO:0030154	-		IPR001298; IPR013783; IPR014756; IPR017868
Caenorhabditis briggsae	glutamyl-tr- amidotransferase subunit a	2	F:GO:0016884; P:GO:0019915	-	EC:6.3.5.0	IPR000120; PTHR11895:SF7 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG19188 [Caenorhabditis briggsae]	0				PTHR10024 (PANTHER)
Caenorhabditis briggsae	major facilitator superfamily domain-containing protein 7	5	C:GO:0016021; P:GO:0000003; P:GO:0040010; P:GO:0006898; P:GO:0055085	-		IPR005828; IPR016196; PTHR10924 (PANTHER), SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	autophagy protein apg6 containing protein	15	P:GO:0035121; P:GO:0040010; P:GO:0008340; P:GO:0009267; P:GO:0035071; P:GO:0040024; P:GO:0040027; P:GO:0040035; C:GO:0031410; P:GO:0040011; P:GO:0030163; P:GO:0009792; P:GO:0040018; P:GO:0006914; C:GO:0005634	-		IPR007243; PTHR12768:SF2 (PANTHER)
Caenorhabditis elegans	39s ribosomal protein l43	1	C:GO:0005840	-		IPR007741; IPR012336; PTHR21396 (PANTHER), PTHR21396:SF1 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	timeless interacting protein	8	P:GO:0009411; C:GO:0000790; P:GO:0000076; P:GO:0031573; F:GO:0005515; P:GO:0033262; P:GO:0008284; C:GO:0005737	-		-
Loa loa	cullin 3	15	P:GO:0008054; P:GO:0007369; P:GO:0035024; C:GO:0005794; F:GO:0004842; P:GO:0016567; P:GO:0001831; C:GO:0005827; P:GO:0043149; P:GO:0000090; F:GO:0030332; C:GO:0005634; P:GO:0016477; C:GO:0031463; P:GO:0000910	-	EC:6.3.2.19	IPR001373; IPR011991; IPR016157; IPR016158; IPR019559; G3DSA:4.10.1030.10 (GENE3D), PTHR11932 (PANTHER), PTHR11932:SF23 (PANTHER), SSF46785 (SUPERFAMILY)

Loa loa	cullin 3	16	P:GO:0008054; P:GO:0007369; P:GO:0035024; C:GO:0005794; F:GO:0004842; F:GO:0031625; P:GO:0016567; P:GO:0001831; C:GO:0005827; P:GO:0043149; P:GO:0000090; F:GO:0030332; C:GO:0005634; P:GO:0016477; C:GO:0031463; P:GO:0000910	-	EC:6.3.2.19	IPR001373; IPR011991; IPR016157; IPR016158; IPR019559; G3DSA:4.10.1030.10 (GENE3D), PTHR11932 (PANTHER), PTHR11932:SF23 (PANTHER), SSF46785 (SUPERFAMILY)
Loa loa	cullin 3	19	P:GO:0008054; P:GO:0007369; P:GO:0008629; P:GO:0035024; C:GO:0005794; P:GO:0007050; P:GO:0008284; F:GO:0004842; P:GO:0016567; P:GO:0001831; C:GO:0005827; P:GO:0000082; P:GO:0043149; P:GO:0000090; F:GO:0030332; C:GO:0005634; P:GO:0016477; C:GO:0031463; P:GO:0000910	-	EC:6.3.2.19	IPR001373; IPR011991; IPR016157; IPR016158; IPR016159; IPR019559; G3DSA:1.20.1310.10 (GENE3D), G3DSA:4.10.1030.10 (GENE3D), PTHR11932 (PANTHER), PTHR11932:SF23 (PANTHER), SSF46785 (SUPERFAMILY)
Loa loa	ring finger protein 207	1	F:GO:0005488	-		IPR000315; IPR001841; IPR013083; G3DSA:4.10.45.10 (GENE3D), PTHR13712 (PANTHER), PTHR13712:SF62 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	thioredoxin domain-containing protein 12 precursor	0		C:GO:0005788; P:GO:0055114; P:GO:0045454; F:GO:0016491; F:GO:0019153		IPR004879; IPR012335; IPR012336; PTHR15337 (PANTHER), PTHR15337:SF2 (PANTHER)
	-	0				-

synthetic construct	g-s complex locus	32	C:GO:0030133; P:GO:0007191; P:GO:0035116; C:GO:0005624; C:GO:0005834; P:GO:0009306; P:GO:0009755; C:GO:0032588; P:GO:0051216; P:GO:0048701; P:GO:0006112; F:GO:0005525; C:GO:0005576; F:GO:0035255; P:GO:0007565; C:GO:0001726; C:GO:0042383; C:GO:0031224; F:GO:0042802; P:GO:0040032; P:GO:0042493; C:GO:0005768; C:GO:0008021; C:GO:0030054; P:GO:0045672; P:GO:0046907;	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000367; IPR001019; IPR011025; G3DSA:3.40.50.300 (GENE3D), PTHR10218:SF36 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	poly polymerase cid (caffein-induced death protein)	0		F:GO:0016779		PTHR12271 (PANTHER), PTHR12271:SF12 (PANTHER), SSF81631 (SUPERFAMILY)
Glossina morsitans morsitans	ring finger protein 185	6	C:GO:0016021; P:GO:0055114; F:GO:0008270; F:GO:0005515; F:GO:0032440; F:GO:0016874	-	EC:1.3.1.74	IPR001841; IPR013083; IPR017907; IPR018957; PTHR12313 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-mfb-1 protein	3	P:GO:0043053; P:GO:0006508; F:GO:0005515	-		-
Caenorhabditis briggsae	proteasome (macropain) 26s non- 6	9	P:GO:0008340; C:GO:0000502; P:GO:0051436; P:GO:0051437; P:GO:0000003; P:GO:0018996; P:GO:0031145; P:GO:0002119; F:GO:0005515	-		IPR000717; IPR011991; IPR019585; PTHR14145 (PANTHER), PTHR14145:SF1 (PANTHER), SSF46785 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	choline ki-se a family member (cka-1)	4	F:GO:0005515; F:GO:0016301; C:GO:0005737; P:GO:0008654	-		IPR002573; IPR011009; G3DSA:3.10.450.110 (GENE3D), G3DSA:3.90.1200.10 (GENE3D), PTHR22603:SF7 (PANTHER)
Caenorhabditis elegans	briggsae cbr-eel-1 protein	2	F:GO:0016874; P:GO:0033227	-		PTHR11254 (PANTHER), PTHR11254:SF67 (PANTHER)

Caenorhabditis briggsae	casein ki-se alpha 1 polypeptide	20	F:GO:0047485; P:GO:0040010; P:GO:0016055; F:GO:0008013; C:GO:0030424; F:GO:0004674; C:GO:0030425; F:GO:0019888; P:GO:0040035; F:GO:0005524; C:GO:0005929; C:GO:0016581; C:GO:0043025; P:GO:0007165; P:GO:0034608; P:GO:0034606; P:GO:0009792; C:GO:0016580; C:GO:0005886; P:GO:0006468	-	EC:2.7.11.0	SignalP (SIGNALP)
Caenorhabditis briggsae	casein ki-se alpha 1 polypeptide	20	F:GO:0047485; P:GO:0040010; P:GO:0016055; F:GO:0008013; C:GO:0030424; F:GO:0004674; C:GO:0030425; F:GO:0019888; P:GO:0040035; F:GO:0005524; C:GO:0005929; C:GO:0016581; C:GO:0043025; P:GO:0007165; P:GO:0034608; P:GO:0034606; P:GO:0009792; C:GO:0016580; C:GO:0005886; P:GO:0006468	-	EC:2.7.11.0	SignalP (SIGNALP)
Caenorhabditis elegans	kiaa1833 partial	1	F:GO:0005488	-		IPR011989
Loa loa	heat repeat-containing protein 5b	4	P:GO:0040007; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		IPR011989; IPR016024; PTHR21663 (PANTHER)
Caenorhabditis briggsae	ubiquitin-conjugating enzyme e2 j2-like	3	P:GO:0019538; C:GO:0044464; F:GO:0019787	-		IPR000608; IPR016135; PTHR11621 (PANTHER), PTHR11621:SF14 (PANTHER)
Caenorhabditis elegans	transmembrane protein 33	2	C:GO:0016020; F:GO:0005515	-		IPR005344; PTHR12703 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	transmembrane protein isoform cra_a	3	C:GO:0016020; C:GO:0042470; F:GO:0005515	-		IPR005344
Caenorhabditis elegans	transmembrane protein 33	3	C:GO:0016020; C:GO:0042470; F:GO:0005515	-		IPR005344; PTHR12703 (PANTHER)
	-	0				-
	-	0				-

Caenorhabditis elegans	sterol regulatory element binding transcription factor 2	1	F:GO:0005515	-		PTHR12565 (PANTHER), PTHR12565:SF3 (PANTHER)
Caenorhabditis briggsae	cop9 sig-losome complex subunit 5	3	C:GO:0005634; F:GO:0005515; F:GO:0008233	-		IPR000555; G3DSA:3.40.140.10 (GENE3D), PTHR10410 (PANTHER), PTHR10410:SF6 (PANTHER), SSF102712 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR001660; IPR010993; IPR013761; IPR021129; PTHR10627 (PANTHER), PTHR10627:SF2 (PANTHER)
Caenorhabditis elegans	zinc finger protein	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		IPR003006; IPR007087; IPR015880
Loa loa	r- polymerase-associated protein ctr9 homolog	4	C:GO:0016593; P:GO:0010390; F:GO:0005515; P:GO:0033523	-		IPR001440; IPR011990; IPR013026; IPR013105; IPR019734; PTHR14027 (PANTHER), PTHR14027:SF2 (PANTHER), SSF48452 (SUPERFAMILY)
Caenorhabditis elegans	6-phosphofructo-2-ki-se fructose- -biphosphatase 3	4	F:GO:0003873; P:GO:0006003; F:GO:0016787; F:GO:0005524	-	EC:2.7.1.105	-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	3	P:GO:0006457; P:GO:0009792; F:GO:0003755	-	EC:5.2.1.8	SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	3	P:GO:0006457; P:GO:0009792; F:GO:0003755	-	EC:5.2.1.8	-
Caenorhabditis elegans	lethal isoform i	6	F:GO:0000827; F:GO:0003993; F:GO:0000832; P:GO:0006020; F:GO:0033857; C:GO:0005829	-	EC:3.1.3.2; EC:2.7.4.24	IPR000560; G3DSA:3.40.50.1240 (GENE3D), PTHR12750 (PANTHER), PTHR12750:SF5 (PANTHER), SSF53254 (SUPERFAMILY)
Caenorhabditis elegans	lethal isoform i	6	F:GO:0000827; F:GO:0003993; F:GO:0000832; P:GO:0006020; F:GO:0033857; C:GO:0005829	-	EC:3.1.3.2; EC:2.7.4.24	IPR000560; G3DSA:3.40.50.1240 (GENE3D), PTHR12750 (PANTHER), PTHR12750:SF5 (PANTHER), SSF53254 (SUPERFAMILY)
Caenorhabditis elegans	lethal isoform i	6	F:GO:0000827; F:GO:0003993; F:GO:0000832; P:GO:0006020; F:GO:0033857; C:GO:0005829	-	EC:3.1.3.2; EC:2.7.4.24	IPR000560; G3DSA:3.40.50.1240 (GENE3D), PTHR12750 (PANTHER), PTHR12750:SF5 (PANTHER), SSF53254 (SUPERFAMILY)
Homo sapiens	ubiquitin b	7	F:GO:0030528; F:GO:0003735; C:GO:0022627; P:GO:0016567; F:GO:0005515; C:GO:0005634; P:GO:0045941	-		-
Homo sapiens	os05g0242100 isoform 2	2	C:GO:0005840; C:GO:0005634	-		-

Brugia malayi	ring zinc finger-containing protein	0		F:GO:0046872; F:GO:0004383; F:GO:0020037; P:GO:0006397; P:GO:0006182; F:GO:0008270; F:GO:0005515		IPR001841; IPR013083; IPR018957; PTHR23350 (PANTHER), SSF57850 (SUPERFAMILY)
Brugia malayi	ring zinc finger-containing protein	0		F:GO:0046872; F:GO:0004383; F:GO:0020037; P:GO:0006397; P:GO:0006182; F:GO:0008270; F:GO:0005515		IPR001841; IPR013083; IPR018957; PTHR23350 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis elegans	3-hydroxyisobutyryl- mitochondrial precursor	6	P:GO:0009792; F:GO:0005515; C:GO:0005759; P:GO:0040010; P:GO:0008152; F:GO:0003860	-	EC:3.1.2.4	IPR001753; G3DSA:3.90.226.10 (GENE3D), PTHR11941 (PANTHER), SSF52096 (SUPERFAMILY)
Caenorhabditis briggsae	basic leucine zipper nuclear factor 1	0		P:GO:0043001; P:GO:0007030		PTHR13066 (PANTHER)
Caenorhabditis elegans	6-phosphofructo-2-ki-se fructose- -bisphosphatase short form	11	F:GO:0003873; C:GO:0043540; F:GO:0019900; P:GO:0016311; F:GO:0004331; F:GO:0070095; F:GO:0042802; P:GO:0046835; F:GO:0005524; P:GO:0033133; P:GO:0006003	-	EC:2.7.1.105 ; EC:3.1.3.46	IPR003094; IPR013078; G3DSA:3.40.50.1240 (GENE3D), PTHR10606:SF11 (PANTHER), SSF53254 (SUPERFAMILY)
Caenorhabditis elegans	peptidyl-prolyl cis-trans isomerase 5	2	F:GO:0003755; P:GO:0006457	-	EC:5.2.1.8	IPR002130; IPR015891; IPR020892; PTHR11071 (PANTHER), PTHR11071:SF62 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	membrane-associated protein gex-3	4	P:GO:0018991; P:GO:0016477; P:GO:0010172; F:GO:0005515	-		SignalP (SIGNALP)
	-	0				PTHR18937 (PANTHER), PTHR18937:SF13 (PANTHER)
Ancylostoma caninum	zinc metallopeptidase	1	F:GO:0008233	-		IPR000718; IPR018497; G3DSA:3.40.390.10 (GENE3D), PTHR11733:SF15 (PANTHER), SSF55486 (SUPERFAMILY)
Loa loa	tata binding protein associated factor	6	F:GO:0008270; P:GO:0006367; P:GO:0006355; F:GO:0016251; F:GO:0008237; C:GO:0005669	-		PTHR15137 (PANTHER), PTHR15137:SF7 (PANTHER), SSF55486 (SUPERFAMILY)

Caenorhabditis briggsae	briggsae cbr-gop-3 protein	6	P:GO:0009792; P:GO:0002119; P:GO:0040010; P:GO:0000003; C:GO:0019867; P:GO:0006898	-		-
Caenorhabditis briggsae	Hypothetical protein CBG14931 [Caenorhabditis briggsae]	0				-
	-	0				-
Canis familiaris	ribosomal protein s19	12	F:GO:0003723; P:GO:0015669; C:GO:0005730; P:GO:0006364; F:GO:0003735; P:GO:0006414; C:GO:0022627; P:GO:0051272; P:GO:0030218; P:GO:0042274; P:GO:0009991; F:GO:0005515	-		IPR001266
Caenorhabditis briggsae	briggsae cbr-adr-2 protein	0		P:GO:0000003; F:GO:0003723; F:GO:0004000; P:GO:0006396; F:GO:0005515; F:GO:0003725; C:GO:0005622		-
	-	0				-
	-	0				-
Caenorhabditis elegans	domain containing protein	2	P:GO:0016998; F:GO:0005515	-		IPR002482; IPR018392; G3DSA:3.10.350.10 (GENE3D), PTHR23354 (PANTHER), PTHR23354:SF4 (PANTHER), SSF54106 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0008565; P:GO:0006886; P:GO:0005975; F:GO:0005524; C:GO:0016020; F:GO:0030246; C:GO:0016459; F:GO:0005509; P:GO:0016998; C:GO:0000139; F:GO:0003824; F:GO:0000166; P:GO:0048280; C:GO:0005737; F:GO:0005488; F:GO:0003779; F:GO:0003774; F:GO:0016740; P:GO:0031424		-
	-	0				-

Caenorhabditis briggsae	prolyl 4-hydroxylase	6	F:GO:0031418; F:GO:0005506; F:GO:0004656; P:GO:0055114; F:GO:0016702; C:GO:0005783	-	EC:1.14.11.2; EC:1.13.11.0	IPR005123; IPR006620; PTHR10869 (PANTHER), PTHR10869:SF13 (PANTHER), PS51471 (PROFILE)
Caenorhabditis briggsae	monocarboxylate transporter	3	P:GO:0000003; P:GO:0040007; P:GO:0002119	-		IPR011701; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11360 (PANTHER), PTHR11360:SF15 (PANTHER), SignalP (SIGNALP)
Heligmosomoides polygyrus	c-type lectin-1	1	F:GO:0005488	-		IPR001304; IPR016186; IPR016187; PTHR22801 (PANTHER), PTHR22801:SF9 (PANTHER)
Danio rerio	regulatory associated protein of complex 1 isoform 1	11	C:GO:0005829; P:GO:0001938; P:GO:0031669; C:GO:0030425; P:GO:0042325; F:GO:0032403; P:GO:0008361; P:GO:0032008; C:GO:0043025; F:GO:0019901; C:GO:0031931	-		IPR004083; PTHR12848:SF6 (PANTHER)
	-	0				-
	-	0				-
Pan troglodytes	ribosomal protein sa	14	P:GO:0016337; F:GO:0003735; C:GO:0005604; F:GO:0005055; P:GO:0006414; C:GO:0022627; F:GO:0043022; C:GO:0005624; F:GO:0043236; P:GO:0030855; C:GO:0043025; P:GO:0007165; C:GO:0005634; C:GO:0005886	-		IPR001865; IPR005707; IPR018130
Caenorhabditis elegans	osteopetrosis associated transmembrane protein 1	0		P:GO:0030316; C:GO:0016021; C:GO:0016020; C:GO:0005829; F:GO:0005515		-
Caenorhabditis elegans	osteopetrosis associated transmembrane protein 1	0		P:GO:0030316; C:GO:0016021; C:GO:0016020; C:GO:0005829; F:GO:0005515		-
Caenorhabditis elegans	briggsae cbr-fox-1 protein	7	F:GO:0003729; F:GO:0003677; P:GO:0007399; F:GO:0005515; F:GO:0000166; P:GO:0007474; P:GO:0045941	-		SignalP (SIGNALP)

Brugia malayi	superkiller viralicidic activity 2-like 2	12	P:GO:0040010; P:GO:0031101; P:GO:0040035; P:GO:0002119; P:GO:0051781; F:GO:0005515; F:GO:0000166; F:GO:0004386; P:GO:0040011; P:GO:0006139; P:GO:0002009; P:GO:0009792	-		IPR001650; IPR012961; IPR018247; G3DSA:3.40.50.300 (GENE3D), PTHR11752 (PANTHER), PTHR11752:SF2 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	surfeit 4 cargo protein	14	P:GO:0040035; P:GO:0009792; P:GO:0002119; C:GO:0012505; C:GO:0005794; P:GO:0032940; C:GO:0031090; P:GO:0040011; P:GO:0019915; P:GO:0040007; C:GO:0005783; C:GO:0044425; C:GO:0044446; P:GO:0002009	-		IPR002995; PTHR23427 (PANTHER), PTHR23427:SF1 (PANTHER)
Caenorhabditis briggsae	surfeit locus protein 4	13	C:GO:0000139; P:GO:0040035; P:GO:0009792; C:GO:0005789; P:GO:0002119; F:GO:0005515; P:GO:0032940; P:GO:0040011; C:GO:0016021; P:GO:0019915; P:GO:0040007; C:GO:0033116; P:GO:0002009	-		IPR002995; PTHR23427 (PANTHER), PTHR23427:SF1 (PANTHER)
Caenorhabditis elegans	glycosylation related family member (gly-5)	3	C:GO:0016021; F:GO:0005515; F:GO:0016740	-		IPR000772; IPR008997; G3DSA:2.80.10.50 (GENE3D), PTHR11675 (PANTHER)
Caenorhabditis elegans	glycosylation related family member (gly-5)	5	C:GO:0016021; C:GO:0005794; F:GO:0005515; F:GO:0016757; F:GO:0005529	-		IPR000772; IPR001173; IPR008997; G3DSA:2.80.10.50 (GENE3D), G3DSA:3.90.550.10 (GENE3D), PTHR11675 (PANTHER), SSF53448 (SUPERFAMILY)
Caenorhabditis elegans	glycosylation related family member (gly-5)	5	C:GO:0016021; C:GO:0005794; F:GO:0005515; F:GO:0016757; F:GO:0005529	-		IPR000772; IPR001173; IPR008997; G3DSA:2.80.10.50 (GENE3D), G3DSA:3.90.550.10 (GENE3D), PTHR11675 (PANTHER), SSF53448 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-bam-2 protein	0		C:GO:0005887		SignalP (SIGNALP)

Caenorhabditis elegans	eph receptor b2	9	F:GO:0005515; P:GO:0007409; F:GO:0004713; C:GO:0044464; P:GO:0051239; P:GO:0023052; P:GO:0007391; P:GO:0050794; F:GO:0004888	-	EC:2.7.10.0	IPR003961; IPR008957; IPR011641; IPR013783; IPR020685; IPR020769; G3DSA:2.170.300.10 (GENE3D)
Branchiostoma floridae	cdw92 antigen	2	P:GO:0006810; C:GO:0016020	-		IPR007603; SignalP (SIGNALP)
Loa loa	tip60	15	P:GO:0040010; F:GO:0016747; F:GO:0008270; P:GO:0006333; P:GO:0045449; P:GO:0000003; P:GO:0040027; P:GO:0010171; C:GO:0000785; P:GO:0006898; P:GO:0002009; P:GO:0009792; F:GO:0003682; C:GO:0005634; P:GO:0006974	-	EC:2.3.1.0	IPR002717; IPR016181; G3DSA:3.30.60.60 (GENE3D), PTHR10615 (PANTHER), PTHR10615:SF30 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-lon-2 protein	0		C:GO:0016020; C:GO:0005578; F:GO:0043395		-
	-	0				-
Brugia malayi	zgc:136346 protein	0		F:GO:0003676; P:GO:0008150; C:GO:0005575		PTHR13468 (PANTHER)
	-	0				-
Caenorhabditis elegans	protein	0		F:GO:0005102; C:GO:0005615; C:GO:0016021; P:GO:0007165		IPR002181; IPR014715; IPR014716; PTHR19143 (PANTHER)
Brugia malayi	mediator of r- polymerase ii transcription subunit 13-like	1	P:GO:0009792	-		IPR021643; PTHR12950 (PANTHER), PTHR12950:SF3 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	briggsae cbr-rsks-1 protein	3	F:GO:0004672; P:GO:0009987; F:GO:0000166	-		G3DSA:3.30.200.20 (GENE3D), PTHR22985 (PANTHER), PTHR22985:SF83 (PANTHER)
Caenorhabditis elegans	hypothetical protein ZC477.5 [Caenorhabditis elegans]	0				IPR021869
Caenorhabditis elegans	znrf2 protein	8	F:GO:0016874; C:GO:0042734; C:GO:0030054; F:GO:0005515; C:GO:0005765; P:GO:0008152; F:GO:0008270; C:GO:0010008	-		-

Caenorhabditis elegans	znrf2 protein	8	F:GO:0016874; C:GO:0042734; C:GO:0030054; F:GO:0005515; C:GO:0005765; P:GO:0008152; F:GO:0008270; C:GO:0010008	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	inin receptor homolog family member (ckr-2)	8	F:GO:0005515; C:GO:0005624; C:GO:0016021; P:GO:0019915; P:GO:0007165; P:GO:0007186; P:GO:0050806; F:GO:0004983	-		IPR000276; IPR009126; IPR017452; G3DSA:1.20.1070.10 (GENE3D), PTHR19264 (PANTHER), PTHR19264:SF283 (PANTHER), SSF81321 (SUPERFAMILY)
Caenorhabditis elegans	ecotropic viral integration site 5	1	F:GO:0005515	-		PTHR22957 (PANTHER), PTHR22957:SF3 (PANTHER)
	-	0				-
Caenorhabditis elegans	hypothetical protein F40F4.6 [Caenorhabditis elegans]	1	P:GO:0040010	-		-
Loa loa	briggsae cbr-sas-4 protein	0		C:GO:0005737; P:GO:0007049; C:GO:0005856; P:GO:0007275; C:GO:0005815		-
Caenorhabditis elegans	bifunctio-l aminoacyl-tr- synthetase	13	C:GO:0005829; F:GO:0004819; F:GO:0003723; C:GO:0005625; P:GO:0006424; C:GO:0016021; F:GO:0004827; P:GO:0006461; F:GO:0005524; F:GO:0005515; P:GO:0016485; F:GO:0004818; P:GO:0006433	-	EC:6.1.1.18; EC:6.1.1.15; EC:6.1.1.17	IPR000924; IPR001412; IPR014729; IPR020058; IPR020061; G3DSA:3.90.800.10 (GENE3D), PTHR10119:SF11 (PANTHER), SSF52374 (SUPERFAMILY)
Caenorhabditis elegans	brm protein	4	P:GO:0040010; F:GO:0005488; P:GO:0040035; P:GO:0009792	-		IPR014978
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	P:GO:0006629; F:GO:0016788	-		SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	atp gtp binding protein 1	3	F:GO:0046872; F:GO:0008237; F:GO:0004180	-		-
Brugia malayi	thioredoxin family protein	4	P:GO:0040035; P:GO:0040010; P:GO:0019915; P:GO:0006898	-		IPR012335; IPR012336; IPR013766; IPR017936; PTHR18929 (PANTHER), SignalP (SIGNALP)

Brugia malayi	thioredoxin family protein	4	P:GO:0040035; P:GO:0040010; P:GO:0019915; P:GO:0006898	-		IPR012335; IPR012336; IPR013766; IPR017936; PTHR18929 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	yl53_caeel ame: full=uncharacterized protein	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	solute carrier family member f1	1	C:GO:0016020	-		IPR009262; PTHR14233:SF2 (PANTHER), PF06027 (PFAM), SSF103481 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	leucine-rich ppr-motif containing	1	P:GO:0007275	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	cation-transporting atpase	7	C:GO:0016021; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0015914; F:GO:0000287; F:GO:0004012	-	EC:3.6.3.1	-
	-	0				-
	-	0				-
Brugia malayi	uncoordi-ted family member (unc-22)	7	C:GO:0030018; F:GO:0005200; P:GO:0006468; F:GO:0008307; F:GO:0004687; P:GO:0007498; F:GO:0005524	-	EC:2.7.11.18	IPR000719; IPR011009; IPR017442; IPR020675; G3DSA:3.30.200.20 (GENE3D)
Caenorhabditis elegans	phenylalanine hydroxylase	17	P:GO:0006979; P:GO:0008340; P:GO:0040002; P:GO:0055114; P:GO:0042438; P:GO:0006559; P:GO:0000003; F:GO:0004510; P:GO:0006911; F:GO:0005515; P:GO:0006569; F:GO:0016597; P:GO:0009792; C:GO:0005811; F:GO:0004505; P:GO:0006726; F:GO:0005506	-	EC:1.14.16.4; EC:1.14.16.1	IPR001273; IPR018301; IPR019774; PS51410 (PROFILE)
Brugia malayi	uncoordi-ted family member (unc-52)	2	P:GO:0030239; C:GO:0005578	-		IPR002049; IPR006210; G3DSA:2.10.25.10 (GENE3D), PTHR10574 (PANTHER), PTHR10574:SF20 (PANTHER), SignalP (SIGNALP), SSF57196 (SUPERFAMILY)
Loa loa	denn domain-containing	0				IPR001194; PTHR13196 (PANTHER), PTHR13196:SF2 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-hex-3 protein	3	F:GO:0004553; F:GO:0005488; P:GO:0044238	-	EC:3.2.1.0	IPR017853; SignalP (SIGNALP)

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	P:GO:0055085; P:GO:0008643; C:GO:0016021; F:GO:0005215	-		IPR005828; IPR016196; PTHR11600 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	5	P:GO:0048856; P:GO:0007275; P:GO:0000003; P:GO:0009987; P:GO:0016043	-		-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG21170 [Caenorhabditis briggsae]	0				PTHR21035 (PANTHER)
	-	0				-
Caenorhabditis elegans	nuclear receptor nhr-31	8	F:GO:0003700; F:GO:0043565; F:GO:0005515; F:GO:0003707; P:GO:0019915; C:GO:0005634; F:GO:0008270; P:GO:0006355	-		IPR000536; IPR008946; IPR015619; PTHR11865 (PANTHER)
Ciona intestinalis	microspherule protein 1	0		C:GO:0005654; C:GO:0005737; C:GO:0071339; F:GO:0005515; C:GO:0005730; C:GO:0005634; P:GO:0006464		-
Ciona intestinalis	microspherule protein 1	0		C:GO:0005654; C:GO:0005737; C:GO:0071339; F:GO:0005515; C:GO:0005730; C:GO:0005634; P:GO:0006464		-
Pan troglodytes	s100 calcium binding protein a6	19	C:GO:0005829; F:GO:0047485; P:GO:0048146; C:GO:0001726; C:GO:0031234; F:GO:0008270; P:GO:0007049; F:GO:0005509; F:GO:0048154; P:GO:0051781; P:GO:0007409; F:GO:0048306; P:GO:0007165; C:GO:0048471; F:GO:0042803; C:GO:0005635; P:GO:0034220; F:GO:0015075; F:GO:0005523	-		IPR001751; IPR011992; IPR013787; IPR018247; IPR018249; PTHR11639 (PANTHER), PTHR11639:SF13 (PANTHER), SSF47473 (SUPERFAMILY)

Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0005524; P:GO:0006468		IPR012877
Demansia vestigiata	venom c-type lectin galactose binding isoform variant 1	1	F:GO:0005488	-		IPR001304; IPR016186; IPR016187; PTHR22801 (PANTHER), PTHR22801:SF9 (PANTHER), SignalP (SIGNALP)
	-	0				-
Nippostrongylus brasiliensis	elegans protein partially confirmed by transcript evidence	2	P:GO:0009792; F:GO:0005515	-		IPR003677; PTHR21593 (PANTHER)
Nippostrongylus brasiliensis	elegans protein partially confirmed by transcript evidence	2	P:GO:0009792; F:GO:0005515	-		IPR003677; PTHR21593 (PANTHER), SignalP (SIGNALP)
Loa loa	protein tyrosine non-receptor type 11-like	31	P:GO:0046825; P:GO:0035265; P:GO:0042445; P:GO:0007409; F:GO:0004726; C:GO:0005624; P:GO:0009755; F:GO:0043274; P:GO:0046676; C:GO:0005829; P:GO:0046887; F:GO:0019904; P:GO:0048609; F:GO:0043560; P:GO:0051463; P:GO:0000077; P:GO:0009967; C:GO:0043234; C:GO:0001725; P:GO:0006470; C:GO:0030054; P:GO:0060125; P:GO:0006641; F:GO:0051428; P:GO:0040014; C:GO:0005625; P:GO:0000187;	-		-

Caenorhabditis elegans	casein ki-se beta polypeptide	31	P:GO:0016246; C:GO:0005929; F:GO:0005102; P:GO:0033211; P:GO:0040010; C:GO:0005956; P:GO:0040011; P:GO:0034606; C:GO:0005737; P:GO:0008285; C:GO:0030425; F:GO:0019904; C:GO:0043025; P:GO:0009792; P:GO:0002009; P:GO:0007249; F:GO:0004674; F:GO:0042802; C:GO:0030424; P:GO:0002119; F:GO:0019887; P:GO:0043623; P:GO:0010171; F:GO:0008233; C:GO:0005886; F:GO:0008134; P:GO:0034608;	-	EC:2.7.11.0	IPR000704; IPR016149
	-	0				-
Caenorhabditis elegans	protein isoform cra_a	0		F:GO:0003674; P:GO:0008150; C:GO:0005575		-
Loa loa	hypothetical protein LOAG_00508 [Loa loa]	0				IPR000210; IPR011333
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	chloride channel protein 3	4	P:GO:0006810; P:GO:0000003; C:GO:0016020; F:GO:0005216	-		IPR001807; IPR014743; PTHR11689:SF21 (PANTHER)
Caenorhabditis elegans	chloride channel protein 3	4	P:GO:0006810; P:GO:0000003; C:GO:0016020; F:GO:0005216	-		IPR001807; IPR014743; PTHR11689:SF21 (PANTHER)
	-	0				-

Brugia malayi	retinoic acid receptor beta	25	F:GO:0003700; P:GO:0008284; F:GO:0003708; F:GO:0046872; P:GO:0007283; P:GO:0045596; P:GO:0030852; P:GO:0007165; P:GO:0045944; F:GO:0010843; P:GO:0071222; C:GO:0005737; P:GO:0007399; F:GO:0016564; F:GO:0005515; P:GO:0000122; P:GO:0001657; P:GO:0055012; C:GO:0030425; P:GO:0060591; C:GO:0005634; C:GO:0043025; P:GO:0061037; P:GO:0032526; P:GO:0045947	-		IPR001628; IPR003078; IPR008946; PTHR11865 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis elegans	transmembrane protein 144	2	P:GO:0009792; P:GO:0000003	-		IPR010651; SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	2	P:GO:0009792; P:GO:0000003	-		SignalP (SIGNALP)
Caenorhabditis briggsae	guanylate ki-se family protein	16	C:GO:0043296; P:GO:0008078; P:GO:0045176; P:GO:0016337; P:GO:0007420; P:GO:0001841; P:GO:0002011; P:GO:0060059; P:GO:0045199; P:GO:0016332; F:GO:0030165; P:GO:0035050; C:GO:0001917; C:GO:0031226; P:GO:0055008; C:GO:0005634	-		IPR008144; IPR008145; G3DSA:3.30.63.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR23122 (PANTHER), PTHR23122:SF4 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	C:GO:0016021; P:GO:0007160; P:GO:0040010; F:GO:0005509	-		IPR003886

Loa loa	transcription initiation factor tfiid subunit 11	9	F:GO:0047485; P:GO:0043923; P:GO:0006367; F:GO:0003677; P:GO:0006368; F:GO:0046966; F:GO:0003713; C:GO:0005669; F:GO:0042809	-		IPR006809; IPR009072; PTHR13218:SF7 (PANTHER)
	-	0				-
Caenorhabditis elegans	transmembrane emp24 domain-containing protein 10 precursor	3	C:GO:0016021; P:GO:0009792; P:GO:0006810	-		IPR000348; IPR009038; IPR015720; PTHR22811 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-npp-12 protein	3	F:GO:0005515; C:GO:0005635; C:GO:0016020	-		PTHR23019 (PANTHER)
Caenorhabditis elegans	beta-carotene -dioxyge-se	3	F:GO:0005515; F:GO:0016702; P:GO:0006721	-	EC:1.13.11.0	IPR004294; PTHR10543:SF4 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG20775 [Caenorhabditis briggsae]	0				-
	-	0				-
Brugia malayi	cell division cycle related family member (cdc-14)	10	P:GO:0040010; P:GO:0000910; C:GO:0030496; P:GO:0060284; F:GO:0004725; C:GO:0005819; P:GO:0045786; P:GO:0009792; C:GO:0005737; P:GO:0006974	-	EC:3.1.3.48	G3DSA:3.90.190.10 (GENE3D), SSF52799 (SUPERFAMILY)
Caenorhabditis elegans	variable abnormal morphology family member (vab-10)	0		F:GO:0005509; P:GO:0007050; F:GO:0003779		IPR002017; IPR018159; G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF38 (PANTHER), SSF46966 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	adenylyl cyclase-associated protein 1	6	P:GO:0008078; P:GO:0007190; P:GO:0007163; F:GO:0003779; P:GO:0007165; P:GO:0016043	-		-
Ornithorhynchus anatinus	ribosomal protein l19	4	F:GO:0003735; F:GO:0003723; C:GO:0022625; P:GO:0006414	-		IPR000196; IPR015972; IPR015974; PTHR10722 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	apolipoprotein o-like	0		C:GO:0005739; F:GO:0005524; P:GO:0006412; F:GO:0004812; C:GO:0005737; P:GO:0006418; C:GO:0005743; C:GO:0005576		IPR001412; IPR019166; PTHR14564 (PANTHER)

	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-frk-1 protein	2	F:GO:0004672; C:GO:0005829	-		IPR001245; IPR011009; IPR020685; IPR020764; G3DSA:3.30.200.20 (GENE3D)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	briggsae cbr-dys-1 protein	2	P:GO:0065007; P:GO:0009987	-		-
Caenorhabditis elegans	udp-n-acetylglucosamine transporter	12	C:GO:0000139; F:GO:0005461; F:GO:0005464; F:GO:0005463; F:GO:0005456; P:GO:0015757; P:GO:0015785; F:GO:0005351; P:GO:0015789; C:GO:0016021; P:GO:0015782; F:GO:0005459	-		IPR007271; PTHR10231:SF13 (PANTHER)
Caenorhabditis elegans	transmembrane protein 134	0		F:GO:0003674; C:GO:0016021; C:GO:0005575		-
Angiostrongylus cantonensis	pre-mr- splicing protein	10	P:GO:0007030; P:GO:0002119; P:GO:0018996; C:GO:0071011; P:GO:0000003; P:GO:0040011; P:GO:0040007; C:GO:0005829; P:GO:0000398; C:GO:0071013	-		PTHR19923 (PANTHER)
Loa loa	structural mainte-nce of chromosome protein	2	P:GO:0009792; P:GO:0045132	-		IPR003395; G3DSA:3.40.50.300 (GENE3D), PTHR19306 (PANTHER), PTHR19306:SF1 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	5	P:GO:0007160; P:GO:0008218; F:GO:0005509; P:GO:0018298; C:GO:0016020	-		IPR000742; IPR002919; IPR006209; IPR006210; IPR011042; IPR013032; G3DSA:2.10.25.10 (GENE3D), G3DSA:2.170.300.10 (GENE3D), PTHR10529 (PANTHER), PTHR10529:SF4 (PANTHER), SSF57196 (SUPERFAMILY)
Brugia malayi	ubiquitin carboxyl-termi-l hydrolase 22	8	P:GO:0016579; P:GO:0016570; F:GO:0008234; F:GO:0003713; P:GO:0048522; P:GO:0045449; C:GO:0005634; P:GO:0007049	-		IPR001394; IPR001607; IPR013083; IPR018200; PTHR10420 (PANTHER), PTHR10420:SF57 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein Y71G10AL.1 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	hypothetical protein Y71G10AL.1 [Caenorhabditis elegans]	0				-

Loa loa	cop9 sig-losome complex subunit 3	0		F:GO:0005488; C:GO:0008180; C:GO:0005737; C:GO:0000502; P:GO:0001701; F:GO:0005515; C:GO:0005634		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Loa loa	e3 ubiquitin	0		F:GO:0046872; F:GO:0016874; P:GO:0008150; F:GO:0008270; F:GO:0005515; C:GO:0005575		IPR006595; PTHR12170 (PANTHER), PTHR12170:SF3 (PANTHER)
Caenorhabditis elegans	prion-like-(q n-rich)-domain-bearing protein family member (pqn-89)	0				-
Caenorhabditis elegans	l80003_1guanylyl cyclase	0				-
Caenorhabditis elegans	protein fam173b	0		F:GO:0003674; C:GO:0016021; C:GO:0016020; P:GO:0008150; C:GO:0005575		G3DSA:3.40.50.150 (GENE3D), PTHR13610 (PANTHER), SignalP (SIGNALP), SSF53335 (SUPERFAMILY)
	-	0				-
Brugia malayi	dead h	0				PTHR12957 (PANTHER), PTHR12957:SF3 (PANTHER)
Caenorhabditis elegans	caax prenyl protease 2	0		P:GO:0006508; C:GO:0030176; C:GO:0016021; C:GO:0016020; F:GO:0004222; F:GO:0008233		IPR003675; PTHR13046 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	caax prenyl protease 2	0		P:GO:0006508; C:GO:0030176; C:GO:0016021; C:GO:0016020; F:GO:0004222; F:GO:0008233		IPR003675; PTHR13046 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	a chain golgi alpha-mannosidase ii in complex with 5-substituted swainsonine a-log: -5- - swainsonine	6	C:GO:0000139; F:GO:0043169; C:GO:0005795; P:GO:0006487; F:GO:0004572; C:GO:0005783	-	EC:3.2.1.114	IPR000602; IPR011330; PTHR11607 (PANTHER), PTHR11607:SF4 (PANTHER)
Brugia malayi	tr--splicing endonuclease subunit sen34	0		P:GO:0006397; C:GO:0005634; F:GO:0016787; P:GO:0000379; F:GO:0003676; C:GO:0000214; F:GO:0000213; P:GO:0006388; C:GO:0005730; F:GO:0004519; F:GO:0004518		IPR006676; IPR006677; IPR011856; PTHR13070 (PANTHER)

Caenorhabditis briggsae	gpi inositol deacylase pgap1	1	P:GO:0009792	-		IPR012908; PTHR15495 (PANTHER), PTHR15495:SF2 (PANTHER)
Caenorhabditis elegans	gdnf family receptor alpha-3	0				-
Caenorhabditis elegans	par-6 at contacts (abnormal early localization of par-6) family member (pac-1)	3	C:GO:0005737; F:GO:0005100; P:GO:0007266	-		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0008061; P:GO:0006030; P:GO:0040011; P:GO:0002119; C:GO:0005576; F:GO:0005515; P:GO:0009405		IPR006150; IPR006210; IPR013032; SignalP (SIGNALP)
Caenorhabditis briggsae	dep domain-containing protein 5	1	P:GO:0040010	-		IPR022046; PTHR13179 (PANTHER)
Caenorhabditis sp. PS1010	uncoordi-ted family member (unc-73)	5	P:GO:0023034; P:GO:0031175; P:GO:0050794; F:GO:0005488; C:GO:0044444	-		PTHR22826 (PANTHER), PTHR22826:SF39 (PANTHER), SSF46966 (SUPERFAMILY)
Apis mellifera	set domain and mariner transposase fusion	0		F:GO:0016740; F:GO:0004803; P:GO:0006313; F:GO:0008168; C:GO:0005634; F:GO:0003677; F:GO:0008270; F:GO:0018024; P:GO:0015074; P:GO:0016568		-
Caenorhabditis briggsae	trans-golgi network protein 2	2	C:GO:0043231; C:GO:0044444	-		PTHR23211 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	F:GO:0005044; F:GO:0005488; C:GO:0016020	-		-
Caenorhabditis elegans	r- binding homolog 2	5	P:GO:0009792; P:GO:0008354; P:GO:0007126; P:GO:0007281; C:GO:0043231	-		IPR001159; IPR014720; PTHR10910 (PANTHER), PTHR10910:SF6 (PANTHER), SSF54768 (SUPERFAMILY)
Homo sapiens	-dh dehydroge-se	14	C:GO:0005654; P:GO:0017148; F:GO:0005515; F:GO:0008137; P:GO:0030262; C:GO:0016021; P:GO:0045892; P:GO:0022900; P:GO:0008624; C:GO:0005747; P:GO:0030308; P:GO:0006606; F:GO:0005524; P:GO:0006800	-	EC:1.6.5.3	-
Brugia malayi	coronin 2a	0				IPR001680; IPR015048; IPR015505; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; SSF117289 (SUPERFAMILY)

Cyathostominae sp. JM-2007a	briggsae cbr-tag-273 protein	2	F:GO:0008270; P:GO:0000003	-		-
Caenorhabditis elegans	aspartyl glutamyl-tr- amidotransferase subunit b	1	F:GO:0016874	-		IPR006075; IPR010916; IPR017958; IPR017959; IPR018027; SSF55931 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	adipokinetic hormone receptor	4	P:GO:0007186; C:GO:0016021; P:GO:0007165; F:GO:0005000	-		IPR000276; IPR017452; G3DSA:1.20.1070.10 (GENE3D), PTHR19264 (PANTHER), PTHR19264:SF50 (PANTHER), SignalP (SIGNALP), SSF81321 (SUPERFAMILY)
	-	0				-
	-	0				-
Loa loa	patched family protein	4	P:GO:0018996; C:GO:0016020; P:GO:0040018; P:GO:0040011	-		-
	-	0				-
Caenorhabditis elegans	cytosolic phosphoglucomutase	13	C:GO:0005829; P:GO:0019388; P:GO:0006874; P:GO:0019255; P:GO:0006011; F:GO:0000287; P:GO:0005992; F:GO:0004614; C:GO:0009507; P:GO:0046686; C:GO:0005634; C:GO:0005886; P:GO:0005978	-	EC:5.4.2.2	G3DSA:3.30.310.50 (GENE3D), SSF55957 (SUPERFAMILY)
Camponotus floridanus	uncharacterized transposase-like protein	0				IPR007087; IPR015880
Caenorhabditis elegans	mothers against decapentaplegic homolog 4	20	P:GO:0007179; P:GO:0006357; P:GO:0051246; P:GO:0007369; P:GO:0043009; P:GO:0090100; P:GO:0072131; P:GO:0051128; P:GO:0040007; P:GO:0042127; C:GO:0005737; P:GO:0048646; P:GO:0009952; C:GO:0005667; F:GO:0003677; P:GO:0030154; P:GO:0048523; P:GO:0045893; P:GO:0051239; F:GO:0046332	-		IPR001132; IPR003619; IPR008984; IPR013019; IPR013790; IPR017855
	-	0				-
	-	0				-

Caenorhabditis elegans	cell division cycle related family member (cdc-)	14	P:GO:0040010; P:GO:0007126; P:GO:0000212; P:GO:0000003; P:GO:0051301; F:GO:0004725; P:GO:0010171; P:GO:0002119; P:GO:0006898; P:GO:0009792; P:GO:0008283; P:GO:0051729; C:GO:0005634; P:GO:0007346	-	EC:3.1.3.48	IPR000751; IPR001763; PTHR10828:SF14 (PANTHER)
Caenorhabditis elegans	neuropeptide-like protein family member (nlp-21)	0				SignalP (SIGNALP)
Brugia malayi	gtpase activating protein and vps9 domains 1	3	P:GO:0009987; P:GO:0050789; C:GO:0044444	-		-
Brugia malayi	hypothetical protein Bm1_22765 [Brugia malayi]	0		P:GO:0000003		-
Brugia malayi	hypothetical protein Bm1_52845 [Brugia malayi]	0				-
Brugia malayi	hypothetical protein Bm1_52845 [Brugia malayi]	0				-
Caenorhabditis briggsae	traf and tnf receptor associated protein	6	P:GO:0030512; F:GO:0005515; F:GO:0004518; P:GO:0007368; P:GO:0060027; P:GO:0006974	-		IPR005135; IPR009060; G3DSA:1.10.8.10 (GENE3D), G3DSA:3.60.10.10 (GENE3D)
Caenorhabditis elegans	mit domain-containing protein 1	0		F:GO:0003674; C:GO:0031902; C:GO:0016020; P:GO:0008150; C:GO:0005768; P:GO:0006810; C:GO:0005575; P:GO:0015031		IPR007330; G3DSA:1.20.58.280 (GENE3D), PTHR21222 (PANTHER), SSF116846 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	P:GO:0006952	-		-
Loa loa	briggsae cbr-pqn-21 protein	0		C:GO:0016021; C:GO:0016020; P:GO:0051973; C:GO:0005768; F:GO:0003676; F:GO:0008270; C:GO:0005794; C:GO:0005575; C:GO:0005622; C:GO:0005886		IPR007087; IPR008162; IPR015880
Loa loa	briggsae cbr-pqn-21 protein	0		C:GO:0016021; C:GO:0016020; P:GO:0051973; C:GO:0005768; F:GO:0003676; F:GO:0008270; C:GO:0005794; C:GO:0005575; C:GO:0005622; C:GO:0005886		IPR007087; IPR008162; IPR015880
Caenorhabditis briggsae	kiaa1738 protein	1	C:GO:0016020	-		IPR019411; PTHR13466 (PANTHER)

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	F:GO:0004872; F:GO:0005515; P:GO:0006350	-		IPR001628; IPR008946; IPR013088; PR00350 (PRINTS), PTHR11865 (PANTHER), PTHR11865:SF218 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		IPR002549
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		IPR002549
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		IPR002549
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		IPR002549
Caenorhabditis elegans	rap ran-gap family protein	0		F:GO:0005096; P:GO:0051056; C:GO:0005622		-
Caenorhabditis briggsae	excision repair cross-complementing rodent repair deficiency complementation group 1	33	P:GO:0000718; C:GO:0005654; P:GO:0009650; P:GO:0006312; P:GO:0010165; P:GO:0009744; P:GO:0032205; P:GO:0048568; F:GO:0003684; F:GO:0008022; P:GO:0035166; P:GO:0006949; C:GO:0000784; P:GO:0001302; P:GO:0007283; P:GO:0008283; P:GO:0008584; P:GO:0010259; F:GO:0003697; P:GO:0006302; F:GO:0019904; P:GO:0006296; C:GO:0000109; P:GO:0007281; P:GO:0048477; P:GO:0006295; P:GO:0035264;	-		IPR004579; IPR010994; IPR011335; G3DSA:1.10.150.20 (GENE3D), PTHR12749 (PANTHER)
Caenorhabditis elegans	zinc metalloprotease	0		P:GO:0006508; F:GO:0008237; F:GO:0004222		IPR000718; IPR008753; G3DSA:1.10.1380.10 (GENE3D), PTHR11733:SF24 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	peptidase family m3 containing protein	3	F:GO:0008233; P:GO:0043170; P:GO:0044238	-		IPR001567; G3DSA:3.40.390.10 (GENE3D), PTHR11804 (PANTHER), PTHR11804:SF4 (PANTHER)
	-	0				-
Caenorhabditis briggsae	btb poz domain containing protein	2	F:GO:0005515; C:GO:0016021	-		-

Caenorhabditis briggsae	translocating chain-associated membrane protein 1	15	F:GO:0046966; F:GO:0004402; C:GO:0043231; F:GO:0047485; P:GO:0030521; P:GO:0019915; F:GO:0016922; F:GO:0003713; C:GO:0044425; P:GO:0045944; F:GO:0004872; P:GO:0006613; C:GO:0044444; P:GO:0032502; F:GO:0050681	-	EC:2.3.1.48	IPR013599; PTHR12371 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	translocation associated membrane protein 1	13	F:GO:0004402; C:GO:0043231; P:GO:0030518; F:GO:0047485; C:GO:0005737; P:GO:0019915; F:GO:0016922; F:GO:0003713; C:GO:0044425; F:GO:0035258; P:GO:0045944; F:GO:0004872; P:GO:0006613	-	EC:2.3.1.48	IPR006634; IPR013599; PTHR12371 (PANTHER), PTHR12371:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	translocation associated membrane protein 1	13	F:GO:0004402; C:GO:0043231; P:GO:0030518; F:GO:0047485; C:GO:0005737; P:GO:0019915; F:GO:0016922; F:GO:0003713; C:GO:0044425; F:GO:0035258; P:GO:0045944; F:GO:0004872; P:GO:0006613	-	EC:2.3.1.48	IPR006634; IPR013599; PTHR12371 (PANTHER), PTHR12371:SF1 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				IPR013032; G3DSA:2.170.300.10 (GENE3D), SSF57196 (SUPERFAMILY)
Caenorhabditis briggsae	triosephosphate isomerase	6	F:GO:0004807; P:GO:0044283; P:GO:0044249; P:GO:0032787; P:GO:0008610; P:GO:0006007	-	EC:5.3.1.1	IPR000652; IPR013785; IPR020861

Caenorhabditis briggsae	ump-cmp ki-se	7	C:GO:0005737; P:GO:0009792; F:GO:0004017; P:GO:0009165; F:GO:0009041; F:GO:0005524; F:GO:0004127	-	EC:2.7.4.3; EC:2.7.4.14	-
Ancylostoma caninum	secreted protein 5 precursor	0		P:GO:0006898; C:GO:0005576		IPR014044
Caenorhabditis elegans	protein phosphatase methylesterase 1	10	F:GO:0008601; P:GO:0009792; P:GO:0002119; F:GO:0051721; F:GO:0051722; P:GO:0006482; F:GO:0004864; P:GO:0000003; P:GO:0008340; P:GO:0040007	-		-
Cooperia oncophora	low-density lipoprotein receptor domain class a containing protein	1	F:GO:0004872	-		IPR002172; PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER)
	-	0				-
	-	0				-
Loa loa	s-p25 fusion protein	9	F:GO:0005483; C:GO:0045202; F:GO:0005484; P:GO:0048172; C:GO:0019717; P:GO:0016082; P:GO:0016081; P:GO:0006893; C:GO:0005886	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	neurofibromin 2 (bilateral acoustic neuroma)	18	C:GO:0044446; P:GO:0042325; P:GO:0031324; C:GO:0043232; P:GO:0046426; P:GO:0044260; P:GO:0010605; C:GO:0043231; C:GO:0042995; C:GO:0005886; C:GO:0044425; P:GO:0080090; P:GO:0009792; F:GO:0005515; P:GO:0007155; P:GO:0030036; C:GO:0044444; P:GO:0048731	-		IPR000798; IPR008954; IPR011259; PTHR23281 (PANTHER), PTHR23281:SF1 (PANTHER)
Caenorhabditis elegans	briggsae cbr-pad-1 protein	0		P:GO:0007275; P:GO:0006810; P:GO:0015031		SignalP (SIGNALP)
Caenorhabditis briggsae	7 transmembrane	4	P:GO:0007186; C:GO:0016021; P:GO:0007165; F:GO:0004930	-		-

Ancylostoma caninum	venom-allergen-like protein family member (vap-1)	0		P:GO:0040011; C:GO:0005576		IPR001283; IPR014044
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	d domain (prokaryotic heat shock protein) family member (dnj-29)	4	P:GO:0006457; C:GO:0016021; F:GO:0051082; F:GO:0031072	-		IPR001623; IPR003095; IPR004179; IPR015609; G3DSA:1.10.150.20 (GENE3D), G3DSA:1.10.3380.10 (GENE3D), G3DSA:2.60.40.150 (GENE3D), PTHR11821:SF7 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	d domain (prokaryotic heat shock protein) family member (dnj-29)	3	P:GO:0006457; C:GO:0016021; F:GO:0051082	-		IPR001623; IPR003095; IPR004179; IPR015609; G3DSA:1.10.150.20 (GENE3D), G3DSA:1.10.3380.10 (GENE3D), G3DSA:2.60.40.150 (GENE3D), PTHR11821:SF7 (PANTHER), SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	actin binding lim protein 1	6	P:GO:0007411; F:GO:0008270; P:GO:0045944; P:GO:0007010; F:GO:0003779; C:GO:0015629	-		IPR001781; PTHR18973 (PANTHER), PTHR18973:SF90 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis briggsae	Hypothetical protein CBG02376 [Caenorhabditis briggsae]	0				IPR021013
Caenorhabditis briggsae	small nuclear ribonucleoprotein g	2	F:GO:0003676; C:GO:0030529	-		IPR001163; IPR006649; IPR010920; G3DSA:2.30.30.100 (GENE3D), PTHR10553 (PANTHER), PTHR10553:SF2 (PANTHER)
Caenorhabditis elegans	pctaire class cell cycle ki-se family member (pct-1)	4	P:GO:0006468; F:GO:0005515; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF103 (PANTHER)
	-	0				-
Caenorhabditis briggsae	cg3714 cg3714-pa	9	P:GO:0006979; C:GO:0005829; F:GO:0004514; P:GO:0009435; P:GO:0040007; P:GO:0040035; F:GO:0004516; P:GO:0002119; P:GO:0009792	-	EC:2.4.2.19; EC:2.4.2.11	IPR002638; IPR006405; IPR007229; IPR015977; G3DSA:3.20.140.10 (GENE3D), PTHR11098 (PANTHER), SSF54675 (SUPERFAMILY)
Caenorhabditis briggsae	cg3714 cg3714-pa	9	P:GO:0006979; C:GO:0005829; F:GO:0004514; P:GO:0009435; P:GO:0040007; P:GO:0040035; F:GO:0004516; P:GO:0002119; P:GO:0009792	-	EC:2.4.2.19; EC:2.4.2.11	-

Caenorhabditis briggsae	briggsae cbr-tag-192 protein	12	P:GO:0009653; C:GO:0000785; P:GO:0007423; P:GO:0006333; F:GO:0004386; F:GO:0003677; P:GO:0009790; P:GO:0050789; F:GO:0003682; C:GO:0005634; F:GO:0005524; P:GO:0003008	-		IPR000330; IPR000953; IPR001005; IPR001650; IPR006576; IPR014001; IPR014021; IPR016197; G3DSA:2.40.50.40 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR10799 (PANTHER), PTHR10799:SF70 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	chromodomain helicase d- binding protein 6	12	P:GO:0009653; C:GO:0000785; P:GO:0007423; P:GO:0006333; F:GO:0004386; F:GO:0003677; P:GO:0009790; P:GO:0050789; F:GO:0003682; C:GO:0005634; F:GO:0005524; P:GO:0003008	-		IPR000330; IPR000953; IPR001650; IPR006576; IPR014001; IPR014021; IPR016197; G3DSA:2.40.50.40 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR10799 (PANTHER), PTHR10799:SF70 (PANTHER), SSF52540 (SUPERFAMILY)
Loa loa	anion exchange protein	3	C:GO:0016021; F:GO:0005452; P:GO:0006820	-		IPR003020; IPR011531
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-unc-95 protein	1	F:GO:0008270	-		IPR001781; PTHR18973 (PANTHER), PTHR18973:SF94 (PANTHER)
Loa loa	probable cation-transporting atpase in chromosome	5	F:GO:0016820; F:GO:0016887; F:GO:0000166; P:GO:0008152; C:GO:0016020	-	EC:3.6.3.0	-
	-	0				-
Caenorhabditis elegans	alanine aminotransferase	7	F:GO:0030170; P:GO:0042851; F:GO:0004021; P:GO:0009058; P:GO:0006103; P:GO:0000003; F:GO:0016847	-	EC:2.6.1.2; EC:4.4.1.14	IPR015422; IPR015424; PTHR11751 (PANTHER), PTHR11751:SF29 (PANTHER)
	-	0				-
Caenorhabditis elegans	ylu4_caeel ame: full=uncharacterized protein	0		P:GO:0006898; P:GO:0002119; P:GO:0040007		-
Caenorhabditis elegans	deah (asp-glu-ala-his) box polypeptide 8	5	P:GO:0006396; F:GO:0004004; F:GO:0003676; F:GO:0005515; F:GO:0000166	-		IPR003029; IPR012340; IPR016027; IPR022967; PTHR15838 (PANTHER)
Caenorhabditis briggsae	minichromosome mainte-nce complex component 3 associated protein	5	P:GO:0019915; P:GO:0000003; P:GO:0010171; C:GO:0005634; P:GO:0002119	-		IPR005062; PTHR12436 (PANTHER), PTHR12436:SF3 (PANTHER)

Caenorhabditis briggsae	minichromosome mainte-nce complex component 3 associated protein	5	P:GO:0019915; P:GO:0000003; P:GO:0010171; C:GO:0005634; P:GO:0002119	-		IPR005062; PTHR12436 (PANTHER), PTHR12436:SF3 (PANTHER)
Caenorhabditis elegans	hypothetical protein H14E04.2 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	serine threonine ki-se cdc2	17	P:GO:0001556; F:GO:0008353; P:GO:0040002; P:GO:0045836; P:GO:0040035; P:GO:0035046; P:GO:0051446; P:GO:0051301; F:GO:0005524; P:GO:0007067; P:GO:0040011; F:GO:0019901; F:GO:0004693; P:GO:0009792; C:GO:0005737; C:GO:0005634; P:GO:0006468	-	EC:2.7.11.23 ; EC:2.7.11.22	IPR000719; IPR002290; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF109 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	nucleoporin 205	0		C:GO:0046930; F:GO:0003674; F:GO:0015288; C:GO:0005635; C:GO:0005575		IPR021827
Caenorhabditis briggsae	polynucleotide ki-se- 3 -phosphatase	4	P:GO:0008340; P:GO:0040007; P:GO:0019915; P:GO:0002119	-		IPR010488; IPR013954; IPR015636; G3DSA:3.40.50.300 (GENE3D), SSF52540 (SUPERFAMILY), SSF56784 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	breast cancer early onset	4	F:GO:0005515; P:GO:0006259; P:GO:0016567; P:GO:0019222	-		IPR001357; IPR001841; IPR011364; IPR013083; IPR017907; IPR018957; G3DSA:3.40.50.10190 (GENE3D), SSF57850 (SUPERFAMILY)
Caenorhabditis elegans	breast cancer early onset	4	F:GO:0005515; P:GO:0006259; P:GO:0016567; P:GO:0019222	-		IPR001357; IPR001841; IPR011364; IPR013083; IPR017907; IPR018957; G3DSA:3.40.50.10190 (GENE3D), SSF57850 (SUPERFAMILY)
Caenorhabditis elegans	adenylosucci-te synthetase	11	P:GO:0040010; F:GO:0004019; P:GO:0006164; P:GO:0040027; P:GO:0040035; F:GO:0000287; P:GO:0040011; P:GO:0006898; P:GO:0009792; C:GO:0005737; F:GO:0005525	-	EC:6.3.4.4	IPR001114; G3DSA:3.90.170.10 (GENE3D), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	ysyf_caeel ame: full=uncharacterized f-box protein	0				-

Caenorhabditis briggsae	Hypothetical protein CBG01593 [Caenorhabditis briggsae]	4	P:GO:0007186; C:GO:0016021; P:GO:0007165; F:GO:0004930	-		-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-pqn-89 protein	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-pqn-89 protein	0				SignalP (SIGNALP)
Toxoplasma gondii GT1	camp-dependent protein ki-se regulatory	0		F:GO:0016740; F:GO:0045735; F:GO:0016787; F:GO:0003676; F:GO:0000166; F:GO:0004715; F:GO:0016301; F:GO:0004692; F:GO:0005509		-
	-	0				-
Caenorhabditis elegans	sh3bgr protein	1	F:GO:0005515	-		-
Caenorhabditis elegans	sh3bgr protein	1	F:GO:0005515	-		-
Caenorhabditis elegans	g in family member (glb-10)	4	F:GO:0020037; F:GO:0005344; P:GO:0015671; F:GO:0019825	-		IPR000971; IPR009050; IPR012292
Caenorhabditis briggsae	amine oxidase	0		P:GO:0055114; F:GO:0005488; F:GO:0016491; P:GO:0008152		IPR002937; PR00419 (PRINTS), G3DSA:3.50.50.60 (GENE3D), PTHR10742 (PANTHER), PTHR10742:SF22 (PANTHER), SignalP (SIGNALP), SSF51905 (SUPERFAMILY)
Loa loa	phosphatidylinositol glycan anchor class v	4	P:GO:0000003; F:GO:0016740; P:GO:0007275; C:GO:0044464	-		IPR007315; PTHR12468:SF1 (PANTHER), PF04188 (PFAM)
Caenorhabditis briggsae	neurogenic locus notch protein	0		F:GO:0005488; P:GO:0040010		-
Ancylostoma ceylanicum	gamma-glutamylcysteine synthetase	4	F:GO:0004357; F:GO:0005515; P:GO:0006750; F:GO:0000166	-	EC:6.3.2.2	SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	amp-activated ki-se family member (aak-2)	4	P:GO:0006468; F:GO:0005515; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR015741; IPR017442; IPR020636; G3DSA:1.10.510.10 (GENE3D)
Macaca mulatta	peptidylprolyl isomerase a	13	P:GO:0006457; P:GO:0019047; P:GO:0045069; F:GO:0042277; F:GO:0046790; F:GO:0051082; C:GO:0005576; C:GO:0005634; F:GO:0008270; C:GO:0005829; F:GO:0003755; P:GO:0044419; P:GO:0019059	-	EC:5.2.1.8	IPR002130; IPR015891; IPR020892; PTHR11071 (PANTHER), PTHR11071:SF74 (PANTHER)
Caenorhabditis briggsae	phospholipase b1	2	F:GO:0016788; P:GO:0006629	-		IPR001087; IPR013830; IPR013831; PTHR21325 (PANTHER)

Caenorhabditis briggsae	phospholipase b1	2	F:GO:0016788; P:GO:0006629	-		IPR001087; IPR013830; IPR013831; PTHR21325 (PANTHER)
Caenorhabditis briggsae	phospholipase b1	2	F:GO:0016788; P:GO:0006629	-		IPR001087; IPR013830; IPR013831; PTHR21325 (PANTHER)
	-	0				-
Caenorhabditis briggsae	ligase atp-dependent	2	P:GO:0006259; F:GO:0005488	-		IPR001510; PTHR10459 (PANTHER), PTHR10459:SF2 (PANTHER), SSF57716 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Brugia malayi	abhydrolase domain containing 2	0		P:GO:0009611; C:GO:0016021; C:GO:0016020; F:GO:0004091; F:GO:0016787; F:GO:0003674; P:GO:0030336; P:GO:0008152; P:GO:0008150		PTHR10794 (PANTHER), PTHR10794:SF9 (PANTHER)
Brugia malayi	mediator of r- polymerase ii transcription subunit 12	5	P:GO:0051239; P:GO:0002119; P:GO:0048513; P:GO:0045927; P:GO:0022414	-		-
Caenorhabditis elegans	ck1 worm6 protein ki-se	0		F:GO:0016301; F:GO:0005524; F:GO:0004672; F:GO:0000166; P:GO:0006468		PTHR11909 (PANTHER), PTHR11909:SF19 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	4	F:GO:0016787; P:GO:0000003; F:GO:0005488; P:GO:0040010	-		-
Caenorhabditis briggsae	exostoses -like 3	6	F:GO:0005515; P:GO:0001558; F:GO:0016758; P:GO:0035138; P:GO:0048522; C:GO:0031227	-	EC:2.4.1.0	IPR015338; G3DSA:3.90.550.10 (GENE3D), PTHR11062 (PANTHER), PTHR11062:SF5 (PANTHER), SSF53448 (SUPERFAMILY)
Brugia malayi	cut domain containing protein	17	P:GO:0007492; P:GO:0000003; P:GO:0030512; P:GO:0001952; P:GO:0010552; P:GO:0030183; P:GO:0045165; P:GO:0031018; F:GO:0016563; F:GO:0043565; P:GO:0006006; P:GO:0042384; F:GO:0003700; P:GO:0030335; C:GO:0005634; P:GO:0048536; P:GO:0002064	-		IPR001356; IPR003350; IPR009057; IPR010982; IPR012287; G3DSA:1.10.260.40 (GENE3D), PTHR14057 (PANTHER), PTHR14057:SF3 (PANTHER)

	-	0				-
	-	0				-
Apis mellifera	serine-type protease inhibitor	0		C:GO:0016020; C:GO:0005886		IPR000601; IPR001000; IPR002859; IPR013032; IPR022409; PTHR10083 (PANTHER), PTHR10083:SF14 (PANTHER), SignalP (SIGNALP)
Apis mellifera	serine-type protease inhibitor	0		C:GO:0016020; C:GO:0005886		IPR000601; IPR001000; IPR002859; IPR013032; IPR022409; PTHR10083 (PANTHER), PTHR10083:SF14 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	major allergen	0				IPR002499
Caenorhabditis briggsae	zinc finger protein	1	F:GO:0008270	-		IPR004457; PTHR10876 (PANTHER)
Caenorhabditis elegans	briggsae cbr-unc-97 protein	2	F:GO:0008270; F:GO:0017022	-		IPR001781; PTHR18973 (PANTHER), PTHR18973:SF93 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis elegans	histidine triad protein member 5	3	P:GO:0000290; F:GO:0016787; F:GO:0005515	-		IPR008594; IPR011145; IPR011146; PF11969 (PFAM)
Caenorhabditis elegans	eukaryotic translation initiation factor 3 subunit 6	14	P:GO:0000184; C:GO:0000785; C:GO:0005852; P:GO:0043473; P:GO:0040007; P:GO:0006898; C:GO:0016605; F:GO:0047485; P:GO:0045947; F:GO:0003743; C:GO:0005829; P:GO:0048703; P:GO:0002119; P:GO:0040035	-		IPR000717; IPR011991; IPR016650; IPR019010; PTHR10317 (PANTHER), SSF46785 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	suppressor of activated let-60 ras family member (sur-7)	0		F:GO:0008324; P:GO:0040027; P:GO:0010043; P:GO:0032502; C:GO:0016020; P:GO:0055085; P:GO:0040010; P:GO:0006812		IPR002524; SignalP (SIGNALP)
Caenorhabditis briggsae	zinc finger	4	F:GO:0008270; C:GO:0005622; F:GO:0005515; F:GO:0003677	-		IPR011705; IPR013089
Loa loa	aqr protein	6	P:GO:0008380; F:GO:0008026; C:GO:0005681; F:GO:0003723; P:GO:0006397; F:GO:0005524	-		PTHR10887 (PANTHER), PTHR10887:SF5 (PANTHER), SSF52540 (SUPERFAMILY)
Phragmatopoma californica	cement precursor protein 3b variant 1	0		P:GO:0016068		-

Taeniopygia guttata	death inducer-obliterator 1	0		F:GO:0046872; P:GO:0006915; C:GO:0005737; P:GO:0006350; F:GO:0008270; F:GO:0005515; C:GO:0005634		-
	-	0				-
Loa loa	cleavage and polyadenylation specificity factor	10	F:GO:0003730; P:GO:0006379; P:GO:0000910; P:GO:0006378; P:GO:0040035; P:GO:0006398; P:GO:0009792; F:GO:0016787; P:GO:0016246; C:GO:0005847	-		IPR022712; PTHR11203 (PANTHER), PTHR11203:SF5 (PANTHER)
Caenorhabditis elegans	abnormal embroygenesis family member (emb-9)	3	F:GO:0005515; C:GO:0005581; F:GO:0005201	-		PTHR10499 (PANTHER)
Brugia malayi	ring finger protein 2	7	P:GO:0000278; P:GO:0009948; C:GO:0071339; C:GO:0016604; F:GO:0046872; P:GO:0006350; F:GO:0003682	-		IPR001841; IPR013083; IPR017907; IPR018957; PTHR10825 (PANTHER), PTHR10825:SF5 (PANTHER), SSF57850 (SUPERFAMILY)
Ancylostoma ceylanicum	serine protei-se	2	F:GO:0004867; F:GO:0008233	-		IPR002223; IPR020901; PTHR10083 (PANTHER), PTHR10083:SF39 (PANTHER)
	-	0				-
Homo sapiens	PREDICTED: hypothetical protein [Homo sapiens]	0				IPR016160; PTHR16484 (PANTHER), PTHR16484:SF2 (PANTHER)
Caenorhabditis elegans	tbc1 domain member 15	2	C:GO:0005622; P:GO:0032313	-		IPR000195; G3DSA:1.10.8.270 (GENE3D), PTHR22957 (PANTHER), PTHR22957:SF34 (PANTHER)
Caenorhabditis elegans	tbc1 domain family member 15	2	C:GO:0005622; P:GO:0032313	-		IPR000195; G3DSA:1.10.8.270 (GENE3D), PTHR22957 (PANTHER), PTHR22957:SF34 (PANTHER)
Ancylostoma caninum	elegans protein partially confirmed by transcript evidence	2	P:GO:0008152; F:GO:0008237	-		IPR000718; IPR008753; G3DSA:3.40.390.10 (GENE3D), PTHR11733:SF15 (PANTHER), SSF55486 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	hypothetical protein F35H10.10 [Caenorhabditis elegans]	4	P:GO:0007186; C:GO:0016021; P:GO:0007165; F:GO:0004930	-		G3DSA:3.40.50.2300 (GENE3D), SignalP (SIGNALP), SSF53822 (SUPERFAMILY)
Caenorhabditis elegans	glucose-6-phosphate dehydroge-se	7	P:GO:0006071; F:GO:0008889; P:GO:0006006; F:GO:0004345; P:GO:0055114; F:GO:0005488; P:GO:0006629	-	EC:3.1.4.46; EC:1.1.1.49	-

Loa loa	bromodomain-containing protein 8	3	C:GO:0031981; P:GO:0050794; P:GO:0016573	-		IPR001487; PTHR15398 (PANTHER)
Loa loa	bromodomain-containing protein 8	3	C:GO:0031981; P:GO:0050794; P:GO:0016573	-		IPR001487; PTHR15398 (PANTHER)
Loa loa	briggsae cbr-vab-9 protein	2	P:GO:0060857; C:GO:0044425	-		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Loa loa	zinc c2h2 type family protein	0		F:GO:0008270; C:GO:0005622		-
Loa loa	zinc c2h2 type family protein	0		F:GO:0008270; C:GO:0005622		-
	-	0				-
Brugia malayi	bromodomain containing protein	0				-
Caenorhabditis briggsae	sumo-activating enzyme subunit 1	8	P:GO:0009792; P:GO:0002119; F:GO:0005488; P:GO:0016925; P:GO:0040019; P:GO:0040007; F:GO:0019948; P:GO:0048477	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	multidrug resistance protein family member (mrp-1)	4	F:GO:0042626; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		IPR017940; G3DSA:1.20.1560.10 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF15 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	ef hand family protein	12	P:GO:0047497; P:GO:0006915; F:GO:0005509; C:GO:0005743; P:GO:0007264; P:GO:0019725; P:GO:0002119; F:GO:0005515; C:GO:0031307; F:GO:0016787; P:GO:0015031; F:GO:0005525	-		IPR001806; IPR005225; IPR013753; IPR020860; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), PTHR11708:SF13 (PANTHER), SSF52540 (SUPERFAMILY)
Drosophila sechellia	isoform a	0		F:GO:0003674; F:GO:0008270; C:GO:0005575		IPR006578
Drosophila sechellia	isoform a	0		F:GO:0003674; F:GO:0008270; C:GO:0005575		IPR006578

Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; C:GO:0016020; P:GO:0055085; F:GO:0005215; P:GO:0006810		SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; C:GO:0016020; P:GO:0055085; F:GO:0005215; P:GO:0006810		IPR005828; IPR016196; G3DSA:1.20.1250.20 (GENE3D), PTHR11600 (PANTHER), PTHR11600:SF27 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	P:GO:0007409	-		SignalP (SIGNALP)
Caenorhabditis briggsae	ww domain containing protein	9	P:GO:0040008; P:GO:0048519; P:GO:0006915; N:GO:2000026; P:GO:0048592; P:GO:0007444; P:GO:0042127; P:GO:0048468; P:GO:0030182	-		IPR001202; IPR011524; G3DSA:2.20.70.10 (GENE3D), PTHR10316 (PANTHER), PTHR10316:SF13 (PANTHER)
Danio rerio	transmembrane receptor notch1 partial	10	P:GO:0031016; P:GO:0048729; P:GO:0009952; P:GO:0042659; P:GO:0043009; P:GO:0016043; P:GO:0010470; P:GO:0060795; P:GO:0030182; P:GO:0021515	-		IPR000742; IPR006210; IPR013032; G3DSA:2.10.25.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF219 (PANTHER), SSF57196 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	kinesin family member 3a	4	P:GO:0007018; F:GO:0005524; F:GO:0003777; C:GO:0005874	-		IPR001752; PTHR16012 (PANTHER), PTHR16012:SF160 (PANTHER), SSF52540 (SUPERFAMILY)
Loa loa	zinc c2h2 type family protein	1	F:GO:0005515	-		IPR015880
	-	0				-
Caenorhabditis elegans	pp-loop atpase superfamily	10	P:GO:0006412; C:GO:0005829; P:GO:0034227; P:GO:0048598; P:GO:0048599; P:GO:0007283; P:GO:0040025; P:GO:0002098; F:GO:0000049; P:GO:0006974	-	EC:3.6.5.3	IPR014729; SSF52402 (SUPERFAMILY)
	-	0				-
Ailuropoda melanoleuca	ribosomal protein l31	5	F:GO:0003735; F:GO:0003723; F:GO:0005515; C:GO:0022625; P:GO:0006414	-		IPR000054; IPR020052

Caenorhabditis briggsae	ferm domain (-ezrin-radixin-moesin) family member (frm-1)	3	C:GO:0008091; F:GO:0008092; C:GO:0005886	-		IPR000299; IPR014352; IPR018979; IPR019748; IPR019749; IPR019750; G3DSA:3.10.20.90 (GENE3D), PTHR23280 (PANTHER), SSF54236 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	protein arginine n-methyltransferase	1	F:GO:0008168	-	EC:2.1.1.0	G3DSA:2.70.160.11 (GENE3D), G3DSA:3.40.50.150 (GENE3D), PTHR11006 (PANTHER), PTHR11006:SF4 (PANTHER), SSF53335 (SUPERFAMILY)
Dictyocaulus viviparus	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	P:GO:0019915; P:GO:0040010	-		PTHR11161 (PANTHER), SignalP (SIGNALP)
	-	0				-
Pan troglodytes	zinc finger protein 91-like	7	P:GO:0045730; P:GO:0006952; C:GO:0005625; P:GO:0006955; P:GO:0007204; C:GO:0045121; C:GO:0005887	-		SignalP (SIGNALP)
Loa loa	elegans protein confirmed by transcript evidence	0		F:GO:0003676; P:GO:0000398; F:GO:0000166; F:GO:0008270; C:GO:0005634; C:GO:0005622		PTHR23106 (PANTHER), PTHR23106:SF1 (PANTHER)
Caenorhabditis elegans	r- polymerase 1-2	13	F:GO:0003899; P:GO:0009303; P:GO:0017126; P:GO:0007566; C:GO:0005736; P:GO:0040007; P:GO:0040035; F:GO:0003677; P:GO:0002119; F:GO:0005515; F:GO:0032549; C:GO:0005654; P:GO:0009792	-	EC:2.7.7.6	IPR007120; IPR007641; IPR015712; G3DSA:2.40.270.10 (GENE3D), PTHR20856:SF5 (PANTHER), SSF64484 (SUPERFAMILY)
Caenorhabditis elegans	px domain containing protein	1	F:GO:0005488	-		IPR001683
Caenorhabditis sp. PS1010	seryl-tr- synthetase	7	C:GO:0005829; F:GO:0004828; C:GO:0005739; P:GO:0006434; F:GO:0005524; F:GO:0005515; P:GO:0001569	-	EC:6.1.1.11	IPR010978; IPR015866

Caenorhabditis elegans	acyl- synthetase long-chain family member 5	17	P:GO:0009749; P:GO:0009744; P:GO:0032869; P:GO:0042178; C:GO:0005743; P:GO:0010867; C:GO:0005741; F:GO:0004467; P:GO:0070723; P:GO:0010747; P:GO:0032000; C:GO:0005783; P:GO:0008654; C:GO:0005886; C:GO:0005625; P:GO:0007584; C:GO:0005778	-	EC:6.2.1.3	IPR000873; IPR020459; IPR020845; G3DSA:2.30.38.10 (GENE3D), G3DSA:3.40.50.980 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF8 (PANTHER), SSF56801 (SUPERFAMILY)
Caenorhabditis elegans	ibr domain containing protein	0		F:GO:0003676; F:GO:0046872; F:GO:0008270; F:GO:0005515; C:GO:0005622		SSF57850 (SUPERFAMILY)
Caenorhabditis elegans	lim domain family member (lim-9)	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	n-acetyltransferase 9-like	1	F:GO:0016740	-		IPR016181; PTHR13256 (PANTHER)
	-	0				-
Caenorhabditis elegans	diacylglycerol ki-se protein isoform partially confirmed by transcript evidence	20	F:GO:0004143; P:GO:0016049; C:GO:0005856; P:GO:0019932; F:GO:0046872; P:GO:0051260; C:GO:0016023; F:GO:0005524; P:GO:0046339; F:GO:0019992; P:GO:0006897; F:GO:0046982; P:GO:0007275; F:GO:0042803; P:GO:0007205; P:GO:0015031; C:GO:0005634; P:GO:0007173; P:GO:0010033; C:GO:0005886	-	EC:2.7.1.107	IPR000756; IPR001206; PTHR11255 (PANTHER), PTHR11255:SF10 (PANTHER)

Caenorhabditis elegans	diacylglycerol ki-se protein isoform partially confirmed by transcript evidence	20	F:GO:0004143; P:GO:0016049; C:GO:0005856; P:GO:0019932; F:GO:0046872; P:GO:0051260; C:GO:0016023; F:GO:0005524; P:GO:0046339; F:GO:0019992; P:GO:0006897; F:GO:0046982; P:GO:0007275; F:GO:0042803; P:GO:0007205; P:GO:0015031; C:GO:0005634; P:GO:0007173; P:GO:0010033; C:GO:0005886	-	EC:2.7.1.107	IPR000756; IPR001206; PTHR11255 (PANTHER), PTHR11255:SF10 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	dehydroge-se reductase (sdr family) member 1	5	C:GO:0043231; P:GO:0040010; C:GO:0044444; P:GO:0008152; F:GO:0003824	-		IPR002198; IPR002347; IPR016040; IPR020904; PTHR19410:SF32 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	exportin 4	1	F:GO:0005488	-		PTHR12596 (PANTHER), PTHR12596:SF3 (PANTHER)
	-	0				-
Caenorhabditis briggsae	briggsae cbr-lss-4 protein	9	P:GO:0040035; P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0001703; P:GO:0018991; P:GO:0040010; P:GO:0006898; P:GO:0002009	-		IPR021906; PTHR12656 (PANTHER)
Caenorhabditis briggsae	atp-dependent r- helicase ddx42	10	P:GO:0045767; P:GO:0040010; F:GO:0003676; F:GO:0008026; P:GO:0000003; F:GO:0005524; F:GO:0005515; C:GO:0005737; P:GO:0008104; C:GO:0005634	-		IPR014014; PTHR10967 (PANTHER), PTHR10967:SF48 (PANTHER)
	-	0				-
Caenorhabditis elegans	yma7_caeel ame: full=uncharacterized protein	1	P:GO:0040011	-		-

Brugia malayi	g protein-coupled receptor ki-se interacting 2	8	F:GO:0048365; F:GO:0008060; P:GO:0032312; C:GO:0043234; F:GO:0008270; C:GO:0016023; F:GO:0019901; C:GO:0005634	-		IPR001164; IPR002110; IPR020683; PTHR23180 (PANTHER), PTHR23180:SF18 (PANTHER)
Angiostrongylus cantonensis	tho complex subunit 2	7	P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0000003; P:GO:0040011; P:GO:0040007; P:GO:0045132	-		IPR021418; PTHR21597 (PANTHER)
Caenorhabditis brenneri	elegans protein confirmed by transcript evidence	0		P:GO:0009792		-
Loa loa	lim domain containing protein	0		P:GO:0007411; F:GO:0009055; C:GO:0043195; P:GO:0048813; F:GO:0003779; F:GO:0008270; P:GO:0055114; F:GO:0016491; F:GO:0003824; P:GO:0016322; P:GO:0045214; P:GO:0008152; F:GO:0046872; C:GO:0005829; C:GO:0005886; F:GO:0004497; F:GO:0005488		IPR022735
Caenorhabditis briggsae	programmed cell death protein 5	1	F:GO:0003677	-		IPR002836
	-	0				-
Caenorhabditis elegans	dead box atp-dependent r- helicase	7	C:GO:0005682; F:GO:0004004; F:GO:0003676; C:GO:0071011; F:GO:0005524; P:GO:0000398; C:GO:0071013	-		IPR000629; IPR001650; IPR011545; IPR014001; IPR014014; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF47 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	map ki-se ki-se ki-se	4	P:GO:0009792; F:GO:0005488; F:GO:0016301; P:GO:0016246	-		IPR000719; IPR011009; IPR015747; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR22986 (PANTHER)
	-	0				-
Caenorhabditis elegans	tetratricopeptide repeat protein 15	0		F:GO:0003674; F:GO:0005488; P:GO:0008150; C:GO:0005575		-

Caenorhabditis elegans	kinetochore l family member (knl-1)	8	C:GO:0000785; P:GO:0007059; P:GO:0030953; P:GO:0045184; F:GO:0032403; C:GO:0000940; P:GO:0051382; P:GO:0051301	-		-
	-	0				-
Caenorhabditis briggsae	adenylate ki-se 3-like 1	4	C:GO:0005737; F:GO:0004017; P:GO:0009165; F:GO:0005524	-	EC:2.7.4.3	IPR000850; IPR007862; G3DSA:3.40.50.300 (GENE3D), PTHR23359:SF22 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	adenylate ki-se 3-like 1	4	C:GO:0005737; F:GO:0004017; P:GO:0009165; F:GO:0005524	-	EC:2.7.4.3	-
Caenorhabditis elegans	adenylate ki-se 3-like 1	4	C:GO:0005737; F:GO:0004017; P:GO:0009165; F:GO:0005524	-	EC:2.7.4.3	IPR000850; IPR007862; G3DSA:3.40.50.300 (GENE3D), PTHR23359:SF22 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	troponin t	3	P:GO:0043050; P:GO:0006952; P:GO:0040017	-		IPR001978; G3DSA:1.20.5.350 (GENE3D), PTHR11521 (PANTHER), PTHR11521:SF1 (PANTHER)
Caenorhabditis briggsae	troponin t	3	P:GO:0043050; P:GO:0006952; P:GO:0040017	-		IPR001978; G3DSA:1.20.5.350 (GENE3D), PTHR11521 (PANTHER), PTHR11521:SF1 (PANTHER)
	-	0				-
Caenorhabditis briggsae	sym-4	4	C:GO:0044444; P:GO:0040011; C:GO:0044446; P:GO:0050789	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR14221 (PANTHER)
Caenorhabditis elegans	hypothetical protein F42A10.7 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein F42A10.7 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR001466; IPR012338; G3DSA:3.40.710.10 (GENE3D), PTHR10566 (PANTHER), PTHR10566:SF6 (PANTHER)
Caenorhabditis elegans	-d-dependent epimerase dehydratase	3	P:GO:0008152; F:GO:0005488; F:GO:0016616	-	EC:1.1.1.0	IPR001509; IPR016040; PTHR10366 (PANTHER), PTHR10366:SF10 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	atp-binding sub-family b (mdr tap) member 9 isoform 1	7	P:GO:0055085; F:GO:0015421; C:GO:0016021; F:GO:0005102; P:GO:0015833; F:GO:0005524; P:GO:0007165	-	EC:3.6.3.23	IPR003439; IPR003593; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF82 (PANTHER), SSF52540 (SUPERFAMILY)

Caenorhabditis briggsae	tap-like abc transporter	15	P:GO:0055085; P:GO:0006629; P:GO:0040010; P:GO:0007041; P:GO:0009851; C:GO:0005765; P:GO:0009792; C:GO:0016021; F:GO:0042626; P:GO:0035264; C:GO:0005624; P:GO:0015833; F:GO:0005524; F:GO:0015197; P:GO:0016246	-		G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF82 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	cg10174 protein	9	P:GO:0018996; P:GO:0009792; P:GO:0000003; C:GO:0005622; P:GO:0040010; P:GO:0006810; P:GO:0002119; P:GO:0040011; P:GO:0060465	-		-
Caenorhabditis briggsae	viral a-type inclusion protein	6	C:GO:0044422; C:GO:0005737; N:GO:0071842; P:GO:0009792; C:GO:0043232; F:GO:0005488	-		PD936484 (PRODOM)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0003676; F:GO:0004523		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0003676; F:GO:0004523		-
Caenorhabditis briggsae	golgi resident protein gcp60	2	C:GO:0005794; F:GO:0005515	-		IPR000582; IPR014352; PTHR22973 (PANTHER), PTHR22973:SF4 (PANTHER)
Caenorhabditis elegans	ubiquitin carboxyl-termi-l hydrolase 5	1	F:GO:0004221	-	EC:3.1.2.15	IPR001394; IPR001607; IPR013083; IPR018200; PTHR10420 (PANTHER), PTHR10420:SF36 (PANTHER), SSF54001 (SUPERFAMILY)
Caenorhabditis elegans	ubiquitin carboxyl-termi-l hydrolase family protein	1	F:GO:0004221	-	EC:3.1.2.15	IPR001394; IPR001607; IPR013083; IPR018200; PTHR10420 (PANTHER), PTHR10420:SF36 (PANTHER), SSF54001 (SUPERFAMILY)
Brugia malayi	hypothetical protein [Brugia malayi]	0		C:GO:0030117; F:GO:0005488; P:GO:0016192; P:GO:0006886; F:GO:0005515		-
	-	0				IPR013854
Brugia malayi	f-box wd repeat-containing protein 9	0		F:GO:0003674; P:GO:0008150; F:GO:0005515		-
Brugia malayi	serine threonine protein ki-se	4	F:GO:0004672; P:GO:0040010; P:GO:0019915; F:GO:0000166	-		-

	-	0				-
	-	0				SignalP (SIGNALP)
Argas monolakensis	10 kda secreted protein	0				-
Caenorhabditis briggsae	par-6 at contacts (abnormal early localization of par-6) family member (pac-1)	3	C:GO:0005737; F:GO:0005100; P:GO:0007266	-		IPR001849; IPR011993; PTHR23175 (PANTHER), PTHR23175:SF3 (PANTHER), SSF50729 (SUPERFAMILY)
Caenorhabditis briggsae	ran binding protein 3	4	P:GO:0009792; P:GO:0010171; P:GO:0006810; P:GO:0040011	-		IPR000156; IPR011993; PTHR23138 (PANTHER), PTHR23138:SF4 (PANTHER), SSF50729 (SUPERFAMILY)
Caenorhabditis elegans	erk1 2 map ki-se	6	F:GO:0004707; P:GO:0006468; P:GO:0040025; F:GO:0005515; F:GO:0004713; F:GO:0005524	-	EC:2.7.11.24; EC:2.7.10.0	-
Caenorhabditis briggsae	ww domain containing protein	1	F:GO:0016874	-		-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	9	P:GO:0040010; P:GO:0040035; P:GO:0040025; F:GO:0005515; P:GO:0042127; P:GO:0007098; P:GO:0040020; C:GO:0005634; P:GO:0009790	-		-
Loa loa	methyltransferase 10 domain containing	10	P:GO:0040010; P:GO:0040035; F:GO:0016740; P:GO:0040025; F:GO:0005515; P:GO:0007098; P:GO:0042127; P:GO:0040020; C:GO:0005634; P:GO:0009790	-		IPR010286; G3DSA:3.40.50.150 (GENE3D), SSF53335 (SUPERFAMILY)
Loa loa	methyltransferase 10 domain containing	9	P:GO:0040010; P:GO:0040035; P:GO:0040025; F:GO:0005515; P:GO:0007098; P:GO:0042127; P:GO:0040020; C:GO:0005634; P:GO:0009790	-		IPR010286; G3DSA:3.40.50.150 (GENE3D), SSF53335 (SUPERFAMILY)

Caenorhabditis elegans	solute carrier family 6 (neurotransmitter glycine) member 5	15	P:GO:0007274; F:GO:0005277; F:GO:0005328; F:GO:0015187; P:GO:0001504; P:GO:0015870; P:GO:0015871; P:GO:0048265; F:GO:0030165; P:GO:0040017; C:GO:0045211; P:GO:0015816; F:GO:0005333; C:GO:0005887; P:GO:0015844	-		SignalP (SIGNALP)
Caenorhabditis elegans	mkiaa1386 protein	0		F:GO:0003676; F:GO:0003723; F:GO:0046872; F:GO:0000166; F:GO:0008270; F:GO:0005515		IPR001878; IPR013032; SSF57850 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein Y49F6B.2 [Caenorhabditis elegans]	0		P:GO:0000003; P:GO:0006898; P:GO:0002119; P:GO:0009792; P:GO:0040007; P:GO:0002009		-
Loa loa	elegans protein partially confirmed by transcript evidence	0		F:GO:0003676; F:GO:0035091; P:GO:0007154; F:GO:0008270; F:GO:0005515		IPR001683
Caenorhabditis elegans	wd-repeat protein	6	P:GO:0018996; C:GO:0044428; P:GO:0000003; P:GO:0040010; P:GO:0002119; P:GO:0040011	-		IPR001680; IPR015943; PTHR22836 (PANTHER)
Brugia malayi	isoform a	6	P:GO:0018996; C:GO:0044428; P:GO:0000003; P:GO:0040010; P:GO:0002119; P:GO:0040011	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; IPR020472; PTHR22836 (PANTHER)
	-	0				-
Sporobolus stapfianus	group 3 lea protein	0		C:GO:0016023; P:GO:0006950; F:GO:0005515		PTHR23241 (PANTHER), PTHR23241:SF11 (PANTHER)
Caenorhabditis elegans	tol-pal system protein	0		C:GO:0016023; F:GO:0005515		PTHR23241 (PANTHER), PTHR23241:SF11 (PANTHER)
Caenorhabditis briggsae	c3orf33 protein	2	F:GO:0003676; F:GO:0016788	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0003676; F:GO:0016788		-

Caenorhabditis briggsae	integrator complex subunit 8	0		P:GO:0006869; C:GO:0032039; F:GO:0005488; P:GO:0016180; F:GO:0005515		-
Caenorhabditis elegans	golgi golgin subfamily 2	1	F:GO:0005515	-		-
Caenorhabditis elegans	golgi golgin subfamily 2	1	F:GO:0005515	-		-
Caenorhabditis elegans	golgi golgin subfamily 2	1	F:GO:0005515	-		-
Tribolium castaneum	adp atp translocase	15	P:GO:0055085; P:GO:0040010; F:GO:0005488; P:GO:0008340; C:GO:0016021; C:GO:0005743; P:GO:0000003; F:GO:0005471; P:GO:0015867; P:GO:0002119; P:GO:0040017; P:GO:0015866; P:GO:0006898; P:GO:0009792; C:GO:0005811	-		IPR001993; IPR002067; IPR002113; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF35 (PANTHER)
Nematostella vectensis	phosphoglucose isomerase	7	C:GO:0005737; P:GO:0009792; P:GO:0006094; F:GO:0004347; F:GO:0005515; P:GO:0008340; P:GO:0006096	-	EC:5.3.1.9	-
Loa loa	zinc c2h2 type family protein	0		F:GO:0008270; C:GO:0005622		IPR007087; IPR015880
Caenorhabditis elegans	protein mon2-like protein	1	P:GO:0006810	-		-
Caenorhabditis briggsae	-dh dehydroge-se 1 alpha assembly factor 1	2	C:GO:0005739; F:GO:0005488	-		IPR008979; IPR013857; PTHR13194 (PANTHER), PTHR13194:SF8 (PANTHER)
Callithrix jacchus	40s ribosomal protein s24-like	10	P:GO:0006413; F:GO:0003735; F:GO:0031369; P:GO:0006364; F:GO:0003743; C:GO:0022627; P:GO:0042274; P:GO:0034101; F:GO:0000166; P:GO:0006414	-		IPR001976; IPR012677; IPR012678; IPR018098
Loa loa	mediator complex subunit 20	1	P:GO:0006350	-		IPR013921; PTHR12465 (PANTHER)

Caenorhabditis elegans	serine long chain base subunit 1	13	P:GO:0046511; P:GO:0040010; C:GO:0016021; P:GO:0046512; F:GO:0004758; P:GO:0006686; F:GO:0016769; P:GO:0040027; C:GO:0035339; F:GO:0005515; P:GO:0040011; P:GO:0009792; F:GO:0030170	-	EC:2.3.1.50	IPR004839; IPR015421; IPR015424; PTHR13693 (PANTHER), PTHR13693:SF2 (PANTHER)
Mus musculus	myosin light polypeptide 6	8	C:GO:0016461; F:GO:0000146; F:GO:0008307; P:GO:0007519; P:GO:0030049; F:GO:0030898; F:GO:0005515; F:GO:0005509	-		-
Caenorhabditis elegans	briggsae cbr-opt-2 protein	5	P:GO:0015833; F:GO:0005515; F:GO:0015198; C:GO:0016021; F:GO:0015293	-		IPR000109; PTHR11654 (PANTHER), PTHR11654:SF11 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	cdc28 protein ki-se regulatory subunit 1b	12	P:GO:0007126; F:GO:0016538; P:GO:0009794; P:GO:0000003; P:GO:0051301; P:GO:0007067; F:GO:0016301; F:GO:0019901; C:GO:0005654; P:GO:0000079; P:GO:0009792; P:GO:0008283	-		IPR000789; PTHR23415 (PANTHER)
Caenorhabditis briggsae	cdc28 protein ki-se regulatory subunit 1b	12	P:GO:0007126; F:GO:0016538; P:GO:0009794; P:GO:0000003; P:GO:0051301; P:GO:0007067; F:GO:0016301; F:GO:0019901; C:GO:0005654; P:GO:0000079; P:GO:0009792; P:GO:0008283	-		IPR000789; PTHR23415 (PANTHER), PTHR23415:SF1 (PANTHER)
Pristionchus pacificus	daf-12 c4	6	F:GO:0003700; F:GO:0043565; F:GO:0003707; C:GO:0005634; F:GO:0008270; P:GO:0006355	-		-

Caenorhabditis elegans	sterol o-acyltransferase	2	C:GO:0016021; F:GO:0008415	-		IPR004299; PTHR10408 (PANTHER), SignalP (SIGNALP)
Vibrio parahaemolyticus 16	peptidase s1 and chymotrypsin hap	0		P:GO:0006508; F:GO:0004252; F:GO:0008236; F:GO:0016787; F:GO:0003824; F:GO:0008233		IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR19355 (PANTHER)
Homo sapiens	enolase 1	15	P:GO:0009615; C:GO:0000015; P:GO:0000122; F:GO:0003714; F:GO:0004252; C:GO:0031430; C:GO:0009986; F:GO:0004634; P:GO:0006096; F:GO:0003677; P:GO:0030308; F:GO:0000287; F:GO:0003700; C:GO:0005886; C:GO:0005634	-	EC:3.4.21.0; EC:4.2.1.11	IPR020810; G3DSA:3.20.20.120 (GENE3D), PTHR11902 (PANTHER), SSF51604 (SUPERFAMILY)
Brugia malayi	cd- sequence	0		P:GO:0055114; F:GO:0016491		IPR013027; G3DSA:3.50.50.60 (GENE3D), PTHR22912 (PANTHER), PTHR22912:SF31 (PANTHER), SSF51905 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-aat-3 protein	6	P:GO:0019915; C:GO:0016021; P:GO:0006865; F:GO:0015171; C:GO:0005886; P:GO:0055085	-		IPR002293; PTHR11785:SF74 (PANTHER)
Caenorhabditis elegans	c7orf55 protein	0				-
Caenorhabditis elegans	x-prolyl aminopeptidase (aminopeptidase p)	1	C:GO:0005739	-		IPR000994; IPR001714; IPR007865; G3DSA:3.40.350.10 (GENE3D), PTHR10804:SF18 (PANTHER), SSF53092 (SUPERFAMILY)
Pongo abelii	PREDICTED: hypothetical protein LOC100433574 [Pongo abelii]	0				-
Caenorhabditis elegans	mitochondrial carnitine acylcarnitine carrier protein	7	P:GO:0009792; F:GO:0005488; C:GO:0005743; P:GO:0055085; P:GO:0006839; C:GO:0016021; F:GO:0005215	-		IPR001993; IPR002113; IPR018108; G3DSA:1.50.40.10 (GENE3D), PTHR11896:SF61 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	coiled-coil-helix-coiled-coil-helix domain containing 3	0		C:GO:0005739; F:GO:0005515		IPR009069
	-	0				-

Caenorhabditis elegans	vacuolar h	12	F:GO:0046961; F:GO:0005515; F:GO:0008553; P:GO:0007557; C:GO:0031410; P:GO:0009790; P:GO:0015986; C:GO:0000221; C:GO:0045177; P:GO:0006200; P:GO:0030728; C:GO:0005886	-	EC:3.6.3.14; EC:3.6.3.6	IPR004907; G3DSA:1.20.1460.10 (GENE3D), SSF118203 (SUPERFAMILY)
Caenorhabditis elegans	sec24 member b (cerevisiae)	11	C:GO:0043231; P:GO:0016044; C:GO:0044446; F:GO:0005515; C:GO:0044425; C:GO:0044444; C:GO:0031090; P:GO:0006888; C:GO:0012505; F:GO:0005215; P:GO:0015031	-		IPR006896; IPR006900; IPR012990; G3DSA:3.40.50.410 (GENE3D), PTHR13803 (PANTHER), SSF53300 (SUPERFAMILY), SSF81995 (SUPERFAMILY), SSF82754 (SUPERFAMILY)
	-	0				-
synthetic construct	serine peptidase kunitz 2	7	C:GO:0005737; C:GO:0005625; P:GO:0010951; P:GO:0006928; F:GO:0004867; C:GO:0016021; C:GO:0005576	-		IPR002223; IPR020901; PTHR10083 (PANTHER), PTHR10083:SF19 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	atp synthase mitochondrial f1 complex assembly factor 2	0		F:GO:0003674; P:GO:0043461; P:GO:0008150; F:GO:0005515; C:GO:0005575		IPR011419; G3DSA:1.10.3580.10 (GENE3D), PTHR21013:SF9 (PANTHER)
Caenorhabditis elegans	kiaa1310 protein	0		F:GO:0003674; P:GO:0008150		PTHR13136 (PANTHER)
Caenorhabditis elegans	cg14224 cg14224-pa	0		P:GO:0043161; F:GO:0003684; P:GO:0006289		-

Caenorhabditis briggsae	briggsae cbr-pyr-1 protein	29	P:GO:0042052; F:GO:0004088; C:GO:0005771; C:GO:0005791; P:GO:0046673; P:GO:0008594; C:GO:0016027; F:GO:0070406; F:GO:0004151; P:GO:0007602; P:GO:0006541; P:GO:0030713; P:GO:0046328; P:GO:0009642; C:GO:0016029; C:GO:0016023; P:GO:0016476; C:GO:0005811; P:GO:0008344; F:GO:0005515; F:GO:0005524; P:GO:0007155; P:GO:0006930; P:GO:0035099; P:GO:0007391; F:GO:0004070; C:GO:0005767;	-	EC:6.3.5.5; EC:3.5.2.3; EC:2.1.3.2	IPR002082; IPR002195; IPR006130; IPR006132; IPR011059; G3DSA:2.30.40.10 (GENE3D), G3DSA:3.40.50.1370 (GENE3D), PTHR11405 (PANTHER), PTHR11405:SF3 (PANTHER), SSF51556 (SUPERFAMILY)
Caenorhabditis elegans	protein phosphatase 1 regulatory inhibitor subunit 16a	8	P:GO:0040035; P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040018; P:GO:0040010; P:GO:0008340; P:GO:0006898	-		IPR002110; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER), PTHR18958:SF165 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG15312 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)
Caenorhabditis briggsae	wd repeats and sof1 domain containing	8	C:GO:0080008; P:GO:0040010; P:GO:0040035; P:GO:0016567; F:GO:0016740; P:GO:0002119; P:GO:0040039; P:GO:0006898	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR22851 (PANTHER)
Caenorhabditis elegans	vacuolar protein sorting-associated protein 52 homolog	2	C:GO:0044464; F:GO:0005515	-		IPR007258; PTHR14190:SF5 (PANTHER)
Haemonchus contortus	nicotinic acetylcholine receptor alpha subunit 38	6	F:GO:0004872; C:GO:0045211; C:GO:0030054; P:GO:0006811; C:GO:0016021; F:GO:0004889	-		-
	-	0				-
Caenorhabditis elegans	hsp20 alpha crystallin family protein	1	F:GO:0042802	-		IPR001436; IPR002068; IPR008978; G3DSA:2.60.40.790 (GENE3D), PTHR11527 (PANTHER), PTHR11527:SF28 (PANTHER)

Caenorhabditis elegans	hsp20 alpha crystallin family protein	1	F:GO:0042802	-		IPR001436; IPR002068; IPR008978; G3DSA:2.60.40.790 (GENE3D), PTHR11527 (PANTHER), PTHR11527:SF28 (PANTHER)
Caenorhabditis elegans	chromaffin granule amine transporter	2	P:GO:0055085; P:GO:0042221	-		IPR011701; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR10074 (PANTHER), PTHR10074:SF32 (PANTHER)
Ailuropoda melanoleuca	nucleobindin 1	6	C:GO:0016020; C:GO:0005615; C:GO:0005793; C:GO:0005794; F:GO:0003677; F:GO:0005509	-		-
Caenorhabditis elegans	blistered cuticle family member (bli-4)	12	C:GO:0016021; P:GO:0040002; P:GO:0040007; P:GO:0018996; P:GO:0006508; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0040011; F:GO:0004252; P:GO:0009792; C:GO:0005634	-	EC:3.4.21.0	IPR000209; IPR002884; IPR008979; IPR009020; IPR015500; IPR022398; G3DSA:2.60.120.260 (GENE3D), G3DSA:3.30.70.850 (GENE3D), PTHR10795:SF13 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	blistered cuticle family member (bli-4)	12	C:GO:0016021; P:GO:0040002; P:GO:0040007; P:GO:0018996; P:GO:0006508; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0040011; F:GO:0004252; P:GO:0009792; C:GO:0005634	-	EC:3.4.21.0	IPR000209; IPR002884; IPR006212; IPR008979; IPR009020; IPR009030; IPR015500; IPR022398; G3DSA:2.10.220.10 (GENE3D), G3DSA:2.60.120.260 (GENE3D), G3DSA:3.30.70.850 (GENE3D), PTHR10795:SF13 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	leucine-rich ppr-motif containing	0		F:GO:0003723; C:GO:0005739; F:GO:0005488; P:GO:0006350; P:GO:0045449; F:GO:0003677; C:GO:0005634; P:GO:0006810		PTHR10483 (PANTHER), PTHR10483:SF3 (PANTHER)
Caenorhabditis briggsae	zinc finger protein 598	1	F:GO:0005488	-		IPR001841; IPR007087; IPR013083; IPR015880; IPR017907; PTHR22938 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis briggsae	zinc finger protein 598	0		F:GO:0046872; F:GO:0008270; F:GO:0005515; C:GO:0005622		IPR001841; IPR007087; IPR013083; IPR015880; IPR017907; PTHR22938 (PANTHER), SSF57850 (SUPERFAMILY)
Caenorhabditis briggsae	zinc finger protein 598	1	F:GO:0005488	-		IPR001841; IPR007087; IPR013083; IPR015880; IPR017907; PTHR22938 (PANTHER), SSF57850 (SUPERFAMILY)

Caenorhabditis briggsae	immunoglobulin domain containing protein	0				IPR003598; IPR007110; IPR013098; IPR013783; PTHR10489 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis briggsae	uncoordi-ted family member (unc-22)	6	C:GO:0030018; P:GO:0006468; F:GO:0008307; P:GO:0007498; F:GO:0005524; F:GO:0004674	-	EC:2.7.11.0	SignalP (SIGNALP)
Caenorhabditis elegans	variable abnormal morphology family member (vab-1)	5	F:GO:0004672; P:GO:0007391; P:GO:0007399; F:GO:0005515; C:GO:0016020	-		IPR001090; IPR008979; IPR020685; G3DSA:2.60.120.260 (GENE3D), PTHR23256:SF59 (PANTHER), SignalP (SIGNALP)
	-	0				-
Loa loa	hypothetical protein LOAG_00970 [Loa loa]	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	osteoclast stimulating factor 1	1	F:GO:0017124	-		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF214 (PANTHER)
Caenorhabditis briggsae	chromosome 19 open reading frame 29	0				IPR018816; IPR019134; PTHR21737 (PANTHER), PTHR21737:SF4 (PANTHER)
Caenorhabditis briggsae	chromosome 19 open reading frame 29	0				IPR018816; IPR019134; PTHR21737 (PANTHER), PTHR21737:SF4 (PANTHER)
Caenorhabditis briggsae	chromosome 19 open reading frame 29	0				IPR018816; IPR019134; PTHR21737 (PANTHER), PTHR21737:SF4 (PANTHER)
Ancylostoma ceylanicum	spindle assembly abnormal protein sas-5	0				-
	-	0				-
Aurelia aurita	serine protease 1	0		P:GO:0006508; F:GO:0004252; F:GO:0003824; F:GO:0008233		IPR003582; SignalP (SIGNALP)
Caenorhabditis briggsae	multidrug resistance protein family member (mrp-5)	10	P:GO:0055085; P:GO:0040010; F:GO:0042626; P:GO:0040002; F:GO:0008514; C:GO:0005624; F:GO:0005524; P:GO:0002119; P:GO:0040017; C:GO:0005887	-		IPR001140; IPR011527; IPR017940; G3DSA:1.20.1560.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF14 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-haf-2 protein	5	F:GO:0016887; P:GO:0006810; C:GO:0016020; F:GO:0000166; F:GO:0005215	-		IPR001140; IPR003439; IPR003593; IPR011527; IPR017871; IPR017940; G3DSA:1.20.1560.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF82 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)

Caenorhabditis elegans	briggsae cbr-haf-2 protein	5	F:GO:0016887; P:GO:0006810; C:GO:0016020; F:GO:0000166; F:GO:0005215	-		IPR001140; IPR003439; IPR003593; IPR011527; IPR017871; IPR017940; G3DSA:1.20.1560.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF82 (PANTHER), SignalP (SIGNALP), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	wd repeat domain 3	1	P:GO:0006898	-		IPR007148; PTHR19853 (PANTHER)
Caenorhabditis briggsae	wd repeat-containing protein 3	1	P:GO:0006898	-		IPR007148; PTHR19853 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		C:GO:0016021; C:GO:0016020; P:GO:0055085; F:GO:0005215; P:GO:0006810		IPR004156; PTHR11388:SF7 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-ife- protein	6	F:GO:0003723; P:GO:0009792; C:GO:0005737; F:GO:0005515; P:GO:0006413; F:GO:0003743	-		IPR001040; IPR019770
Caenorhabditis elegans	transcription initiation factor iia subunit 2	11	P:GO:0010552; P:GO:0051091; C:GO:0005672; F:GO:0016251; P:GO:0006368; F:GO:0017025; P:GO:0051123; F:GO:0046982; F:GO:0003713; F:GO:0042803; P:GO:0032568	-		IPR003194; IPR009083; IPR009088; IPR015871; IPR015872
	-	0				-
Caenorhabditis elegans	#NAME?	10	P:GO:0006952; F:GO:0008667; C:GO:0005739; P:GO:0055114; F:GO:0008670; P:GO:0019915; P:GO:0006635; F:GO:0070402; P:GO:0051289; P:GO:0009239	-	EC:1.3.1.28; EC:1.3.1.34	IPR002198; IPR002347; IPR016040; PTHR19410:SF117 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-elo-8 protein	0		C:GO:0016021		SignalP (SIGNALP)
Loa loa	atp-dependent r- helicase an3	8	P:GO:0009792; P:GO:0002119; F:GO:0008026; C:GO:0043186; P:GO:0042006; F:GO:0003723; F:GO:0005524; P:GO:0040007	-		-

Bombyx mori	ap- isoform b	11	P:GO:0006901; P:GO:0010552; P:GO:0014032; P:GO:0048489; F:GO:0043565; P:GO:0008104; P:GO:0048728; P:GO:0045807; C:GO:0030136; C:GO:0005886; P:GO:0016348	-		IPR004979; IPR013854; PTHR10812:SF4 (PANTHER)
	-	0				-
Pongo abelii	cytoplasmic dynein 1 heavy chain 1	12	F:GO:0003777; C:GO:0005829; P:GO:0006810; C:GO:0005874; F:GO:0042623; P:GO:0006200; P:GO:0007052; C:GO:0005868; F:GO:0005524; P:GO:0007018; F:GO:0005515; C:GO:0005794	-		-
Caenorhabditis briggsae	yl15_caeel ame: full=uncharacterized homeobox protein	0		P:GO:0006915; F:GO:0030414; F:GO:0004867; C:GO:0005576		-
Brugia malayi	dedicator of cytokinesis family protein	3	F:GO:0005085; F:GO:0005525; F:GO:0051020	-		IPR010703; PTHR23317 (PANTHER), PTHR23317:SF27 (PANTHER)
	-	0				-
Strongylocentrotus purpuratus	cyclin b	0		F:GO:0016301; F:GO:0004672; F:GO:0005524; P:GO:0007049; P:GO:0006468; P:GO:0051301; P:GO:0007067; C:GO:0005634		-
Strongylocentrotus purpuratus	cyclin b3	0		F:GO:0016301; F:GO:0004672; F:GO:0005524; P:GO:0007049; P:GO:0006468; P:GO:0051301; P:GO:0007067; C:GO:0005634		IPR006670; IPR006671; IPR011028; IPR013763
Strongylocentrotus purpuratus	cyclin b	0		F:GO:0016301; F:GO:0004672; F:GO:0005524; P:GO:0007049; P:GO:0006468; P:GO:0051301; P:GO:0007067; C:GO:0005634		IPR006670; IPR011028; IPR013763

Caenorhabditis elegans	filamin abp280 repeat family protein	0		F:GO:0003779; P:GO:0009612		IPR001298; IPR013783; IPR014756; IPR017868; PTHR11915 (PANTHER), PTHR11915:SF55 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	huntingtin interacting protein e	4	F:GO:0005488; F:GO:0070733; P:GO:0034259; C:GO:0016021	-		IPR003812; IPR011990; IPR013026; G3DSA:1.10.3290.10 (GENE3D), PTHR13504 (PANTHER), PTHR13504:SF11 (PANTHER), PS51459 (PROFILE), SignalP (SIGNALP), SSF140931 (SUPERFAMILY), SSF48452 (SUPERFAMILY)
Caenorhabditis briggsae	prohibitin	2	C:GO:0005811; C:GO:0016020	-		IPR000163; IPR001107; SSF117892 (SUPERFAMILY)
Caenorhabditis briggsae	atp-binding sub-family b (mdr tap) member 9	21	P:GO:0001916; F:GO:0046979; C:GO:0042825; C:GO:0043190; P:GO:0002474; C:GO:0005743; P:GO:0015031; F:GO:0042288; C:GO:0005765; C:GO:0005769; F:GO:0046978; P:GO:0015833; F:GO:0022891; F:GO:0015421; P:GO:0055085; F:GO:0042605; F:GO:0042803; P:GO:0006200; C:GO:0005886; F:GO:0005524; F:GO:0046980	-	EC:3.6.3.23	IPR003439; IPR003593; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF82 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-pcp- protein	2	P:GO:0006508; F:GO:0008236	-		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	carkd protein	0		C:GO:0005739; F:GO:0003674; P:GO:0008150; C:GO:0005575		IPR000631; IPR017953; G3DSA:3.40.1190.20 (GENE3D), PTHR12592 (PANTHER), SignalP (SIGNALP), SSF53613 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	14 kda phosphohistidine phosphatase	0		P:GO:0008150; C:GO:0005575		-
	-	0				-

Caenorhabditis briggsae	coatomer protein subunit beta 1	8	F:GO:0005515; P:GO:0032940; P:GO:0016192; P:GO:0000003; P:GO:0008340; P:GO:0006886; C:GO:0030126; F:GO:0005198	-		IPR002553; IPR011989; IPR016024; PTHR10635 (PANTHER)
Caenorhabditis elegans	transmembrane protein 147	4	C:GO:0016020; P:GO:0000003; P:GO:0040010; F:GO:0005515	-		IPR019164; PTHR12869 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	beta3 protein	7	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0006810; P:GO:0007040; P:GO:0019915; P:GO:0040007	-		IPR002553; IPR011989; IPR016024; PTHR11134 (PANTHER), PTHR11134:SF1 (PANTHER)
Caenorhabditis elegans	beta3 protein	10	P:GO:0009792; P:GO:0010171; P:GO:0002119; F:GO:0005488; C:GO:0044444; P:GO:0016192; P:GO:0007040; P:GO:0019915; P:GO:0040007; P:GO:0015031	-		IPR002553; IPR011989; PTHR11134 (PANTHER), PTHR11134:SF1 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	af17 c	0		F:GO:0005179; P:GO:0007218; C:GO:0005576		-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	nucleoporin 210	3	F:GO:0005515; C:GO:0005635; C:GO:0016020	-		IPR003343; IPR008964; G3DSA:2.60.40.1080 (GENE3D), PTHR23019 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
Ancylostoma ceylanicum	zinc metallopeptidase	6	C:GO:0016021; F:GO:0004222; F:GO:0003676; P:GO:0032259; P:GO:0006508; F:GO:0008168	-	EC:3.4.24.0; EC:2.1.1.0	-
Loa loa	nuclear receptor nhr-31	6	F:GO:0046872; F:GO:0004879; F:GO:0003677; P:GO:0045449; F:GO:0005515; P:GO:0019915	-		IPR000536; IPR008946; PTHR11865 (PANTHER), PTHR11865:SF197 (PANTHER)
Caenorhabditis elegans	- h exchanger family member (nhx-8)	5	F:GO:0015385; P:GO:0055085; P:GO:0006812; P:GO:0006885; C:GO:0016021	-		IPR006153; IPR018409; IPR018422; SignalP (SIGNALP)

Caenorhabditis elegans	28s ribosomal protein mitochondrial	7	P:GO:0040035; P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; P:GO:0006898; P:GO:0006412	-	EC:3.6.5.3	-
	-	0				-
Caenorhabditis briggsae	bud13_caeel ame: full=bud13 homolog	0		P:GO:0006898; P:GO:0000003; P:GO:0002119; P:GO:0002009; P:GO:0040011; P:GO:0040007; P:GO:0040035; P:GO:0007126; P:GO:0045132		-
	-	0				-
	-	0				-
Caenorhabditis elegans	single-strand binding protein	2	F:GO:0003677; F:GO:0005515	-		IPR000424; IPR011344; IPR012340; IPR016027
Caenorhabditis briggsae	d- replication licensing factor mcm6	15	P:GO:0006268; F:GO:0016851; F:GO:0003697; P:GO:0015995; P:GO:0030174; P:GO:0009792; F:GO:0042802; C:GO:0042555; P:GO:0045449; F:GO:0003682; F:GO:0005524; F:GO:0003678; P:GO:0040035; P:GO:0007049; P:GO:0000910	-	EC:6.6.1.1	IPR001208; IPR008049; IPR012340; IPR016027; IPR018525; G3DSA:3.40.50.300 (GENE3D), PTHR11630 (PANTHER), PTHR11630:SF43 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	d- replication licensing factor mcm6	15	P:GO:0006268; F:GO:0016851; F:GO:0003697; P:GO:0015995; P:GO:0030174; P:GO:0009792; F:GO:0042802; C:GO:0042555; P:GO:0045449; F:GO:0003682; F:GO:0005524; F:GO:0003678; P:GO:0040035; P:GO:0007049; P:GO:0000910	-	EC:6.6.1.1	-

Caenorhabditis briggsae	d- replication licensing factor mcm6	15	P:GO:0006268; F:GO:0016851; F:GO:0003697; P:GO:0015995; P:GO:0030174; P:GO:0009792; F:GO:0042802; C:GO:0042555; P:GO:0045449; F:GO:0003682; F:GO:0005524; F:GO:0003678; P:GO:0040035; P:GO:0007049; P:GO:0000910	-	EC:6.6.1.1	-
Caenorhabditis briggsae	d- replication licensing factor mcm6	15	P:GO:0006268; F:GO:0016851; F:GO:0003697; P:GO:0015995; P:GO:0030174; P:GO:0009792; F:GO:0042802; C:GO:0042555; P:GO:0045449; F:GO:0003682; F:GO:0005524; F:GO:0003678; P:GO:0040035; P:GO:0007049; P:GO:0000910	-	EC:6.6.1.1	-
Caenorhabditis briggsae	d- replication licensing factor mcm6	15	P:GO:0006268; F:GO:0016851; F:GO:0003697; P:GO:0015995; P:GO:0030174; P:GO:0009792; F:GO:0042802; C:GO:0042555; P:GO:0045449; F:GO:0003682; F:GO:0005524; F:GO:0003678; P:GO:0040035; P:GO:0007049; P:GO:0000910	-	EC:6.6.1.1	-

Caenorhabditis briggsae	d- replication licensing factor mcm6	15	P:GO:0006268; F:GO:0016851; F:GO:0003697; P:GO:0015995; P:GO:0030174; P:GO:0009792; F:GO:0042802; C:GO:0042555; P:GO:0045449; F:GO:0003682; F:GO:0005524; F:GO:0003678; P:GO:0040035; P:GO:0007049; P:GO:0000910	-	EC:6.6.1.1	-
	-	0				-
	-	0				-
Caenorhabditis briggsae	histidine acid phosphatase family protein	5	P:GO:0009792; P:GO:0002119; P:GO:0000003; P:GO:0040007; P:GO:0006898	-		IPR000560; G3DSA:3.40.50.1240 (GENE3D), PTHR11567 (PANTHER), PTHR11567:SF17 (PANTHER), SignalP (SIGNALP), SSF53254 (SUPERFAMILY)
Caenorhabditis elegans	uncoordi-ted family member (unc-89)	0		P:GO:0045214; P:GO:0006936; C:GO:0005829; F:GO:0005509; P:GO:0043056; F:GO:0004713; P:GO:0051592; P:GO:0007076; P:GO:0035023; C:GO:0031674; C:GO:0031672; P:GO:0001701; P:GO:0055008; F:GO:0004674; P:GO:0030241; P:GO:0030240; F:GO:0004672; P:GO:0055003; P:GO:0055002; F:GO:0051015; C:GO:0005622; F:GO:0051393; C:GO:0030018; F:GO:0042802; F:GO:0005524; C:GO:0030017; F:GO:0043621;		IPR007110; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)

Caenorhabditis elegans	acetoacetyl- synthetase	18	P:GO:0071394; C:GO:0005829; P:GO:0014074; P:GO:0006629; P:GO:0042594; P:GO:0010243; P:GO:0050872; P:GO:0045471; P:GO:0001889; P:GO:0007584; P:GO:0071333; P:GO:0060612; P:GO:0071397; P:GO:0034201; P:GO:0042493; F:GO:0047760; P:GO:0032024; F:GO:0030729	-	EC:6.2.1.2; EC:6.2.1.16	IPR000873; IPR020845; G3DSA:3.40.50.980 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF40 (PANTHER), SSF56801 (SUPERFAMILY)
Caenorhabditis elegans	n -dimethylguanosine tr- methyltransferase	1	F:GO:0008168	-	EC:2.1.1.0	IPR002905; G3DSA:3.40.50.150 (GENE3D), SSF53335 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	coenzyme q biosynthesis protein	2	C:GO:0005743; P:GO:0006744	-		IPR007715; PTHR12922 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Ancylostoma ceylanicum	secreted protein 5 precursor	0		C:GO:0005576		IPR014044
Ancylostoma ceylanicum	secreted protein 5 precursor	0		C:GO:0005576		IPR014044
	-	0				-
Caenorhabditis elegans	atrial -triuretic peptide clearance	8	P:GO:0007194; P:GO:0007589; F:GO:0001653; C:GO:0044464; F:GO:0042562; P:GO:0007186; P:GO:0048015; P:GO:0003008	-		IPR001170; IPR001828; G3DSA:3.40.50.2300 (GENE3D), PTHR11920 (PANTHER), PTHR11920:SF2 (PANTHER), SSF53822 (SUPERFAMILY)
Brugia malayi	vacuolar protein sorting-associated protein 33b	1	F:GO:0005515	-		IPR001619; PTHR11679:SF1 (PANTHER)
Caenorhabditis elegans	kunitz bovine pancreatic trypsin inhibitor domain containing protein	0		F:GO:0004867		SignalP (SIGNALP)
Caenorhabditis elegans	phytanoyl- dioxyge-se domain containing 1	3	P:GO:0055114; F:GO:0046872; F:GO:0016702	-	EC:1.13.11.0	IPR008775; G3DSA:2.60.120.620 (GENE3D), PTHR20883 (PANTHER), SSF51197 (SUPERFAMILY)
Caenorhabditis elegans	surfeit locus protein 1	4	P:GO:0006811; C:GO:0016020; C:GO:0005739; F:GO:0004129	-	EC:1.9.3.1	-
Oceanicola granulosus HTCC2516	helicase, putative [Oceanicola granulosus HTCC2516]	0		F:GO:0003676; F:GO:0004386; F:GO:0005524		-
Oceanicola granulosus HTCC2516	helicase, putative [Oceanicola granulosus HTCC2516]	0		F:GO:0003676; F:GO:0004386; F:GO:0005524		-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-

Caenorhabditis elegans	purine-rich element binding protein b	17	C:GO:0005662; C:GO:0000784; P:GO:0006270; P:GO:0006268; F:GO:0003697; P:GO:0045892; C:GO:0005737; C:GO:0030425; P:GO:0008284; C:GO:0043025; F:GO:0003705; P:GO:0007399; F:GO:0003691; F:GO:0008134; P:GO:0045637; F:GO:0003729; F:GO:0046332	-		SignalP (SIGNALP)
Loa loa	ssd- and r--binding protein	0		F:GO:0016563; F:GO:0003697		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0004672; F:GO:0005524; P:GO:0006915		-
Caenorhabditis briggsae	lysosomal phospholipase a2	10	C:GO:0005764; P:GO:0006631; F:GO:0004607; F:GO:0047499; C:GO:0005625; C:GO:0005739; P:GO:0046470; P:GO:0019915; P:GO:0006672; F:GO:0004622	-	EC:2.3.1.43; EC:3.1.1.5	IPR003386; G3DSA:3.40.50.1820 (GENE3D), PTHR11440:SF15 (PANTHER), SSF53474 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				PTHR15410 (PANTHER)
Caenorhabditis elegans	leucine-rich transmembrane	0		F:GO:0004872; F:GO:0016787; C:GO:0016021; F:GO:0005515; F:GO:0004721		SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-unc-36 protein	4	C:GO:0016021; F:GO:0005262; P:GO:0006816; F:GO:0005244	-		PTHR10166 (PANTHER), PTHR10166:SF5 (PANTHER)
	-	0				-

Angiostrongylus cantonensis	bzip transcription factor family protein	24	P:GO:0009648; P:GO:0001666; F:GO:0003690; P:GO:0048146; P:GO:0009409; P:GO:0006355; P:GO:0009636; P:GO:0007565; P:GO:0007623; P:GO:0043434; F:GO:0043565; F:GO:0046983; P:GO:0007568; F:GO:0003700; P:GO:0014070; P:GO:0034097; P:GO:0032355; P:GO:0032570; P:GO:0051591; C:GO:0005634; P:GO:0006366; P:GO:0045941; P:GO:0009612; P:GO:0030431	-		IPR000837; IPR004827; IPR011616; G3DSA:1.20.5.170 (GENE3D), PTHR23351 (PANTHER), PTHR23351:SF1 (PANTHER)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	P:GO:0040007	-		-
						-
Caenorhabditis elegans	autocrine motility factor receptor	2	F:GO:0005488; C:GO:0044464	-		IPR001841; IPR003892; IPR013083; PTHR12477 (PANTHER), PTHR12477:SF2 (PANTHER), SignalP (SIGNALP), SSF57850 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0005488		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0005488		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0005488		-
Caenorhabditis briggsae	integrin beta subunit (agap000815-pa)	6	C:GO:0008305; P:GO:0007160; F:GO:0004872; P:GO:0007275; F:GO:0005488; P:GO:0007229	-		SignalP (SIGNALP)
Caenorhabditis elegans	ylz5_caeel ame: full=uncharacterized protein	0		F:GO:0003676; F:GO:0046983		-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0008152; C:GO:0016021		-

Caenorhabditis elegans	lissencephaly-1 homolog b	56	P:GO:0048814; C:GO:0000235; C:GO:0031512; P:GO:0021766; F:GO:0030234; F:GO:0042803; C:GO:0005869; P:GO:0008090; P:GO:0050885; P:GO:0007312; P:GO:0008298; P:GO:0000132; C:GO:0031252; P:GO:0051301; P:GO:0045494; P:GO:0007268; P:GO:0030381; P:GO:0007405; C:GO:0000776; P:GO:0051081; P:GO:0045176; P:GO:0051383; P:GO:0007611; P:GO:0021540; P:GO:0048135; C:GO:0030424; P:GO:0045478; P:GO:0016319;	-		IPR001680; IPR006594; IPR011046; IPR013720; IPR015943; IPR017986; IPR019781; IPR019782; PTHR22847 (PANTHER), PTHR22847:SF51 (PANTHER), SSF109925 (SUPERFAMILY)
Caenorhabditis briggsae	proteasome (macropain) activator subunit 4	0		P:GO:0030154; F:GO:0005488; C:GO:0000502; P:GO:0007275; P:GO:0007283; C:GO:0005634		IPR011989; IPR016024; IPR021843
Caenorhabditis elegans	transcription initiation factor small	10	P:GO:0040010; F:GO:0008026; P:GO:0000003; F:GO:0000166; P:GO:0006898; P:GO:0002009; P:GO:0009792; C:GO:0005634; F:GO:0003702; P:GO:0006366	-		IPR003196; IPR011039; IPR011991; SSF46785 (SUPERFAMILY)
Caenorhabditis elegans	mitochondrial gtpase 1 precursor	3	C:GO:0005622; F:GO:0005515; F:GO:0000166	-		IPR002917; IPR006073; IPR023179; G3DSA:3.40.50.300 (GENE3D), PTHR11089 (PANTHER), PTHR11089:SF4 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical upf0195 protein in chromosome	0		F:GO:0003674; P:GO:0008150		IPR002744; PTHR12377 (PANTHER), SSF117916 (SUPERFAMILY)
Loa loa	ring finger and wd repeat domain 3	1	F:GO:0005488	-		IPR001680; IPR001841; IPR011046; IPR013083; IPR015943; IPR018378; IPR018957; PTHR16047 (PANTHER), PTHR16047:SF7 (PANTHER), SSF57850 (SUPERFAMILY)
	-	0				-

Caenorhabditis briggsae	d- replication licensing factor mcm2	18	C:GO:0000785; P:GO:0008340; F:GO:0005515; P:GO:0006974; P:GO:0040010; P:GO:0006268; C:GO:0005737; P:GO:0030174; P:GO:0006350; P:GO:0009792; F:GO:0003677; P:GO:0042325; P:GO:0002119; C:GO:0042555; F:GO:0016887; F:GO:0003682; F:GO:0005524; P:GO:0040035	-			IPR001208; IPR003593; IPR008045; IPR012340; IPR016027; IPR018525; IPR021092; G3DSA:3.30.1640.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR11630 (PANTHER), PTHR11630:SF44 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	d- replication licensing factor mcm2	18	C:GO:0000785; P:GO:0008340; F:GO:0005515; P:GO:0006974; P:GO:0040010; P:GO:0006268; C:GO:0005737; P:GO:0030174; P:GO:0006350; P:GO:0009792; F:GO:0003677; P:GO:0042325; P:GO:0002119; C:GO:0042555; F:GO:0016887; F:GO:0003682; F:GO:0005524; P:GO:0040035	-			IPR001208; IPR003593; IPR008045; IPR012340; IPR016027; IPR018525; IPR021092; G3DSA:3.30.1640.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR11630 (PANTHER), PTHR11630:SF44 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	d- replication licensing factor mcm2	18	C:GO:0000785; P:GO:0008340; F:GO:0005515; P:GO:0006974; P:GO:0040010; P:GO:0006268; C:GO:0005737; P:GO:0030174; P:GO:0006350; P:GO:0009792; F:GO:0003677; P:GO:0042325; P:GO:0002119; C:GO:0042555; F:GO:0016887; F:GO:0003682; F:GO:0005524; P:GO:0040035	-			IPR001208; IPR003593; IPR008045; IPR012340; IPR016027; IPR018525; IPR021092; G3DSA:3.30.1640.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR11630 (PANTHER), PTHR11630:SF44 (PANTHER), SSF52540 (SUPERFAMILY)

Caenorhabditis briggsae	d- replication licensing factor mcm2	18	C:GO:0000785; P:GO:0008340; F:GO:0005515; P:GO:0006974; P:GO:0040010; P:GO:0006268; C:GO:0005737; P:GO:0030174; P:GO:0006350; P:GO:0009792; F:GO:0003677; P:GO:0042325; P:GO:0002119; C:GO:0042555; F:GO:0016887; F:GO:0003682; F:GO:0005524; P:GO:0040035	-		IPR001208; IPR003593; IPR008045; IPR012340; IPR016027; IPR018525; IPR021092; G3DSA:3.30.1640.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR11630 (PANTHER), PTHR11630:SF44 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	d- replication licensing factor mcm2	18	C:GO:0000785; P:GO:0008340; F:GO:0005515; P:GO:0006974; P:GO:0040010; P:GO:0006268; C:GO:0005737; P:GO:0030174; P:GO:0006350; P:GO:0009792; F:GO:0003677; P:GO:0042325; P:GO:0002119; C:GO:0042555; F:GO:0016887; F:GO:0003682; F:GO:0005524; P:GO:0040035	-		IPR001208; IPR003593; IPR008045; IPR012340; IPR016027; IPR018525; IPR021092; G3DSA:3.30.1640.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR11630 (PANTHER), PTHR11630:SF44 (PANTHER), SSF52540 (SUPERFAMILY)
Trichostrongylus colubriformis	glbh_trico ame: full=globin-like host-protective antigen flags: precursor	5	F:GO:0020037; C:GO:0005615; F:GO:0005344; P:GO:0015671; F:GO:0019825	-		-
Caenorhabditis briggsae	carboxylase:pyruvate acetyl-coa propionyl-coa	9	C:GO:0005875; F:GO:0004736; F:GO:0009374; P:GO:0009252; F:GO:0005524; P:GO:0006094; C:GO:0005759; C:GO:0005811; F:GO:0008716	-	EC:6.4.1.1; EC:6.3.2.4	IPR000891; IPR003379; IPR012287; IPR013785; PTHR18866 (PANTHER), PTHR18866:SF10 (PANTHER), SSF51569 (SUPERFAMILY), SSF89000 (SUPERFAMILY)
Caenorhabditis elegans	vacuolar protein sorting 13d	3	P:GO:0040010; P:GO:0002119; P:GO:0040011	-		-

Pongo abelii	proteasome (macropain) 26s non- 8	7	C:GO:0005730; P:GO:0051436; P:GO:0051437; C:GO:0005838; P:GO:0031145; F:GO:0005515; C:GO:0005737	-		-
Loa loa	prolyl oligopeptidase (s09 family)	0		P:GO:0006508; F:GO:0004252; F:GO:0016787		IPR002470; IPR004106; G3DSA:2.130.10.120 (GENE3D), PTHR11757:SF2 (PANTHER)
Loa loa	major sperm protein	2	C:GO:0005856; F:GO:0005198	-		IPR000535; IPR008962; PTHR10809 (PANTHER)
Caenorhabditis briggsae	filamin abp280 repeat family protein	8	P:GO:0009792; P:GO:0010171; C:GO:0005840; F:GO:0003735; F:GO:0003779; P:GO:0007126; P:GO:0000003; P:GO:0006412	-	EC:3.6.5.3	IPR001298; IPR013783; IPR014756; IPR017868; PTHR11915 (PANTHER), PTHR11915:SF24 (PANTHER)
Brugia malayi	elegans protein partially confirmed by transcript evidence	2	P:GO:0051179; P:GO:0009987	-		-
Caenorhabditis elegans	beta-galactosidase	2	P:GO:0048102; F:GO:0016787	-		IPR001944; IPR008979; G3DSA:2.60.120.260 (GENE3D)
Caenorhabditis elegans	tgf-beta resistance-associated protein trag	0				SignalP (SIGNALP)
Brugia malayi	kiaa0732 protein	6	P:GO:0044260; P:GO:0090304; F:GO:0003677; C:GO:0044446; P:GO:0065007; C:GO:0005634	-		IPR006596; G3DSA:3.40.50.1010 (GENE3D), SignalP (SIGNALP), SSF88723 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Brugia malayi	kiaa1530 protein	0		F:GO:0005488		IPR018610
Loa loa	wgr domain containing protein	6	F:GO:0005488; P:GO:0044238; P:GO:0044260; F:GO:0016740; C:GO:0005634; P:GO:0006974	-		IPR008893; IPR012982; PTHR15447 (PANTHER), SSF142921 (SUPERFAMILY)
Caenorhabditis briggsae	peptidyl-prolyl cis-trans isomerase cwc27 homolog	2	F:GO:0016853; C:GO:0005634	-		IPR002130; IPR015891; PTHR11071 (PANTHER), PTHR11071:SF33 (PANTHER)
Brugia malayi	arginine-tr--protein c terminus containing protein	4	C:GO:0005737; F:GO:0004057; P:GO:0016598; C:GO:0005634	-	EC:2.3.2.8	IPR007472; IPR016181; PTHR21367 (PANTHER)
Caenorhabditis briggsae	fructose- -bisphosphatase	3	P:GO:0016051; C:GO:0005737; F:GO:0042132	-	EC:3.1.3.11	IPR000146; IPR020548; G3DSA:3.30.540.10 (GENE3D), G3DSA:3.40.190.80 (GENE3D), SSF56655 (SUPERFAMILY)
Caenorhabditis briggsae	yl4m_caeel ame: full=uncharacterized protein	0				SignalP (SIGNALP)
Loa loa	kelch domain containing 3	5	C:GO:0005737; F:GO:0003682; F:GO:0005515; P:GO:0000003; C:GO:0000790	-		IPR006652; IPR011498; IPR015915; PTHR23244 (PANTHER), PTHR23244:SF33 (PANTHER), SSF117281 (SUPERFAMILY)

Loa loa	kelch domain containing 3	5	C:GO:0005737; F:GO:0003682; F:GO:0005515; P:GO:0000003; C:GO:0000790	-		IPR006652; IPR011498; IPR015915; PTHR23244 (PANTHER), PTHR23244:SF33 (PANTHER), SSF117281 (SUPERFAMILY)
Loa loa	kelch domain containing 3	5	C:GO:0005737; F:GO:0003682; F:GO:0005515; P:GO:0000003; C:GO:0000790	-		IPR006652; IPR011498; IPR015915; PTHR23244 (PANTHER), PTHR23244:SF33 (PANTHER), SSF117281 (SUPERFAMILY)
	-	0				-
Homo sapiens	mhc class i antigen	7	P:GO:0006955; F:GO:0032393; P:GO:0044419; C:GO:0005887; P:GO:0002474; F:GO:0005515; C:GO:0042612	-		
Homo sapiens	mhc class i antigen	9	F:GO:0032393; C:GO:0005887; C:GO:0005624; P:GO:0006952; F:GO:0005515; P:GO:0002474; P:GO:0006955; P:GO:0044419; C:GO:0042612	-		IPR001039; IPR003597; IPR007110; IPR011161; IPR011162; IPR013783; PTHR16675 (PANTHER), PTHR16675:SF53 (PANTHER), SSF48726 (SUPERFAMILY)
Homo sapiens	mhc class i antigen	7	P:GO:0006955; F:GO:0032393; C:GO:0005576; P:GO:0044419; C:GO:0005887; P:GO:0002474; C:GO:0042612	-		IPR001039; IPR003597; IPR007110; IPR011161; IPR011162; IPR013783; PTHR16675 (PANTHER), PTHR16675:SF53 (PANTHER), SSF48726 (SUPERFAMILY)
Homo sapiens	mhc class i antigen	9	C:GO:0000139; F:GO:0032393; C:GO:0005887; F:GO:0005515; C:GO:0031901; P:GO:0002474; P:GO:0006955; P:GO:0044419; C:GO:0042612	-		IPR001039; IPR003597; IPR007110; IPR011161; IPR011162; IPR013783; PTHR16675 (PANTHER), PTHR16675:SF53 (PANTHER), SSF48726 (SUPERFAMILY)
Homo sapiens	mhc class i antigen	9	F:GO:0032393; C:GO:0005887; C:GO:0005624; P:GO:0006952; F:GO:0005515; P:GO:0002474; P:GO:0006955; P:GO:0044419; C:GO:0042612	-		IPR001039; IPR011161; IPR011162; PTHR16675 (PANTHER), PTHR16675:SF53 (PANTHER)
Homo sapiens	mhc class i antigen	0				IPR001039; IPR011161; IPR011162; PTHR16675 (PANTHER), PTHR16675:SF53 (PANTHER)

Homo sapiens	mhc class i antigen	9	C:GO:0000139; F:GO:0032393; C:GO:0005887; F:GO:0005515; C:GO:0031901; P:GO:0002474; P:GO:0006955; P:GO:0044419; C:GO:0042612	-		IPR001039; IPR011161; IPR011162; PTHR16675 (PANTHER), PTHR16675:SF53 (PANTHER)
Homo sapiens	mhc class i antigen	9	F:GO:0032393; C:GO:0005887; C:GO:0005624; P:GO:0006952; F:GO:0005515; P:GO:0002474; P:GO:0006955; P:GO:0044419; C:GO:0042612	-		IPR001039; IPR003597; IPR007110; IPR011161; IPR011162; IPR013783; PTHR16675 (PANTHER), PTHR16675:SF53 (PANTHER), SSF48726 (SUPERFAMILY)
Homo sapiens	mhc class i antigen	9	C:GO:0000139; F:GO:0032393; C:GO:0005887; F:GO:0005515; C:GO:0031901; P:GO:0002474; P:GO:0006955; P:GO:0044419; C:GO:0042612	-		IPR001039; IPR003597; IPR007110; IPR011161; IPR011162; IPR013783; PTHR16675 (PANTHER), PTHR16675:SF53 (PANTHER), SSF48726 (SUPERFAMILY)
Pan troglodytes	mhc class i antigen	7	P:GO:0006955; F:GO:0032393; C:GO:0005576; P:GO:0044419; C:GO:0005887; P:GO:0002474; C:GO:0042612	-		IPR001039; IPR011161; IPR011162; PTHR16675 (PANTHER), PTHR16675:SF53 (PANTHER)
Caenorhabditis briggsae	transmembrane protein 85	4	P:GO:0009792; P:GO:0000003; P:GO:0040007; P:GO:0002119	-		IPR009445; PTHR19315:SF6 (PANTHER)
Ancylostoma ceylanicum	metalloprotease 1 precursor	2	F:GO:0046872; F:GO:0008237	-		IPR000859; IPR013032; PTHR10127 (PANTHER), PTHR10127:SF60 (PANTHER)
Caenorhabditis elegans	wd repeat domain 74	3	P:GO:0040035; P:GO:0002119; P:GO:0040007	-		IPR001680; IPR011046; IPR015943; IPR019781; PTHR16038 (PANTHER)
Caenorhabditis elegans	wd repeat domain 74	3	P:GO:0040035; P:GO:0002119; P:GO:0040007	-		IPR001680; IPR011046; IPR015943; IPR019781; PTHR16038 (PANTHER)
Dysdercus peruvianus	facilitative hexose transporter	0		C:GO:0016021; F:GO:0022891; C:GO:0016020; P:GO:0055085; F:GO:0005215; P:GO:0006810		IPR005828; PTHR11600 (PANTHER), SignalP (SIGNALP)
	-	0				-

Loa loa	cdk5 regulatory subunit associated protein 1	10	P:GO:0045736; P:GO:0009451; F:GO:0051536; P:GO:0045664; P:GO:0007420; P:GO:0009058; F:GO:0016874; F:GO:0019901; P:GO:0008283; F:GO:0019887	-		IPR005839; IPR013848; IPR018247
Loa loa	cdk5 regulatory subunit associated protein 1	9	P:GO:0045736; P:GO:0009451; P:GO:0045664; P:GO:0007420; F:GO:0004326; F:GO:0051539; F:GO:0005524; F:GO:0042808; P:GO:0009396	-	EC:6.3.2.17	IPR005839; IPR006638; IPR007197; IPR013848; IPR018247; IPR020612; G3DSA:3.80.30.20 (GENE3D), SSF102114 (SUPERFAMILY)
Loa loa	cdk5 regulatory subunit associated protein 1	9	P:GO:0045736; P:GO:0009451; P:GO:0045664; P:GO:0007420; F:GO:0004326; F:GO:0051539; F:GO:0005524; F:GO:0042808; P:GO:0009396	-	EC:6.3.2.17	IPR005839; IPR006638; IPR007197; IPR013848; IPR018247; IPR020612; G3DSA:3.80.30.20 (GENE3D), SSF102114 (SUPERFAMILY)
	-	0				-
	-	0				-
Loa loa	resistance to inhibitors of cholinesterase 8 homolog a	1	F:GO:0005488	-		IPR008376; IPR019318; PTHR12425 (PANTHER)
	-	0				-
Caenorhabditis briggsae	mitochondrial 39s ribosomal protein l50	3	P:GO:0007275; P:GO:0000003; P:GO:0040007	-		-
Caenorhabditis elegans	host cell factor 1	6	P:GO:0009987; C:GO:0035097; P:GO:0050789; P:GO:0019046; F:GO:0003713; C:GO:0005737	-		IPR008957; IPR013783
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	P:GO:0002119	-		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	P:GO:0002119	-		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	P:GO:0002119	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		C:GO:0005634		IPR012580
Caenorhabditis briggsae	organic cation transporter	4	P:GO:0006810; P:GO:0009987; C:GO:0016020; F:GO:0005215	-		IPR011701; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11600 (PANTHER), PTHR11600:SF35 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		C:GO:0016021		IPR013838; SignalP (SIGNALP)
Caenorhabditis elegans	dtw domain containing 1	1	C:GO:0016021	-		IPR005636; PTHR15627 (PANTHER), PTHR15627:SF8 (PANTHER)
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	phosphogluco-te dehydroge-se	28	P:GO:0006541; F:GO:0005515; C:GO:0005792; P:GO:0009448; P:GO:0010468; F:GO:0031406; P:GO:0031175; P:GO:0019322; C:GO:0005737; P:GO:0018996; F:GO:0050661; P:GO:0019530; P:GO:0009051; F:GO:0005529; P:GO:0006544; P:GO:0022402; F:GO:0051287; P:GO:0021510; P:GO:0002119; P:GO:0055114; F:GO:0004617; P:GO:0006566; C:GO:0005625; F:GO:0004616; P:GO:0021915; P:GO:0021782; P:GO:0019521	-	EC:1.1.1.95; EC:1.1.1.44	IPR006113; IPR006114; IPR006115; IPR006183; IPR006184; IPR008927; IPR013328; IPR016040; PTHR11811 (PANTHER), SSF51735 (SUPERFAMILY)
Caenorhabditis elegans	transducin -like 3	6	P:GO:0040010; P:GO:0045132; P:GO:0000003; P:GO:0006898; P:GO:0009792; C:GO:0044424	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; IPR020472; PTHR19854 (PANTHER), PTHR19854:SF2 (PANTHER)
Caenorhabditis briggsae	vacuolar protein sorting 52 (cerevisiae)	3	C:GO:0044444; F:GO:0005515; C:GO:0043231	-		IPR007258; PTHR14190:SF5 (PANTHER)

Caenorhabditis briggsae	briggsae cbr-apr-1 protein	30	P:GO:0048468; P:GO:0030177; P:GO:0007052; C:GO:0043005; P:GO:0048699; F:GO:0047485; P:GO:0040027; P:GO:0007420; C:GO:0043234; C:GO:0044430; P:GO:0040003; F:GO:0008013; P:GO:0040010; C:GO:0005912; P:GO:0045944; P:GO:0051656; P:GO:0016476; P:GO:0006611; P:GO:0030178; P:GO:0000003; P:GO:0001700; P:GO:0007155; P:GO:0010171; P:GO:0003002; P:GO:0008356; C:GO:0045177; P:GO:0001714;	-		IPR011989; IPR016024; PTHR12607 (PANTHER), PTHR12607:SF4 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	9	P:GO:0009792; P:GO:0002119; F:GO:0030528; F:GO:0003676; P:GO:0045449; P:GO:0040010; P:GO:0000003; P:GO:0006898; F:GO:0008270	-		SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	9	P:GO:0009792; P:GO:0002119; F:GO:0030528; F:GO:0003676; P:GO:0045449; P:GO:0040010; P:GO:0000003; P:GO:0006898; F:GO:0008270	-		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		IPR006578

Caenorhabditis elegans	kinesin-like protein 2	14	F:GO:0008017; P:GO:0000910; P:GO:0045132; C:GO:0000922; P:GO:0090307; C:GO:0005873; C:GO:0005813; F:GO:0003677; P:GO:0007067; P:GO:0051299; F:GO:0000166; P:GO:0008283; P:GO:0009792; F:GO:0008574	-	EC:3.6.4.4	IPR001752; IPR019821; PTHR16012 (PANTHER), PTHR16012:SF71 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				IPR013786
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-ekl-1 protein	0		P:GO:0000003; F:GO:0003676; P:GO:0016246; P:GO:0009792		IPR002999; IPR008191; G3DSA:2.30.30.140 (GENE3D), SSF63748 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0044238; P:GO:0040010; F:GO:0016757	-		IPR002213; SSF53756 (SUPERFAMILY)
Caenorhabditis briggsae	activating sig-l cointegrator 1 complex subunit 3	4	F:GO:0008026; F:GO:0003677; C:GO:0005622; F:GO:0005524	-		IPR001650; IPR004179; G3DSA:1.10.3380.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR11752 (PANTHER), PTHR11752:SF8 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	utp11-like u3 small nucleolar ribonucleoprotein variant 1	7	P:GO:0006412; P:GO:0040010; P:GO:0000003; P:GO:0002119; C:GO:0030529; P:GO:0006898; P:GO:0009792	-	EC:3.6.5.3	IPR007144
						IPR003599; IPR007110; IPR013098; IPR013783; IPR018281; PTHR19897 (PANTHER), PTHR19897:SF9 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis briggsae	nuclear vcp-like	2	F:GO:0017111; F:GO:0005524	-	EC:3.6.1.15	G3DSA:1.10.8.60 (GENE3D), PTHR23077 (PANTHER), PTHR23077:SF16 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	ubiquitin carboxyl-termi-l hydrolase 30	1	F:GO:0008233	-		IPR001394; IPR018200; PTHR10420 (PANTHER), PTHR10420:SF41 (PANTHER), SignalP (SIGNALP), SSF54001 (SUPERFAMILY)
Caenorhabditis elegans	ubiquitin specific protease 30	1	F:GO:0016787	-		IPR001394; IPR018200; PTHR10420 (PANTHER), PTHR10420:SF41 (PANTHER), SignalP (SIGNALP), SSF54001 (SUPERFAMILY)

Caenorhabditis elegans	mitochondrial ribosomal	9	P:GO:0006412; P:GO:0040010; C:GO:0005840; P:GO:0008340; F:GO:0003735; P:GO:0040035; P:GO:0002119; P:GO:0006898; P:GO:0009792	-	EC:3.6.5.3	SignalP (SIGNALP)
	-	0				-
Loa loa	novel protein vertebrate pctaire protein ki-se 2	6	P:GO:0009987; F:GO:0004674; F:GO:0005515; P:GO:0007275; P:GO:0009653; C:GO:0044464	-	EC:2.7.11.0	G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF7 (PANTHER)
Brugia malayi	testis-expressed sequence 2 protein	1	C:GO:0016020	-		-
Caenorhabditis elegans	anillin rhotekin	1	P:GO:0009987	-		-
Caenorhabditis elegans	anillin rhotekin	1	P:GO:0009987	-		-
Caenorhabditis elegans	anillin rhotekin	1	P:GO:0009987	-		-
Caenorhabditis elegans	anillin rhotekin	1	P:GO:0009987	-		-
Caenorhabditis elegans	anillin rhotekin	1	P:GO:0009987	-		-
Caenorhabditis elegans	surfeit locus protein 1	0		C:GO:0005739; F:GO:0004129; P:GO:0021522; C:GO:0016021; C:GO:0016020; P:GO:0048568; C:GO:0005743		IPR002994; PTHR23427 (PANTHER), PTHR23427:SF2 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				IPR007588
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-ttll-12 protein	0		F:GO:0016874; F:GO:0004835; P:GO:0006464		IPR004344; G3DSA:2.170.270.10 (GENE3D), PTHR12241:SF5 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	6	P:GO:0006412; C:GO:0005840; C:GO:0005739; F:GO:0003735; F:GO:0005524; F:GO:0016887	-	EC:3.6.5.3	PTHR21610 (PANTHER), PTHR21610:SF4 (PANTHER), SSF53300 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	peroxisomal membrane protein pex13	7	P:GO:0016477; C:GO:0005779; C:GO:0005624; P:GO:0007399; P:GO:0016560; F:GO:0005515; P:GO:0007610	-		IPR007223; PTHR19332 (PANTHER)
Caenorhabditis briggsae	yms5_caeel ame: full=uncharacterized protein flags: precursor	2	C:GO:0016021; P:GO:0007160	-		PTHR13802 (PANTHER), PTHR13802:SF1 (PANTHER)
Caenorhabditis brenneri	elegans protein confirmed by transcript evidence	0				IPR001534; SignalP (SIGNALP)
	-	0				-

Loa loa	briggsae cbr-smu-1 protein	3	C:GO:0071011; C:GO:0071013; F:GO:0016905	-	EC:2.7.11.7	IPR006594; IPR006595; PTHR22848 (PANTHER)
Caenorhabditis elegans	ubiquitin associated and sh3 domain a	0		P:GO:0050860		IPR013078; G3DSA:3.40.50.1240 (GENE3D), PTHR16469 (PANTHER), SSF53254 (SUPERFAMILY)
Caenorhabditis briggsae	ubiquitin associated and sh3 domain a	2	P:GO:0050789; C:GO:0044424	-		IPR013078; G3DSA:3.40.50.1240 (GENE3D), PTHR16469 (PANTHER), SSF53254 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-prpf-4 protein	14	P:GO:0040010; F:GO:0004674; P:GO:0008360; C:GO:0071011; P:GO:0040035; F:GO:0005524; P:GO:0007155; P:GO:0002119; P:GO:0040011; P:GO:0000398; C:GO:0071013; P:GO:0002009; P:GO:0009792; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF17 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-prpf-4 protein	14	P:GO:0040010; F:GO:0004674; P:GO:0008360; C:GO:0071011; P:GO:0040035; F:GO:0005524; P:GO:0007155; P:GO:0002119; P:GO:0040011; P:GO:0000398; C:GO:0071013; P:GO:0002009; P:GO:0009792; P:GO:0006468	-	EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF17 (PANTHER)
	-	0				-
Caenorhabditis briggsae	t-complex protein 1 subunit gamma	4	P:GO:0006457; C:GO:0005737; F:GO:0051082; F:GO:0005524	-		IPR002194; IPR002423; IPR012719; IPR017998; G3DSA:1.10.560.10 (GENE3D), G3DSA:3.30.260.10 (GENE3D), G3DSA:3.50.7.10 (GENE3D), SignalP (SIGNALP), SSF52029 (SUPERFAMILY), SSF54849 (SUPERFAMILY)
Acyrthosiphon pisum	cullin 5	11	C:GO:0005829; P:GO:0048523; P:GO:0022402; C:GO:0031461; F:GO:0004872; C:GO:0005624; P:GO:0006970; F:GO:0005515; P:GO:0008283; P:GO:0051480; C:GO:0005634	-		IPR001373; IPR016159; G3DSA:1.20.1310.10 (GENE3D), PTHR11932 (PANTHER), PTHR11932:SF7 (PANTHER)

Brugia malayi	glucosidase 2 subunit beta	4	C:GO:0005622; F:GO:0005509; P:GO:0048793; F:GO:0005080	-		IPR002172; PTHR12630 (PANTHER), PTHR12630:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	tachykinin receptor 1	16	F:GO:0005515; P:GO:0065008; P:GO:0009612; P:GO:0010033; P:GO:0044057; C:GO:0016021; F:GO:0004995; P:GO:0019915; P:GO:0007610; P:GO:0007217; P:GO:0007165; P:GO:0048522; P:GO:0050877; P:GO:0051240; P:GO:0006954; C:GO:0005886	-		IPR000276; IPR017452; G3DSA:1.20.1070.10 (GENE3D), PTHR19264 (PANTHER), PTHR19264:SF235 (PANTHER), SSF81321 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-unc-104 protein	10	F:GO:0003777; P:GO:0007411; P:GO:0048490; P:GO:0007528; C:GO:0005874; P:GO:0008345; P:GO:0047496; F:GO:0005524; P:GO:0016188; C:GO:0005871	-		IPR000253; IPR001752; IPR008984; IPR019821; PTHR16012 (PANTHER), PTHR16012:SF104 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-unc-104 protein	20	P:GO:0007411; P:GO:0048490; C:GO:0030659; F:GO:0005515; P:GO:0008089; F:GO:0016491; P:GO:0008345; C:GO:0005874; F:GO:0003777; P:GO:0047496; P:GO:0007528; P:GO:0016188; P:GO:0047497; P:GO:0007274; F:GO:0016887; P:GO:0006200; P:GO:0007270; C:GO:0005871; F:GO:0005524; C:GO:0005739	-		IPR000253; IPR001752; IPR008984; IPR019821; PTHR16012 (PANTHER), PTHR16012:SF104 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	briggsae cbr-ctg-1 protein	4	C:GO:0005829; P:GO:0045542; F:GO:0008047; F:GO:0016765	-		IPR001251; PTHR23324 (PANTHER), PTHR23324:SF9 (PANTHER)
Brugia malayi	frizzled homolog 10	2	P:GO:0007166; F:GO:0004888	-		SignalP (SIGNALP)

Caenorhabditis briggsae	methylase-like protein	0		F:GO:0008168; P:GO:0008152		IPR013216; G3DSA:3.40.50.150 (GENE3D), PTHR10108 (PANTHER), PTHR10108:SF26 (PANTHER), SSF53335 (SUPERFAMILY)
Caenorhabditis briggsae	diacylglycerol ki-se epsilon	2	F:GO:0005488; F:GO:0016740	-		IPR002219; G3DSA:3.30.60.20 (GENE3D), PTHR11255 (PANTHER), PTHR11255:SF7 (PANTHER), SignalP (SIGNALP), SSF57889 (SUPERFAMILY)
Caenorhabditis elegans	cell polarity protein	0				-
Brugia malayi	proteophosphoglycan ppg4	0		F:GO:0046872; F:GO:0005515; C:GO:0005575		-
Brugia malayi	proteophosphoglycan ppg4	0		F:GO:0004674; F:GO:0004672; P:GO:0006468; F:GO:0000166; F:GO:0005524; C:GO:0005575; P:GO:0006886; F:GO:0005515; F:GO:0046872		-
Brugia malayi	proteophosphoglycan ppg4	0		F:GO:0005515		-
Harpegnathos saltator	dephospho- ki-se	4	C:GO:0005737; P:GO:0015937; F:GO:0005524; F:GO:0004140	-	EC:2.7.1.24	IPR001977; G3DSA:3.40.50.300 (GENE3D), SSF52540 (SUPERFAMILY)
Loa loa	ph domain containing protein	0		C:GO:0005634; F:GO:0005159; F:GO:0005158; F:GO:0042169; C:GO:0005737; C:GO:0005792; P:GO:0007165; P:GO:0048009; F:GO:0004871; F:GO:0043548; P:GO:0008286		IPR011993; PTHR10614 (PANTHER), PTHR10614:SF6 (PANTHER)
	-	0				-
Caenorhabditis briggsae	zinc cchc domain containing 11	2	P:GO:0008340; F:GO:0005515	-		-
Caenorhabditis briggsae	neutral alpha-glucosidase ab-like	9	P:GO:0009792; P:GO:0002119; F:GO:0004553; P:GO:0005975; F:GO:0030246; F:GO:0005515; C:GO:0043231; C:GO:0044444; P:GO:0040007	-	EC:3.2.1.0	IPR000322; IPR011013; PTHR22762:SF7 (PANTHER)
Tetraodon nigroviridis	phd and ring finger domains 1	1	F:GO:0005488	-		IPR001841; IPR001965; IPR011011; IPR013083; IPR019786; IPR019787; PTHR10615 (PANTHER), PTHR10615:SF20 (PANTHER), SSF57850 (SUPERFAMILY)

Homo sapiens	-dh dehydroge-se subunit 5	9	P:GO:0001666; P:GO:0006810; F:GO:0008137; P:GO:0010243; C:GO:0005747; C:GO:0016021; P:GO:0006120; C:GO:0019717; P:GO:0042542	-	EC:1.6.5.3	-
	-	0				-
Angiostrongylus cantonensis	tnf receptor-associated protein 1	8	P:GO:0006457; P:GO:0034599; C:GO:0043231; P:GO:0040010; C:GO:0044444; F:GO:0005524; F:GO:0051082; F:GO:0005164	-		IPR001404; IPR020568; IPR020576; PTHR11528:SF24 (PANTHER)
Loa loa	briggsae cbr-pqn-27 protein	0		F:GO:0005488; P:GO:0016070; F:GO:0005515		SignalP (SIGNALP)
	-	0				IPR018545
Caenorhabditis elegans	coiled-coil domain-containing protein 94	4	P:GO:0000003; P:GO:0040010; P:GO:0006898; P:GO:0002119	-		IPR007590
Caenorhabditis elegans	coiled-coil domain-containing protein 94	4	P:GO:0000003; P:GO:0040010; P:GO:0006898; P:GO:0002119	-		IPR007590
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	P:GO:0040010; F:GO:0005515	-		IPR002781; SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	2	P:GO:0040010; F:GO:0005515	-		IPR002781; SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-sulp-6 protein	0		P:GO:0008272; C:GO:0016021; F:GO:0008271; C:GO:0016020; P:GO:0055085; P:GO:0006810; F:GO:0005215		IPR002645; PTHR11814 (PANTHER), PTHR11814:SF10 (PANTHER)
Caenorhabditis elegans	dead (asp-glu-ala-asp) box polypeptide 49	3	F:GO:0003676; F:GO:0005524; F:GO:0008026	-		IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF12 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	set (trithorax polycomb) domain containing family member (set-3)	0		P:GO:0002119		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis elegans	sh2 domain containing protein	2	F:GO:0005515; P:GO:0007298	-		IPR000980; PTHR23101 (PANTHER), PTHR23101:SF3 (PANTHER), SSF55550 (SUPERFAMILY)

Strongylocentrotus purpuratus	rad50-interacting protein 1	0		P:GO:0007049; P:GO:0016192; C:GO:0005783; C:GO:0016020; P:GO:0006810; P:GO:0015031		-
Strongylocentrotus purpuratus	rad50-interacting protein 1	0		P:GO:0007049; P:GO:0016192; C:GO:0005783; C:GO:0016020; P:GO:0006810; P:GO:0015031		-
Brugia malayi	kinetochore-associated protein 1	0		P:GO:0051301; P:GO:0007067; P:GO:0007096; C:GO:0005634; P:GO:0007093; C:GO:0005694; F:GO:0003674; C:GO:0000777; P:GO:0006461; C:GO:0000776; P:GO:0007049; P:GO:0008150; C:GO:0005737; C:GO:0000922; C:GO:0005828; C:GO:0005856; F:GO:0005515; C:GO:0005575		IPR019527
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				IPR017964
Caenorhabditis briggsae	ser thr protein phosphatase family protein	0		F:GO:0046872; C:GO:0016021; F:GO:0016787; C:GO:0016020; P:GO:0008150		IPR004843; G3DSA:3.60.21.10 (GENE3D), SignalP (SIGNALP), SSF56300 (SUPERFAMILY)
Trypanosoma brucei	pyruvate ki-se	2	F:GO:0046872; F:GO:0016301	-		IPR001697; IPR011037; IPR015793; IPR015806
	-	0				-
Caenorhabditis briggsae	small subunit processome homolog	0		F:GO:0003674; P:GO:0008150		IPR006984
Brugia malayi	mitochondrial elongation factor g2	5	F:GO:0003746; P:GO:0032790; F:GO:0005525; P:GO:0070125; F:GO:0003924	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000795; IPR005225; G3DSA:3.40.50.300 (GENE3D), PTHR23115 (PANTHER), PTHR23115:SF13 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	c-myc promoter-binding protein irlb	1	F:GO:0005515	-		IPR001194; IPR005113; PTHR12296 (PANTHER), PTHR12296:SF3 (PANTHER)
Caenorhabditis briggsae	cyclin fold protein 1 variant b	0				-
Haemonchus contortus	intesti-l prolyl carboxypeptidase 2	2	F:GO:0005515; F:GO:0070011	-		IPR008758; G3DSA:3.40.50.1820 (GENE3D), PTHR11010:SF4 (PANTHER), SSF53474 (SUPERFAMILY)
Haemonchus contortus	intesti-l prolyl carboxypeptidase 2	2	F:GO:0005515; F:GO:0070011	-		IPR008758; G3DSA:3.40.50.1820 (GENE3D), PTHR11010:SF4 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)

Caenorhabditis elegans	carnitine o-octanoyltransferase	8	C:GO:0005625; P:GO:0042493; P:GO:0010243; F:GO:0008458; P:GO:0044237; P:GO:0006810; C:GO:0005782; C:GO:0005739	-	EC:2.3.1.137	IPR000542; PTHR22589:SF9 (PANTHER), SSF52777 (SUPERFAMILY)
Caenorhabditis elegans	carnitine o-octanoyltransferase	8	C:GO:0005625; P:GO:0042493; P:GO:0010243; F:GO:0008458; P:GO:0044237; P:GO:0006810; C:GO:0005782; C:GO:0005739	-	EC:2.3.1.137	IPR000542; PTHR22589:SF9 (PANTHER), SSF52777 (SUPERFAMILY)
Caenorhabditis elegans	breast carcinoma amplified sequence 3	1	F:GO:0005515	-		IPR001680; IPR015943; PTHR13268 (PANTHER), SSF101908 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	u2 small nuclear	8	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0005488; P:GO:0040010; P:GO:0008340; P:GO:0040011; P:GO:0006898	-		PTHR12097 (PANTHER)
Caenorhabditis elegans	bardet-biedl syndrome 7	10	P:GO:0032402; C:GO:0043005; P:GO:0035058; P:GO:0051877; C:GO:0034464; P:GO:0001947; F:GO:0005515; P:GO:0007368; P:GO:0048546; P:GO:0045444	-		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0016884; C:GO:0016021		IPR000120; PTHR11895:SF5 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	cell death abnormality family member (ced-7)	6	P:GO:0043652; F:GO:0042626; C:GO:0005886; F:GO:0005524; P:GO:0012501; C:GO:0016021	-		G3DSA:3.40.50.300 (GENE3D), PTHR19229 (PANTHER), PTHR19229:SF18 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	cwf19-like protein 1	1	F:GO:0016787	-		IPR006768; IPR011146; IPR011151; PTHR12072 (PANTHER)
Caenorhabditis elegans	mitochondrial atpase	0		F:GO:0005524		IPR005654; G3DSA:3.40.50.300 (GENE3D)

Caenorhabditis elegans	r--binding protein 24-b	5	C:GO:0005737; F:GO:0003676; F:GO:0005515; F:GO:0000166; P:GO:0006396	-		IPR000504; IPR012677; IPR015463; PTHR10432 (PANTHER), SSF54928 (SUPERFAMILY)
Caenorhabditis briggsae	wd repeat domain 18	2	P:GO:0007275; P:GO:0042254	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR18763 (PANTHER)
Caenorhabditis briggsae	wd repeat domain 18	2	P:GO:0007275; P:GO:0042254	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR18763 (PANTHER)
Drosophila persimilis	GL25064 [Drosophila persimilis]	0		F:GO:0008061; P:GO:0006030; C:GO:0005576		-
Caenorhabditis briggsae	Hypothetical protein CBG14163 [Caenorhabditis briggsae]	1	P:GO:0040010	-		IPR000742
Caenorhabditis elegans	hypothetical protein Y4C6B.7 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein R12C12.10 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	briggsae cbr-rlbp-1 protein	1	P:GO:0009987	-		IPR000198; IPR008936; PTHR12783 (PANTHER), PTHR12783:SF1 (PANTHER)
Loa loa	briggsae cbr-apa-2 protein	16	C:GO:0005829; F:GO:0008565; P:GO:0040010; F:GO:0008022; P:GO:0000003; F:GO:0008289; C:GO:0030131; C:GO:0005905; C:GO:0030666; P:GO:0050690; P:GO:0040011; P:GO:0006898; P:GO:0006886; C:GO:0030141; P:GO:0009792; C:GO:0005886	-		IPR002553; IPR011989; IPR016024; PTHR22780 (PANTHER), PTHR22780:SF4 (PANTHER)
Loa loa	alpha gamma epsilon	15	C:GO:0005829; F:GO:0008565; P:GO:0040010; F:GO:0008022; P:GO:0000003; F:GO:0008289; C:GO:0030131; C:GO:0005905; C:GO:0030666; P:GO:0050690; P:GO:0040011; P:GO:0006898; P:GO:0006886; P:GO:0009792; C:GO:0005886	-		IPR002553; IPR011989; IPR016024; PTHR22780 (PANTHER), PTHR22780:SF4 (PANTHER)
Caenorhabditis briggsae	hect domain and rld 3	1	P:GO:0000003	-		IPR000408; IPR009091; PTHR11254 (PANTHER), PTHR11254:SF8 (PANTHER)
	-	0				SignalP (SIGNALP)

Caenorhabditis briggsae	glycine dehydroge-se	4	F:GO:0004375; F:GO:0030170; P:GO:0055114; P:GO:0006544	-	EC:1.4.4.2	IPR015424; IPR020580; IPR020581
Caenorhabditis elegans	set domain containing 4	0		F:GO:0003674; P:GO:0008150		IPR001214; G3DSA:3.90.1410.10 (GENE3D), PTHR13271 (PANTHER), SSF82199 (SUPERFAMILY)
Caenorhabditis elegans	death associated protein 3	9	C:GO:0015935; P:GO:0040007; C:GO:0005761; C:GO:0045202; F:GO:0001540; P:GO:0008637; P:GO:0002119; P:GO:0009792; C:GO:0016020	-		IPR008092; IPR019368; PTHR12810 (PANTHER)
Caenorhabditis briggsae	hypothetical kda protein in rnr3-arc15 intergenic	0		F:GO:0008168; F:GO:0003674; F:GO:0016740; P:GO:0008152; P:GO:0008150; P:GO:0032259; C:GO:0005575		PTHR12843 (PANTHER)
Caenorhabditis briggsae	hypothetical kda protein in rnr3-arc15 intergenic	0		F:GO:0008168; F:GO:0003674; F:GO:0016740; P:GO:0008152; P:GO:0008150; P:GO:0032259; C:GO:0005575		-
Caenorhabditis elegans	scavenger receptor class member 1	8	P:GO:0007155; C:GO:0044425; P:GO:0030301; P:GO:0050789; P:GO:0016043; C:GO:0005886; F:GO:0005488; P:GO:0040035	-		IPR002159; PTHR11923:SF1 (PANTHER), SignalP (SIGNALP)
Loa loa	eukaryotic translation initiation factor 3 subunit 8	5	C:GO:0005829; P:GO:0000003; P:GO:0006412; C:GO:0005852; F:GO:0003743	-	EC:3.6.5.3	IPR008905; PTHR13937 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	mgc68765 protein	3	C:GO:0005875; F:GO:0003779; P:GO:0007498	-		IPR001715; PTHR11915 (PANTHER)
Caenorhabditis elegans	isoform d	1	C:GO:0005875	-		IPR001715; PTHR11915 (PANTHER)
	-	0				-
Caenorhabditis elegans	roundabout 1	0				-
Caenorhabditis elegans	roundabout 1	0				-
Caenorhabditis elegans	roundabout 1	0				-

Brugia malayi	cap-gly domain containing protein	2	C:GO:0005737; C:GO:0043229	-		IPR000938; IPR023092; PTHR18916 (PANTHER), PTHR18916:SF2 (PANTHER)
Ailuropoda melanoleuca	ubiquitin-activating enzyme e1	6	P:GO:0008219; F:GO:0005524; F:GO:0008641; F:GO:0005515; P:GO:0006464; F:GO:0016874	-		IPR000594; IPR009036; IPR016040; PTHR10953 (PANTHER), PTHR10953:SF4 (PANTHER)
Caenorhabditis briggsae	thymidylate synthase	11	P:GO:0009792; P:GO:0010171; C:GO:0005625; F:GO:0005542; P:GO:0046078; P:GO:0006231; P:GO:0000003; P:GO:0032259; F:GO:0048037; F:GO:0004799; F:GO:0000166	-	EC:2.1.1.45	IPR000398; IPR020940; PTHR11549 (PANTHER)
Angiostrongylus cantonensis	elegans protein confirmed by transcript evidence	4	P:GO:0019915; P:GO:0006952; P:GO:0010171; F:GO:0005515	-		IPR008160; PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER)
Haemonchus contortus	acetylcholine regulator unc-	21	P:GO:0032229; P:GO:0007412; F:GO:0030347; P:GO:0006944; P:GO:0070527; P:GO:0006904; F:GO:0047485; P:GO:0050821; P:GO:0060292; P:GO:0043524; C:GO:0031091; F:GO:0019904; P:GO:0016188; F:GO:0042802; C:GO:0043234; P:GO:0010807; P:GO:0002576; F:GO:0017075; P:GO:0007274; C:GO:0005886; C:GO:0005739	-		-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein Y71G12B.8 [Caenorhabditis elegans]	0		F:GO:0004386; F:GO:0005524; P:GO:0040010; P:GO:0002119; P:GO:0040007; F:GO:0008026		-

Loa loa	protein red	6	P:GO:0006355; P:GO:0051239; C:GO:0005622; P:GO:0048522; P:GO:0002521; F:GO:0005488	-		IPR012492; IPR012916; PTHR12765 (PANTHER)
Loa loa	protein red	6	P:GO:0006355; P:GO:0051239; C:GO:0005622; P:GO:0048522; P:GO:0002521; F:GO:0005488	-		IPR012492; IPR012916; PTHR12765 (PANTHER)
Loa loa	protein red	6	P:GO:0006355; P:GO:0051239; C:GO:0005622; P:GO:0048522; P:GO:0002521; F:GO:0005488	-		IPR012492; IPR012916; PTHR12765 (PANTHER)
Caenorhabditis elegans	hypothetical protein Y71G12B.8 [Caenorhabditis elegans]	2	P:GO:0002119; P:GO:0040010	-		-
Loa loa	protein red	6	P:GO:0006355; P:GO:0051239; C:GO:0005622; P:GO:0048522; P:GO:0002521; F:GO:0005488	-		IPR012492; IPR012916; PTHR12765 (PANTHER)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	rio ki-se 3	2	F:GO:0005488; F:GO:0004672	-		-
Caenorhabditis elegans	hypothetical protein K02F3.9 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	yv31_caeel ame: full=upf0057 membrane protein	1	C:GO:0016021	-		IPR000612; SignalP (SIGNALP)
Homo sapiens	tryptophanyl-tr- isoform cra_a	8	C:GO:0005625; F:GO:0004830; P:GO:0008285; P:GO:0006436; F:GO:0005524; F:GO:0005515; P:GO:0045765; C:GO:0005737	-	EC:6.1.1.2	IPR002306; IPR014729; SSF52374 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				IPR004988
	-	0				-
Caenorhabditis elegans	briggsae cbr-sos-1 protein	0		P:GO:0051056; P:GO:0007264; F:GO:0005089; P:GO:0035023; F:GO:0003677; F:GO:0005085; C:GO:0005622		IPR011993
Caenorhabditis elegans	zinc c2h2 type family protein	5	F:GO:0030528; F:GO:0003676; P:GO:0009790; P:GO:0045449; P:GO:0002521	-		IPR007087; IPR013087; IPR015880; PTHR23223 (PANTHER), PTHR23223:SF15 (PANTHER), SSF57667 (SUPERFAMILY)
Brugia malayi	zinc c2h2 type family protein	0		F:GO:0003676; F:GO:0008270; C:GO:0005622		-
	-	0				-

Caenorhabditis elegans	zinc c2h2 type family protein	5	F:GO:0030528; F:GO:0003676; P:GO:0009790; P:GO:0045449; P:GO:0002521	-		IPR007087; IPR013087; IPR015880; PTHR23223 (PANTHER), PTHR23223:SF15 (PANTHER), SSF57667 (SUPERFAMILY)
	-	0				-
Brugia malayi	cyclin-g-associated ki-se	3	C:GO:0005737; F:GO:0016301; F:GO:0030332	-		IPR000719; IPR011009; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR22967 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	actin family protein	6	P:GO:0002119; F:GO:0005515; P:GO:0000003; P:GO:0040007; P:GO:0006898; C:GO:0044424	-		IPR004000; G3DSA:3.30.420.40 (GENE3D), G3DSA:3.90.640.10 (GENE3D), PTHR11937:SF19 (PANTHER), SSF53067 (SUPERFAMILY)
Caenorhabditis elegans	cleavage and polyadenylation specificity factor subunit 1	4	P:GO:0006378; C:GO:0005847; F:GO:0003723; P:GO:0006379	-		PTHR10644 (PANTHER), PTHR10644:SF2 (PANTHER)
Caenorhabditis briggsae	rrs1 protein	7	P:GO:0009792; P:GO:0002119; P:GO:0042254; P:GO:0040010; P:GO:0000003; P:GO:0040019; C:GO:0005634	-		IPR007023
Loa loa	ancient conserved domain protein 4	0				-
Brugia malayi	retinoblastoma 1	9	F:GO:0005515; P:GO:0065009; P:GO:0051329; P:GO:0006355; P:GO:0045786; P:GO:0023052; P:GO:0048856; P:GO:0030154; C:GO:0044451	-		IPR002719; IPR002720; IPR011028; IPR013763; PTHR13742 (PANTHER), PTHR13742:SF7 (PANTHER)
	-	0				IPR013032; SignalP (SIGNALP)
Loa loa	creb-binding protein	5	P:GO:0044260; P:GO:0007275; P:GO:0044238; P:GO:0050789; F:GO:0005488	-		IPR000197; PTHR13808 (PANTHER)
	-	0				-
	-	0				IPR005018
Caenorhabditis briggsae	briggsae cbr-lpr-2 protein	0		F:GO:0005488; C:GO:0016021		-
Naegleria gruberi	te-scin-x precursor	0		F:GO:0030414; F:GO:0005509; F:GO:0004867; C:GO:0005576		-
Naegleria gruberi	te-scin-x precursor	0		F:GO:0030414; F:GO:0005509; F:GO:0004867; C:GO:0005576		-

Naegleria gruberi	te-scin-x precursor	0		F:GO:0030414; F:GO:0005509; F:GO:0004867; C:GO:0005576		IPR014044; SignalP (SIGNALP)
Naegleria gruberi	te-scin-x precursor	0		F:GO:0030414; F:GO:0005509; F:GO:0004867; C:GO:0005576		-
Nectria haematococca mpVI 77-13-4	conidiospore surface protein	0		F:GO:0030414; F:GO:0005509; F:GO:0004867; C:GO:0005576		SignalP (SIGNALP)
Ancylostoma caninum	scp-like extracellular protein	0		C:GO:0005576		SignalP (SIGNALP)
Ancylostoma caninum	venom allergen antigen-like protein 1	0		C:GO:0005576		-
Naegleria gruberi	te-scin-x precursor	0		F:GO:0030414; F:GO:0005509; F:GO:0004867; C:GO:0005576		-
Caenorhabditis elegans	set domain containing 3	0		F:GO:0003674; P:GO:0008150		-
Caenorhabditis elegans	guanine nucleotide-	2	P:GO:0015031; F:GO:0005488	-		-
Caenorhabditis sp. PS1010	fat tumor suppressor homolog 1	2	P:GO:0009987; C:GO:0016020	-		-
Brugia malayi	tm2 domain-containing protein cg10795 precursor	0				IPR007829; PTHR21016 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	prematurely termi-ted mr- decay factor-like	0		F:GO:0004386; C:GO:0016021; C:GO:0016020; F:GO:0003677; F:GO:0016787; F:GO:0000166; C:GO:0005737; F:GO:0005524; F:GO:0017111; F:GO:0008270; P:GO:0000184		PTHR10887 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein Y73B6BL.1 [Caenorhabditis elegans]	0		F:GO:0046872; F:GO:0016491; P:GO:0008152		-
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Caenorhabditis elegans	n-acetyltransferase 6	2	F:GO:0008415; P:GO:0008152	-		IPR000182; IPR016181; PTHR13538 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	vab-10a protein	0		F:GO:0005509; P:GO:0007050; F:GO:0003779		IPR001101; G3DSA:3.90.1290.10 (GENE3D), SSF75399 (SUPERFAMILY)
Caenorhabditis elegans	propionyl-coenzyme a alpha polypeptide	9	F:GO:0004658; P:GO:0009062; F:GO:0019899; F:GO:0009374; P:GO:0009252; F:GO:0005524; C:GO:0005759; P:GO:0009063; F:GO:0008716	-	EC:6.4.1.3; EC:6.3.2.4	IPR000089; IPR001882; IPR005479; IPR005481; IPR005482; IPR011053; IPR011054; IPR011761; IPR011764; IPR013815; IPR013816; IPR013817; IPR016185; G3DSA:2.40.50.100 (GENE3D), PTHR18866 (PANTHER), PTHR18866:SF13 (PANTHER), SignalP (SIGNALP), SSF56059 (SUPERFAMILY)

						-
Caenorhabditis elegans	briggsae cbr-tgt-1 protein	3	F:GO:0008479; F:GO:0046872; P:GO:0008616	-	EC:2.4.2.29	IPR002616
	-	0				-
	-	0				-
Caenorhabditis elegans	zinc finger protein	2	F:GO:0003676; F:GO:0008270	-		IPR000571; G3DSA:4.10.1000.10 (GENE3D), PTHR12547 (PANTHER), PTHR12547:SF17 (PANTHER), SSF90229 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	lin-5 interacting protein family member (lfi-1)	5	P:GO:0009987; C:GO:0043234; F:GO:0005515; C:GO:0005694; C:GO:0044430	-		IPR009053; PD936484 (PRODOM), PTHR18937 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	glutamate synthase	10	P:GO:0006537; P:GO:0009792; F:GO:0045181; P:GO:0002119; F:GO:0051536; F:GO:0005506; F:GO:0010181; P:GO:0040010; P:GO:0055114; F:GO:0050660	-		IPR000583; IPR006982; IPR013785; IPR017932; G3DSA:3.60.20.10 (GENE3D), PTHR11938 (PANTHER), PTHR11938:SF1 (PANTHER), SSF51395 (SUPERFAMILY), SSF56235 (SUPERFAMILY)
synthetic construct	glyceraldehyde-3-phosphate dehydroge-se	7	F:GO:0051287; F:GO:0005515; P:GO:0055114; P:GO:0006096; C:GO:0016020; F:GO:0004365; C:GO:0048471	-	EC:1.2.1.12	IPR006424; IPR016040; IPR020828; IPR020829; IPR020830; IPR020831; G3DSA:3.30.360.10 (GENE3D), SSF51735 (SUPERFAMILY), SSF55347 (SUPERFAMILY)
Caenorhabditis elegans	mitochondrial intermediate peptidase	1	F:GO:0008233	-		IPR001567; G3DSA:1.10.1370.10 (GENE3D), G3DSA:3.40.390.10 (GENE3D), PTHR11804 (PANTHER), PTHR11804:SF5 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	mitochondrial intermediate peptidase	1	F:GO:0008233	-		IPR001567; G3DSA:1.10.1370.10 (GENE3D), G3DSA:3.40.390.10 (GENE3D), PTHR11804 (PANTHER), PTHR11804:SF5 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis brenneri	williams-beuren syndrome critical region protein 20 copy a	0		F:GO:0005381; P:GO:0006827		-
Caenorhabditis elegans	hypothetical protein C53H9.3 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				PTHR11600 (PANTHER), SignalP (SIGNALP)

Brugia malayi	importin beta-3	10	C:GO:0005829; P:GO:0040010; C:GO:0005875; P:GO:0000003; P:GO:0018996; P:GO:0002119; F:GO:0005515; P:GO:0006898; P:GO:0009792; P:GO:0001703	-		IPR000357; IPR001494; IPR011989; IPR016024; IPR021133; PTHR10527 (PANTHER), PTHR10527:SF5 (PANTHER)
Caenorhabditis elegans	hypothetical protein Y71G12A.2 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	runt-related transcription factor 1	24	P:GO:0001501; P:GO:0048666; P:GO:0001649; P:GO:0007417; P:GO:0045766; P:GO:0032526; P:GO:0035162; P:GO:0030853; P:GO:0048266; F:GO:0070491; F:GO:0005509; C:GO:0005730; F:GO:0016563; F:GO:0046982; P:GO:0060216; F:GO:0003677; F:GO:0003700; P:GO:0016481; P:GO:0030854; P:GO:0045944; F:GO:0042803; P:GO:0001889; F:GO:0008134; P:GO:0001701	-		-
Loa loa	thyroid transcription factor 1-associated protein 26 homolog	0		P:GO:0045449; F:GO:0005515; C:GO:0005634		IPR000169; IPR009149; IPR013730
Mus musculus	ribosomal protein l17	4	F:GO:0003735; C:GO:0015934; C:GO:0005829; P:GO:0006414	-		IPR001063; IPR005721
Caenorhabditis elegans	eukaryotic translation initiation factor 3 subunit l	4	C:GO:0005737; F:GO:0005515; F:GO:0003743; P:GO:0006412	-	EC:3.6.5.3	SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	transmembrane amino acid transporter protein	1	C:GO:0016020	-		IPR013057; PTHR22950 (PANTHER), PTHR22950:SF5 (PANTHER)
Caenorhabditis elegans	transmembrane amino acid transporter protein	1	C:GO:0016020	-		IPR013057; PTHR22950 (PANTHER), PTHR22950:SF5 (PANTHER)
Caenorhabditis elegans	transmembrane amino acid transporter protein	1	C:GO:0016020	-		IPR013057; PTHR22950 (PANTHER), PTHR22950:SF5 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-lin-25 protein	4	P:GO:0032501; C:GO:0044424; P:GO:0030154; P:GO:0022414	-		-
Caenorhabditis elegans	hypothetical protein Y4C6B.1 [Caenorhabditis elegans]	0				-

Loa loa	myosin xviiia	7	P:GO:0009987; F:GO:0017111; C:GO:0005856; C:GO:0005730; F:GO:0042802; F:GO:0000166; C:GO:0005794	-	EC:3.6.1.15	IPR001609; G3DSA:4.10.270.10 (GENE3D), PTHR13140 (PANTHER), PTHR13140:SF23 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	briggsae cbr-npp-15 protein	0		F:GO:0003674; C:GO:0016021; P:GO:0040010		IPR018247; PTHR13405 (PANTHER), PTHR13405:SF6 (PANTHER)
Homo sapiens	mhc class ii antigen	14	C:GO:0005789; C:GO:0005769; C:GO:0042613; C:GO:0005771; C:GO:0005794; P:GO:0019886; F:GO:0005515; C:GO:0009897; C:GO:0005765; C:GO:0016021; F:GO:0032395; C:GO:0010008; P:GO:0006955; F:GO:0042605	-		IPR000353; IPR003597; IPR007110; IPR013783; PTHR19944 (PANTHER), PTHR19944:SF26 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	hypothetical protein D1007.15 [Caenorhabditis elegans]	0				-
Caenorhabditis elegans	diphthamide biosynthesis protein 1	4	C:GO:0044424; P:GO:0000003; P:GO:0040010; P:GO:0002119	-		IPR002728; PTHR10762:SF1 (PANTHER)
Caenorhabditis elegans	diphthamide biosynthesis protein 1	4	C:GO:0044424; P:GO:0000003; P:GO:0040010; P:GO:0002119	-		IPR002728; PTHR10762:SF1 (PANTHER)
	-	0				-
	-	0				-
	-	0				IPR008139; IPR011001; SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	microtubule associated serine threonine ki-se 2	14	P:GO:0000003; F:GO:0000166; P:GO:0044237; F:GO:0004672; F:GO:0046872; C:GO:0000776; F:GO:0008017; P:GO:0009792; C:GO:0005813; P:GO:0043170; C:GO:0005876; P:GO:0000087; P:GO:0031111; C:GO:0005938	-		IPR015022; IPR023142; PTHR22985 (PANTHER), PTHR22985:SF42 (PANTHER)

Caenorhabditis elegans	microtubule associated serine threonine ki-se 2	9	C:GO:0005856; F:GO:0004672; F:GO:0046872; P:GO:0000003; P:GO:0043170; F:GO:0005515; F:GO:0000166; P:GO:0009792; P:GO:0044237	-		IPR015022; IPR023142; PTHR22985 (PANTHER), PTHR22985:SF42 (PANTHER)
Brugia malayi	elegans protein confirmed by transcript evidence	7	P:GO:0009792; P:GO:0010171; P:GO:0002119; P:GO:0040011; P:GO:0019915; P:GO:0040007; P:GO:0006898	-		-
	-	0				-
Caenorhabditis briggsae	mitochondrial ribosomal protein l37	0		F:GO:0045182; F:GO:0003735; C:GO:0005739; P:GO:0006412; C:GO:0005761; C:GO:0005840		-
Caenorhabditis briggsae	mitochondrial ribosomal protein l37	2	C:GO:0044444; C:GO:0043229	-		-
Caenorhabditis elegans	briggsae cbr-mog-5 protein	7	F:GO:0003723; F:GO:0004004; C:GO:0071011; P:GO:0000381; F:GO:0005524; F:GO:0005515; C:GO:0071013	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Loa loa	fizzy cell division cycle 20 related 1	6	P:GO:0044267; P:GO:0009792; P:GO:0007067; P:GO:0007126; P:GO:0050794; C:GO:0005634	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		F:GO:0001851; C:GO:0005634; P:GO:0030449; C:GO:0005737; F:GO:0003674; C:GO:0005576; C:GO:0005575; F:GO:0043499; F:GO:0008201; P:GO:0006957; C:GO:0005886; P:GO:0008150; C:GO:0005615		IPR000436; IPR016060; PTHR19325 (PANTHER), PTHR19325:SF25 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis briggsae	briggsae cbr-cnt-1 protein	5	F:GO:0046872; P:GO:0019915; P:GO:0002119; F:GO:0005515; P:GO:0050794	-		SSF103657 (SUPERFAMILY)
Caenorhabditis elegans	ubiquitin specific protease 32	3	P:GO:0009792; F:GO:0016787; P:GO:0008152	-		IPR001125; IPR001394; IPR002048; IPR006615; IPR011992; IPR018247; IPR018249; PTHR10420 (PANTHER), PTHR10420:SF70 (PANTHER), SSF143791 (SUPERFAMILY), SSF47473 (SUPERFAMILY), SSF54001 (SUPERFAMILY)
Caenorhabditis elegans	fatty acid synthetase family member (acs-14)	16	P:GO:0048666; F:GO:0000166; P:GO:0008610; C:GO:0005792; C:GO:0005741; F:GO:0004467; C:GO:0044425; P:GO:0006637; P:GO:0048522; P:GO:0006641; C:GO:0005783; C:GO:0005886; P:GO:0009725; P:GO:0015908; C:GO:0005778; P:GO:0044249	-	EC:6.2.1.3	-
	-	0				SignalP (SIGNALP)
	-	0				IPR022353
Caenorhabditis briggsae	tim44-like domain containing protein	2	C:GO:0030529; C:GO:0005739	-		SignalP (SIGNALP)
Caenorhabditis briggsae	deah (asp-glu-ala-his) box polypeptide 9	11	F:GO:0003723; C:GO:0070937; P:GO:0070934; C:GO:0005730; P:GO:0008380; C:GO:0005813; F:GO:0005515; F:GO:0000166; F:GO:0004386; C:GO:0030529; P:GO:0034605	-		IPR001650; IPR002464; IPR007502; IPR011709; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR18934 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	nips-p protein	2	F:GO:0016791; P:GO:0008152	-	EC:3.1.3.0	IPR011008; IPR012577; G3DSA:3.30.70.900 (GENE3D), PTHR21017 (PANTHER), PTHR21017:SF5 (PANTHER)
Caenorhabditis elegans	jhd1_caeel ame: full= domain-containing histone demethylation protein 1 ame: full= -lysine-36 demethylase 1	4	P:GO:0000003; F:GO:0016491; P:GO:0008152; P:GO:0006974	-		-
Caenorhabditis briggsae	protein ki-se domain containing protein	7	P:GO:0040010; F:GO:0004674; P:GO:0044260; P:GO:0005975; F:GO:0005515; F:GO:0000166; C:GO:0044464	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR22686 (PANTHER)

Drosophila grimshawi	GH24427 [Drosophila grimshawi]	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	d- replication licensing factor mcm5	16	P:GO:0000278; P:GO:0040010; P:GO:0006268; P:GO:0000910; C:GO:0042555; F:GO:0003677; F:GO:0005524; C:GO:0000785; F:GO:0016887; F:GO:0005515; P:GO:0030174; P:GO:0009792; P:GO:0043066; P:GO:0001703; P:GO:0006350; F:GO:0003682	-		IPR001208; IPR008048; IPR012340; IPR016027; IPR018525; G3DSA:3.30.1640.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR11630 (PANTHER), PTHR11630:SF42 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	d- replication licensing factor mcm5	16	P:GO:0000278; P:GO:0040010; P:GO:0006268; P:GO:0000910; C:GO:0042555; F:GO:0003677; F:GO:0005524; C:GO:0000785; F:GO:0016887; F:GO:0005515; P:GO:0030174; P:GO:0009792; P:GO:0043066; P:GO:0001703; P:GO:0006350; F:GO:0003682	-		IPR001208; IPR008048; IPR012340; IPR016027; IPR018525; G3DSA:3.30.1640.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR11630 (PANTHER), PTHR11630:SF42 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	metallophosphoesterase domain containing 1	1	F:GO:0016787	-		PTHR12905 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	P:GO:0019915	-		SignalP (SIGNALP)
Caenorhabditis elegans	sugar transporter	6	C:GO:0016021; P:GO:0009792; P:GO:0040007; P:GO:0055085; F:GO:0005215; P:GO:0002119	-		IPR011701; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11600 (PANTHER), PTHR11600:SF42 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	abnormal cell migration family member (mig-15)	0		F:GO:0005083; F:GO:0005524; F:GO:0004672; P:GO:0006468; F:GO:0005515; F:GO:0004674		PTHR22986 (PANTHER), PTHR22986:SF83 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	catenin (cadherin-associated protein) alpha-like 1	7	P:GO:0007266; P:GO:0007155; C:GO:0016021; C:GO:0005829; C:GO:0015629; F:GO:0045296; F:GO:0005198	-		IPR001033; IPR006077; G3DSA:1.20.120.230 (GENE3D), PTHR18914 (PANTHER), PTHR18914:SF8 (PANTHER)

Caenorhabditis elegans	par-6 gamma	8	C:GO:0005737; P:GO:0007163; P:GO:0040001; F:GO:0005515; P:GO:0007155; P:GO:0007369; C:GO:0016021; P:GO:0008406	-		IPR000270; G3DSA:3.10.20.240 (GENE3D), PTHR14102 (PANTHER), PTHR14102:SF2 (PANTHER), SSF54277 (SUPERFAMILY)
	-	0				-
Brugia malayi	tho complex subunit 6 homolog isoform 1	3	C:GO:0000346; P:GO:0006406; C:GO:0000347	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR22847 (PANTHER), PTHR22847:SF3 (PANTHER)
Caenorhabditis elegans	c2 domain containing protein	2	P:GO:0009792; C:GO:0016021	-		PTHR10774 (PANTHER), PTHR10774:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	c2 domain containing protein	2	P:GO:0009792; C:GO:0016021	-		PTHR10774 (PANTHER), PTHR10774:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	set (trithorax polycomb) domain containing family member (set-18)	1	F:GO:0005515	-		-
	-	0				SignalP (SIGNALP)
Loa loa	hypothetical protein LOAG_02385 [Loa loa]	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		P:GO:0000003; P:GO:0006898; P:GO:0009792; P:GO:0002119; P:GO:0040007		-
Caenorhabditis elegans	o ant response abnormal family member (odr-4)	0		P:GO:0055114; F:GO:0016491; F:GO:0008270		-
Caenorhabditis briggsae	gyf domain-containing protein	0		C:GO:0016021; C:GO:0016020; F:GO:0008158		IPR003169; G3DSA:3.30.1490.40 (GENE3D), PTHR14445 (PANTHER), PTHR14445:SF4 (PANTHER)
Caenorhabditis briggsae	gyf domain-containing protein	0				IPR003169; G3DSA:3.30.1490.40 (GENE3D), PTHR14445 (PANTHER), PTHR14445:SF4 (PANTHER)
Caenorhabditis briggsae	gyf domain-containing protein	0		C:GO:0016021; C:GO:0016020; F:GO:0008158		IPR003169; G3DSA:3.30.1490.40 (GENE3D), PTHR14445 (PANTHER), PTHR14445:SF4 (PANTHER)
Caenorhabditis briggsae	gyf domain-containing protein	0				IPR003169; G3DSA:3.30.1490.40 (GENE3D), PTHR14445 (PANTHER), PTHR14445:SF4 (PANTHER)
Caenorhabditis briggsae	gyf domain-containing protein	0		C:GO:0016021; C:GO:0016020; F:GO:0008158		IPR003169; G3DSA:3.30.1490.40 (GENE3D), PTHR14445 (PANTHER), PTHR14445:SF4 (PANTHER)
Caenorhabditis elegans	phosphoethanolamine ransferase family member (pmt-1)	9	P:GO:0009792; P:GO:0002119; F:GO:0008757; P:GO:0032940; P:GO:0009058; P:GO:0040017; P:GO:0040010; P:GO:0000003; P:GO:0044238	-		PTHR10108 (PANTHER), PTHR10108:SF3 (PANTHER)
	-	0				IPR022559; SignalP (SIGNALP)

Caenorhabditis elegans	homolog subfamily c member 12	0		F:GO:0051082; P:GO:0006457; F:GO:0031072		IPR001623; IPR015609; PTHR11821:SF52 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG20503 [Caenorhabditis briggsae]	0				-
Caenorhabditis elegans	bifunctio-l protein ncoat	1	F:GO:0016798	-		IPR011496; IPR017853; PTHR13170 (PANTHER), PTHR13170:SF5 (PANTHER)
synthetic construct	beta-galactoside-binding lectin precursor	24	F:GO:0004871; P:GO:0071333; F:GO:0005534; F:GO:0043236; P:GO:0033555; P:GO:0007157; F:GO:0016936; C:GO:0005615; P:GO:0045445; P:GO:0034120; C:GO:0005737; C:GO:0009986; F:GO:0001948; P:GO:0043123; C:GO:0005578; P:GO:0010812; P:GO:0048678; F:GO:0030395; P:GO:0042493; P:GO:0010977; P:GO:0071407; F:GO:0042803; P:GO:0042981; C:GO:0005634	-		SignalP (SIGNALP)
	-	0				IPR002223; IPR020901; PTHR10083 (PANTHER), PTHR10083:SF17 (PANTHER), SignalP (SIGNALP)
Brugia malayi	uncoordi-ted family member (unc-89)	4	F:GO:0004674; F:GO:0005524; P:GO:0009792; P:GO:0006468	-	EC:2.7.11.0	IPR013098; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-reps-1 protein	0		F:GO:0005509		IPR000261; IPR011992; IPR018247; IPR018249; PTHR11216 (PANTHER), PTHR11216:SF33 (PANTHER), SSF47473 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein W04C9.2 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
	-	0				-
Loa loa	round spermatid basic protein 1-like	0		C:GO:0005634		PTHR13354 (PANTHER)
Saccoglossus kowalevskii	lipophorin receptor	0		C:GO:0005905; F:GO:0005509; F:GO:0004872; C:GO:0016021; C:GO:0016020; P:GO:0006897		-

Caenorhabditis elegans	cytochrome family subfamily polypeptide 24	12	P:GO:0043651; F:GO:0003958; F:GO:0071614; F:GO:0008404; C:GO:0005792; F:GO:0016712; P:GO:0014070; F:GO:0008405; P:GO:0019373; F:GO:0005506; C:GO:0016020; C:GO:0005783	-	EC:1.6.2.4; EC:1.14.14.0	-
Loa loa	lim domain containing protein	2	P:GO:0048468; C:GO:0044464	-		IPR001781; PTHR18973 (PANTHER), PTHR18973:SF106 (PANTHER), SSF57716 (SUPERFAMILY)
Loa loa	lim domain containing protein	2	P:GO:0048468; C:GO:0044464	-		IPR001781; PTHR18973 (PANTHER), PTHR18973:SF106 (PANTHER), SSF57716 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	C:GO:0005634	-		PTHR12202 (PANTHER)
Caenorhabditis briggsae	glutathione synthetase	7	P:GO:0009792; F:GO:0016874; P:GO:0002119; F:GO:0005515; P:GO:0040010; P:GO:0000003; F:GO:0000166	-		-
Brugia malayi	zinc finger	1	P:GO:0019915	-		IPR000210; IPR006652; IPR011333; IPR011705; IPR013069; IPR013089; IPR015916; PTHR23230:SF147 (PANTHER), SSF117281 (SUPERFAMILY)
Caenorhabditis briggsae	5-oxoproli-se (atp-hydrolysing)	3	F:GO:0017168; P:GO:0006749; F:GO:0000166	-	EC:3.5.2.9	IPR003692; PTHR11365 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	mgc137510 protein	4	F:GO:0046872; P:GO:0007165; C:GO:0005622; F:GO:0005070	-		IPR000980; IPR015778; IPR020685; SSF55550 (SUPERFAMILY)
Caenorhabditis briggsae	transformation transcription domain-associated protein	1	P:GO:0009987	-		IPR000403; IPR003152; IPR011009; PTHR11139 (PANTHER), PTHR11139:SF2 (PANTHER)
Caenorhabditis briggsae	transformation transcription domain-associated protein	1	P:GO:0009987	-		-
	-	0				-
Caenorhabditis elegans	phosphoethanolamine ransferase family member (pmt-1)	6	P:GO:0009792; P:GO:0002119; P:GO:0032940; P:GO:0040017; P:GO:0040010; P:GO:0000003	-		-
Caenorhabditis briggsae	upf0378 protein kiaa0100	0				IPR019443; PTHR15678 (PANTHER)
Caenorhabditis briggsae	heat-responsive protein 12	4	F:GO:0004519; P:GO:0006449; C:GO:0005634; C:GO:0005739	-		IPR006056; IPR006175; IPR013813; IPR019897

	-	0				-
Caenorhabditis briggsae	briggsae cbr-grl-17 protein	0				SignalP (SIGNALP)
Zea mays	briggsae cbr-pqn-22 protein	0		F:GO:0005515		-
Zea mays	briggsae cbr-pqn-22 protein	0		F:GO:0005515		-
	-	0				-
	-	0				-
Caenorhabditis elegans	c5orf44 protein	1	F:GO:0005515	-		-
Caenorhabditis elegans	enoyl- hydratase	5	F:GO:0004872; P:GO:0002119; P:GO:0040010; F:GO:0003824; P:GO:0023052	-		IPR001753; IPR014748; G3DSA:3.90.226.10 (GENE3D), PTHR11941 (PANTHER), SSF52096 (SUPERFAMILY)
Caenorhabditis elegans	enoyl- hydratase	5	F:GO:0004872; P:GO:0002119; P:GO:0040010; F:GO:0003824; P:GO:0023052	-		IPR001753; IPR014748; G3DSA:3.90.226.10 (GENE3D), PTHR11941 (PANTHER), SSF52096 (SUPERFAMILY)
Caenorhabditis briggsae	vesicle-fusing atpase	15	P:GO:0040007; P:GO:0000003; P:GO:0006911; F:GO:0005524; P:GO:0048172; P:GO:0002119; F:GO:0016887; F:GO:0005515; P:GO:0007030; P:GO:0016082; P:GO:0006888; P:GO:0040011; P:GO:0006898; P:GO:0009792; C:GO:0005737	-		IPR003959; IPR003960; G3DSA:3.40.50.300 (GENE3D), PTHR23078 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	c9orf7 homolog	1	F:GO:0005515	-		IPR019365; PTHR13314 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-ltd-1 protein	1	F:GO:0008270	-		-
Caenorhabditis sp. PS1010	briggsae cbr-mel-28 protein	0		P:GO:0006355; F:GO:0003677		-
	-	0				-
Polysphondylium pallidum PN500	checkpoint with forkhead and ring finger domains	4	P:GO:0000278; F:GO:0016874; F:GO:0005488; P:GO:0044267	-		-
Polysphondylium pallidum PN500	checkpoint with forkhead and ring finger domains	4	P:GO:0000278; F:GO:0016874; F:GO:0005488; P:GO:0044267	-		-
	-	0				SignalP (SIGNALP)
	-	0				PTHR22979 (PANTHER), PTHR22979:SF1 (PANTHER), SignalP (SIGNALP)
Loa loa	three prime repair exonuclease 2	0		F:GO:0003676		IPR012337; G3DSA:3.30.420.10 (GENE3D), PTHR13058 (PANTHER), PTHR13058:SF1 (PANTHER)

Caenorhabditis briggsae	golgi-specific brefeldin a resistance factor 1	7	P:GO:0006892; C:GO:0000139; P:GO:0006890; F:GO:0005086; P:GO:0032012; F:GO:0005515; P:GO:0048205	-			IPR000904; G3DSA:1.10.1000.11 (GENE3D), G3DSA:1.10.220.20 (GENE3D), PTHR10663 (PANTHER), PTHR10663:SF8 (PANTHER)
Caenorhabditis briggsae	golgi-specific brefeldin a-resistance guanine nucleotide exchange factor 1	7	P:GO:0006892; C:GO:0000139; P:GO:0006890; F:GO:0005086; P:GO:0032012; F:GO:0005515; P:GO:0048205	-			IPR000904; G3DSA:1.10.1000.11 (GENE3D), G3DSA:1.10.220.20 (GENE3D), PTHR10663 (PANTHER), PTHR10663:SF8 (PANTHER)
Caenorhabditis briggsae	golgi-specific brefeldin a resistance factor 1	7	P:GO:0006892; C:GO:0000139; P:GO:0006890; F:GO:0005086; P:GO:0032012; F:GO:0005515; P:GO:0048205	-			IPR000904; G3DSA:1.10.1000.11 (GENE3D), G3DSA:1.10.220.20 (GENE3D), PTHR10663 (PANTHER), PTHR10663:SF8 (PANTHER)
Caenorhabditis briggsae	golgi-specific brefeldin a resistance factor 1	7	P:GO:0006892; C:GO:0000139; P:GO:0006890; F:GO:0005086; P:GO:0032012; F:GO:0005515; P:GO:0048205	-			IPR000904; G3DSA:1.10.1000.11 (GENE3D), G3DSA:1.10.220.20 (GENE3D), PTHR10663 (PANTHER), PTHR10663:SF8 (PANTHER)
Caenorhabditis elegans	golgi-specific brefeldin a-resistance guanine nucleotide exchange factor 1	15	F:GO:0005515; C:GO:0005788; C:GO:0005777; F:GO:0016563; C:GO:0005829; C:GO:0005801; P:GO:0048193; F:GO:0003677; P:GO:0032012; C:GO:0005795; F:GO:0005086; P:GO:0045449; C:GO:0005634; P:GO:0046903; C:GO:0005739	-			PTHR10663 (PANTHER), PTHR10663:SF8 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	golgi-specific brefeldin a resistance factor 1	7	P:GO:0006892; C:GO:0000139; P:GO:0006890; F:GO:0005086; P:GO:0032012; F:GO:0005515; P:GO:0048205	-			IPR000904; G3DSA:1.10.1000.11 (GENE3D), G3DSA:1.10.220.20 (GENE3D), PTHR10663 (PANTHER), PTHR10663:SF8 (PANTHER)

Caenorhabditis elegans	golgi-specific brefeldin a-resistance guanine nucleotide exchange factor 1	15	F:GO:0005515; C:GO:0005788; C:GO:0005777; F:GO:0016563; C:GO:0005829; C:GO:0005801; P:GO:0048193; F:GO:0003677; P:GO:0032012; C:GO:0005795; F:GO:0005086; P:GO:0045449; C:GO:0005634; P:GO:0046903; C:GO:0005739	-		PTHR10663 (PANTHER), PTHR10663:SF8 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	golgi-specific brefeldin a-resistance guanine nucleotide exchange factor 1	19	F:GO:0004871; F:GO:0005515; C:GO:0005788; P:GO:0008610; F:GO:0005525; C:GO:0005777; C:GO:0005829; F:GO:0016563; C:GO:0005801; F:GO:0003677; P:GO:0032012; C:GO:0005795; F:GO:0005086; P:GO:0007186; P:GO:0045449; F:GO:0003824; C:GO:0005634; P:GO:0046903; C:GO:0005739	-		IPR001019; IPR011025; G3DSA:3.40.50.300 (GENE3D), PTHR10218:SF63 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	golgi-specific brefeldin a resistance factor 1	7	P:GO:0006892; C:GO:0000139; P:GO:0006890; F:GO:0005086; P:GO:0032012; F:GO:0005515; P:GO:0048205	-		IPR000904; G3DSA:1.10.1000.11 (GENE3D), G3DSA:1.10.220.20 (GENE3D), PTHR10663 (PANTHER), PTHR10663:SF8 (PANTHER)
Caenorhabditis elegans	glycerol ki-se	7	C:GO:0005625; P:GO:0006072; F:GO:0042393; F:GO:0004370; P:GO:0045471; C:GO:0005634; C:GO:0005739	-	EC:2.7.1.30	-
	-	0				-
	-	0				-

Loa loa	dead box atp-dependent r- helicase	10	P:GO:0009792; P:GO:0002119; F:GO:0008026; P:GO:0040010; F:GO:0005524; P:GO:0000003; P:GO:0008340; P:GO:0040011; F:GO:0003743; P:GO:0019915	-		IPR011545; IPR014001; IPR014014; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF2 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein F01G4.6 [Caenorhabditis elegans]	6	P:GO:0040035; P:GO:0009792; P:GO:0002119; P:GO:0006810; P:GO:0040010; C:GO:0016020	-		-
Caenorhabditis elegans	beta 5	6	F:GO:0008060; P:GO:0032312; F:GO:0008270; P:GO:0019915; P:GO:0002119; F:GO:0005515	-		IPR001164; IPR001849; IPR011993; PTHR23180 (PANTHER), PTHR23180:SF20 (PANTHER), SSF50729 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Loa loa	baculoviral iap repeat-containing 2	1	F:GO:0005488	-		IPR001841; PTHR10044 (PANTHER), PTHR10044:SF9 (PANTHER)
Caenorhabditis elegans	vitellogenin structural genes (yolk protein genes) family member (vit-2)	4	P:GO:0009792; P:GO:0008340; P:GO:0040010; F:GO:0005515	-		IPR000215; IPR001747; IPR015816; IPR015819; PTHR23345 (PANTHER)
Caenorhabditis elegans	vitellogenin structural genes (yolk protein genes) family member (vit-2)	4	P:GO:0009792; P:GO:0008340; P:GO:0040010; F:GO:0005515	-		IPR000215; IPR015816; IPR015819; PTHR23345 (PANTHER)
Oscheius sp. (strain CEW1)	vitellogenin structural genes (yolk protein genes) family member (vit-2)	4	P:GO:0009792; F:GO:0005515; P:GO:0040010; P:GO:0008340	-		SignalP (SIGNALP)
Caenorhabditis elegans	vitellogenin structural genes (yolk protein genes) family member (vit-2)	4	P:GO:0009792; F:GO:0005515; P:GO:0040010; P:GO:0008340	-		IPR001747; IPR015816; IPR015819; PTHR23345 (PANTHER)
Caenorhabditis elegans	vitellogenin structural genes (yolk protein genes) family member (vit-2)	4	P:GO:0009792; F:GO:0005515; P:GO:0040010; P:GO:0008340	-		IPR001747; IPR015816; IPR015819; PTHR23345 (PANTHER)
Caenorhabditis elegans	vitellogenin structural genes (yolk protein genes) family member (vit-2)	4	P:GO:0009792; F:GO:0005515; P:GO:0040010; P:GO:0008340	-		IPR000215

Angiostrongylus cantonensis	mediator of r- polymerase ii transcription subunit 6	12	P:GO:0006357; P:GO:0040007; P:GO:0040027; P:GO:0040035; P:GO:0007283; F:GO:0016455; F:GO:0005515; P:GO:0007281; C:GO:0016592; P:GO:0048477; P:GO:0009792; P:GO:0008406	-		SignalP (SIGNALP)
Arabidopsis lyrata subsp. lyrata	serine threonine ki-se	0		F:GO:0003824; P:GO:0030154; P:GO:0033993; F:GO:0048185; F:GO:0004872; F:GO:0004871; P:GO:0006355; C:GO:0005886; F:GO:0004713; P:GO:0007368; F:GO:0004712; P:GO:0009749; P:GO:0001541; C:GO:0016021; C:GO:0016020; P:GO:0001701; F:GO:0004674; F:GO:0004672; C:GO:0048179; F:GO:0004709; P:GO:0007165; F:GO:0005524; F:GO:0016301; F:GO:0000166; F:GO:0016361; P:GO:0021549; P:GO:0006468; C:GO:0009986;		IPR000719; IPR011009; IPR017441; IPR017442; G3DSA:3.30.200.20 (GENE3D), PTHR23257 (PANTHER), PTHR23257:SF80 (PANTHER), SignalP (SIGNALP)

Homo sapiens	AF113217_1MSTP037 [Homo sapiens]	20	C:GO:0005829; F:GO:0005158; P:GO:0007043; C:GO:0032587; C:GO:0043231; P:GO:0007016; F:GO:0017166; F:GO:0030274; P:GO:0007044; C:GO:0005813; P:GO:0007155; C:GO:0005925; P:GO:0030866; C:GO:0005911; F:GO:0003779; C:GO:0015629; P:GO:0006928; F:GO:0005200; C:GO:0005576; P:GO:0006936	-		IPR007921; SignalP (SIGNALP)
Caenorhabditis briggsae	hyphally-regulated cell wall protein	0		P:GO:0060271; F:GO:0008061; F:GO:0005488; P:GO:0060041; P:GO:0006030; P:GO:0010842; P:GO:0007018; C:GO:0005576		-
Caenorhabditis briggsae	mucin- partial	0				-
Caenorhabditis briggsae	major facilitator superfamily protein	6	C:GO:0016021; P:GO:0009792; P:GO:0040007; P:GO:0055085; F:GO:0005215; P:GO:0002119	-		SignalP (SIGNALP)
Loa loa	phd-finger family protein	1	F:GO:0005488	-		IPR001965; IPR011011; IPR013083; IPR019786; IPR019787; PTHR13793 (PANTHER), PTHR13793:SF9 (PANTHER)
Equus caballus	survival of motor neuron telomeric	5	C:GO:0005737; F:GO:0005488; C:GO:0005654; P:GO:0000398; P:GO:0022618	-		IPR002999; IPR010304; IPR018351; G3DSA:2.30.30.140 (GENE3D), PTHR12664 (PANTHER), SSF63748 (SUPERFAMILY)
Caenorhabditis briggsae	4-coumarate- ligase-like protein	2	F:GO:0003824; P:GO:0008152	-		-
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	P:GO:0040010	-		IPR006621; PTHR11161 (PANTHER)
	-	0				-

Caenorhabditis elegans	acp1 protein	8	F:GO:0004725; F:GO:0042802; F:GO:0003993; C:GO:0019717; P:GO:0016311; P:GO:0007268; P:GO:0044267; F:GO:0017124	-	EC:3.1.3.48; EC:3.1.3.2	IPR000106; IPR002115; IPR017867; G3DSA:3.40.50.270 (GENE3D), PTHR11717:SF7 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	ubiquitin fusion degradation (yeast ufd homolog) family member (ufd-1)	0		F:GO:0005515; P:GO:0006511		-
Caenorhabditis elegans	ubiquitin fusion degradation protein 1 homolog	1	F:GO:0005515	-		-
Caenorhabditis elegans	ubiquitin fusion degradation protein 1 homolog	1	F:GO:0005515	-		-
	-	0				-
Brugia malayi	male sterility protein	6	P:GO:0008610; F:GO:0050062; F:GO:0005515; C:GO:0005782; P:GO:0044237; C:GO:0016020	-	EC:1.2.1.50	IPR004262; PTHR11011 (PANTHER), PTHR11011:SF8 (PANTHER)
Ornithorhynchus anatinus	snrnp core protein smx5d	0				SignalP (SIGNALP)
Drosophila erecta	GG20442 [Drosophila erecta]	0				-
Drosophila erecta	GG20442 [Drosophila erecta]	0				-
Caenorhabditis briggsae	nucleolar gtp-binding protein 1	17	P:GO:0008156; P:GO:0000003; P:GO:0030336; F:GO:0005515; P:GO:0040010; P:GO:0050821; F:GO:0005525; P:GO:0000079; P:GO:0008285; P:GO:0022408; P:GO:0009792; P:GO:0002119; P:GO:0031397; C:GO:0048471; F:GO:0003924; P:GO:0033342; C:GO:0005634	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	PTHR11702 (PANTHER), PTHR11702:SF4 (PANTHER)
	-	0				-
Caenorhabditis briggsae	krr1 small subunit processome component homolog	6	P:GO:0010171; P:GO:0002119; F:GO:0003723; P:GO:0018991; P:GO:0040007; C:GO:0005634	-		SignalP (SIGNALP)
Brugia malayi	d domain (prokaryotic heat shock protein) family member (dnj-5)	1	F:GO:0005515	-		IPR001623; IPR006162; IPR015609; PTHR11821:SF36 (PANTHER)
Brugia malayi	d domain (prokaryotic heat shock protein) family member (dnj-5)	0		F:GO:0051082; P:GO:0006457; C:GO:0016021; F:GO:0031072		IPR001623; IPR006162; IPR015609; PTHR11821:SF36 (PANTHER), SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	dymeclin isoform 1	5	P:GO:0009792; C:GO:0005737; P:GO:0000003; F:GO:0005515; P:GO:0002119	-		IPR019142; PTHR12895 (PANTHER), PTHR12895:SF2 (PANTHER)
Pan troglodytes	guanylate binding protein interferon-inducible	4	P:GO:0006955; F:GO:0003924; C:GO:0005886; F:GO:0005525	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR003191; PTHR10751 (PANTHER), PTHR10751:SF2 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	4	F:GO:0047750; P:GO:0016125; C:GO:0016021; C:GO:0005783	-	EC:5.3.3.5	SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Hydra magnipapillata	zinc finger lsd1 subclass family protein	0		F:GO:0008061; P:GO:0006030; F:GO:0004872; F:GO:0045735; C:GO:0005576		-
Hydra magnipapillata	alpha beta hydrolase fold-1 domain-containing protein	0				-
Hydra magnipapillata	zinc finger lsd1 subclass family protein	0		C:GO:0005737; P:GO:0007288; F:GO:0004872; F:GO:0045735		-
	-	0				-
	-	0				-
Caenorhabditis brenneri	splicing arginine serine-rich 17a	5	P:GO:0016070; F:GO:0005515; P:GO:0050794; P:GO:0010467; C:GO:0005634	-		PTHR12484 (PANTHER)
Caenorhabditis elegans	ethanolaminephosphotransferase 1	1	F:GO:0016780	-	EC:2.7.8.0	-
Brugia malayi	cation transporting atpase protein isoform partially confirmed by transcript evidence	5	C:GO:0016021; F:GO:0015662; P:GO:0006754; F:GO:0005524; P:GO:0006812	-		IPR001757; PTHR11939:SF54 (PANTHER), SSF81665 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0005506; F:GO:0031418; F:GO:0016705; F:GO:0016702; P:GO:0000003; P:GO:0055114; F:GO:0016491; F:GO:0004656; C:GO:0005783; F:GO:0005488		IPR006620; PTHR10869 (PANTHER), PTHR10869:SF4 (PANTHER)
Caenorhabditis elegans	selenophosphate synthetase	5	P:GO:0007444; F:GO:0004756; P:GO:0016260; P:GO:0008283; F:GO:0005524	-	EC:2.7.9.3	IPR000728; IPR004536; IPR010918; IPR016188; IPR017964; G3DSA:3.30.1330.10 (GENE3D), G3DSA:3.90.650.10 (GENE3D), PTHR10256 (PANTHER)
Brugia malayi	udp-glucose:glycoprotein glucosyltransferase containing protein	1	F:GO:0016740	-		IPR009448; SignalP (SIGNALP)

	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	mitotic phosphoprotein 44	1	P:GO:0006810	-		IPR007846; PTHR21527 (PANTHER), PTHR21527:SF1 (PANTHER), PS51472 (PROFILE), SSF54928 (SUPERFAMILY)
Drosophila pseudoobscura pseudoobscura	serine threonine-protein ki-se grp	15	P:GO:0007348; P:GO:0000003; P:GO:0040010; F:GO:0004672; P:GO:0040011; P:GO:0051225; P:GO:0016321; P:GO:0009792; P:GO:0000077; P:GO:0002119; P:GO:0010171; F:GO:0031151; P:GO:0051299; C:GO:0005634; P:GO:0019538	-		IPR000719; IPR011009; IPR015729; IPR017442; IPR020636; G3DSA:1.10.510.10 (GENE3D)
Harpegnathos saltator	novel protein (zgc:56093)	4	P:GO:0000075; P:GO:0007275; F:GO:0016740; P:GO:0042770	-		IPR000719; IPR011009; IPR015729; IPR017442; IPR020636; G3DSA:1.10.510.10 (GENE3D)
	-	0				-
	-	0				-
Caenorhabditis briggsae	syntaxin 1a	18	P:GO:0008286; F:GO:0005484; P:GO:0007349; P:GO:0040011; P:GO:0007317; C:GO:0016021; P:GO:0006936; P:GO:0006886; P:GO:0007482; P:GO:0016081; P:GO:0031629; F:GO:0042302; P:GO:0042335; P:GO:0019722; P:GO:0007399; C:GO:0005886; P:GO:0040014; P:GO:0000910	-		IPR000727; IPR006011; IPR006012; IPR010989; G3DSA:1.20.58.70 (GENE3D), PTHR19957 (PANTHER), PTHR19957:SF33 (PANTHER)

Caenorhabditis elegans	syntaxin 1a	18	P:GO:0008286; F:GO:0005484; P:GO:0007349; P:GO:0040011; P:GO:0007317; C:GO:0016021; P:GO:0006936; P:GO:0006886; P:GO:0007482; P:GO:0016081; P:GO:0031629; F:GO:0042302; P:GO:0042335; P:GO:0019722; P:GO:0007399; C:GO:0005886; P:GO:0040014; P:GO:0000910	-		SignalP (SIGNALP)
Caenorhabditis briggsae	syntaxin 1a	18	P:GO:0008286; F:GO:0005484; P:GO:0007349; P:GO:0040011; P:GO:0007317; C:GO:0016021; P:GO:0006936; P:GO:0006886; P:GO:0007482; P:GO:0016081; P:GO:0031629; F:GO:0042302; P:GO:0042335; P:GO:0019722; P:GO:0007399; C:GO:0005886; P:GO:0040014; P:GO:0000910	-		SignalP (SIGNALP)
Caenorhabditis elegans	variable abnormal morphology family member (vab-10)	1	F:GO:0003779	-		IPR002017; IPR018159; G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF49 (PANTHER), SSF46966 (SUPERFAMILY)
Brugia malayi	cg15644	0		P:GO:0000003; P:GO:0040035; F:GO:0008270; P:GO:0002119; P:GO:0040007		PTHR21330 (PANTHER), PTHR21330:SF1 (PANTHER), PF11789 (PFAM)
Brugia malayi	5 -nucleotidase	4	F:GO:0008253; F:GO:0005488; P:GO:0046085; C:GO:0005739	-	EC:3.1.3.5	IPR006434; PF05822 (PFAM), SSF56784 (SUPERFAMILY)
	-	0				-

Strongylocentrotus purpuratus	host cell factor 1	9	C:GO:0071339; P:GO:0007049; P:GO:0043254; P:GO:0045449; F:GO:0042802; P:GO:0019046; C:GO:0070688; F:GO:0003713; C:GO:0005737	-		-
	-	0				-
Caenorhabditis briggsae	glutaryl-coenzyme a dehydroge-se	8	F:GO:0004361; F:GO:0000062; C:GO:0005743; P:GO:0055114; F:GO:0005515; P:GO:0019395; F:GO:0050660; P:GO:0046949	-	EC:1.3.99.7	IPR006089; IPR006090; IPR006091; IPR009075; PTHR10909 (PANTHER), PTHR10909:SF10 (PANTHER)
Caenorhabditis elegans	glutaryl-coenzyme a dehydroge-se	9	F:GO:0004361; F:GO:0000062; C:GO:0005743; P:GO:0055114; F:GO:0005515; C:GO:0005759; P:GO:0019395; F:GO:0050660; P:GO:0046949	-	EC:1.3.99.7	IPR006089; IPR006090; IPR006091; IPR006092; IPR009075; IPR009100; IPR013786; PTHR10909 (PANTHER), PTHR10909:SF10 (PANTHER)
Caenorhabditis elegans	uridine phosphorylase 2	4	C:GO:0005737; F:GO:0004850; C:GO:0045098; P:GO:0009116	-	EC:2.4.2.3	IPR000845; IPR010059; IPR018017; G3DSA:3.40.50.1580 (GENE3D), SSF53167 (SUPERFAMILY)
Caenorhabditis elegans	vacuolar protein sorting-associated protein 45	8	C:GO:0000139; P:GO:0002119; P:GO:0018996; P:GO:0000003; P:GO:0051649; P:GO:0006898; C:GO:0010008; P:GO:0015031	-		-
Caenorhabditis elegans	hed family member (ptc-3)	8	P:GO:0009792; P:GO:0002119; F:GO:0008158; P:GO:0040018; P:GO:0018996; P:GO:0000003; P:GO:0040011; C:GO:0016021	-		IPR003392; PTHR10796 (PANTHER), PTHR10796:SF34 (PANTHER), SSF82866 (SUPERFAMILY)
Caenorhabditis briggsae	temporarily assigned gene -me family member (tag-51)	0				-
Caenorhabditis elegans	r- binding motif protein 7	3	P:GO:0002119; F:GO:0005488; P:GO:0040010	-		IPR000504; IPR012677; PTHR13798 (PANTHER), SSF54928 (SUPERFAMILY)
Loa loa	prefoldin subunit 4	0		F:GO:0051082; P:GO:0006457; C:GO:0016272		IPR002777; G3DSA:1.10.287.370 (GENE3D), PTHR21100 (PANTHER), PTHR21100:SF3 (PANTHER)
	-	0				-

Caenorhabditis briggsae	reactive oxygen species modulator 1	6	P:GO:0001302; P:GO:0008284; P:GO:0010670; P:GO:0034614; C:GO:0016020; C:GO:0005739	-		-
Brugia malayi	protein tyrosine non-receptor type 11	27	P:GO:0048011; F:GO:0004725; P:GO:0046825; P:GO:0035265; P:GO:0042445; P:GO:0007409; P:GO:0009755; F:GO:0043274; P:GO:0046676; C:GO:0005829; P:GO:0046887; F:GO:0019904; P:GO:0048609; F:GO:0043560; P:GO:0051463; P:GO:0009967; C:GO:0043234; P:GO:0006470; P:GO:0060125; P:GO:0006641; F:GO:0051428; P:GO:0040014; C:GO:0005625; P:GO:0000187; F:GO:0005158; P:GO:0042593; C:GO:0005739	-	EC:3.1.3.48	IPR000242; IPR000980; G3DSA:3.90.190.10 (GENE3D), PTHR19134 (PANTHER), PTHR19134:SF64 (PANTHER), SSF52799 (SUPERFAMILY), SSF55550 (SUPERFAMILY)
Loa loa	cation transport regulator-like protein 2	0		F:GO:0003674; P:GO:0008150; C:GO:0005575		IPR006840
	-	0				-
Caenorhabditis briggsae	ribosome biogenesis protein bop1	10	P:GO:0040010; P:GO:0051726; C:GO:0070545; P:GO:0040035; P:GO:0000463; P:GO:0002119; F:GO:0005515; P:GO:0006898; C:GO:0005654; P:GO:0009792	-		IPR001680; IPR011046; IPR012953; IPR015943; IPR017986; IPR018087; IPR019781; IPR019782; PTHR17605 (PANTHER)
Caenorhabditis elegans	chch domain containing protein	0				IPR010625
Brugia malayi	ankyrin repeat domain-containing protein 13c	0				IPR021832; PTHR12447 (PANTHER)
Haemonchus contortus	modulation of locomotion defective family member (mod-1)	5	C:GO:0016021; C:GO:0030054; C:GO:0045211; F:GO:0005230; P:GO:0006811	-		IPR006028; IPR006029; IPR006201; IPR006202; IPR018000; G3DSA:1.20.120.370 (GENE3D), PTHR18945:SF13 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				SignalP (SIGNALP)

Caenorhabditis briggsae	hect domain and rld 4	4	F:GO:0016874; C:GO:0005622; P:GO:0000003; P:GO:0009987	-		IPR000569; PTHR11254 (PANTHER), PTHR11254:SF8 (PANTHER)
Caenorhabditis elegans	rap guanine nucleotide exchange factor 6	4	F:GO:0005085; C:GO:0005622; P:GO:0051056; F:GO:0005515	-		IPR000595; IPR014710; IPR018490; SignalP (SIGNALP)
	-	0				IPR000488; IPR011029
Homo sapiens	hCG1989828 [Homo sapiens]	0				-
	-	0				-
Caenorhabditis elegans	cleavage and polyadenylation specific factor isoform cra_a	3	C:GO:0005654; F:GO:0003723; P:GO:0006397	-		PTHR10644 (PANTHER), PTHR10644:SF2 (PANTHER)
	-	0				PTHR13902 (PANTHER), PTHR13902:SF12 (PANTHER)
	-	0				-
Caenorhabditis elegans	metallophosphoesterase domain-containing	2	F:GO:0005515; F:GO:0016787	-		-
Ancylostoma caninum	venom-allergen-like protein family member (vap-1)	1	P:GO:0040011	-		IPR001283; IPR014044; PTHR10334:SF11 (PANTHER)
Brugia malayi	hypothetical protein Bm1_07715 [Brugia malayi]	0				-
	-	0				-
Loa loa	vacuolar protein sorting 37b	0		C:GO:0031902; C:GO:0016020; C:GO:0005768; P:GO:0015031		-
Caenorhabditis elegans	28s ribosomal protein mitochondrial precursor	2	C:GO:0044444; C:GO:0043229	-		SignalP (SIGNALP)
Brugia malayi	mediator of r- polymerase ii transcription subunit 10	10	P:GO:0040010; P:GO:0006357; P:GO:0040035; F:GO:0016455; P:GO:0002119; P:GO:0040017; P:GO:0040039; C:GO:0016592; P:GO:0002009; P:GO:0009792	-		IPR019145; PTHR13345 (PANTHER), PTHR13345:SF2 (PANTHER)
Brugia malayi	speckle-type poz protein	3	P:GO:0000003; P:GO:0006397; F:GO:0005515	-		IPR000210; IPR011333; IPR013069; IPR013089; PTHR23230:SF94 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-cpg-4 protein	0				SignalP (SIGNALP)
Caenorhabditis elegans	animal haem peroxidase family protein	0		P:GO:0055114; F:GO:0020037; P:GO:0006979; F:GO:0004601		-
	-	0				-
Caenorhabditis elegans	af316599_1 paracaspase	0		P:GO:0000003; P:GO:0006508; F:GO:0005515; F:GO:0004197		-
Caenorhabditis elegans	af316599_1 paracaspase	0		P:GO:0000003; P:GO:0006508; F:GO:0005515; F:GO:0004197		IPR007110; IPR013783; PTHR22576 (PANTHER), PTHR22576:SF1 (PANTHER), SSF48726 (SUPERFAMILY)
Xenopus (Silurana) tropicalis	loc779458 protein	0				-

Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
Brugia malayi	estrogen receptor binding site associated antigen 9-like	0				IPR008610; SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-lpd-6 protein	0				PTHR12661 (PANTHER), PTHR12661:SF1 (PANTHER)
Brugia malayi	briggsae cbr-mdt-17 protein	0				-
	-	0				-
Loa loa	c1orf149 homolog	1	P:GO:0009987	-		IPR015418; PTHR13476 (PANTHER)
Loa loa	c1orf149 homolog	1	P:GO:0009987	-		IPR015418; PTHR13476 (PANTHER)
Caenorhabditis elegans	map ki-se activating protein c22orf5	1	F:GO:0016301	-		IPR005178; PTHR23423:SF2 (PANTHER)
Caenorhabditis elegans	map ki-se activating protein c22orf5	1	F:GO:0016301	-		IPR005178; PTHR23423:SF2 (PANTHER)
Caenorhabditis elegans	map ki-se activating protein c22orf5	1	F:GO:0016301	-		IPR005178; PTHR23423:SF2 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	F:GO:0003677	-		IPR003656
Caenorhabditis elegans	polybromodomain protein	10	P:GO:0009987; P:GO:0040010; F:GO:0005488; C:GO:0005622; P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0040011; P:GO:0002009; P:GO:0009792	-		IPR001487; PTHR10799 (PANTHER), PTHR10799:SF76 (PANTHER)
Loa loa	molecular chaperone	0		F:GO:0005216; P:GO:0006816; C:GO:0016021; C:GO:0016020; F:GO:0032440; P:GO:0006811; P:GO:0006810; F:GO:0031072; P:GO:0055114; F:GO:0005262; F:GO:0016491; P:GO:0055085; F:GO:0005488		IPR002110; IPR020683; PTHR18958 (PANTHER), PTHR18958:SF298 (PANTHER)
Caenorhabditis elegans	n-acetylglucosaminyl-phosphatidylinositol de-n-acetylase	0		F:GO:0000225; F:GO:0016787		IPR003737; G3DSA:3.40.50.10320 (GENE3D), PTHR12993:SF2 (PANTHER), SignalP (SIGNALP), SSF102588 (SUPERFAMILY)
Caenorhabditis elegans	sulfide quinone reductase	1	C:GO:0005743	-		IPR015904; G3DSA:3.50.50.60 (GENE3D), SSF51905 (SUPERFAMILY)
Loa loa	transportin 3	1	F:GO:0005515	-		IPR016024; PTHR12363 (PANTHER), PTHR12363:SF5 (PANTHER), SignalP (SIGNALP)

Caenorhabditis elegans	polymerase i polypeptide 30kda	7	F:GO:0003899; C:GO:0005654; F:GO:0016757; F:GO:0003677; C:GO:0005736; F:GO:0046983; P:GO:0006360	-	EC:2.7.7.6	IPR011261; IPR011262; IPR011263; G3DSA:3.30.1360.10 (GENE3D), PTHR11800 (PANTHER), PTHR11800:SF13 (PANTHER)
Loa loa	ran binding protein 17	4	F:GO:0005488; P:GO:0055085; P:GO:0006886; C:GO:0005634	-		-
Caenorhabditis elegans	rho gtpase activating protein 1	5	F:GO:0005100; C:GO:0043231; P:GO:0007264; C:GO:0005813; F:GO:0005515	-		IPR000198; IPR001251; IPR008936; PTHR23176 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0043169; F:GO:0016787; P:GO:0016998; P:GO:0005975; F:GO:0003824; P:GO:0008340; F:GO:0005515; P:GO:0009253; P:GO:0008152; F:GO:0003796; F:GO:0016798		PTHR23208 (PANTHER), PTHR23208:SF13 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0		F:GO:0043169; F:GO:0016787; P:GO:0016998; P:GO:0005975; F:GO:0003824; P:GO:0008340; F:GO:0005515; P:GO:0009253; P:GO:0008152; F:GO:0003796; F:GO:0016798		PTHR23208 (PANTHER), PTHR23208:SF13 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		IPR013781; IPR017853; PTHR23208 (PANTHER), PTHR23208:SF13 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		IPR013781; IPR017853; PTHR23208 (PANTHER), PTHR23208:SF13 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	ubiquitin carboxyl-termi-l hydrolase family protein	0		F:GO:0016787; F:GO:0008234; F:GO:0008233; F:GO:0004221; P:GO:0006511		-
Caenorhabditis elegans	ubiquitin carboxyl-termi-l hydrolase family protein	0		F:GO:0016787; F:GO:0008234; F:GO:0008233; F:GO:0004221; P:GO:0006511		-
	-	0				-
	-	0				-

Caenorhabditis elegans	dihydropyrimidine dehydroge-se	17	C:GO:0005829; F:GO:0004158; P:GO:0006145; P:GO:0006212; F:GO:0046872; P:GO:0055114; F:GO:0009055; F:GO:0017113; F:GO:0051539; P:GO:0006222; P:GO:0006210; F:GO:0042803; F:GO:0050660; P:GO:0006207; F:GO:0050661; P:GO:0006214; F:GO:0010181	-	EC:1.3.3.1; EC:1.3.1.2	IPR012135; IPR013785; IPR017896; IPR017900; G3DSA:3.30.70.20 (GENE3D), PTHR11938 (PANTHER), PTHR11938:SF6 (PANTHER), SSF51395 (SUPERFAMILY), SSF54862 (SUPERFAMILY)
Loa loa	r- polymerase ii 140kd subunit	10	F:GO:0003899; P:GO:0040010; P:GO:0008340; P:GO:0000003; C:GO:0005665; F:GO:0003677; P:GO:0002119; F:GO:0032549; P:GO:0009792; P:GO:0006366	-	EC:2.7.7.6	IPR007642; IPR007644; IPR015712; G3DSA:3.90.1100.10 (GENE3D), PTHR20856:SF1 (PANTHER), SSF64484 (SUPERFAMILY)
Caenorhabditis elegans	cholinergic receptor nicotinic alpha polypeptide 1	6	F:GO:0004872; C:GO:0045211; C:GO:0030054; P:GO:0006811; C:GO:0016021; F:GO:0004889	-		-
	-	0				-
	-	0				-
Angiostrongylus cantonensis	myelin transcription factor 1-like	0				PD120929 (PRODOM)
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	udp-glucose:glycoprotein glucosyltransferase containing protein	6	F:GO:0003980; C:GO:0005788; C:GO:0005793; P:GO:0051084; P:GO:0006486; F:GO:0051082	-		IPR009448; G3DSA:3.90.550.10 (GENE3D), SSF53448 (SUPERFAMILY)
Caenorhabditis briggsae	yo85_caeel ame: full=uncharacterized protein	1	P:GO:0009792	-		PD131032 (PRODOM)
Caenorhabditis elegans	swi snf matrix actin dependent regulator of subfamily a-like 1	13	F:GO:0003678; P:GO:0001525; P:GO:0051216; P:GO:0006357; F:GO:0003676; P:GO:0006259; P:GO:0022402; P:GO:0030097; P:GO:0048589; F:GO:0000166; F:GO:0008094; P:GO:0010172; C:GO:0005634	-		IPR000330; IPR001650; IPR003593; IPR010003; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10799 (PANTHER), PTHR10799:SF43 (PANTHER), SSF52540 (SUPERFAMILY)

Caenorhabditis elegans	swi snf matrix actin dependent regulator of subfamily a-like 1	13	F:GO:0003678; P:GO:0001525; P:GO:0051216; P:GO:0006357; F:GO:0003676; P:GO:0006259; P:GO:0022402; P:GO:0030097; P:GO:0048589; F:GO:0000166; F:GO:0008094; P:GO:0010172; C:GO:0005634	-		IPR000330; IPR001650; IPR003593; IPR010003; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10799 (PANTHER), PTHR10799:SF43 (PANTHER), SSF52540 (SUPERFAMILY)
	succi-te dehydroge-se	13	P:GO:0006810; P:GO:0006105; F:GO:0048039; F:GO:0051537; C:GO:0005749; F:GO:0046872; F:GO:0009055; P:GO:0006099; F:GO:0051539; F:GO:0051538; P:GO:0022904; F:GO:0005515; F:GO:0008177	-	EC:1.3.5.1	IPR001041; IPR004489; IPR006058; IPR009051; IPR012285; IPR012675; PTHR11921 (PANTHER)
	succi-te dehydroge-se	13	P:GO:0006810; P:GO:0006105; F:GO:0048039; F:GO:0051537; C:GO:0005749; F:GO:0046872; F:GO:0009055; P:GO:0006099; F:GO:0051539; F:GO:0051538; P:GO:0022904; F:GO:0005515; F:GO:0008177	-	EC:1.3.5.1	-
Caenorhabditis briggsae	briggsae cbr-sdhb-1 protein	12	P:GO:0006810; C:GO:0005875; F:GO:0048039; F:GO:0051537; C:GO:0005749; F:GO:0046872; F:GO:0009055; P:GO:0006099; F:GO:0051539; F:GO:0051538; P:GO:0006121; F:GO:0008177	-	EC:1.3.5.1	-

Caenorhabditis briggsae	apical junction molecule family member (ajm-1)	8	P:GO:0009792; C:GO:0043296; P:GO:0045216; F:GO:0008092; C:GO:0005913; P:GO:0040010; P:GO:0040011; F:GO:0008270	-		-
Caenorhabditis elegans	peroxin-3 family protein	0		P:GO:0040010; C:GO:0005779; P:GO:0007031		-
Caenorhabditis briggsae	ribosomal protein l14p l23e containing protein	3	P:GO:0009792; P:GO:0000003; C:GO:0030529	-		-
	-	0				-
Loa loa	frap-related protein	4	F:GO:0016772; F:GO:0005515; P:GO:0044237; P:GO:0006974	-		IPR000276; IPR003151; IPR014009
Loa loa	phosphatidylinositol 3- and 4-ki-se family protein	8	P:GO:0044260; F:GO:0016772; F:GO:0005515; C:GO:0016020; P:GO:0006974; P:GO:0044238; C:GO:0043229; P:GO:0065007	-		IPR000276; IPR003151; IPR014009
Loa loa	coronin 2a	1	C:GO:0017053	-		IPR015049; IPR015505; IPR015943; SSF101908 (SUPERFAMILY)
Loa loa	coronin 2a	1	C:GO:0017053	-		IPR015049; IPR015505; IPR015943; SSF101908 (SUPERFAMILY)
Caenorhabditis elegans	vitellogenin receptor	5	F:GO:0005488; C:GO:0005615; P:GO:0050794; P:GO:0008152; C:GO:0044464	-		-
Myxicola infundibulum	intermediate filament	0		P:GO:0051258; C:GO:0005882; F:GO:0005102; F:GO:0005198; P:GO:0007165; F:GO:0030674; C:GO:0005577; P:GO:0030168		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	3	P:GO:0055085; C:GO:0016021; F:GO:0005215	-		IPR000390; IPR005828; IPR005829; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11600 (PANTHER), PTHR11600:SF27 (PANTHER)
Caenorhabditis elegans	gamma-tubulin interacting protein family member (gip-1)	1	P:GO:0000226	-		-
Caenorhabditis briggsae	Hypothetical protein CBG16936 [Caenorhabditis briggsae]	0				IPR000436; IPR016060; PTHR19325 (PANTHER), PTHR19325:SF25 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-

Loa loa	dual specificity phosphatase 22	2	P:GO:0006796; F:GO:0004721	-	EC:3.1.3.16	IPR000340; IPR000387; IPR016130; IPR020422; G3DSA:3.90.190.10 (GENE3D), PTHR10159 (PANTHER), SSF52799 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	protein ki-se domain containing protein	3	P:GO:0009987; P:GO:0050896; P:GO:0019915	-		-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG16326 [Caenorhabditis briggsae]	0				-
	-	0				-
Monodelphis domestica	cellulosomal scaffoldin anchoring	0				-
Monodelphis domestica	cellulosomal scaffoldin anchoring	0				-
	-	0				-
Nematostella vectensis	protein	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	uncoordi-ted family member (unc-87)	1	F:GO:0005515	-		IPR000557; PTHR18959 (PANTHER)
Homo sapiens	prosaposin	19	P:GO:0055085; F:GO:0008047; P:GO:0043065; P:GO:0006687; P:GO:0045161; C:GO:0016021; C:GO:0005743; C:GO:0043202; C:GO:0005615; F:GO:0008289; P:GO:0006869; F:GO:0005515; P:GO:0009966; P:GO:0007585; F:GO:0005319; C:GO:0005578; F:GO:0005529; P:GO:0006919; C:GO:0005794	-		SignalP (SIGNALP)
Caenorhabditis elegans	small subunit processome component 20 homolog	3	F:GO:0005488; C:GO:0031981; P:GO:0006364	-		IPR016024; PTHR17695 (PANTHER)
	-	0				-
Caenorhabditis briggsae	bzip transcription factor family protein	3	C:GO:0043231; P:GO:0045449; F:GO:0003677	-		IPR004827; IPR008917; IPR011616; G3DSA:1.20.5.170 (GENE3D), PTHR22952 (PANTHER), PTHR22952:SF6 (PANTHER)
Caenorhabditis briggsae	bzip transcription factor family protein	3	C:GO:0043231; P:GO:0045449; F:GO:0003677	-		IPR004827; IPR008917; IPR011616; G3DSA:1.20.5.170 (GENE3D), PTHR22952 (PANTHER), PTHR22952:SF6 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				IPR003582; PTHR21724 (PANTHER)
Saccoglossus kowalevskii	r--directed d- polymerase (reverse transcriptase)	3	F:GO:0003723; F:GO:0003964; P:GO:0006278	-	EC:2.7.7.49	IPR000477; IPR015706; PTHR19446:SF101 (PANTHER)
Caenorhabditis elegans	tb2 hva22 family protein	0		F:GO:0004872; F:GO:0005515		IPR004345; PTHR12300:SF13 (PANTHER)

	-	0				SignalP (SIGNALP)
Brugia malayi	iws1 c-terminus family protein	4	P:GO:0006351; F:GO:0003676; P:GO:0000003; C:GO:0005634	-		IPR017923
Brugia malayi	iws1 c-terminus family protein	3	P:GO:0006351; F:GO:0003676; C:GO:0005634	-		IPR017923
Caenorhabditis elegans	sft2 domain containing 2	1	P:GO:0006810	-		IPR007305; IPR011691
Caenorhabditis elegans	sft2 domain containing 2	1	P:GO:0006810	-		IPR007305; IPR011691
Caenorhabditis elegans	sy-ptotagmin ix	4	C:GO:0016021; C:GO:0008021; P:GO:0006810; F:GO:0005215	-		IPR000008; IPR001565; IPR008973; IPR018029; IPR020477; G3DSA:2.60.40.150 (GENE3D), PTHR10024 (PANTHER), PTHR10024:SF41 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	d-j homolog subfamily c member 25	2	C:GO:0016021; F:GO:0031072	-		IPR001623; IPR015609; IPR018253; PTHR11821:SF28 (PANTHER)
Angiostrongylus cantonensis	dynein heavy chain	8	P:GO:0007018; C:GO:0030286; F:GO:0016887; C:GO:0005794; F:GO:0005515; F:GO:0005524; C:GO:0005829; F:GO:0003777	-		IPR004273; PTHR10676 (PANTHER), PTHR10676:SF28 (PANTHER)
	-	0				-
Caenorhabditis elegans	potential d--binding protein c17orf49 homolog	1	F:GO:0005515	-		PTHR21397 (PANTHER)
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis briggsae	briggsae cbr-snf-1 protein	3	C:GO:0016021; P:GO:0006810; F:GO:0015293	-		IPR000175; PTHR11616:SF12 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	bed-type zinc finger transcription factor family member (bed-2)	2	F:GO:0005515; F:GO:0003677	-		PTHR21709 (PANTHER)
Caenorhabditis elegans	briggsae cbr-elo-2 protein	2	C:GO:0016021; P:GO:0007283	-		IPR002076
Caenorhabditis elegans	briggsae cbr-elo-2 protein	2	C:GO:0016021; P:GO:0007283	-		IPR002076
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				IPR001910; IPR023186
Caenorhabditis briggsae	5 - cytosolic iii	5	F:GO:0008253; P:GO:0055086; F:GO:0008665; F:GO:0005488; C:GO:0005783	-	EC:3.1.3.5	IPR006434; PF05822 (PFAM), SSF56784 (SUPERFAMILY)
Caenorhabditis elegans	phosphoribosylformylglyci-midine synthase	4	P:GO:0040010; P:GO:0009168; F:GO:0005515; F:GO:0004642	-	EC:6.3.5.3	IPR010918; IPR016188; PTHR10099 (PANTHER)
Caenorhabditis briggsae	potassium channel tetramerisation domain containing 8	4	C:GO:0005886; F:GO:0005515; P:GO:0006813; F:GO:0005216	-		IPR003131; IPR011333; PTHR14499 (PANTHER), PTHR14499:SF9 (PANTHER)

	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-smgl-2 protein	2	F:GO:0005488; F:GO:0016787	-		IPR011709
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	jmjc domain-containing protein 8	0		F:GO:0003674; P:GO:0008150		IPR003347; IPR014710; IPR022777; PTHR12480 (PANTHER), SSF51197 (SUPERFAMILY)
Caenorhabditis briggsae	yqvw_caeel ame: full=uncharacterized protein	1	P:GO:0040011	-		-
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG18919 [Caenorhabditis briggsae]	4	F:GO:0005488; P:GO:0040010; P:GO:0040011; P:GO:0001703	-		IPR015880
Brugia malayi	riken cd- 2310021p13 gene	0		F:GO:0046872; F:GO:0003674; P:GO:0008150; F:GO:0008270		IPR007527; PTHR22619 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG13933 [Caenorhabditis briggsae]	2	P:GO:0040010; P:GO:0006898	-		IPR013136
Caenorhabditis briggsae	Hypothetical protein CBG13933 [Caenorhabditis briggsae]	2	P:GO:0040010; P:GO:0006898	-		IPR013136
Caenorhabditis briggsae	upstream of 140	1	P:GO:0000003	-		PTHR13002 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				SignalP (SIGNALP)

Caenorhabditis elegans	-+ k+ alpha 1 polypeptide	28	F:GO:0043548; P:GO:0045989; P:GO:0045822; F:GO:0003869; P:GO:0015988; C:GO:0005792; C:GO:0016323; C:GO:0042470; F:GO:0043531; F:GO:0031402; P:GO:0006754; F:GO:0019904; C:GO:0042383; F:GO:0005391; P:GO:0045823; P:GO:0042493; P:GO:0031947; C:GO:0005768; P:GO:0010107; P:GO:0016311; C:GO:0005890; P:GO:0002026; C:GO:0005901; P:GO:0006200; F:GO:0005524; P:GO:0008217; F:GO:0030955	-	EC:3.1.3.41; EC:3.6.3.9	IPR001757; IPR008250; G3DSA:1.20.1110.10 (GENE3D), PTHR11939:SF100 (PANTHER)
Brugia malayi	surfeit locus protein 5 containing protein	12	P:GO:0040010; P:GO:0006357; P:GO:0040035; F:GO:0016455; P:GO:0010171; P:GO:0002119; F:GO:0005515; P:GO:0040017; P:GO:0006898; C:GO:0016592; P:GO:0009792; P:GO:0040018	-		IPR009332; PTHR12434:SF2 (PANTHER), PF06179 (PFAM)
Caenorhabditis briggsae	actin-related protein 2 3 complex subunit 1a	9	P:GO:0030833; C:GO:0005885; P:GO:0040010; P:GO:0000003; P:GO:0002119; F:GO:0003779; P:GO:0040011; P:GO:0009792; P:GO:0040018	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR10709 (PANTHER), PTHR10709:SF6 (PANTHER)
Caenorhabditis briggsae	cell differentiation protein rcd1 homolog	5	P:GO:0019221; P:GO:0045449; F:GO:0005515; P:GO:0007548; C:GO:0005634	-		IPR007216; IPR011989
Caenorhabditis elegans	yrrc_caeel ame: full=uncharacterized protein	0				PTHR21824 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)

Loa loa	zinc matrin type 2	4	P:GO:0019915; F:GO:0003676; C:GO:0005634; F:GO:0008270	-		IPR000690; IPR003604; IPR007087; IPR015880; IPR022755; SSF57667 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	protein disulfide isomerase associated 3	10	F:GO:0004629; F:GO:0003756; P:GO:0043065; P:GO:0006606; P:GO:0045454; F:GO:0004197; C:GO:0005788; F:GO:0005515; P:GO:0007165; P:GO:0006621	-	EC:5.3.4.1; EC:3.4.22.0	IPR005746; IPR012335; IPR012336; IPR013766; IPR017936; IPR017937; PTHR18929 (PANTHER)
Brugia malayi	prostaglandin reductase 2	3	P:GO:0055114; F:GO:0016491; F:GO:0008270	-		IPR002085; IPR011032; G3DSA:3.90.180.10 (GENE3D), PTHR11695:SF5 (PANTHER)
Caenorhabditis briggsae	coiled-coil domain containing 132	0				IPR019514; PTHR13258 (PANTHER)
Ancylostoma caninum	venom allergen antigen-like protein 1	0		P:GO:0040011; C:GO:0005576		IPR001283; IPR002413; IPR013032; IPR014044; IPR018244; PTHR10334:SF11 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Caenorhabditis elegans	cbp p300 homolog family member (cbp-1)	27	P:GO:0006915; P:GO:0010035; C:GO:0032991; F:GO:0046872; P:GO:0007283; P:GO:0018076; P:GO:0040039; F:GO:0008013; P:GO:0040010; P:GO:0008340; P:GO:0001666; P:GO:0032270; F:GO:0003713; P:GO:0045944; P:GO:0010033; P:GO:0043967; C:GO:0005737; P:GO:0040026; P:GO:0007399; P:GO:0009792; F:GO:0003677; P:GO:0018996; P:GO:0040035; P:GO:0010171; F:GO:0004402; C:GO:0005730; P:GO:0051091	-	EC:2.3.1.48	IPR000197; PTHR13808 (PANTHER)

Caenorhabditis elegans	cbp p300 homolog family member (cbp-1)	13	P:GO:0008340; P:GO:0040010; F:GO:0003712; P:GO:0040026; P:GO:0007283; P:GO:0018996; C:GO:0005737; P:GO:0040039; P:GO:0009792; P:GO:0010171; P:GO:0045944; C:GO:0005634; P:GO:0040035	-		IPR000197; PTHR13808 (PANTHER)
Caenorhabditis elegans	defective p granules and sterile family member (deps-1)	0				-
Loa loa	dynein heavy chain	2	F:GO:0017111; F:GO:0000166	-	EC:3.6.1.15	IPR013594; PTHR10676 (PANTHER), PTHR10676:SF4 (PANTHER)
Caenorhabditis elegans	novel protein	2	F:GO:0005515; P:GO:0009890	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	Hypothetical protein CBG14775 [Caenorhabditis briggsae]	0				-
	-	0				-
Loa loa	elegans protein partially confirmed by transcript evidence	5	F:GO:0005488; P:GO:0006520; F:GO:0008483; P:GO:0019915; F:GO:0016846	-	EC:2.6.1.0	IPR004839; IPR015421; IPR015422; IPR015424; PTHR11751 (PANTHER), PTHR11751:SF38 (PANTHER)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0006629; C:GO:0016021; F:GO:0016787; F:GO:0004806		IPR002921; G3DSA:3.40.50.1820 (GENE3D), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
Caenorhabditis brenneri	propionyl coenzyme a carboxylase beta subunit family member (pccb-1)	1	F:GO:0005515	-		PS51257 (PROFILE)
Caenorhabditis elegans	f-box and leucine-rich repeat protein 11	9	P:GO:0016568; F:GO:0051864; F:GO:0046872; P:GO:0055114; P:GO:0045449; P:GO:0000003; F:GO:0016702; C:GO:0005634; P:GO:0006974	-	EC:1.14.11.27; EC:1.13.11.0	-
Caenorhabditis elegans	threonine dehydroge-se	6	P:GO:0006694; F:GO:0003854; P:GO:0045226; F:GO:0003978; F:GO:0050662; F:GO:0008831	-	EC:1.1.1.145; EC:5.1.3.2; EC:1.1.1.133	IPR001509; IPR016040; PTHR10366 (PANTHER), PTHR10366:SF12 (PANTHER), SSF51735 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis briggsae	Hypothetical protein CBG22835 [Caenorhabditis briggsae]	0		F:GO:0046872; P:GO:0055114; F:GO:0009055; F:GO:0016491; F:GO:0020037; F:GO:0005506; F:GO:0004497		-

Caenorhabditis briggsae	Hypothetical protein CBG14902 [Caenorhabditis briggsae]	6	P:GO:0010171; P:GO:0040018; P:GO:0018991; P:GO:0040017; P:GO:0040010; P:GO:0007413	-		-
	-	0				-
Caenorhabditis elegans	prolyl carboxy peptidase like family member (pcp-3)	2	F:GO:0005515; F:GO:0070011	-		IPR008758; PTHR11010:SF4 (PANTHER)
Caenorhabditis briggsae	prolyl carboxy peptidase like family member (pcp-3)	2	F:GO:0005515; F:GO:0070011	-		IPR008758; PTHR11010:SF4 (PANTHER)
Caenorhabditis briggsae	myosin heavy chain	4	C:GO:0032982; F:GO:0003779; F:GO:0005524; F:GO:0003774	-		IPR002928; IPR015650; PTHR13140 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis briggsae	acetyl- acetyltransferase	4	P:GO:0010171; F:GO:0008415; P:GO:0040011; P:GO:0008152	-		IPR002155; IPR016038; IPR016039; IPR020616
	-	0				-
Caenorhabditis briggsae	glutamate synthase	10	F:GO:0045181; P:GO:0040010; F:GO:0051536; P:GO:0055114; P:GO:0006537; P:GO:0002119; F:GO:0050660; P:GO:0009792; F:GO:0010181; F:GO:0005506	-		-
Caenorhabditis elegans	hypothetical protein F49C12.15 [Caenorhabditis elegans]	0				-
Brugia malayi	ring and yy1 binding protein	2	C:GO:0005622; F:GO:0008270	-		-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	serine palmitoyltransferase	1	F:GO:0016740	-		PTHR13693 (PANTHER), PTHR13693:SF3 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	uncharacterized protein c12orf4	0				IPR019311
	-	0				SignalP (SIGNALP)

Rattus norvegicus	aminoadipate-semialdehyde dehydroge-se	0		F:GO:0016874; P:GO:0006629; F:GO:0000036; P:GO:0006810; F:GO:0000166; F:GO:0005524; F:GO:0003674; P:GO:0055114; F:GO:0031177; F:GO:0016491; F:GO:0003824; C:GO:0005575; F:GO:0048037; P:GO:0008152; P:GO:0008150; F:GO:0004043		IPR011047
	-	0				-
Caenorhabditis briggsae	briggsae cbr-oct-2 protein	4	P:GO:0019915; C:GO:0016021; P:GO:0055085; F:GO:0005215	-		-
Brugia malayi	replication protein a 70 kda d--binding subunit	3	P:GO:0009987; F:GO:0005515; C:GO:0005634	-		IPR004365; IPR012340; IPR016027; PTHR23273 (PANTHER)
Acyrthosiphon pisum	briggsae cbr-spt-5 protein	1	P:GO:0007275	-		-
Caenorhabditis elegans	atp-dependent d- helicase pif1	2	F:GO:0005488; F:GO:0017111	-	EC:3.6.1.15	IPR010285; PTHR23274 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	glioma tumor suppressor candidate region gene 2	4	P:GO:0000003; P:GO:0040007; P:GO:0006898; P:GO:0002119	-		IPR011687; PTHR14211:SF6 (PANTHER)
Caenorhabditis elegans	glioma tumor suppressor candidate region gene 2	4	P:GO:0000003; P:GO:0040007; P:GO:0006898; P:GO:0002119	-		IPR011687; PTHR14211:SF6 (PANTHER)
Caenorhabditis elegans	glioma tumor suppressor candidate region gene 2	4	P:GO:0000003; P:GO:0040007; P:GO:0006898; P:GO:0002119	-		IPR011687; PTHR14211:SF6 (PANTHER)
	-	0				-
Caenorhabditis briggsae	histone acetyltransferase type b catalytic subunit	4	P:GO:0044238; F:GO:0016747; P:GO:0044260; P:GO:0009792	-	EC:2.3.1.0	IPR016181; PTHR12046 (PANTHER)
Caenorhabditis sp. PS1010	briggsae cbr-cdh-4 protein	7	P:GO:0007411; P:GO:0007163; P:GO:0007155; P:GO:0007413; P:GO:0048513; C:GO:0016323; P:GO:0048546	-		IPR002126; IPR015919; IPR020894; PTHR10596 (PANTHER), PTHR10596:SF74 (PANTHER)
Ciona intestinalis	uncharacterized transposase-like protein	0		F:GO:0046872; P:GO:0055114; F:GO:0009055; F:GO:0016491; F:GO:0020037; F:GO:0005506; F:GO:0004497		IPR007087; IPR015880

Caenorhabditis briggsae	cerebral endothelial cell adhesion molecule 1	8	P:GO:0009103; P:GO:0040010; P:GO:0040035; F:GO:0005515; P:GO:0040011; P:GO:0002009; F:GO:0016757; C:GO:0005783	-		IPR002654; PTHR10730 (PANTHER)
Caenorhabditis elegans	isoform cra_a	0		P:GO:0055114; P:GO:0006099; C:GO:0005576; F:GO:0008924		IPR019443; PTHR15678 (PANTHER)
Haemonchus contortus	ilin (drosophila ecm protein) homolog family member (ppn-1)	5	F:GO:0004222; F:GO:0004867; C:GO:0005578; F:GO:0008270; F:GO:0005515	-	EC:3.4.24.0	IPR000884; G3DSA:2.20.100.10 (GENE3D), PTHR13723 (PANTHER), PTHR13723:SF18 (PANTHER)
Loa loa	family with sequence similarity member a	2	C:GO:0005622; F:GO:0005515	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	F:GO:0005515; F:GO:0008233	-		IPR006150; PTHR10083 (PANTHER), PTHR10083:SF21 (PANTHER)
	-	0				-
Caenorhabditis elegans	eukaryotic translation initiation factor 3 subunit m	8	F:GO:0003743; P:GO:0006413; C:GO:0008180; C:GO:0005852; P:GO:0030154; F:GO:0005515; P:GO:0007275; P:GO:0048477	-		IPR000717; IPR011991; PTHR15350 (PANTHER), PTHR15350:SF3 (PANTHER), SSF46785 (SUPERFAMILY)
Caenorhabditis elegans	eukaryotic translation initiation factor 3 subunit m	8	F:GO:0003743; P:GO:0006413; C:GO:0008180; C:GO:0005852; P:GO:0030154; F:GO:0005515; P:GO:0007275; P:GO:0048477	-		IPR000717; IPR011991; PTHR15350 (PANTHER), PTHR15350:SF3 (PANTHER), SSF46785 (SUPERFAMILY)
Caenorhabditis elegans	dendritic cell protein	9	P:GO:0009987; C:GO:0043231; C:GO:0043234; P:GO:0000003; P:GO:0032501; C:GO:0044446; F:GO:0005515; C:GO:0044444; P:GO:0032502	-		IPR000717; PTHR15350 (PANTHER), PTHR15350:SF3 (PANTHER), SSF46785 (SUPERFAMILY)
Caenorhabditis elegans	dendritic cell protein	9	P:GO:0009987; C:GO:0043231; C:GO:0043234; P:GO:0000003; P:GO:0032501; C:GO:0044446; F:GO:0005515; C:GO:0044444; P:GO:0032502	-		IPR000717; PTHR15350 (PANTHER), PTHR15350:SF3 (PANTHER), SSF46785 (SUPERFAMILY)

Macaca mulatta	ribosomal protein l3	6	C:GO:0005730; F:GO:0003735; F:GO:0003723; F:GO:0005515; C:GO:0022625; P:GO:0006414	-		-
Caenorhabditis briggsae	briggsae cbr-lem-2 protein	0		C:GO:0005635		IPR003887; IPR011015; PTHR12019 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-lem-2 protein	0		C:GO:0031965; C:GO:0005637; P:GO:0008283; C:GO:0005635; C:GO:0005634; F:GO:0003677; C:GO:0005694; F:GO:0005521; C:GO:0016021; C:GO:0016020; P:GO:0031047; F:GO:0000166; C:GO:0005737; C:GO:0000785; P:GO:0045449; P:GO:0031053; C:GO:0005654; F:GO:0005515		IPR003887; IPR011015; PTHR12019 (PANTHER)
	-	0				-
Anopheles gambiae str. PEST	mannosyl-oligosaccharide alpha- -mannosidase	4	C:GO:0016020; P:GO:0008152; F:GO:0004571; F:GO:0005509	-	EC:3.2.1.113	-
Caenorhabditis briggsae	leucine-rich ppr-motif containing	5	P:GO:0009792; P:GO:0000003; P:GO:0040007; P:GO:0006898; P:GO:0002119	-		-
	-	0				-
Caenorhabditis briggsae	ribosomal protein s11 containing protein	6	P:GO:0009792; C:GO:0005840; F:GO:0003735; P:GO:0040010; P:GO:0006898; P:GO:0006412	-	EC:3.6.5.3	IPR001971; PTHR11759:SF4 (PANTHER), SSF53137 (SUPERFAMILY)
Caenorhabditis briggsae	slit-robo rho gtpase activating protein	4	P:GO:0045132; P:GO:0007165; C:GO:0005622; F:GO:0005515	-		IPR000198; IPR008936; PTHR14166 (PANTHER), PTHR14166:SF2 (PANTHER)
Caenorhabditis elegans	crumbs homolog 3	0				-
	-	0				-
Brugia malayi	run and fyve domain containing 1	1	F:GO:0005488	-		IPR000306; IPR004012; IPR011011; IPR013083; IPR017455; PTHR22835 (PANTHER), PTHR22835:SF37 (PANTHER), SignalP (SIGNALP), SSF140741 (SUPERFAMILY)

Caenorhabditis briggsae	#NAME?	9	C:GO:0005737; P:GO:0009792; F:GO:0046872; C:GO:0005886; P:GO:0019509; F:GO:0005515; P:GO:0055114; C:GO:0005634; F:GO:0051213	-		IPR004313; IPR011051; IPR014710
Caenorhabditis elegans	uncoordi-ted family member (unc-52)	7	P:GO:0001525; P:GO:0051216; C:GO:0005604; P:GO:0030239; P:GO:0060350; P:GO:0007519; F:GO:0005515	-		IPR003598; IPR007110; IPR013151; IPR013783; PTHR10574 (PANTHER), PTHR10574:SF20 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis briggsae	patched family protein	3	P:GO:0040025; P:GO:0040018; P:GO:0040011	-		IPR003392; PTHR10796 (PANTHER), PTHR10796:SF14 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-dnj-16 protein	3	P:GO:0006457; F:GO:0051082; F:GO:0031072	-		IPR001623; IPR015609; IPR018253; PTHR11821:SF20 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	isoform cra_a	1	F:GO:0005488	-		IPR000357; IPR011989
Brugia malayi	ubiquitin-like protein 5	0		F:GO:0003674; P:GO:0008150; C:GO:0005575		-
Caenorhabditis elegans	d-se domain containing 2	0		F:GO:0016888; F:GO:0016787; P:GO:0008150; F:GO:0004518; C:GO:0005634; C:GO:0005575		-
	-	0				-
Caenorhabditis elegans	phosphatidylinositol synthase	3	C:GO:0016021; P:GO:0000003; F:GO:0016780	-	EC:2.7.8.0	PTHR15362 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	phosphatidylinositol synthase	3	C:GO:0016021; P:GO:0000003; F:GO:0016780	-	EC:2.7.8.0	PTHR15362 (PANTHER), SignalP (SIGNALP)
Brugia malayi	innexin family protein	5	P:GO:0040035; P:GO:0040010; P:GO:0040011; C:GO:0044425; P:GO:0002009	-		IPR000990
Caenorhabditis elegans	transmembrane protein 68	1	F:GO:0003824	-		-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	chromosome 20 open reading frame 43	6	P:GO:0009792; P:GO:0040007; P:GO:0010171; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		IPR006735; PF04641 (PFAM)

Caenorhabditis briggsae	chromosome 20 open reading frame 43	6	P:GO:0009792; P:GO:0040007; P:GO:0010171; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		SignalP (SIGNALP)
Caenorhabditis briggsae	zgc:55448 protein	6	P:GO:0009792; P:GO:0040007; P:GO:0010171; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		IPR006735; PF04641 (PFAM)
Caenorhabditis briggsae	zgc:55448 protein	6	P:GO:0009792; P:GO:0040007; P:GO:0010171; P:GO:0006898; P:GO:0002119; P:GO:0040011	-		IPR006735; PF04641 (PFAM)
	-	0				-
Caenorhabditis elegans	yqy2_caeel ame: full=uncharacterized protein	0		P:GO:0008152; F:GO:0008080		-
	-	0				SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	actin related protein 2 3 complex subunit 2	13	F:GO:0003899; C:GO:0005885; F:GO:0003723; P:GO:0006396; C:GO:0031252; C:GO:0042995; C:GO:0005925; F:GO:0003779; P:GO:0006928; F:GO:0005200; C:GO:0005794; F:GO:0000175; P:GO:0030838	-	EC:2.7.7.6	IPR007188; G3DSA:3.30.1460.20 (GENE3D), SSF69645 (SUPERFAMILY)
Caenorhabditis elegans	cyclin b	1	F:GO:0005515	-		IPR004367; IPR006670; IPR006671; IPR011028; IPR013763; IPR014400; PTHR10177 (PANTHER), PTHR10177:SF21 (PANTHER)
Caenorhabditis elegans	hypothetical protein K04G7.1 [Caenorhabditis elegans]	3	P:GO:0009792; P:GO:0000003; P:GO:0006898	-		-
Caenorhabditis briggsae	mannosyl-oligosaccharide glucosidase	5	C:GO:0016021; P:GO:0040010; F:GO:0004573; P:GO:0009311; P:GO:0040011	-	EC:3.2.1.106	IPR004888; PTHR10412 (PANTHER)
Loa loa	integrin alpha fg-gap repeat containing 2	0		P:GO:0007229		PTHR16317 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	serine protease	1	F:GO:0016787	-		IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR19355 (PANTHER), PTHR19355:SF174 (PANTHER)

Monodelphis domestica	suppression of tumorigenicity 14 (colon carcinoma)	0		P:GO:0016477; F:GO:0004252; C:GO:0016021; C:GO:0016020; F:GO:0016787; C:GO:0019897; F:GO:0008236; F:GO:0003824; C:GO:0005576; F:GO:0005044; F:GO:0008233; C:GO:0016323; P:GO:0006508; P:GO:0008152; C:GO:0005887; C:GO:0005886; C:GO:0005615		IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR19355 (PANTHER), PTHR19355:SF174 (PANTHER)
Caenorhabditis briggsae	serine protease	1	F:GO:0016787	-		IPR001254; IPR001314; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR19355 (PANTHER), PTHR19355:SF174 (PANTHER)
Caenorhabditis briggsae	transmembrane amino acid transporter protein	1	C:GO:0016020	-		IPR013057; SignalP (SIGNALP)
	-	0				-
Haemonchus contortus	daf-16b transcription factor	4	F:GO:0003700; F:GO:0043565; C:GO:0005634; P:GO:0006355	-		-
	-	0				-
Caenorhabditis elegans	titin isoform n2-a	2	P:GO:0009792; P:GO:0000003	-		IPR003599; IPR003961; IPR007110; IPR008957; IPR013098; IPR013783; PTHR10489 (PANTHER), SSF48726 (SUPERFAMILY)
Loa loa	elegans protein partially confirmed by transcript evidence	0				-
	-	0				-
Aedes aegypti	dopa decarboxylase	3	P:GO:0044237; F:GO:0016831; P:GO:0044281	-	EC:4.1.1.0	-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0008270; C:GO:0005622		IPR007087
	-	0				SignalP (SIGNALP)
Loa loa	mob1 phocein family protein	0				-
Brugia malayi	cationic amino acid transporter	6	P:GO:0019915; C:GO:0016021; P:GO:0006865; F:GO:0015171; C:GO:0005886; P:GO:0055085	-		IPR002293; PTHR11785:SF74 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	riken cd- 2610029g23 gene	0		F:GO:0003674; P:GO:0008150; C:GO:0005575		-
	-	0				-
Caenorhabditis elegans	beta-galactosidase	1	F:GO:0016787	-		IPR001944; IPR013781; IPR017853
Heterodera glycines	venom allergen-like protein	0		F:GO:0009055; P:GO:0019646; P:GO:0006898; C:GO:0005576		IPR001283; IPR014044; PTHR10334:SF11 (PANTHER)
	-	0				-

Ancylostoma caninum	secreted protein 5 precursor	0		P:GO:0040011; C:GO:0005576		IPR001283; IPR002413; IPR014044; PTHR10334:SF11 (PANTHER)
Caenorhabditis elegans	hypothetical protein T12D8.9 [Caenorhabditis elegans]	0				-
	-	0				-
Loa loa	multiple pdz domain protein family member (mpz-1)	2	F:GO:0005515; C:GO:0016021	-		-
Caenorhabditis briggsae	udp-glucose pyrophosphatase	0		F:GO:0046872; F:GO:0016787; F:GO:0016818		IPR000086; IPR015797; PTHR11839 (PANTHER), PTHR11839:SF2 (PANTHER), PS51462 (PROFILE)
Caenorhabditis elegans	uroca-se domain containing 1	2	P:GO:0006548; F:GO:0016153	-	EC:4.2.1.49	IPR000193
Brugia malayi	zinc finger protein dhhc domain containing	2	C:GO:0016020; F:GO:0008270	-		IPR001594; PTHR22883 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	2	P:GO:0040018; P:GO:0040011	-		IPR000615; IPR021134; SignalP (SIGNALP)
Caenorhabditis elegans	briggsae cbr-zyg-9 protein	1	F:GO:0005515	-		PTHR12609 (PANTHER)
Caenorhabditis elegans	rnp-1 like r--binding protein	4	C:GO:0005622; P:GO:0009792; F:GO:0000166; F:GO:0003723	-		IPR000504; IPR012677; IPR015465; PTHR10432 (PANTHER), SSF54928 (SUPERFAMILY)
Haemochus contortus	galectin	3	F:GO:0005515; F:GO:0005529; P:GO:0000003	-		SignalP (SIGNALP)
	-	0				-
	-	0				IPR018271; SignalP (SIGNALP)
Caenorhabditis elegans	isoform cra_a	1	P:GO:0009987	-		-
Caenorhabditis elegans	isoform cra_a	1	P:GO:0009987	-		-
Caenorhabditis elegans	domon domain containing protein	0		F:GO:0030246; F:GO:0004500; C:GO:0016021; F:GO:0003824; P:GO:0006548; P:GO:0016052		-
Drosophila melanogaster	mucin 68d	0		F:GO:0008061; P:GO:0006030; C:GO:0005576		-
Caenorhabditis briggsae	pap 25a associated domain containing protein	4	P:GO:0040035; P:GO:0009792; P:GO:0007281; P:GO:0040010	-		PTHR23092 (PANTHER), PTHR23092:SF4 (PANTHER), SSF81631 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	loss of heterozygosity 12 chromosomal region 1	3	P:GO:0002119; F:GO:0005515; P:GO:0040007	-		IPR018780
Brugia malayi	elegans protein confirmed by transcript evidence	0				-

Homo sapiens	nucleoside diphosphate ki-se b	31	C:GO:0030027; F:GO:0005515; P:GO:0002762; P:GO:0070593; F:GO:0004550; P:GO:0006241; C:GO:0005792; P:GO:0006355; P:GO:0030819; P:GO:0007162; C:GO:0016021; C:GO:0005882; P:GO:0016338; F:GO:0046872; P:GO:0006165; C:GO:0001726; P:GO:0007156; F:GO:0003677; P:GO:0045618; P:GO:0006183; P:GO:0006228; P:GO:0050679; F:GO:0003700; C:GO:0048471; C:GO:0005886; C:GO:0005625; C:GO:0005634;	-	EC:2.7.4.6	IPR001564
Caenorhabditis elegans	tyrosine-protein ki-se pr2	6	P:GO:0042059; P:GO:0040027; F:GO:0004713; F:GO:0000166; P:GO:0048102; P:GO:0009792	-	EC:2.7.10.0	-
	-	0				SignalP (SIGNALP)
Brugia malayi	variant sh3 domain containing protein	9	P:GO:0007427; C:GO:0044441; P:GO:0046425; C:GO:0005768; P:GO:0043409; F:GO:0005515; P:GO:0048013; P:GO:0006886; F:GO:0008268	-		IPR002014; IPR008942; IPR018205; PTHR13856 (PANTHER), PTHR13856:SF22 (PANTHER)
	-	0				-
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis elegans	phosphoglycerate mutase	0				IPR013078; G3DSA:3.40.50.1240 (GENE3D), PTHR23029 (PANTHER), SSF53254 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	sda1 domain containing 1	7	C:GO:0005730; P:GO:0002119; F:GO:0005515; P:GO:0042254; P:GO:0040007; P:GO:0006898; P:GO:0051729	-		IPR007949; IPR016024; PTHR12730 (PANTHER)

Brugia malayi	histone h3	1	C:GO:0043229	-		IPR000164; IPR007125; IPR009072
	-	0				-
	-	0				-
Caenorhabditis elegans	i in family member (inx-1)	3	C:GO:0005921; C:GO:0016021; P:GO:0040011	-		IPR000990
Caenorhabditis elegans	p38 mapk	7	P:GO:0044238; P:GO:0007243; P:GO:0044260; F:GO:0005515; F:GO:0008339; P:GO:0006950; C:GO:0005634	-		IPR011009; G3DSA:1.10.510.10 (GENE3D), PTHR11909 (PANTHER), PTHR11909:SF7 (PANTHER)
Caenorhabditis briggsae	yl54_caeel ame: full=uncharacterized protein	0				-
Loa loa	hypothetical protein LOAG_03906 [Loa loa]	1	P:GO:0000003	-		-
Loa loa	ribonuclease iii	3	F:GO:0003723; P:GO:0031053; C:GO:0005622	-		IPR001159; IPR014720; PTHR11207 (PANTHER), SSF54768 (SUPERFAMILY)
Caenorhabditis elegans	neuro-l calcium sensor 2	3	F:GO:0016491; P:GO:0000003; F:GO:0005509	-		IPR001125; IPR002048; IPR011992; IPR018247; IPR018248; IPR018249; PTHR23055 (PANTHER), PTHR23055:SF19 (PANTHER), SSF47473 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-age-1 protein	7	P:GO:0008340; P:GO:0007611; P:GO:0000003; P:GO:0050920; P:GO:0043053; F:GO:0016301; P:GO:0009792	-		IPR002420; IPR008973; G3DSA:2.60.40.150 (GENE3D)
Caenorhabditis briggsae	nematode cuticle collagen n-termi-l domain containing protein	2	F:GO:0042302; C:GO:0016021	-		PTHR10499 (PANTHER), PTHR10499:SF58 (PANTHER)
	-	0				-
Caenorhabditis elegans	hypothetical protein F21F3.7 [Caenorhabditis elegans]	0				IPR008590
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		PTHR22746 (PANTHER), PTHR22746:SF6 (PANTHER)
Drosophila grimshawi	myst histone acetyltransferase	2	F:GO:0016747; C:GO:0005622	-	EC:2.3.1.0	-

Caenorhabditis briggsae	briggsae cbr-unc-70 protein	20	P:GO:0016199; P:GO:0007026; F:GO:0005546; C:GO:0031594; P:GO:0030721; P:GO:0007009; C:GO:0008091; C:GO:0045170; F:GO:0003779; F:GO:0008017; C:GO:0016328; C:GO:0045169; C:GO:0030424; P:GO:0045478; P:GO:0042062; C:GO:0016327; P:GO:0007274; C:GO:0005811; P:GO:0048790; F:GO:0005200	-		IPR001605; IPR001849; IPR002017; IPR011993; IPR018159; G3DSA:1.20.58.60 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF48 (PANTHER), SSF46966 (SUPERFAMILY), SSF50729 (SUPERFAMILY)
Caenorhabditis elegans	protein	1	F:GO:0016740	-		IPR019410; G3DSA:3.40.50.150 (GENE3D), PTHR14614 (PANTHER), SSF53335 (SUPERFAMILY)
Caenorhabditis briggsae	atp-dependent r- helicase ddx54	11	F:GO:0030331; P:GO:0040010; F:GO:0003723; P:GO:0006396; F:GO:0004004; C:GO:0005730; C:GO:0016021; P:GO:0045449; P:GO:0006200; F:GO:0005524; F:GO:0003714	-		IPR000629; IPR011545; IPR014001; IPR014014; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF17 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	immunoglobulin-binding protein 1	17	P:GO:0043154; P:GO:0018991; F:GO:0005515; P:GO:0040007; P:GO:0040017; P:GO:0032873; P:GO:0010553; P:GO:0009792; P:GO:0002009; P:GO:0034612; C:GO:0005813; P:GO:0002119; F:GO:0008601; P:GO:0010171; P:GO:0070555; P:GO:0060632; P:GO:0040035	-		IPR007304; PTHR10933:SF8 (PANTHER)

Caenorhabditis briggsae	dephospho- ki-se family protein	0		F:GO:0016301; P:GO:0009058; F:GO:0005524; P:GO:0015937; F:GO:0016779; C:GO:0005737; F:GO:0004140; F:GO:0003824		-
	-	0				-
Loa loa	ran binding protein 10	0		F:GO:0008536; C:GO:0005881; P:GO:0000226; F:GO:0048487; F:GO:0005087		IPR006595; IPR013144; IPR019589; PTHR12864 (PANTHER), PTHR12864:SF1 (PANTHER)
Loa loa	ran-binding protein 10	0		C:GO:0005737; C:GO:0005634		IPR006595; IPR013144; IPR019589; PTHR12864 (PANTHER), PTHR12864:SF1 (PANTHER)
Loa loa	ran binding protein 10	0		F:GO:0008536; C:GO:0005881; P:GO:0000226; F:GO:0048487; F:GO:0005087		IPR006595; IPR013144; IPR019589; PTHR12864 (PANTHER), PTHR12864:SF1 (PANTHER)
Pan troglodytes	ribosomal protein s19	12	F:GO:0003723; P:GO:0015669; C:GO:0005730; P:GO:0006364; F:GO:0003735; P:GO:0006414; C:GO:0022627; P:GO:0051272; P:GO:0030218; P:GO:0042274; P:GO:0009991; F:GO:0005515	-		SignalP (SIGNALP)

Caenorhabditis briggsae	myosin heavy chain	35	P:GO:0006941; P:GO:0007626; P:GO:0046664; P:GO:0045200; C:GO:0016461; P:GO:0035159; P:GO:0031036; P:GO:0035072; P:GO:0007443; P:GO:0007395; P:GO:0045214; P:GO:0035017; P:GO:0007297; C:GO:0031672; P:GO:0046663; F:GO:0003779; F:GO:0000146; P:GO:0001736; F:GO:0008307; F:GO:0032027; P:GO:0008258; P:GO:0051259; P:GO:0016203; C:GO:0032154; C:GO:0045179; P:GO:0045184; C:GO:0005863; P:GO:0035317;	-		-
Macaca mulatta	ribosomal protein l35a	9	C:GO:0005840; P:GO:0042273; F:GO:0003735; F:GO:0005515; P:GO:0006364; C:GO:0005829; C:GO:0005739; F:GO:0000049; P:GO:0006414	-		IPR001780; IPR009000; IPR018266
Brugia malayi	glucosamine-6-phosphate n-acetyltransferase	4	P:GO:0000910; P:GO:0000003; F:GO:0008080; F:GO:0005515	-		-
Brugia malayi	glucosamine-6-phosphate n-acetyltransferase	4	P:GO:0000910; P:GO:0000003; F:GO:0008080; F:GO:0005515	-		IPR000182; IPR016181; PTHR13355 (PANTHER)
	-	0				-
Caenorhabditis briggsae	periodic tryptophan protein 1 homolog	0		F:GO:0003674; F:GO:0008415; F:GO:0016740; F:GO:0004402; P:GO:0008150; C:GO:0005634; C:GO:0005575		IPR001680; IPR011046; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR14091 (PANTHER)
Loa loa	hypothetical protein LOAG_06803 [Loa loa]	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	mgc84616 protein	2	P:GO:0008152; F:GO:0016757	-		IPR007235; G3DSA:3.40.50.2000 (GENE3D), PTHR12867 (PANTHER), SignalP (SIGNALP)

Caenorhabditis briggsae	briggsae cbr-twk-25 protein	0		C:GO:0016021; C:GO:0016020; F:GO:0005267; P:GO:0006813; P:GO:0006811; F:GO:0005216; P:GO:0006810		-
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein D2024.5 [Caenorhabditis elegans]	4	P:GO:0002119; P:GO:0009792; P:GO:0040007; P:GO:0040011	-		-
Loa loa	esr1 protein	16	P:GO:0008156; C:GO:0005654; P:GO:0043517; F:GO:0032405; F:GO:0032407; P:GO:0034446; F:GO:0004674; P:GO:0000077; P:GO:0034644; P:GO:0071480; C:GO:0031527; F:GO:0051015; C:GO:0031258; P:GO:0031532; F:GO:0005518; F:GO:0004888	-	EC:2.7.11.0	IPR000403; IPR003152; IPR011009; IPR014009; IPR018936; G3DSA:3.30.1010.10 (GENE3D), PTHR11139 (PANTHER), PTHR11139:SF8 (PANTHER)
Loa loa	esr1 protein	17	P:GO:0000075; F:GO:0004672; P:GO:0007346; F:GO:0032404; P:GO:0071478; P:GO:0042770; P:GO:0009653; P:GO:0007127; P:GO:0006260; P:GO:0006302; P:GO:0006310; C:GO:0044428; P:GO:0065008; P:GO:0030036; P:GO:0007275; P:GO:0051276; C:GO:0031253	-		IPR000403; IPR003151; IPR003152; IPR011009; IPR014009; IPR018936; G3DSA:3.30.1010.10 (GENE3D), PTHR11139 (PANTHER), PTHR11139:SF8 (PANTHER)
Loa loa	esr1 protein	11	F:GO:0004672; C:GO:0031253; P:GO:0042770; P:GO:0071478; C:GO:0044428; P:GO:0016043; F:GO:0032404; P:GO:0048523; P:GO:0032502; P:GO:0006260; P:GO:0007049	-		IPR000403; IPR003151; IPR003152; IPR011009; IPR014009; IPR018936; G3DSA:3.30.1010.10 (GENE3D), PTHR11139 (PANTHER), PTHR11139:SF8 (PANTHER)

Loa loa	esr1 protein	11	F:GO:0004672; C:GO:0031253; P:GO:0042770; P:GO:0071478; C:GO:0044428; P:GO:0016043; F:GO:0032404; P:GO:0048523; P:GO:0032502; P:GO:0006260; P:GO:0007049	-		IPR000403; IPR003151; IPR003152; IPR011009; IPR014009; IPR018936; G3DSA:3.30.1010.10 (GENE3D), PTHR11139 (PANTHER), PTHR11139:SF8 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-pgp-10 protein	4	F:GO:0042626; P:GO:0055085; F:GO:0005524; C:GO:0016021	-		PTHR19242 (PANTHER), PTHR19242:SF62 (PANTHER), SignalP (SIGNALP)
Homo sapiens	-dh dehydroge-se subunit 1	0				-
Caenorhabditis elegans	gex interacting protein family member (gei-4)	1	F:GO:0005515	-		-
Caenorhabditis elegans	gex interacting protein family member (gei-4)	1	F:GO:0005515	-		-
Drosophila sechellia	darkener of isoform l	20	P:GO:0031987; P:GO:0000381; P:GO:0001964; P:GO:0007548; F:GO:0000166; P:GO:0008362; P:GO:0046777; F:GO:0004712; P:GO:0045494; P:GO:0008407; F:GO:0004674; P:GO:0035071; P:GO:0007350; C:GO:0005875; C:GO:0005783; P:GO:0042051; P:GO:0030717; C:GO:0005634; P:GO:0048854; P:GO:0000165	-	EC:2.7.112.1; EC:2.7.11.0	IPR000719; IPR008271; IPR011009; IPR017441; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR11295 (PANTHER), PTHR11295:SF33 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein C24B9.3 [Caenorhabditis elegans]	0				IPR002035; G3DSA:3.40.50.410 (GENE3D), SignalP (SIGNALP), SSF53300 (SUPERFAMILY)
Brugia malayi	lariat debranching enzyme	9	P:GO:0040010; P:GO:0000375; P:GO:0000003; P:GO:0040011; P:GO:0006898; F:GO:0008419; P:GO:0006397; P:GO:0009792; C:GO:0005634	-		IPR004843; IPR007708; G3DSA:3.60.21.10 (GENE3D), PTHR12849 (PANTHER), SSF56300 (SUPERFAMILY)
Caenorhabditis elegans	eya (drosophila eyes absent) homolog family member (eya-1)	1	F:GO:0005515	-		PTHR10190 (PANTHER), PTHR10190:SF3 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)

	-	0				IPR003618
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	phospholipase group ib	23	P:GO:0002446; P:GO:0030593; P:GO:0010524; P:GO:0048146; P:GO:0010552; P:GO:0046470; P:GO:0032637; F:GO:0005102; P:GO:0032612; P:GO:0015758; C:GO:0005615; F:GO:0032052; P:GO:0050482; P:GO:0045740; P:GO:0032869; P:GO:0051092; P:GO:0050778; F:GO:0043498; P:GO:0044240; F:GO:0047498; F:GO:0005509; P:GO:0000187; P:GO:0019370	-		-
Caenorhabditis elegans	phospholipase group ib	23	P:GO:0002446; P:GO:0030593; P:GO:0010524; P:GO:0048146; P:GO:0010552; P:GO:0046470; P:GO:0032637; F:GO:0005102; P:GO:0032612; P:GO:0015758; C:GO:0005615; F:GO:0032052; P:GO:0050482; P:GO:0045740; P:GO:0032869; P:GO:0051092; P:GO:0050778; F:GO:0043498; P:GO:0044240; F:GO:0047498; F:GO:0005509; P:GO:0000187; P:GO:0019370	-		IPR001211; IPR013090; IPR016090; PTHR11716:SF2 (PANTHER), SignalP (SIGNALP)
Caenorhabditis remanei	phosphoglucomutase 1	4	P:GO:0006006; C:GO:0005829; F:GO:0000287; F:GO:0004614	-	EC:5.4.2.2	IPR005841; IPR005844; IPR005845; IPR005846; IPR016055; IPR016066; G3DSA:3.30.310.50 (GENE3D), PTHR22573 (PANTHER), PTHR22573:SF5 (PANTHER), SSF55957 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein F18A1.6 [Caenorhabditis elegans]	0				-

Caenorhabditis elegans	elegans protein confirmed by transcript evidence	4	F:GO:0016757; P:GO:0044237; P:GO:0040010; P:GO:0044238	-		IPR002213; G3DSA:3.40.50.2000 (GENE3D), SSF53756 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	1-acyl-sn-glycerol-3-phosphate acyltransferase epsilon	4	P:GO:0044255; F:GO:0046027; C:GO:0005829; C:GO:0005739	-	EC:2.3.1.158	-
Caenorhabditis briggsae	uncoordi-ted family member (unc-83)	0				-
Loa loa	chimerin 2	4	F:GO:0046872; P:GO:0007165; C:GO:0005622; F:GO:0005515	-		IPR000198; IPR002219; IPR008936; IPR020454; G3DSA:3.30.60.20 (GENE3D), PTHR23178 (PANTHER), SSF57889 (SUPERFAMILY)
Caenorhabditis elegans	briggsae cbr-mel-47 protein	0		C:GO:0005634; P:GO:0006260; F:GO:0003676; F:GO:0000166; P:GO:0051301; F:GO:0003674; F:GO:0003723; P:GO:0007275; P:GO:0007049		IPR000504; IPR008191; IPR012677; PTHR15597 (PANTHER), PTHR15597:SF10 (PANTHER), SSF54928 (SUPERFAMILY), SSF63748 (SUPERFAMILY)
Caenorhabditis briggsae	regulator of g-protein sig-ling 7	6	C:GO:0005834; F:GO:0004871; P:GO:0023034; P:GO:0006397; P:GO:0007186; C:GO:0005634	-	EC:3.6.5.1	IPR000591; IPR011991; SSF46785 (SUPERFAMILY)
Caenorhabditis briggsae	d--repair protein rad13	0		F:GO:0003697; P:GO:0006281; P:GO:0006289; F:GO:0003824; F:GO:0004519; F:GO:0004518; C:GO:0005634; F:GO:0003677		IPR006084; IPR006086; IPR008918; IPR020045; G3DSA:1.10.150.20 (GENE3D), G3DSA:3.40.50.1010 (GENE3D), PTHR11081:SF4 (PANTHER), SSF88723 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-sur-6 protein	5	F:GO:0008601; C:GO:0000159; P:GO:0007165; P:GO:0008219; C:GO:0005741	-		IPR000009; IPR011046; IPR015943; IPR019781
Caenorhabditis briggsae	briggsae cbr-sur-6 protein	5	F:GO:0008601; C:GO:0000159; P:GO:0007165; P:GO:0008219; C:GO:0005741	-		IPR000009; IPR011046; IPR015943; IPR019781

Caenorhabditis elegans	fork head domain containing protein	34	P:GO:0007224; P:GO:0061030; P:GO:0050728; P:GO:0002053; P:GO:0010552; P:GO:0001701; P:GO:0060441; P:GO:0071345; P:GO:0045198; P:GO:0016337; P:GO:0048617; P:GO:0051150; P:GO:0048566; P:GO:0010811; P:GO:0071407; F:GO:0016563; P:GO:0048371; P:GO:0030198; P:GO:0030335; P:GO:0060463; P:GO:0001570; P:GO:0060438; P:GO:0001756; F:GO:0043565; F:GO:0003702; P:GO:0043305; P:GO:0090131;	-		IPR001766; IPR011991; IPR018122; SSF46785 (SUPERFAMILY)
Caenorhabditis briggsae	myosin heavy chain	4	C:GO:0032982; F:GO:0003779; F:GO:0005524; F:GO:0003774	-		IPR001609; IPR015650; PTHR13140 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis elegans	hippocampus abundant transcript 1	5	P:GO:0015904; P:GO:0055085; C:GO:0016021; P:GO:0046677; F:GO:0015520	-		PTHR10074 (PANTHER), PTHR10074:SF17 (PANTHER)
Caenorhabditis elegans	hippocampus abundant transcript 1	5	P:GO:0015904; P:GO:0055085; C:GO:0016021; P:GO:0046677; F:GO:0015520	-		PTHR10074 (PANTHER), PTHR10074:SF17 (PANTHER)
Caenorhabditis elegans	ferm domain (-ezrin-radixin-moesin) family member (frm-8)	1	F:GO:0005515	-		IPR000299; IPR019748; PTHR13436 (PANTHER), PTHR13436:SF1 (PANTHER)
Ailuropoda melanoleuca	ribosomal protein l22	6	F:GO:0008201; P:GO:0046632; F:GO:0003735; F:GO:0003723; C:GO:0022625; P:GO:0006414	-		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0		P:GO:0000003; P:GO:0040011; P:GO:0010171; P:GO:0040010; P:GO:0006898; P:GO:0002119		-
Caenorhabditis elegans	copine family protein	0				IPR002035; IPR010734; PTHR10857 (PANTHER), SSF53300 (SUPERFAMILY)

	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-ttll-5 protein	0		F:GO:0004835; P:GO:0006464		-
Loa loa	myc and mondo-like family member (mml-1)	6	P:GO:0009987; P:GO:0006810; C:GO:0043231; P:GO:0050789; P:GO:0040007; P:GO:0007275	-		PTHR15741 (PANTHER), PTHR15741:SF1 (PANTHER)
Loa loa	mediator of r- polymerase ii transcription subunit 17	4	F:GO:0003712; F:GO:0016563; C:GO:0005634; P:GO:0006366	-		IPR019313; PTHR13114 (PANTHER)
Caenorhabditis briggsae	atp-dependent r- helicase	7	P:GO:0009987; P:GO:0040010; F:GO:0008266; P:GO:0000003; P:GO:0002119; C:GO:0044464; F:GO:0016787	-		-
	-	0				-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	C:GO:0016021; P:GO:0015986; P:GO:0040013	-		IPR002490; PTHR11629:SF23 (PANTHER)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	C:GO:0016021; P:GO:0015986; P:GO:0040013	-		IPR002490; PTHR11629:SF23 (PANTHER)
Pongo abelii	ribosomal protein l5	8	C:GO:0005730; P:GO:0006364; P:GO:0042273; F:GO:0003735; P:GO:0006414; F:GO:0005515; C:GO:0022625; F:GO:0008097	-		IPR005484; IPR005485; G3DSA:3.30.420.100 (GENE3D), SSF53137 (SUPERFAMILY)
	-	0				-
	-	0				-
	-	0				-
Bursaphelenchus xylophilus	ribosomal protein l5	12	P:GO:0040010; P:GO:0044238; P:GO:0044260; F:GO:0019843; P:GO:0040035; P:GO:0010171; P:GO:0002119; P:GO:0042254; C:GO:0030529; P:GO:0010467; P:GO:0009792; C:GO:0005737	-		IPR005484; IPR005485; G3DSA:3.30.420.100 (GENE3D), PTHR23410:SF1 (PANTHER), SSF53137 (SUPERFAMILY)

Caenorhabditis elegans	chromodomain-helicase-d--binding protein 1	5	F:GO:0003676; C:GO:0044427; F:GO:0000166; F:GO:0004386; P:GO:0006325	-		IPR001650; G3DSA:3.40.50.300 (GENE3D), PTHR10799 (PANTHER), PTHR10799:SF70 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	hypothetical protein C18C4.5 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				-
Caenorhabditis briggsae	altered response to gravity	3	P:GO:0050896; F:GO:0005515; C:GO:0016020	-		IPR015609; PTHR11821:SF20 (PANTHER)
Caenorhabditis elegans	-d-dependent adp-ribosyltransferase sirtuin-4	8	F:GO:0005515; P:GO:0006974; C:GO:0005759; P:GO:0046676; F:GO:0003950; F:GO:0034979; F:GO:0046872; P:GO:0045449	-	EC:2.4.2.30	IPR003000; G3DSA:3.30.1600.10 (GENE3D), G3DSA:3.40.50.1220 (GENE3D), SSF52467 (SUPERFAMILY)
Ancylostoma ceylanicum	secreted protein 5 precursor	0		P:GO:0006898; C:GO:0005576		IPR014044; SignalP (SIGNALP)
Ancylostoma ceylanicum	secreted protein 5 precursor	0		P:GO:0006898; C:GO:0005576		IPR014044; SignalP (SIGNALP)
Ancylostoma ceylanicum	secreted protein 5 precursor	0		C:GO:0005576		IPR014044
Ancylostoma ceylanicum	secreted protein 5 precursor	0		P:GO:0006898; C:GO:0005576		IPR014044; SignalP (SIGNALP)
Ancylostoma ceylanicum	secreted protein 5 precursor	0		P:GO:0006898; C:GO:0005576		IPR014044; SignalP (SIGNALP)
Ancylostoma caninum	secreted protein asp-2	0		C:GO:0005576		IPR014044
Ancylostoma ceylanicum	secreted protein 5 precursor	0		P:GO:0006898; C:GO:0005576		IPR014044; SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
	-	0				-
Ancylostoma ceylanicum	secreted protein 5 precursor	0		P:GO:0006898; C:GO:0005576		IPR014044; SignalP (SIGNALP)
Caenorhabditis elegans	egg sterile protein partially confirmed by transcript evidence	0		F:GO:0005515		
	-	0				-
	-	0				-
Caenorhabditis briggsae	thiamine pyrophosphate central domain containing protein	6	F:GO:0030976; C:GO:0016021; P:GO:0009792; P:GO:0008152; F:GO:0000287; F:GO:0016740	-		IPR014044; SignalP (SIGNALP)
	-	0				IPR014044
Caenorhabditis briggsae	Hypothetical protein CBG14163 [Caenorhabditis briggsae]	1	P:GO:0040010	-		-

Caenorhabditis briggsae	39s ribosomal protein mitochondrial	8	P:GO:0009792; C:GO:0005840; F:GO:0003676; F:GO:0003735; F:GO:0005515; C:GO:0005634; F:GO:0008270; P:GO:0006412	-	EC:3.6.5.3	IPR001857; IPR008991; PTHR15680:SF3 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG07071 [Caenorhabditis briggsae]	1	C:GO:0016020	-		SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	3	C:GO:0034703; F:GO:0005261; P:GO:0055080	-		-
Caenorhabditis elegans	zinc transporter zip1	6	F:GO:0046873; C:GO:0005886; P:GO:0006829; P:GO:0055085; C:GO:0016021; F:GO:0008270	-		-
Brugia malayi	la domain containing protein	0		F:GO:0003676; F:GO:0000166		PTHR22792 (PANTHER), PTHR22792:SF7 (PANTHER)
Caenorhabditis elegans	cell 12a endogluca-se	0		F:GO:0004725; P:GO:0006629; F:GO:0004721; F:GO:0016787; P:GO:0006470; P:GO:0000272; F:GO:0003824; F:GO:0004872; F:GO:0004553; F:GO:0008810; F:GO:0008970		-
Caenorhabditis elegans	cell 12a endogluca-se	0		F:GO:0004725; P:GO:0006629; F:GO:0004721; F:GO:0016787; P:GO:0006470; C:GO:0019867; P:GO:0000272; F:GO:0003824; F:GO:0004872; F:GO:0004553; P:GO:0009405; F:GO:0008810; F:GO:0008970		-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	F:GO:0016627; P:GO:0006631	-		IPR002655; IPR009075; IPR012258; PTHR10909 (PANTHER)
Ciona intestinalis	uncharacterized transposase-like protein	0				-
	-	0				-
	-	0				-
Callithrix jacchus	ribosomal protein s3a	9	P:GO:0006413; F:GO:0003723; P:GO:0006917; C:GO:0005730; F:GO:0003735; P:GO:0006414; C:GO:0022627; P:GO:0030154; F:GO:0005515	-		IPR001593; IPR018281

Dictyocaulus viviparus	elegans protein confirmed by transcript evidence	1	F:GO:0005515	-		-
Caenorhabditis elegans	glycerol ki-se	2	F:GO:0004370; P:GO:0006072	-	EC:2.7.1.30	IPR000577; IPR005999; IPR018483; IPR018484; G3DSA:3.30.420.40 (GENE3D), SSF53067 (SUPERFAMILY)
Caenorhabditis elegans	uncharacterized protein kiaa0467	0				-
Saccoglossus kowalevskii	rho gtpase-activating protein 5	0		F:GO:0005179; F:GO:0005525; P:GO:0007264; P:GO:0007165; C:GO:0005576; P:GO:0019915; C:GO:0005622		-
						IPR000742; IPR006209; IPR006210; IPR013032; IPR013111; G3DSA:2.10.25.10 (GENE3D), PTHR11201 (PANTHER), PTHR11201:SF220 (PANTHER), SignalP (SIGNALP), SSF57196 (SUPERFAMILY)
Caenorhabditis briggsae	exportin 7	4	F:GO:0005488; P:GO:0006810; P:GO:0033036; C:GO:0044424	-		IPR011989; IPR014877; PTHR12596 (PANTHER), PTHR12596:SF2 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	exportin 7	4	F:GO:0005488; P:GO:0006810; P:GO:0033036; C:GO:0044424	-		IPR011989; IPR014877; PTHR12596 (PANTHER), PTHR12596:SF2 (PANTHER), SignalP (SIGNALP)
Loa loa	f-box wd repeat-containing protein 1a	17	P:GO:0000209; P:GO:0033598; P:GO:0051437; P:GO:0016055; C:GO:0005829; P:GO:0006511; P:GO:0008285; F:GO:0004842; P:GO:0051726; P:GO:0071407; N:GO:0061136; F:GO:0008013; P:GO:0060444; C:GO:0005634; F:GO:0045309; P:GO:0043122; P:GO:0044419	-	EC:6.3.2.19	IPR001680; IPR015943; IPR017986; IPR019775; IPR019781; IPR019782; PTHR22844 (PANTHER), PTHR22844:SF10 (PANTHER)
Caenorhabditis elegans	ras gtp exchange son of	4	F:GO:0005089; C:GO:0043229; F:GO:0003677; P:GO:0035023	-		IPR001895; IPR008937; IPR015759
	-	0				-
	-	0				-
Dinoroseobacter shibae DFL 12	acyl- synthetases (amp-forming) amp-acid ligases ii	1	F:GO:0003824	-		IPR000873; IPR020845; G3DSA:3.40.50.980 (GENE3D), PTHR11968 (PANTHER), PTHR11968:SF43 (PANTHER), SSF56801 (SUPERFAMILY)
Brugia malayi	lsm domain-containing protein 1	0		F:GO:0003676; C:GO:0030529		IPR010920; G3DSA:2.30.30.100 (GENE3D), PTHR21617 (PANTHER)

Caenorhabditis elegans	hypothetical protein C02B10.5 [Caenorhabditis elegans]	0		P:GO:0010171; P:GO:0009792; F:GO:0005515		-
Caenorhabditis briggsae	Hypothetical protein CBG19977 [Caenorhabditis briggsae]	0		P:GO:0010171; P:GO:0009792; F:GO:0005515		PTHR23194 (PANTHER), PTHR23194:SF1 (PANTHER)
Loa loa	low-density lipoprotein receptor repeat class b containing protein	0		P:GO:0008283; C:GO:0016021; C:GO:0016020; P:GO:0006898; P:GO:0006897; C:GO:0030139; C:GO:0005783; F:GO:0005509; C:GO:0031526; F:GO:0004872; C:GO:0005768; C:GO:0005764; C:GO:0005794; C:GO:0005905; C:GO:0005624; P:GO:0006766; P:GO:0006486; P:GO:0006629; F:GO:0005515; C:GO:0016324; F:GO:0017124; P:GO:0030900		IPR006210; G3DSA:2.10.25.10 (GENE3D), PTHR10529 (PANTHER), PTHR10529:SF2 (PANTHER), SSF57196 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein C27A12.9 [Caenorhabditis elegans]	0		P:GO:0008152; F:GO:0003824		SignalP (SIGNALP)
Loa loa	hypothetical protein LOAG_03903 [Loa loa]	0		P:GO:0008152; F:GO:0003824		SignalP (SIGNALP)
Caenorhabditis elegans	ef hand family protein	1	F:GO:0005509	-		-
Brugia malayi	8-oxoguanine d-	11	F:GO:0034039; F:GO:0008017; F:GO:0003684; C:GO:0005739; P:GO:0045471; P:GO:0045007; P:GO:0071276; P:GO:0051593; P:GO:0032355; P:GO:0042493; C:GO:0005654	-		IPR012294; IPR012904; G3DSA:1.10.340.30 (GENE3D), PTHR10242 (PANTHER)
	-	0				IPR016197; G3DSA:2.40.50.40 (GENE3D)
Caenorhabditis elegans	ectonucleoside triphosphate diphosphohydrolase 4	4	C:GO:0005794; P:GO:0007275; F:GO:0016787; C:GO:0016020	-		IPR000407; PTHR11782:SF5 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-ooc-3 protein	0				PS51257 (PROFILE), SignalP (SIGNALP)
Caenorhabditis briggsae	briggsae cbr-ooc-3 protein	0				PS51257 (PROFILE), SignalP (SIGNALP)

Caenorhabditis elegans	small subunit ribosomal protein 24	9	P:GO:0040035; P:GO:0009792; P:GO:0002119; C:GO:0005840; F:GO:0003735; P:GO:0008340; P:GO:0040007; P:GO:0006412; F:GO:0000166	-	EC:3.6.5.3	IPR001976; IPR012677; IPR012678
Brugia malayi	replication factor c subunit 3	13	P:GO:0040010; P:GO:0046683; P:GO:0006260; P:GO:0040035; P:GO:0006297; F:GO:0003677; F:GO:0016887; F:GO:0005515; F:GO:0000166; P:GO:0040011; C:GO:0005654; P:GO:0009792; C:GO:0005663	-		-
Brugia malayi	replication factor c subunit 3	13	P:GO:0040010; P:GO:0046683; P:GO:0006260; P:GO:0040035; P:GO:0006297; F:GO:0003677; F:GO:0016887; F:GO:0005515; F:GO:0000166; P:GO:0040011; C:GO:0005654; P:GO:0009792; C:GO:0005663	-		-
Brugia malayi	replication factor c subunit 3	13	P:GO:0040010; P:GO:0046683; P:GO:0006260; P:GO:0040035; P:GO:0006297; F:GO:0003677; F:GO:0016887; F:GO:0005515; F:GO:0000166; P:GO:0040011; C:GO:0005654; P:GO:0009792; C:GO:0005663	-		-

Brugia malayi	replication factor c subunit 3	13	P:GO:0040010; P:GO:0046683; P:GO:0006260; P:GO:0040035; P:GO:0006297; F:GO:0003677; F:GO:0016887; F:GO:0005515; F:GO:0000166; P:GO:0040011; C:GO:0005654; P:GO:0009792; C:GO:0005663	-		-
Caenorhabditis elegans	peroxisomal biogenesis factor 5	5	F:GO:0005515; P:GO:0051179; P:GO:0006996; C:GO:0044444; P:GO:0032501	-		IPR001440; IPR011990; IPR013026; IPR019734; PTHR10130 (PANTHER), SSF48452 (SUPERFAMILY)
Loa loa	major allergen	0				SignalP (SIGNALP)
Loa loa	golgin subfamily a member 7	0		F:GO:0003674; P:GO:0008150		IPR019383; PTHR13254 (PANTHER)
Loa loa	golgi golgin subfamily 7	0		F:GO:0003674; C:GO:0016020; C:GO:0000139; C:GO:0005794; P:GO:0008150		IPR019383; PTHR13254 (PANTHER)
Caenorhabditis elegans	rieske-domain protein neverland	4	F:GO:0051537; P:GO:0055114; F:GO:0046872; F:GO:0016491	-		IPR017941; PTHR21266 (PANTHER), PTHR21266:SF19 (PANTHER)
Brugia malayi	smc c-termi-l domain containing protein	1	F:GO:0005488	-		IPR003395; IPR017871; G3DSA:3.40.50.300 (GENE3D), PTHR18937 (PANTHER), PTHR18937:SF13 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0019915		SignalP (SIGNALP)
Blastocystis hominis	un-med protein product [Blastocystis hominis]	0				-
	-	0				-
Caenorhabditis briggsae	briggsae cbr-lin-25 protein	0		P:GO:0030154; C:GO:0005737; P:GO:0007275; P:GO:0007618; P:GO:0001708; C:GO:0005634; P:GO:0018991		-
	-	0				-
Brugia malayi	hypothetical protein Bm1_49545 [Brugia malayi]	0				-

Caenorhabditis elegans	phosphatidylinositol 3- alpha polypeptide	16	P:GO:0008340; P:GO:0043491; C:GO:0005942; F:GO:0043560; F:GO:0046934; P:GO:0007611; P:GO:0000003; P:GO:0050920; P:GO:0043053; P:GO:0006916; F:GO:0016303; P:GO:0006006; P:GO:0009792; C:GO:0030027; P:GO:0040014; P:GO:0006468	-	EC:2.7.1.153 ; EC:2.7.1.137	IPR000403; IPR011009; IPR015433; PTHR10048:SF14 (PANTHER)
	-	0				-
Caenorhabditis elegans	uncharacterized protein c22orf9-like protein	0				IPR019141; PTHR21477 (PANTHER), PTHR21477:SF5 (PANTHER)
	-	0				-
Nematostella vectensis	zinc transporter zip12	4	P:GO:0030001; C:GO:0016021; F:GO:0046873; P:GO:0055085	-		IPR003689; PTHR16950 (PANTHER), PTHR16950:SF1 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	serine threonine-protein ki-se d3	9	F:GO:0046872; P:GO:0045087; F:GO:0005524; F:GO:0004697; F:GO:0005515; C:GO:0005737; P:GO:0007205; C:GO:0016020; P:GO:0006468	-	EC:2.7.11.13	IPR002219; IPR015727; IPR020454; G3DSA:3.30.60.20 (GENE3D), SSF57889 (SUPERFAMILY)
	-	0				-
Apis mellifera	probable phospholipid-transporting atpase id	6	F:GO:0043492; F:GO:0022892; F:GO:0016820; F:GO:0000166; P:GO:0008152; C:GO:0016020	-	EC:3.6.3.0	-
Loa loa	riken cd- 1700019e19	0				-
Loa loa	hypothetical protein LOAG_07497 [Loa loa]	0				-
Loa loa	hypothetical protein LOAG_07497 [Loa loa]	0				-
Caenorhabditis elegans	vitellogenin structural genes (yolk protein genes) family member (vit-2)	4	P:GO:0009792; P:GO:0008340; P:GO:0040010; F:GO:0005515	-		IPR011030; SignalP (SIGNALP)

Caenorhabditis elegans	corepressor interacting with rbpj 1	13	P:GO:0006396; C:GO:0005730; P:GO:0040007; C:GO:0016607; P:GO:0040035; F:GO:0016564; C:GO:0000118; P:GO:0000122; P:GO:0010171; P:GO:0002119; P:GO:0001703; C:GO:0005737; F:GO:0042826	-		IPR019339; PTHR13151 (PANTHER)
Caenorhabditis elegans	cbf1 interacting corepressor	14	P:GO:0006396; C:GO:0005730; P:GO:0040007; C:GO:0016607; P:GO:0040035; C:GO:0000118; P:GO:0000122; P:GO:0010171; F:GO:0003714; P:GO:0002119; F:GO:0003700; P:GO:0001703; C:GO:0005737; F:GO:0042826	-		IPR019339; PTHR13151 (PANTHER)
Caenorhabditis elegans	corepressor interacting with rbpj 1	13	P:GO:0006396; C:GO:0005730; P:GO:0040007; C:GO:0016607; P:GO:0040035; F:GO:0016564; C:GO:0000118; P:GO:0000122; P:GO:0010171; P:GO:0002119; P:GO:0001703; C:GO:0005737; F:GO:0042826	-		IPR019339; PTHR13151 (PANTHER)
Caenorhabditis briggsae	phospholipase c gamma	5	F:GO:0004871; F:GO:0005515; F:GO:0004435; P:GO:0009395; P:GO:0007165	-	EC:3.1.4.11	IPR000909; IPR001192; IPR017946; PTHR10336 (PANTHER), PTHR10336:SF22 (PANTHER)
Loa loa	inositol hexakisphosphate and diphosphoinositol-pentakisphosphate ki-se	5	F:GO:0000827; F:GO:0000832; P:GO:0006020; F:GO:0033857; C:GO:0005829	-	EC:2.7.4.24	IPR000560; PTHR12750 (PANTHER), PTHR12750:SF5 (PANTHER), SSF53254 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	pleckstrin homology domain family h (with 4 domain) member 1	2	P:GO:0008340; P:GO:0040010	-		IPR001849; IPR011993; PTHR22903 (PANTHER), PTHR22903:SF2 (PANTHER), SSF50729 (SUPERFAMILY)
Caenorhabditis elegans	smg-associated and lethal protein partially confirmed by transcript evidence	0				SignalP (SIGNALP)

Callithrix jacchus	coatomer protein subunit epsilon	8	C:GO:0030126; C:GO:0005829; P:GO:0006890; P:GO:0006891; F:GO:0005515; P:GO:0048205; F:GO:0005198; P:GO:0015031	-		-
Caenorhabditis elegans	coiled-coil domain-containing protein 124	2	C:GO:0005634; F:GO:0003677	-		IPR000910; IPR010422
	-	0				-
Haemonchus contortus	beta-tubulin isotype 1	6	P:GO:0007018; F:GO:0005525; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000217; IPR002453; IPR003008; IPR008280; IPR017975; IPR018316; IPR023123; SignalP (SIGNALP)
Cooperia oncophora	beta-tubulin isotype 2	6	P:GO:0007018; F:GO:0005525; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000217; IPR002453; IPR003008; IPR008280; IPR017975; IPR018316; IPR023123; SignalP (SIGNALP)
Cooperia oncophora	beta-tubulin isotype 2	6	P:GO:0007018; F:GO:0005525; P:GO:0051258; F:GO:0005198; F:GO:0003924; C:GO:0005874	-	EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR000217; IPR002453; IPR003008; IPR008280; IPR017975; IPR018316; IPR023123; SignalP (SIGNALP)
Caenorhabditis elegans	temporarily assigned gene -me family member (tag-260)	1	F:GO:0005515	-		IPR013083; IPR022750; SSF57850 (SUPERFAMILY)
Caenorhabditis elegans	temporarily assigned gene -me family member (tag-260)	2	F:GO:0008270; F:GO:0005515	-		IPR013083; IPR022750; SSF57850 (SUPERFAMILY)
Caenorhabditis elegans	ribonucleoside-diphosphate reductase large chain	0		P:GO:0006260; F:GO:0005524; P:GO:0055114; F:GO:0016491; F:GO:0004748; F:GO:0005515; C:GO:0005971		-
Caenorhabditis elegans	briggsae cbr-qui-1 protein	1	F:GO:0003824	-		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR19871 (PANTHER)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Homo sapiens	light polypeptide	10	C:GO:0008043; F:GO:0008199; P:GO:0006892; P:GO:0055114; F:GO:0042802; C:GO:0022627; P:GO:0006879; P:GO:0016044; F:GO:0016491; P:GO:0006826	-		-

Brugia malayi	u2-associated sr140 protein	0		F:GO:0003676; F:GO:0003723; F:GO:0000166; P:GO:0006396; C:GO:0005575		IPR018522
	-	0				-
Caenorhabditis brenneri	purity of essence	6	P:GO:0042066; P:GO:0007291; F:GO:0005516; F:GO:0008270; P:GO:0006260; F:GO:0004842	-	EC:6.3.2.19	PTHR21725 (PANTHER)
						IPR003599; IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	glutamate synthase	10	P:GO:0006537; P:GO:0009792; F:GO:0045181; P:GO:0002119; F:GO:0051536; F:GO:0005506; F:GO:0010181; P:GO:0040010; P:GO:0055114; F:GO:0050660	-		IPR002489; IPR002932; IPR013785; PTHR11938 (PANTHER), PTHR11938:SF1 (PANTHER), SSF51395 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	origin recognition complex subunit 2 family protein	4	P:GO:0009987; P:GO:0006810; C:GO:0043234; C:GO:0044427	-		IPR007220
Caenorhabditis elegans	microneme protein 4	4	F:GO:0005488; P:GO:0044237; P:GO:0007155; F:GO:0003824	-		SignalP (SIGNALP)
Caenorhabditis elegans	microneme protein 4	6	F:GO:0005488; P:GO:0007155; F:GO:0004888; F:GO:0003824; P:GO:0044237; C:GO:0016020	-		SignalP (SIGNALP)
	-	0				-
Caenorhabditis briggsae	cysteinyl-tr- synthetase	5	C:GO:0005737; P:GO:0006423; F:GO:0005524; F:GO:0000049; F:GO:0004817	-	EC:6.1.1.16	IPR014729; IPR015803; SignalP (SIGNALP), SSF52374 (SUPERFAMILY)
Caenorhabditis briggsae	wd repeat domain 89	0		F:GO:0003674; P:GO:0008150; C:GO:0005575		IPR001680; IPR011046; IPR015943; IPR017986; IPR019781; IPR019782; PTHR19857 (PANTHER), PTHR19857:SF3 (PANTHER)
	-	0				-
Caenorhabditis elegans	briggsae cbr-tag-189 protein	4	C:GO:0000139; C:GO:0005789; P:GO:0006506; F:GO:0008565	-		-

Caenorhabditis elegans	adenylate cyclase	9	C:GO:0016021; F:GO:0004016; P:GO:0007188; P:GO:0009190; P:GO:0002119; F:GO:0000166; P:GO:0040011; P:GO:0040015; C:GO:0005886	-	EC:4.6.1.1	PTHR11920 (PANTHER), PTHR11920:SF12 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	karyopherin alpha 2	8	F:GO:0008565; P:GO:0046015; P:GO:0006259; P:GO:0006606; C:GO:0005643; P:GO:0022403; C:GO:0005737; F:GO:0042826	-		IPR000225; IPR002652; IPR011989; IPR016024; PTHR23316 (PANTHER)
Caenorhabditis elegans	importin subunit alpha-3	5	F:GO:0008565; P:GO:0006606; F:GO:0008022; C:GO:0005643; C:GO:0005737	-		IPR000225; IPR002652; IPR011989; IPR016024; PTHR23316 (PANTHER)
Caenorhabditis elegans	importin subunit alpha-3	5	F:GO:0008565; P:GO:0006606; F:GO:0008022; C:GO:0005643; C:GO:0005737	-		IPR000225; IPR002652; IPR011989; IPR016024; PTHR23316 (PANTHER)
Caenorhabditis elegans	importin subunit alpha-3	5	F:GO:0008565; P:GO:0006606; F:GO:0008022; C:GO:0005643; C:GO:0005737	-		IPR000225; IPR002652; IPR011989; IPR016024; PTHR23316 (PANTHER)
Caenorhabditis briggsae	cation-transporting atpase	2	F:GO:0016820; F:GO:0016887	-	EC:3.6.3.0	SignalP (SIGNALP)
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	3	P:GO:0009792; P:GO:0008152; P:GO:0000003	-		IPR015324
	-	0				-
	-	0				-
Loa loa	variant sh3 domain containing protein	11	P:GO:0043087; P:GO:0006909; F:GO:0005515; P:GO:0006955; P:GO:0007229; C:GO:0005829; P:GO:0008624; P:GO:0042110; P:GO:0045785; F:GO:0030676; C:GO:0005886	-		IPR000219; PTHR22826 (PANTHER), PTHR22826:SF53 (PANTHER)
Loa loa	amine oxidase (flavin containing) domain 1	0		P:GO:0055114; F:GO:0016491; F:GO:0046592; F:GO:0008270		-
Caenorhabditis briggsae	erv1 alr family protein	3	P:GO:0045454; F:GO:0016972; P:GO:0055114	-	EC:1.8.3.2	PTHR22897 (PANTHER), PTHR22897:SF4 (PANTHER)

Equus caballus	proteoglycan 3	0		F:GO:0046872; F:GO:0005488; F:GO:0005529; C:GO:0005576; P:GO:0009405		IPR001304; IPR016186; IPR016187; PTHR22801 (PANTHER), SignalP (SIGNALP)
Struthio camelus	venom c-type lectin mannose binding isoform 3	0		F:GO:0046872; F:GO:0005488; F:GO:0005529; C:GO:0005578; C:GO:0005576; P:GO:0009405		IPR001304; IPR016186; IPR016187; PTHR22801 (PANTHER), PTHR22801:SF9 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	transaldolase	8	P:GO:0009052; F:GO:0004801; P:GO:0032231; P:GO:0035107; P:GO:0007424; P:GO:0009792; C:GO:0005737; P:GO:0002064	-	EC:2.2.1.2	-
Caenorhabditis elegans	novel protein	0		F:GO:0005515		-
Caenorhabditis briggsae	briggsae cbr-hsr-9 protein	1	P:GO:0032502	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	intraflagellar transport 57 homolog	13	C:GO:0035085; F:GO:0005198; F:GO:0005515; P:GO:0006919; P:GO:0042073; P:GO:0007635; P:GO:0032006; P:GO:0042462; P:GO:0008104; P:GO:0001539; P:GO:0007368; C:GO:0005932; P:GO:0035058	-		IPR019530
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	mospd2 protein	0		C:GO:0005856; C:GO:0016021; F:GO:0005198		PTHR19993 (PANTHER)
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	uncoordi-ted family member (unc-89)	2	F:GO:0004672; C:GO:0044464	-		IPR003598; IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), PTHR19897:SF5 (PANTHER), SSF48726 (SUPERFAMILY)
Caenorhabditis elegans	phosphoserine aminotransferase	3	F:GO:0030170; F:GO:0004648; P:GO:0006564	-	EC:2.6.1.52	IPR015422; IPR015424; PTHR21152 (PANTHER), PTHR21152:SF1 (PANTHER)
	-	0				-
	-	0				-
Caenorhabditis elegans	adenylate cyclase type 5	4	F:GO:0004016; P:GO:0009190; C:GO:0016021; F:GO:0000166	-	EC:4.6.1.1	IPR001054; PTHR11920 (PANTHER), PTHR11920:SF14 (PANTHER), SignalP (SIGNALP)

Caenorhabditis briggsae	er lumen protein retaining receptor	9	F:GO:0005046; C:GO:0016021; P:GO:0006890; F:GO:0004872; P:GO:0006891; C:GO:0030140; P:GO:0006621; C:GO:0005789; P:GO:0015031	-		IPR000133; PTHR10585:SF10 (PANTHER), SignalP (SIGNALP)
	-	0				-
	-	0				-
Brugia malayi	sex comb on midleg homolog 1	0		P:GO:0045449; C:GO:0005634		-
Loa loa	pwwp domain containing protein	3	P:GO:0000003; F:GO:0003677; P:GO:0006898	-		PTHR12550 (PANTHER), PTHR12550:SF3 (PANTHER)
Caenorhabditis briggsae	spectrin alpha chain	2	F:GO:0004725; F:GO:0005509	-	EC:3.1.3.48	IPR001452; IPR002017; IPR013315; IPR018159; G3DSA:1.20.58.60 (GENE3D), G3DSA:2.30.30.40 (GENE3D), PTHR11915 (PANTHER), PTHR11915:SF6 (PANTHER), SSF46966 (SUPERFAMILY)
	-	0				-
Caenorhabditis elegans	major sperm protein	0		C:GO:0005856; F:GO:0005198; C:GO:0044297; C:GO:0031143; P:GO:0019915		IPR000535; IPR008962; PTHR22947 (PANTHER)
Caenorhabditis elegans	histone methyltransferase-like family member (met-1)	0		F:GO:0016740; F:GO:0008168; P:GO:0006259; F:GO:0003677; C:GO:0005634; F:GO:0018024; P:GO:0006281; F:GO:0003824; F:GO:0005515; F:GO:0004518		-
Caenorhabditis elegans	pqq enzyme repeat family protein	0		C:GO:0016021; C:GO:0016020; P:GO:0006898; F:GO:0005515		IPR011047; PTHR21573 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	tropomyosin	6	C:GO:0005737; P:GO:0009790; P:GO:0007015; P:GO:0034609; P:GO:0040011; F:GO:0051015	-		-
	-	0				-

Caenorhabditis vulgaris	briggsae cbr-let-23 protein	0		F:GO:0016740; C:GO:0016020; F:GO:0004672; P:GO:0006468; F:GO:0000166; P:GO:0007169; F:GO:0005524; F:GO:0004714; F:GO:0016301; F:GO:0004713; F:GO:0004872; F:GO:0005515		-
Caenorhabditis briggsae	briggsae cbr-unc-62 protein	0		P:GO:0006355; P:GO:0007275; F:GO:0043565; P:GO:0045449; F:GO:0003677; F:GO:0003700; C:GO:0005634		-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	muscle positioning protein 4	2	F:GO:0005509; F:GO:0005515	-		IPR000082
Caenorhabditis briggsae	sushi domain	0		F:GO:0030414; P:GO:0007155; C:GO:0016020; C:GO:0005576		IPR000436; IPR016060
Brugia malayi	arginine-glutamic acid dipeptide repeats	4	P:GO:0007163; P:GO:0030334; F:GO:0005515; C:GO:0005634	-		IPR000679; IPR000949; IPR001005; IPR001025; IPR009057; IPR013088; PTHR13859 (PANTHER), PTHR13859:SF2 (PANTHER), SSF57716 (SUPERFAMILY)
Brugia malayi	arginine-glutamic acid dipeptide repeats	4	P:GO:0007163; P:GO:0030334; F:GO:0005515; C:GO:0005634	-		IPR000679; IPR000949; IPR001005; IPR001025; IPR009057; IPR013088; PTHR13859 (PANTHER), PTHR13859:SF2 (PANTHER), SSF57716 (SUPERFAMILY)
Caenorhabditis elegans	mitochondrial ribosomal protein s22	4	P:GO:0002119; P:GO:0000003; P:GO:0040007; P:GO:0006898	-		IPR019374; PTHR13071 (PANTHER)
Caenorhabditis elegans	hypothetical protein F19C7.1 [Caenorhabditis elegans]	0				-
	-	0				-
	-	0				SignalP (SIGNALP)
	-	0				-
Brugia malayi	cut5-related partial	0		F:GO:0005488; C:GO:0005622; F:GO:0016853		IPR001357; G3DSA:3.40.50.10190 (GENE3D)
	-	0				-

Caenorhabditis briggsae	crooked neck	18	P:GO:0008366; P:GO:0007417; F:GO:0005488; C:GO:0071011; P:GO:0000381; P:GO:0007443; P:GO:0040007; P:GO:0008347; C:GO:0016607; P:GO:0000003; P:GO:0018996; P:GO:0002119; P:GO:0007422; P:GO:0048663; P:GO:0007405; C:GO:0071013; P:GO:0009792; P:GO:0007438	-		IPR003107; IPR011990; PTHR11246 (PANTHER), PTHR11246:SF3 (PANTHER), SSF48452 (SUPERFAMILY)
Drosophila erecta	activin receptor type ii	8	P:GO:0048666; F:GO:0005515; C:GO:0016020; P:GO:0007178; F:GO:0005024; P:GO:0048513; P:GO:0002009; P:GO:0048598	-		IPR000719; IPR008271; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), G3DSA:2.10.60.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), PTHR23255 (PANTHER), SignalP (SIGNALP), SSF57302 (SUPERFAMILY)
Caenorhabditis elegans	hypothetical protein Y37E11AL.2 [Caenorhabditis elegans]	0		F:GO:0004864; P:GO:0043666; P:GO:0009966		SignalP (SIGNALP)
	-	0				-
	-	0				SignalP (SIGNALP)
Brugia malayi	zinc finger ccch-type containing 12b	0		F:GO:0003676; F:GO:0046872; F:GO:0016787; F:GO:0008270; F:GO:0004519		IPR021869; PTHR12876 (PANTHER)
	-	0				-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	splicing factor 3b subunit 5	3	P:GO:0007052; C:GO:0071011; P:GO:0000398	-		-
Loa loa	mucin-like protein	0		F:GO:0004553; F:GO:0005525; F:GO:0030248; F:GO:0003924; P:GO:0005975; C:GO:0005576		-
	-	0				SignalP (SIGNALP)
Caenorhabditis elegans	ppm1b protein	2	F:GO:0046872; F:GO:0004721	-	EC:3.1.3.16	-
	-	0				-
Loa loa	smr domain containing protein	0				-
Caenorhabditis elegans	kinesin family member 1a	5	P:GO:0008089; F:GO:0005524; P:GO:0008152; F:GO:0003777; C:GO:0005874	-		IPR001752; PTHR16012 (PANTHER), PTHR16012:SF104 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-

Caenorhabditis briggsae	briggsae cbr-mup-4 protein	2	F:GO:0005509; F:GO:0005515	-		IPR000152; IPR000742; IPR006210; IPR013091; G3DSA:2.10.25.10 (GENE3D), PTHR22992 (PANTHER), PTHR22992:SF12 (PANTHER), SSF57196 (SUPERFAMILY)
Caenorhabditis elegans	ph domain containing protein	0		C:GO:0005634; P:GO:0007067; C:GO:0005737; P:GO:0051301; F:GO:0003779; F:GO:0005515; C:GO:0005938; P:GO:0007049; C:GO:0005856		-
Caenorhabditis elegans	ph domain containing protein	0		C:GO:0005634; P:GO:0007067; C:GO:0005737; P:GO:0051301; F:GO:0003779; F:GO:0005515; C:GO:0005938; P:GO:0007049; C:GO:0005856		-
Caenorhabditis elegans	ph domain containing protein	0		C:GO:0005634; P:GO:0007067; C:GO:0005737; P:GO:0051301; F:GO:0003779; F:GO:0005515; C:GO:0005938; P:GO:0007049; C:GO:0005856		IPR001849; IPR011993; PTHR21538 (PANTHER), PTHR21538:SF11 (PANTHER), SSF50729 (SUPERFAMILY)
Loa loa	hypothetical protein LOAG_10739 [Loa loa]	0				-
	-	0				-
Caenorhabditis briggsae	inositol -trisphosphate receptor	11	P:GO:0055085; P:GO:0000280; P:GO:0006979; P:GO:0051209; P:GO:0007629; C:GO:0016021; P:GO:0016319; F:GO:0005220; P:GO:0007591; C:GO:0005789; P:GO:0030322	-		IPR015925; PTHR13715:SF2 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	zinc finger ccch domain-containing protein 14	0		F:GO:0003723; F:GO:0046872; F:GO:0003676; F:GO:0008270; C:GO:0005634		-
	-	0				-
	-	0				IPR004827
	-	0				-
	-	0				-
	-	0				-

Caenorhabditis brenneri	atp-binding sub-family d member 4	1	F:GO:0017111	-	EC:3.6.1.15	IPR010509; IPR011527; IPR017940; G3DSA:1.20.1560.10 (GENE3D), PTHR11384 (PANTHER), PTHR11384:SF3 (PANTHER), SignalP (SIGNALP)
Loa loa	myeloid lymphoid or mixed-lineage leukemia (trithorax drosophila) translocated 10	5	C:GO:0005730; P:GO:0045944; F:GO:0046872; F:GO:0005515; C:GO:0005737	-		IPR001965; IPR011011; IPR013083; IPR019786; IPR019787; PTHR13793 (PANTHER), PTHR13793:SF23 (PANTHER)
Loa loa	gag protein	3	C:GO:0005737; P:GO:0001708; F:GO:0005488	-		IPR001878; IPR013084; PTHR11544 (PANTHER), PTHR11544:SF3 (PANTHER), SSF57756 (SUPERFAMILY)
Loa loa	r--binding protein lin-28	3	C:GO:0005737; P:GO:0001708; F:GO:0005488	-		IPR001878; IPR013084; SSF57756 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		F:GO:0005488; C:GO:0016021; C:GO:0016020; P:GO:0040010; P:GO:0055085; C:GO:0005743; P:GO:0006810		PTHR11662 (PANTHER), PTHR11662:SF9 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	g-patch domain containing protein	1	C:GO:0005622	-		IPR000467; PTHR23329 (PANTHER), PTHR23329:SF1 (PANTHER)
Caenorhabditis elegans	-t10 protein	10	P:GO:0040035; C:GO:0005730; P:GO:0009792; P:GO:0002119; F:GO:0008080; F:GO:0005515; F:GO:0005524; P:GO:0040011; P:GO:0008152; P:GO:0040007	-		IPR007807; PTHR10925 (PANTHER), PTHR10925:SF5 (PANTHER)
Caenorhabditis briggsae	n-acetyltransferase 10	10	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0008080; F:GO:0005515; P:GO:0040011; P:GO:0008152; P:GO:0040007; C:GO:0005634; F:GO:0000166	-		IPR007807; IPR016181; PTHR10925 (PANTHER), PTHR10925:SF5 (PANTHER)
Brugia malayi	g10 protein	11	P:GO:0008340; C:GO:0071011; P:GO:0040007; P:GO:0040035; P:GO:0019915; P:GO:0002119; P:GO:0000398; P:GO:0040011; P:GO:0006898; C:GO:0071013; P:GO:0009792	-		IPR001748; IPR018230
	-	0				-

Pristionchus pacificus	small subunit ribosomal protein 28	3	C:GO:0005840; F:GO:0003735; P:GO:0006412	-	EC:3.6.5.3	IPR000289; IPR012340; IPR016027; PTHR10769:SF1 (PANTHER)
Caenorhabditis briggsae	class member 2	2	F:GO:0004553; F:GO:0005488	-	EC:3.2.1.0	SignalP (SIGNALP)
Caenorhabditis briggsae	class member 2	2	F:GO:0004553; F:GO:0005488	-	EC:3.2.1.0	SignalP (SIGNALP)
Caenorhabditis briggsae	zinc finger protein 291	0		F:GO:0008270; C:GO:0005622		-
Caenorhabditis briggsae	zinc finger protein 291	0		F:GO:0008270; C:GO:0005622		-
Caenorhabditis elegans	ubiquitin-conjugating enzyme variant	0		C:GO:0016021		IPR019547; PTHR11621 (PANTHER), PTHR11621:SF1 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-ora-1 protein	0				IPR003677; PTHR21593 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-ora-1 protein	0				IPR003677; PTHR21593 (PANTHER)
Caenorhabditis briggsae	briggsae cbr-ora-1 protein	0				IPR003677; PTHR21593 (PANTHER)
Caenorhabditis briggsae	uncoordi-ted family member (unc-89)	0		F:GO:0005089; P:GO:0035023; C:GO:0005622		IPR003598; IPR007110; IPR013098; IPR013783; PTHR19897 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
	-	0				-
Brugia malayi	exosome complex exonuclease rrp4	0		F:GO:0003723; F:GO:0004527		IPR003029; IPR022967; PTHR21321 (PANTHER), PTHR21321:SF2 (PANTHER)
Caenorhabditis elegans	cg34118 cg34118-pa	0				IPR016017; SSF110035 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	5	F:GO:0003676; P:GO:0000003; F:GO:0005515; P:GO:0009792; P:GO:0006350	-		PS51257 (PROFILE)
Macaca mulatta	hepatitis b virus x interacting protein	4	F:GO:0005515; P:GO:0006916; C:GO:0005829; P:GO:0043154	-		PTHR13342 (PANTHER)
Caenorhabditis briggsae	clathrin coat assembly protein ap-1	5	P:GO:0016192; P:GO:0040025; F:GO:0005515; P:GO:0006886; C:GO:0030121	-		IPR008968; G3DSA:2.60.40.1170 (GENE3D), PTHR11998 (PANTHER), PTHR11998:SF11 (PANTHER)
Brugia malayi	hypothetical protein Bm1_12375 [Brugia malayi]	0				-
Caenorhabditis elegans	translation initiation factor eif-2b subunit beta	10	P:GO:0000003; P:GO:0040010; P:GO:0006898; P:GO:0040018; P:GO:0044237; P:GO:0050896; P:GO:0009792; P:GO:0002119; P:GO:0010171; F:GO:0005488	-		IPR000649; G3DSA:3.40.50.10470 (GENE3D), PTHR10233:SF9 (PANTHER), SSF100950 (SUPERFAMILY)
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	2	P:GO:0009987; P:GO:0008152	-		IPR003886; SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	protein son-like	2	C:GO:0005622; F:GO:0003725	-		SignalP (SIGNALP)
	-	0				-
	-	0				-

	-	0				-
Caenorhabditis elegans	hypothetical protein F45E4.3 [Caenorhabditis elegans]	0		P:GO:0040011		-
Loa loa	activator c11orf59-like	0				PTHR13401 (PANTHER), SignalP (SIGNALP)
Caenorhabditis briggsae	member ras oncogene family	10	P:GO:0007264; P:GO:0006355; P:GO:0006913; F:GO:0005524; F:GO:0008134; P:GO:0006886; C:GO:0005737; C:GO:0005634; F:GO:0005525; C:GO:0005886	-		IPR001806; IPR002078; IPR003579; IPR005225; IPR013753; IPR015598; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	member ras oncogene family	10	P:GO:0007264; P:GO:0006355; P:GO:0006913; F:GO:0005524; F:GO:0008134; P:GO:0006886; C:GO:0005737; C:GO:0005634; F:GO:0005525; C:GO:0005886	-		IPR001806; IPR002078; IPR003579; IPR005225; IPR013753; IPR015598; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	29kda protein from anisakis simplex	2	C:GO:0031672; C:GO:0055120	-		-
Caenorhabditis briggsae	Hypothetical protein CBG09826 [Caenorhabditis briggsae]	0				SignalP (SIGNALP)
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	ankyrin unc44	1	F:GO:0005488	-		IPR002110; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER)
Angiostrongylus cantonensis	hypothetical protein [Angiostrongylus cantonensis]	1	F:GO:0005488	-		-
Caenorhabditis elegans	rm23_caeel ame: full=probable 39s ribosomal protein mitochondrial short=l23mt short=mrp-l23	0		F:GO:0003735; P:GO:0006898; C:GO:0030529; C:GO:0005739; F:GO:0000166; P:GO:0006412; P:GO:0000003; P:GO:0002119; P:GO:0009792; C:GO:0005840; P:GO:0002009; C:GO:0005622; P:GO:0040010; P:GO:0040007; P:GO:0040035		-
Caenorhabditis briggsae	polymerase iii (d- directed) polypeptide 155kda	8	F:GO:0003899; F:GO:0008270; P:GO:0032728; P:GO:0045087; F:GO:0003677; F:GO:0032549; P:GO:0006351; C:GO:0005666	-	EC:2.7.7.6	IPR007081; IPR015700; PTHR19376 (PANTHER), SSF64484 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	ribosomal protein s5	11	P:GO:0006413; F:GO:0003729; P:GO:0008340; P:GO:0040007; F:GO:0003735; P:GO:0006450; P:GO:0000003; C:GO:0022627; P:GO:0002119; F:GO:0005515; P:GO:0009792	-		IPR000235; IPR005716; IPR020606
Caenorhabditis briggsae	briggsae cbr-apb-3 protein	31	C:GO:0000785; P:GO:0008156; C:GO:0030117; P:GO:0008340; P:GO:0000122; P:GO:0051101; C:GO:0035189; P:GO:0000080; P:GO:0007307; P:GO:0031396; P:GO:0040007; F:GO:0008565; P:GO:0007113; P:GO:0006727; P:GO:0016183; P:GO:0007040; C:GO:0005794; P:GO:0006886; P:GO:0008285; P:GO:0019915; P:GO:0009792; P:GO:0042023; P:GO:0002119; C:GO:0008021; P:GO:0010171; F:GO:0010843; F:GO:0008134;	-		IPR002553; IPR011989; PTHR11134 (PANTHER), PTHR11134:SF1 (PANTHER)
Caenorhabditis elegans	2-acylglycerol o-acyltransferase 1	3	F:GO:0016747; P:GO:0044238; C:GO:0044425	-	EC:2.3.1.0	IPR007130
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	0		P:GO:0006508; F:GO:0008168		-
Caenorhabditis elegans	elegans protein confirmed by transcript evidence	0				-
Loa loa	hypothetical protein LOAG_11699 [Loa loa]	0				-
Caenorhabditis elegans	n-deacetylase n-sulfotransferase	3	C:GO:0016020; C:GO:0005794; F:GO:0008146	-	EC:2.8.2.0	IPR021930; PTHR10605 (PANTHER), PTHR10605:SF2 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	n-deacetylase n-sulfotransferase	3	C:GO:0016020; C:GO:0005794; F:GO:0008146	-	EC:2.8.2.0	IPR021930; PTHR10605 (PANTHER), PTHR10605:SF2 (PANTHER), SignalP (SIGNALP)
	-	0				-

Caenorhabditis elegans	integral membrane protein gpr180	0		C:GO:0016021; C:GO:0016020; F:GO:0004930; P:GO:0007165; P:GO:0050909; F:GO:0004872; F:GO:0004871; P:GO:0007186; C:GO:0005886		IPR019336; PTHR23252 (PANTHER), PTHR23252:SF3 (PANTHER)
Caenorhabditis briggsae	paz domain containing protein	1	P:GO:0000003	-		-
Caenorhabditis elegans	hypothetical protein M04B2.6 [Caenorhabditis elegans]	0				SignalP (SIGNALP)
Brugia malayi	o-linked n-acetylglucosamine ogt	5	P:GO:0035220; F:GO:0005488; P:GO:0006486; F:GO:0008375; C:GO:0005634	-		PTHR23083 (PANTHER), PTHR23083:SF21 (PANTHER), SignalP (SIGNALP), SSF48452 (SUPERFAMILY)
Loa loa	mediator complex subunit rgr-1	6	P:GO:0006357; P:GO:0040007; F:GO:0016455; P:GO:0002119; C:GO:0016592; P:GO:0009792	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Brugia malayi	isoform a	0		F:GO:0003674; P:GO:0008150; C:GO:0005575		-
Caenorhabditis briggsae	briggsae cbr-dnj-15 protein	1	P:GO:0006974	-		IPR009073
Caenorhabditis elegans	pyridoxamine 5 -phosphate oxidase	4	P:GO:0008615; P:GO:0055114; F:GO:0004733; F:GO:0010181	-	EC:1.4.3.5	IPR000659; IPR009002; IPR011576; IPR012349; IPR019576; IPR019740
Caenorhabditis elegans	pyridoxamine 5 -phosphate oxidase	4	P:GO:0008615; F:GO:0016638; P:GO:0055114; F:GO:0010181	-		IPR000659; IPR009002; IPR011576; IPR012349
Caenorhabditis elegans	pyridoxamine 5 -phosphate oxidase	4	P:GO:0008615; P:GO:0055114; F:GO:0004733; F:GO:0010181	-	EC:1.4.3.5	IPR000659; IPR009002; IPR011576; IPR012349; IPR019576; IPR019740
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
Caenorhabditis elegans	zinc finger ccch type containing 6	8	P:GO:0040035; P:GO:0009792; P:GO:0002119; F:GO:0046872; P:GO:0040018; P:GO:0040010; P:GO:0040019; P:GO:0040011	-		IPR000571; IPR003006; G3DSA:4.10.1000.10 (GENE3D), PTHR13119 (PANTHER), PTHR13119:SF5 (PANTHER), SSF90229 (SUPERFAMILY)
	-	0				SignalP (SIGNALP)
Brugia malayi	proteasome (macropain) 26s non- 5	1	F:GO:0005488	-		IPR011989; IPR016024; IPR019538; PTHR13554 (PANTHER), PTHR13554:SF6 (PANTHER)
Brugia malayi	protein	0		F:GO:0004872; F:GO:0004497		-
Brugia malayi	protein	2	P:GO:0055114; F:GO:0070330	-		-

Brugia malayi	protein	2	P:GO:0055114; F:GO:0070330	-		-
Caenorhabditis elegans	probable atp-dependent r- helicase ddx56	4	F:GO:0003676; C:GO:0005730; F:GO:0000166; F:GO:0004386	-		IPR001650; IPR011545; IPR014001; IPR014021; G3DSA:3.40.50.300 (GENE3D), PTHR10967 (PANTHER), PTHR10967:SF29 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	amidase family protein	1	C:GO:0005811	-		IPR000120; PTHR11895:SF5 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	hypothetical protein R05G6.1 [Caenorhabditis elegans]	0				-
Caenorhabditis briggsae	elegans fln-2 isoform partially confirmed by transcript evidence	0		F:GO:0003779		IPR001298; IPR013783; IPR014756; IPR017868; PTHR11915 (PANTHER), PTHR11915:SF24 (PANTHER)
Camponotus floridanus	cullin 4b	4	P:GO:0071600; P:GO:0035118; P:GO:0045750; P:GO:0045732	-		IPR001373; IPR016159; G3DSA:1.20.1310.10 (GENE3D)
Brugia malayi	ubiquitin carboxyl-termi-l hydrolase 28	9	F:GO:0004221; P:GO:0010212; P:GO:0042771; F:GO:0004843; F:GO:0005515; P:GO:0000077; P:GO:0016579; C:GO:0005654; P:GO:0008283	-	EC:3.1.2.15	IPR001394; PTHR10420 (PANTHER), PTHR10420:SF18 (PANTHER), SSF54001 (SUPERFAMILY)
Loa loa	transcription elongation factor spt4	12	F:GO:0003746; P:GO:0008340; F:GO:0008270; P:GO:0045944; P:GO:0000122; F:GO:0008159; F:GO:0008148; P:GO:0006368; F:GO:0003700; F:GO:0046982; C:GO:0005654; P:GO:0006338	-		IPR016046; IPR022800; SSF63393 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-cyn-16 protein	1	F:GO:0016853	-		-
Brugia malayi	hypothetical protein Bm1_20725 [Brugia malayi]	0				-
Caenorhabditis briggsae	3-oxo-5-alpha-steroid 4-dehydroge-se 3-like	4	F:GO:0016627; P:GO:0006629; C:GO:0005737; P:GO:0044237	-		PTHR14624 (PANTHER), SignalP (SIGNALP)
	-	0				-
Caenorhabditis elegans	melanocortin 4 receptor	4	F:GO:0004871; P:GO:0023052; P:GO:0065007; C:GO:0016020	-		IPR000276; IPR017452; G3DSA:1.20.1070.10 (GENE3D), PTHR19264 (PANTHER), PTHR19264:SF10 (PANTHER), SSF81321 (SUPERFAMILY)
Homo sapiens	-dh dehydroge-se	5	F:GO:0008565; C:GO:0005747; C:GO:0016021; P:GO:0022900; P:GO:0015031	-		-
Caenorhabditis briggsae	phosphatidylinositol transfer protein	2	C:GO:0005622; P:GO:0006810	-		IPR001666; G3DSA:3.30.530.20 (GENE3D), PTHR10658:SF8 (PANTHER), SSF55961 (SUPERFAMILY)

Caenorhabditis elegans	sugar transporter family protein	2	P:GO:0006810; C:GO:0044464	-		IPR005828; IPR005829; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11600 (PANTHER), PTHR11600:SF100 (PANTHER), SignalP (SIGNALP)
Brugia malayi	conserved oligomeric golgi complex subunit 4	3	N:GO:0071842; P:GO:0048193; C:GO:0044431	-		-
	-	0				SignalP (SIGNALP)
Caenorhabditis briggsae	ectonucleoside triphosphate diphosphohydrolase isoform cra_b	2	P:GO:0008152; F:GO:0016787	-		IPR000407; PTHR11782:SF7 (PANTHER)
Caenorhabditis briggsae	1-aminocyclopropane-1-carboxylate synthase	1	F:GO:0003824	-		IPR001176; IPR004839; IPR015421; IPR015424; PTHR11751 (PANTHER), PTHR11751:SF26 (PANTHER)
	-	0				-
Caenorhabditis elegans	atp-binding sub-family b (mdr tap) member 6	13	C:GO:0005774; P:GO:0071585; P:GO:0070574; F:GO:0015086; F:GO:0020037; F:GO:0015562; C:GO:0005794; P:GO:0015886; F:GO:0015439; C:GO:0005886; P:GO:0006779; F:GO:0005524; C:GO:0031307	-	EC:3.6.3.41	IPR001140; IPR003439; IPR003593; IPR011527; IPR017871; IPR017940; G3DSA:1.20.1560.10 (GENE3D), G3DSA:3.40.50.300 (GENE3D), PTHR19242 (PANTHER), PTHR19242:SF69 (PANTHER), SSF52540 (SUPERFAMILY)
	-	0				-
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0006629; C:GO:0016021; F:GO:0016787; F:GO:0004806		IPR002921; G3DSA:3.40.50.1820 (GENE3D), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0		P:GO:0006629; C:GO:0016021; F:GO:0016787; F:GO:0004806		IPR002921; G3DSA:3.40.50.1820 (GENE3D), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis briggsae	elegans protein partially confirmed by transcript evidence	1	F:GO:0005515	-		-
Caenorhabditis briggsae	briggsae cbr-ddr-2 protein	1	P:GO:0040010	-		IPR020685; IPR020742; G3DSA:3.30.200.20 (GENE3D)
Taeniopygia guttata	ubiquitin specific peptidase 5 (isopeptidase t)	3	F:GO:0008233; P:GO:0006511; F:GO:0005488	-		-
Taeniopygia guttata	ubiquitin specific peptidase 5 (isopeptidase t)	3	F:GO:0008233; P:GO:0006511; F:GO:0005488	-		-
Nematostella vectensis	sphingosine-1-phosphate phosphatase 1	9	P:GO:0006915; C:GO:0005624; C:GO:0005794; P:GO:0006668; P:GO:0006670; C:GO:0005783; C:GO:0015629; C:GO:0005739; F:GO:0042392	-		IPR000326; IPR016118; PTHR14969 (PANTHER), PTHR14969:SF4 (PANTHER)

Caenorhabditis elegans	adenosine deami-se	15	P:GO:0034656; P:GO:0046700; P:GO:0048534; P:GO:0009168; P:GO:0002684; F:GO:0004000; P:GO:0009792; P:GO:0030154; P:GO:0048523; P:GO:0048522; P:GO:0050896; P:GO:0042278; P:GO:0046649; P:GO:0051239; C:GO:0016020	-	EC:3.5.4.4	SignalP (SIGNALP)
Caenorhabditis elegans	adenosine deami-se	15	P:GO:0034656; P:GO:0046700; P:GO:0048534; P:GO:0009168; P:GO:0002684; F:GO:0004000; P:GO:0009792; P:GO:0030154; P:GO:0048523; P:GO:0048522; P:GO:0050896; P:GO:0042278; P:GO:0046649; P:GO:0051239; C:GO:0016020	-	EC:3.5.4.4	SignalP (SIGNALP)
Caenorhabditis briggsae	protein c14orf166	0		F:GO:0005515; F:GO:0042802; F:GO:0003677		-
Caenorhabditis briggsae	hypothetical kda protein in chromosome	1	F:GO:0005515	-		IPR020830; PTHR23136 (PANTHER), PTHR23136:SF1 (PANTHER)
Caenorhabditis briggsae	aldo-keto reductase	3	P:GO:0040010; P:GO:0002119; P:GO:0040011	-		IPR001395; IPR018170; IPR020471; IPR023210; PTHR11732:SF34 (PANTHER)
Caenorhabditis briggsae	mitochondrial processing peptidase beta subunit	8	P:GO:0009792; P:GO:0002119; F:GO:0004222; P:GO:0040010; P:GO:0000003; P:GO:0008340; P:GO:0006508; F:GO:0008270	-	EC:3.4.24.0	IPR001431; IPR007863; IPR011237; IPR011249; IPR011765; PTHR11851 (PANTHER), PTHR11851:SF58 (PANTHER), SignalP (SIGNALP)

Caenorhabditis briggsae	insulin-degrading enzyme	21	P:GO:0051603; P:GO:0051291; F:GO:0031626; F:GO:0008270; P:GO:0051289; F:GO:0043559; C:GO:0031597; C:GO:0005615; F:GO:0001540; C:GO:0009986; P:GO:0045861; F:GO:0004222; P:GO:0050435; F:GO:0016887; F:GO:0042803; P:GO:0006200; C:GO:0005634; C:GO:0005782; F:GO:0005524; P:GO:0042447; C:GO:0005739	-	EC:3.4.24.0	IPR001431; IPR007863; IPR011237; IPR011249; IPR011765; IPR018247; PTHR11851 (PANTHER), PTHR11851:SF64 (PANTHER), SignalP (SIGNALP)
Brugia malayi	enhancer of rudimentary homolog	4	P:GO:0007049; P:GO:0042742; P:GO:0006213; F:GO:0005515	-		IPR000781; SSF143875 (SUPERFAMILY)
Brugia malayi	enhancer of rudimentary homolog	4	P:GO:0007049; P:GO:0042742; P:GO:0006213; F:GO:0005515	-		-
Caenorhabditis elegans	ankyrin repeat domain protein	1	F:GO:0005515	-		IPR002110; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER), PTHR18958:SF273 (PANTHER)
Glossina morsitans morsitans	serine protease easter	0		P:GO:0006508; F:GO:0004252; F:GO:0008236; P:GO:0006911; F:GO:0016787; F:GO:0003824; F:GO:0008233		IPR001254; IPR009003; IPR018114; G3DSA:2.40.10.10 (GENE3D), PTHR19355 (PANTHER), PTHR19355:SF82 (PANTHER)
	-	0				-
Pongo abelii	ribosomal protein s10	4	C:GO:0005730; F:GO:0005515; C:GO:0022627; P:GO:0006414	-		-
	-	0				SignalP (SIGNALP)
	-	0				-
Haemonchus contortus	myosin heavy chain	6	C:GO:0032982; F:GO:0003779; F:GO:0005524; F:GO:0003774; C:GO:0031672; P:GO:0007626	-		SignalP (SIGNALP)
Brugia malayi	hypothetical kda protein in chromosome	1	C:GO:0016020	-		PTHR21191 (PANTHER), PTHR21191:SF3 (PANTHER), SignalP (SIGNALP)
Bombyx mori	sericin 2 isoform 1 precursor	0				-
	-	0				-
	-	0				-

Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	0				-
	-	0				-
Brugia malayi	hypothetical protein Bm1_38255 [Brugia malayi]	0				-
Caenorhabditis elegans	hatching enzyme	2	F:GO:0008233; P:GO:0007413	-		IPR001506; IPR006026; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF73 (PANTHER), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	hatching enzyme	2	F:GO:0016787; P:GO:0007413	-		IPR001506; IPR006026; G3DSA:3.40.390.10 (GENE3D), PTHR10127 (PANTHER), PTHR10127:SF73 (PANTHER), SignalP (SIGNALP), SSF55486 (SUPERFAMILY)
Caenorhabditis elegans	pten induced ki-se 1	16	P:GO:0090200; P:GO:0031396; P:GO:0033603; C:GO:0005743; C:GO:0005829; C:GO:0005741; F:GO:0055131; F:GO:0010857; P:GO:0043123; P:GO:0018105; F:GO:0004674; F:GO:0000287; P:GO:0032226; P:GO:0006950; P:GO:0043254; F:GO:0005524	-	EC:2.7.11.0	IPR000719; IPR011009; IPR017442; G3DSA:1.10.510.10 (GENE3D), PTHR22972 (PANTHER)
Trichomonas vaginalis G3	heavy polypeptide non- isoform cra_a	0		C:GO:0043025; P:GO:0006930; C:GO:0005886; P:GO:0008152; F:GO:0000146; P:GO:0021680; F:GO:0043531; P:GO:0001701; P:GO:0001764; P:GO:0055003; F:GO:0051015; P:GO:0006928; C:GO:0005819; C:GO:0030496; P:GO:0007420; F:GO:0005524; P:GO:0030048; P:GO:0021678; P:GO:0006887; F:GO:0000166; P:GO:0007097; P:GO:0030239; P:GO:0021670; C:GO:0001725; C:GO:0005938; P:GO:0007512;		-

Caenorhabditis elegans	f-box only protein	6	P:GO:0060966; F:GO:0008270; P:GO:0070923; F:GO:0004842; F:GO:0005515; C:GO:0048471	-	EC:6.3.2.19	IPR006626; IPR011050; IPR012334; IPR022441; PTHR22990 (PANTHER), PTHR22990:SF6 (PANTHER)
	-	0				-
Caenorhabditis elegans	ortholog of drosophila d a gene family member (drsh-1)	10	F:GO:0004525; F:GO:0003723; P:GO:0000910; P:GO:0031053; P:GO:0007052; P:GO:0019953; P:GO:0042254; P:GO:0009792; P:GO:0016072; C:GO:0005634	-	EC:3.1.26.3	IPR000999; PTHR11207 (PANTHER)
Caenorhabditis elegans	neural stem cell-derived dendrite regulator	1	F:GO:0005515	-		G3DSA:3.40.50.1820 (GENE3D), PTHR21493 (PANTHER), PTHR21493:SF6 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
Caenorhabditis elegans	neural stem cell-derived dendrite regulator	2	F:GO:0016787; F:GO:0005515	-		G3DSA:3.40.50.1820 (GENE3D), PTHR21493 (PANTHER), PTHR21493:SF6 (PANTHER), SignalP (SIGNALP), SSF53474 (SUPERFAMILY)
	-	0				-
						IPR003599; IPR003961; IPR007110; IPR008957; IPR013098; IPR013783; PR00014 (PRINTS), PTHR19900 (PANTHER), PTHR19900:SF7 (PANTHER), SSF48726 (SUPERFAMILY)
	-	0				-
	-	0				-
Caenorhabditis elegans	cleavage and polyadenylation specificity factor	3	F:GO:0016787; P:GO:0016180; C:GO:0032039	-		-
Loa loa	late secretory pathway protein avl9 homolog	1	C:GO:0016021	-		IPR001194; IPR018307
Caenorhabditis briggsae	elegans protein confirmed by transcript evidence	5	P:GO:0006633; F:GO:0016717; F:GO:0005515; F:GO:0020037; P:GO:0055114	-	EC:1.14.19.0	IPR001199; IPR005804; PTHR19353 (PANTHER)
	-	0				SignalP (SIGNALP)
	-	0				-
Brugia malayi	topoisomerase iii alpha	5	P:GO:0006259; P:GO:0007276; P:GO:0007126; P:GO:0071103; F:GO:0003916	-		-
Angiostrongylus cantonensis	tumor suppressing subtransferable candidate 1	0		F:GO:0003674; F:GO:0005515		IPR001680; IPR015943; IPR017986; IPR019781; IPR019782; PTHR14205 (PANTHER), PTHR14205:SF6 (PANTHER), SSF101908 (SUPERFAMILY)
	-	0				-

Caenorhabditis elegans	cbp p300 homolog family member (cbp-1)	13	F:GO:0008270; F:GO:0004402; P:GO:0040010; F:GO:0003712; P:GO:0040026; P:GO:0007283; P:GO:0018996; C:GO:0005737; P:GO:0040039; P:GO:0009792; P:GO:0045944; C:GO:0005634; P:GO:0040035	-	EC:2.3.1.48	IPR001487; IPR010303; IPR019786; PTHR13808 (PANTHER)
	-	0				-
Ailuropoda melanoleuca	alpha 1 type i collagen preproprotein isoform 2	31	P:GO:0060351; P:GO:0001957; P:GO:0071363; P:GO:0007605; P:GO:0034505; P:GO:0042542; P:GO:0001649; P:GO:0009612; P:GO:0001568; P:GO:0060325; F:GO:0005201; C:GO:0005615; P:GO:0048706; P:GO:0015031; F:GO:0048407; C:GO:0005737; P:GO:0043434; P:GO:0071300; P:GO:0007601; P:GO:0010812; C:GO:0005584; F:GO:0042802; P:GO:0060346; P:GO:0032964; P:GO:0030199; P:GO:0051591;	-		IPR008160; PTHR10499 (PANTHER), PTHR10499:SF122 (PANTHER)
	-	0				-
Caenorhabditis elegans	proteasome subunit alpha type 3	9	C:GO:0015630; P:GO:0051436; P:GO:0051437; F:GO:0042802; F:GO:0004298; P:GO:0031145; C:GO:0019773; C:GO:0005737; C:GO:0005634	-	EC:3.4.25.0	-
Homo sapiens	fam128b protein	4	C:GO:0005819; C:GO:0005813; F:GO:0005515; C:GO:0008274	-		-

Caenorhabditis briggsae	major facilitator superfamily protein	15	P:GO:0055085; P:GO:0015893; F:GO:0015238; C:GO:0016021; P:GO:0040007; P:GO:0070715; P:GO:0052106; C:GO:0031526; F:GO:0030165; P:GO:0002119; C:GO:0016324; P:GO:0060731; P:GO:0015879; P:GO:0009792; F:GO:0015226	-		IPR011701; IPR016196; IPR020846; G3DSA:1.20.1250.20 (GENE3D), PTHR11600 (PANTHER), PTHR11600:SF42 (PANTHER), SignalP (SIGNALP)
Caenorhabditis elegans	d--directed r- polymerase i subunit rpa1	7	F:GO:0003899; P:GO:0009303; C:GO:0005654; F:GO:0003677; C:GO:0005736; F:GO:0005515; F:GO:0008270	-	EC:2.7.7.6	-
Loa loa	drim protein	11	C:GO:0005730; C:GO:0030688; P:GO:0000472; P:GO:0008285; C:GO:0030686; F:GO:0005515; C:GO:0032040; P:GO:0000480; C:GO:0005654; C:GO:0005737; P:GO:0000447	-		-
Caenorhabditis brenneri	d--directed r- polymerase iii subunit rpc10	9	F:GO:0003899; P:GO:0050896; F:GO:0030528; F:GO:0008270; P:GO:0006383; P:GO:0045449; F:GO:0003677; C:GO:0005666; C:GO:0005737	-	EC:2.7.7.6	IPR001222; G3DSA:2.20.25.10 (GENE3D), PTHR11239 (PANTHER), PTHR11239:SF2 (PANTHER), SSF57783 (SUPERFAMILY)
Loa loa	paired amphipathic helix repeat family protein	4	F:GO:0051287; F:GO:0016616; C:GO:0005634; P:GO:0006355	-	EC:1.1.1.0	IPR003822; PTHR12346 (PANTHER), PS51477 (PROFILE)
Loa loa	paired amphipathic helix repeat family protein	4	F:GO:0051287; F:GO:0016616; C:GO:0005634; P:GO:0006355	-	EC:1.1.1.0	IPR003822; PTHR12346 (PANTHER), PS51477 (PROFILE)
Caenorhabditis briggsae	s-adenosylmethionine decarboxylase	5	P:GO:0006597; P:GO:0008295; F:GO:0016831; P:GO:0040011; P:GO:0007413	-	EC:4.1.1.0	IPR001985; IPR016067
Brugia malayi	dehydroge-se reductase sdr family member 7b	3	C:GO:0044464; P:GO:0008152; F:GO:0003824	-		IPR002198; IPR002347; IPR016040; PTHR19410:SF44 (PANTHER), SignalP (SIGNALP), SSF51735 (SUPERFAMILY)

	-	0				-
	-	0				-
Caenorhabditis elegans	elegans protein partially confirmed by transcript evidence	0				-
Caenorhabditis elegans	briggsae cbr-acbp-5 protein	0		F:GO:0005488; F:GO:0000062; P:GO:0010288		IPR000582; IPR002110; IPR020683; PR01415 (PRINTS), PTHR18958 (PANTHER), PTHR18958:SF176 (PANTHER)
Caenorhabditis briggsae	alpha-amylase	1	F:GO:0003824	-		IPR013781; IPR017853
Caenorhabditis briggsae	propionyl- carboxylase	8	P:GO:0009792; P:GO:0002119; F:GO:0003723; F:GO:0004485; P:GO:0040010; F:GO:0004525; F:GO:0004658; P:GO:0006396	-	EC:6.4.1.4; EC:3.1.26.3; EC:6.4.1.3	IPR000022; IPR011763; G3DSA:3.90.226.10 (GENE3D), PTHR22855 (PANTHER), PTHR22855:SF13 (PANTHER), SSF52096 (SUPERFAMILY)
Brugia malayi	hypothetical zinc finger protein in chromosome	3	F:GO:0003676; C:GO:0005622; F:GO:0008270	-		IPR007087; IPR013087; IPR015880; PTHR11389 (PANTHER), SSF57667 (SUPERFAMILY)
Loa loa	ubiquitin	5	C:GO:0005737; P:GO:0000003; P:GO:0040007; C:GO:0005634; P:GO:0002119	-		IPR000626; IPR019954; IPR019955; IPR019956; G3DSA:3.10.20.90 (GENE3D), PTHR10666 (PANTHER), PTHR10666:SF9 (PANTHER), SignalP (SIGNALP), SSF54236 (SUPERFAMILY)
Caenorhabditis briggsae	phospholipase b-like lami- ancestor	0		P:GO:0008150; C:GO:0005575		IPR007000; SignalP (SIGNALP)
	-	0				-
Strongylocentrotus purpuratus	autophagy related protein atg12-like protein	4	C:GO:0005737; C:GO:0005625; C:GO:0005624; P:GO:0006914	-		-
	-	0				-
Caenorhabditis briggsae	member ras oncogene isoform cra_a	19	P:GO:0008103; C:GO:0000139; P:GO:0018125; P:GO:0006913; P:GO:0001745; C:GO:0005626; F:GO:0005525; F:GO:0004767; P:GO:0006887; P:GO:0006886; F:GO:0001671; F:GO:0051117; P:GO:0007264; P:GO:0009792; P:GO:0050790; F:GO:0003924; C:GO:0005634; P:GO:0007293; P:GO:0045451	-	EC:3.1.4.12; EC:3.6.5.1; EC:3.6.5.2; EC:3.6.5.3; EC:3.6.5.4	IPR001806; IPR003579; IPR005225; IPR013753; IPR015600; IPR020851; G3DSA:3.40.50.300 (GENE3D), PTHR11708 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	briggsae cbr-imp-3 protein	0		F:GO:0004190; C:GO:0016021		PS51257 (PROFILE), SignalP (SIGNALP)
Brugia malayi	hypothetical protein [Brugia malayi]	0				PTHR13673 (PANTHER)
Caenorhabditis briggsae	Hypothetical protein CBG14950 [Caenorhabditis briggsae]	3	P:GO:0040018; P:GO:0040035; P:GO:0002119	-		-
	-	0				-

Brugia malayi	ribosomal protein s29	13	P:GO:0006412; P:GO:0001525; P:GO:0040010; C:GO:0005840; P:GO:0001570; P:GO:0051726; F:GO:0046872; F:GO:0003735; P:GO:0000003; P:GO:0010171; P:GO:0002119; P:GO:0060218; P:GO:0009792	-	EC:3.6.5.3	-
Haemonchus contortus	myosin heavy chain	6	C:GO:0032982; F:GO:0003779; F:GO:0005524; F:GO:0003774; C:GO:0031672; P:GO:0007626	-		IPR001609; IPR002928; IPR009053; IPR015650; PD936484 (PRODOM), G3DSA:4.10.270.10 (GENE3D), PTHR13140 (PANTHER), SSF52540 (SUPERFAMILY)
Haemonchus contortus	myosin heavy chain	6	C:GO:0032982; F:GO:0003779; F:GO:0005524; F:GO:0003774; C:GO:0031672; P:GO:0007626	-		IPR001609; IPR002928; IPR004009; IPR009053; IPR015650; PD936484 (PRODOM), G3DSA:4.10.270.10 (GENE3D), PTHR13140 (PANTHER), SSF52540 (SUPERFAMILY)
Caenorhabditis briggsae	profilin iii	18	P:GO:0009653; P:GO:0008340; P:GO:0003006; P:GO:0048610; C:GO:0015629; P:GO:0007283; P:GO:0040011; P:GO:0048468; C:GO:0005737; P:GO:0051179; F:GO:0003779; P:GO:0045927; P:GO:0009792; P:GO:0008361; P:GO:0007015; P:GO:0048477; P:GO:0007399; P:GO:0000910	-		-
Caenorhabditis elegans	proton-coupled amino acid transporter 1	0		C:GO:0016021; C:GO:0016020		-
	-	0				-
Caenorhabditis briggsae	-dh dehydroge-se	7	P:GO:0009792; P:GO:0002119; C:GO:0005743; C:GO:0070469; P:GO:0006810; P:GO:0040007; P:GO:0022900	-		PTHR15223 (PANTHER), SignalP (SIGNALP)

Caenorhabditis briggsae	-dh dehydroge-se	7	P:GO:0009792; P:GO:0002119; C:GO:0005743; C:GO:0070469; P:GO:0006810; P:GO:0040007; P:GO:0022900	-		-
Caenorhabditis briggsae	e3 ubiquitin-protein ligase ubr2	1	F:GO:0005488	-		PTHR21497 (PANTHER), PTHR21497:SF6 (PANTHER), SignalP (SIGNALP)
Brugia malayi	saga-associated factor 29-like protein	0				IPR010750; PTHR21539 (PANTHER)
Caenorhabditis elegans	28s ribosomal protein mitochondrial	7	P:GO:0040010; C:GO:0005840; P:GO:0008340; P:GO:0040035; P:GO:0002119; P:GO:0006898; P:GO:0009792	-		IPR000754; IPR014721; IPR020568
Caenorhabditis briggsae	briggsae cbr-pif-1 protein	0		F:GO:0016887		-
Caenorhabditis briggsae	glutamine-dependent -d(+) synthetase	4	F:GO:0016810; F:GO:0005524; F:GO:0003952; P:GO:0009435	-	EC:6.3.5.1	-
	-	0				-
	-	0				-