Supplementary Information

Proteomic analysis of MYB-regulated secretome identifies functional pathways and biomarkers: potential pathobiological and clinical implications

Haseeb Zubair[1,2,^], Girijesh Kumar Patel[2,^], Mohammad Aslam Khan[1,2], Shafquat Azim[2], Asif Zubair[3], Seema Singh[1,2,4,], Sanjeev Kumar Srivastava[1,2], Ajay Pratap Singh[1,2,4,*]

[1]Department of Pathology, College of Medicine, University of South Alabama, Mobile, AL 36617; [2]Mitchell Cancer Institute, University of South Alabama, Mobile, AL 36604; [3]Molecular and Computational Biology, School of Biological Sciences, Dornsife College of Letters, Arts and Sciences, University of Southern California, Los Angeles, CA 90089, USA, [4]Department of Biochemistry and Molecular Biology, College of Medicine, University of South Alabama, Mobile, AL 36688

Running title: MYB-regulated pancreatic cancer secretome

***Correspondence to:**
Ajay Pratap Singh, PhD
Professor and Director of Research
Department of Pathology, College of Medicine
Program Leader, Cancer Biology
Mitchell Cancer Institute, University of South Alabama
1660 Springhill Avenue, Mobile, AL 36604
Tel: +1 251-445-9843, Fax: +1 251-460-6994
Email: asingh@health.southalabama.edu

Supplementary Table 1 (A): List of proteins identified in MiaPaCa (-Scr and -shMYB) cell lines

Checked	Master	Protein Gro	Accession	Descriptio	Coverage	# Peptides	# PSMs	# Unique P	# Protein G	# AAs	MW [kDa]	calc. pI	Found in Sa	Found in Sa	Found in Sa	Found in Sa	Found in Sa	Found in Sa	Modificatio	Area: F73:	Area: F72:	Area: F71:	Area: F70:	Area: F69:	Area: F68:	Score Sequ	# Peptides	Score Masc	# Peptides
FALSE	Master Pro	228	578798587	PREDICTED	26	8	262	7	1	434	47.3	6.99	High	High	High	High	High	High		1.29E+08	1.37E+08	1.26E+08	3.09E+08	3.06E+08	3E+08	388.88	8	4612	8
FALSE	Master Pro	228	4503571	alpha-enol	26	8	262	7	1	434	47.1	7.39	High	High	High	High	High	High		1.29E+08	1.37E+08	1.26E+08	3.09E+08	3.06E+08	3E+08	388.88	8	4612	8
FALSE	None	228	319996655	c-myc pror	21	5	203	5	1	341	36.9	6.28	High	High	High	High	High	High		82333167	91290240	86790573	2.07E+08	2.07E+08	2E+08	311.62	5	3609	5
FALSE	Master Pro	32	578818565	PREDICTED	32	16	225	16	1	466	53.6	5.12	High	High	High	High	High	High		1.14E+08	1.8E+08	1.3E+08	3.54E+08	3.37E+08	3.39E+08	280.18	16	2317	16
FALSE	Master Pro	129	5729877	heat shock	22	12	123	9	1	646	70.9	5.52	High	High	High	High	High	High		20890168	27685375	26494201	73763112	74908156	78199314	172.69	12	1153	12
FALSE	None	129	24234686	heat shock	27	11	121	8	1	493	53.5	5.86	High	High	High	High	High	High		20890168	27685375	26494201	73763112	74908156	78199314	169.51	11	1121	11
FALSE	Master Pro	104	530405975	PREDICTED	22	9	107	9	1	591	64.5	8.02	High	High	High	High	High	High		24813598	27340954	25478573	81104672	79444507	82468918	166.53	9	1502	9
FALSE	Master Pro	104	578827087	PREDICTED	22	9	107	9	1	605	65.8	7.99	High	High	High	High	High	High		24813598	27340954	25478573	81104672	79444507	82468918	166.53	9	1502	9
FALSE	Master Pro	104	530405979	PREDICTED	25	9	107	9	1	531	57.9	7.84	High	High	High	High	High	High		24813598	27340954	25478573	81104672	79444507	82468918	166.53	9	1502	9
FALSE	None	104	332164777	pyruvate ki	23	7	98	7	1	457	49.9	7.83	High	High	High	High	High	High		24813598	27340954	25478573	81104672	79444507	80546775	155.31	7	1466	7
FALSE	None	104	33286422	pyruvate ki	22	8	97	8	1	531	58	7.71	High	High	High	High	High	High		24813598	27340954	25478573	81104672	79444507	82468918	150.81	8	1369	8
FALSE	None	104	332164775	pyruvate ki	19	8	97	8	1	605	65.9	7.87	High	High	High	High	High	High		24813598	27340954	25478573	81104672	79444507	82468918	150.81	8	1369	8
FALSE	None	104	332164781	pyruvate ki	21	8	97	8	1	536	58.5	7.71	High	High	High	High	High	High		24813598	27340954	25478573	81104672	79444507	82468918	150.81	8	1369	8
FALSE	Master Pro	276	87196339	collagen al	11	8	105	8	1	1028	108.5	5.43	High	High	High	High	High	High		20732869	10874694	23926961	54041052	59383617	62979196	149.74	7	1448	8
FALSE	Master Pro	106	372466577	keratin, typ	22	9	105	8	1	483	53.7	5.59	High	High	High	High	High	High		43857838	70905342	66588358	1.08E+08	1.01E+08	1.08E+08	149.2	9	1189	9
FALSE	Master Pro	106	372466572	keratin, typ	21	9	105	8	1	511	56.6	5.43	High	High	High	High	High	High		43857838	70905342	66588358	1.08E+08	1.01E+08	1.08E+08	149.2	9	1189	9
FALSE	Master Pro	160	16507237	78 kDa gluc	20	9	100	8	1	654	72.3	5.16	High	High	High	High	High	High		17008489	19056623	19060088	36189495	37265125	38837912	148.81	9	1196	9
FALSE	None	104	332164779	pyruvate ki	20	7	88	7	1	516	56.2	8.44	High	High	High	High	High	High		17448659	19019658	17469354	49541687	47527729	47746676	141.8	7	1403	7
FALSE	Master Pro	15	578831328	PREDICTED	19	12	114	3	1	468	51.2	7.2	High	High	High	High	High	High		1.99E+08	3.9E+08	3.37E+08	6.82E+08	4.62E+08	1.03E+08	139.94	12	825	12
FALSE	Master Pro	15	316659409	actin, cytop	23	12	114	3	1	375	41.8	5.48	High	High	High	High	High	High		1.99E+08	3.9E+08	3.37E+08	6.82E+08	4.62E+08	1.03E+08	139.94	12	825	12
FALSE	Master Pro	15	4501885	actin, cytop	23	12	114	3	1	375	41.7	5.48	High	High	High	High	High	High		1.99E+08	3.9E+08	3.37E+08	6.82E+08	4.62E+08	1.03E+08	139.94	12	825	12
FALSE	Master Pro	170	4826898	profilin-1 [I	47	5	94	5	1	140	15	8.27	High	High	High	High	High	High		1.04E+08	1.2E+08	1.14E+08	2.04E+08	1.91E+08	1.94E+08	134.11	5	979	5
FALSE	Master Pro	182	10863927	peptidyl-pr	27	5	88	5	1	165	18	7.81	High	High	High	High	High	High		28545881	33080452	47839263	63692296	66535493	63996503	132.54	5	870	5
FALSE	Master Pro	195	4501881	actin, alpha	20	10	106	1	1	377	42	5.39	High	High	High	High	High	High		5419644	52425915	6618548	1.2E+08	1.2E+08	1.2E+08	132.33	10	636	10
FALSE	Master Pro	195	4885049	actin, alpha	20	10	106	1	1	377	42	5.39	High	High	High	High	High	High		5419644	52425915	6618548	1.2E+08	1.2E+08	1.2E+08	132.33	10	636	10
FALSE	Master Pro	102	530381931	PREDICTED	18	9	80	4	1	724	83.2	5.03	High	High	High	High	High	High		15236431	11809113	10395922	56637045	59692069	60260306	127.03	9	1109	9
FALSE	Master Pro	102	431822408	heat shock	18	9	80	4	1	714	82.3	5.06	High	High	High	High	High	High		15236431	11809113	10395922	56637045	59692069	60260306	127.03	9	1109	9
FALSE	None	102	431822406	heat shock	17	8	76	4	1	676	78.2	5.05	High	High	High	High	High	High		15236431	11809113	10395922	56637045	59692069	60260306	123.04	8	1109	8
FALSE	Master Pro	136	50845388	annexin A2	24	7	85	7	1	357	40.4	8.37	High	High	High	High	High	High		13731097	12526806	13261599	60342687	59397175	61361367	122.9	7	825	7
FALSE	Master Pro	136	209862831	annexin A2	25	7	85	7	1	339	38.6	7.75	High	High	High	High	High	High		13731097	12526806	13261599	60342687	59397175	61361367	122.9	7	825	7
FALSE	Master Pro	277	5031863	galectin-3-	13	7	94	7	1	585	65.3	5.27	High	High	High	High	High	High		14599441	17881428	16790266	42293652	40777506	47418684	121.86	7	981	7
FALSE	Master Pro	114	5031635	cofilin-1 [H	25	4	74	4	1	166	18.5	8.09	High	High	High	High	High	High		65190216	73532310	68494266	1.2E+08	98086493	1.01E+08	117.92	4	881	4
FALSE	Master Pro	221	4504183	glutathione	21	3	64	3	1	210	23.3	5.64	High	High	High	High	High	High		27040325	26990660	26072930	52254207	50606668	49995630	117.73	3	1473	3
FALSE	Master Pro	113	530391067	PREDICTED	20	6	68	6	1	440	48.5	5.54	High	High	High	High	High	High		8674278	7756359	4865779	16554978	20518027	20763516	109.29	6	970	6
FALSE	Master Pro	113	14165435	heterogene	19	6	68	6	1	463	50.9	5.54	High	High	High	High	High	High		8674278	7756359	4865779	16554978	20518027	20763516	109.29	6	970	6
FALSE	Master Pro	113	530391071	PREDICTED	20	6	68	6	1	439	48.5	5.92	High	High	High	High	High	High		8674278	7756359	4865779	16554978	20518027	20763516	109.29	6	970	6
FALSE	Master Pro	113	14165439	heterogene	19	6	68	6	1	464	51	5.33	High	High	High	High	High	High		8674278	7756359	4865779	16554978	20518027	20763516	109.29	6	970	6
FALSE	None	195	4501889	actin, gam	17	8	90	1	1	376	41.9	5.48	High	High	High	High	High	High		5419644	52425915	6618548	1.2E+08	1.2E+08	1.2E+08	108.85	8	582	8
FALSE	None	195	4501883	actin, aorti	17	8	90	1	1	377	42	5.39	High	High	High	High	High	High		5419644	52425915	6618548	1.2E+08	1.2E+08	1.2E+08	108.85	8	582	8
FALSE	None	114	343887344	cofilin-2 isc	19	3	65	3	1	149	16.9	8.62	High	High	High	High	High	High		56982976	64437088	60430589	1.2E+08	1.27E+08	1.32E+08	108.79	3	837	3
FALSE	None	114	33946278	cofilin-2 isc	17	3	65	3	1	166	18.7	7.88	High	High	High	High	High	High		56982976	64437088	60430589	1.2E+08	1.27E+08	1.32E+08	108.79	3	837	3
FALSE	Master Pro	51	24119203	tropomyos	24	6	63	5	1	248	29	4.78	High	High	High	High	High	High		17009738	23208005	20960128	20946541	20368394	22616412	107.8	6	826	6
FALSE	Master Pro	51	499137520	tropomyos	26	6	63	5	1	227	26.4	4.78	High	High	High	High	High	High		17009738	23208005	20960128	20946541	20368394	22616412	107.8	6	826	6
FALSE	Master Pro	51	114155144	tropomyos	24	6	63	5	1	248	28.9	4.75	High	High	High	High	High	High		17009738	23208005	20960128	20946541	20368394	22616412	107.8	6	826	6
FALSE	Master Pro	51	114155146	tropomyos	24	6	63	5	1	247	28.9	4.81	High	High	High	High	High	High		17009738	23208005	20960128	20946541	20368394	22616412	107.8	6	826	6
FALSE	Master Pro	51	499137518	tropomyos	24	6	63	5	1	248	28.9	4.75	High	High	High	High	High	High		17009738	23208005	20960128	20946541	20368394	22616412	107.8	6	826	6
FALSE	Master Pro	51	114155148	tropomyos	24	6	63	5	1	247	28.8	4.77	High	High	High	High	High	High		17009738	23208005	20960128	20946541	20368394	22616412	107.8	6	826	6
FALSE	Master Pro	51	578801453	PREDICTED	24	6	63	5	1	248	28.8	4.72	High	High	High	High	High	High		17009738	23208005	20960128	20946541	20368394	22616412	107.8	6	826	6
FALSE	Master Pro	280	226529917	triosephos	21	5	71	5	1	286	30.8	5.92	High	High	High	High	High	High		32275361	43032641	46955863	1.37E+08	1.26E+08	1.32E+08	99.89	5	875	5
FALSE	Master Pro	280	4507645	triosephos	24	5	71	5	1	249	26.7	6.9	High	High	High	High	High	High		32275361	43032641	46955863	1.37E+08	1.26E+08	1.32E+08	99.89	5	875	5
FALSE	Master Pro	121	4505763	phosphogly	22	6	68	6	1	417	44.6	8.1	High	High	High	High	High	High		5006647	9824913	4708359	96453594	1.04E+08	94716953	99.65	6	867	6
FALSE	None	270	58761496	heterogene	17	4	57	4	1	320	34.2	9	High	High	High	High	High	High		14448718	15002386	16032948	35625541	32527830	31356976	99.53	4	1010	4
FALSE	Master Pro	270	530400152	PREDICTED	15	5	59	5	1	372	38.7	9.13	High	High	High	High	High	High		15391069	15002386	17516010	35625541	32527830	31356976	99.53	4	1010	5
FALSE	Master Pro	270	4504445	heterogene	18	5	59	5	1	320	34.2	9.23	High	High	High	High	High	High		15391069	15002386	17516010	35625541	32527830	31356976	99.53	4	1010	5
FALSE	Master Pro	165	578813467	PREDICTED	18	4	61	4	1	313	33.9	9.03	High	High	High	High	High	High		49403265	53734137	56194491	67065649	1E+08	61391820	98.79	4	1277	4
FALSE	Master Pro	165	530384720	PREDICTED	16	4	61	4	1	353	37.4	8.95	High	High	High	High	High	High		49403265	53734137	56194491	67065649	1E+08	61391820	98.79	4	1277	4
FALSE	Master Pro	165	4504447	heterogene	16	4	61	4	1	341	36	8.65	High	High	High	High	High	High		49403265	53734137	56194491	67065649	1E+08	61391820	98.79	4	1277	4
FALSE	None	276	578836441	PREDICTED	6	4	69	4	1	841	88.1	5.31	High	High	High	High	High	High		6676136	8008788	6493389	36626590	39676085	39432815	97.24	4	957	4
FALSE	Master Pro	238	13325075	sulfhydryl	10	6	68	6	1	747	82.5	8.92	High	High	High	High	High	High		10395107	11677688	4395542	24772677	24477720	24138111	93.76	6	726	6
FALSE	Master Pro	154	27436946	lamin isofo	17	9	66	9	1	664	74.1	7.02	High	High	High	High	High	High		13306653	16559642	12470931	49349474	49088267	49986737	92.73	9	526	9
FALSE	Master Pro	127	161702986	ezrin [Hom	12	6	72	6	1	586	69.4	6.27	High	High	High	High	High	High		29865284	32037913	30932909	66861345	66526683	67616840	90.92	6	905	6
FALSE	Master Pro	101	21735621	malate deh	13	3	48	3	1	338	35.5	8.68	High	High	High	High	High	High		5843009	5668696	6370116	36039507	27966063	30259594	90.09	3	965	3
FALSE	None	15	578831330	PREDICTED	20	7	71	2	1	253	27.5	9.28	High	High	High	High	High	High		1.99E+08	3.9E+08	3.37E+08	6.82E+08	6.9E+08	1.5E+08	88.68	7	394	7
FALSE	Master Pro	156	7669492	glyceraldeh	16	4	66	4	1	335	36	8.46	High	High	High	High	High	High		1.25E+08	1.39E+08	1.39E+08	2.51E+08	2.88E+08	2.95E+08	88.4	4	1140	4
FALSE	Master Pro	156	378404908	glyceraldeh	18	4	66	4	1	293	31.5	7.61	High	High	High	High	High	High		1.25E+08	1.39E+08	1.39E+08	2.51E+08	2.88E+08	2.95E+08	88.4	4	1140	4
FALSE	None	238	51873067	sulfhydryl	10	5	64	5	1	604	66.8	8.56	High	High	High	High	High	High		10395107	11677688	4351524	24772677	24477720	24138111	88.02	5	711	5
FALSE	None	154	544063468	lamin isofo	16	8	62	8	1	614	69.2	6.64	High	High	High	High	High	High		12464133	16559642	12307428	49349474	49088267	49986737	84.95	8	406	8
FALSE	None	154	544063466	lamin isofo	17	8	62	8	1	572	65.1	6.84	High	High	High	High	High	High		12464133	16559642	12307428	49349474	49088267	49986737	84.95	8	406	8
FALSE	Master Pro	204	15617199	histone H2	27	3	56	3	1	130	14.1	11.05	High	High	High	High	High	High		1.45E+08	1.58E+08	1.32E+08	1.59E+08	1.61E+08	1.57E+08	83.91	3	468	3
FALSE	Master Pro	204	10800144	histone clu	27	3	56	3	1	128	13.9	10.89	High	High	High	High	High	High		1.45E+08	1.58E+08	1.32E+08	1.59E+08	1.61E+08	1.57E+08	83.91	3	468	3
FALSE	Master Pro	204	19557656	histone H2	27	3	56	3	1	130	14.1	11.05	High	High	High	High	High	High		1.45E+08	1.58E+08	1.32E+08	1.59E+08	1.61E+08	1.57E+08	83.91	3	468	3
FALSE	Master Pro	204	25092737	histone H2	27	3	56	3	1	131	14.2	10.86	High	High	High	High	High	High		1.45E+08	1.58E+08	1.32E+08	1.59E+08	1.61E+08	1.57E+08	83.91	3	468	3
FALSE	Master Pro	204	29553970	histone H2	27	3	56	3	1	129	14	10.9	High	High	High	High	High	High		1.45E+08	1.58E+08	1.32E+08	1.59E+08	1.61E+08	1.57E+08	83.91	3	468	3
FALSE	Master Pro	204	10800130	histone H2	27	3	56	3	1	130	14.1	10.9	High	High	High	High	High	High		1.45E+08	1.58E+08	1.32E+08	1.59E+08	1.61E+08	1.57E+08	83.91	3	468	3
FALSE	Master Pro	204	4504245	histone H2	27	3	56	3	1	130	14.1	11.05	High	High	High	High	High	High		1.45E+08	1.58E+08	1.32E+08	1.59E+08	1.61E+08	1.57E+08	83.91	3	468	3
FALSE	Master Pro	204	4504253	histone H2	24	3	56	3	1	143	15.1	10.74	High	High	High	High	High	High		1.45E+08	1.58E+08	1.32E+08	1.59E+08	1.61E+08	1.57E+08	83.91	3	468	3
FALSE	Master Pro	204	24638446	histone H2	27	3	56	3	1	129	14	10.9	High	High	High	High	High	High		1.45E+08	1.58E+08	1.32E+08	1.59E+08	1.61E+08	1.57E+08	83.91	3	468	3

FALSE	Master Pro	204	4504249	histone H2	27	3	56	3	1	130	14.1	10.9	High	High	High	High	High	High		1.45E+08	1.58E+08	1.32E+08	1.59E+08	1.61E+08	1.57E+08	83.91	3	468	3
FALSE	Master Pro	204	18105045	histone H2	27	3	56	3	1	128	13.9	10.89	High	High	High	High	High	High		1.45E+08	1.58E+08	1.32E+08	1.59E+08	1.61E+08	1.57E+08	83.91	3	468	3
FALSE	Master Pro	204	106775678	histone H2	27	3	56	3	1	130	14.1	10.9	High	High	High	High	High	High		1.45E+08	1.58E+08	1.32E+08	1.59E+08	1.61E+08	1.57E+08	83.91	3	468	3
FALSE	None	15;195	153791352	POTE anky	4	8	72	0	2	1075	121.4	6.2	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								82.14	8	565	8
FALSE	None	15;195	134133226	POTE anky	4	8	72	0	2	1075	121.3	6.2	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								82.14	8	565	8
FALSE	None	15;195	578804361	PREDICTED	7	8	72	0	2	675	76.6	5.16	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								82.14	8	565	8
FALSE	Master Pro	196	296080693	glucose-6-	11	4	52	4	1	569	64.3	8.91	High	High	High	High	High	High		4909534	4765156	5631891	42187861	38510199	38666642	81.34	4	957	4
FALSE	Master Pro	196	530416227	PREDICTED	10	4	52	4	1	597	67.2	8.97	High	High	High	High	High	High		4909534	4765156	5631891	42187861	38510199	38666642	81.34	4	957	4
FALSE	Master Pro	196	530416229	PREDICTED	11	4	52	4	1	558	63.1	8.32	High	High	High	High	High	High		4909534	4765156	5631891	42187861	38510199	38666642	81.34	4	957	4
FALSE	None	204	28195394	histone H2	22	2	51	2	1	130	14	10.89	High	High	High	High	High	High		1.45E+08	1.58E+08	1.58E+08	1.59E+08	1.61E+08	1.57E+08	80.06	2	467	2
FALSE	None	127	578812963	PREDICTED	11	5	61	5	1	543	64	6.01	High	High	High	High	High	High		24536958	31235044	26308772	63280634	61985340	63749418	79.26	5	771	5
FALSE	None	101	538919685	malate deh	11	2	38	2	1	296	30.9	8.43	High	High	High	High	High	High		7050525	6503875	6370116	41708198	27472507	30930153	78.83	2	965	2
FALSE	None	154	27436948	lamin isofo	16	8	56	8	1	634	70.6	8.4	High	High	High	High	High	High		13306653	16559642	12470931	49349474	49088267	49986737	78.6	8	422	8
FALSE	Master Pro	218	39725934	pigment ep	19	6	52	6	1	418	46.3	6.38	High	High	High	High	High	High		14532662	17815781	16101465	41597570	24194940	38189837	76.07	6	358	6
FALSE	Master Pro	110	4557888	keratin, typ	21	7	53	7	1	430	48	5.45	High	High	High	High	High	High		31565923	65607183	64877392	40052156	38826241	36983685	75.72	7	551	7
FALSE	None	154	383792150	lamin isofo	18	8	56	8	1	574	63.9	6.74	High	High	High	High	High	High		7734747	13336050	9310165	49349474	49088267	49986737	75.11	8	472	8
FALSE	Master Pro	13	153792590	heat shock	11	7	46	3	1	854	98.1	5.16	High	Not Found	Not Found	High	High	High		7246692			33125428	34822802	26395731	70.94	7	645	7
FALSE	Master Pro	13	154146191	heat shock	12	7	46	3	1	732	84.6	5.02	High	Not Found	Not Found	High	High	High		7246692			33125428	34822802	26395731	70.94	7	645	7
FALSE	Master Pro	198	55956788	nucleolin [	10	6	57	6	1	710	76.6	4.7	High	High	High	High	High	High		34738929	43918631	35402166	39469001	71815933	55517058	70.78	6	483	6
FALSE	Master Pro	162	117189975	heterogene	16	4	50	2	1	306	33.7	5.08	High	High	High	High	High	High		17885757	12888207	13111218	44324773	43174846	41306784	68.79	4	460	4
FALSE	Master Pro	162	117190174	heterogene	16	4	50	2	1	293	32.3	5.08	High	High	High	High	High	High		17885757	12888207	13111218	44324773	43174846	41306784	68.79	4	460	4
FALSE	Master Pro	162	578825750	PREDICTED	16	4	50	2	1	301	33.3	8.53	High	High	High	High	High	High		17885757	12888207	13111218	44324773	43174846	41306784	68.79	4	460	4
FALSE	None	154	544063464	lamin isofo	17	7	52	7	1	491	55.7	7.02	High	High	High	High	High	High		8408092	13336050	10322035	49349474	49088267	49986737	67.33	7	352	7
FALSE	Master Pro	137	4503471	elongation	9	4	61	4	1	462	50.1	9.01	High	High	High	High	High	High		82897985	1.19E+08	1.15E+08	2.67E+08	2.62E+08	2.84E+08	66.85	4	409	4
FALSE	Master Pro	271	183227678	protein DJ-	10	1	31	1	1	189	19.9	6.79	High	High	High	High	High	High		2871828	2860633	2378801	8338607	7762414	6503442	66.12	1	925	1
FALSE	Master Pro	240	29788785	tubulin bet	22	7	51	3	1	444	49.6	4.89	High	High	High	High	Not Found	Not Found		6607369	7112406	5443881	17527291			65.98	7	380	7
FALSE	Master Pro	126	14389309	tubulin alp	9	3	39	3	1	449	49.9	5.1	High	High	High	High	High	High		16015814	20891640	23802201	48925102	58437752	46724143	64.8	3	387	3
FALSE	Master Pro	126	393715095	tubulin alp	10	3	39	3	1	416	46.3	5.08	High	High	High	High	High	High		16015814	20891640	23802201	48925102	58437752	46724143	64.8	3	387	3
FALSE	Master Pro	126	57013276	tubulin alp	9	3	39	3	1	451	50.1	5.06	High	High	High	High	High	High		16015814	20891640	23802201	48925102	58437752	46724143	64.8	3	387	3
FALSE	Master Pro	126	393715091	tubulin alp	9	3	39	3	1	451	50.1	5.06	High	High	High	High	High	High		16015814	20891640	23802201	48925102	58437752	46724143	64.8	3	387	3
FALSE	None	15;195	315570273	actin, gam	14	7	63	0	2	333	37.1	5.54	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								64.46	7	563	7
FALSE	None	129	13676857	heat shock	8	5	50	2	1	639	70	5.74	High	High	High	High	High	High		5783174	14623984	11365270	33034300	33314035	32675629	64.28	5	478	5
FALSE	Master Pro	40	170763500	protein SET	12	3	41	3	1	290	33.5	4.32	High	High	High	High	High	High		42798544	20466914	49108967	64696040	26682403	68161954	63.81	3	435	3
FALSE	Master Pro	40	170763498	protein SET	13	3	41	3	1	277	32.1	4.22	High	High	High	High	High	High		42798544	20466914	49108967	64696040	26682403	68161954	63.81	3	435	3
FALSE	Master Pro	40	351721324	protein SET	13	3	41	3	1	266	31.1	4.23	High	High	High	High	High	High		42798544	20466914	49108967	64696040	26682403	68161954	63.81	3	435	3
FALSE	Master Pro	40	351721296	protein SET	13	3	41	3	1	268	31.3	4.21	High	High	High	High	High	High		42798544	20466914	49108967	64696040	26682403	68161954	63.81	3	435	3
FALSE	Master Pro	259	41406057	amyloid be	10	5	46	5	1	695	78.6	4.82	High	High	High	High	High	High		27428946	34333353	27561803	1.05E+08	1.01E+08	99421577	63.49	5	571	5
FALSE	Master Pro	259	209862833	amyloid be	10	5	46	5	1	746	84.5	4.75	High	High	High	High	High	High		27428946	34333353	27561803	1.05E+08	1.01E+08	99421577	63.49	5	571	5
FALSE	Master Pro	259	209915570	amyloid be	11	5	46	5	1	639	72.5	4.82	High	High	High	High	High	High		27428946	34333353	27561803	1.05E+08	1.01E+08	99421577	63.49	5	571	5
FALSE	Master Pro	259	324021736	amyloid be	10	5	46	5	1	733	82.9	4.78	High	High	High	High	High	High		27428946	34333353	27561803	1.05E+08	1.01E+08	99421577	63.49	5	571	5
FALSE	Master Pro	259	324021740	amyloid be	10	5	46	5	1	677	76.7	4.81	High	High	High	High	High	High		27428946	34333353	27561803	1.05E+08	1.01E+08	99421577	63.49	5	571	5
FALSE	Master Pro	259	4502167	amyloid be	9	5	46	5	1	770	86.9	4.82	High	High	High	High	High	High		27428946	34333353	27561803	1.05E+08	1.01E+08	99421577	63.49	5	571	5
FALSE	Master Pro	259	41406055	amyloid be	9	5	46	5	1	751	84.8	4.79	High	High	High	High	High	High		27428946	34333353	27561803	1.05E+08	1.01E+08	99421577	63.49	5	571	5
FALSE	Master Pro	259	324021738	amyloid be	9	5	46	5	1	752	85	4.81	High	High	High	High	High	High		27428946	34333353	27561803	1.05E+08	1.01E+08	99421577	63.49	5	571	5
FALSE	Master Pro	259	209915573	amyloid be	10	5	46	5	1	714	80.8	4.82	High	High	High	High	High	High		27428946	34333353	27561803	1.05E+08	1.01E+08	99421577	63.49	5	571	5
FALSE	Master Pro	259	209915575	amyloid be	11	5	46	5	1	660	75.1	4.84	High	High	High	High	High	High		27428946	34333353	27561803	1.05E+08	1.01E+08	99421577	63.49	5	571	5
FALSE	Master Pro	140	29550838	Golgi mem	15	5	46	5	1	401	45.3	4.97	High	High	High	High	High	High		6086715	15853680	12949488	22862416	27887201	8391811	63.31	5	412	5
FALSE	Master Pro	77	119395750	keratin, typ	9	5	46	4	1	644	66	8.12	High	High	High	High	High	High		6611158	7495992	6846045	19726503	14321482	16467112	62.19	5	575	5
FALSE	Master Pro	199	355594753	clusterin p	9	3	40	3	1	449	52.5	6.27	High	High	High	High	High	High		8197401	10083892	11175771	8822967	8070459	8101383	59.79	3	609	3
FALSE	Master Pro	199	578815184	PREDICTED	8	3	40	3	1	501	57.8	6.68	High	High	High	High	High	High		8197401	10083892	11175771	8822967	8070459	8101383	59.79	3	609	3
FALSE	Master Pro	122	5803011	gamma-en	8	2	43	1	1	434	47.2	5.03	Not Found	Not Found	Not Found	Not Found	High	High						5072908	4677521	59.17	2	839	2
FALSE	Master Pro	34	11321593	insulin-like	6	1	36	1	1	240	25.3	7.81	High	High	High	High	High	High		36122863	1.42E+08	1.31E+08	1.89E+08	1.76E+08	1.14E+08	57.99	1	965	1
FALSE	None	240	29788768	tubulin bet	16	5	42	1	1	445	49.9	4.89	High	Not Found	High	Not Found	Not Found	Not Found		7276982		7915590				57.22	5	362	5
FALSE	None	240	4507729	tubulin bet	16	5	42	1	1	445	49.9	4.89	High	Not Found	High	Not Found	Not Found	Not Found		7276982		7915590				57.22	5	362	5
FALSE	Master Pro	47	50592996	tubulin bet	16	5	42	1	1	450	50.4	4.93	Not Found	Not Found	Not Found	High	Not Found	High					5982631		5014711	56.5	5	369	5
FALSE	Master Pro	175	260099723	L-lactate d	19	5	42	5	1	361	39.8	8.43	High	High	High	High	High	High			8777567		40549073	35174589	70259028	56.42	5	641	5
FALSE	Master Pro	175	5031857	L-lactate d	20	5	42	5	1	332	36.7	8.27	High	High	High	High	High	High			8777567		40549073	35174589	70259028	56.42	5	641	5
FALSE	Master Pro	173	4503477	elongation	12	2	30	2	1	225	24.7	4.67	High	High	High	High	High	High		11208088	13689264	16126193	14009390	19994114	16843233	55.44	2	590	2
FALSE	None	175	260099725	L-lactate d	21	4	40	4	1	274	30	8	High	High	High	High	High	High			8777567		40549073	35174589	37726478	54.54	4	632	4
FALSE	None	175	260099727	L-lactate d	24	4	40	4	1	241	26.7	8.15	High	High	High	High	High	High			8777567		40549073	35174589	37726478	54.54	4	632	4
FALSE	None	240	5174735	tubulin bet	12	4	38	1	1	445	49.8	4.89	High	Not Found	High	Not Found	Not Found	Not Found		7276982		7915590				54.4	4	336	4
FALSE	Master Pro	85	67191208	polyubiquit	33	2	39	2	1	685	77	7.66	High	High	High	High	High	High		4.2E+08	4.8E+08	4.33E+08	6.69E+08	6.53E+08	6.51E+08	54.2	2	286	2
FALSE	Master Pro	85	528524477	polyubiquit	33	2	39	2	1	229	25.7	7.43	High	High	High	High	High	High		4.2E+08	4.8E+08	4.33E+08	6.69E+08	6.53E+08	6.51E+08	54.2	2	286	2
FALSE	Master Pro	85	530415146	PREDICTED	14	2	39	2	1	175	19.4	9.22	High	High	High	High	High	High		4.2E+08	4.8E+08	4.33E+08	6.69E+08	6.53E+08	6.51E+08	54.2	2	286	2
FALSE	Master Pro	85	4507761	ubiquitin-6	20	2	39	2	1	128	14.7	9.83	High	High	High	High	High	High		4.2E+08	4.8E+08	4.33E+08	6.69E+08	6.53E+08	6.51E+08	54.2	2	286	2
FALSE	Master Pro	85	530415150	PREDICTED	16	2	39	2	1	156	17.5	9.57	High	High	High	High	High	High		4.2E+08	4.8E+08	4.33E+08	6.69E+08	6.53E+08	6.51E+08	54.2	2	286	2
FALSE	Master Pro	85	530415144	PREDICTED	12	2	39	2	1	203	22.2	8.94	High	High	High	High	High	High		4.2E+08	4.8E+08	4.33E+08	6.69E+08	6.53E+08	6.51E+08	54.2	2	286	2
FALSE	Master Pro	85	208022622	ubiquitin-4	16	2	39	2	1	156	18	9.64	High	High	High	High	High	High		4.2E+08	4.8E+08	4.33E+08	6.69E+08	6.53E+08	6.51E+08	54.2	2	286	2
FALSE	None	47	308235963	tubulin bet	16	4	38	1	1	378	42.4	4.96	Not Found	Not Found	Not Found	High	Not Found	High					5982631		5014711	53.68	4	343	4
FALSE	Master Pro	279	58218968	calmodulin	22	3	33	3	1	149	16.8	4.22	High	High	High	High	High	High		5567161	19665727	8712484	62983952	35861185	35467804	51.85	3	448	3
FALSE	Master Pro	279	578826144	PREDICTED	22	3	33	3	1	150	17	4.22	High	High	High	High	High	High		5567161	19665727	8712484	62983952	35861185	35467804	51.85	3	448	3
FALSE	None	122;228	301897479	beta-enola	5	1	39	0	2	391	42.2	7.97	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								51.45	1	778	1
FALSE	None	122;228	530410063	PREDICTED	4	1	39	0	2	443	48	8.16	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								51.45	1	778	1
FALSE	None	122;228	301897477	beta-enola	4	1	39	0	2	434	47	7.71	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								51.45	1	778	1
FALSE	Master Pro	186	578811108	PREDICTED	8	2	32	1	1	452	49.1	6.92	High	High	High	High	High	High		3719404	5902483	4884231	17144975	14182573	16673603	51.39	2	539	2
FALSE	Master Pro	186	578811110	PREDICTED	8	2	32	1	1	429	47.1	6.34	High	High	High	High	High	High		3719404	5902483	4884231	17144975	14182573	16673603	51.39	2	539	2
FALSE	Master Pro	186	530381015	PREDICTED	7	2	32	1	1	472	51.2	6.8	High	High	High	High	High	High		3719404	5902483	4884231	17144975	14182573	16673603	51.39	2	539	2
FALSE	Master Pro	186	381342476	heterogene	8	2	32	1	1	449	49.2	6.3	High	High	High	High	High	High		3719404	5902483	4884231	17144975	14182573	16673603	51.39	2	539	2
FALSE	None	15	578813594	PREDICTED	15	5	43	1	1	253	28.2	5.34	Not Found	Not Found	Not Found	Not Found	High	High						7066445	10209447	51.25	5	458	5

FALSE	Master Prc	210	4502101	annexin A1	17	4	41	4	1	346	38.7	7.02	High	High	High	High	High	High		4669011	4471245	6120916	13605682	7193137	7906737	50.6	4	399	4
FALSE	Master Prc	150	342187211	fructose-bi	10	3	33	3	1	418	45.2	8.25	High	High	High	High	High	High		76256591	1.03E+08	95008656	1.26E+08	1.1E+08	1.81E+08	50.47	3	431	3
FALSE	Master Prc	150	4557305	fructose-bi	11	3	33	3	1	364	39.4	8.09	High	High	High	High	High	High		76256591	1.03E+08	95008656	1.26E+08	1.1E+08	1.81E+08	50.47	3	431	3
FALSE	Master Prc	45	58761500	obg-like AT	10	3	29	3	1	396	44.7	7.81	High	High	High	High	High	High		9191094	5100092	9146937	11552279	11698734	13883666	50.43	3	694	3
FALSE	Master Prc	244	4507585	tumor necr	18	4	36	4	1	300	32.7	8.24	High	High	High	High	High	High		14249107	26134067	24646245	22128555	21706509	23456959	50.33	3	315	4
FALSE	Master Prc	35	163965364	nascent po	20	3	30	3	1	215	23.4	4.56	High	High	High	High	High	High		12792230	14966184	6749932	19701649	18521915	24154728	50.12	3	533	3
FALSE	Master Prc	35	578823766	PREDICTED	2	3	30	3	1	2082	205.6	9.6	High	High	High	High	High	High		12792230	14966184	6749932	19701649	18521915	24154728	50.12	3	533	3
FALSE	Master Prc	35	578823770	PREDICTED	2	3	30	3	1	2059	203.6	9.57	High	High	High	High	High	High		12792230	14966184	6749932	19701649	18521915	24154728	50.12	3	533	3
FALSE	Master Prc	35	333033787	nascent po	5	3	30	3	1	925	94.6	5.14	High	High	High	High	High	High		12792230	14966184	6749932	19701649	18521915	24154728	50.12	3	533	3
FALSE	Master Prc	35	578823768	PREDICTED	2	3	30	3	1	2078	205.3	9.58	High	High	High	High	High	High		12792230	14966184	6749932	19701649	18521915	24154728	50.12	3	533	3
FALSE	Master Prc	35	578823772	PREDICTED	2	3	30	3	1	2035	201.3	9.55	High	High	High	High	High	High		12792230	14966184	6749932	19701649	18521915	24154728	50.12	3	533	3
FALSE	Master Prc	35	578823778	PREDICTED	19	3	30	3	1	219	23.7	4.59	High	High	High	High	High	High		12792230	14966184	6749932	19701649	18521915	24154728	50.12	3	533	3
FALSE	Master Prc	149	530415128	PREDICTED	14	4	32	3	1	248	28.6	4.7	High	High	High	High	High	High		3398679	9526211	7371355		16768081	17074824	49.91	4	311	4
FALSE	Master Prc	149	4507651	tropomyos	14	4	32	3	1	248	28.5	4.69	High	High	High	High	High	High		3398679	9526211	7371355		16768081	17074824	49.91	4	311	4
FALSE	Master Prc	108	39777597	protein-glu	6	3	38	3	1	687	77.3	5.22	High	High	High	High	High	High		7498575	7132735	7420309	14853683	11305333	12898559	49.1	3	295	3
FALSE	None	32	55749932	desmin [Hc	3	2	30	2	1	470	53.5	5.27	High	High	High	High	High	High		39412688	59194171	46489965	41363460	39862769	6463263	48.7	2	366	2
FALSE	Master Prc	12	66392203	NME1-NMI	27	3	42	3	1	267	30.1	8.92	High	High	High	High	High	High		22306834	18310787	19704327	59006527	58210547	55696055	48.24	3	232	3
FALSE	Master Prc	12	4505409	nucleoside	29	3	42	3	1	152	17.3	8.41	High	High	High	High	High	High		22306834	18310787	19704327	59006527	58210547	55696055	48.24	3	232	3
FALSE	Master Prc	272	4757900	calreticulin	10	4	41	4	1	417	48.1	4.44	High	High	High	High	High	High		29417323	15266302	31991954	32470688	31974030	22346728	47.78	4	415	4
FALSE	None	40	567757558	SET-like pr	8	2	29	2	1	302	34.9	4.31	High	High	High	High	High	High		53324841	16972543	61820282	81581815	30531802	86175106	47.71	2	411	2
FALSE	None	280	384475517	triosephos	17	2	33	2	1	167	17.9	5.58	High	High	High	High	High	High		69777125	59379805	59161891	1.73E+08	1.61E+08	1.69E+08	46.77	2	324	2
FALSE	Master Prc	89	4758638	peroxiredo	23	4	34	4	1	224	25	6.38	High	High	High	High	High	High		18193900	29925549	26783242	24677026	19621984	48685608	46.77	4	338	4
FALSE	Master Prc	217	5032057	protein S1(	15	1	28	1	1	105	11.7	7.12	High	High	High	High	High	High		23909412	24231844	26933020	30446882	29211469	26245877	46.61	1	592	1
FALSE	Master Prc		63055057	beta-actin-	9	4	38	0	0	376	42	5.59	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								45.95	4	384	4
FALSE	Master Prc	52	4507509	metallopro	10	2	38	2	1	207	23.2	8.1	High	High	High	High	High	High		4.93E+08	5.43E+08	4.19E+08	6.13E+08	6.08E+08	6.45E+08	45.53	2	198	2
FALSE	Master Prc	98	4505863	urokinase-	11	4	53	4	1	431	48.5	8.41	High	High	High	High	High	High		18230889	28381598	34835207	38758425	54943432	58352792	43.74	4	206	4
FALSE	Master Prc	98	222537759	urokinase-	11	4	53	4	1	414	46.9	8.44	High	High	High	High	High	High		18230889	28381598	34835207	38758425	54943432	58352792	43.74	4	206	4
FALSE	Master Prc	214	10835063	nucleopho	5	1	28	1	1	294	32.6	4.78	High	High	High	High	High	High		7447687	6291018	5388215	13645667	10651596	13871601	43.54	1	268	1
FALSE	Master Prc	214	40353734	nucleopho	5	1	28	1	1	265	29.4	4.61	High	High	High	High	High	High		7447687	6291018	5388215	13645667	10651596	13871601	43.54	1	268	1
FALSE	None	32	21264345	peripherin	4	2	34	2	1	470	53.6	5.47	High	High	High	High	High	High		40690058	98480632	44352724	2.17E+08	1.11E+08	1.16E+08	43.52	2	239	2
FALSE	None	32	530400571	PREDICTED	4	2	34	2	1	471	53.7	5.47	High	High	High	High	High	High		40690058	98480632	44352724	2.17E+08	1.11E+08	1.16E+08	43.52	2	239	2
FALSE	None	51	578801437	PREDICTED	11	3	33	2	1	285	33.2	4.77	Not Found	Not Found	High	High	High	High				4170426	17662123	17578023	17607685	43.48	3	132	3
FALSE	None	51	578801445	PREDICTED	11	3	33	2	1	285	33	4.74	Not Found	Not Found	High	High	High	High				4170426	17662123	17578023	17607685	43.48	3	132	3
FALSE	None	51	578801447	PREDICTED	11	3	33	2	1	284	33.1	4.79	Not Found	Not Found	High	High	High	High				4170426	17662123	17578023	17607685	43.48	3	132	3
FALSE	None	51	578801441	PREDICTED	11	3	33	2	1	285	33.1	4.74	Not Found	Not Found	High	High	High	High				4170426	17662123	17578023	17607685	43.48	3	132	3
FALSE	None	51	578801449	PREDICTED	11	3	33	2	1	284	33	4.77	Not Found	Not Found	High	High	High	High				4170426	17662123	17578023	17607685	43.48	3	132	3
FALSE	None	51	114155140	tropomyos	11	3	33	2	1	285	32.9	4.72	Not Found	Not Found	High	High	High	High				4170426	17662123	17578023	17607685	43.48	3	132	3
FALSE	None	51	578801439	PREDICTED	11	3	33	2	1	285	33.1	4.74	Not Found	Not Found	High	High	High	High				4170426	17662123	17578023	17607685	43.48	3	132	3
FALSE	Master Prc	135	4505621	phosphatic	18	2	24	2	1	187	21	7.53	High	High	High	High	High	High		30555797	38699437	30732387	47397786	47401064	49866196	43.21	2	717	2
FALSE	None	137	4503475	elongation	7	3	43	3	1	463	50.4	9.03	High	High	High	High	High	High		1.59E+08	1.73E+08	1.15E+08	2.42E+08	2.35E+08	2.58E+08	42.67	3	240	3
FALSE	Master Prc	48	578810781	PREDICTED	8	2	22	2	1	466	52.1	5.52	High	High	High	High	High	High		2461826	2593221	2038195	1441495	6184971	7994451	42.16	2	359	2
FALSE	None	15;195	475808427	POTE anky	3	5	40	0	2	1075	121.2	6.21	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								40.99	5	207	5
FALSE	Master Prc	220	4507511	metallopro	7	2	24	2	1	220	24.4	7.49	High	High	High	High	High	High		53484255	71565094	70170293	74604086	71592726	74801975	40.86	2	467	2
FALSE	Master Prc	100	66346679	plasminoge	8	2	22	2	1	408	44.9	8.65	High	High	High	High	Not Found	Not Found		12617408	11612700	4831045	3404454			40.28	2	500	2
FALSE	Master Prc	100	66346681	plasminoge	8	2	22	2	1	402	44.2	8.66	High	High	High	High	Not Found	Not Found		12617408	11612700	4831045	3404454			40.28	2	500	2
FALSE	Master Prc	100	66346685	plasminoge	9	2	22	2	1	387	42.4	8.44	High	High	High	High	Not Found	Not Found		12617408	11612700	4831045	3404454			40.28	2	500	2
FALSE	Master Prc	100	66346683	plasminoge	9	2	22	2	1	393	43.1	8.44	High	High	High	High	Not Found	Not Found		12617408	11612700	4831045	3404454			40.28	2	500	2
FALSE	Master Prc	172	4504323	histone H4	41	4	40	4	1	103	11.4	11.36	High	High	High	High	High	High		1.19E+08	1.79E+08	1.28E+08	1.42E+08	1.02E+08	1.04E+08	40.02	4	198	4
FALSE	Master Prc	242	6598323	rab GDP di	7	2	24	2	1	445	50.6	6.47	Not Found	Not Found	High	High	High	High				5603756	2843112	4753351	10850701	39.71	2	213	2
FALSE	Master Prc	44	34098946	nuclease-s	10	2	21	2	1	324	35.9	9.88	High	High	High	High	High	High		14128290	17431752	5771428	8644132	9122102	9631546	38.22	2	399	2
FALSE	Master Prc	44	224586882	Y-box-bind	9	2	21	2	1	372	40.1	9.77	High	High	High	High	High	High		14128290	17431752	5771428	8644132	9122102	9631546	38.22	2	399	2
FALSE	Master Prc	44	156415990	Y-box-bind	9	2	21	2	1	364	38.5	10.8	High	High	High	High	High	High		14128290	17431752	5771428	8644132	9122102	9631546	38.22	2	399	2
FALSE	Master Prc	44	224586884	Y-box-bind	11	2	21	2	1	303	31.9	9.66	High	High	High	High	High	High		14128290	17431752	5771428	8644132	9122102	9631546	38.22	2	399	2
FALSE	None	98	578819560	PREDICTED	10	3	42	3	1	375	42.4	8.29	High	High	High	High	High	High		26517528	28381598	34835207	52666919	54943432	58352792	37.21	3	199	3
FALSE	Master Prc	68	258645150	RNA-bindir	14	2	23	2	1	196	22.2	5.26	High	High	High	High	High	High		12764305	12327768	11751049	37037790	33940605	36498190	36.84	2	325	2
FALSE	Master Prc	68	242117971	RNA bindir	7	2	23	2	1	390	42.1	9.89	High	High	High	High	High	High		12764305	12327768	11751049	37037790	33940605	36498190	36.84	2	325	2
FALSE	Master Prc	68	56699409	RNA-bindir	7	2	23	2	1	391	42.3	10.05	High	High	High	High	High	High		12764305	12327768	11751049	37037790	33940605	36498190	36.84	2	325	2
FALSE	None	175	15082234	L-lactate d	7	2	21	2	1	381	41.9	8.65	Not Found	Not Found	Not Found	High	High	High					20116409	14479991	17152997	36.22	2	513	2
FALSE	Master Prc	252	530370872	PREDICTED	10	3	27	3	1	408	46.8	7.12	High	High	High	High	High	High		7359067	6392202	4295627	5617840	7040764		35.15	3	280	3
FALSE	Master Prc	226	73760405	thymopoie	9	3	22	3	1	454	50.6	9.38	High	High	High	High	High	High		10728079	12793839	10340889	15981535	15138572	13513743	35.14	3	352	3
FALSE	Master Prc	226	530400792	PREDICTED	10	3	22	3	1	414	46.3	9.03	High	High	High	High	High	High		10728079	12793839	10340889	15981535	15138572	13513743	35.14	3	352	3
FALSE	Master Prc	226	73760401	thymopoie	12	3	22	3	1	345	38.7	9.16	High	High	High	High	High	High		10728079	12793839	10340889	15981535	15138572	13513743	35.14	3	352	3
FALSE	Master Prc	226	4507555	thymopoie	6	3	22	3	1	694	75.4	7.66	High	High	High	High	High	High		10728079	12793839	10340889	15981535	15138572	13513743	35.14	3	352	3
FALSE	Master Prc	226	530400796	PREDICTED	11	3	22	3	1	382	42.9	9.41	High	High	High	High	High	High		10728079	12793839	10340889	15981535	15138572	13513743	35.14	3	352	3
FALSE	Master Prc	123	567757609	chloride in	12	2	20	2	1	241	26.9	5.17	High	High	High	High	High	High		3887711	5340530	4944973	13733026	9771128	12563537	34.11	2	361	2
FALSE	Master Prc	207	32455266	peroxiredo	32	6	29	5	1	199	22.1	8.13	High	High	High	High	High	High		87297778	54708204	96084022	1.5E+08	1.52E+08	1.07E+08	33.98	6	149	6
FALSE	Master Prc	27	530396010	PREDICTED	3	2	32	2	1	702	77	5.39	High	High	High	High	High	High		6965699	29283905	71726609	1.49E+08	1.47E+08	1.42E+08	33.93	2	301	2
FALSE	Master Prc	27	578820966	PREDICTED	3	2	32	2	1	741	81.4	5.33	High	High	High	High	High	High		6965699	29283905	71726609	1.49E+08	1.47E+08	1.42E+08	33.93	2	301	2
FALSE	Master Prc	27	48255935	CD44 antig	3	2	32	2	1	742	81.5	5.33	High	High	High	High	High	High		6965699	29283905	71726609	1.49E+08	1.47E+08	1.42E+08	33.93	2	301	2
FALSE	Master Prc	27	48255939	CD44 antig	4	2	32	2	1	493	53.4	5.4	High	High	High	High	High	High		6965699	29283905	71726609	1.49E+08	1.47E+08	1.42E+08	33.93	2	301	2
FALSE	Master Prc	27	321400138	CD44 antig	5	2	32	2	1	429	46.5	5.74	High	High	High	High	High	High		6965699	29283905	71726609	1.49E+08	1.47E+08	1.42E+08	33.93	2	301	2
FALSE	Master Prc	27	321400142	CD44 antig	7	2	32	2	1	294	32.1	5.21	High	High	High	High	High	High		6965699	29283905	71726609	1.49E+08	1.47E+08	1.42E+08	33.93	2	301	2
FALSE	Master Prc	27	530396022	PREDICTED	4	2	32	2	1	535	58	5.02	High	High	High	High	High	High		6965699	29283905	71726609	1.49E+08	1.47E+08	1.42E+08	33.93	2	301	2
FALSE	Master Prc	27	578820976	PREDICTED	5	2	32	2	1	397	44.4	5.36	High	High	High	High	High	High		6965699	29283905	71726609	1.49E+08	1.47E+08	1.42E+08	33.93	2	301	2
FALSE	Master Prc	27	530396012	PREDICTED	3	2	32	2	1	700	76.6	5.27	High	High	High	High	High	High		6965699	29283905	71726609	1.49E+08	1.47E+08	1.42E+08	33.93	2	301	2
FALSE	Master Prc	27	578820968	PREDICTED	3	2	32	2	1	735	80.8	5.33	High	High	High	High	High	High		6965699	29283905	71726609	1.49E+08	1.47E+08	1.42E+08	33.93	2	301	2
FALSE	Master Prc	27	321400140	CD44 antig	6	2	32	2	1	340	37.3	5.52	High	High	High	High	High	High		6965699	29283905	71726609	1.49E+08	1.47E+08	1.42E+08	33.93	2	301	2
FALSE	Master Prc	27	530396020	PREDICTED	4	2	32	2	1	578	62.9	5.08	High	High	High	High	High	High		6965699	29283905	71726609	1.49E+08	1.47E+08	1.42E+08	33.93	2	301	2
FALSE	Master Prc	27	48255937	CD44 antig	3	2	32	2	1	699	76.6	5.27	High	High	High	High	High	High		6965699	29283905	71726609	1.49E+08	1.47E+08	1.42E+08	33.93	2	301	2

FALSE	Master Pro	27	530396018	PREDICTED	4	2	32	2	1	580	63.1	5.71	High	High	High	High	High	High		6965699	29283905	71726609	1.49E+08	1.47E+08	1.42E+08	33.93	2	301	2
FALSE	Master Pro	27	530396008	PREDICTED	3	2	32	2	1	703	77	5.39	High	High	High	High	High	High		6965699	29283905	71726609	1.49E+08	1.47E+08	1.42E+08	33.93	2	301	2
FALSE	Master Pro	27	530396004	PREDICTED	3	2	32	2	1	743	81.6	5.33	High	High	High	High	High	High		6965699	29283905	71726609	1.49E+08	1.47E+08	1.42E+08	33.93	2	301	2
FALSE	Master Pro	27	48255941	CD44 antig	6	2	32	2	1	361	39.4	5.41	High	High	High	High	High	High		6965699	29283905	71726609	1.49E+08	1.47E+08	1.42E+08	33.93	2	301	2
FALSE	Master Pro	27	530396006	PREDICTED	3	2	32	2	1	742	81.5	5.33	High	High	High	High	High	High		6965699	29283905	71726609	1.49E+08	1.47E+08	1.42E+08	33.93	2	301	2
FALSE	None	186	9624998	heterogene	4	1	18	1	1	449	49.2	6.3	High	High	High	High	High	High		3719404	5902483	4884231	17144975	14182573	16673603	33.88	1	326	1
FALSE	Master Pro	200	194239727	elongation	13	3	24	3	1	281	31.1	5.01	High	High	High	High	High	High		5555464	7304853	5829654	9835958	7441664	8877615	33.56	3	308	3
FALSE	Master Pro	200	578839684	PREDICTED	6	3	24	3	1	647	71.4	6.42	High	High	High	High	High	High		5555464	7304853	5829654	9835958	7441664	8877615	33.56	3	308	3
FALSE	Master Pro	200	578815864	PREDICTED	5	3	24	3	1	687	75.5	6.43	High	High	High	High	High	High		5555464	7304853	5829654	9835958	7441664	8877615	33.56	3	308	3
FALSE	Master Pro	200	578839680	PREDICTED	6	3	24	3	1	664	73	6.34	High	High	High	High	High	High		5555464	7304853	5829654	9835958	7441664	8877615	33.56	3	308	3
FALSE	Master Pro	200	304555581	elongation	6	3	24	3	1	647	71.4	6.42	High	High	High	High	High	High		5555464	7304853	5829654	9835958	7441664	8877615	33.56	3	308	3
FALSE	Master Pro	200	530388819	PREDICTED	5	3	24	3	1	688	75.6	6.43	High	High	High	High	High	High		5555464	7304853	5829654	9835958	7441664	8877615	33.56	3	308	3
FALSE	Master Pro	200	194239729	elongation	14	3	24	3	1	257	28.5	4.92	High	High	High	High	High	High		5555464	7304853	5829654	9835958	7441664	8877615	33.56	3	308	3
FALSE	Master Pro	200	578839682	PREDICTED	6	3	24	3	1	648	71.5	6.42	High	High	High	High	High	High		5555464	7304853	5829654	9835958	7441664	8877615	33.56	3	308	3
FALSE	Master Pro	178	578800215	PREDICTED	13	3	29	1	1	293	32	5.68	High	High	High	High	Not Found	High		32663131	34889794	33706511	99961742		18427645	33.11	3	201	3
FALSE	Master Pro	178	578839320	PREDICTED	13	3	29	1	1	293	32	5.68	High	High	High	High	Not Found	High		32663131	34889794	33706511	99961742		18427645	33.11	3	201	3
FALSE	Master Pro	178	61966711	heterogene	13	3	29	1	1	293	32.1	5.06	High	High	High	High	Not Found	High		32663131	34889794	33706511	99961742		18427645	33.11	3	201	3
FALSE	Master Pro	96	153791632	eukaryotic	8	1	29	1	1	154	16.8	5	High	High	High	High	High	High		13593895	12080744	16382313	59744676	48272417	54102951	32.91	1	141	1
FALSE	Master Pro	96	9966867	eukaryotic	8	1	29	1	1	153	16.8	5.58	High	High	High	High	High	High		13593895	12080744	16382313	59744676	48272417	54102951	32.91	1	141	1
FALSE	Master Pro	96	219555707	eukaryotic	7	1	29	1	1	184	20.2	7.01	High	High	High	High	High	High		13593895	12080744	16382313	59744676	48272417	54102951	32.91	1	141	1
FALSE	Master Pro	96	530410036	PREDICTED	8	1	29	1	1	154	16.8	5.24	High	High	High	High	High	High		13593895	12080744	16382313	59744676	48272417	54102951	32.91	1	141	1
FALSE	Master Pro	262	32189392	peroxiredo	19	4	29	3	1	198	21.9	5.97	High	High	High	High	High	High		3672220	2184850	2297653	7201142	9589403	2762721	32.79	4	295	4
FALSE	Master Pro	235	7657441	28 kDa hea	16	2	22	2	1	181	20.6	8.87	High	High	High	High	High	High		21194601	23201477	22159052	32784107	33524667	31362372	32.2	2	250	2
FALSE	Master Pro	30	374671789	single-strar	30	3	22	3	1	148	17.2	9.6	Not Found	Not Found	Not Found	High	High	High					14664166	17183184	16121419	32.16	3	342	3
FALSE	Master Pro	94	578817383	PREDICTED	8	4	23	4	1	820	89.5	6.57	High	High	High	High	High	High		8593479	7165005	7736092	21066627	34193840	36310970	31.79	3	288	4
FALSE	Master Pro	94	189083776	gelsolin iso	9	4	23	4	1	731	80.6	5.85	High	High	High	High	High	High		8593479	7165005	7736092	21066627	34193840	36310970	31.79	3	288	4
FALSE	Master Pro	94	4504165	gelsolin iso	9	4	23	4	1	782	85.6	6.28	High	High	High	High	High	High		8593479	7165005	7736092	21066627	34193840	36310970	31.79	3	288	4
FALSE	Master Pro	94	427918083	gelsolin iso	9	4	23	4	1	739	81.4	5.85	High	High	High	High	High	High		8593479	7165005	7736092	21066627	34193840	36310970	31.79	3	288	4
FALSE	Master Pro	94	530391018	PREDICTED	9	4	23	4	1	752	82.8	5.85	High	High	High	High	High	High		8593479	7165005	7736092	21066627	34193840	36310970	31.79	3	288	4
FALSE	Master Pro	94	390517030	gelsolin iso	9	4	23	4	1	767	84.7	5.83	High	High	High	High	High	High		8593479	7165005	7736092	21066627	34193840	36310970	31.79	3	288	4
FALSE	Master Pro	94	384475528	gelsolin iso	9	4	23	4	1	748	82.5	5.63	High	High	High	High	High	High		8593479	7165005	7736092	21066627	34193840	36310970	31.79	3	288	4
FALSE	Master Pro	94	578817385	PREDICTED	9	4	23	4	1	742	81.9	5.85	High	High	High	High	High	High		8593479	7165005	7736092	21066627	34193840	36310970	31.79	3	288	4
FALSE	None	129	530427787	PREDICTED	5	2	24	0	1	641	70.4	6.29	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								31.44	2	333	2
FALSE	None	129	530381921	PREDICTED	4	2	24	0	1	705	77.5	7.66	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								31.44	2	333	2
FALSE	None	129	530429266	PREDICTED	4	2	24	0	1	705	77.5	7.66	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								31.44	2	333	2
FALSE	None	129	530427783	PREDICTED	4	2	24	0	1	705	77.5	8.06	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								31.44	2	333	2
FALSE	None	129	530429270	PREDICTED	5	2	24	0	1	641	70.4	6.02	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								31.44	2	333	2
FALSE	None	129	530381923	PREDICTED	5	2	24	0	1	641	70.3	6.02	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								31.44	2	333	2
FALSE	None	182	530384859	PREDICTED	14	2	21	2	1	105	11.4	7.9	High	High	High	High	High	High		7586637	15764291	17147761	13099425	14255673	12878153	31.16	2	145	2
FALSE	None	15;195	459352730	POTE anky	2	3	23	0	2	1038	117.3	5.97	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								29.93	3	102	3
FALSE	Master Pro	61	11056044	inorganic p	6	1	14	1	1	289	32.6	5.86	High	High	High	Not Found	Not Found	High		2527666	2324697	1967201				29.86	1	317	1
FALSE	Master Pro	237	4758950	peptidyl-pr	16	3	30	3	1	216	23.7	9.41	High	High	High	High	High	High		22380356	21564664	21286835	45423190	44432064	40439193	29.34	3	212	3
FALSE	Master Pro	284	20070228	nucleobind	12	4	30	4	1	461	53.8	5.25	Not Found	High	High	High	High	High			14452772	13266549	19206281	22852034	20865655	29.21	4	110	3
FALSE	Master Pro	116	4504523	10 kDa hea	25	2	20	2	1	102	10.9	8.92	High	High	High	High	High	High		30213494	35938416	35248167	25009896	22995140	32904294	28.98	2	446	2
FALSE	Master Pro	24	4505753	phosphogly	13	2	26	2	1	254	28.8	7.18	High	High	High	High	High	High		15953323	14948481		65787461	63567569	57483101	28.91	2	210	2
FALSE	Master Pro	260	46276863	parathymo	11	1	20	1	1	102	11.5	4.16	High	High	High	High	High	High		1219163	45588353	31289071	61977621	49701173	56020815	28.71	1	260	1
FALSE	Master Pro	46	57242757	calsynteni	3	3	23	3	1	981	109.7	4.91	High	High	High	High	High	High		20130869	21685725	18409410	23564146	27072296	24414709	28.68	3	206	3
FALSE	Master Pro	46	530360505	PREDICTED	3	3	23	3	1	962	107.7	4.97	High	High	High	High	High	High		20130869	21685725	18409410	23564146	27072296	24414709	28.68	3	206	3
FALSE	Master Pro	46	57242755	calsynteni	3	3	23	3	1	971	108.6	4.93	High	High	High	High	High	High		20130869	21685725	18409410	23564146	27072296	24414709	28.68	3	206	3
FALSE	Master Pro	79	4506669	60S acidic	14	1	22	1	1	114	11.5	4.32	High	High	High	High	High	High		10969722	11120970	8360999	32165803	26691571	28556196	27.85	1	243	1
FALSE	Master Pro	14	530421539	PREDICTED	7	5	23	5	1	1109	123.1	5.85	Not Found	Not Found	Not Found	High	High	High					14237522	13360598	15237710	27.03	5	123	5
FALSE	Master Pro	14	530421541	PREDICTED	7	5	23	5	1	1064	118.5	5.81	Not Found	Not Found	Not Found	High	High	High					14237522	13360598	15237710	27.03	5	123	5
FALSE	Master Pro	14	23510340	ubiquitin-li	7	5	23	5	1	1058	117.8	5.76	Not Found	Not Found	Not Found	High	High	High					14237522	13360598	15237710	27.03	5	123	5
FALSE	Master Pro	138	12025678	alpha-actin	5	4	20	4	1	911	104.8	5.44	Not Found	Not Found	Not Found	High	High	High					13065512	13209708	8419374	26.67	4	210	4
FALSE	Master Pro	138	194097352	alpha-actin	5	4	20	4	1	887	102.6	5.5	Not Found	Not Found	Not Found	High	High	High					13065512	13209708	8419374	26.67	4	210	4
FALSE	Master Pro	138	578834952	PREDICTED	5	4	20	4	1	911	104.8	5.44	Not Found	Not Found	Not Found	High	High	High					13065512	13209708	8419374	26.67	4	210	4
FALSE	Master Pro	138	4501891	alpha-actin	5	4	20	4	1	892	103	5.41	Not Found	Not Found	Not Found	High	High	High					13065512	13209708	8419374	26.67	4	210	4
FALSE	Master Pro	138	530417302	PREDICTED	5	4	20	4	1	906	104.3	5.5	Not Found	Not Found	Not Found	High	High	High					13065512	13209708	8419374	26.67	4	210	4
FALSE	Master Pro	138	530417304	PREDICTED	5	4	20	4	1	906	104.3	5.5	Not Found	Not Found	Not Found	High	High	High					13065512	13209708	8419374	26.67	4	210	4
FALSE	Master Pro	138	194097350	alpha-actin	5	4	20	4	1	914	105.5	5.41	Not Found	Not Found	Not Found	High	High	High					13065512	13209708	8419374	26.67	4	210	4
FALSE	Master Pro	2	5031973	protein dis	7	2	21	2	1	440	48.1	5.08	Not Found	High	High	High	High	High			4727859		9942726	9250320	8398233	26.46	2	200	2
FALSE	Master Pro	2	544186040	protein dis	7	2	21	2	1	437	47.8	5.08	Not Found	High	High	High	High	High			4727859		9942726	9250320	8398233	26.46	2	200	2
FALSE	Master Pro	2	544186032	protein dis	6	2	21	2	1	492	53.9	5.33	Not Found	High	High	High	High	High			4727859		9942726	9250320	8398233	26.46	2	200	2
FALSE	Master Pro	2	578802476	PREDICTED	6	2	21	2	1	491	53.5	6.14	Not Found	High	High	High	High	High			4727859		9942726	9250320	8398233	26.46	2	200	2
FALSE	Master Pro	2	530366876	PREDICTED	6	2	21	2	1	447	49.1	5.71	Not Found	High	High	High	High	High			4727859		9942726	9250320	8398233	26.46	2	200	2
FALSE	Master Pro	2	544186046	protein dis	6	2	21	2	1	488	53.2	5.53	Not Found	High	High	High	High	High			4727859		9942726	9250320	8398233	26.46	2	200	2
FALSE	Master Pro	2	544186036	protein dis	7	2	21	2	1	445	48.6	5.08	Not Found	High	High	High	High	High			4727859		9942726	9250320	8398233	26.46	2	200	2
FALSE	None	51	499137516	tropomyos	11	2	19	2	1	182	21.3	4.93	Not Found	Not Found	High	High	High	High				4170426	17662123	17578023	17607685	26.41	2	114	2
FALSE	None	51	499137522	tropomyos	13	2	19	2	1	158	18.6	4.74	Not Found	Not Found	High	High	High	High				4170426	17662123	17578023	17607685	26.41	2	114	2
FALSE	None	126	46409270	tubulin alp	4	1	14	1	1	450	49.9	5.1	High	High	High	High	High	High		22633248	24397981	23582818	56745423	56657977	59322316	26.41	1	160	1
FALSE	None	126	17921993	tubulin alp	4	1	14	1	1	450	49.9	5.1	High	High	High	High	High	High		22633248	24397981	23582818	56745423	56657977	59322316	26.41	1	160	1
FALSE	None	126	17921989	tubulin alp	4	1	14	1	1	448	49.9	5.06	High	High	High	High	High	High		22633248	24397981	23582818	56745423	56657977	59322316	26.41	1	160	1
FALSE	None	126	9507215	tubulin alp	4	1	14	1	1	449	50.1	5.06	High	High	High	High	High	High		22633248	24397981	23582818	56745423	56657977	59322316	26.41	1	160	1
FALSE	None	126	530370916	PREDICTED	4	1	14	1	1	433	48.3	5.01	High	High	High	High	High	High		22633248	24397981	23582818	56745423	56657977	59322316	26.41	1	160	1
FALSE	None	126	530357774	PREDICTED	14	1	14	1	1	128	14.3	4.41	High	High	High	High	High	High		22633248	24397981	23582818	56745423	56657977	59322316	26.41	1	160	1
FALSE	None	126	301171345	tubulin alp	5	1	14	1	1	383	42.9	5.08	High	High	High	High	High	High		22633248	24397981	23582818	56745423	56657977	59322316	26.41	1	160	1
FALSE	Master Pro	33	4502027	serum albu	4	3	27	3	1	609	69.3	6.28	High	High	High	High	High	High		28215156	33763099	30848402	1.41E+08	2.76E+08	1.51E+08	25.82	3	290	3
FALSE	Master Pro	82	4885381	histone H1	10	3	30	3	1	226	22.6	10.92	High	High	High	High	High	High		1.27E+08	1.58E+08	1.45E+08	1.41E+08	1.47E+08	1.42E+08	25.63	3	205	3
FALSE	Master Pro	112	515869342	hsc70-inte	10	3	21	3	1	359	40.1	5.3	High	High	High	High	High	High		11934621	14398391	13925772	25610209	24015433	23861196	25.45	3	110	3

FALSE	Master Pro	112	19923193	hsc70-inte	10	3	21	3	1	369	41.3	5.27	High	High	High	High	High	High		11934621	14398391	13925772	25610209	24015433	23861196	25.45	3	110	3
FALSE	Master Pro	5	4503481	elongation	8	4	21	4	1	437	50.1	6.67	High	High	High	High	High	High		7901745	12970506	10861329	20490977	22511115	20530979	25.45	4	247	4
FALSE	Master Pro	125	530394328	PREDICTED	7	6	24	6	1	1135	123.9	5.71	Not Found	Not Found	Not Found	High	High	High					18003014	18922668	19068544	25.43	6	152	6
FALSE	Master Pro	125	530394330	PREDICTED	7	6	24	6	1	1067	116.8	6.16	Not Found	Not Found	Not Found	High	High	High					18003014	18922668	19068544	25.43	6	152	6
FALSE	Master Pro	125	4507877	vinculin iso	7	6	24	6	1	1066	116.6	6.09	Not Found	Not Found	Not Found	High	High	High					18003014	18922668	19068544	25.43	6	152	6
FALSE	Master Pro	125	7669550	vinculin iso	7	6	24	6	1	1134	123.7	5.66	Not Found	Not Found	Not Found	High	High	High					18003014	18922668	19068544	25.43	6	152	6
FALSE	None	162;178	282396082	heterogene	7	2	20	0	2	293	32	5.43	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								25.08	2	201	2
FALSE	Master Pro	157	21464101	14-3-3 prot	13	3	22	3	1	247	28.3	4.89	High	High	High	High	High	High		10574784	12483617	6783402	55725572	80760292	59535908	25.07	3	235	3
FALSE	None	127	4506467	radixin isof	3	2	23	2	1	583	68.5	6.37	High	High	High	High	High	High		27316685	40799747	28580998	59860077	58370982	56297532	24.74	2	232	2
FALSE	None	127	386781571	radixin isof	3	2	23	2	1	604	71	6.71	High	High	High	High	High	High		27316685	40799747	28580998	59860077	58370982	56297532	24.74	2	232	2
FALSE	None	127	4505257	moesin [Ho	3	2	23	2	1	577	67.8	6.4	High	High	High	High	High	High		27316685	40799747	28580998	59860077	58370982	56297532	24.74	2	232	2
FALSE	None	127	386781587	radixin isof	4	2	23	2	1	447	52.6	6.16	High	High	High	High	High	High		27316685	40799747	28580998	59860077	58370982	56297532	24.74	2	232	2
FALSE	None	127	530421753	PREDICTED	3	2	23	2	1	578	67.9	6.28	High	High	High	High	High	High		27316685	40799747	28580998	59860077	58370982	56297532	24.74	2	232	2
FALSE	None	149	530390127	PREDICTED	9	2	20	1	1	213	24.7	4.74	Not Found	Not Found	Not Found	High	High	High						16768081	17074824	24.74	2	63	2
FALSE	None	149	223555975	tropomyos	7	2	20	1	1	284	32.7	4.73	Not Found	Not Found	Not Found	High	High	High						16768081	17074824	24.74	2	63	2
FALSE	None	149	42476296	tropomyos	7	2	20	1	1	284	32.8	4.7	Not Found	Not Found	Not Found	High	High	High						16768081	17074824	24.74	2	63	2
FALSE	None	149	530390119	PREDICTED	7	2	20	1	1	303	34.1	5.1	Not Found	Not Found	Not Found	High	High	High						16768081	17074824	24.74	2	63	2
FALSE	None	149	530390125	PREDICTED	7	2	20	1	1	284	32.8	4.68	Not Found	Not Found	Not Found	High	High	High						16768081	17074824	24.74	2	63	2
FALSE	None	149	47519616	tropomyos	7	2	20	1	1	284	33	4.67	Not Found	Not Found	Not Found	High	High	High						16768081	17074824	24.74	2	63	2
FALSE	None	149	578833543	PREDICTED	7	2	20	1	1	284	32.8	4.73	Not Found	Not Found	Not Found	High	High	High						16768081	17074824	24.74	2	63	2
FALSE	None	149	530390123	PREDICTED	7	2	20	1	1	284	33	4.69	Not Found	Not Found	Not Found	High	High	High						16768081	17074824	24.74	2	63	2
FALSE	None	51	530406390	PREDICTED	7	2	20	1	1	287	33.1	4.81	Not Found	Not Found	Not Found	High	High	High					14568511	14647778	14809722	24.43	2	44	2
FALSE	None	51	530406388	PREDICTED	7	2	20	1	1	287	32.9	4.79	Not Found	Not Found	Not Found	High	High	High					14568511	14647778	14809722	24.43	2	44	2
FALSE	None	51	578827355	PREDICTED	7	2	20	1	1	284	32.8	4.77	Not Found	Not Found	Not Found	High	High	High					14568511	14647778	14809722	24.43	2	44	2
FALSE	None	51	530406412	PREDICTED	8	2	20	1	1	248	28.7	4.79	Not Found	Not Found	Not Found	High	High	High					14568511	14647778	14809722	24.43	2	44	2
FALSE	None	51	63252904	tropomyos	8	2	20	1	1	245	28.4	4.77	Not Found	Not Found	Not Found	High	High	High					14568511	14647778	14809722	24.43	2	44	2
FALSE	None	51	530406394	PREDICTED	7	2	20	1	1	287	33	4.79	Not Found	Not Found	Not Found	High	High	High					14568511	14647778	14809722	24.43	2	44	2
FALSE	None	51	63252900	tropomyos	7	2	20	1	1	284	32.9	4.78	Not Found	Not Found	Not Found	High	High	High					14568511	14647778	14809722	24.43	2	44	2
FALSE	None	51	530406406	PREDICTED	8	2	20	1	1	251	28.8	4.83	Not Found	Not Found	Not Found	High	High	High					14568511	14647778	14809722	24.43	2	44	2
FALSE	None	51	530406410	PREDICTED	8	2	20	1	1	248	28.6	4.79	Not Found	Not Found	Not Found	High	High	High					14568511	14647778	14809722	24.43	2	44	2
FALSE	None	51	530406404	PREDICTED	7	2	20	1	1	275	31.7	4.89	Not Found	Not Found	Not Found	High	High	High					14568511	14647778	14809722	24.43	2	44	2
FALSE	None	51	530406400	PREDICTED	7	2	20	1	1	284	32.6	4.73	Not Found	Not Found	Not Found	High	High	High					14568511	14647778	14809722	24.43	2	44	2
FALSE	None	51	530406416	PREDICTED	8	2	20	1	1	248	28.7	4.82	Not Found	Not Found	Not Found	High	High	High					14568511	14647778	14809722	24.43	2	44	2
FALSE	None	51	63252898	tropomyos	7	2	20	1	1	284	32.7	4.74	Not Found	Not Found	Not Found	High	High	High					14568511	14647778	14809722	24.43	2	44	2
FALSE	None	51	530406402	PREDICTED	7	2	20	1	1	281	32.5	4.74	Not Found	Not Found	Not Found	High	High	High					14568511	14647778	14809722	24.43	2	44	2
FALSE	None	51	63252896	tropomyos	7	2	20	1	1	284	32.7	4.75	Not Found	Not Found	Not Found	High	High	High					14568511	14647778	14809722	24.43	2	44	2
FALSE	None	51	63252906	tropomyos	7	2	20	1	1	284	32.8	4.75	Not Found	Not Found	Not Found	High	High	High					14568511	14647778	14809722	24.43	2	44	2
FALSE	None	51	530406418	PREDICTED	8	2	20	1	1	245	28.5	4.78	Not Found	Not Found	Not Found	High	High	High					14568511	14647778	14809722	24.43	2	44	2
FALSE	None	51	530406414	PREDICTED	8	2	20	1	1	248	28.7	4.79	Not Found	Not Found	Not Found	High	High	High					14568511	14647778	14809722	24.43	2	44	2
FALSE	None	51	530406398	PREDICTED	7	2	20	1	1	284	32.6	4.73	Not Found	Not Found	Not Found	High	High	High					14568511	14647778	14809722	24.43	2	44	2
FALSE	None	51	63252902	tropomyos	7	2	20	1	1	284	32.7	4.74	Not Found	Not Found	Not Found	High	High	High					14568511	14647778	14809722	24.43	2	44	2
FALSE	None	51	27597085	tropomyos	7	2	20	1	1	284	32.8	4.77	Not Found	Not Found	Not Found	High	High	High					14568511	14647778	14809722	24.43	2	44	2
FALSE	None	51	530406386	PREDICTED	6	2	20	1	1	326	37.4	4.72	Not Found	Not Found	Not Found	High	High	High					14568511	14647778	14809722	24.43	2	44	2
FALSE	None	51	530406408	PREDICTED	8	2	20	1	1	248	28.6	4.77	Not Found	Not Found	Not Found	High	High	High					14568511	14647778	14809722	24.43	2	44	2
FALSE	None	51	530406392	PREDICTED	7	2	20	1	1	287	32.9	4.77	Not Found	Not Found	Not Found	High	High	High					14568511	14647778	14809722	24.43	2	44	2
FALSE	Master Pro	185	4503117	cystatin-B [	24	2	18	2	1	98	11.1	7.56	High	High	High	High	High	High		12317933	16752194	14443968	33996386	33693132	34412022	23.64	2	181	2
FALSE	Master Pro	169	24797067	HLA class I	7	2	16	2	1	365	40.8	6	High	High	High	High	High	High		22651040	24578780	12986287	29336741	26966766	28162206	23.62	2	224	2
FALSE	Master Pro	169	578841851	PREDICTED	6	2	16	2	1	434	47.8	6.6	High	High	High	High	High	High		22651040	24578780	12986287	29336741	26966766	28162206	23.62	2	224	2
FALSE	Master Pro	169	337752170	HLA class I	7	2	16	2	1	365	40.8	6.54	High	High	High	High	High	High		22651040	24578780	12986287	29336741	26966766	28162206	23.62	2	224	2
FALSE	Master Pro	169	578841853	PREDICTED	7	2	16	2	1	405	44.5	6.16	High	High	High	High	High	High		22651040	24578780	12986287	29336741	26966766	28162206	23.62	2	224	2
FALSE	Master Pro	169	530428926	PREDICTED	7	2	16	2	1	391	43.8	6.74	High	High	High	High	High	High		22651040	24578780	12986287	29336741	26966766	28162206	23.62	2	224	2
FALSE	Master Pro	229	41399285	60 kDa hea	9	4	23	4	1	573	61	5.87	Not Found	Not Found	Not Found	High	High	High					29251388	30355112	30329654	23.36	4	115	4
FALSE	Master Pro	37	4757768	rho GDP-di	15	2	21	2	1	204	23.2	5.11	High	High	High	High	High	High		23257393	36564586	29189092	50980702	57960469	57677072	23.25	2	243	2
FALSE	None	121	31543397	phosphogly	8	2	16	2	1	417	44.8	8.54	Not Found	Not Found	Not Found	High	High	High					1.19E+08	1.08E+08	74933658	23.21	2	211	2
FALSE	Master Pro	132	22208967	high mobili	15	3	24	3	1	107	11.7	10.32	High	High	High	High	High	High		23576479	62046515	47715396	31166080	27342657	27262662	23.07	3	232	3
FALSE	Master Pro	275	4506715	40S riboso	17	1	20	1	1	69	7.8	10.7	High	High	High	High	High	High		26294671	25159694	24324322		5559044	6922701	23.02	1	194	1
FALSE	None	47;240	574584818	tubulin bet	6	2	22	0	2	372	41.6	4.94	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								22.82	2	47	2
FALSE	None	47;240	574584811	tubulin bet	5	2	22	0	2	489	53.8	4.98	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								22.82	2	47	2
FALSE	None	47;240	574584803	tubulin bet	5	2	22	0	2	495	54.4	5.02	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								22.82	2	47	2
FALSE	None	47;240	14210536	tubulin bet	5	2	22	0	2	446	49.8	4.88	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								22.82	2	47	2
FALSE	None	47;240	530424971	PREDICTED	8	2	22	0	2	300	34.1	4.84	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								22.82	2	47	2
FALSE	None	47;240	21361322	tubulin bet	5	2	22	0	2	444	49.6	4.88	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								22.82	2	47	2
FALSE	Master Pro	16	10835159	plasminoge	9	3	22	3	1	402	45	7.2	High	High	High	Not Found	High	High			41435163	12449532		14228761	16684016	22.41	3	80	3
FALSE	Master Pro	145	4504483	hypoxanth	17	3	23	3	1	218	24.6	6.68	High	High	High	High	High	High		1414619	6589995	6933971	7567378	12269550	10665328	22.09	3	180	3
FALSE	Master Pro	42	578821728	PREDICTED	3	4	21	4	1	4596	489.1	6.29	High	High	High	High	High	High		5227071	5972002	6055745	15087716	27869679	14472443	21.93	4	100	4
FALSE	Master Pro	42	530397285	PREDICTED	4	4	21	4	1	5762	615	6.15	High	High	High	High	High	High		5227071	5972002	6055745	15087716	27869679	14472443	21.93	4	100	4
FALSE	Master Pro	42	530397283	PREDICTED	4	4	21	4	1	5762	614.7	6.19	High	High	High	High	High	High		5227071	5972002	6055745	15087716	27869679	14472443	21.93	4	100	4
FALSE	Master Pro	42	530397279	PREDICTED	4	4	21	4	1	5890	628.7	6.15	High	High	High	High	High	High		5227071	5972002	6055745	15087716	27869679	14472443	21.93	4	100	4
FALSE	Master Pro	42	530397287	PREDICTED	4	4	21	4	1	5762	614.8	6.18	High	High	High	High	High	High		5227071	5972002	6055745	15087716	27869679	14472443	21.93	4	100	4
FALSE	Master Pro	42	530397289	PREDICTED	4	4	21	4	1	5438	580.3	6.14	High	High	High	High	High	High		5227071	5972002	6055745	15087716	27869679	14472443	21.93	4	100	4
FALSE	None	77	47132620	keratin, typ	2	1	12	1	1	639	65.4	8	High	High	High	High	High	High		8521313	9236485	9500909	26844613	26049660	25637028	21.6	1	249	1
FALSE	None	77	194018511	keratin, typ	2	1	12	1	1	578	61.9	5.99	High	High	High	High	High	High		8521313	9236485	9500909	26844613	26049660	25637028	21.6	1	249	1
FALSE	Master Pro	152	4826734	RNA-bindin	5	3	16	3	1	526	53.4	9.36	High	High	High	High	High	High		7874221	11435326	10015085	16970069	16862840	19110476	21.24	3	135	3
FALSE	Master Pro	152	283135173	RNA-bindin	5	3	16	3	1	522	53.2	9.36	High	High	High	High	High	High		7874221	11435326	10015085	16970069	16862840	19110476	21.24	3	135	3
FALSE	Master Pro	152	283135201	RNA-bindin	5	3	16	3	1	525	53.3	9.36	High	High	High	High	High	High		7874221	11435326	10015085	16970069	16862840	19110476	21.24	3	135	3
FALSE	Master Pro	152	530407875	PREDICTED	8	3	16	3	1	321	33.2	9.17	High	High	High	High	High	High		7874221	11435326	10015085	16970069	16862840	19110476	21.24	3	135	3
FALSE	Master Pro	9	38455402	neutrophil	8	1	10	1	1	198	22.6	8.91	High	High	High	High	Not Found	High		6337834	8748809	9604193	18868623		19155511	21.02	1	208	1
FALSE	Master Pro	180	148470406	heterogene	8	2	16	1	1	415	45.6	5.58	Not Found	Not Found	Not Found	High	Not Found	Not Found					5079355			20.93	2	241	2
FALSE	Master Pro	4	386869503	40S riboso	10	2	14	2	1	259	28.5	9.73	High	High	High	High	High	High		4438669	4487196	5365041	18343687	19215909	13894165	20.89	2	200	2

FALSE	Master Prc	4	378548190	40S ribosor	11	2	14	2	1	243	26.7	9.66	High	High	High	High	High	High		4438669	4487196	5365041	18343687	19215909	13894165	20.89	2	200	2
FALSE	Master Prc	213	4505641	proliferatir	5	1	12	1	1	261	28.8	4.69	High	High	High	High	High	High		6214403		6082034	15787868	14040281	14631102	20.87	1	282	1
FALSE	Master Prc	144	217330646	activated R	19	2	21	2	1	127	14.4	9.6	High	High	High	High	High	High		24853437	21695458	21202878	24079122	14891410	14687966	20.75	2	234	2
FALSE	Master Prc	187	115430223	galectin-3 i	14	3	27	3	1	250	26.1	8.56	Not Found	Not Found	High	High	High	High				18590507	50004353	50625623	44018002	20.45	3	75	3
FALSE	Master Prc	59	4506901	serine/argi	9	1	16	1	1	164	19.3	11.65	High	High	High	High	Not Found	Not Found		9253220	8397431	7580984	13855674			20.37	1	166	1
FALSE	Master Prc	59	530367944	PREDICTED	6	1	16	1	1	235	26.9	11.85	High	High	High	High	Not Found	Not Found		9253220	8397431	7580984	13855674			20.37	1	166	1
FALSE	Master Prc	59	306482694	serine/argi	6	1	16	1	1	226	26	11.77	High	High	High	High	Not Found	Not Found		9253220	8397431	7580984	13855674			20.37	1	166	1
FALSE	Master Prc	59	530367946	PREDICTED	6	1	16	1	1	223	25.6	11.8	High	High	High	High	Not Found	Not Found		9253220	8397431	7580984	13855674			20.37	1	166	1
FALSE	Master Prc	59	530367948	PREDICTED	10	1	16	1	1	137	15.8	9.8	High	High	High	High	Not Found	Not Found		9253220	8397431	7580984	13855674			20.37	1	166	1
FALSE	Master Prc	59	72534660	serine/argi	6	1	16	1	1	238	27.4	11.82	High	High	High	High	Not Found	Not Found		9253220	8397431	7580984	13855674			20.37	1	166	1
FALSE	Master Prc	57	578800842	PREDICTED	24	2	17	2	1	136	15.1	9.82	High	High	High	High	High	High		8020556	6637279	6667476	8213457	8224431	8244191	20.34	1	110	2
FALSE	Master Prc	57	4758516	hepatoma-	14	2	17	2	1	240	26.8	4.73	High	High	High	High	High	High		8020556	6637279	6667476	8213457	8224431	8244191	20.34	1	110	2
FALSE	Master Prc	57	578800844	PREDICTED	28	2	17	2	1	120	13.7	9.6	High	High	High	High	High	High		8020556	6637279	6667476	8213457	8224431	8244191	20.34	1	110	2
FALSE	Master Prc	57	186928819	hepatoma-	13	2	17	2	1	256	28.2	4.79	High	High	High	High	High	High		8020556	6637279	6667476	8213457	8224431	8244191	20.34	1	110	2
FALSE	Master Prc	57	186928821	hepatoma-	14	2	17	2	1	233	25.5	4.55	High	High	High	High	High	High		8020556	6637279	6667476	8213457	8224431	8244191	20.34	1	110	2
FALSE	Master Prc	184	4885375	histone H1	10	3	17	3	1	213	21.4	10.93	High	High	High	High	High	High		61646498	62959053	33854361	1.2E+08	1.5E+08	53072735	20.24	3	106	3
FALSE	Master Prc	184	4885379	histone H1	10	3	17	3	1	219	21.9	11.03	High	High	High	High	High	High		61646498	62959053	33854361	1.2E+08	1.5E+08	53072735	20.24	3	106	3
FALSE	Master Prc	184	4885377	histone H1	10	3	17	3	1	221	22.3	11.02	High	High	High	High	High	High		61646498	62959053	33854361	1.2E+08	1.5E+08	53072735	20.24	3	106	3
FALSE	None	175	207028494	L-lactate de	15	3	21	3	1	274	30.2	7.15	High	High	High	High	High	High			8777567		44725613	40095415	70259028	20.21	3	151	3
FALSE	Master Prc	87	4507149	superoxide	9	1	14	1	1	154	15.9	6.13	High	High	High	High	High	High		1.06E+08	1.25E+08	1.08E+08	1.7E+08	1.74E+08	1.73E+08	20.06	1	237	1
FALSE	Master Prc	54	11056061	thymosin b	41	2	19	2	1	44	5.1	5.06	High	High	High	Not Found	Not Found	High		7177948	4.98E+08	3.68E+08			8589289	19.4	2	144	2
FALSE	Master Prc	7	7706495	dnaJ homo	8	2	12	2	1	358	40.5	6.18	High	High	High	Not Found	Not Found	Not Found		5290964	9754559	9665594				19.35	2	146	2
FALSE	Master Prc	176	4502491	complemer	10	3	17	3	1	282	31.3	4.84	Not Found	Not Found	Not Found	High	High	High					27462942	29463617	20934479	19.31	3	187	3
FALSE	Master Prc	201	4503483	elongation	2	1	17	1	1	858	95.3	6.83	High	High	High	High	High	High			1343601		5133240	7235540	5529606	19.14	1	139	1
FALSE	None	200	304555588	elongation	5	1	12	1	1	262	29.1	5.03	High	High	High	Not Found	Not Found	High		5669260		5595049			8877615	19.11	1	190	1
FALSE	None	13;102	155722983	heat shock	2	1	12	0	2	704	80.1	8.21	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								19.1	1	203	1
FALSE	None	13;102	440309857	heat shock	2	1	12	0	2	651	74.2	7.87	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								19.1	1	203	1
FALSE	Master Prc	19	4507677	endoplasm	3	2	14	1	1	803	92.4	4.84	High	Not Found	Not Found	Not Found	Not Found	Not Found		3825282						19.1	2	190	2
FALSE	Master Prc	183	21700763	hematolog	15	2	12	2	1	190	20.1	9.26	High	High	High	Not Found	Not Found	Not Found		9499850	10950027	10513499				18.96	2	166	2
FALSE	Master Prc	263	528078355	proteasom	10	2	14	2	1	236	27.2	5.83	Not Found	High	High	High	High	High			1610027	2017222	11333078	3985831	6722078	18.81	2	119	2
FALSE	Master Prc	263	5453990	proteasom	10	2	14	2	1	249	28.7	6.02	Not Found	High	High	High	High	High			1610027	2017222	11333078	3985831	6722078	18.81	2	119	2
FALSE	Master Prc	191	222144324	myosin reg	12	2	15	2	1	172	19.8	4.84	High	High	High	High	High	High		11346495	11291541	12489775	16041184	16558556	22487289	18.6	2	221	2
FALSE	Master Prc	191	530424791	PREDICTED	12	2	15	2	1	177	20.4	4.75	High	High	High	High	High	High		11346495	11291541	12489775	16041184	16558556	22487289	18.6	2	221	2
FALSE	Master Prc	191	5453740	myosin reg	12	2	15	2	1	171	19.8	4.81	High	High	High	High	High	High		11346495	11291541	12489775	16041184	16558556	22487289	18.6	2	221	2
FALSE	Master Prc	49	4504517	heat shock	16	2	13	2	1	205	22.8	6.4	High	High	High	Not Found	High	Not Found		12687206	11477469	11097990		22317508		18.56	1	165	2
FALSE	Master Prc	211	9951915	adenosylhc	6	2	14	2	1	432	47.7	6.34	High	High	High	High	High	High		6124881	7499405	8079690	8532945	9479469	13712092	18.46	1	219	2
FALSE	Master Prc	211	530417910	PREDICTED	7	2	14	2	1	404	44.6	6.47	High	High	High	High	High	High		6124881	7499405	8079690	8532945	9479469	13712092	18.46	1	219	2
FALSE	Master Prc	189	578817861	PREDICTED	11	1	12	1	1	115	13.1	8.07	High	High	High	High	High	High		95585722	88112418	82493801	1.54E+08	1.69E+08	1.56E+08	17.95	1	226	1
FALSE	Master Prc	189	50592994	thioredoxir	12	1	12	1	1	105	11.7	4.92	High	High	High	High	High	High		95585722	88112418	82493801	1.54E+08	1.69E+08	1.56E+08	17.95	1	226	1
FALSE	Master Prc	189	349732256	thioredoxir	15	1	12	1	1	85	9.4	6.04	High	High	High	High	High	High		95585722	88112418	82493801	1.54E+08	1.69E+08	1.56E+08	17.95	1	226	1
FALSE	Master Prc	3	21956645	myotrophir	14	1	8	1	1	118	12.9	5.52	High	High	High	Not Found	High	Not Found		12012945	11038182	12029478		15380108		17.8	1	207	1
FALSE	None	101	538919948	malate deh	11	2	16	2	1	231	24.6	7.99	High	High	Not Found	High	High	High		4635493	4833517		30370817	22495394	25172310	17.74	2	39	2
FALSE	Master Prc	225	4505011	lysyl oxidas	3	2	19	2	1	774	86.7	6.38	High	High	High	Not Found	High	Not Found		5515459	8538473	9063143		9019231		17.69	2	121	2
FALSE	Master Prc	92	578833388	PREDICTED	6	3	14	3	1	536	60.4	4.45	High	High	High	Not Found	Not Found	Not Found		7039991	9181461	8541413				17.65	3	166	3
FALSE	Master Prc	92	574280088	glucosidase	6	3	14	3	1	525	59.1	4.42	High	High	High	Not Found	Not Found	Not Found		7039991	9181461	8541413				17.65	3	166	3
FALSE	Master Prc	92	48255889	glucosidase	6	3	14	3	1	528	59.4	4.41	High	High	High	Not Found	Not Found	Not Found		7039991	9181461	8541413				17.65	3	166	3
FALSE	Master Prc	92	578833384	PREDICTED	6	3	14	3	1	543	61.2	4.46	High	High	High	Not Found	Not Found	Not Found		7039991	9181461	8541413				17.65	3	166	3
FALSE	Master Prc	92	574280236	glucosidase	6	3	14	3	1	535	60.2	4.41	High	High	High	Not Found	Not Found	Not Found		7039991	9181461	8541413				17.65	3	166	3
FALSE	Master Prc	92	578833390	PREDICTED	6	3	14	3	1	533	60.1	4.46	High	High	High	Not Found	Not Found	Not Found		7039991	9181461	8541413				17.65	3	166	3
FALSE	Master Prc	236	555290167	aspartate a	9	3	18	3	1	387	43	9.29	Not Found	High	Not Found	High	High	High			6005632		25897188	24932412	26622857	17.54	3	124	3
FALSE	Master Prc	236	73486658	aspartate a	8	3	18	3	1	430	47.5	9.01	Not Found	High	Not Found	High	High	High			6005632		25897188	24932412	26622857	17.54	3	124	3
FALSE	None	68	153252068	RNA-bindir	4	1	11	1	1	392	42.8	10.32	High	High	High	High	High	High		8960092	8528657	8596346	27292395	21789301	29286310	17.54	1	150	1
FALSE	None	68	223890219	RNA-bindir	1	1	11	1	1	1067	114.9	9.1	High	High	High	High	High	High		8960092	8528657	8596346	27292395	21789301	29286310	17.54	1	150	1
FALSE	None	180;186	530381031	PREDICTED	7	1	14	0	2	251	26.3	6.79	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								17.51	1	234	1
FALSE	None	180;186	530381027	PREDICTED	6	1	14	0	2	271	28.5	6.64	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								17.51	1	234	1
FALSE	Master Prc	261	55956919	heterogene	4	1	12	1	1	332	35.9	6.95	High	High	High	High	High	High		27760583	32860114	30604845	44881926	48100955	47818772	17.5	1	118	1
FALSE	Master Prc	261	55956921	heterogene	5	1	12	1	1	285	30.6	7.91	High	High	High	High	High	High		27760583	32860114	30604845	44881926	48100955	47818772	17.5	1	118	1
FALSE	None	169	578841864	PREDICTED	4	1	12	1	1	346	38.9	5.83	High	High	High	High	High	High		22651040	24578780	24652166	29336741	26966766	28162206	17.47	1	167	1
FALSE	None	169	62912479	HLA class I	4	1	12	1	1	358	40	5.83	High	High	High	High	High	High		22651040	24578780	24652166	29336741	26966766	28162206	17.47	1	167	1
FALSE	None	169	530429221	PREDICTED	4	1	12	1	1	362	40.3	6.76	High	High	High	High	High	High		22651040	24578780	24652166	29336741	26966766	28162206	17.47	1	167	1
FALSE	None	169	4504415	HLA class I	4	1	12	1	1	338	38.2	5.69	High	High	High	High	High	High		22651040	24578780	24652166	29336741	26966766	28162206	17.47	1	167	1
FALSE	None	169	17986001	major histc	4	1	12	1	1	362	40.4	5.85	High	High	High	High	High	High		22651040	24578780	24652166	29336741	26966766	28162206	17.47	1	167	1
FALSE	None	169	530381866	PREDICTED	3	1	12	1	1	391	43.9	6.47	High	High	High	High	High	High		22651040	24578780	24652166	29336741	26966766	28162206	17.47	1	167	1
FALSE	None	169	530429585	PREDICTED	4	1	12	1	1	343	38.6	5.66	High	High	High	High	High	High		22651040	24578780	24652166	29336741	26966766	28162206	17.47	1	167	1
FALSE	None	169	530429219	PREDICTED	3	1	12	1	1	391	43.6	7.14	High	High	High	High	High	High		22651040	24578780	24652166	29336741	26966766	28162206	17.47	1	167	1
FALSE	None	169	578842315	PREDICTED	3	1	12	1	1	448	51.1	7.2	High	High	High	High	High	High		22651040	24578780	24652166	29336741	26966766	28162206	17.47	1	167	1
FALSE	None	169	578842321	PREDICTED	3	1	12	1	1	394	44.4	6.16	High	High	High	High	High	High		22651040	24578780	24652166	29336741	26966766	28162206	17.47	1	167	1
FALSE	None	169	530429558	PREDICTED	3	1	12	1	1	405	44.6	6.05	High	High	High	High	High	High		22651040	24578780	24652166	29336741	26966766	28162206	17.47	1	167	1
FALSE	None	169	578839603	PREDICTED	4	1	12	1	1	346	38.9	5.83	High	High	High	High	High	High		22651040	24578780	24652166	29336741	26966766	28162206	17.47	1	167	1
FALSE	None	169	530428630	PREDICTED	3	1	12	1	1	405	44.6	6.21	High	High	High	High	High	High		22651040	24578780	24652166	29336741	26966766	28162206	17.47	1	167	1
FALSE	None	169	578842319	PREDICTED	3	1	12	1	1	431	49.2	6.99	High	High	High	High	High	High		22651040	24578780	24652166	29336741	26966766	28162206	17.47	1	167	1
FALSE	None	169	530429247	PREDICTED	4	1	12	1	1	352	39.7	5.67	High	High	High	High	High	High		22651040	24578780	24652166	29336741	26966766	28162206	17.47	1	167	1
FALSE	None	169	578842317	PREDICTED	3	1	12	1	1	435	48.9	5.9	High	High	High	High	High	High		22651040	24578780	24652166	29336741	26966766	28162206	17.47	1	167	1
FALSE	Master Prc	158	294997292	dystroglyca	2	1	16	1	1	895	97.5	8.56	High	High	High	High	High	High			26046664	24991289	34109619	26620018	29520302	17.24	1	187	1
FALSE	None	116	321117267	HSPE1-MO	5	1	12	1	1	261	29.7	6.16	High	High	High	High	High	High		30213494	35938416	35248167	30544328	27302947	27543370	17.11	1	308	1
FALSE	None	204	4504255	histone H2	13	2	16	2	1	128	13.5	10.58	High	High	High	High	High	High		1.63E+08	1.94E+08	1.35E+08	1.73E+08	1.91E+08	1.81E+08	16.99	2	109	2
FALSE	None	204	6912616	histone H2	13	2	16	2	1	128	13.5	10.58	High	High	High	High	High	High		1.63E+08	1.94E+08	1.35E+08	1.73E+08	1.91E+08	1.81E+08	16.99	2	109	2
FALSE	None	204	20357599	histone H2	14	2	16	2	1	114	12.1	10.46	High	High	High	High	High	High		1.63E+08	1.94E+08	1.35E+08	1.73E+08	1.91E+08	1.81E+08	16.99	2	109	2
FALSE	None	204	530377637	PREDICTED	11	2	16	2	1	152	16.6	10.65	High	High	High	High	High	High		1.63E+08	1.94E+08	1.35E+08	1.73E+08	1.91E+08	1.81E+08	16.99	2	109	2

FALSE	Master Pro	161	7669503	lysosome-a	5	2	17	2	1	410	44.9	5.69	High	High	High	High	High	High		4791960	4125814		9392596	6656276	8548075	16.92	2	134	2
FALSE	Master Pro	161	169790833	lysosome-a	5	2	17	2	1	411	45.1	5.91	High	High	High	High	High	High		4791960	4125814		9392596	6656276	8548075	16.92	2	134	2
FALSE	Master Pro	161	4504957	lysosome-a	5	2	17	2	1	410	44.9	5.63	High	High	High	High	High	High		4791960	4125814		9392596	6656276	8548075	16.92	2	134	2
FALSE	None	152	4507353	TATA-bindi	4	2	12	2	1	589	61.5	8.02	High	High	High	High	High	High		7874221	11435326	10015085	17123280	16862840	18871356	16.38	2	137	2
FALSE	None	152	21327701	TATA-bindi	4	2	12	2	1	592	61.8	8.02	High	High	High	High	High	High		7874221	11435326	10015085	17123280	16862840	18871356	16.38	2	137	2
FALSE	Master Pro	171	21361657	protein dis	4	2	15	2	1	505	56.7	6.35	High	High	High	High	High	High				3154553	9312282	7643153	8445556	16.16	2	117	2
FALSE	Master Pro	39	88853069	vitronectin	3	1	13	1	1	478	54.3	5.8	High	Not Found	High	High	High	High				4290591	14247036	12959866	13086296	16.01	1	98	1
FALSE	Master Pro	115	530368148	PREDICTED	4	1	12	1	1	348	38.5	6.19	High	Not Found	High	High	High	High		3341963			17655896	14474402	11128199	15.82	1	225	1
FALSE	Master Pro	115	371502127	macrophag	4	1	12	1	1	333	36.8	7.2	High	Not Found	High	High	High	High		3341963			17655896	14474402	11128199	15.82	1	225	1
FALSE	None	77;106	196115290	glial fibrilla	3	1	13	0	2	431	49.5	6.13	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								15.32	1	177	1
FALSE	None	77;106	125628636	keratin, typ	2	1	13	0	2	452	50.5	5.67	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								15.32	1	177	1
FALSE	None	77;106	331999954	keratin, typ	2	1	13	0	2	520	56.1	6.61	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								15.32	1	177	1
FALSE	None	77;106	125628632	keratin, typ	3	1	13	0	2	422	47.2	5.3	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								15.32	1	177	1
FALSE	None	77;106	530399826	PREDICTED	2	1	13	0	2	550	60.8	5.68	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								15.32	1	177	1
FALSE	None	77;106	530399828	PREDICTED	2	1	13	0	2	487	54.2	5.33	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								15.32	1	177	1
FALSE	None	77;106	4503979	glial fibrilla	3	1	13	0	2	432	49.9	5.52	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								15.32	1	177	1
FALSE	None	77;106	334688844	glial fibrilla	3	1	13	0	2	438	50.3	5.67	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								15.32	1	177	1
FALSE	None	77;106	67782365	keratin, typ	2	1	13	0	2	469	51.4	5.48	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								15.32	1	177	1
FALSE	Master Pro	206	14110420	heterogene	4	1	11	1	1	355	38.4	7.81	High	High	High	High	High	High		26323066	30636727	27914875	59240800	65192411	62152225	15.16	1	167	1
FALSE	Master Pro	206	51477708	heterogene	5	1	11	1	1	287	30.7	8.41	High	High	High	High	High	High		26323066	30636727	27914875	59240800	65192411	62152225	15.16	1	167	1
FALSE	Master Pro	206	14110417	heterogene	4	1	11	1	1	336	36.2	8.1	High	High	High	High	High	High		26323066	30636727	27914875	59240800	65192411	62152225	15.16	1	167	1
FALSE	Master Pro	206	14110414	heterogene	5	1	11	1	1	306	32.8	8.16	High	High	High	High	High	High		26323066	30636727	27914875	59240800	65192411	62152225	15.16	1	167	1
FALSE	Master Pro	141	530413651	PREDICTED	11	2	13	2	1	224	25	8.76	High	High	High	High	Not Found	Not Found		7164527	10694582	8636158	32979429			15.15	2	184	2
FALSE	Master Pro	141	68303561	proteasom	10	2	13	2	1	256	28.5	8.98	High	High	High	High	Not Found	Not Found		7164527	10694582	8636158	32979429			15.15	2	184	2
FALSE	Master Pro	141	68303563	proteasom	10	2	13	2	1	250	27.8	8.98	High	High	High	High	Not Found	Not Found		7164527	10694582	8636158	32979429			15.15	2	184	2
FALSE	Master Pro	141	4506189	proteasom	10	2	13	2	1	248	27.9	8.46	High	High	High	High	Not Found	Not Found		7164527	10694582	8636158	32979429			15.15	2	184	2
FALSE	Master Pro	141	68303565	proteasom	12	2	13	2	1	212	23.7	9.11	High	High	High	High	Not Found	Not Found		7164527	10694582	8636158	32979429			15.15	2	184	2
FALSE	Master Pro	282	11128019	cytochrom	18	2	15	2	1	105	11.7	9.57	High	High	Not Found	High	High	High		11302067	11525180		39740845	40143717	41719636	15.11	2	82	2
FALSE	Master Pro	134	228008400	heterogene	2	1	13	1	1	562	62.6	7.56	High	Not Found	High	High	High	High		4384381		6194014	16747728	12238391	15472241	14.99	1	87	1
FALSE	Master Pro	134	228008396	heterogene	3	1	13	1	1	464	52	9.16	High	Not Found	High	High	High	High		4384381		6194014	16747728	12238391	15472241	14.99	1	87	1
FALSE	Master Pro	134	228008291	heterogene	2	1	13	1	1	623	69.6	8.59	High	Not Found	High	High	High	High		4384381		6194014	16747728	12238391	15472241	14.99	1	87	1
FALSE	Master Pro	134	530382968	PREDICTED	2	1	13	1	1	561	62.5	7.56	High	Not Found	High	High	High	High		4384381		6194014	16747728	12238391	15472241	14.99	1	87	1
FALSE	Master Pro	134	228008295	heterogene	2	1	13	1	1	588	65.6	8.6	High	Not Found	High	High	High	High		4384381		6194014	16747728	12238391	15472241	14.99	1	87	1
FALSE	Master Pro	134	359338991	heterogene	3	1	13	1	1	410	46.3	8.88	High	Not Found	High	High	High	High		4384381		6194014	16747728	12238391	15472241	14.99	1	87	1
FALSE	Master Pro	134	530382970	PREDICTED	2	1	13	1	1	525	59	9.36	High	Not Found	High	High	High	High		4384381		6194014	16747728	12238391	15472241	14.99	1	87	1
FALSE	Master Pro	134	228008398	heterogene	2	1	13	1	1	527	58.7	7.56	High	Not Found	High	High	High	High		4384381		6194014	16747728	12238391	15472241	14.99	1	87	1
FALSE	Master Pro	223	5453710	LIM and SH	5	1	12	1	1	261	29.7	7.05	High	High	High	High	High	High		23150603	22838585	20501021	23073011	21877002	22011284	14.93	1	133	1
FALSE	Master Pro	223	410444379	LIM and SH	6	1	12	1	1	205	23.2	4.94	High	High	High	High	High	High		23150603	22838585	20501021	23073011	21877002	22011284	14.93	1	133	1
FALSE	Master Pro	197	530402322	PREDICTED	9	2	19	2	1	158	18.3	9.7	High	High	High	High	High	High			9021840	8044202	14282800	60469510	1.12E+08	14.7	2	69	2
FALSE	Master Pro	197	530402316	PREDICTED	7	2	19	2	1	215	24.9	5.74	High	High	High	High	High	High			9021840	8044202	14282800	60469510	1.12E+08	14.7	2	69	2
FALSE	None	42	578821732	PREDICTED	3	3	15	3	1	3489	368.2	6.58	High	High	High	High	High	Not Found		5227071	5972002	6055745	15370859	41716251		14.49	3	90	3
FALSE	None	42	578821730	PREDICTED	4	3	15	3	1	4001	423.5	6.34	High	High	High	High	High	Not Found		5227071	5972002	6055745	15370859	41716251		14.49	3	90	3
FALSE	None	42	530397291	PREDICTED	4	3	15	3	1	4506	478.7	6.28	High	High	High	High	High	Not Found		5227071	5972002	6055745	15370859	41716251		14.49	3	90	3
FALSE	None	30	530387113	PREDICTED	17	2	10	2	1	159	18.5	10.1	Not Found	Not Found	Not Found	High	High	High					15690446	22378893	18504975	14.43	2	188	2
FALSE	Master Pro	258	24431933	reticulon-4	9	2	13	2	1	373	40.3	4.78	High	High	High	High	High	Not Found		9824606	13017258	15548356	15389797	51767382		14.34	2	180	2
FALSE	Master Pro	258	24431935	reticulon-4	3	2	13	2	1	1192	129.9	4.5	High	High	High	High	High	Not Found		9824606	13017258	15548356	15389797	51767382		14.34	2	180	2
FALSE	Master Pro	258	47519490	reticulon-4	9	2	13	2	1	392	42.2	4.74	High	High	High	High	High	Not Found		9824606	13017258	15548356	15389797	51767382		14.34	2	180	2
FALSE	None	12	4557797	nucleoside	19	2	14	2	1	152	17.1	6.19	High	High	High	High	High	High		14898776	19778806	23332452	65128401	70317858	63751186	14.34	2	43	2
FALSE	None	12	38045913	nucleoside	16	2	14	2	1	177	19.6	5.58	High	High	High	High	High	High		14898776	19778806	23332452	65128401	70317858	63751186	14.34	2	43	2
FALSE	Master Pro	193	4507521	transketola	3	1	8	1	1	623	67.8	7.66	Not Found	High	High	Not Found	High	High			7484845			25756629	23592617	14.23	1	142	1
FALSE	Master Pro	193	384475521	transketola	3	1	8	1	1	631	68.8	7.52	Not Found	High	High	Not Found	High	High			7484845			25756629	23592617	14.23	1	142	1
FALSE	Master Pro	193	578806532	PREDICTED	3	1	8	1	1	630	68.8	7.88	Not Found	High	High	Not Found	High	High			7484845			25756629	23592617	14.23	1	142	1
FALSE	Master Pro	174	38372925	basigin isof	11	2	13	2	1	269	29.2	5.64	Not Found	High	High	High	High	High			10741873	10856660	37836984	37038616	34879876	14.16	2	139	2
FALSE	Master Pro	67	4506193	proteasom	10	2	11	2	1	241	26.5	8.13	High	High	High	Not Found	Not Found	Not Found		8735443	6997470	5553969				14.13	2	175	2
FALSE	Master Pro	177	40068512	plasma alp	5	2	12	2	1	467	54	6.25	High	High	High	High	High	Not Found		3296074	5875871	6741677	7441023	8327112		14.01	2	70	2
FALSE	Master Pro	241	5453555	GTP-bindin	10	2	14	2	1	216	24.4	7.49	High	High	High	Not Found	High	Not Found		10574030	11760252	12025926		15386073		13.66	2	90	2
FALSE	Master Pro	215	32171249	prostaglan	8	1	6	1	1	190	21	7.8	Not Found	Not Found	Not Found	High	High	High					14152517	15197865	15123190	13.62	1	149	1
FALSE	Master Pro	111	23110935	proteasom	4	1	12	1	1	269	30.2	6.99	High	High	High	High	High	High		13516908	15591390	17994090	23035055	20370776	24273566	13.5	1	167	1
FALSE	Master Pro	111	4506179	proteasom	5	1	12	1	1	263	29.5	6.61	High	High	High	High	High	High		13516908	15591390	17994090	23035055	20370776	24273566	13.5	1	167	1
FALSE	Master Pro	222	171543879	CD99 antig	24	2	8	2	1	169	17.1	4.56	High	Not Found	High	High	Not Found	High		4719686		4900356	13711490		14910948	13.27	2	166	2
FALSE	Master Pro	222	530421140	PREDICTED	24	2	8	2	1	168	17	4.56	High	Not Found	High	High	Not Found	High		4719686		4900356	13711490		14910948	13.27	2	166	2
FALSE	Master Pro	222	578837893	PREDICTED	18	2	8	2	1	217	22.3	5.69	High	Not Found	High	High	Not Found	High		4719686		4900356	13711490		14910948	13.27	2	166	2
FALSE	Master Pro	222	530421138	PREDICTED	22	2	8	2	1	184	18.8	4.75	High	Not Found	High	High	Not Found	High		4719686		4900356	13711490		14910948	13.27	2	166	2
FALSE	Master Pro	222	578837898	PREDICTED	23	2	8	2	1	177	17.7	4.82	High	Not Found	High	High	Not Found	High		4719686		4900356	13711490		14910948	13.27	2	166	2
FALSE	Master Pro	222	4505183	CD99 antig	22	2	8	2	1	185	18.8	4.75	High	Not Found	High	High	Not Found	High		4719686		4900356	13711490		14910948	13.27	2	166	2
FALSE	Master Pro	222	530423040	PREDICTED	18	2	8	2	1	218	22.5	5.69	High	Not Found	High	High	Not Found	High		4719686		4900356	13711490		14910948	13.27	2	166	2
FALSE	Master Pro	222	530423044	PREDICTED	20	2	8	2	1	202	20.7	5.27	High	Not Found	High	High	Not Found	High		4719686		4900356	13711490		14910948	13.27	2	166	2
FALSE	Master Pro	222	530423050	PREDICTED	25	2	8	2	1	160	16	4.7	High	Not Found	High	High	Not Found	High		4719686		4900356	13711490		14910948	13.27	2	166	2
FALSE	Master Pro	222	578837896	PREDICTED	22	2	8	2	1	181	18.2	5.1	High	Not Found	High	High	Not Found	High		4719686		4900356	13711490		14910948	13.27	2	166	2
FALSE	Master Pro	119	530368056	PREDICTED	3	1	8	1	1	497	55.6	7.88	Not Found	Not Found	Not Found	High	High	High					5914718	5068655	6368079	13.16	1	34	1
FALSE	Master Pro	119	48255966	UTP--gluco	3	1	8	1	1	508	56.9	8.15	Not Found	Not Found	Not Found	High	High	High					5914718	5068655	6368079	13.16	1	34	1
FALSE	None	204	41406069	histone H2	14	1	11	1	1	66	6.9	11.06	High	High	High	High	High	High		1.63E+08	1.94E+08	1.88E+08	1.73E+08	1.91E+08	1.81E+08	13.13	1	109	1
FALSE	Master Pro	148	14165466	polypyrimi	4	1	6	1	1	531	57.2	9.17	Not Found	Not Found	Not Found	Not Found	High	High							4416362	12.72	1	196	1
FALSE	Master Pro	148	14165464	polypyrimi	3	1	6	1	1	550	59	9.16	Not Found	Not Found	Not Found	Not Found	High	High							4416362	12.72	1	196	1
FALSE	Master Pro	148	4506243	polypyrimi	3	1	6	1	1	557	59.6	9.16	Not Found	Not Found	Not Found	Not Found	High	High							4416362	12.72	1	196	1
FALSE	Master Pro	148	530425327	PREDICTED	4	1	6	1	1	533	57.4	9.32	Not Found	Not Found	Not Found	Not Found	High	High							4416362	12.72	1	196	1
FALSE	Master Pro	148	530425325	PREDICTED	3	1	6	1	1	559	59.8	9.31	Not Found	Not Found	Not Found	Not Found	High	High							4416362	12.72	1	196	1
FALSE	Master Pro	25	4505185	macrophag	10	1	12	1	1	115	12.5	7.88	High	High	High	High	High	High		16792823	19772671	18907976	47291903	48486451	47578692	12.43	1	96	1
FALSE	None	12	310923127	nucleoside	15	1	8	1	1	82	9.6	9.7	Not Found	High	High	High	High	High			18676092	24708091	65128401	70317858	63751186	12.25	1	32	1

FALSE	Master Prc	41	6005942	transitiona	2	1	8	1	1	806	89.3	5.26	Not Found	Not Found	Not Found	High	High	High					3265652	4645965		12.14	1	110	1
FALSE	Master Prc	58	7524346	adenylate l	6	1	8	1	1	232	25.6	7.88	High	High	Not Found	High	Not Found	High		4363366	4491233		8373538		9462180	12.04	1	95	1
FALSE	Master Prc	58	4502013	adenylate l	5	1	8	1	1	239	26.5	7.81	High	High	Not Found	High	Not Found	High		4363366	4491233		8373538		9462180	12.04	1	95	1
FALSE	Master Prc	58	312836806	adenylate l	6	1	8	1	1	224	24.6	6.7	High	High	Not Found	High	Not Found	High		4363366	4491233		8373538		9462180	12.04	1	95	1
FALSE	Master Prc	21	34740329	heterogene	3	1	8	1	1	378	39.6	9.01	High	High	High	Not Found	Not Found	Not Found		6111656	6133900	6388223				11.87	1	161	1
FALSE	Master Prc	21	530369994	PREDICTED	3	1	8	1	1	341	35.9	8.95	High	High	High	Not Found	Not Found	Not Found		6111656	6133900	6388223				11.87	1	161	1
FALSE	Master Prc	21	578803915	PREDICTED	3	1	8	1	1	331	35.4	9.17	High	High	High	Not Found	Not Found	Not Found		6111656	6133900	6388223				11.87	1	161	1
FALSE	Master Prc	21	530369992	PREDICTED	3	1	8	1	1	356	37	8.31	High	High	High	Not Found	Not Found	Not Found		6111656	6133900	6388223				11.87	1	161	1
FALSE	Master Prc	36	578800054	PREDICTED	3	1	6	1	1	643	67.4	7.61	Not Found	Not Found	Not Found	High	High	High					8157305	8256693	9619025	11.67	1	230	1
FALSE	Master Prc	36	578800052	PREDICTED	3	1	6	1	1	664	69.7	7.36	Not Found	Not Found	Not Found	High	High	High					8157305	8256693	9619025	11.67	1	230	1
FALSE	Master Prc	36	17402900	far upstrea	3	1	6	1	1	644	67.5	7.61	Not Found	Not Found	Not Found	High	High	High					8157305	8256693	9619025	11.67	1	230	1
FALSE	Master Prc	36	530363548	PREDICTED	3	1	6	1	1	665	69.8	7.36	Not Found	Not Found	Not Found	High	High	High					8157305	8256693	9619025	11.67	1	230	1
FALSE	Master Prc	74	34419635	heat shock	6	3	13	1	1	643	71	6.14	Not Found	Not Found	Not Found	Not Found	Not Found	High							4589697	11.48	2	132	3
FALSE	Master Prc	203	124494254	proliferatic	7	2	8	2	1	394	43.8	6.55	High	Not Found	Not Found	High	High	High		5802805			24028974	23275332	26156341	10.95	2	54	2
FALSE	Master Prc	97	20070125	protein dis	8	3	8	3	1	508	57.1	4.87	Not Found	Not Found	High	High	High	High				9257326	9740563	7350423	21029337	10.89	3	94	2
FALSE	Master Prc	8	4504347	hemoglobi	11	1	10	1	1	142	15.2	8.68	High	High	Not Found	High	High	High		3065627	5109548		15728400	13969701	16948979	10.71	1	0	1
FALSE	Master Prc	84	4757826	beta-2-mic	11	1	8	1	1	119	13.7	6.52	High	High	High	Not Found	Not Found	Not Found		14160385	22051158	17684746				10.7	1	53	1
FALSE	Master Prc	84	530406197	PREDICTED	11	1	8	1	1	122	14	7.44	High	High	High	Not Found	Not Found	Not Found		14160385	22051158	17684746				10.7	1	53	1
FALSE	Master Prc	128	167234419	thyroid hoı	2	2	9	2	1	955	108.6	10.15	High	High	High	Not Found	Not Found	Not Found		8431291	6942093					10.49	2	79	2
FALSE	Master Prc	239	21624607	coactosin-l	11	1	8	1	1	142	15.9	5.67	Not Found	High	High	High	Not Found	High			1642429	1607710	2493980		1982573	10.48	1	112	1
FALSE	Master Prc	23	289547526	rab11 fami	1	1	9	1	1	649	70.9	9.31	High	High	Not Found	High	High	High		25441358	32097110		49509038	54236594	46661956	10.45	1	0	1
FALSE	Master Prc	23	289547524	rab11 fami	1	1	9	1	1	1283	137.1	5.43	High	High	Not Found	High	High	High		25441358	32097110		49509038	54236594	46661956	10.45	1	0	1
FALSE	Master Prc	88	45935371	serglycin p	8	1	6	1	1	158	17.6	4.96	High	High	High	Not Found	Not Found	Not Found		5417234	5356656	5209297				9.99	1	68	1
FALSE	None	207	5453549	peroxiredo	3	1	7	1	1	271	30.5	6.29	High	Not Found	Not Found	High	High	High		68569179			1.1E+08	1.1E+08	1.16E+08	9.97	1	49	1
FALSE	None	207	530420948	PREDICTED	3	1	7	1	1	257	29.3	5.69	High	Not Found	Not Found	High	High	High		68569179			1.1E+08	1.1E+08	1.16E+08	9.97	1	49	1
FALSE	Master Prc		242332527	uncharacte	0	1	8	0	0	3197	361.5	6.99	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								9.97	1	65	1
FALSE	Master Prc		530378906	PREDICTED	0	1	8	0	0	3250	367.2	6.92	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								9.97	1	65	1
FALSE	Master Prc		530378904	PREDICTED	0	1	8	0	0	3251	367.3	6.92	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								9.97	1	65	1
FALSE	Master Prc		530378914	PREDICTED	0	1	8	0	0	3208	362.5	6.93	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								9.97	1	65	1
FALSE	Master Prc		530378908	PREDICTED	0	1	8	0	0	3250	367.2	6.93	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								9.97	1	65	1
FALSE	Master Prc		578809969	PREDICTED	0	1	8	0	0	2792	316	6.95	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								9.97	1	65	1
FALSE	Master Prc		530378912	PREDICTED	0	1	8	0	0	3214	363.4	6.93	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								9.97	1	65	1
FALSE	Master Prc	20	4506597	60S riboso	10	1	8	1	1	165	17.8	9.42	High	High	High	Not Found	Not Found	Not Found		4972729	4133519	4304492				9.9	1	79	1
FALSE	Master Prc	147	6679625	chymotryp	6	1	7	1	1	270	29.2	6.28	Not Found	Not Found	Not Found	High	High	High					2410712	1518087		9.86	1	135	1
FALSE	Master Prc	147	236460050	chymotryp	6	1	7	1	1	270	29.5	6.9	Not Found	Not Found	Not Found	High	High	High					2410712	1518087		9.86	1	135	1
FALSE	Master Prc	22	9845502	40S riboso	6	1	6	1	1	295	32.8	4.87	High	High	Not Found	Not Found	Not Found	Not Found		8119726	7476526					9.75	1	89	1
FALSE	Master Prc	153	212549555	interleukin	3	2	11	2	1	706	76.5	7.91	Not Found	Not Found	Not Found	High	High	High					16068125	15780785	14630310	9.66	2	79	2
FALSE	Master Prc	153	24234753	interleukin	3	2	11	2	1	702	76	7.75	Not Found	Not Found	Not Found	High	High	High					16068125	15780785	14630310	9.66	2	79	2
FALSE	Master Prc	153	212549553	interleukin	2	2	11	2	1	898	95.7	8.81	Not Found	Not Found	Not Found	High	High	High					16068125	15780785	14630310	9.66	2	79	2
FALSE	Master Prc	153	578833231	PREDICTED	2	2	11	2	1	855	91.9	8.78	Not Found	Not Found	Not Found	High	High	High					16068125	15780785	14630310	9.66	2	79	2
FALSE	Master Prc	153	24234750	interleukin	2	2	11	2	1	894	95.3	8.76	Not Found	Not Found	Not Found	High	High	High					16068125	15780785	14630310	9.66	2	79	2
FALSE	Master Prc	153	24234756	interleukin	3	2	11	2	1	690	74.6	8.24	Not Found	Not Found	Not Found	High	High	High					16068125	15780785	14630310	9.66	2	79	2
FALSE	Master Prc	91	5031877	lamin-B1 is	4	2	8	2	1	586	66.4	5.16	High	High	High	Not Found	Not Found	Not Found		8841341	6766444	9651441				9.63	2	52	2
FALSE	Master Prc	251	578806085	PREDICTED	1	2	10	2	1	2320	248.2	6.25	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	578806117	PREDICTED	3	2	10	2	1	1135	119.9	5.24	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	578806092	PREDICTED	1	2	10	2	1	2311	247.4	6.43	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	578806067	PREDICTED	1	2	10	2	1	2352	251.5	6.32	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	578806111	PREDICTED	3	2	10	2	1	1207	127.2	5.57	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	578806122	PREDICTED	4	2	10	2	1	865	91.4	8.72	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	578806113	PREDICTED	3	2	10	2	1	1178	124.2	5.53	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	578806094	PREDICTED	1	2	10	2	1	2309	246.4	6.21	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	578806104	PREDICTED	1	2	10	2	1	2280	244.3	5.95	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	530372482	PREDICTED	2	2	10	2	1	2256	241.1	6.34	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	578806096	PREDICTED	1	2	10	2	1	2300	246.4	6.35	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	530372504	PREDICTED	4	2	10	2	1	906	95.4	9.07	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	578806081	PREDICTED	1	2	10	2	1	2326	248.2	6.23	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	578806108	PREDICTED	1	2	10	2	1	2268	242.9	5.91	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	578806102	PREDICTED	1	2	10	2	1	2282	244.4	6.43	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	578806083	PREDICTED	1	2	10	2	1	2323	248.6	6.3	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	578806075	PREDICTED	1	2	10	2	1	2335	249.7	6.3	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	578806100	PREDICTED	1	2	10	2	1	2283	244.4	5.96	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	197276600	microtubul	3	2	10	2	1	1135	119.9	6.23	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	578806069	PREDICTED	1	2	10	2	1	2351	251.5	6.32	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	530372458	PREDICTED	1	2	10	2	1	2314	247.1	6.23	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	578806090	PREDICTED	1	2	10	2	1	2314	247.7	6.14	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	578806071	PREDICTED	1	2	10	2	1	2340	250.4	6.32	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	578806077	PREDICTED	1	2	10	2	1	2335	249.7	6.32	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	530372498	PREDICTED	3	2	10	2	1	1129	118.7	5.45	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	530372502	PREDICTED	3	2	10	2	1	975	102.5	9.28	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	578806106	PREDICTED	1	2	10	2	1	2274	243.1	6.27	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	530372506	PREDICTED	4	2	10	2	1	903	95.2	8.94	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	47519639	microtubul	3	2	10	2	1	1152	120.9	5.43	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	530372466	PREDICTED	1	2	10	2	1	2297	245.3	6.21	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	578806115	PREDICTED	3	2	10	2	1	1155	122	5.57	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	Master Prc	251	578806073	PREDICTED	1	2	10	2	1	2337	250	6.25	High	High	High	Not Found	Not Found	High		10310347	9685947	9678741			20479115	9.36	2	122	2
FALSE	None	24	71274132	phosphogl	6	1	14	1	1	254	28.8	6.65	High	High	High	High	High	Not Found		15953323	14948481		76567790	69873333		9.31	1	77	1
FALSE	None	24	50593010	phosphogl	6	1	14	1	1	253	28.7	8.88	High	High	High	High	High	Not Found		15953323	14948481		76567790	69873333		9.31	1	77	1
FALSE	Master Prc	190	157743259	homeobox	4	1	8	1	1	357	37.8	8.12	High	High	High	Not Found	Not Found	Not Found		29729188	39097182	37501084				9.25	1	122	1
FALSE	Master Prc	142	14141161	heterogene	3	2	9	2	1	806	88.9	5.78	High	Not Found	High	High	High	Not Found		11308846		11087012	35517259	67167451		9.19	2	34	2

FALSE	Master Pro	142	74136883	heterogene	3	2	9	2	1	825	90.5	6	High	Not Found	High	High	High	Not Found		11308846		11087012	35517259	67167451		9.19	2	34	2
FALSE	None	37	297374785	rho GDP-di	10	1	10	1	1	160	18.2	5.19	High	High	High	High	Not Found	Not Found		13817810		26572531	44112055			8.96	1	107	1
FALSE	Master Pro	81	11968182	40S riboso	5	1	12	1	1	152	17.7	10.99	High	Not Found	High	High	High	High		3246030		2936472		6556644	4845285	8.88	1	0	1
FALSE	Master Pro	155	532691774	proteasom	6	1	6	1	1	227	25.3	7.11	High	High	High	Not Found	Not Found	Not Found		6968732	7075259	6901721				8.78	1	144	1
FALSE	Master Pro	155	23110944	proteasom	5	1	6	1	1	246	27.4	6.76	High	High	High	Not Found	Not Found	Not Found		6968732	7075259	6901721				8.78	1	144	1
FALSE	Master Pro	99	6031162	calretinin i	6	1	6	1	1	192	22.1	5.03	Not Found	Not Found	Not Found	High	High	High					18246564	17266119	19234949	8.77	1	94	1
FALSE	Master Pro	99	153946409	calretinin i	4	1	6	1	1	271	31.5	5.15	Not Found	Not Found	Not Found	High	High	High					18246564	17266119	19234949	8.77	1	94	1
FALSE	None	4	386869506	40S riboso	11	1	6	1	1	117	12.6	9.28	Not Found	Not Found	Not Found	High	High	High					18343687	19215909	19243019	8.58	1	44	1
FALSE	None	202	4505303	myosin ligh	6	1	6	1	1	208	22.8	5.73	High	High	High	Not Found	Not Found	Not Found		15394781	18226079	16599444				8.05	1	86	1
FALSE	Master Pro	202	88999583	myosin ligh	19	2	8	2	1	151	17	4.55	High	High	High	Not Found	Not Found	Not Found		15394781	18226079	9127350				8.05	2	86	2
FALSE	Master Pro	202	17986258	myosin ligh	19	2	8	2	1	151	16.9	4.65	High	High	High	Not Found	Not Found	Not Found		15394781	18226079	9127350				8.05	2	86	2
FALSE	Master Pro	247	4506407	ran-specifi	5	1	6	1	1	201	23.3	5.29	High	High	High	Not Found	Not Found	Not Found		7924757	8700707	7931065				7.96	1	86	1
FALSE	Master Pro	247	520975484	ran-specifi	6	1	6	1	1	200	23.2	5.29	High	High	High	Not Found	Not Found	Not Found		7924757	8700707	7931065				7.96	1	86	1
FALSE	Master Pro	247	520975477	ran-specifi	4	1	6	1	1	278	31.9	8.75	High	High	High	Not Found	Not Found	Not Found		7924757	8700707	7931065				7.96	1	86	1
FALSE	Master Pro	247	578837318	PREDICTED	4	1	6	1	1	271	30.9	6.68	High	High	High	Not Found	Not Found	Not Found		7924757	8700707	7931065				7.96	1	86	1
FALSE	Master Pro	118	21703710	protein shi	3	1	7	1	1	240	25.6	6.68	High	High	High	Not Found	Not Found	High		19463245	21259330	19905268			10497222	7.94	1	33	1
FALSE	Master Pro	118	441418791	protein shi	3	1	7	1	1	209	22.4	6.25	High	High	High	Not Found	Not Found	High		19463245	21259330	19905268			10497222	7.94	1	33	1
FALSE	Master Pro	256	7706573	45 kDa calc	7	2	11	2	1	348	39.6	5.11	High	High	High	Not Found	Not Found	High		6187551	14554114	15990038			16082529	7.94	2	58	2
FALSE	Master Pro	256	18699732	45 kDa calc	7	2	11	2	1	362	41.8	4.86	High	High	High	Not Found	Not Found	High		6187551	14554114	15990038			16082529	7.94	2	58	2
FALSE	Master Pro	18	4759212	tubulin-spe	14	1	8	1	1	108	12.8	5.29	High	High	High	Not Found	Not Found	Not Found		8829313	14906622	11857405				7.69	1	20	1
FALSE	Master Pro	131	4504151	granulins p	5	2	9	2	1	593	63.5	6.83	High	High	High	High	Not Found	High		5457852	5157394	5365240			28404173	7.66	2	55	2
FALSE	None	74	167466173	heat shock	5	2	9	1	1	641	70	5.66	Not Found	Not Found	Not Found	Not Found	Not Found	High							4589697	7.6	1	130	2
FALSE	None	127	578800142	PREDICTED	0	1	6	1	1	1945	220.7	5.58	Not Found	Not Found	Not Found	High	High	High					70121749	68715386	78653189	7.56	1	55	1
FALSE	None	127	578800146	PREDICTED	0	1	6	1	1	1737	196.6	5.57	Not Found	Not Found	Not Found	High	High	High					70121749	68715386	78653189	7.56	1	55	1
FALSE	None	127	578800144	PREDICTED	0	1	6	1	1	1918	217	5.6	Not Found	Not Found	Not Found	High	High	High					70121749	68715386	78653189	7.56	1	55	1
FALSE	None	127	578800140	PREDICTED	0	1	6	1	1	1972	223.3	5.62	Not Found	Not Found	Not Found	High	High	High					70121749	68715386	78653189	7.56	1	55	1
FALSE	None	127	153791497	rootletin [H	0	1	6	1	1	2017	228.4	5.5	Not Found	Not Found	Not Found	High	High	High					70121749	68715386	78653189	7.56	1	55	1
FALSE	None	127	578800138	PREDICTED	0	1	6	1	1	1979	224.1	5.59	Not Found	Not Found	Not Found	High	High	High					70121749	68715386	78653189	7.56	1	55	1
FALSE	None	175	578820360	PREDICTED	3	1	6	1	1	332	36.5	6.99	Not Found	Not Found	Not Found	High	High	High					32195992	25332939	24393717	7.53	1	50	1
FALSE	None	175	578820358	PREDICTED	3	1	6	1	1	356	39.1	7.44	Not Found	Not Found	Not Found	High	High	High					32195992	25332939	24393717	7.53	1	50	1
FALSE	Master Pro	212	568599832	cystatin-C p	11	1	4	1	1	146	15.8	8.75	High	High	Not Found	Not Found	Not Found	Not Found		5744756	7079170					7.48	1	113	1
FALSE	Master Pro	278	11559923	eukaryotic	5	1	6	1	1	248	27.4	7.23	High	High	High	Not Found	Not Found	Not Found			7326127	8663418				7.47	1	132	1
FALSE	Master Pro	278	14702180	eukaryotic	6	1	6	1	1	228	25.2	8.09	High	High	High	Not Found	Not Found	Not Found			7326127	8663418				7.47	1	132	1
FALSE	None	182	113428306	PREDICTED	5	1	7	1	1	186	20.4	6.42	Not Found	Not Found	High	High	High	High				59846998	91897613	98763109	89609439	7.46	1	53	1
FALSE	None	77	119703753	keratin, typ	2	1	6	1	1	564	60	8	High	High	High	Not Found	Not Found	Not Found		6489272	8331514	7425039				7.37	1	84	1
FALSE	None	51	578827359	PREDICTED	6	1	6	1	1	161	18.7	4.78	Not Found	Not Found	Not Found	High	High	High					14568511	14647778	14809722	7.36	1	0	1
FALSE	Master Pro	181	31542331	protein CYI	3	1	14	1	1	381	42	8.21	High	High	High	High	High	High		11286947	12482169	9634817	48163613	48955889	44941907	7.28	1	145	1
FALSE	Master Pro	56	322303127	40S riboso	8	2	6	2	1	165	18.9	10.15	Not Found	High	Not Found	Not Found	High	High			7915643			6293188	7143278	7.1	2	83	2
FALSE	Master Pro	65	41327712	adapter mo	9	2	6	2	1	304	33.8	5.55	High	Not Found	High	High	Not Found	Not Found		3059477		3362491	2501547			7.1	2	99	2
FALSE	Master Pro	65	41327710	adapter mo	14	2	6	2	1	204	22.9	5.48	High	Not Found	High	High	Not Found	Not Found		3059477		3362491	2501547			7.1	2	99	2
FALSE	Master Pro	103	556695502	small ubiqu	9	1	6	1	1	141	15.8	6.92	High	High	High	Not Found	Not Found	Not Found		3920194	9840005	7561139				7.06	1	68	1
FALSE	Master Pro	103	54792071	small ubiqu	17	1	6	1	1	71	8.1	5.41	High	High	High	Not Found	Not Found	Not Found		3920194	9840005	7561139				7.06	1	68	1
FALSE	Master Pro	103	50400081	small ubiqu	13	1	6	1	1	95	10.6	7.18	High	High	High	Not Found	Not Found	Not Found		3920194	9840005	7561139				7.06	1	68	1
FALSE	Master Pro	103	48928058	small ubiqu	12	1	6	1	1	103	11.6	5.49	High	High	High	Not Found	Not Found	Not Found		3920194	9840005	7561139				7.06	1	68	1
FALSE	Master Pro	103	54792069	small ubiqu	13	1	6	1	1	95	10.9	5.5	High	High	High	Not Found	Not Found	Not Found		3920194	9840005	7561139				7.06	1	68	1
FALSE	Master Pro	168	4506661	60S riboso	4	1	6	1	1	266	30	10.61	High	High	High	Not Found	Not Found	Not Found		6806851	6470088	7466381				6.81	1	34	1
FALSE	Master Pro	267	13775198	SH3 domai	16	1	4	1	1	93	10.4	4.93	Not Found	Not Found	Not Found	High	Not Found	High					9036431		11185543	6.8	1	86	1
FALSE	Master Pro	230	67782307	superoxide	13	2	8	2	1	222	24.7	8.25	High	Not Found	High	High	Not Found	High		1274027		2407535	5642666		7572043	6.76	2	28	2
FALSE	Master Pro	230	67782309	superoxide	16	2	8	2	1	183	20.7	8.25	High	Not Found	High	High	Not Found	High		1274027		2407535	5642666		7572043	6.76	2	28	2
FALSE	Master Pro	93	578794950	PREDICTED	6	1	6	1	1	191	21	7.72	High	High	High	Not Found	Not Found	Not Found		7007082	6299792	6854261				6.73	1	28	1
FALSE	Master Pro	93	5802966	destrin iso	7	1	6	1	1	165	18.5	7.85	High	High	High	Not Found	Not Found	Not Found		7007082	6299792	6854261				6.73	1	28	1
FALSE	Master Pro	93	58530848	destrin iso	7	1	6	1	1	148	16.6	8.34	High	High	High	Not Found	Not Found	Not Found		7007082	6299792	6854261				6.73	1	28	1
FALSE	Master Pro	93	578843371	PREDICTED	6	1	6	1	1	191	21.1	7.77	High	High	High	Not Found	Not Found	Not Found		7007082	6299792	6854261				6.73	1	28	1
FALSE	Master Pro	93	578806939	PREDICTED	6	1	6	1	1	178	19.5	7.12	High	High	High	Not Found	Not Found	Not Found		7007082	6299792	6854261				6.73	1	28	1
FALSE	Master Pro	255	32455262	peroxiredo	14	1	4	1	1	125	12.8	9.14	Not Found	Not Found	High	Not Found	Not Found	Not Found				1609110				6.71	1	67	1
FALSE	Master Pro	255	6912238	peroxiredo	8	1	4	1	1	214	22	8.57	Not Found	Not Found	High	Not Found	Not Found	Not Found				1609110				6.71	1	67	1
FALSE	Master Pro	255	32455260	peroxiredo	10	1	4	1	1	170	17.4	8.76	Not Found	Not Found	High	Not Found	Not Found	Not Found				1609110				6.71	1	67	1
FALSE	Master Pro	255	530396544	PREDICTED	7	1	4	1	1	251	25.5	10.35	Not Found	Not Found	High	Not Found	Not Found	Not Found				1609110				6.71	1	67	1
FALSE	Master Pro	254	189458817	transferrin	2	1	6	1	1	760	84.8	6.61	Not Found	Not Found	Not Found	High	High	High					7183472	6319535	5423099	6.66	1	142	1
FALSE	Master Pro	283	578804378	PREDICTED	8	2	7	2	1	428	49.4	7.36	Not Found	High	Not Found	High	High	Not Found					5569154	1529634		6.59	2	22	2
FALSE	Master Pro	283	56549640	septin-2 iso	9	2	7	2	1	361	41.5	6.6	Not Found	High	Not Found	High	High	Not Found					5569154	1529634		6.59	2	22	2
FALSE	Master Pro	283	545478466	septin-2 iso	8	2	7	2	1	396	45.4	6.89	Not Found	High	Not Found	High	High	Not Found					5569154	1529634		6.59	2	22	2
FALSE	Master Pro	283	545478822	septin-2 iso	9	2	7	2	1	371	42.7	6.86	Not Found	High	Not Found	High	High	Not Found					5569154	1529634		6.59	2	22	2
FALSE	Master Pro	283	578804380	PREDICTED	8	2	7	2	1	423	48.8	7.17	Not Found	High	Not Found	High	High	Not Found					5569154	1529634		6.59	2	22	2
FALSE	Master Pro	130	38327039	heat shock	2	1	6	1	1	840	94.3	5.19	Not Found	Not Found	Not Found	High	High	High					12868303	13140843	13953342	6.55	1	53	1
FALSE	Master Pro	11	300360534	glutathione	5	1	10	1	1	213	24.8	6.1	Not Found	High	High	High	High	High			7111790	6923140	16221974	14162775	14975230	6.52	1	86	1
FALSE	Master Pro	11	4758484	glutathione	4	1	10	1	1	241	27.5	6.6	Not Found	High	High	High	High	High			7111790	6923140	16221974	14162775	14975230	6.52	1	86	1
FALSE	Master Pro	43	530422766	PREDICTED	6	1	7	1	1	220	25.5	9.06	High	High	High	High	Not Found	Not Found		16829542	19842219	20788172	30082458			6.51	1	51	1
FALSE	Master Pro	43	530422768	PREDICTED	7	1	7	1	1	200	23	8.37	High	High	High	High	Not Found	Not Found		16829542	19842219	20788172	30082458			6.51	1	51	1
FALSE	Master Pro	43	530422764	PREDICTED	6	1	7	1	1	222	25.6	8.12	High	High	High	High	Not Found	Not Found		16829542	19842219	20788172	30082458			6.51	1	51	1
FALSE	Master Pro	105	50363221	alpha-1-an	10	3	9	3	1	418	46.7	5.59	Not Found	Not Found	Not Found	Not Found	High	High						18193194	19323358	6.51	2	79	3
FALSE	Master Pro	245	530418509	PREDICTED	5	1	4	1	1	314	36.2	5.48	Not Found	High	High	Not Found	Not Found	Not Found			2301425	3183233				6.43	1	76	1
FALSE	Master Pro	245	29826335	eukaryotic	5	1	4	1	1	333	38.4	5.8	Not Found	High	High	Not Found	Not Found	Not Found			2301425	3183233				6.43	1	76	1
FALSE	None	169	578841947	PREDICTED	4	1	4	1	1	362	40.6	6.99	High	Not Found	High	Not Found	Not Found	Not Found				1320408				6.15	1	81	1
FALSE	None	169	578841731	PREDICTED	4	1	4	1	1	394	44.2	6.3	High	Not Found	High	Not Found	Not Found	Not Found				1320408				6.15	1	81	1
FALSE	None	169	530429121	PREDICTED	4	1	4	1	1	391	44	6.64	High	Not Found	High	Not Found	Not Found	Not Found				1320408				6.15	1	81	1
FALSE	None	169	578842421	PREDICTED	4	1	4	1	1	326	37	5.99	High	Not Found	High	Not Found	Not Found	Not Found				1320408				6.15	1	81	1
FALSE	None	169	578842189	PREDICTED	4	1	4	1	1	394	44.4	6.2	High	Not Found	High	Not Found	Not Found	Not Found				1320408				6.15	1	81	1
FALSE	None	169	578842419	PREDICTED	4	1	4	1	1	365	41	6.47	High	Not Found	High	Not Found	Not Found	Not Found				1320408				6.15	1	81	1

FALSE	None	169	578841489	PREDICTED	4	1	4	1	1	365	40.9	6.99	High	Not Found	High	Not Found	Not Found	Not Found				1320408				6.15	1	81	1
FALSE	None	169	578841735	PREDICTED	4	1	4	1	1	326	36.8	6.19	High	Not Found	High	Not Found	Not Found	Not Found				1320408				6.15	1	81	1
FALSE	None	169	578841733	PREDICTED	4	1	4	1	1	365	40.8	6.73	High	Not Found	High	Not Found	Not Found	Not Found				1320408				6.15	1	81	1
FALSE	None	169	578841487	PREDICTED	4	1	4	1	1	394	44.3	6.64	High	Not Found	High	Not Found	Not Found	Not Found				1320408				6.15	1	81	1
FALSE	None	169	578842191	PREDICTED	4	1	4	1	1	365	41	6.54	High	Not Found	High	Not Found	Not Found	Not Found				1320408				6.15	1	81	1
FALSE	None	169	578842417	PREDICTED	4	1	4	1	1	394	44.4	6.11	High	Not Found	High	Not Found	Not Found	Not Found				1320408				6.15	1	81	1
FALSE	Master Prc	73	4826972	RNA-bindi	6	1	6	1	1	174	19.9	5.72	High	High	High	Not Found	Not Found	Not Found		7486964	12005138	9856891				5.78	1	27	1
FALSE	Master Prc	224	4503529	eukaryotic	2	1	6	1	1	406	46.1	5.48	Not Found	Not Found	Not Found	High	High	High					14414793	15893766	12602110	5.75	1	55	1
FALSE	Master Prc	224	83700235	eukaryotic	2	1	6	1	1	407	46.4	5.48	Not Found	Not Found	Not Found	High	High	High					14414793	15893766	12602110	5.75	1	55	1
FALSE	Master Prc	281	110611233	collagen al	1	1	4	1	1	1336	135.4	6.47	Not Found	Not Found	Not Found	Not Found	High	High						16866454	15370786	5.7	1	143	1
FALSE	Master Prc	281	110611235	collagen al	1	1	4	1	1	1516	153.7	5.68	Not Found	Not Found	Not Found	Not Found	High	High						16866454	15370786	5.7	1	143	1
FALSE	None	157	578840292	PREDICTED	8	2	10	2	1	240	27.4	4.89	Not Found	Not Found	High	High	High	High				1929297	63659747	1.22E+08	67703890	5.7	2	0	2
FALSE	None	157	5803227	14-3-3 pro	7	2	10	2	1	245	27.7	4.78	Not Found	Not Found	High	High	High	High				1929297	63659747	1.22E+08	67703890	5.7	2	0	2
FALSE	None	157	4507949	14-3-3 pro	7	2	10	2	1	246	28.1	4.83	Not Found	Not Found	High	High	High	High				1929297	63659747	1.22E+08	67703890	5.7	2	0	2
FALSE	None	157	5454052	14-3-3 pro	7	2	10	2	1	248	27.8	4.74	Not Found	Not Found	High	High	High	High				1929297	63659747	1.22E+08	67703890	5.7	2	0	2
FALSE	None	157	5803225	14-3-3 pro	7	2	10	2	1	255	29.2	4.74	Not Found	Not Found	High	High	High	High				1929297	63659747	1.22E+08	67703890	5.7	2	0	2
FALSE	None	157	4507951	14-3-3 pro	7	2	10	2	1	246	28.2	4.84	Not Found	Not Found	High	High	High	High				1929297	63659747	1.22E+08	67703890	5.7	2	0	2
FALSE	None	157	530389315	PREDICTED	5	2	10	2	1	384	42.5	5.22	Not Found	Not Found	High	High	High	High				1929297	63659747	1.22E+08	67703890	5.7	2	0	2
FALSE	None	157	530389319	PREDICTED	7	2	10	2	1	245	27.7	4.79	Not Found	Not Found	High	High	High	High				1929297	63659747	1.22E+08	67703890	5.7	2	0	2
FALSE	Master Prc	209	578842331	PREDICTED	8	1	6	1	1	179	19.1	5.5	High	High	Not Found	High	High	Not Found		4104963	4138493		8313166	8186103		5.6	1	21	1
FALSE	Master Prc	209	62198241	protein Cu	7	1	6	1	1	198	20.9	5.48	High	High	Not Found	High	High	Not Found		4104963	4138493		8313166	8186103		5.6	1	21	1
FALSE	Master Prc	209	7706244	protein Cu	9	1	6	1	1	156	16.8	5.21	High	High	Not Found	High	High	Not Found		4104963	4138493		8313166	8186103		5.6	1	21	1
FALSE	Master Prc	194	5032051	40S riboso	9	1	4	1	1	151	16.3	10.05	Not Found	High	High	Not Found	Not Found	Not Found			6356778	5811383				5.57	1	76	1
FALSE	Master Prc	243	578832893	PREDICTED	5	1	6	1	1	222	26.1	5.97	Not Found	Not Found	Not Found	High	High	High					15915228	13432088	14655308	5.57	1	46	1
FALSE	Master Prc	243	21040371	ATP-depen	2	1	6	1	1	427	49.1	5.68	Not Found	Not Found	Not Found	High	High	High					15915228	13432088	14655308	5.57	1	46	1
FALSE	Master Prc	243	4758112	spliceosom	2	1	6	1	1	428	49	5.67	Not Found	Not Found	Not Found	High	High	High					15915228	13432088	14655308	5.57	1	46	1
FALSE	Master Prc	250	5453597	F-actin-cap	9	2	4	2	1	286	32.9	5.69	High	Not Found	High	Not Found	Not Found	Not Found		3905587		6735898				5.44	2	61	2
FALSE	Master Prc	78	16579885	60S riboso	6	2	8	2	1	427	47.7	11.06	High	High	Not Found	High	Not Found	High		5820054	13491903				44655881	5.42	2	30	2
FALSE	None	153	530414822	PREDICTED	2	1	6	1	1	633	66.3	9.39	Not Found	Not Found	Not Found	High	High	High					19017826	19522937	18212722	5.41	1	43	1
FALSE	None	138	507588250	alpha-acti	2	1	4	1	1	686	79.6	5.57	Not Found	Not Found	Not Found	High	Not Found	High					8247809		8252610	5.4	1	0	1
FALSE	None	138	4501893	alpha-acti	1	1	4	1	1	894	103.8	5.45	Not Found	Not Found	Not Found	High	Not Found	High					8247809		8252610	5.4	1	0	1
FALSE	None	138	507588248	alpha-acti	1	1	4	1	1	894	103.9	5.52	Not Found	Not Found	Not Found	High	Not Found	High					8247809		8252610	5.4	1	0	1
FALSE	None	263	528078353	proteasom	5	1	4	1	1	233	26.9	5.78	Not Found	Not Found	Not Found	High	Not Found	High					11333078		9737148	5.19	1	0	1
FALSE	None	263	30581141	proteasom	5	1	4	1	1	250	28.6	6.71	Not Found	Not Found	Not Found	High	Not Found	High					11333078		9737148	5.19	1	0	1
FALSE	None	242	169646441	rab GDP di	3	1	4	1	1	400	45.6	6.24	Not Found	Not Found	High	Not Found	Not Found	High				5603756			17673457	5.17	1	53	1
FALSE	Master Prc	10	530403617	PREDICTED	6	1	4	1	1	301	33.8	7.91	Not Found	Not Found	Not Found	High	Not Found	High					2229496		2695978	4.97	1	56	1
FALSE	Master Prc	10	346644849	DNA-(apur	5	1	4	1	1	318	35.5	8.12	Not Found	Not Found	Not Found	High	Not Found	High					2229496		2695978	4.97	1	56	1
FALSE	Master Prc	17	16933546	60S acidic	5	1	4	1	1	317	34.3	5.97	Not Found	Not Found	Not Found	Not Found	High	High						5372353	7907243	4.86	1	44	1
FALSE	Master Prc	268	22538442	cathepsin	4	1	4	1	1	303	33.8	7.11	High	Not Found	High	Not Found	Not Found	Not Found		6037006		7041790				4.78	1	63	1
FALSE	Master Prc	75	5174539	malate de	4	1	3	1	1	334	36.4	7.36	Not Found	Not Found	Not Found	Not Found	High	Not Found						12303759		4.61	1	0	1
FALSE	Master Prc	75	312283703	malate de	5	1	3	1	1	245	27	9.11	Not Found	Not Found	Not Found	Not Found	High	Not Found						12303759		4.61	1	0	1
FALSE	Master Prc	75	312283701	malate de	3	1	3	1	1	352	38.6	7.71	Not Found	Not Found	Not Found	Not Found	High	Not Found						12303759		4.61	1	0	1
FALSE	Master Prc	120	118498359	ribosomal	3	1	4	1	1	490	54.9	10.13	High	Not Found	High	Not Found	Not Found	Not Found		5216409		5831928				4.47	1	28	1
FALSE	Master Prc	265	4506387	UV excisio	2	1	4	1	1	409	43.1	4.84	High	Not Found	High	Not Found	Not Found	Not Found		15208591		18794955				4.46	1	0	1
FALSE	Master Prc	63	118402586	lactoylglut	9	1	5	1	1	184	20.8	5.31	High	High	Not Found	Not Found	Not Found	High		4117732	3334658				5226221	4.44	1	18	1
FALSE	Master Prc	257	530374897	PREDICTED	9	2	6	2	1	258	27.4	6.4	High	High	High	Not Found	Not Found	Not Found		20054934	15337236	19221679				4.33	2	69	2
FALSE	Master Prc	257	530374895	PREDICTED	8	2	6	2	1	259	27.5	6.4	High	High	High	Not Found	Not Found	Not Found		20054934	15337236	19221679				4.33	2	69	2
FALSE	None	257	530374903	PREDICTED	9	1	2	1	1	157	17.4	5.95	Not Found	High	Not Found	Not Found	Not Found	Not Found			6523011					4.33	1	69	1
FALSE	None	257	530374907	PREDICTED	9	1	2	1	1	156	17.4	5.95	Not Found	High	Not Found	Not Found	Not Found	Not Found			6523011					4.33	1	69	1
FALSE	Master Prc	257	530374899	PREDICTED	9	2	6	2	1	257	27.2	6.4	High	High	High	Not Found	Not Found	Not Found		20054934	15337236	19221679				4.33	2	69	2
FALSE	Master Prc	257	8923710	protein CD	9	2	6	2	1	258	27.3	6.4	High	High	High	Not Found	Not Found	Not Found		20054934	15337236	19221679				4.33	2	69	2
FALSE	None	257	544346300	protein CD	9	1	2	1	1	156	17.3	5.95	Not Found	High	Not Found	Not Found	Not Found	Not Found			6523011					4.33	1	69	1
FALSE	Master Prc	273	578809271	PREDICTED	4	1	4	1	1	334	38.1	6.39	High	Not Found	Not Found	Not Found	Not Found	High		2048727					4164037	4.33	1	46	1
FALSE	Master Prc	273	9994187	platelet-de	3	1	4	1	1	345	39	6.14	High	Not Found	Not Found	Not Found	Not Found	High		2048727					4164037	4.33	1	46	1
FALSE	Master Prc	253	530410965	PREDICTED	4	1	4	1	1	451	48.4	8.21	Not Found	Not Found	Not Found	High	Not Found	High					6557718		4685731	4.26	1	0	1
FALSE	Master Prc	253	530410969	PREDICTED	4	1	4	1	1	364	39.4	6.87	Not Found	Not Found	Not Found	High	Not Found	High					6557718		4685731	4.26	1	0	1
FALSE	Master Prc	31	4507835	uridine 5'-	2	1	4	1	1	480	52.2	7.24	Not Found	Not Found	Not Found	High	High	Not Found					34661214	28298809		4.11	1	45	1
FALSE	Master Prc	107	530360777	PREDICTED	3	1	3	1	1	494	55.7	9.23	Not Found	Not Found	Not Found	Not Found	High	High						7592781	7764882	4.09	1	0	1
FALSE	Master Prc	107	5031755	heterogen	2	1	3	1	1	633	70.9	8.13	Not Found	Not Found	Not Found	Not Found	High	High						7592781	7764882	4.09	1	0	1
FALSE	Master Prc	107	530360775	PREDICTED	2	1	3	1	1	595	66.9	8.29	Not Found	Not Found	Not Found	Not Found	High	High						7592781	7764882	4.09	1	0	1
FALSE	Master Prc	107	156151396	heterogen	2	1	3	1	1	535	59.9	9.16	Not Found	Not Found	Not Found	Not Found	High	High						7592781	7764882	4.09	1	0	1
FALSE	Master Prc	107	156151394	heterogen	2	1	3	1	1	636	71.2	8.13	Not Found	Not Found	Not Found	Not Found	High	High						7592781	7764882	4.09	1	0	1
FALSE	Master Prc	107	156151392	heterogen	2	1	3	1	1	532	59.6	9.16	Not Found	Not Found	Not Found	Not Found	High	High						7592781	7764882	4.09	1	0	1
FALSE	Master Prc	55	224451142	stathmin is	7	1	8	1	1	174	19.8	7.02	High	High	High	High	High	High		23249019	20556346	19806563	11090678	8627359	10170040	4	1	76	1
FALSE	Master Prc	55	44890052	stathmin is	9	1	8	1	1	149	17.3	5.97	High	High	High	High	High	High		23249019	20556346	19806563	11090678	8627359	10170040	4	1	76	1
FALSE	Master Prc	266	4506671	60S acidic	10	1	4	1	1	115	11.7	4.54	Not Found	Not Found	Not Found	High	High	Not Found					14178541	13715985		3.98	1	59	1
FALSE	None	110	24234699	keratin, typ	2	1	3	1	1	400	44.1	5.14	Not Found	High	High	Not Found	Not Found	Not Found			1.17E+08	1.16E+08				3.9	1	0	1
FALSE	None	204	41406067	histone H2	7	1	5	1	1	102	11	10.23	Not Found	High	High	Not Found	Not Found	Not Found				82093418				3.86	1	31	1
FALSE	None	204	41406071	histone H2	8	1	5	1	1	90	9.4	10.49	Not Found	High	High	Not Found	Not Found	Not Found				82093418				3.86	1	31	1
FALSE	Master Prc	38	5453595	adenylyl cy	7	2	7	2	1	475	51.6	8.02	Not Found	High	Not Found	High	High	Not Found			3454764		16962478	14769211		3.79	2	0	2
FALSE	None	38	578798235	PREDICTED	3	1	4	1	1	475	51.9	8.06	Not Found	High	Not Found	Not Found	High	Not Found			3454764			9225396		3.79	1	0	1
FALSE	Master Prc	232	17105394	60S riboso	8	1	6	1	1	156	17.7	10.45	High	High	High	Not Found	Not Found	Not Found		5642425	5790488	5318987				3.71	1	57	1
FALSE	Master Prc	80	530389395	PREDICTED	2	1	4	1	1	560	61.5	9.33	High	Not Found	High	Not Found	Not Found	Not Found		4881973		5566629				3.67	1	55	1
FALSE	Master Prc	80	530389397	PREDICTED	2	1	4	1	1	549	60.1	9.48	High	Not Found	High	Not Found	Not Found	Not Found		4881973		5566629				3.67	1	55	1
FALSE	Master Prc	80	223555917	protein LY	2	1	4	1	1	582	63.8	9.32	High	Not Found	High	Not Found	Not Found	Not Found		4881973		5566629				3.67	1	55	1
FALSE	None	187	294345475	galectin-3	6	1	8	1	1	200	20.5	8.57	Not Found	Not Found	Not Found	High	High	High					39939161	39316865	41025858	3.66	1	25	1
FALSE	Master Prc	72	20149540	protein-lys	2	1	4	1	1	417	46.9	8.09	Not Found	Not Found	Not Found	High	High	Not Found					18571021	18056493		3.6	1	61	1
FALSE	Master Prc	139	110224476	prosaposin	3	1	4	1	1	527	58.4	5.14	Not Found	Not Found	Not Found	High	Not Found	High					2744909			3.59	1	65	1
FALSE	Master Prc	139	110224479	prosaposin	3	1	4	1	1	526	58.3	5.14	Not Found	Not Found	Not Found	High	Not Found	High					2744909			3.59	1	65	1

FALSE	Master Pr	139	11386147	prosaposin	3	1	4	1	1	524	58.1	5.17	Not Found	Not Found	Not Found	High	Not Found	High					2744909			3.59	1	65	1
FALSE	None	241	530401711	PREDICTED	8	1	6	1	1	128	14.7	6.32	High	High	High	Not Found	Not Found	Not Found		12364259	15038909	16005704				3.55	1	38	1
FALSE	Master Pr	163	303227928	matrin-3 is	3	1	2	1	1	559	62.5	6.01	Not Found	Not Found	Not Found	Not Found	High	Not Found						3357849		3.54	1	36	1
FALSE	Master Pr	163	303227924	matrin-3 is	2	1	2	1	1	847	94.6	6.25	Not Found	Not Found	Not Found	Not Found	High	Not Found						3357849		3.54	1	36	1
FALSE	Master Pr	163	533112484	matrin-3 is	4	1	2	1	1	509	56.7	5.86	Not Found	Not Found	Not Found	Not Found	High	Not Found						3357849		3.54	1	36	1
FALSE	Master Pr	208	540344563	protein ph	6	1	2	1	1	317	36.8	5.2	Not Found	Not Found	Not Found	High	Not Found	Not Found					1304498			3.38	1	61	1
FALSE	Master Pr	208	540344569	protein ph	5	1	2	1	1	344	39.8	4.96	Not Found	Not Found	Not Found	High	Not Found	Not Found					1304498			3.38	1	61	1
FALSE	Master Pr	208	539845980	protein ph	6	1	2	1	1	301	35.1	5.31	Not Found	Not Found	Not Found	High	Not Found	Not Found					1304498			3.38	1	61	1
FALSE	Master Pr	208	4506013	protein ph	5	1	2	1	1	360	41.5	4.91	Not Found	Not Found	Not Found	High	Not Found	Not Found					1304498			3.38	1	61	1
FALSE	Master Pr	208	540344567	protein ph	8	1	2	1	1	237	27.3	4.93	Not Found	Not Found	Not Found	High	Not Found	Not Found					1304498			3.38	1	61	1
FALSE	Master Pr	208	539846291	protein ph	8	1	2	1	1	221	25.6	5.02	Not Found	Not Found	Not Found	High	Not Found	Not Found					1304498			3.38	1	61	1
FALSE	Master Pr	208	540344565	protein ph	6	1	2	1	1	280	32	4.73	Not Found	Not Found	Not Found	High	Not Found	Not Found					1304498			3.38	1	61	1
FALSE	Master Pr	83	302191611	cysteine ar	8	1	2	1	1	187	20	8.48	Not Found	Not Found	High	Not Found	Not Found	Not Found				3172903				3.35	1	0	1
FALSE	Master Pr	83	302191615	cysteine ar	8	1	2	1	1	193	20.6	8.57	Not Found	Not Found	High	Not Found	Not Found	Not Found				3172903				3.35	1	0	1
FALSE	Master Pr	53	10863955	phosphose	3	1	4	1	1	324	35.2	6.68	Not Found	Not Found	Not Found	High	High	High					22456394	22841874	21414697	3.21	1	48	1
FALSE	Master Pr	53	17402893	phosphose	3	1	4	1	1	370	40.4	7.66	Not Found	Not Found	Not Found	High	High	High					22456394	22841874	21414697	3.21	1	48	1
FALSE	Master Pr	86	5729953	nuclear mi	6	2	3	2	1	331	38.2	5.38	High	Not Found	High	Not Found	Not Found	Not Found		1944538		3666802				2.99	1	43	2
FALSE	None	128	530363679	PREDICTED	2	1	3	1	1	568	65.7	9.5	Not Found	High	High	Not Found	Not Found	Not Found			3181708					2.99	1	34	1
FALSE	Master Pr	246	164698500	septin-9 is	4	1	2	1	1	422	47.5	6.48	Not Found	High	Not Found	Not Found	Not Found	Not Found			3380888					2.84	1	46	1
FALSE	Master Pr	246	116256489	septin-9 is	3	1	2	1	1	568	63.6	8.4	Not Found	High	Not Found	Not Found	Not Found	Not Found			3380888					2.84	1	46	1
FALSE	Master Pr	246	164698498	septin-9 is	3	1	2	1	1	579	64.6	7.58	Not Found	High	Not Found	Not Found	Not Found	Not Found			3380888					2.84	1	46	1
FALSE	Master Pr	246	164698494	septin-9 is	3	1	2	1	1	586	65.4	8.97	Not Found	High	Not Found	Not Found	Not Found	Not Found			3380888					2.84	1	46	1
FALSE	Master Pr	95	530390549	PREDICTED	4	1	2	1	1	333	37.5	5.45	High	Not Found	Not Found	Not Found	Not Found	Not Found		19907647						2.81	1	0	1
FALSE	Master Pr	143	578831222	PREDICTED	3	1	2	1	1	491	54.1	5.38	Not Found	High	Not Found	Not Found	Not Found	Not Found			882656.2					2.78	1	41	1
FALSE	Master Pr	143	192448443	peptidyl-pr	3	1	2	1	1	582	64.2	5.62	Not Found	High	Not Found	Not Found	Not Found	Not Found			882656.2					2.78	1	41	1
FALSE	Master Pr	28	194688133	high mobili	7	1	2	1	1	209	24	7.81	Not Found	Not Found	Not Found	Not Found	High	Not Found						1.3E+08		2.75	1	23	1
FALSE	Master Pr	264	4506455	reticulocall	5	1	2	1	1	331	38.9	5	Not Found	Not Found	High	Not Found	Not Found	Not Found				2521232				2.69	1	79	1
FALSE	Master Pr	64	5902102	small nucle	11	1	2	1	1	119	13.3	11.56	Not Found	Not Found	Not Found	High	Not Found	Not Found					9568882			2.65	1	34	1
FALSE	Master Pr	269	578830368	PREDICTED	4	1	2	1	1	401	44.8	6.09	Not Found	Not Found	High	Not Found	Not Found	Not Found				2931439				2.61	1	48	1
FALSE	Master Pr	216	4507797	ubiquitin-c	7	1	4	1	1	145	16.4	8.09	High	High	High	Not Found	Not Found	Not Found		15299700	19390213	18846012				2.55	1	66	1
FALSE	Master Pr	216	40806167	ubiquitin-c	6	1	4	1	1	170	19.3	8.54	High	High	High	Not Found	Not Found	Not Found		15299700	19390213	18846012				2.55	1	66	1
FALSE	Master Pr	216	543583766	ubiquitin-c	16	1	4	1	1	64	6.9	4.78	High	High	High	Not Found	Not Found	Not Found		15299700	19390213	18846012				2.55	1	66	1
FALSE	Master Pr	216	383872507	ubiquitin-c	10	1	4	1	1	105	11.8	5.52	High	High	High	Not Found	Not Found	Not Found		15299700	19390213	18846012				2.55	1	66	1
FALSE	Master Pr	216	383872501	ubiquitin-c	7	1	4	1	1	144	16.2	6.7	High	High	High	Not Found	Not Found	Not Found		15299700	19390213	18846012				2.55	1	66	1
FALSE	Master Pr	216	40806190	TMEM189-	3	1	4	1	1	370	42.2	6.61	High	High	High	Not Found	Not Found	Not Found		15299700	19390213	18846012				2.55	1	66	1
FALSE	Master Pr	216	73765546	ubiquitin-c	7	1	4	1	1	147	16.5	7.93	High	High	High	Not Found	Not Found	Not Found		15299700	19390213	18846012				2.55	1	66	1
FALSE	Master Pr	219	308818195	dihydropyr	2	1	2	1	1	677	73.5	6.35	Not Found	High	Not Found	Not Found	Not Found	Not Found								2.54	1	41	1
FALSE	Master Pr	26	55741750	zinc transp	2	1	9	1	1	831	94.1	6.76	Not Found	Not Found	Not Found	High	High	High					15089741		19680318	2.53	1	0	1
FALSE	Master Pr	26	530370623	PREDICTED	2	1	9	1	1	898	101	7.01	Not Found	Not Found	Not Found	High	High	High					15089741		19680318	2.53	1	0	1
FALSE	Master Pr	50	4502419	flavin redu	7	1	2	1	1	206	22.1	7.65	Not Found	Not Found	High	Not Found	Not Found	Not Found				1300723				2.47	1	49	1
FALSE	Master Pr	1	530384474	PREDICTED	14	1	2	1	1	101	11.9	9.63	Not Found	High	Not Found	Not Found	Not Found	Not Found			21095352					2.47	1	0	1
FALSE	Master Pr	1	15082258	chromobo	8	1	2	1	1	183	20.8	5.33	Not Found	High	Not Found	Not Found	Not Found	Not Found			21095352					2.47	1	0	1
FALSE	Master Pr	179	4506141	serine prot	2	1	2	1	1	480	51.3	7.83	Not Found	Not Found	Not Found	Not Found	High	Not Found						10916694		2.41	1	23	1
FALSE	Master Pr	6	578832961	PREDICTED	5	1	2	1	1	297	31.9	9.61	Not Found	High	Not Found	Not Found	Not Found	Not Found			2073808					2.41	1	0	1
FALSE	Master Pr	6	4502847	cold-induci	8	1	2	1	1	172	18.6	9.51	Not Found	High	Not Found	Not Found	Not Found	Not Found			2073808					2.41	1	0	1
FALSE	Master Pr	6	578832966	PREDICTED	8	1	2	1	1	168	18.1	9.64	Not Found	High	Not Found	Not Found	Not Found	Not Found			2073808					2.41	1	0	1
FALSE	None	174	38372919	basigin iso	4	1	4	1	1	385	42.2	5.66	Not Found	High	High	Not Found	Not Found	Not Found			2859053	2862996				2.4	1	26	1
FALSE	None	174	38372923	basigin iso	7	1	4	1	1	205	22.8	5.47	Not Found	High	High	Not Found	Not Found	Not Found			2859053	2862996				2.4	1	26	1
FALSE	None	174	38372921	basigin iso	8	1	4	1	1	176	19.4	6.68	Not Found	High	High	Not Found	Not Found	Not Found			2859053	2862996				2.4	1	26	1
FALSE	Master Pr	188	48762934	collagen al	1	1	2	1	1	1366	129.2	8.95	Not Found	Not Found	High	Not Found	Not Found	Not Found				2453438				2.36	1	22	1
FALSE	Master Pr	159	392513662	interleukin	4	1	2	1	1	352	38.9	4.94	Not Found	Not Found	Not Found	High	Not Found	Not Found					6592566			2.3	1	28	1
FALSE	Master Pr	159	24234747	interleukin	4	1	2	1	1	390	43	5.26	Not Found	Not Found	Not Found	High	Not Found	Not Found					6592566			2.3	1	28	1
FALSE	Master Pr	66	530371951	PREDICTED	2	1	2	1	1	713	81.9	7.96	Not Found	Not Found	High	Not Found	Not Found	Not Found								2.29	1	0	1
FALSE	Master Pr	66	578805705	PREDICTED	1	1	2	1	1	1172	133.2	6.8	Not Found	Not Found	High	Not Found	Not Found	Not Found								2.29	1	0	1
FALSE	Master Pr	66	578805707	PREDICTED	1	1	2	1	1	1162	132	6.8	Not Found	Not Found	High	Not Found	Not Found	Not Found								2.29	1	0	1
FALSE	Master Pr	66	578805719	PREDICTED	2	1	2	1	1	709	81.3	8.05	Not Found	Not Found	High	Not Found	Not Found	Not Found								2.29	1	0	1
FALSE	Master Pr	66	578805716	PREDICTED	2	1	2	1	1	1115	126.7	6.74	Not Found	Not Found	High	Not Found	Not Found	Not Found								2.29	1	0	1
FALSE	Master Pr	66	207029299	serine/thre	2	1	2	1	1	712	81.6	7.97	Not Found	Not Found	High	Not Found	Not Found	Not Found								2.29	1	0	1
FALSE	Master Pr	66	578805709	PREDICTED	1	1	2	1	1	1162	132	6.62	Not Found	Not Found	High	Not Found	Not Found	Not Found								2.29	1	0	1
FALSE	Master Pr	66	578805714	PREDICTED	2	1	2	1	1	1125	127.9	6.74	Not Found	Not Found	High	Not Found	Not Found	Not Found								2.29	1	0	1
FALSE	Master Pr	66	578805711	PREDICTED	1	1	2	1	1	1158	131.4	6.6	Not Found	Not Found	High	Not Found	Not Found	Not Found								2.29	1	0	1
FALSE	Master Pr	90	578827458	PREDICTED	6	1	2	1	1	208	24.2	4.02	Not Found	High	Not Found	Not Found	Not Found	Not Found			3314183					2.29	1	0	1
FALSE	Master Pr	90	5454088	acidic leuci	5	1	2	1	1	251	28.8	4.06	Not Found	High	Not Found	Not Found	Not Found	Not Found			3314183					2.29	1	0	1
FALSE	Master Pr	90	5453880	acidic leuci	5	1	2	1	1	249	28.6	4.09	Not Found	High	Not Found	Not Found	Not Found	Not Found			3314183					2.29	1	0	1
FALSE	Master Pr	60	4503349	deoxyribo	3	1	2	1	1	360	39.6	8.05	Not Found	High	Not Found	Not Found	Not Found	Not Found			7328886					2.25	1	41	1
FALSE	None	45	58761502	obg-like AT	5	1	2	1	1	238	27.6	9.28	Not Found	High	Not Found	Not Found	Not Found	Not Found			1244291					2.25	1	0	1
FALSE	Master Pr	71	4506743	40S riboso	5	1	2	1	1	208	24.2	10.32	Not Found	Not Found	Not Found	Not Found	Not Found	High							99748746	2.2	1	0	1
FALSE	Master Pr	71	578826508	PREDICTED	5	1	2	1	1	208	24.2	9.86	Not Found	Not Found	Not Found	Not Found	Not Found	High							99748746	2.2	1	0	1
FALSE	Master Pr	71	578796949	PREDICTED	5	1	2	1	1	208	24.2	9.91	Not Found	Not Found	Not Found	Not Found	Not Found	High							99748746	2.2	1	0	1
FALSE	Master Pr	274	38201714	ELAV-like p	3	1	2	1	1	326	36.1	9.17	Not Found	High	Not Found	Not Found	Not Found	Not Found								2.19	1	0	1
FALSE	None	250	5453599	F-actin-cap	3	1	2	1	1	286	32.9	5.85	Not Found	Not Found	High	Not Found	Not Found	Not Found				6735898				2.19	1	0	1
FALSE	None	283	578804386	PREDICTED	9	1	2	1	1	194	22.6	6.55	Not Found	Not Found	Not Found	High	Not Found	Not Found					7262263			2.13	1	0	1
FALSE	Master Pr	70	4557553	emerin [H	5	1	5	1	1	254	29	5.5	Not Found	Not Found	Not Found	High	High	High					15403449	10436474	12561389	2.13	1	34	1
FALSE	Master Pr	29	115527062	collagen al	1	1	2	1	1	1019	108.5	6.21	Not Found	Not Found	High	Not Found	Not Found	Not Found				1050207				2.12	1	32	1
FALSE	Master Pr	29	115527066	collagen al	1	1	2	1	1	918	97.4	5.55	Not Found	Not Found	High	Not Found	Not Found	Not Found				1050207				2.12	1	32	1
FALSE	Master Pr	29	115527070	collagen al	1	1	2	1	1	828	87.2	5.92	Not Found	Not Found	High	Not Found	Not Found	Not Found				1050207				2.12	1	32	1
FALSE	None	91	310689049	lamin-B1 is	3	1	2	1	1	376	43	5.12	Not Found	High	Not Found	Not Found	Not Found	Not Found			4098761					2.01	1	0	1
FALSE	Master Pr	234	530400295	PREDICTED	2	1	5	1	1	463	53.8	4.46	Not Found	High	High	High	Not Found	Not Found			2504776	2552977	2199250			2.01	1	27	1
FALSE	Master Pr	234	578823791	PREDICTED	3	1	5	1	1	339	39.3	4.55	Not Found	High	High	High	Not Found	Not Found			2504776	2552977	2199250			2.01	1	27	1

FALSE	Master Prc	234	21327708	nucleosom	3	1	5	1	1	391	45.3	4.46	Not Found	High	High	High	Not Found	Not Found			2504776	2552977	2199250			2.01	1	27	1
FALSE	Master Prc	234	578823785	PREDICTED	2	1	5	1	1	452	52.7	4.48	Not Found	High	High	High	Not Found	Not Found			2504776	2552977	2199250			2.01	1	27	1
FALSE	Master Prc	234	578823788	PREDICTED	3	1	5	1	1	402	46.5	4.46	Not Found	High	High	High	Not Found	Not Found			2504776	2552977	2199250			2.01	1	27	1
FALSE	Master Prc	234	578823793	PREDICTED	3	1	5	1	1	328	38.2	4.56	Not Found	High	High	High	Not Found	Not Found			2504776	2552977	2199250			2.01	1	27	1
FALSE	Master Prc	76	17136148	V-type pro	4	1	2	1	1	470	52	6.14	High	Not Found	Not Found	Not Found	Not Found	Not Found		858439.3						1.98	1	0	1
FALSE	Master Prc	124	4506765	protein S1	11	1	8	1	1	101	11.7	6.11	Not Found	Not Found	Not Found	High	High	High					98357449	1.04E+08	98741134	1.98	1	0	1
FALSE	None	47;240	42558279	tubulin bet	2	1	4	0	2	444	49.7	4.89	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								1.96	1	35	1
FALSE	None	47;240	13562114	tubulin bet	2	1	4	0	2	451	50.3	5.17	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								1.96	1	35	1
FALSE	Master Prc	166	4506623	60S riboso	7	1	3	1	1	136	15.8	10.56	Not Found	Not Found	Not Found	Not Found	High	High						18961332	18694449	1.93	1	28	1
FALSE	Master Prc	227	24234688	stress-70 p	2	1	2	1	1	679	73.6	6.16	Not Found	Not Found	Not Found	High	Not Found	Not Found					5670576			1.91	1	33	1
FALSE	Master Prc		578836138	PREDICTED	1	1	2	0	0	720	82.6	5.9	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								1.9	1	0	1
FALSE	Master Prc	62	16445393	cadherin-1	2	1	4	1	1	794	88.3	4.81	High	Not Found	High	Not Found	Not Found	Not Found		332678		46108495				1.86	1	0	1
FALSE	Master Prc	109	4557831	pterin-4-al	15	1	2	1	1	104	12	6.8	Not Found	Not Found	Not Found	Not Found	Not Found	High							1617438	1.72	1	0	1
FALSE	None	27	48255943	CD44 antig	6	1	4	1	1	139	15.6	8.48	High	High	High	Not Found	Not Found	Not Found		11784062	33208191	37951081				1.61	1	42	1
FALSE	Master Prc	164	4503507	eukaryotic	3	1	5	1	1	472	51.1	8.4	Not Found	Not Found	Not Found	High	High	High					10775904	11649959	11636440	0	1	63	1
FALSE	Master Prc	69	160420317	filamin-A is	1	2	3	2	1	2647	280.6	6.06	High	Not Found	Not Found	Not Found	Not Found	High		1808669					10339430	0	1	0	2
FALSE	None	257	197313672	protein CD	4	1	4	1	1	213	22.1	5.81	High	High	High	Not Found	Not Found	Not Found		20054934	24151460	19221679				0	1	0	1
FALSE	Master Prc	69	116063573	filamin-A is	1	2	3	2	1	2639	279.8	6.05	High	Not Found	Not Found	Not Found	Not Found	High		1808669					10339430	0	1	0	2
FALSE	None	257	530374901	PREDICTED	4	1	4	1	1	210	21.7	5.54	High	High	High	Not Found	Not Found	Not Found		20054934	24151460	19221679				0	1	0	1
FALSE	Master Prc	249	530400234	PREDICTED	5	1	3	1	1	295	32.5	5.62	High	High	Not Found	Not Found	Not Found	Not Found								0	1	0	1
FALSE	Master Prc	167	373432684	ubiquitin-c	7	1	1	1	1	212	24	8.75	Not Found	Not Found	Not Found	High	Not Found	Not Found					6048827			0	1		
FALSE	Master Prc	167	373432682	ubiquitin-c	12	1	1	1	1	122	14.1	8.92	Not Found	Not Found	Not Found	High	Not Found	Not Found					6048827			0	1		
FALSE	Master Prc	146	544063423	stress-indu	3	1	2	1	1	590	68	7.74	High	Not Found	High	Not Found	Not Found	Not Found		1006880		1979874				0	1		
FALSE	Master Prc	146	5803181	stress-indu	3	1	2	1	1	543	62.6	6.8	High	Not Found	High	Not Found	Not Found	Not Found		1006880		1979874				0	1		
FALSE	Master Prc	167	4507789	ubiquitin-c	10	1	1	1	1	154	17.9	8.51	Not Found	Not Found	Not Found	High	Not Found	Not Found					6048827			0	1		
FALSE	Master Prc	133	4506607	60S riboso	7	1	1	1	1	188	21.6	11.72	Not Found	High	Not Found	Not Found	Not Found	Not Found										41	1
FALSE	Master Prc	133	395132436	60S riboso	8	1	1	1	1	159	18.1	11.84	Not Found	High	Not Found	Not Found	Not Found	Not Found										41	1
FALSE	Master Prc	248	46367787	polyadenyl	2	1	2	1	1	636	70.6	9.5	Not Found	Not Found	Not Found	Not Found	High	High						15398210	16255916			18	1
FALSE	Master Prc	248	45238849	polyadenyl	2	1	2	1	1	631	70	9.67	Not Found	Not Found	Not Found	Not Found	High	High						15398210	16255916			18	1
FALSE	Master Prc	151	4758280	ephrin type	1	1	3	1	1	986	109.8	6.61	Not Found	High	High	Not Found	Not Found	Not Found			9793539	9604328						0	1
FALSE	Master Prc	117	6005956	dual specif	5	1	1	1	1	340	37.7	6.84	Not Found	Not Found	Not Found	Not Found	High	Not Found						11251093				0	1
FALSE	Master Prc	151	530369978	PREDICTED	1	1	3	1	1	949	105.6	6.19	Not Found	High	High	Not Found	Not Found	Not Found			9793539	9604328						0	1
FALSE	Master Prc	192	12667788	myosin-9 [	1	1	1	1	1	1960	226.4	5.6	Not Found	Not Found	Not Found	Not Found	Not Found	High							4803428			0	1

Mascot

Supplementary Table 1 (B): List of proteins identified in BxPC3 (-Neo and -MYB) cell lines

Checked	Master	Protein Group IDs	Accession	Description	Coverage	# Peptides	# PSMs	# Unique P	# Protein G	# AAs	MW [kDa]	calc. pI	Found in S	Found in S	Found in S	Found in S	Found in S	Found in S	Modificatio	Area: F67:	Area: F66:	Area: F65:	Area: F64:	Area: F63:	Area: F62:	Score Sequ	# Peptides	Score Masc	# Peptides Mascot
FALSE	Master Protein Candidate Rejected		530378906	PREDICTED: uncharacterized protein C5orf42 isoform X2 [Homo sapiens]	0	1	10	0	0	3250	367.2	6.92	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								12.79	1	44	1
FALSE	Master Protein Candidate Rejected		530378912	PREDICTED: uncharacterized protein C5orf42 isoform X5 [Homo sapiens]	0	1	10	0	0	3214	363.4	6.93	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								12.79	1	44	1
FALSE	Master Protein Candidate Rejected		530381923	PREDICTED: heat shock 70 kDa protein 1-like isoform X2 [Homo sapiens]	8	4	34	0	0	641	70.3	6.02	High	High	Not Found	Not Found	Not Found	Not Found		48916036	54695029					44.4	4	303	4
FALSE	Master Protein Rejected		530378904	PREDICTED: uncharacterized protein C5orf42 isoform X1 [Homo sapiens]	0	1	10	0	0	3251	367.3	6.92	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								12.79	1	44	1
FALSE	Master Protein Candidate Rejected		578830721	PREDICTED: fatty acid desaturase 6 isoform X2 [Homo sapiens]	4	1	1	0	0	368	41.8	7.3	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								2.47	1		
FALSE	Master Protein Candidate Rejected		530429266	PREDICTED: heat shock 70 kDa protein 1-like isoform X2 [Homo sapiens]	7	4	34	0	0	705	77.5	7.66	High	High	Not Found	Not Found	Not Found	Not Found		48916036	54695029					44.4	4	303	4
FALSE	Master Protein Candidate Rejected		530378908	PREDICTED: uncharacterized protein C5orf42 isoform X3 [Homo sapiens]	0	1	10	0	0	3250	367.2	6.93	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								12.79	1	44	1
FALSE	Master Protein Rejected		126090909	homeobox protein engrailed-1 [Homo sapiens]	5	1	1	0	0	392	40.1	9.5	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found										0	1
FALSE	Master Protein Candidate Rejected		578809969	PREDICTED: uncharacterized protein C5orf42 isoform X12 [Homo sapiens]	0	1	10	0	0	2792	316	6.95	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								12.79	1	44	1
FALSE	Master Protein Rejected		530381921	PREDICTED: heat shock 70 kDa protein 1-like isoform X1 [Homo sapiens]	7	4	34	0	0	705	77.5	7.66	High	High	Not Found	Not Found	Not Found	Not Found		48916036	54695029					44.4	4	303	4
FALSE	Master Protein Candidate Rejected		530429270	PREDICTED: heat shock 70 kDa protein 1-like isoform X4 [Homo sapiens]	8	4	34	0	0	641	70.4	6.02	High	High	Not Found	Not Found	Not Found	Not Found		48916036	54695029					44.4	4	303	4
FALSE	Master Protein Candidate Rejected		530427783	PREDICTED: heat shock 70 kDa protein 1-like isoform X2 [Homo sapiens]	7	4	34	0	0	705	77.5	8.06	High	High	Not Found	Not Found	Not Found	Not Found		48916036	54695029					44.4	4	303	4
FALSE	Master Protein Rejected		578830719	PREDICTED: fatty acid desaturase 6 isoform X1 [Homo sapiens]	4	1	1	0	0	382	43.3	7.3	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								2.47	1		
FALSE	Master Protein Rejected		119703753	keratin, type II cytoskeletal 6B [Homo sapiens]	16	8	100	0	0	564	60	8	High	High	High	High	High	High		40342425	55328330	43852312	72398151	49052208	52260451	118.17	8	788	8
FALSE	Master Protein Rejected		34419635	heat shock 70 kDa protein 6 [Homo sapiens]	8	4	36	0	0	643	71	6.14	High	High	High	High	High	High		82367243	87562595	87769489	2.01E+08	2.18E+08	1.9E+08	49.61	4	377	4
FALSE	Master Protein Candidate Rejected		530378914	PREDICTED: uncharacterized protein C5orf42 isoform X6 [Homo sapiens]	0	1	10	0	0	3208	362.5	6.93	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								12.79	1	44	1
FALSE	Master Protein Rejected		29788785	tubulin beta chain [Homo sapiens]	15	5	37	0	0	444	49.6	4.89	High	High	High	High	High	High		20171292	20326000	19755876	84431920	90904650	87299383	51.09	5	373	5
FALSE	Master Protein Candidate Rejected		242332527	uncharacterized protein C5orf42 [Homo sapiens]	0	1	10	0	0	3197	361.5	6.99	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								12.79	1	44	1
FALSE	Master Protein Rejected		47132620	keratin, type II cytoskeletal 2 epidermal [Homo sapiens]	5	3	49	0	0	639	65.4	8	High	High	High	Not Found	Not Found	Not Found		37167279	40336236	37620215				55.11	3	475	3
FALSE	Master Protein Candidate Rejected		530427787	PREDICTED: heat shock 70 kDa protein 1-like isoform X4 [Homo sapiens]	8	4	34	0	0	641	70.4	6.29	High	High	Not Found	Not Found	Not Found	Not Found		48916036	54695029					44.4	4	303	4
FALSE	Master Protein Candidate Rejected		116812626	fatty acid desaturase 6 [Homo sapiens]	5	1	1	0	0	350	39.7	8.32	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								2.47	1		
FALSE	Master Protein Rejected		533112494	mucin-19 precursor [Homo sapiens]	0	1	2	0	0	8384	804.8	5.01	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								5.77	1		
FALSE	None	1	187960037	chromobox protein homolog 1 [Homo sapiens]	9	1	2	1	1	185	21.4	4.93	Not Found	Not Found	Not Found	Not Found	High	Not Found						32030806		3.72	1	71	1
FALSE	None	1	530384474	PREDICTED: chromobox protein homolog 3 isoform X2 [Homo sapiens]	14	2	17	2	1	101	11.9	9.63	High	High	High	High	High	High		44556057	43033444	39042035	67573865	63125414	81214497	38.28	2	387	2
FALSE	Master Protein	1	15082258	chromobox protein homolog 3 [Homo sapiens]	23	4	31	4	1	183	20.8	5.33	High	High	High	High	High	High		48634685	47405568	46556288	76017015	78003275	86597265	67.3	4	540	4
FALSE	Master Protein Candidate	10	341604768	60S ribosomal protein L13 isoform 2 [Homo sapiens]	6	1	2	1	1	192	22.2	11.65	Not Found	Not Found	Not Found	High	Not Found	Not Found					240300.9			1.85	1	0	1
FALSE	Master Protein	10	15431295	60S ribosomal protein L13 isoform 1 [Homo sapiens]	5	1	2	1	1	211	24.2	11.65	Not Found	Not Found	Not Found	High	Not Found	Not Found					240300.9			1.85	1	0	1
FALSE	Master Protein	100	4507129	small nuclear ribonucleoprotein E [Homo sapiens]	12	1	1	1	1	92	10.8	9.44	Not Found	Not Found	Not Found	High	Not Found	Not Found					30998233					28	1
FALSE	Master Protein Candidate	101	4504383	hepatocyte growth factor activator preproprotein [Homo sapiens]	2	1	2	1	1	655	70.6	7.24	Not Found	Not Found	Not Found	High	Not Found	High					14168617		15112685	1.64	1		
FALSE	Master Protein	101	530376064	PREDICTED: hepatocyte growth factor activator isoform X1 [Homo sapiens]	2	1	2	1	1	662	71.4	7.05	Not Found	Not Found	Not Found	High	Not Found	High					14168617		15112685	1.64	1		
FALSE	None	102	194018511	keratin, type II cytoskeletal 1b [Homo sapiens]	2	1	6	1	1	578	61.9	5.99	High	High	High	Not Found	Not Found	Not Found		37167279	40336236	37620215				9.59	1	124	1
FALSE	Master Protein	102	119395750	keratin, type II cytoskeletal 1 [Homo sapiens]	11	6	119	5	1	644	66	8.12	High	High	High	High	High	High		79042764	1.1E+08	78098735	1.82E+08	1.49E+08	1.14E+08	135.51	6	1049	6
FALSE	Master Protein	103	4506669	60S acidic ribosomal protein P1 isoform 1 [Homo sapiens]	14	1	14	1	1	114	11.5	4.32	High	High	High	High	High	High		9354364	7455792	8365657	38531318	40588846	38438210	17.64	1	131	1
FALSE	Master Protein Candidate	104	530404198	PREDICTED: legumain isoform X1 [Homo sapiens]	5	1	2	1	1	376	42.9	6.37	Not Found	Not Found	Not Found	Not Found	Not Found	High							28077642	3.96	1	26	1
FALSE	Master Protein	104	56682964	legumain preproprotein [Homo sapiens]	4	1	2	1	1	433	49.4	6.55	Not Found	Not Found	Not Found	Not Found	Not Found	High							28077642	3.96	1	26	1
FALSE	Master Protein Candidate	104	530404200	PREDICTED: legumain isoform X2 [Homo sapiens]	5	1	2	1	1	372	42	6.2	Not Found	Not Found	Not Found	Not Found	Not Found	High							28077642	3.96	1	26	1
FALSE	Master Protein	105	11968182	40S ribosomal protein S18 [Homo sapiens]	5	1	2	1	1	152	17.7	10.99	Not Found	Not Found	High	Not Found	Not Found	Not Found				12998774				2.25	1	31	1
FALSE	Master Protein Candidate	106	302191611	cysteine and glycine-rich protein 1 isoform 3 [Homo sapiens]	8	1	12	1	1	187	20	8.48	High	High	High	High	High	High		36686095	38989141	36398344	67627379	70736013	59859968	16.44	1	91	1
FALSE	Master Protein	106	302191615	cysteine and glycine-rich protein 1 isoform 1 [Homo sapiens]	8	1	12	1	1	193	20.6	8.57	High	High	High	High	High	High		36686095	38989141	36398344	67627379	70736013	59859968	16.44	1	91	1
FALSE	Master Protein Candidate	107	40805862	tumor protein D54 isoform f [Homo sapiens]	5	1	3	1	1	186	19.9	5.48	High	High	Not Found	Not Found	Not Found	Not Found		16274367	16791288					1.99	1	90	1
FALSE	Master Protein Candidate	107	345197268	tumor protein D54 isoform i [Homo sapiens]	6	1	3	1	1	152	16.3	4.92	High	High	Not Found	Not Found	Not Found	Not Found		16274367	16791288					1.99	1	90	1
FALSE	Master Protein Candidate	107	345197262	tumor protein D54 isoform g [Homo sapiens]	5	1	3	1	1	181	19.5	6.6	High	High	Not Found	Not Found	Not Found	Not Found		16274367	16791288					1.99	1	90	1
FALSE	Master Protein Candidate	107	345197264	tumor protein D54 isoform h [Homo sapiens]	6	1	3	1	1	163	17.5	6.6	High	High	Not Found	Not Found	Not Found	Not Found		16274367	16791288					1.99	1	90	1
FALSE	Master Protein Candidate	107	40805860	tumor protein D54 isoform e [Homo sapiens]	4	1	3	1	1	206	22.2	5.36	High	High	Not Found	Not Found	Not Found	Not Found		16274367	16791288					1.99	1	90	1
FALSE	Master Protein Candidate	107	40805868	tumor protein D54 isoform c [Homo sapiens]	4	1	3	1	1	220	23.8	5.73	High	High	Not Found	Not Found	Not Found	Not Found		16274367	16791288					1.99	1	90	1
FALSE	Master Protein	107	40805864	tumor protein D54 isoform a [Homo sapiens]	4	1	3	1	1	229	24.8	6.42	High	High	Not Found	Not Found	Not Found	Not Found		16274367	16791288					1.99	1	90	1
FALSE	Master Protein Candidate	107	40805870	tumor protein D54 isoform d [Homo sapiens]	5	1	3	1	1	200	21.4	5.99	High	High	Not Found	Not Found	Not Found	Not Found		16274367	16791288					1.99	1	90	1
FALSE	Master Protein Candidate	107	345198270	tumor protein D54 isoform j [Homo sapiens]	4	1	3	1	1	222	23.8	6.55	High	High	Not Found	Not Found	Not Found	Not Found		16274367	16791288					1.99	1	90	1
FALSE	Master Protein Candidate	107	40805866	tumor protein D54 isoform b [Homo sapiens]	4	1	3	1	1	209	22.5	6.7	High	High	Not Found	Not Found	Not Found	Not Found		16274367	16791288					1.99	1	90	1
FALSE	Master Protein Candidate	108	4757826	beta-2-microglobulin precursor [Homo sapiens]	19	3	31	3	1	119	13.7	6.52	High	High	High	High	High	High		4643233		4334019	5554755	6277682	8820217	33.46	3	67	3
FALSE	Master Protein	108	530406197	PREDICTED: beta-2-microglobulin isoform X1 [Homo sapiens]	19	3	31	3	1	122	14	7.44	High	High	High	High	High	High		4643233		4334019	5554755	6277682	8820217	33.46	3	67	3
FALSE	Master Protein Candidate	109	528524477	polyubiquitin-B precursor [Homo sapiens]	33	2	24	2	1	229	25.7	7.43	High	High	High	High	High	High		9.4E+08	9.67E+08	9.53E+08	1.93E+09	9.96E+08	9.62E+08	36.61	2	186	2
FALSE	Master Protein Candidate	109	530415146	PREDICTED: ubiquitin-60S ribosomal protein L40 isoform X2 [Homo sapiens]	14	2	24	2	1	175	19.4	9.22	High	High	High	High	High	High		9.4E+08	9.67E+08	9.53E+08	1.93E+09	9.96E+08	9.62E+08	36.61	2	186	2
FALSE	Master Protein Candidate	109	4507761	ubiquitin-60S ribosomal protein L40 precursor [Homo sapiens]	20	2	24	2	1	128	14.7	9.83	High	High	High	High	High	High		9.4E+08	9.67E+08	9.53E+08	1.93E+09	9.96E+08	9.62E+08	36.61	2	186	2
FALSE	Master Protein Candidate	109	530415150	PREDICTED: ubiquitin-60S ribosomal protein L40 isoform X4 [Homo sapiens]	16	2	24	2	1	156	17.5	9.57	High	High	High	High	High	High		9.4E+08	9.67E+08	9.53E+08	1.93E+09	9.96E+08	9.62E+08	36.61	2	186	2
FALSE	Master Protein Candidate	109	208022622	ubiquitin-40S ribosomal protein S27a precursor [Homo sapiens]	16	2	24	2	1	156	18	9.64	High	High	High	High	High	High		9.4E+08	9.67E+08	9.53E+08	1.93E+09	9.96E+08	9.62E+08	36.61	2	186	2
FALSE	Master Protein Candidate	109	67191208	polyubiquitin-C [Homo sapiens]	33	2	24	2	1	685	77	7.66	High	High	High	High	High	High		9.4E+08	9.67E+08	9.53E+08	1.93E+09	9.96E+08	9.62E+08	36.61	2	186	2
FALSE	Master Protein	109	530415144	PREDICTED: ubiquitin-60S ribosomal protein L40 isoform X1 [Homo sapiens]	12	2	24	2	1	203	22.2	8.94	High	High	High	High	High	High		9.4E+08	9.67E+08	9.53E+08	1.93E+09	9.96E+08	9.62E+08	36.61	2	186	2
FALSE	Master Protein Candidate	11	300360534	glutathione S-transferase omega-1 isoform 3 [Homo sapiens]	16	3	28	3	1	213	24.8	6.1	High	High	High	High	High	High		91399256	98228980	95994034	2.71E+08	2.73E+08	2.67E+08	32.39	3	209	3
FALSE	None	11	300360532	glutathione S-transferase omega-1 isoform 2 [Homo sapiens]	4	1	6	1	1	208	23.7	7.17	High	High	High	Not Found	Not Found	Not Found		1.21E+08	1.14E+08	1.14E+08				6.15	1	32	1
FALSE	Master Protein	11	4758484	glutathione S-transferase omega-1 isoform 1 [Homo sapiens]	14	3	28	3	1	241	27.5	6.6	High	High	High	High	High	High		91399256	98228980	95994034	2.71E+08	2.73E+08	2.67E+08	32.39	3	209	3
FALSE	Master Protein	111	31317307	proprotein convertase subtilisin/kexin type 9 preproprotein [Homo sapiens]	8	4	19	4	1	692	74.2	6.61	Not Found	Not Found	High	High	High	High				19294344	60020201	52380441	62571734	26.44	4	253	4
FALSE	Master Protein	112	40254924	leucine-rich repeat-containing protein 59 [Homo sapiens]	4	1	1	1	1	307	34.9	9.57	Not Found	Not Found	Not Found	Not Found	High	Not Found						56069504		0	1		
FALSE	Master Protein	113	5729953	nuclear migration protein nudC [Homo sapiens]	5	1	6	1	1	331	38.2	5.38	Not Found	Not Found	Not Found	High	High	High					47018847	47942646	43850041	9.61	1	169	1
FALSE	Master Protein	114	4507951	14-3-3 protein eta [Homo sapiens]	13	3	18	1	1	246	28.2	4.84	High	Not Found	Not Found	Not Found	Not Found	Not Found		26430188						13.3	3	91	3
FALSE	Master Protein	116	4507149	superoxide dismutase [Cu-Zn] [Homo sapiens]	9	1	12	1	1	154	15.9	6.13	High	High	High	High	High	High		1.43E+08	1.37E+08	1.48E+08	3.14E+08	3.19E+08	2.93E+08	19.98	1	219	1
FALSE	None	117	578799098	PREDICTED: agrin isoform X6 [Homo sapiens]	3	5	36	5	1	1766	184.9	6	High	High	High	High	High	High		56713060	69423297	71507093	1.14E+08	1.13E+08	1.16E+08	42.17	5	412	5
FALSE	Master Protein	117	530360311	PREDICTED: agrin isoform X2 [Homo sapiens]	4	6	44	6	1	2049	215.2	6.51	High	High	High	High	High	High		74182193	74133939	75952771	1.14E+08	1.13E+08	1.51E+08	54.16	6	453	6
FALSE	None	117	578799094	PREDICTED: agrin isoform X4 [Homo sapiens]	3	5	36	5	1	2053	215.6	6.34	High	High	High	High	High	High		56713060	69423297	71507093	1.14E+08	1.13E+08	1.16E+08	42.17	5	412	5
FALSE	Master Protein Candidate	117	54873613	agrin precursor [Homo sapiens]	4	6	44	6	1	2045	214.7	6.4	High	High	High	High	High	High		74182193	74133939	75952771	1.14E+08	1.13E+08	1.51E+08	54.16	6	453	6
FALSE	None	117	578799100	PREDICTED: agrin isoform X7 [Homo sapiens]	4	5	36	5	1	1479	154.3	6.23	High	High	High	High	High	High		56713060	69423297	71507093	1.14E+08	1.13E+08	1.16E+08	42.17	5	412	5
FALSE	None	117	578799096	PREDICTED: agrin isoform X5 [Homo sapiens]	3	4	25	4	1	1907	200	6.39	High	High	High	High	High	High		50779431	70809079	73588362	89074036	1.02E+08	90791839	29.03	4	322	4
FALSE	None	117	578799092	PREDICTED: agrin isoform X3 [Homo sapiens]	3	5	36	5	1	2057	216.1	6.44	High	High	High	High	High	High		56713060	69423297	71507093	1.14E+08	1.13E+08	1.16E+08	42.17	5	412	5
FALSE	Master Protein Candidate	118	41327736	epidermal growth factor receptor isoform d precursor [Homo sapiens]	4	2	18	2	1	705	77.3	6.96	High	High	High	High	High	High			9918792	14316374	38525373	41529934	39928075	23.46	2	114	2
FALSE	Master Protein	118	29725609	epidermal growth factor receptor isoform a precursor [Homo sapiens]	2	2	18	2	1	1210	134.2	6.68	High	High	High	High	High	High			9918792	14316374	38525373	41529934	39928075	23.46	2	114	2
FALSE	Master Protein Candidate	118	41327734	epidermal growth factor receptor isoform c precursor [Homo sapiens]	7	2	18	2	1	405	44.6	7.01	High	High	High	High	High	High			9918792	14316374	38525373	41529934	39928075	23.46	2	114	2
FALSE	Master Protein Candidate	118	41327732	epidermal growth factor receptor isoform b precursor [Homo sapiens]	4	2	18	2	1	628	69.2	7.05	High	High	High	High	High	High			9918792	14316374	38525373	41529934	39928075	23.46	2	114	2
FALSE	Master Protein	119	4758638	peroxiredoxin-6 [Homo sapiens]	19	3	20	3	1	224	25	6.38	High	High	High	High	High	High		91339961	95041254	83663352	1.08E+08	1.69E+08	1.59E+08	23.33	2	158	3
FALSE	None	12	4505409	nucleoside diphosphate kinase B isoform a [Homo sapiens]	36	4	34	4	1	152	17.3	8.41	High	High	High	High	High	High		1.19E+08	2.57E+08	1.73E+08	3.9E+08	4.12E+08	2.3E+08	29.6	4	149	4
FALSE	Master Protein	12	66392203	NME1-NME2 protein [Homo sapiens]	39	6	41	6	1	267	30.1	8.92	High	High	High	High	High	High		1.19E+08	2.57E+08	1.73E+08	3.9E+08	1.98E+08	1.85E+08	31.41	6	166	6
FALSE	None	12	310923127	nucleoside diphosphate kinase B isoform b [Homo sapiens]	27	2	11	2	1	82	9.6	9.7	High	High	High	High	Not Found	Not Found		73800812	2.62E+08	65031048	3.27E+08			8.74	2	0	2
FALSE	None	12	4557797	nucleoside diphosphate kinase A isoform b [Homo sapiens]	32	4	19	4	1	152	17.1	6.19	High	High	High	Not Found	High	High		1.01E+08	2.23E+08	1.56E+08		91146073	63404259	6.39	4	53	4
FALSE	None	12	38045913	nucleoside diphosphate kinase A isoform a [Homo sapiens]	28	4	19	4	1	177	19.6	5.58	High	High	High	Not Found	High	High		1.01E+08	2.23E+08	1.56E+08		91146073	63404259	6.39	4	53	4
FALSE	Master Protein	120	530384074	PREDICTED: NKG2D ligand 2 isoform X1 [Homo sapiens]	4	1	4	1	1	246	27.4	7.3	Not Found	High	High	Not Found	Not Found	Not Found			57741856	55566867				4.54	1	74	1
FALSE	Master Protein	121	4505585	platelet-activating factor acetylhydrolase IB subunit beta isoform a [Homo sapiens]	4	1	2	1	1	229	25.6	5.92	Not Found	Not Found	Not Found	High	Not Found	Not Found					72636707			1.97	1	34	1
FALSE	None	122	21071028	acidic leucine-rich nuclear phosphoprotein 32 family member D [Homo sapiens]	9	2	7	2	1	131	14.8	5.02	High	High	High	High	Not Found	Not Found		16326706	11362431	16400711	36461330			10.4	2	25	2
FALSE	None	122	6912604	acidic leucine-rich nuclear phosphoprotein 32 family member C [Homo sapiens]	5	1	2	1	1	234	26.7	4.21	Not Found	Not Found	Not Found	High	Not Found	Not Found					36461330			2.13	1	0	1
FALSE	Master Protein	122	5454088	acidic leucine-rich nuclear phosphoprotein 32 family member B [Homo sapiens]	14	4	23	4	1	251	28.8	4.06	High	High	High	High	High	High		1.08E+08	1.08E+08	1.46E+08	2.67E+08	5.06E+08	4.51E+08	30.06	4	105	4
FALSE	None	122	5453880	acidic leucine-rich nuclear phosphoprotein 32 family member A [Homo sapiens]	5	2	7	2	1	249	28.6	4.09	High	High	High	High	Not Found	Not Found		16326706	11362431	16400711	36461330			10.4	2	25	2
FALSE	Master Protein	123	62868215	laminin subunit beta-3 precursor [Homo sapiens]	3	3	13	3	1	1172	129.5	7.21	High	High	Not Found	High	High	High		29991114	27746975		56947351	74273262	38353598	14.41	3	98	3
FALSE	Master Protein	124	23110942	proteasome subunit alpha type-5 isoform 1 [Homo sapiens]	13	2	13	2	1	241	26.4	4.79	Not Found	Not Found	Not Found	High	High	High					2.17E+08	1.35E+08	1.47E+08	13.17	2	193	2
FALSE	None	124	315138985	proteasome subunit alpha type-5 isoform 2 [Homo sapiens]	10	1	10	1	1	183	20	4.73	Not Found	Not Found	Not Found	High	High	High					2.17E+08	2.02E+08	2.2E+08	10.61	1	186	1
FALSE	Master Protein	125	7657033	5'(3')-deoxyribonucleotidase, cytosolic type isoform 1 [Homo sapiens]	9	1	2	1	1	201	23.4	6.64	Not Found	Not Found	Not Found	Not Found	Not Found	High								1.78	1	0	1
FALSE	Master Protein Candidate	125	578830793	PREDICTED: 5'(3')-deoxyribonucleotidase, cytosolic type isoform X1 [Homo sapiens]	10	1	2	1	1	182	20.4	5.82	Not Found	Not Found	Not Found	Not Found	Not Found	High								1.78	1	0	1
FALSE	Master Protein Candidate	125	356874780	5'(3')-deoxyribonucleotidase, cytosolic type isoform 2 [Homo sapiens]	11	1	2	1	1	161	18.7	6.79	Not Found	Not Found	Not Found	Not Found	Not Found	High								1.78	1	0	1
FALSE	Master Protein Candidate	125	578830796	PREDICTED: 5'(3')-deoxyribonucleotidase, cytosolic type isoform X2 [Homo sapiens]	14	1	2	1	1	125	14.2	6.79	Not Found	Not Found	Not Found	Not Found	Not Found	High								1.78	1	0	1
FALSE	Master Protein	126	4505209	collagenase 3 preproprotein [Homo sapiens]	3	1	2	1	1	471	53.8	5.6	Not Found	High	High	Not Found	Not Found	Not Found			11678742	13127821						0	1
FALSE	Master Protein Candidate	127	217416386	uncharacterized aarF domain-containing protein kinase 4 isoform b [Homo sapiens]	3	1	2	1	1	503	55.8	7.43	Not Found	Not Found	Not Found	High	Not Found	Not Found					40296372			2.31	1	0	1
FALSE	Master Protein Candidate	127	578834923	PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X6 [Homo sapiens]	2	1	2	1	1	544	60	7.23	Not Found	Not Found	Not Found	High	Not Found	Not Found					40296372			2.31	1	0	1
FALSE	Master Protein	127	530417278	PREDICTED: uncharacterized aarF domain-containing protein kinase 4 isoform X1 [Homo sapiens]	2	1	2	1	1	628	69.6	8.21	Not Found	Not Found	Not Found	High	Not Found	Not Found					40296372			2.31	1	0	1
FALSE	Master Protein	128	578833384	PREDICTED: glucosidase 2 subunit beta isoform X1 [Homo sapiens]	2	1	4	1	1	543	61.2	4.46	High	High	Not Found	Not Found	Not Found	Not Found		50582392	49827155					4.49	1	0	1
FALSE	Master Protein Candidate	128	574280236	glucosidase 2 subunit beta isoform 3 precursor [Homo sapiens]	2	1	4	1	1	535	60.2	4.41	High	High	Not Found	Not Found	Not Found	Not Found		50582392	49827155					4.49	1	0	1
FALSE	Master Protein Candidate	128	578833388	PREDICTED: glucosidase 2 subunit beta isoform X3 [Homo sapiens]	2	1	4	1	1	536	60.4	4.45	High	High	Not Found	Not Found	Not Found	Not Found		50582392	49827155					4.49	1	0	1
FALSE	Master Protein Candidate	128	578833390	PREDICTED: glucosidase 2 subunit beta isoform X4 [Homo sapiens]	2	1	4	1	1	533	60.1	4.46	High	High	Not Found	Not Found	Not Found	Not Found		50582392	49827155					4.49	1	0	1
FALSE	Master Protein Candidate	128	48255889	glucosidase 2 subunit beta isoform 1 precursor [Homo sapiens]	2	1	4	1	1	528	59.4	4.41	High	High	Not Found	Not Found	Not Found	Not Found		50582392	49827155					4.49	1	0	1
FALSE	Master Protein Candidate	128	574280088	glucosidase 2 subunit beta isoform 2 precursor [Homo sapiens]	2	1	4	1	1	525	59.1	4.42	High	High	Not Found	Not Found	Not Found	Not Found		50582392	49827155					4.49	1	0	1
FALSE	Master Protein Candidate	129	578806939	PREDICTED: destrin-like [Homo sapiens]	6	1	12	1	1	178	19.5	7.12	High	High	High	High	High	High		48981588	50505158	52065467	98520077	96730052	91435812	12.75	1	74	1
FALSE	Master Protein	129	578794950	PREDICTED: destrin-like [Homo sapiens]	6	1	12	1	1	191	21	7.72	High	High	High	High	High	High		48981588	50505158	52065467	98520077	96730052	91435812	12.75	1	74	1
FALSE	Master Protein Candidate	129	5802966	destrin isoform a [Homo sapiens]	7	1	12	1	1	165	18.5	7.85	High	High	High	High	High	High		48981588	50505158	52065467	98520077	96730052	91435812	12.75	1	74	1
FALSE	Master Protein Candidate	129	578843371	PREDICTED: destrin-like [Homo sapiens]	6	1	12	1	1	191	21.1	7.77	High	High	High	High	High	High		48981588	50505158	52065467	98520077	96730052	91435812	12.75	1	74	1
FALSE	Master Protein Candidate	129	58530848	destrin isoform b [Homo sapiens]	7	1	12	1	1	148	16.6	8.34	High	High	High	High	High	High		48981588	50505158	52065467	98520077	96730052	91435812	12.75	1	74	1

FALSE	Master Protein	13	67782365	keratin, type II cytoskeletal 7 [Homo sapiens]	22	9	172	8	1	469	51.4	5.48	High	High	High	High	High	High		1.3E+08	1.54E+08	1.51E+08	2.44E+08	2.42E+08	2.41E+08	209.54	8	1858	9
FALSE	None	13;102;148	125628632	keratin, type II cytoskeletal 80 isoform K80.1 [Homo sapiens]	3	1	96	0	3	422	47.2	5.3	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								104.26	1	869	1
FALSE	None	13;102;148	334688844	glial fibrillary acidic protein isoform 3 [Homo sapiens]	3	1	96	0	3	438	50.3	5.67	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								104.26	1	869	1
FALSE	None	13;102;148	125628636	keratin, type II cytoskeletal 80 isoform K80 [Homo sapiens]	2	1	96	0	3	452	50.5	5.67	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								104.26	1	869	1
FALSE	None	13;102;148	530399826	PREDICTED: keratin, type II cytoskeletal 80 isoform X1 [Homo sapiens]	2	1	96	0	3	550	60.8	5.68	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								104.26	1	869	1
FALSE	None	13;102;148	4503979	glial fibrillary acidic protein isoform 1 [Homo sapiens]	3	1	96	0	3	432	49.9	5.52	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								104.26	1	869	1
FALSE	None	13;102;148	196115290	glial fibrillary acidic protein isoform 2 [Homo sapiens]	3	1	96	0	3	431	49.5	6.13	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								104.26	1	869	1
FALSE	None	13;102;148	331999954	keratin, type II cytoskeletal 4 [Homo sapiens]	2	1	96	0	3	520	56.1	6.61	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								104.26	1	869	1
FALSE	None	13;102;148	530399828	PREDICTED: keratin, type II cytoskeletal 80 isoform X2 [Homo sapiens]	2	1	96	0	3	487	54.2	5.33	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								104.26	1	869	1
FALSE	Master Protein Candidate	130	530401159	PREDICTED: polyadenylate-binding protein 4-like [Homo sapiens]	10	1	2	1	1	160	17.1	8.79	Not Found	Not Found	Not Found	Not Found	High	High						16526772	21586025	0	1	0	1
FALSE	Master Protein Candidate	130	208431836	polyadenylate-binding protein 4 isoform 3 [Homo sapiens]	3	1	2	1	1	631	69.5	9.52	Not Found	Not Found	Not Found	Not Found	High	High						16526772	21586025	0	1	0	1
FALSE	Master Protein	130	208431833	polyadenylate-binding protein 4 isoform 1 [Homo sapiens]	2	1	2	1	1	660	72.3	9.35	Not Found	Not Found	Not Found	Not Found	High	High						16526772	21586025	0	1	0	1
FALSE	Master Protein Candidate	130	4504715	polyadenylate-binding protein 4 isoform 2 [Homo sapiens]	2	1	2	1	1	644	70.7	9.26	Not Found	Not Found	Not Found	Not Found	High	High						16526772	21586025	0	1	0	1
FALSE	Master Protein	131	578817383	PREDICTED: gelsolin isoform X7 [Homo sapiens]	2	1	8	1	1	820	89.5	6.57	High	Not Found	Not Found	High	High	Not Found		26800925			55135988	60542552		12.15	1	88	1
FALSE	Master Protein Candidate	131	384475528	gelsolin isoform d [Homo sapiens]	2	1	8	1	1	748	82.5	5.63	High	Not Found	Not Found	High	High	Not Found		26800925			55135988	60542552		12.15	1	88	1
FALSE	Master Protein Candidate	131	530391018	PREDICTED: gelsolin isoform X1 [Homo sapiens]	2	1	8	1	1	752	82.8	5.85	High	Not Found	Not Found	High	High	Not Found		26800925			55135988	60542552		12.15	1	88	1
FALSE	Master Protein Candidate	131	578817385	PREDICTED: gelsolin isoform X8 [Homo sapiens]	2	1	8	1	1	742	81.9	5.85	High	Not Found	Not Found	High	High	Not Found		26800925			55135988	60542552		12.15	1	88	1
FALSE	Master Protein Candidate	131	189083776	gelsolin isoform b [Homo sapiens]	2	1	8	1	1	731	80.6	5.85	High	Not Found	Not Found	High	High	Not Found		26800925			55135988	60542552		12.15	1	88	1
FALSE	Master Protein Candidate	131	427918083	gelsolin isoform e [Homo sapiens]	2	1	8	1	1	739	81.4	5.85	High	Not Found	Not Found	High	High	Not Found		26800925			55135988	60542552		12.15	1	88	1
FALSE	Master Protein Candidate	131	4504165	gelsolin isoform a precursor [Homo sapiens]	2	1	8	1	1	782	85.6	6.28	High	Not Found	Not Found	High	High	Not Found		26800925			55135988	60542552		12.15	1	88	1
FALSE	Master Protein Candidate	131	390517030	gelsolin isoform f [Homo sapiens]	2	1	8	1	1	767	84.7	5.83	High	Not Found	Not Found	High	High	Not Found		26800925			55135988	60542552		12.15	1	88	1
FALSE	Master Protein	132	530390549	PREDICTED: cathepsin L1 isoform X1 [Homo sapiens]	8	2	15	2	1	333	37.5	5.45	High	High	High	High	High	High		77443978	87966387	54181776	95667566	1.29E+08	1.36E+08	25.68	2	187	2
FALSE	None	133	9966867	eukaryotic translation initiation factor 5A-2 [Homo sapiens]	8	1	24	1	1	153	16.8	5.58	High	High	High	High	High	High		1.59E+08	1.79E+08	1.75E+08	3.15E+08	3.42E+08	3.62E+08	31.02	1	156	1
FALSE	Master Protein Candidate	133	153791632	eukaryotic translation initiation factor 5A-1-like [Homo sapiens]	19	3	44	3	1	154	16.8	5	High	High	High	High	High	High		1.3E+08	1.34E+08	99850154	2.1E+08	2.15E+08	2.24E+08	53.63	3	172	3
FALSE	Master Protein	133	219555707	eukaryotic translation initiation factor 5A-1 isoform A [Homo sapiens]	16	3	44	3	1	184	20.2	7.01	High	High	High	High	High	High		1.3E+08	1.34E+08	99850154	2.1E+08	2.15E+08	2.24E+08	53.63	3	172	3
FALSE	Master Protein Candidate	133	530410036	PREDICTED: eukaryotic translation initiation factor 5A-1 isoform X5 [Homo sapiens]	19	3	44	3	1	154	16.8	5.24	High	High	High	High	High	High		1.3E+08	1.34E+08	99850154	2.1E+08	2.15E+08	2.24E+08	53.63	3	172	3
FALSE	Master Protein	134	20070125	protein disulfide-isomerase precursor [Homo sapiens]	10	4	17	4	1	508	57.1	4.87	High	High	High	High	High	High		20277193	16558157	20427144	41025951	49633199	64118705	11.64	4	30	4
FALSE	None	135	387912532	serpin B7 isoform 2 [Homo sapiens]	3	1	12	1	1	363	41.1	6.74	High	High	High	High	High	High		15467867	16033498	15880817	61430718	63730185	65501614	12.09	1	30	1
FALSE	None	135	387912530	serpin B7 isoform 1 [Homo sapiens]	3	1	12	1	1	380	42.9	6.8	High	High	High	High	High	High		15467867	16033498	15880817	61430718	63730185	65501614	12.09	1	30	1
FALSE	Master Protein	135	219689110	plasminogen activator inhibitor 2 [Homo sapiens]	18	7	59	7	1	415	46.6	5.63	High	High	High	High	High	High		33882073	30686235	31415224	1.1E+08	1.08E+08	1.1E+08	62.47	7	170	7
FALSE	Master Protein Candidate	136	4502049	aldose reductase [Homo sapiens]	3	1	2	1	1	316	35.8	6.98	Not Found	Not Found	Not Found	High	Not Found	Not Found					30382811			1.84	1	0	1
FALSE	Master Protein	136	320202986	alcohol dehydrogenase [NADP(+)] [Homo sapiens]	3	1	2	1	1	325	36.6	6.79	Not Found	Not Found	Not Found	High	Not Found	Not Found					30382811			1.84	1	0	1
FALSE	Master Protein	137	4505863	urokinase-type plasminogen activator isoform 1 preproprotein [Homo sapiens]	2	1	6	1	1	431	48.5	8.41	Not Found	Not Found	Not Found	High	High	High					28491680	33717236	31504192	7.7	1	42	1
FALSE	Master Protein Candidate	137	222537759	urokinase-type plasminogen activator isoform 2 [Homo sapiens]	2	1	6	1	1	414	46.9	8.44	Not Found	Not Found	Not Found	High	High	High					28491680	33717236	31504192	7.7	1	42	1
FALSE	Master Protein Candidate	137	578819560	PREDICTED: urokinase-type plasminogen activator isoform X1 [Homo sapiens]	3	1	6	1	1	375	42.4	8.29	Not Found	Not Found	Not Found	High	High	High					28491680	33717236	31504192	7.7	1	42	1
FALSE	Master Protein	138	12408675	prefoldin subunit 2 [Homo sapiens]	9	1	6	1	1	154	16.6	6.58	High	Not Found	Not Found	Not Found	High	High								8.59	1	45	1
FALSE	None	139	578832543	PREDICTED: serpin B5 isoform X1 [Homo sapiens]	11	2	10	2	1	204	23.1	6.54	High	High	High	Not Found	High	High		52929674	52106817	54034955		1.31E+08	84037891	5.66	2	0	1
FALSE	Master Protein	139	167860126	serpin B5 [Homo sapiens]	18	5	36	5	1	375	42.1	6.05	High	High	High	High	High	High		56466957	52106817	57872675	92208281	1.09E+08	1.04E+08	36	5	171	4
FALSE	Master Protein	14	13775200	splicing factor 3B subunit 5 [Homo sapiens]	15	1	6	1	1	86	10.1	6.35	High	High	High	Not Found	Not Found	Not Found		11466696	14774738	14714178				8.19	1	36	1
FALSE	Master Protein Candidate	140	66346681	plasminogen activator inhibitor 1 RNA-binding protein isoform 2 [Homo sapiens]	4	1	2	1	1	402	44.2	8.66	High	High	Not Found	Not Found	Not Found	Not Found		19035265	21182905					0	1		
FALSE	Master Protein	140	66346679	plasminogen activator inhibitor 1 RNA-binding protein isoform 1 [Homo sapiens]	4	1	2	1	1	408	44.9	8.65	High	High	Not Found	Not Found	Not Found	Not Found		19035265	21182905					0	1		
FALSE	Master Protein Candidate	140	66346685	plasminogen activator inhibitor 1 RNA-binding protein isoform 4 [Homo sapiens]	4	1	2	1	1	387	42.4	8.44	High	High	Not Found	Not Found	Not Found	Not Found		19035265	21182905					0	1		
FALSE	Master Protein Candidate	140	66346683	plasminogen activator inhibitor 1 RNA-binding protein isoform 3 [Homo sapiens]	4	1	2	1	1	393	43.1	8.44	High	High	Not Found	Not Found	Not Found	Not Found		19035265	21182905					0	1		
FALSE	None	141	538919948	malate dehydrogenase, mitochondrial isoform 3 [Homo sapiens]	26	4	37	4	1	231	24.6	7.99	High	High	High	High	High	High		34655594	39629234	25081786	59255737	45054177	62981301	48.97	4	367	4
FALSE	Master Protein	141	21735621	malate dehydrogenase, mitochondrial isoform 1 precursor [Homo sapiens]	26	6	71	6	1	338	35.5	8.68	High	High	High	High	High	High		61945124	49371827	52954942	1.1E+08	1.08E+08	1.17E+08	99.38	6	717	6
FALSE	None	141	538919685	malate dehydrogenase, mitochondrial isoform 2 precursor [Homo sapiens]	20	4	53	4	1	296	30.9	8.43	High	High	High	High	High	High		61945124	61043725	66891520	1.1E+08	1.02E+08	1.17E+08	73.18	4	541	4
FALSE	Master Protein Candidate	142	20162550	protein phosphatase 1 regulatory subunit 14B [Homo sapiens]	9	1	22	1	1	147	15.9	4.86	High	High	High	High	High	High		3790050	3712939	4460895	11438371	12314797	8435253	27.1	1	147	1
FALSE	Master Protein	142	73390140	LIM domain kinase 2 isoform 1 [Homo sapiens]	2	1	22	1	1	686	77.8	7.05	High	High	High	High	High	High		3790050	3712939	4460895	11438371	12314797	8435253	27.1	1	147	1
FALSE	Master Protein Candidate	143	431822408	heat shock protein HSP 90-beta isoform c [Homo sapiens]	11	6	32	3	1	714	82.3	5.06	High	High	High	High	High	High		35697806	28967033	31304231	52208513	54703884	74267839	40.08	6	250	6
FALSE	None	143	431822406	heat shock protein HSP 90-beta isoform b [Homo sapiens]	10	5	26	3	1	676	78.2	5.05	High	High	High	High	High	High		35697806	28967033	31304231	52208513	54703884	74267839	33.14	5	237	5
FALSE	Master Protein	143	530381931	PREDICTED: heat shock protein HSP 90-beta isoform X1 [Homo sapiens]	11	6	32	3	1	724	83.2	5.03	High	High	High	High	High	High		35697806	28967033	31304231	52208513	54703884	74267839	40.08	6	250	6
FALSE	None	143	4507677	endoplasmin precursor [Homo sapiens]	1	1	5	1	1	803	92.4	4.84	High	High	High	Not Found	Not Found	Not Found		35697806	32841872	33405703				5.11	1	39	1
FALSE	Master Protein	144	4757960	cadherin-1 preproprotein [Homo sapiens]	5	3	18	3	1	882	97.4	4.73	High	High	High	High	High	High		29413296	30099201	36030598	1.01E+08	1.07E+08	88855447	25.61	2	167	3
FALSE	Master Protein	145	42822870	ribonuclease inhibitor [Homo sapiens]	3	1	4	1	1	461	49.9	4.82	Not Found	Not Found	Not Found	High	Not Found	High					39358856		45377954	6.06	1	116	1
FALSE	Master Protein Candidate	146	530405975	PREDICTED: pyruvate kinase PKM isoform X1 [Homo sapiens]	29	13	300	13	1	591	64.5	8.02	High	High	High	High	High	High		2.53E+08	2.18E+08	1.43E+08	6.84E+08	6.44E+08	7.52E+08	431.31	13	3429	13
FALSE	None	146	32967597	pyruvate kinase PKLR isoform 2 [Homo sapiens]	2	1	4	1	1	543	58.5	7.05	High	Not Found	Not Found	Not Found	Not Found	High		3.13E+08					9.44E+08	4.28	1	43	1
FALSE	Master Protein Candidate	146	530405979	PREDICTED: pyruvate kinase PKM isoform X3 [Homo sapiens]	33	13	300	13	1	531	57.9	7.84	High	High	High	High	High	High		2.53E+08	2.18E+08	1.43E+08	6.84E+08	6.44E+08	7.52E+08	431.31	13	3429	13
FALSE	None	146	33286422	pyruvate kinase PKM isoform b [Homo sapiens]	30	12	274	12	1	531	58	7.71	High	High	High	High	High	High		2.53E+08	2.18E+08	1.38E+08	6.84E+08	6.44E+08	7.52E+08	409.32	12	3215	12
FALSE	None	146	332164775	pyruvate kinase PKM isoform c [Homo sapiens]	26	12	274	12	1	605	65.9	7.87	High	High	High	High	High	High		2.53E+08	2.18E+08	1.38E+08	6.84E+08	6.44E+08	7.52E+08	409.32	12	3215	12
FALSE	None	146	332164779	pyruvate kinase PKM isoform e [Homo sapiens]	28	11	277	11	1	516	56.2	8.44	High	High	High	High	High	High		2.26E+08	1.97E+08	1.43E+08	5.46E+08	5.68E+08	6.91E+08	396.07	11	3283	11
FALSE	None	146	332164777	pyruvate kinase PKM isoform d [Homo sapiens]	29	10	269	10	1	457	49.9	7.83	High	High	High	High	High	High		2.53E+08	2.18E+08	1.43E+08	6.84E+08	6.44E+08	7.52E+08	383.71	10	3169	10
FALSE	Master Protein	146	578827087	PREDICTED: pyruvate kinase PKM isoform X4 [Homo sapiens]	29	13	300	13	1	605	65.8	7.99	High	High	High	High	High	High		2.53E+08	2.18E+08	1.43E+08	6.84E+08	6.44E+08	7.52E+08	431.31	13	3429	13
FALSE	None	146	578801114	PREDICTED: pyruvate kinase PKLR isoform X2 [Homo sapiens]	2	1	4	1	1	510	54.9	7.05	High	Not Found	Not Found	Not Found	Not Found	High		3.13E+08					9.44E+08	4.28	1	43	1
FALSE	None	146	530364927	PREDICTED: pyruvate kinase PKLR isoform X1 [Homo sapiens]	2	1	4	1	1	627	68	8.79	High	Not Found	Not Found	Not Found	Not Found	High		3.13E+08					9.44E+08	4.28	1	43	1
FALSE	None	146	332164781	pyruvate kinase PKM isoform f [Homo sapiens]	29	12	274	12	1	536	58.5	7.71	High	High	High	High	High	High		2.53E+08	2.18E+08	1.38E+08	6.84E+08	6.44E+08	7.52E+08	409.32	12	3215	12
FALSE	None	146	10835121	pyruvate kinase PKLR isoform 1 [Homo sapiens]	2	1	4	1	1	574	61.8	7.74	High	Not Found	Not Found	Not Found	Not Found	High		3.13E+08					9.44E+08	4.28	1	43	1
FALSE	Master Protein Candidate	147	578821434	PREDICTED: unconventional myosin-VIIa isoform X4 [Homo sapiens]	1	1	1	1	1	2190	251.2	8.54	High	Not Found	Not Found	Not Found	Not Found	Not Found		1.11E+08								24	1
FALSE	Master Protein Candidate	147	530396816	PREDICTED: unconventional myosin-VIIa isoform X2 [Homo sapiens]	1	1	1	1	1	2176	250.2	8.66	High	Not Found	Not Found	Not Found	Not Found	Not Found		1.11E+08								24	1
FALSE	Master Protein Candidate	147	578821436	PREDICTED: unconventional myosin-VIIa isoform X5 [Homo sapiens]	1	1	1	1	1	2189	251.1	8.54	High	Not Found	Not Found	Not Found	Not Found	Not Found		1.11E+08								24	1
FALSE	Master Protein Candidate	147	189083798	unconventional myosin-VIIa isoform 1 [Homo sapiens]	1	1	1	1	1	2215	254.2	8.57	High	Not Found	Not Found	Not Found	Not Found	Not Found		1.11E+08								24	1
FALSE	Master Protein	147	578821432	PREDICTED: unconventional myosin-VIIa isoform X3 [Homo sapiens]	1	1	1	1	1	2225	255.2	8.66	High	Not Found	Not Found	Not Found	Not Found	Not Found		1.11E+08								24	1
FALSE	Master Protein Candidate	147	256355179	unconventional myosin-VIIa isoform 3 [Homo sapiens]	1	1	1	1	1	1178	135.7	8.63	High	Not Found	Not Found	Not Found	Not Found	Not Found		1.11E+08								24	1
FALSE	Master Protein Candidate	147	189083802	unconventional myosin-VIIa isoform 2 [Homo sapiens]	1	1	1	1	1	2175	250.1	8.63	High	Not Found	Not Found	Not Found	Not Found	Not Found		1.11E+08								24	1
FALSE	Master Protein Candidate	147	578821438	PREDICTED: unconventional myosin-VIIa isoform X6 [Homo sapiens]	1	1	1	1	1	2177	250.3	8.66	High	Not Found	Not Found	Not Found	Not Found	Not Found		1.11E+08								24	1
FALSE	Master Protein	148	372466572	keratin, type II cytoskeletal 8 isoform 1 [Homo sapiens]	24	11	189	9	1	511	56.6	5.43	High	High	High	High	High	High		1.41E+08	1.43E+08	1.44E+08	3.18E+08	3.26E+08	3.25E+08	229.37	11	1816	11
FALSE	Master Protein Candidate	148	372466577	keratin, type II cytoskeletal 8 isoform 2 [Homo sapiens]	25	11	189	9	1	483	53.7	5.59	High	High	High	High	High	High		1.41E+08	1.43E+08	1.44E+08	3.18E+08	3.26E+08	3.25E+08	229.37	11	1816	11
FALSE	Master Protein Candidate	149	156151396	heterogeneous nuclear ribonucleoprotein R isoform 3 [Homo sapiens]	4	2	12	1	1	535	59.9	9.16	Not Found	Not Found	Not Found	High	Not Found	Not Found					14962936			12.85	2	61	1
FALSE	Master Protein Candidate	149	5031755	heterogeneous nuclear ribonucleoprotein R isoform 2 [Homo sapiens]	3	2	12	1	1	633	70.9	8.13	Not Found	Not Found	Not Found	High	Not Found	Not Found					14962936			12.85	2	61	1
FALSE	Master Protein Candidate	149	156151392	heterogeneous nuclear ribonucleoprotein R isoform 4 [Homo sapiens]	4	2	12	1	1	532	59.6	9.16	Not Found	Not Found	Not Found	High	Not Found	Not Found					14962936			12.85	2	61	1
FALSE	Master Protein Candidate	149	530360777	PREDICTED: heterogeneous nuclear ribonucleoprotein R isoform X4 [Homo sapiens]	4	2	12	1	1	494	55.7	9.23	Not Found	Not Found	Not Found	High	Not Found	Not Found					14962936			12.85	2	61	1
FALSE	Master Protein Candidate	149	530360775	PREDICTED: heterogeneous nuclear ribonucleoprotein R isoform X3 [Homo sapiens]	4	2	12	1	1	595	66.9	8.29	Not Found	Not Found	Not Found	High	Not Found	Not Found					14962936			12.85	2	61	1
FALSE	Master Protein	149	156151394	heterogeneous nuclear ribonucleoprotein R isoform 1 [Homo sapiens]	3	2	12	1	1	636	71.2	8.13	Not Found	Not Found	Not Found	High	Not Found	Not Found					14962936			12.85	2	61	1
FALSE	Master Protein Candidate	15	343478153	amyloid-like protein 2 isoform 5 [Homo sapiens]	2	1	2	1	1	761	87.2	4.88	Not Found	Not Found	Not Found	Not Found	High	Not Found						17374711		2.13	1	0	1
FALSE	Master Protein	15	4502147	amyloid-like protein 2 isoform 1 precursor [Homo sapiens]	2	1	2	1	1	763	86.9	4.79	Not Found	Not Found	Not Found	Not Found	High	Not Found						17374711		2.13	1	0	1
FALSE	Master Protein Candidate	15	214010185	amyloid-like protein 2 isoform 4 precursor [Homo sapiens]	2	1	2	1	1	522	59.1	5.59	Not Found	Not Found	Not Found	Not Found	High	Not Found						17374711		2.13	1	0	1
FALSE	Master Protein Candidate	15	214010181	amyloid-like protein 2 isoform 2 precursor [Homo sapiens]	2	1	2	1	1	751	85.4	4.77	Not Found	Not Found	Not Found	Not Found	High	Not Found						17374711		2.13	1	0	1
FALSE	Master Protein Candidate	15	214010183	amyloid-like protein 2 isoform 3 precursor [Homo sapiens]	2	1	2	1	1	695	79.2	4.72	Not Found	Not Found	Not Found	Not Found	High	Not Found						17374711		2.13	1	0	1
FALSE	Master Protein	150	145309326	laminin subunit gamma-1 precursor [Homo sapiens]	2	2	10	2	1	1609	177.5	5.12	High	High	High	High	High	Not Found		9695800	10028244	11442587	29197524	31662984		16.21	2	236	2
FALSE	Master Protein	151	30425438	out at first protein homolog precursor [Homo sapiens]	6	1	2	1	1	273	30.7	6.84	Not Found	Not Found	High	Not Found	Not Found	Not Found				10844407				4.16	1	51	1
FALSE	Master Protein Candidate	151	578822044	PREDICTED: out at first protein homolog isoform X1 [Homo sapiens]	11	1	2	1	1	157	18.1	7.64	Not Found	Not Found	High	Not Found	Not Found	Not Found				10844407				4.16	1	51	1
FALSE	Master Protein	152	4557888	keratin, type I cytoskeletal 18 [Homo sapiens]	10	3	35	3	1	430	48	5.45	High	High	High	High	High	High		81271540	1.19E+08	78963837	96866927	1.53E+08	1.3E+08	53.18	3	627	3
FALSE	Master Protein Candidate	153	4506179	proteasome subunit alpha type-1 isoform 2 [Homo sapiens]	19	4	24	4	1	263	29.5	6.61	High	High	High	High	High	High		85514763	80600104	94466306	1.3E+08	1.34E+08	1.08E+08	18.96	4	86	4
FALSE	None	153	221316716	proteasome subunit alpha type-1 isoform 3 [Homo sapiens]	29	3	18	3	1	130	14.6	8.51	Not Found	Not Found	High	High	High	High				80397025	1.3E+08	1.34E+08	1.08E+08	13.73	3	67	3
FALSE	Master Protein	153	23110935	proteasome subunit alpha type-1 isoform 1 [Homo sapiens]	19	4	24	4	1	269	30.2	6.99	High	High	High	High	High	High		85514763	80600104	94466306	1.3E+08	1.34E+08	1.08E+08	18.96	4	86	4
FALSE	Master Protein Candidate	154	515869342	hsc70-interacting protein isoform 2 [Homo sapiens]	4	1	4	1	1	359	40.1	5.3	Not Found	Not Found	Not Found	High	Not Found	High					32144525		37657545	4.84	1	47	1
FALSE	Master Protein	154	19923193	hsc70-interacting protein isoform 1 [Homo sapiens]	4	1	4	1	1	369	41.3	5.27	Not Found	Not Found	Not Found	High	Not Found	High					32144525		37657545	4.84	1	47	1
FALSE	Master Protein	155	189083844	dipeptidyl peptidase 1 isoform a preproprotein [Homo sapiens]	5	2	13	2	1	463	51.8	6.99	High	High	High	High	High	High			49420877	45663542	79529047	66013968	82424313	9.71	2	31	2
FALSE	Master Protein	156	14165439	heterogeneous nuclear ribonucleoprotein K isoform a [Homo sapiens]	19	6	60	6	1	464	51	5.33	High	High	High	High	High	High		74533894	56387531	80751299	1.75E+08	1.79E+08	1.65E+08	91.33	6	711	6
FALSE	Master Protein Candidate	156	530391071	PREDICTED: heterogeneous nuclear ribonucleoprotein K isoform X7 [Homo sapiens]	20	6	60	6	1	439	48.5	5.92	High	High	High	High	High	High		74533894	56387531	80751299	1.75E+08	1.79E+08	1.65E+08	91.33	6	711	6
FALSE	Master Protein Candidate	156	14165435	heterogeneous nuclear ribonucleoprotein K isoform b [Homo sapiens]	19	6	60	6	1	463	50.9	5.54	High	High	High	High	High	High		74533894	56387531	80751299	1.75E+08	1.79E+08	1.65E+08	91.33	6	711	6
FALSE	Master Protein Candidate	156	530391067	PREDICTED: heterogeneous nuclear ribonucleoprotein K isoform X5 [Homo sapiens]	20	6	60	6	1	440	48.5	5.54	High	High	High	High	High	High		74533894	56387531	80751299	1.75E+08	1.79E+08	1.65E+08	91.33	6	711	6
FALSE	Master Protein	157	5031635	cofilin-1 [Homo sapiens]	29	5	50	5	1	166	18.5	8.09	High	High	High	High	High	High		1.05E+08	1.06E+08	1.77E+08	2.09E+08	2.02E+08	2.13E+08	80.45	5	706	5
FALSE	None	157	343887344	cofilin-2 isoform 2 [Homo sapiens]	19	3	36	3	1	149	16.9	8.62	High	High	High	High	High	High		1.39E+08	1.46E+08	1.77E+08	1.97E+08	1.94E+08	2.01E+08	58.28	3	563	3
FALSE	None	157	33946278	cofilin-2 isoform 1 [Homo sapiens]	17	3	36	3	1	166	18.7	7.88	High	High	High	High	High	High		1.39E+08	1.46E+08	1.77E+08	1.97E+08	1.94E+08	2.01E+08	58.28	3	563	3
FALSE	Master Protein	158	4504523	10 kDa heat shock protein, mitochondrial [Homo sapiens]	25	2	14	2	1	102	10.9	8.92	High	High	High	High	High	Not Found		29363899	38700538	32148491	52386957	41884488		13.83	2	47	2
FALSE	None	158	321117267	HSPE1-MOB4 protein [Homo sapiens]	5	1	8	1	1	261	29.7	6.16	High	Not Found	High	High	High	Not Found		22032759		26941636	52386957	41884488		9.22	1	47	1
FALSE	Master Protein	159	530418164	PREDICTED: phospholipid transfer protein isoform X1 [Homo sapiens]	7	3	27	3	1	513	56.6	6.64	High	High	High	High	High	High		26288855	27514455	27518335	83924833	1.26E+08	1.18E+08	44.32	3	202	3
FALSE	Master Protein Candidate	159	33356541	phospholipid transfer protein isoform b precursor [Homo sapiens]	8	3	27	3	1	441	49.2	6.55	High	High	High	High	High	High		26288855	27514455	27518335	83924833	1.26E+08	1.18E+08	44.32	3	202	3
FALSE	None	159	339275810	phospholipid transfer protein isoform d [Homo sapiens]	5	2	24	2	1	405	44.8	8.53	High	High	High	High	High	High		26288855	27514455	27518335	83924833	79204584	78755586	38.89	2	202	2
FALSE	Master Protein Candidate	159	5453914	phospholipid transfer protein isoform a precursor [Homo sapiens]	8	3	27	3	1	493	54.7	7.01	High	High	High	High	High	High		26288855	27514455	27518335	83924833	1.26E+08	1.18E+08	44.32	3	202	3
FALSE	Master Protein Candidate	159	339275807	phospholipid transfer protein isoform c precursor [Homo sapiens]	9	3	27	3	1	398	44.1	6.55	High	High	High	High	High	High		26288855	27514455	27518335	83924833	1.26E+08	1.18E+08	44.32	3	202	3
FALSE	Master Protein Candidate	16	154146191	heat shock protein HSP 90-alpha isoform 2 [Homo sapiens]	11	6	33	3	1	732	84.6	5.02	Not Found	Not Found	Not Found	High	High	High					81439373	96684906	71239499	47.47	6	407	6
FALSE	Master Protein	16	153792590	heat shock protein HSP 90-alpha isoform 1 [Homo sapiens]	10	6	33	3	1	854	98.1	5.16	Not Found	Not Found	Not Found	High	High	High					81439373	96684906	71239499	47.47	6	407	6

FALSE	None	16;143	155722983	heat shock protein 75 kDa, mitochondrial isoform 1 precursor [Homo sapiens]	2	1	4	0	2	704	80.1	8.21	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								5.92	1	86	1
FALSE	None	16;143	440309857	heat shock protein 75 kDa, mitochondrial isoform 2 [Homo sapiens]	2	1	4	0	2	651	74.2	7.87	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								5.92	1	86	1
FALSE	Master Protein	160	4505763	phosphoglycerate kinase 1 [Homo sapiens]	21	7	68	7	1	417	44.6	8.1	High	High	High	High	High	High		1.92E+08	2.15E+08	2.23E+08	3.76E+08	2.9E+08	3.99E+08	80.94	7	631	6
FALSE	None	160	31543397	phosphoglycerate kinase 2 [Homo sapiens]	8	3	24	3	1	417	44.8	8.54	High	High	High	High	High	High		1.24E+08	1.15E+08	1.87E+08	2.18E+08	71181347	2.17E+08	20.47	3	193	3
FALSE	Master Protein Candidate	161	315139006	proteasome subunit beta type-2 isoform 2 [Homo sapiens]	9	1	4	1	1	176	20.2	7.44	Not Found	Not Found	Not Found	High	High	Not Found					37970789	41066618		5.77	1	68	1
FALSE	Master Protein	161	4506195	proteasome subunit beta type-2 isoform 1 [Homo sapiens]	7	1	4	1	1	201	22.8	7.02	Not Found	Not Found	Not Found	High	High	Not Found					37970789	41066618		5.77	1	68	1
FALSE	Master Protein	162	530365268	PREDICTED: protein S100-A13 isoform X2 [Homo sapiens]	12	1	4	1	1	98	11.5	6.16	Not Found	High	Not Found	Not Found	Not Found	High			18631921				92705325	2.49	1	0	1
FALSE	Master Protein Candidate	163	5031839	keratin, type II cytoskeletal 6A [Homo sapiens]	17	8	103	3	1	564	60	8	High	High	High	High	High	High		1.85E+08	2.04E+08	1.47E+08	80368683	70484386	83067911	125.18	8	1033	8
FALSE	Master Protein	163	155969697	keratin, type II cytoskeletal 6C [Homo sapiens]	17	8	103	3	1	564	60	8	High	High	High	High	High	High		1.85E+08	2.04E+08	1.47E+08	80368683	70484386	83067911	125.18	8	1033	8
FALSE	None	163;367	578823708	PREDICTED: keratin, type II cytoskeletal 3 isoform X3 [Homo sapiens]	2	1	37	0	2	580	60.6	6.25	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								38.1	1	344	1
FALSE	None	163;367	153791670	keratin, type II cytoskeletal 2 oral [Homo sapiens]	2	1	37	0	2	638	65.8	8.12	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								38.1	1	344	1
FALSE	None	163;367	578823706	PREDICTED: keratin, type II cytoskeletal 3 isoform X2 [Homo sapiens]	2	1	37	0	2	616	63.4	6.48	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								38.1	1	344	1
FALSE	None	163;367	32567786	keratin, type II cytoskeletal 79 [Homo sapiens]	4	2	43	0	2	535	57.8	7.2	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								45.52	2	387	2
FALSE	None	163;367	109148552	keratin, type II cytoskeletal 3 [Homo sapiens]	2	1	37	0	2	628	64.4	6.48	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								38.1	1	344	1
FALSE	None	163;367	153791158	keratin, type II cytoskeletal 75 [Homo sapiens]	4	2	43	0	2	551	59.5	7.74	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								45.52	2	387	2
FALSE	None	163;367	530400221	PREDICTED: keratin, type II cytoskeletal 3 isoform X1 [Homo sapiens]	2	1	37	0	2	606	62.5	6.06	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								38.1	1	344	1
FALSE	Master Protein Candidate	164	32483377	thioredoxin-dependent peroxide reductase, mitochondrial isoform b [Homo sapiens]	10	2	17	2	1	238	25.8	7.46	High	High	High	High	High	High		20856998	20694936	23915997	35948857	37254157	37917998	13.54	2	51	2
FALSE	Master Protein	164	5802974	thioredoxin-dependent peroxide reductase, mitochondrial isoform a precursor [Homo sapiens]	9	2	17	2	1	256	27.7	7.78	High	High	High	High	High	High		20856998	20694936	23915997	35948857	37254157	37917998	13.54	2	51	2
FALSE	Master Protein	165	567757609	chloride intracellular channel protein 1 [Homo sapiens]	12	2	15	2	1	241	26.9	5.17	High	High	High	High	High	High		59752709	64123413	58086084	1.06E+08	1.14E+08	1.05E+08	19.28	2	107	2
FALSE	Master Protein	166	56676393	rho GDP-dissociation inhibitor 2 [Homo sapiens]	13	2	26	2	1	201	23	5.21	High	High	High	High	High	High		1.32E+08	1.33E+08	1.58E+08	2.34E+08	2.75E+08	2.35E+08	34.28	2	326	2
FALSE	Master Protein Candidate	167	530394330	PREDICTED: vinculin isoform X2 [Homo sapiens]	2	2	11	2	1	1067	116.8	6.16	High	High	High	Not Found	Not Found	Not Found		24501181	23404398	22844948				3.8	2	0	2
FALSE	Master Protein	167	530394328	PREDICTED: vinculin isoform X1 [Homo sapiens]	2	2	11	2	1	1135	123.9	5.71	High	High	High	Not Found	Not Found	Not Found		24501181	23404398	22844948				3.8	2	0	2
FALSE	Master Protein Candidate	167	4507877	vinculin isoform VCL [Homo sapiens]	2	2	11	2	1	1066	116.6	6.09	High	High	High	Not Found	Not Found	Not Found		24501181	23404398	22844948				3.8	2	0	2
FALSE	Master Protein Candidate	167	7669550	vinculin isoform meta-VCL [Homo sapiens]	2	2	11	2	1	1134	123.7	5.66	High	High	High	Not Found	Not Found	Not Found		24501181	23404398	22844948				3.8	2	0	2
FALSE	Master Protein Candidate	168	57013276	tubulin alpha-1B chain [Homo sapiens]	19	7	66	7	1	451	50.1	5.06	High	High	High	High	High	High		54605903	57821521	53522701	2.27E+08	2.21E+08	2.23E+08	80.42	7	312	7
FALSE	None	168	530370916	PREDICTED: tubulin alpha-4A chain isoform X1 [Homo sapiens]	14	4	33	4	1	433	48.3	5.01	High	High	High	High	High	High		46368684	49982665	46688312	1.66E+08	1.67E+08	1.35E+08	37.65	4	179	4
FALSE	None	168	17921993	tubulin alpha-3C/D chain [Homo sapiens]	13	4	33	4	1	450	49.9	5.1	High	High	High	High	High	High		46368684	49982665	46688312	1.66E+08	1.67E+08	1.35E+08	37.65	4	179	4
FALSE	None	168	17921989	tubulin alpha-4A chain isoform 1 [Homo sapiens]	13	4	33	4	1	448	49.9	5.06	High	High	High	High	High	High		46368684	49982665	46688312	1.66E+08	1.67E+08	1.35E+08	37.65	4	179	4
FALSE	Master Protein Candidate	168	14389309	tubulin alpha-1C chain [Homo sapiens]	19	7	66	7	1	449	49.9	5.1	High	High	High	High	High	High		54605903	57821521	53522701	2.27E+08	2.21E+08	2.23E+08	80.42	7	312	7
FALSE	None	168	9507215	tubulin alpha-8 chain isoform 1 [Homo sapiens]	10	3	27	3	1	449	50.1	5.06	High	High	High	High	High	High		46368684	49982665	46688312	1.45E+08	1.43E+08	1.35E+08	30.81	3	179	3
FALSE	None	168	46409270	tubulin alpha-3E chain [Homo sapiens]	13	4	33	4	1	450	49.9	5.1	High	High	High	High	High	High		46368684	49982665	46688312	1.66E+08	1.67E+08	1.35E+08	37.65	4	179	4
FALSE	Master Protein	168	393715091	tubulin alpha-1A chain isoform 1 [Homo sapiens]	19	7	66	7	1	451	50.1	5.06	High	High	High	High	High	High		54605903	57821521	53522701	2.27E+08	2.21E+08	2.23E+08	80.42	7	312	7
FALSE	None	168	301171345	tubulin alpha-8 chain isoform 2 [Homo sapiens]	11	3	27	3	1	383	42.9	5.08	High	High	High	High	High	High		46368684	49982665	46688312	1.45E+08	1.43E+08	1.35E+08	30.81	3	179	3
FALSE	None	168	530357774	PREDICTED: tubulin alpha-3E chain-like [Homo sapiens]	14	1	12	1	1	128	14.3	4.41	High	High	High	High	High	High		51800457	54719444	53339086	1.99E+08	1.8E+08	1.89E+08	21.82	1	124	1
FALSE	Master Protein Candidate	168	393715095	tubulin alpha-1A chain isoform 2 [Homo sapiens]	20	7	66	7	1	416	46.3	5.08	High	High	High	High	High	High		54605903	57821521	53522701	2.27E+08	2.21E+08	2.23E+08	80.42	7	312	7
FALSE	None	169	153791497	rootletin [Homo sapiens]	0	1	4	1	1	2017	228.4	5.5	High	Not Found	High	Not Found	Not Found	Not Found		40908312		64408799				4.64	1	56	1
FALSE	None	169	578800144	PREDICTED: rootletin isoform X4 [Homo sapiens]	0	1	4	1	1	1918	217	5.6	High	Not Found	High	Not Found	Not Found	Not Found		40908312		64408799				4.64	1	56	1
FALSE	None	169	578800140	PREDICTED: rootletin isoform X2 [Homo sapiens]	0	1	4	1	1	1972	223.3	5.62	High	Not Found	High	Not Found	Not Found	Not Found		40908312		64408799				4.64	1	56	1
FALSE	None	169	578800142	PREDICTED: rootletin isoform X3 [Homo sapiens]	0	1	4	1	1	1945	220.7	5.58	High	Not Found	High	Not Found	Not Found	Not Found		40908312		64408799				4.64	1	56	1
FALSE	None	169	578812963	PREDICTED: ezrin isoform X1 [Homo sapiens]	18	9	89	5	1	543	64	6.01	High	High	High	High	High	High		45329245	87328223	57201715	98063198	98909536	1.03E+08	119.36	8	941	9
FALSE	None	169	578800146	PREDICTED: rootletin isoform X5 [Homo sapiens]	0	1	4	1	1	1737	196.6	5.57	High	Not Found	High	Not Found	Not Found	Not Found		40908312		64408799				4.64	1	56	1
FALSE	None	169	578800138	PREDICTED: rootletin isoform X1 [Homo sapiens]	0	1	4	1	1	1979	224.1	5.59	High	Not Found	High	Not Found	Not Found	Not Found		40908312		64408799				4.64	1	56	1
FALSE	Master Protein	169	161702986	ezrin [Homo sapiens]	19	10	101	6	1	586	69.4	6.27	High	High	High	High	High	High		82523904	1.02E+08	90875514	1.9E+08	1.86E+08	1.82E+08	136.45	9	1212	10
FALSE	None	169;284	4506467	radixin isoform 2 [Homo sapiens]	5	4	43	0	2	583	68.5	6.37	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								53.97	4	392	4
FALSE	None	169;284	32451486	merlin isoform 2 [Homo sapiens]	1	1	7	0	2	590	69	6.73	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								3.76	1	56	1
FALSE	None	169;284	386781587	radixin isoform 3 [Homo sapiens]	4	3	36	0	2	447	52.6	6.16	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								50.22	3	370	3
FALSE	None	169;284	386781609	radixin isoform 5 [Homo sapiens]	4	1	7	0	2	200	23.4	8.32	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								3.76	1	56	1
FALSE	None	169;284	32967268	merlin isoform 8 [Homo sapiens]	4	1	7	0	2	165	19.2	7.33	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								3.76	1	56	1
FALSE	None	169;284	32967260	merlin isoform 5 [Homo sapiens]	1	1	7	0	2	548	64	6.21	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								3.76	1	56	1
FALSE	None	169;284	386781571	radixin isoform 1 [Homo sapiens]	4	4	43	0	2	604	71	6.71	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								53.97	4	392	4
FALSE	None	169;284	4557795	merlin isoform 1 [Homo sapiens]	1	1	7	0	2	595	69.6	6.47	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								3.76	1	56	1
FALSE	Master Protein Candidate	17	4501885	actin, cytoplasmic 1 [Homo sapiens]	23	7	70	1	1	375	41.7	5.48	High	High	High	High	High	High		1.2E+08	1.14E+09	1.16E+09	2.71E+09	2.68E+09	3.19E+08	90.12	6	502	7
FALSE	Master Protein	17	578831328	PREDICTED: actin, cytoplasmic 2 isoform X1 [Homo sapiens]	18	7	70	1	1	468	51.2	7.2	High	High	High	High	High	High		1.2E+08	1.14E+09	1.16E+09	2.71E+09	2.68E+09	3.19E+08	90.12	6	502	7
FALSE	Master Protein Candidate	17	316659409	actin, cytoplasmic 2 [Homo sapiens]	23	7	70	1	1	375	41.8	5.48	High	High	High	High	High	High		1.2E+08	1.14E+09	1.16E+09	2.71E+09	2.68E+09	3.19E+08	90.12	6	502	7
FALSE	None	17	578831330	PREDICTED: actin, cytoplasmic 2 isoform X2 [Homo sapiens]	20	4	42	1	1	253	27.5	9.28	High	High	High	High	High	High		1.2E+08	1.14E+09	1.16E+09	2.71E+09	2.68E+09	3.19E+08	56.82	3	369	4
FALSE	None	17;245	578813594	PREDICTED: actin, cytoplasmic 1 isoform X1 [Homo sapiens]	14	3	28	0	2	253	28.2	5.34	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								33.3	3	159	3
FALSE	None	17;245	315570273	actin, gamma-enteric smooth muscle isoform 2 precursor [Homo sapiens]	17	5	38	0	2	333	37.1	5.54	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								39.36	4	272	5
FALSE	None	17;245	578804361	PREDICTED: POTE ankyrin domain family member E isoform X1 [Homo sapiens]	7	4	45	0	2	675	76.6	5.16	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								51.93	3	318	4
FALSE	None	17;245	134133226	POTE ankyrin domain family member E [Homo sapiens]	4	4	45	0	2	1075	121.3	6.2	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								51.93	3	318	4
FALSE	None	17;245	475808427	POTE ankyrin domain family member I [Homo sapiens]	3	3	25	0	2	1075	121.2	6.21	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								26.76	2	213	3
FALSE	None	17;245	459352730	POTE ankyrin domain family member J [Homo sapiens]	2	2	16	0	2	1038	117.3	5.97	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								20.7	1	100	2
FALSE	None	17;245	153791352	POTE ankyrin domain family member F [Homo sapiens]	4	4	45	0	2	1075	121.4	6.2	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								51.93	3	318	4
FALSE	None	170	13676857	heat shock-related 70 kDa protein 2 [Homo sapiens]	10	7	80	4	1	639	70	5.74	High	High	High	High	High	High		74383996	91238071	91160944	3.42E+08	3.66E+08	3.41E+08	95.03	7	508	7
FALSE	None	170	24234686	heat shock cognate 71 kDa protein isoform 2 [Homo sapiens]	34	16	181	13	1	493	53.5	5.86	High	High	High	High	High	High		1.38E+08	1.34E+08	1.34E+08	4.12E+08	4.41E+08	3.99E+08	236.52	16	1245	16
FALSE	Master Protein	170	5729877	heat shock cognate 71 kDa protein isoform 1 [Homo sapiens]	28	17	193	14	1	646	70.9	5.52	High	High	High	High	High	High		1.38E+08	1.34E+08	1.34E+08	4.12E+08	4.41E+08	3.99E+08	252.04	17	1402	17
FALSE	Master Protein Candidate	171	47607492	plectin isoform 1c [Homo sapiens]	4	12	67	12	1	4574	518.2	5.74	High	High	High	High	High	High		29045259	33868156	33274448	68114722	73779847	66817843	84.73	12	449	11
FALSE	Master Protein Candidate	171	41322912	plectin isoform 1f [Homo sapiens]	4	12	67	12	1	4533	514.5	5.73	High	High	High	High	High	High		29045259	33868156	33274448	68114722	73779847	66817843	84.73	12	449	11
FALSE	Master Protein Candidate	171	41322919	plectin isoform 1b [Homo sapiens]	4	12	67	12	1	4547	516	5.78	High	High	High	High	High	High		29045259	33868156	33274448	68114722	73779847	66817843	84.73	12	449	11
FALSE	Master Protein Candidate	171	41322908	plectin isoform 1e [Homo sapiens]	4	12	67	12	1	4525	513.4	5.76	High	High	High	High	High	High		29045259	33868156	33274448	68114722	73779847	66817843	84.73	12	449	11
FALSE	Master Protein Candidate	171	578816049	PREDICTED: plectin isoform X11 [Homo sapiens]	4	12	67	12	1	4529	514.1	5.74	High	High	High	High	High	High		29045259	33868156	33274448	68114722	73779847	66817843	84.73	12	449	11
FALSE	Master Protein Candidate	171	41322923	plectin isoform 1a [Homo sapiens]	4	12	67	12	1	4547	515.9	5.8	High	High	High	High	High	High		29045259	33868156	33274448	68114722	73779847	66817843	84.73	12	449	11
FALSE	Master Protein Candidate	171	41322916	plectin isoform 1 [Homo sapiens]	4	12	67	12	1	4684	531.5	5.96	High	High	High	High	High	High		29045259	33868156	33274448	68114722	73779847	66817843	84.73	12	449	11
FALSE	Master Protein Candidate	171	530389147	PREDICTED: plectin isoform X3 [Homo sapiens]	4	12	67	12	1	4556	516.8	5.77	High	High	High	High	High	High		29045259	33868156	33274448	68114722	73779847	66817843	84.73	12	449	11
FALSE	Master Protein Candidate	171	530389151	PREDICTED: plectin isoform X5 [Homo sapiens]	4	12	67	12	1	4552	516.6	5.81	High	High	High	High	High	High		29045259	33868156	33274448	68114722	73779847	66817843	84.73	12	449	11
FALSE	Master Protein Candidate	171	578816045	PREDICTED: plectin isoform X10 [Homo sapiens]	4	12	67	12	1	4579	518.8	5.76	High	High	High	High	High	High		29045259	33868156	33274448	68114722	73779847	66817843	84.73	12	449	11
FALSE	None	171	578816054	PREDICTED: plectin isoform X13 [Homo sapiens]	3	8	45	8	1	3562	401.8	6.37	High	High	High	High	High	High		28426525	33333856	34031466	63523864	68329592	66817843	58.54	8	375	7
FALSE	Master Protein Candidate	171	578816051	PREDICTED: plectin isoform X12 [Homo sapiens]	4	12	67	12	1	4529	513.8	5.77	High	High	High	High	High	High		29045259	33868156	33274448	68114722	73779847	66817843	84.73	12	449	11
FALSE	Master Protein Candidate	171	530389159	PREDICTED: plectin isoform X9 [Homo sapiens]	4	12	67	12	1	4520	513	5.78	High	High	High	High	High	High		29045259	33868156	33274448	68114722	73779847	66817843	84.73	12	449	11
FALSE	Master Protein Candidate	171	530389153	PREDICTED: plectin isoform X6 [Homo sapiens]	4	12	67	12	1	4538	515.1	5.73	High	High	High	High	High	High		29045259	33868156	33274448	68114722	73779847	66817843	84.73	12	449	11
FALSE	Master Protein Candidate	171	530389145	PREDICTED: plectin isoform X2 [Homo sapiens]	4	12	67	12	1	4685	531.7	5.96	High	High	High	High	High	High		29045259	33868156	33274448	68114722	73779847	66817843	84.73	12	449	11
FALSE	Master Protein	171	530389143	PREDICTED: plectin isoform X1 [Homo sapiens]	4	12	67	12	1	4689	532.1	5.97	High	High	High	High	High	High		29045259	33868156	33274448	68114722	73779847	66817843	84.73	12	449	11
FALSE	Master Protein Candidate	171	41322910	plectin isoform 1d [Homo sapiens]	4	12	67	12	1	4515	512.3	5.77	High	High	High	High	High	High		29045259	33868156	33274448	68114722	73779847	66817843	84.73	12	449	11
FALSE	Master Protein Candidate	171	530389157	PREDICTED: plectin isoform X8 [Homo sapiens]	4	12	67	12	1	4524	513.4	5.73	High	High	High	High	High	High		29045259	33868156	33274448	68114722	73779847	66817843	84.73	12	449	11
FALSE	Master Protein Candidate	171	41322914	plectin isoform 1g [Homo sapiens]	4	12	67	12	1	4551	516.2	5.76	High	High	High	High	High	High		29045259	33868156	33274448	68114722	73779847	66817843	84.73	12	449	11
FALSE	Master Protein Candidate	171	530389155	PREDICTED: plectin isoform X7 [Homo sapiens]	4	12	67	12	1	4530	514.1	5.77	High	High	High	High	High	High		29045259	33868156	33274448	68114722	73779847	66817843	84.73	12	449	11
FALSE	Master Protein Candidate	171	530389149	PREDICTED: plectin isoform X4 [Homo sapiens]	4	12	67	12	1	4552	516.6	5.8	High	High	High	High	High	High		29045259	33868156	33274448	68114722	73779847	66817843	84.73	12	449	11
FALSE	Master Protein	173	530405491	PREDICTED: deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial isoform X1 [Homo sapiens]	5	1	12	1	1	263	28.2	9.89	High	High	High	High	High	High		24587854	25872518	23168213	82872462	74139978	85168381	17.67	1	190	1
FALSE	Master Protein Candidate	173	70906441	deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial isoform 1 precursor [Homo sapiens]	5	1	12	1	1	252	26.5	9.36	High	High	High	High	High	High		24587854	25872518	23168213	82872462	74139978	85168381	17.67	1	190	1
FALSE	Master Protein Candidate	173	4503423	deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial isoform 2 [Homo sapiens]	7	1	12	1	1	164	17.7	6.57	High	High	High	High	High	High		24587854	25872518	23168213	82872462	74139978	85168381	17.67	1	190	1
FALSE	Master Protein Candidate	173	70906444	deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial isoform 3 [Homo sapiens]	9	1	12	1	1	141	15.4	6.57	High	High	High	High	High	High		24587854	25872518	23168213	82872462	74139978	85168381	17.67	1	190	1
FALSE	Master Protein	174	4504151	granulins precursor [Homo sapiens]	3	2	14	2	1	593	63.5	6.83	High	High	Not Found	High	High	High		1.01E+08	1.07E+08		2.42E+08	2.24E+08	2.51E+08	4.46	2	24	2
FALSE	Master Protein Candidate	175	359338991	heterogeneous nuclear ribonucleoprotein Q isoform 7 [Homo sapiens]	5	2	19	1	1	410	46.3	8.88	Not Found	High	Not Found	High	High	High			17426001		51432259	52765378	49635538	22.81	2	149	2
FALSE	Master Protein Candidate	175	228008398	heterogeneous nuclear ribonucleoprotein Q isoform 3 [Homo sapiens]	4	2	19	1	1	527	58.7	7.56	Not Found	High	Not Found	High	High	High			17426001		51432259	52765378	49635538	22.81	2	149	2
FALSE	Master Protein	175	228008291	heterogeneous nuclear ribonucleoprotein Q isoform 1 [Homo sapiens]	3	2	19	1	1	623	69.6	8.59	Not Found	High	Not Found	High	High	High			17426001		51432259	52765378	49635538	22.81	2	149	2
FALSE	Master Protein Candidate	175	228008400	heterogeneous nuclear ribonucleoprotein Q isoform 6 [Homo sapiens]	4	2	19	1	1	562	62.6	7.56	Not Found	High	Not Found	High	High	High			17426001		51432259	52765378	49635538	22.81	2	149	2
FALSE	Master Protein Candidate	175	228008396	heterogeneous nuclear ribonucleoprotein Q isoform 2 [Homo sapiens]	5	2	19	1	1	464	52	9.16	Not Found	High	Not Found	High	High	High			17426001		51432259	52765378	49635538	22.81	2	149	2
FALSE	Master Protein Candidate	175	530382968	PREDICTED: heterogeneous nuclear ribonucleoprotein Q isoform X1 [Homo sapiens]	4	2	19	1	1	561	62.5	7.56	Not Found	High	Not Found	High	High	High			17426001		51432259	52765378	49635538	22.81	2	149	2
FALSE	Master Protein Candidate	175	228008295	heterogeneous nuclear ribonucleoprotein Q isoform 4 [Homo sapiens]	4	2	19	1	1	588	65.6	8.6	Not Found	High	Not Found	High	High	High			17426001		51432259	52765378	49635538	22.81	2	149	2
FALSE	Master Protein Candidate	175	530382970	PREDICTED: heterogeneous nuclear ribonucleoprotein Q isoform X2 [Homo sapiens]	4	2	19	1	1	525	59	9.36	Not Found	High	Not Found	High	High	High			17426001		51432259	52765378	49635538	22.81	2	149	2
FALSE	Master Protein	176	4504067	aspartate aminotransferase, cytoplasmic [Homo sapiens]	3	1	8	1	1	413	46.2	7.01	Not Found	Not Found	High	High	High	High				10083481		17572909	22378986	9.15	1	74	1
FALSE	Master Protein	177	4505621	phosphatidylethanolamine-binding protein 1 preproprotein [Homo sapiens]	33	4	32	4	1	187	21	7.53	High	High	High	High	High	High		56747844	56788362	62422163	1.54E+08	1.25E+08	1.22E+08	54.93	4	723	3
FALSE	Master Protein	178	50845388	annexin A2 isoform 1 [Homo sapiens]	40	14	222	14	1	357	40.4	8.37	High	High	High	High	High	High		5.91E+08	6.53E+08	6.66E+08	1.08E+09	1.05E+09	1.12E+09	287.9	14	2063	14
FALSE	Master Protein Candidate	178	209862831	annexin A2 isoform 2 [Homo sapiens]	42	14	222	14	1	339	38.6	7.75	High	High	High	High	High	High		5.91E+08	6.53E+08	6.66E+08	1.08E+09	1.05E+09	1.12E+09	287.9	14	2063	14
FALSE	Master Protein	179	4503471	elongation factor 1-alpha 1 [Homo sapiens]	13	5	71	5	1	462	50.1	9.01	High	High	High	High	High	High		1.99E+08	1.98E+08	1.97E+08	1.99E+08	2.05E+08	1.98E+08	84.9	5	415	5
FALSE	None	179	4503475	elongation factor 1-alpha 2 [Homo sapiens]	10	4	47	4	1	463	50.4	9.03	High	High	High	High	High	High		2.3E+08	2.18E+08	1.67E+08	91871521	86843233	90508901	53.33	4	154	4
FALSE	Master Protein	18	10835159	plasminogen activator inhibitor 1 precursor [Homo sapiens]	8	3	10	3	1	402	45	7.2	Not Found	High	High	High	High	High			44927881	23813611	22262778	59984147	24323787	7.47	2	48	3
FALSE	Master Protein Candidate	180	4501891	alpha-actinin-1 isoform b [Homo sapiens]	14	10	86	2	1	892	103	5.41	Not Found	High	Not Found	High	High	High			8061562		36547713	52384289	51760470	96.26	10	797	10
FALSE	Master Protein	180	194097350	alpha-actinin-1 isoform a [Homo sapiens]	13	10	86	2	1	914	105.5	5.41	Not Found	High	Not Found	High	High	High			8061562		36547713	52384289	51760470	96.26	10	797	10
FALSE	Master Protein Candidate	180	194097352	alpha-actinin-1 isoform c [Homo sapiens]	14	10	86	2	1	887	102.6	5.5	Not Found	High	Not Found	High	High	High			8061562		36547713	52384289	51760470	96.26	10	797	10
FALSE	None	180;248	4501893	alpha-actinin-2 isoform 1 [Homo sapiens]	7	5	44	0	2	894	103.8	5.45	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								46.36	5	312	5
FALSE	None	180;248	385648244	alpha-actinin-3 isoform 2 [Homo sapiens]	3	2	18	0	2	944	107.6	6.46	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								27.61	2	299	2
FALSE	None	180;248	4557241	alpha-actinin-3 isoform 1 [Homo sapiens]	4	3	23	0	2	901	103.2	5.57	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								31.63	3	299	3
FALSE	None	180;248	507588248	alpha-actinin-2 isoform 2 [Homo sapiens]	7	5	44	0	2	894	103.9	5.52	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								46.36	5	312	5

FALSE	None	180;248	507588250	alpha-actinin-2 isoform 3 [Homo sapiens]	4	2	21	0	2	686	79.6	5.57	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								14.73	2	42	2
FALSE	Master Protein	181	131412225	keratin, type I cytoskeletal 13 isoform a [Homo sapiens]	9	4	72	2	1	458	49.5	4.96	Not Found	Not Found	Not Found	Not Found	High	High							26933823	83.55	4	109	4
FALSE	Master Protein Candidate	181	131412228	keratin, type I cytoskeletal 13 isoform b [Homo sapiens]	9	4	72	2	1	420	45.8	4.88	Not Found	Not Found	Not Found	Not Found	High	High							26933823	83.55	4	109	4
FALSE	None	181	153945736	keratin, type I cytoskeletal 27 [Homo sapiens]	3	2	4	2	1	459	49.8	5.05	Not Found	Not Found	Not Found	Not Found	High	High							26933823	1.64	2	35	2
FALSE	None	181	192807292	keratin, type I cytoskeletal 24 [Homo sapiens]	2	1	2	1	1	525	55.1	4.96	Not Found	Not Found	Not Found	Not Found	High	Not Found								1.64	1	25	1
FALSE	None	181	195972866	keratin, type I cytoskeletal 10 [Homo sapiens]	2	2	4	2	1	584	58.8	5.21	Not Found	Not Found	Not Found	Not Found	High	High							26933823	1.64	2	35	2
FALSE	None	181	578830527	PREDICTED: keratin, type I cytoskeletal 24 isoform X1 [Homo sapiens]	3	1	2	1	1	427	46.1	4.91	Not Found	Not Found	Not Found	Not Found	High	Not Found								1.64	1	25	1
FALSE	None	181	530412176	PREDICTED: keratin, type I cytoskeletal 10 isoform X1 [Homo sapiens]	2	2	4	2	1	624	63.3	5.26	Not Found	Not Found	Not Found	Not Found	High	High							26933823	1.64	2	35	2
FALSE	Master Protein	182	217330646	activated RNA polymerase II transcriptional coactivator p15 [Homo sapiens]	19	2	14	2	1	127	14.4	9.6	High	High	High	High	High	High		1.73E+08	1.51E+08	1.74E+08	3.23E+08	3.32E+08	3.15E+08	19.04	2	138	2
FALSE	Master Protein	183	4504483	hypoxanthine-guanine phosphoribosyltransferase [Homo sapiens]	16	3	10	3	1	218	24.6	6.68	Not Found	Not Found	High	High	High	High				19669555	26274364	22515820	40828735	12.78	3	115	3
FALSE	Master Protein	184	34147513	ras-related protein Rab-7a [Homo sapiens]	18	3	16	3	1	207	23.5	6.7	Not Found	High	High	High	High	High				16342176	88827149	66986535	92300248	19.65	3	171	3
FALSE	None	185	555943820	translationally-controlled tumor protein isoform 3 [Homo sapiens]	9	1	4	1	1	138	15.6	5.07	High	Not Found	High	Not Found	Not Found	Not Found		24941930		26623167				4.4	1	0	1
FALSE	Master Protein Candidate	185	4507669	translationally-controlled tumor protein isoform 2 [Homo sapiens]	16	2	16	2	1	172	19.6	4.93	High	High	High	High	High	High		37048359	49973331	40588710	1.16E+08	1.2E+08	1E+08	27.16	2	243	2
FALSE	None	185	254553403	TPT1-like protein [Homo sapiens]	9	1	4	1	1	140	15.8	6.19	High	Not Found	High	Not Found	Not Found	Not Found		24941930		26623167				4.4	1	0	1
FALSE	Master Protein	185	555943903	translationally-controlled tumor protein isoform 1 [Homo sapiens]	14	2	16	2	1	197	22.6	5.24	High	High	High	High	High	High		37048359	49973331	40588710	1.16E+08	1.2E+08	1E+08	27.16	2	243	2
FALSE	Master Protein	187	10834982	insulin-like growth factor-binding protein 5 precursor [Homo sapiens]	5	1	11	1	1	272	30.6	8.21	High	High	High	High	High	High		70020012	85384818		1.03E+08	81157124	1.74E+08	4.46	1	25	1
FALSE	Master Protein Candidate	188	170763500	protein SET isoform 1 [Homo sapiens]	8	2	25	2	1	290	33.5	4.32	High	High	High	High	High	High		3.06E+08	3.15E+08	3.08E+08	7.11E+08	7.08E+08	7.19E+08	37.22	2	188	2
FALSE	Master Protein Candidate	188	351721324	protein SET isoform 4 [Homo sapiens]	9	2	25	2	1	266	31.1	4.23	High	High	High	High	High	High		3.06E+08	3.15E+08	3.08E+08	7.11E+08	7.08E+08	7.19E+08	37.22	2	188	2
FALSE	Master Protein	188	567757558	SET-like protein [Homo sapiens]	8	2	25	2	1	302	34.9	4.31	High	High	High	High	High	High		3.06E+08	3.15E+08	3.08E+08	7.11E+08	7.08E+08	7.19E+08	37.22	2	188	2
FALSE	Master Protein Candidate	188	170763498	protein SET isoform 2 [Homo sapiens]	9	2	25	2	1	277	32.1	4.22	High	High	High	High	High	High		3.06E+08	3.15E+08	3.08E+08	7.11E+08	7.08E+08	7.19E+08	37.22	2	188	2
FALSE	Master Protein Candidate	188	351721296	protein SET isoform 3 [Homo sapiens]	9	2	25	2	1	268	31.3	4.21	High	High	High	High	High	High		3.06E+08	3.15E+08	3.08E+08	7.11E+08	7.08E+08	7.19E+08	37.22	2	188	2
FALSE	Master Protein	189	236460050	chymotrypsin-like elastase family member 3A preproprotein [Homo sapiens]	6	1	2	1	1	270	29.5	6.9	Not Found	High	Not Found	Not Found	Not Found	Not Found								1.7	1	0	1
FALSE	Master Protein Candidate	189	6679625	chymotrypsin-like elastase family member 3B preproprotein [Homo sapiens]	6	1	2	1	1	270	29.2	6.28	Not Found	High	Not Found	Not Found	Not Found	Not Found								1.7	1	0	1
FALSE	Master Protein Candidate	19	324711034	tubulointerstitial nephritis antigen-like isoform 2 precursor [Homo sapiens]	12	4	47	4	1	436	48.8	7.33	High	High	High	High	High	High		94802109	97395876	95997975	1.49E+08	1.49E+08	1.53E+08	62.77	4	604	4
FALSE	None	19	530363130	PREDICTED: tubulointerstitial nephritis antigen-like isoform X1 [Homo sapiens]	2	1	12	1	1	440	48.4	7.43	High	High	High	High	High	High		66748370	68263281	63953951	1.13E+08	1.23E+08	1.24E+08	15.88	1	102	1
FALSE	Master Protein	19	11545918	tubulointerstitial nephritis antigen-like isoform 1 precursor [Homo sapiens]	11	4	47	4	1	467	52.4	6.99	High	High	High	High	High	High		94802109	97395876	95997975	1.49E+08	1.49E+08	1.53E+08	62.77	4	604	4
FALSE	Master Protein Candidate	19	530363132	PREDICTED: tubulointerstitial nephritis antigen-like isoform X2 [Homo sapiens]	15	4	47	4	1	362	40.8	6.96	High	High	High	High	High	High		94802109	97395876	95997975	1.49E+08	1.49E+08	1.53E+08	62.77	4	604	4
FALSE	Master Protein Candidate	190	578825597	PREDICTED: nidogen-2 isoform X4 [Homo sapiens]	1	1	2	1	1	1386	152.6	5.29	High	High	Not Found	Not Found	Not Found	Not Found								2.18	1	0	1
FALSE	Master Protein Candidate	190	144953895	nidogen-2 precursor [Homo sapiens]	1	1	2	1	1	1375	151.2	5.29	High	High	Not Found	Not Found	Not Found	Not Found								2.18	1	0	1
FALSE	Master Protein Candidate	190	530403250	PREDICTED: nidogen-2 isoform X2 [Homo sapiens]	1	1	2	1	1	1354	149.5	5.24	High	High	Not Found	Not Found	Not Found	Not Found								2.18	1	0	1
FALSE	Master Protein	190	530403248	PREDICTED: nidogen-2 isoform X1 [Homo sapiens]	1	1	2	1	1	1402	154.2	5.26	High	High	Not Found	Not Found	Not Found	Not Found								2.18	1	0	1
FALSE	Master Protein Candidate	190	530403252	PREDICTED: nidogen-2 isoform X3 [Homo sapiens]	1	1	2	1	1	1327	146.4	5.26	High	High	Not Found	Not Found	Not Found	Not Found								2.18	1	0	1
FALSE	Master Protein Candidate	191	262527235	lysosomal protective protein isoform c precursor [Homo sapiens]	3	1	7	1	1	481	54.2	6.98	High	High	Not Found	High	High	Not Found		11160601	12523413		27446242	28417628		8.79	1	91	1
FALSE	Master Protein Candidate	191	189163485	lysosomal protective protein isoform b precursor [Homo sapiens]	3	1	7	1	1	480	54.4	6.61	High	High	Not Found	High	High	Not Found		11160601	12523413		27446242	28417628		8.79	1	91	1
FALSE	Master Protein	191	119395729	lysosomal protective protein isoform a precursor [Homo sapiens]	3	1	7	1	1	498	56.2	6.61	High	High	Not Found	High	High	Not Found		11160601	12523413		27446242	28417628		8.79	1	91	1
FALSE	Master Protein Candidate	192	4557305	fructose-bisphosphate aldolase A isoform 1 [Homo sapiens]	28	7	62	7	1	364	39.4	8.09	High	High	High	High	High	High		3.28E+08	2.05E+08	2.72E+08	2.2E+08	1.78E+08	2.5E+08	91.21	7	743	7
FALSE	Master Protein	192	342187211	fructose-bisphosphate aldolase A isoform 2 [Homo sapiens]	24	7	62	7	1	418	45.2	8.25	High	High	High	High	High	High		3.28E+08	2.05E+08	2.72E+08	2.2E+08	1.78E+08	2.5E+08	91.21	7	743	7
FALSE	Master Protein	193	4826734	RNA-binding protein FUS isoform 1 [Homo sapiens]	5	2	20	2	1	526	53.4	9.36	High	High	High	High	High	High		51635528	45127824	53452275	1.24E+08	1.22E+08	1.2E+08	24.53	2	135	2
FALSE	Master Protein Candidate	193	283135201	RNA-binding protein FUS isoform 2 [Homo sapiens]	5	2	20	2	1	525	53.3	9.36	High	High	High	High	High	High		51635528	45127824	53452275	1.24E+08	1.22E+08	1.2E+08	24.53	2	135	2
FALSE	None	193	21327701	TATA-binding protein-associated factor 2N isoform 1 [Homo sapiens]	2	1	6	1	1	592	61.8	8.02	High	High	High	Not Found	Not Found	Not Found		51635528	45127824	45112202				6.72	1	44	1
FALSE	Master Protein Candidate	193	283135173	RNA-binding protein FUS isoform 3 [Homo sapiens]	5	2	20	2	1	522	53.2	9.36	High	High	High	High	High	High		51635528	45127824	53452275	1.24E+08	1.22E+08	1.2E+08	24.53	2	135	2
FALSE	Master Protein Candidate	193	530407875	PREDICTED: RNA-binding protein FUS isoform X3 [Homo sapiens]	8	2	20	2	1	321	33.2	9.17	High	High	High	High	High	High		51635528	45127824	53452275	1.24E+08	1.22E+08	1.2E+08	24.53	2	135	2
FALSE	None	193	4507353	TATA-binding protein-associated factor 2N isoform 2 [Homo sapiens]	2	1	6	1	1	589	61.5	8.02	High	High	High	Not Found	Not Found	Not Found		51635528	45127824	45112202				6.72	1	44	1
FALSE	Master Protein	194	212549553	interleukin enhancer-binding factor 3 isoform d [Homo sapiens]	5	4	25	4	1	898	95.7	8.81	High	High	High	High	High	High		15582308	21069847	22740860	53430494	54729403	59677396	25.73	4	98	4
FALSE	Master Protein Candidate	194	24234756	interleukin enhancer-binding factor 3 isoform c [Homo sapiens]	6	4	25	4	1	690	74.6	8.24	High	High	High	High	High	High		15582308	21069847	22740860	53430494	54729403	59677396	25.73	4	98	4
FALSE	Master Protein Candidate	194	24234753	interleukin enhancer-binding factor 3 isoform b [Homo sapiens]	6	4	25	4	1	702	76	7.75	High	High	High	High	High	High		15582308	21069847	22740860	53430494	54729403	59677396	25.73	4	98	4
FALSE	Master Protein Candidate	194	24234750	interleukin enhancer-binding factor 3 isoform a [Homo sapiens]	5	4	25	4	1	894	95.3	8.76	High	High	High	High	High	High		15582308	21069847	22740860	53430494	54729403	59677396	25.73	4	98	4
FALSE	Master Protein Candidate	194	212549555	interleukin enhancer-binding factor 3 isoform e [Homo sapiens]	6	4	25	4	1	706	76.5	7.91	High	High	High	High	High	High		15582308	21069847	22740860	53430494	54729403	59677396	25.73	4	98	4
FALSE	None	194	530414822	PREDICTED: interleukin enhancer-binding factor 3 isoform X2 [Homo sapiens]	5	3	17	3	1	633	66.3	9.39	Not Found	High	High	High	High	High			21069847	22740860	57608954	58769171	59677396	18.32	3	81	3
FALSE	Master Protein Candidate	194	578833231	PREDICTED: interleukin enhancer-binding factor 3 isoform X3 [Homo sapiens]	5	4	25	4	1	855	91.9	8.78	High	High	High	High	High	High		15582308	21069847	22740860	53430494	54729403	59677396	25.73	4	98	4
FALSE	Master Protein Candidate	195	578846900	PREDICTED: histone H2B type F-S-like [Homo sapiens]	12	1	14	1	1	126	13.9	10.32	High	High	High	High	High	High		20858879	20860618	23203356	36487927	34070348	40442514	26.09	1	348	1
FALSE	Master Protein Candidate	195	66912162	histone H2B type 2-F isoform a [Homo sapiens]	12	1	14	1	1	126	13.9	10.32	High	High	High	High	High	High		20858879	20860618	23203356	36487927	34070348	40442514	26.09	1	348	1
FALSE	Master Protein Candidate	195	578800968	PREDICTED: histone H2B type 2-F isoform X2 [Homo sapiens]	12	1	14	1	1	128	14.2	10.29	High	High	High	High	High	High		20858879	20860618	23203356	36487927	34070348	40442514	26.09	1	348	1
FALSE	Master Protein Candidate	195	20336754	histone H2B type 1-J [Homo sapiens]	12	1	14	1	1	126	13.9	10.32	High	High	High	High	High	High		20858879	20860618	23203356	36487927	34070348	40442514	26.09	1	348	1
FALSE	Master Protein Candidate	195	28173554	histone H2B type 3-B [Homo sapiens]	12	1	14	1	1	126	13.9	10.32	High	High	High	High	High	High		20858879	20860618	23203356	36487927	34070348	40442514	26.09	1	348	1
FALSE	Master Protein Candidate	195	4504261	histone H2B type 1-N [Homo sapiens]	12	1	14	1	1	126	13.9	10.32	High	High	High	High	High	High		20858879	20860618	23203356	36487927	34070348	40442514	26.09	1	348	1
FALSE	Master Protein Candidate	195	18105048	histone H2B type 1-K [Homo sapiens]	12	1	14	1	1	126	13.9	10.32	High	High	High	High	High	High		20858879	20860618	23203356	36487927	34070348	40442514	26.09	1	348	1
FALSE	Master Protein Candidate	195	4504263	histone H2B type 1-M [Homo sapiens]	12	1	14	1	1	126	14	10.32	High	High	High	High	High	High		20858879	20860618	23203356	36487927	34070348	40442514	26.09	1	348	1
FALSE	Master Protein Candidate	195	4504259	histone H2B type 1-L [Homo sapiens]	12	1	14	1	1	126	13.9	10.32	High	High	High	High	High	High		20858879	20860618	23203356	36487927	34070348	40442514	26.09	1	348	1
FALSE	Master Protein	195	530381854	PREDICTED: histone H2B type 1-D isoform X1 [Homo sapiens]	10	1	14	1	1	150	16.3	10.32	High	High	High	High	High	High		20858879	20860618	23203356	36487927	34070348	40442514	26.09	1	348	1
FALSE	Master Protein Candidate	195	20336752	histone H2B type 1-D [Homo sapiens]	12	1	14	1	1	126	13.9	10.32	High	High	High	High	High	High		20858879	20860618	23203356	36487927	34070348	40442514	26.09	1	348	1
FALSE	Master Protein Candidate	195	4504277	histone H2B type 2-E [Homo sapiens]	12	1	14	1	1	126	13.9	10.32	High	High	High	High	High	High		20858879	20860618	23203356	36487927	34070348	40442514	26.09	1	348	1
FALSE	Master Protein Candidate	195	16306566	histone H2B type 1-O [Homo sapiens]	12	1	14	1	1	126	13.9	10.32	High	High	High	High	High	High		20858879	20860618	23203356	36487927	34070348	40442514	26.09	1	348	1
FALSE	Master Protein Candidate	195	21166389	histone H2B type 1-C/E/F/G/I [Homo sapiens]	12	1	14	1	1	126	13.9	10.32	High	High	High	High	High	High		20858879	20860618	23203356	36487927	34070348	40442514	26.09	1	348	1
FALSE	Master Protein Candidate	195	238624110	histone H2B type 2-F isoform b [Homo sapiens]	11	1	14	1	1	134	14.8	10.35	High	High	High	High	High	High		20858879	20860618	23203356	36487927	34070348	40442514	26.09	1	348	1
FALSE	Master Protein Candidate	195	578836330	PREDICTED: histone H2B type F-S-like [Homo sapiens]	12	1	14	1	1	126	13.9	10.37	High	High	High	High	High	High		20858879	20860618	23203356	36487927	34070348	40442514	26.09	1	348	1
FALSE	Master Protein Candidate	195	10800140	histone H2B type 1-B [Homo sapiens]	12	1	14	1	1	126	13.9	10.32	High	High	High	High	High	High		20858879	20860618	23203356	36487927	34070348	40442514	26.09	1	348	1
FALSE	Master Protein Candidate	195	4504269	histone H2B type 1-H [Homo sapiens]	12	1	14	1	1	126	13.9	10.32	High	High	High	High	High	High		20858879	20860618	23203356	36487927	34070348	40442514	26.09	1	348	1
FALSE	Master Protein Candidate	195	578800966	PREDICTED: histone H2B type 2-F isoform X1 [Homo sapiens]	10	1	14	1	1	147	16.1	9.96	High	High	High	High	High	High		20858879	20860618	23203356	36487927	34070348	40442514	26.09	1	348	1
FALSE	None	196	383792150	lamin isoform D [Homo sapiens]	29	16	182	16	1	574	63.9	6.74	High	High	High	High	High	High		2.47E+08	2.08E+08	2.2E+08	6.1E+08	4.39E+08	6.02E+08	239.04	16	2119	16
FALSE	None	196	544063464	lamin isoform E [Homo sapiens]	31	15	168	15	1	491	55.7	7.02	High	High	High	High	High	High		2.47E+08	2.08E+08	2.2E+08	6.1E+08	4.36E+08	6.02E+08	214.82	15	1683	15
FALSE	Master Protein	196	27436946	lamin isoform A [Homo sapiens]	29	18	202	18	1	664	74.1	7.02	High	High	High	High	High	High		2.47E+08	2.08E+08	2.2E+08	6.1E+08	4.39E+08	6.02E+08	264.34	18	2270	18
FALSE	None	196	544063466	lamin isoform C [Homo sapiens]	31	17	188	17	1	572	65.1	6.84	High	High	High	High	High	High		2.47E+08	2.08E+08	2.2E+08	6.1E+08	4.36E+08	6.02E+08	240.12	17	1834	17
FALSE	None	196	544063468	lamin isoform A-delta50 [Homo sapiens]	29	17	188	17	1	614	69.2	6.64	High	High	High	High	High	High		2.47E+08	2.08E+08	2.2E+08	6.1E+08	4.36E+08	6.02E+08	240.12	17	1834	17
FALSE	None	196	27436948	lamin isoform A-delta10 [Homo sapiens]	28	17	192	17	1	634	70.6	8.4	High	High	High	High	High	High		2.47E+08	2.06E+08	2.2E+08	6.1E+08	3.86E+08	6.02E+08	252.33	17	2182	17
FALSE	Master Protein	197	23110944	proteasome subunit alpha type-6 isoform a [Homo sapiens]	9	2	9	2	1	246	27.4	6.76	High	High	High	Not Found	Not Found	Not Found		41926349	29113866	48815369				8.69	2	44	2
FALSE	None	197	532691774	proteasome subunit alpha type-6 isoform c [Homo sapiens]	6	1	4	1	1	227	25.3	7.11	High	Not Found	High	Not Found	Not Found	Not Found		55466784		58414953				4.88	1	44	1
FALSE	Master Protein	198	7669492	glyceraldehyde-3-phosphate dehydrogenase isoform 1 [Homo sapiens]	34	12	140	12	1	335	36	8.46	High	High	High	High	High	High		3.14E+08	3.2E+08	8.68E+08	1.93E+09	1.96E+09	1.86E+09	172.08	10	1994	12
FALSE	None	198	378404908	glyceraldehyde-3-phosphate dehydrogenase isoform 2 [Homo sapiens]	35	11	139	11	1	293	31.5	7.61	High	High	High	High	High	High		3.14E+08	3.2E+08	8.68E+08	1.93E+09	1.96E+09	1.86E+09	172.08	10	1994	11
FALSE	Master Protein	199	21464101	14-3-3 protein gamma [Homo sapiens]	13	3	22	1	1	247	28.3	4.89	High	High	High	Not Found	Not Found	Not Found		77733356	91253226	81772100				22.13	3	192	3
FALSE	Master Protein	2	21956645	myotrophin [Homo sapiens]	25	2	20	2	1	118	12.9	5.52	High	High	High	High	High	High		65006201	64884363	1.05E+08	1.31E+08	1.27E+08	1.29E+08	29.93	2	315	2
FALSE	Master Protein	20	16933546	60S acidic ribosomal protein P0 [Homo sapiens]	3	1	10	1	1	317	34.3	5.97	Not Found	High	High	High	High	High			19344492	20007048	62630846	72754903	61484767	13.67	1	115	1
FALSE	Master Protein	200	294997292	dystroglycan preproprotein [Homo sapiens]	3	2	16	2	1	895	97.5	8.56	High	High	High	High	High	High		99551254	1.09E+08	1.01E+08	1.4E+08	1.29E+08	2.27E+08	21.07	2	210	2
FALSE	Master Protein	201	16507237	78 kDa glucose-regulated protein precursor [Homo sapiens]	30	15	166	13	1	654	72.3	5.16	High	High	High	High	High	High		1.51E+08	1.43E+08	1.59E+08	2.33E+08	2.07E+08	2.37E+08	237.95	15	1838	15
FALSE	Master Protein Candidate	202	4504957	lysosome-associated membrane glycoprotein 2 isoform A precursor [Homo sapiens]	2	1	10	1	1	410	44.9	5.63	High	High	High	High	High	Not Found		22055286	26158316	26095426	38434975	41536418		7.62	1	72	1
FALSE	Master Protein	202	169790833	lysosome-associated membrane glycoprotein 2 isoform C precursor [Homo sapiens]	2	1	10	1	1	411	45.1	5.91	High	High	High	High	High	Not Found		22055286	26158316	26095426	38434975	41536418		7.62	1	72	1
FALSE	Master Protein Candidate	202	7669503	lysosome-associated membrane glycoprotein 2 isoform B precursor [Homo sapiens]	2	1	10	1	1	410	44.9	5.69	High	High	High	High	High	Not Found		22055286	26158316	26095426	38434975	41536418		7.62	1	72	1
FALSE	None	203	282396082	heterogeneous nuclear ribonucleoprotein C-like [Homo sapiens]	8	3	24	3	1	293	32	5.43	High	High	High	High	High	High		1.25E+08	1.26E+08	1.24E+08	1.69E+08	1.71E+08	1.58E+08	30.82	3	227	3
FALSE	None	203	578800215	PREDICTED: heterogeneous nuclear ribonucleoprotein C-like 1-like [Homo sapiens]	8	3	24	3	1	293	32	5.68	High	High	High	High	High	High		1.25E+08	1.26E+08	1.24E+08	1.69E+08	1.71E+08	1.58E+08	30.82	3	227	3
FALSE	Master Protein Candidate	203	117190174	heterogeneous nuclear ribonucleoproteins C1/C2 isoform b [Homo sapiens]	17	5	48	5	1	293	32.3	5.08	High	High	High	High	High	High		87041204	87012596	85396512	2.48E+08	2.54E+08	2.48E+08	57.18	5	295	5
FALSE	None	203	61966711	heterogeneous nuclear ribonucleoprotein C-like 1 [Homo sapiens]	8	3	24	3	1	293	32.1	5.06	High	High	High	High	High	High		1.25E+08	1.26E+08	1.24E+08	1.69E+08	1.71E+08	1.58E+08	30.82	3	227	3
FALSE	Master Protein Candidate	203	578825750	PREDICTED: heterogeneous nuclear ribonucleoproteins C1/C2 isoform X1 [Homo sapiens]	17	5	48	5	1	301	33.3	8.53	High	High	High	High	High	High		87041204	87012596	85396512	2.48E+08	2.54E+08	2.48E+08	57.18	5	295	5
FALSE	None	203	578839320	PREDICTED: heterogeneous nuclear ribonucleoprotein C-like 1-like [Homo sapiens]	8	3	24	3	1	293	32	5.68	High	High	High	High	High	High		1.25E+08	1.26E+08	1.24E+08	1.69E+08	1.71E+08	1.58E+08	30.82	3	227	3
FALSE	Master Protein	203	117189975	heterogeneous nuclear ribonucleoproteins C1/C2 isoform a [Homo sapiens]	17	5	48	5	1	306	33.7	5.08	High	High	High	High	High	High		87041204	87012596	85396512	2.48E+08	2.54E+08	2.48E+08	57.18	5	295	5
FALSE	Master Protein Candidate	204	315221152	60S ribosomal protein L11 isoform 2 [Homo sapiens]	8	1	2	1	1	177	20.1	9.6	Not Found	Not Found	Not Found	Not Found	Not Found	High								2.85	1	0	1
FALSE	Master Protein	204	15431290	60S ribosomal protein L11 isoform 1 [Homo sapiens]	8	1	2	1	1	178	20.2	9.6	Not Found	Not Found	Not Found	Not Found	Not Found	High								2.85	1	0	1
FALSE	Master Protein	205	530384720	PREDICTED: heterogeneous nuclear ribonucleoproteins A2/B1 isoform X1 [Homo sapiens]	16	5	83	4	1	353	37.4	8.95	High	High	High	High	High	High		2.13E+08	2.23E+08	1.39E+08	3.5E+08	3.47E+08	4.95E+08	101.8	5	1094	4
FALSE	Master Protein Candidate	205	578813467	PREDICTED: heterogeneous nuclear ribonucleoproteins A2/B1 isoform X5 [Homo sapiens]	19	5	83	4	1	313	33.9	9.03	High	High	High	High	High	High		2.13E+08	2.23E+08	1.39E+08	3.5E+08	3.47E+08	4.95E+08	101.8	5	1094	4
FALSE	Master Protein Candidate	205	4504447	heterogeneous nuclear ribonucleoproteins A2/B1 isoform A2 [Homo sapiens]	17	5	83	4	1	341	36	8.65	High	High	High	High	High	High		2.13E+08	2.23E+08	1.39E+08	3.5E+08	3.47E+08	4.95E+08	101.8	5	1094	4
FALSE	Master Protein	206	225579152	insulin-like growth factor-binding protein complex acid labile subunit isoform 1 precursor [Homo sapiens]	2	1	1	1	1	643	70.2	6.93	Not Found	Not Found	High	Not Found	Not Found	Not Found				87364948				0	1		
FALSE	Master Protein Candidate	206	4826772	insulin-like growth factor-binding protein complex acid labile subunit isoform 2 precursor [Homo sapiens]	2	1	1	1	1	605	66	6.79	Not Found	Not Found	High	Not Found	Not Found	Not Found				87364948				0	1		
FALSE	Master Protein Candidate	207	530419397	PREDICTED: pyridoxal kinase isoform X4 [Homo sapiens]	6	1	2	1	1	272	30.6	6.65	Not Found	Not Found	High	Not Found	Not Found	Not Found				2651803				2.28	1	0	1
FALSE	Master Protein Candidate	207	530419393	PREDICTED: pyridoxal kinase isoform X2 [Homo sapiens]	5	1	2	1	1	321	36	6.86	Not Found	Not Found	High	Not Found	Not Found	Not Found				2651803				2.28	1	0	1
FALSE	Master Protein Candidate	207	4505701	pyridoxal kinase [Homo sapiens]	5	1	2	1	1	312	35.1	6.13	Not Found	Not Found	High	Not Found	Not Found	Not Found				2651803				2.28	1	0	1
FALSE	Master Protein	207	530419391	PREDICTED: pyridoxal kinase isoform X1 [Homo sapiens]	4	1	2	1	1	364	40.4	7.27	Not Found	Not Found	High	Not Found	Not Found	Not Found				2651803				2.28	1	0	1
FALSE	Master Protein Candidate	207	530419399	PREDICTED: pyridoxal kinase isoform X5 [Homo sapiens]	7	1	2	1	1	239	26.8	6.54	Not Found	Not Found	High	Not Found	Not Found	Not Found				2651803				2.28	1	0	1
FALSE	Master Protein	208	6912494	microtubule-associated protein RP/EB family member 1 [Homo sapiens]	4	1	12	1	1	268	30	5.14	High	High	High	High	High	High		14555698	14873601	14077496	27626276	26512188	27194926	20.33	1	189	1
FALSE	Master Protein	209	4506623	60S ribosomal protein L27 [Homo sapiens]	7	1	10	1	1	136	15.8	10.56	High	High	High	High	Not Found	High		42794280	41735226	39981912	1.06E+08		96959008	8.46	1	29	1
FALSE	Master Protein	21	6912238	peroxiredoxin-5, mitochondrial isoform a precursor [Homo sapiens]	27	4	58	4	1	214	22	8.57	High	High	High	High	High	High		27641263	27159004	36883814	84844815	96943426	79967087	80.89	4	571	4
FALSE	None	21	32455260	peroxiredoxin-5, mitochondrial isoform b precursor [Homo sapiens]	25	3	48	3	1	170	17.4	8.76	High	High	High	High	High	High		27641263	27159004	27866491	76563344	78173440	74826916	69.22	3	533	3
FALSE	None	21	530396544	PREDICTED: peroxiredoxin-5, mitochondrial isoform X1 [Homo sapiens]	12	2	34	2	1	251	25.5	10.35	High	High	High	High	High	High		17512140	19467929	27342002	58279399	77673228	55592139	44.72	2	401	2
FALSE	None	21	32455262	peroxiredoxin-5, mitochondrial isoform c precursor [Homo sapiens]	14	1	24	1	1	125	12.8	9.14	High	High	High	High	High	High		17512140	19467929	13816018	45857192	49518248	47881883	33.05	1	362	1
FALSE	Master Protein	210	13929462	beta-1,4-galactosyltransferase 1 [Homo sapiens]	2	1	8	1	1	398	43.9	8.65	High	Not Found	High	High	High	High		27232928		29380419	55445253	58522155	60493181	8.61	1	38	1

FALSE	Master Protein Candidate	210	530389856	PREDICTED: beta-1,4-galactosyltransferase 1 isoform X1 [Homo sapiens]	2	1	8	1	1	357	39.3	9.07	High	Not Found	High	High	High	High		27232928		29380419	55445253	58522155	60493181	8.61	1	38	1
FALSE	Master Protein Candidate	210	4757828	beta-1,4-galactosyltransferase 5 [Homo sapiens]	2	1	8	1	1	388	45.1	8.15	High	Not Found	High	High	High	High		27232928		29380419	55445253	58522155	60493181	8.61	1	38	1
FALSE	Master Protein Candidate	211	4507789	ubiquitin-conjugating enzyme E2 L3 isoform 1 [Homo sapiens]	10	1	2	1	1	154	17.9	8.51	Not Found	Not Found	High	Not Found	Not Found	Not Found								0	1	0	1
FALSE	Master Protein Candidate	211	373432682	ubiquitin-conjugating enzyme E2 L3 isoform 3 [Homo sapiens]	12	1	2	1	1	122	14.1	8.92	Not Found	Not Found	High	Not Found	Not Found	Not Found								0	1	0	1
FALSE	Master Protein	211	373432684	ubiquitin-conjugating enzyme E2 L3 isoform 4 [Homo sapiens]	7	1	2	1	1	212	24	8.75	Not Found	Not Found	High	Not Found	Not Found	Not Found								0	1	0	1
FALSE	Master Protein	212	4506661	60S ribosomal protein L7a [Homo sapiens]	5	1	2	1	1	266	30	10.61	Not Found	Not Found	Not Found	High	Not Found	Not Found					38182438			2.26	1	0	1
FALSE	Master Protein	213	4826898	profilin-1 [Homo sapiens]	56	6	306	6	1	140	15	8.27	High	High	High	High	High	High		7.52E+08	7.67E+08	9.83E+08	1.1E+09	1.93E+09	1.63E+09	488.84	5	4560	6
FALSE	Master Protein	214	21361657	protein disulfide-isomerase A3 precursor [Homo sapiens]	17	8	65	8	1	505	56.7	6.35	High	High	High	High	High	High		59876607	64870687	66478645	1.36E+08	1.48E+08	1.32E+08	75.86	8	308	8
FALSE	Master Protein	215	4504323	histone H4 [Homo sapiens]	29	3	21	3	1	103	11.4	11.36	High	High	High	High	High	High		1.97E+08	2.27E+08	2.32E+08	2.58E+08	2.18E+08	72491253	22.13	3	136	3
FALSE	Master Protein	216	4503477	elongation factor 1-beta [Homo sapiens]	12	2	16	2	1	225	24.7	4.67	High	High	High	High	High	High		79264185	1.12E+08	1.05E+08	2.94E+08	3.05E+08	2.06E+08	32.38	2	312	2
FALSE	Master Protein	217	14211889	protein dpy-30 homolog [Homo sapiens]	16	1	3	1	1	99	11.2	4.88	High	Not Found	Not Found	Not Found	Not Found	High		1526583					8827879	0	1	0	1
FALSE	Master Protein	218	4826643	annexin A3 [Homo sapiens]	29	8	81	8	1	323	36.4	5.92	High	High	High	High	High	High		71429063	73734111	68482604	1.22E+08	1.2E+08	1.22E+08	96.56	8	715	8
FALSE	None	219	15082234	L-lactate dehydrogenase A-like 6B [Homo sapiens]	4	1	28	1	1	381	41.9	8.65	High	High	High	High	High	High		15997455	14950262	16258427	66176935	66015231	61129933	50.74	1	562	1
FALSE	Master Protein	219	260099723	L-lactate dehydrogenase A chain isoform 3 [Homo sapiens]	17	5	57	5	1	361	39.8	8.43	High	High	High	High	High	High		29572333	46613606	44101415	98327309	96860737	1.29E+08	84.33	5	739	5
FALSE	Master Protein Candidate	219	5031857	L-lactate dehydrogenase A chain isoform 1 [Homo sapiens]	18	5	57	5	1	332	36.7	8.27	High	High	High	High	High	High		29572333	46613606	44101415	98327309	96860737	1.29E+08	84.33	5	739	5
FALSE	None	219	207028494	L-lactate dehydrogenase A chain isoform 2 [Homo sapiens]	16	4	29	4	1	274	30.2	7.15	High	High	High	High	High	High		43147211	41950859	58022909	1.14E+08	1.12E+08	1.29E+08	33.59	4	205	4
FALSE	None	219	260099727	L-lactate dehydrogenase A chain isoform 5 [Homo sapiens]	17	3	51	3	1	241	26.7	8.15	High	High	High	High	High	High		29572333	46613606	44101415	98327309	96860737	1E+08	76.95	3	736	3
FALSE	None	219	260099725	L-lactate dehydrogenase A chain isoform 4 [Homo sapiens]	15	3	51	3	1	274	30	8	High	High	High	High	High	High		29572333	46613606	44101415	98327309	96860737	1E+08	76.95	3	736	3
FALSE	Master Protein	22	4759212	tubulin-specific chaperone A [Homo sapiens]	24	3	8	3	1	108	12.8	5.29	Not Found	Not Found	Not Found	High	High	High					50181129	44056004	46876243	6.96	3	41	3
FALSE	None	22	530379470	PREDICTED: tubulin-specific chaperone A isoform X2 [Homo sapiens]	9	2	4	2	1	129	15.8	9.35	Not Found	Not Found	Not Found	High	High	Not Found					54257377	47784805		4.64	2	42	2
FALSE	Master Protein	220	149999611	signal recognition particle 14 kDa protein [Homo sapiens]	10	1	2	1	1	136	14.6	10.04	Not Found	Not Found	Not Found	High	Not Found	Not Found					31884450			3.77	1	40	1
FALSE	Master Protein	221	4502491	complement component 1 Q subcomponent-binding protein, mitochondrial precursor [Homo sapiens]	5	1	6	1	1	282	31.3	4.84	High	High	High	High	Not Found	Not Found		27404585	27304865	28928161	47376402			0	1	27	1
FALSE	Master Protein	222	530363142	PREDICTED: splicing factor, proline- and glutamine-rich isoform X2 [Homo sapiens]	4	2	14	2	1	707	76.1	9.44	Not Found	High	Not Found	High	High	High			9376640		40408604	33893089	38614107	18.53	2	123	2
FALSE	Master Protein Candidate	222	530363150	PREDICTED: splicing factor, proline- and glutamine-rich isoform X6 [Homo sapiens]	4	2	14	2	1	669	72.2	9.23	Not Found	High	Not Found	High	High	High			9376640		40408604	33893089	38614107	18.53	2	123	2
FALSE	Master Protein	223	14249348	thioredoxin domain-containing protein 17 [Homo sapiens]	20	2	26	2	1	123	13.9	5.52	High	High	High	High	High	High			326649.4		82961824		48960105	8.6	2	32	2
FALSE	Master Protein	224	4885165	cystatin-A [Homo sapiens]	12	1	4	1	1	98	11	5.5	Not Found	High	High	Not Found	Not Found	Not Found			23071441	22298878				4.68	1	28	1
FALSE	Master Protein	225	13994151	PDZ and LIM domain protein 1 [Homo sapiens]	3	1	6	1	1	329	36	7.02	High	High	High	Not Found	Not Found	Not Found		39592005	43120626	40728779				5.95	1	38	1
FALSE	Master Protein	226	4506141	serine protease HTRA1 precursor [Homo sapiens]	2	1	6	1	1	480	51.3	7.83	Not Found	Not Found	Not Found	High	High	High					44397526	52462860	49601066	7.17	1	84	1
FALSE	Master Protein Candidate	227	4506691	40S ribosomal protein S16 [Homo sapiens]	8	1	6	1	1	146	16.4	10.21	Not Found	High	High	High	Not Found	Not Found			24255002	22398648	26412806			8.17	1	135	1
FALSE	Master Protein	227	530417000	PREDICTED: 40S ribosomal protein S16 isoform X1 [Homo sapiens]	7	1	6	1	1	152	17.1	10.96	Not Found	High	High	High	Not Found	Not Found			24255002	22398648	26412806			8.17	1	135	1
FALSE	Master Protein	228	578834659	PREDICTED: kallikrein-10 isoform X5 [Homo sapiens]	9	2	11	2	1	276	30.2	8.59	High	High	High	Not Found	Not Found	Not Found		55728081	61430778	58665000				15.9	2	36	2
FALSE	Master Protein	229	110611218	ribosome-binding protein 1 [Homo sapiens]	2	1	6	1	1	977	108.6	5.54	Not Found	Not Found	Not Found	High	High	High					25612003	21376985	28318964	8.23	1	35	1
FALSE	Master Protein	23	153266822	aldehyde dehydrogenase family 1 member A3 [Homo sapiens]	3	1	1	1	1	512	56.1	7.25	Not Found	Not Found	Not Found	Not Found	Not Found	High										0	1
FALSE	None	230	530384859	PREDICTED: peptidyl-prolyl cis-trans isomerase A isoform X1 [Homo sapiens]	27	3	39	3	1	105	11.4	7.9	High	High	High	High	High	High		1.53E+08	1.32E+08	1.55E+08	1.56E+08	3.31E+08	1.52E+08	60.63	3	495	3
FALSE	Master Protein	230	10863927	peptidyl-prolyl cis-trans isomerase A [Homo sapiens]	35	7	90	7	1	165	18	7.81	High	High	High	High	High	High		1.87E+08	1.86E+08	1.91E+08	2.32E+08	3.82E+08	2.26E+08	123.92	7	922	7
FALSE	None	230	113428306	PREDICTED: peptidyl-prolyl cis-trans isomerase A-like [Homo sapiens]	5	1	11	1	1	186	20.4	6.42	High	High	High	High	High	High		1.24E+08	1.27E+08	1.31E+08	2.35E+08	2.27E+08	2.29E+08	12.65	1	88	1
FALSE	Master Protein Candidate	231	578812900	PREDICTED: receptor-type tyrosine-protein phosphatase kappa isoform X11 [Homo sapiens]	2	1	5	1	1	893	99.6	6.96	High	High	High	Not Found	Not Found	Not Found		26572426	27463008	26551094				4.9	1	75	1
FALSE	Master Protein Candidate	231	578812905	PREDICTED: receptor-type tyrosine-protein phosphatase kappa isoform X13 [Homo sapiens]	2	1	5	1	1	869	96.9	6.62	High	High	High	Not Found	Not Found	Not Found		26572426	27463008	26551094				4.9	1	75	1
FALSE	Master Protein Candidate	231	578812898	PREDICTED: receptor-type tyrosine-protein phosphatase kappa isoform X10 [Homo sapiens]	1	1	5	1	1	1081	123.2	6.46	High	High	High	Not Found	Not Found	Not Found		26572426	27463008	26551094				4.9	1	75	1
FALSE	Master Protein Candidate	231	530383930	PREDICTED: receptor-type tyrosine-protein phosphatase kappa isoform X2 [Homo sapiens]	1	1	5	1	1	1464	165.4	6.15	High	High	High	Not Found	Not Found	Not Found		26572426	27463008	26551094				4.9	1	75	1
FALSE	Master Protein Candidate	231	578839565	PREDICTED: receptor-type tyrosine-protein phosphatase kappa isoform X7 [Homo sapiens]	2	1	5	1	1	866	96	6.38	High	High	High	Not Found	Not Found	Not Found		26572426	27463008	26551094				4.9	1	75	1
FALSE	Master Protein Candidate	231	18860902	receptor-type tyrosine-protein phosphatase kappa isoform b precursor [Homo sapiens]	1	1	5	1	1	1440	162.1	5.9	High	High	High	Not Found	Not Found	Not Found		26572426	27463008	26551094				4.9	1	75	1
FALSE	Master Protein Candidate	231	530383938	PREDICTED: receptor-type tyrosine-protein phosphatase kappa isoform X6 [Homo sapiens]	2	1	5	1	1	890	99.3	6.77	High	High	High	Not Found	Not Found	Not Found		26572426	27463008	26551094				4.9	1	75	1
FALSE	Master Protein Candidate	231	578839561	PREDICTED: receptor-type tyrosine-protein phosphatase kappa isoform X5 [Homo sapiens]	1	1	5	1	1	1057	119.9	6.14	High	High	High	Not Found	Not Found	Not Found		26572426	27463008	26551094				4.9	1	75	1
FALSE	Master Protein Candidate	231	208431815	receptor-type tyrosine-protein phosphatase kappa isoform a precursor [Homo sapiens]	1	1	5	1	1	1446	162.9	5.91	High	High	High	Not Found	Not Found	Not Found		26572426	27463008	26551094				4.9	1	75	1
FALSE	Master Protein Candidate	231	578839563	PREDICTED: receptor-type tyrosine-protein phosphatase kappa isoform X6 [Homo sapiens]	2	1	5	1	1	869	96.3	6.54	High	High	High	Not Found	Not Found	Not Found		26572426	27463008	26551094				4.9	1	75	1
FALSE	Master Protein Candidate	231	578839567	PREDICTED: receptor-type tyrosine-protein phosphatase kappa isoform X8 [Homo sapiens]	2	1	5	1	1	845	93.6	6.21	High	High	High	Not Found	Not Found	Not Found		26572426	27463008	26551094				4.9	1	75	1
FALSE	Master Protein	231	578812892	PREDICTED: receptor-type tyrosine-protein phosphatase kappa isoform X7 [Homo sapiens]	1	1	5	1	1	1470	166.2	6.15	High	High	High	Not Found	Not Found	Not Found		26572426	27463008	26551094				4.9	1	75	1
FALSE	Master Protein Candidate	231	578839557	PREDICTED: receptor-type tyrosine-protein phosphatase kappa isoform X3 [Homo sapiens]	1	1	5	1	1	1375	155.3	6.2	High	High	High	Not Found	Not Found	Not Found		26572426	27463008	26551094				4.9	1	75	1
FALSE	Master Protein Candidate	232	578835708	PREDICTED: endothelial protein C receptor isoform X1 [Homo sapiens]	4	1	5	1	1	240	27.3	7.53	Not Found	High	High	High	High	Not Found			38726316	35892636	53313776	65039130		1.71	1	22	1
FALSE	Master Protein Candidate	232	34335272	endothelial protein C receptor precursor [Homo sapiens]	4	1	5	1	1	238	26.7	7.18	Not Found	High	High	High	High	Not Found			38726316	35892636	53313776	65039130		1.71	1	22	1
FALSE	Master Protein	232	578835706	PREDICTED: endothelial protein C receptor isoform X2 [Homo sapiens]	3	1	5	1	1	275	30.7	8.48	Not Found	High	High	High	High	Not Found			38726316	35892636	53313776	65039130		1.71	1	22	1
FALSE	Master Protein Candidate	233	52632385	heterogeneous nuclear ribonucleoprotein L isoform b [Homo sapiens]	4	1	4	1	1	456	50.5	7.5	Not Found	Not Found	Not Found	High	High	Not Found					48228642	39802372		2.21	1	43	1
FALSE	Master Protein	233	52632383	heterogeneous nuclear ribonucleoprotein L isoform a [Homo sapiens]	3	1	4	1	1	589	64.1	8.22	Not Found	Not Found	Not Found	High	High	Not Found					48228642	39802372		2.21	1	43	1
FALSE	Master Protein	234	4503117	cystatin-B [Homo sapiens]	12	1	12	1	1	98	11.1	7.56	High	High	High	High	High	High		55435760	53159576	54467762	97239858	93446313	89557770	18.09	1	199	1
FALSE	Master Protein	235	7657069	ERO1-like protein alpha precursor [Homo sapiens]	2	1	4	1	1	468	54.4	5.68	Not Found	Not Found	Not Found	High	Not Found	High					15462561		18380665	0	1	31	1
FALSE	Master Protein Candidate	236	578811108	PREDICTED: heterogeneous nuclear ribonucleoprotein H isoform X10 [Homo sapiens]	8	2	34	2	1	452	49.1	6.92	High	High	High	High	High	High		22159196	23356543	23734171	48603700	54524519	52759859	55.67	2	425	2
FALSE	Master Protein Candidate	236	381342476	heterogeneous nuclear ribonucleoprotein H [Homo sapiens]	8	2	34	2	1	449	49.2	6.3	High	High	High	High	High	High		22159196	23356543	23734171	48603700	54524519	52759859	55.67	2	425	2
FALSE	None	236	148470406	heterogeneous nuclear ribonucleoprotein F [Homo sapiens]	4	1	16	1	1	415	45.6	5.58	High	High	High	High	High	High		15458802	17165911	15596835	42856881	44574763	44496404	24.34	1	231	1
FALSE	None	236	530381027	PREDICTED: heterogeneous nuclear ribonucleoprotein H isoform X7 [Homo sapiens]	6	1	16	1	1	271	28.5	6.64	High	High	High	High	High	High		15458802	17165911	15596835	42856881	44574763	44496404	24.34	1	231	1
FALSE	None	236	530381031	PREDICTED: heterogeneous nuclear ribonucleoprotein H isoform X9 [Homo sapiens]	7	1	16	1	1	251	26.3	6.79	High	High	High	High	High	High		15458802	17165911	15596835	42856881	44574763	44496404	24.34	1	231	1
FALSE	None	236	9624998	heterogeneous nuclear ribonucleoprotein H2 [Homo sapiens]	4	1	18	1	1	449	49.2	6.3	High	High	High	High	High	High		28859591	29547175	31871507	54350519	64474275	61023313	31.32	1	214	1
FALSE	Master Protein	236	530381015	PREDICTED: heterogeneous nuclear ribonucleoprotein H isoform X1 [Homo sapiens]	7	2	34	2	1	472	51.2	6.8	High	High	High	High	High	High		22159196	23356543	23734171	48603700	54524519	52759859	55.67	2	425	2
FALSE	Master Protein Candidate	236	578811110	PREDICTED: heterogeneous nuclear ribonucleoprotein H isoform X11 [Homo sapiens]	8	2	34	2	1	429	47.1	6.34	High	High	High	High	High	High		22159196	23356543	23734171	48603700	54524519	52759859	55.67	2	425	2
FALSE	Master Protein	237	115430223	galectin-3 isoform 1 [Homo sapiens]	10	2	10	2	1	250	26.1	8.56	High	High	Not Found	High	High	High		17372718	19618563		74680512	79601053	79279212	8.71	2	41	2
FALSE	Master Protein Candidate	238	27894328	interleukin-1 receptor-like 1 isoform 2 precursor [Homo sapiens]	4	1	6	1	1	328	37	8.1	Not Found	Not Found	Not Found	High	High	High					46539986	37639348	46068391	8.36	1	117	1
FALSE	Master Protein	238	27894324	interleukin-1 receptor-like 1 isoform 1 precursor [Homo sapiens]	2	1	6	1	1	556	63.3	8.35	Not Found	Not Found	Not Found	High	High	High					46539986	37639348	46068391	8.36	1	117	1
FALSE	Master Protein	239	167466173	heat shock 70 kDa protein 1A/1B [Homo sapiens]	16	9	80	7	1	641	70	5.66	High	High	High	High	High	High		58886884	62644567	61055632	1.46E+08	1.42E+08	1.29E+08	107.79	9	675	9
FALSE	Master Protein	24	4506597	60S ribosomal protein L12 [Homo sapiens]	24	3	23	3	1	165	17.8	9.42	High	High	High	High	High	High		57642779	59797581	64101706	1.91E+08	1.91E+08	1.87E+08	23.48	3	98	3
FALSE	Master Protein Candidate	240	222144324	myosin regulatory light chain 12B [Homo sapiens]	12	2	15	2	1	172	19.8	4.84	High	High	Not Found	High	High	High		31581676	32319275		93006499	92655642	86765182	18.04	2	202	2
FALSE	Master Protein	240	530424791	PREDICTED: myosin regulatory light chain 12A isoform X2 [Homo sapiens]	12	2	15	2	1	177	20.4	4.75	High	High	Not Found	High	High	High		31581676	32319275		93006499	92655642	86765182	18.04	2	202	2
FALSE	Master Protein Candidate	240	5453740	myosin regulatory light chain 12A [Homo sapiens]	12	2	15	2	1	171	19.8	4.81	High	High	Not Found	High	High	High		31581676	32319275		93006499	92655642	86765182	18.04	2	202	2
FALSE	Master Protein Candidate	241	24497601	endothelial differentiation-related factor 1 isoform beta [Homo sapiens]	11	1	12	1	1	139	15.5	9.77	High	High	High	High	High	High		17948569	27298330	23999790	22416064	19516267	28554118	8.02	1	34	1
FALSE	Master Protein Candidate	241	526253088	endothelial differentiation-related factor 1 isoform 4 [Homo sapiens]	12	1	12	1	1	127	14.1	9.8	High	High	High	High	High	High		17948569	27298330	23999790	22416064	19516267	28554118	8.02	1	34	1
FALSE	Master Protein	241	4503453	endothelial differentiation-related factor 1 isoform alpha [Homo sapiens]	10	1	12	1	1	148	16.4	9.95	High	High	High	High	High	High		17948569	27298330	23999790	22416064	19516267	28554118	8.02	1	34	1
FALSE	Master Protein Candidate	241	526253090	endothelial differentiation-related factor 1 isoform 5 [Homo sapiens]	12	1	12	1	1	130	14.4	9.86	High	High	High	High	High	High		17948569	27298330	23999790	22416064	19516267	28554118	8.02	1	34	1
FALSE	Master Protein Candidate	241	526253086	endothelial differentiation-related factor 1 isoform 3 [Homo sapiens]	11	1	12	1	1	141	15.6	9.88	High	High	High	High	High	High		17948569	27298330	23999790	22416064	19516267	28554118	8.02	1	34	1
FALSE	Master Protein	242	578840688	PREDICTED: D-dopachrome decarboxylase isoform X1 [Homo sapiens]	12	2	24	2	1	209	22.5	6.54	High	High	High	High	High	High		47718728	52966191	53056953	1.26E+08	1.34E+08	1.49E+08	37.75	2	253	2
FALSE	Master Protein Candidate	242	578840685	PREDICTED: D-dopachrome decarboxylase-like protein isoform X2 [Homo sapiens]	22	2	24	2	1	112	11.7	5.78	High	High	High	High	High	High		47718728	52966191	53056953	1.26E+08	1.34E+08	1.49E+08	37.75	2	253	2
FALSE	Master Protein Candidate	242	4503291	D-dopachrome decarboxylase [Homo sapiens]	21	2	24	2	1	118	12.7	7.3	High	High	High	High	High	High		47718728	52966191	53056953	1.26E+08	1.34E+08	1.49E+08	37.75	2	253	2
FALSE	None	242	222136649	D-dopachrome decarboxylase related protein [Homo sapiens]	10	1	12	1	1	123	13.1	7.34	High	High	High	High	High	High		48740805	47852469	49969488	1.08E+08	1.03E+08		17.5	1	72	1
FALSE	Master Protein Candidate	242	145386559	D-dopachrome decarboxylase-like protein [Homo sapiens]	19	2	24	2	1	134	14.2	6.29	High	High	High	High	High	High		47718728	52966191	53056953	1.26E+08	1.34E+08	1.49E+08	37.75	2	253	2
FALSE	Master Protein Candidate	242	530419451	PREDICTED: D-dopachrome decarboxylase-like protein isoform X1 [Homo sapiens]	23	2	24	2	1	107	11.3	6.28	High	High	High	High	High	High		47718728	52966191	53056953	1.26E+08	1.34E+08	1.49E+08	37.75	2	253	2
FALSE	None	243	578806532	PREDICTED: transketolase isoform X1 [Homo sapiens]	5	2	20	2	1	630	68.8	7.88	High	High	High	High	High	High		45098541	71578563	46824159	1.19E+08	1.75E+08	1.12E+08	29.64	2	205	2
FALSE	Master Protein	243	384475521	transketolase isoform 2 [Homo sapiens]	7	3	23	3	1	631	68.8	7.52	High	High	High	High	High	High		45098541	71578563	46824159	95704745	1.15E+08	91003242	29.64	2	210	3
FALSE	Master Protein Candidate	243	4507521	transketolase isoform 1 [Homo sapiens]	7	3	23	3	1	623	67.8	7.66	High	High	High	High	High	High		45098541	71578563	46824159	95704745	1.15E+08	91003242	29.64	2	210	3
FALSE	Master Protein Candidate	244	94721252	vesicle-associated membrane protein-associated protein A isoform 2 [Homo sapiens]	5	1	12	1	1	249	27.9	8.62	High	High	High	High	High	High		44127469	44093762	42806464	90229066	91360018	87933701	14	1	150	1
FALSE	Master Protein	244	94721250	vesicle-associated membrane protein-associated protein A isoform 1 [Homo sapiens]	4	1	12	1	1	294	32.6	8.91	High	High	High	High	High	High		44127469	44093762	42806464	90229066	91360018	87933701	14	1	150	1
FALSE	Master Protein Candidate	244	307574674	vesicle-associated membrane protein-associated protein B/C isoform 2 [Homo sapiens]	12	1	12	1	1	99	11.1	8.54	High	High	High	High	High	High		44127469	44093762	42806464	90229066	91360018	87933701	14	1	150	1
FALSE	Master Protein Candidate	244	4759302	vesicle-associated membrane protein-associated protein B/C isoform 1 [Homo sapiens]	5	1	12	1	1	243	27.2	7.3	High	High	High	High	High	High		44127469	44093762	42806464	90229066	91360018	87933701	14	1	150	1
FALSE	Master Protein	245	4501881	actin, alpha skeletal muscle [Homo sapiens]	22	7	64	1	1	377	42	5.39	High	High	High	Not Found	Not Found	High		4.32E+08	4.64E+08	4.64E+08			1.17E+09	79.43	6	346	7
FALSE	None	245	4501889	actin, gamma-enteric smooth muscle isoform 1 precursor [Homo sapiens]	19	6	49	1	1	376	41.9	5.48	High	High	High	Not Found	Not Found	High		4.32E+08	4.64E+08	4.64E+08			1.17E+09	58.73	5	272	6
FALSE	None	245	4501883	actin, aortic smooth muscle [Homo sapiens]	19	6	49	1	1	377	42	5.39	High	High	High	Not Found	Not Found	High		4.32E+08	4.64E+08	4.64E+08			1.17E+09	58.73	5	272	6
FALSE	Master Protein Candidate	245	4885049	actin, alpha cardiac muscle 1 proprotein [Homo sapiens]	22	7	64	1	1	377	42	5.39	High	High	High	Not Found	Not Found	High		4.32E+08	4.64E+08	4.64E+08			1.17E+09	79.43	6	346	7
FALSE	Master Protein	246	8922331	protein mago nashi homolog 2 [Homo sapiens]	10	1	10	1	1	148	17.3	6.39	High	Not Found	High	High	High	High		17507403			38548227	46266535	42976935	2.48	1	0	1
FALSE	Master Protein Candidate	246	4505087	protein mago nashi homolog [Homo sapiens]	10	1	10	1	1	146	17.2	6.11	High	Not Found	High	High	High	High		17507403			38548227	46266535	42976935	2.48	1	0	1
FALSE	Master Protein	247	4506619	60S ribosomal protein L24 [Homo sapiens]	8	1	2	1	1	157	17.8	11.25	Not Found	Not Found	High	Not Found	Not Found	Not Found				13718524				2.75	1	0	1
FALSE	None	248	578834952	PREDICTED: alpha-actinin-4 isoform X3 [Homo sapiens]	30	20	165	12	1	911	104.8	5.44	High	High	High	High	High	High		66133300	60885286	61837157	1.34E+08	1.28E+08	1.24E+08	220.73	18	1758	20
FALSE	Master Protein Candidate	248	530417302	PREDICTED: alpha-actinin-4 isoform X1 [Homo sapiens]	32	21	172	13	1	906	104.3	5.5	High	High	High	High	High	High		72215982	68664983	69750950	1.62E+08	1.57E+08	1.24E+08	223.45	19	1771	21
FALSE	Master Protein	248	12025678	alpha-actinin-4 [Homo sapiens]	32	21	172	13	1	911	104.8	5.44	High	High	High	High	High	High		72215982	68664983	69750950	1.62E+08	1.57E+08	1.24E+08	223.45	19	1771	21
FALSE	None	248	530417304	PREDICTED: alpha-actinin-4 isoform X2 [Homo sapiens]	30	20	165	12	1	906	104.3	5.5	High	High	High	High	High	High		66133300	60885286	61837157	1.34E+08	1.28E+08	1.24E+08	220.73	18	1758	20
FALSE	None	248	115430237	spectrin beta chain, non-erythrocytic 4 isoform sigma1 [Homo sapiens]	0	1	13	1	1	2564	288.8	6.01	High	Not Found	High	High	High	High		28239881		32611776	52792769	64063012	56662871	7.96	1	97	1
FALSE	None	248	578834710	PREDICTED: spectrin beta chain, non-erythrocytic 4 isoform X1 [Homo sapiens]	0	1	13	1	1	2394	270.1	5.67	High	Not Found	High	High	High	High		28239881		32611776	52792769	64063012	56662871	7.96	1	97	1
FALSE	Master Protein	249	24497583	aldo-keto reductase family 1 member C3 isoform 1 [Homo sapiens]	2	1	6	1	1	323	36.8	7.94	High	High	High	Not Found	Not Found	Not Found		29554228	31617578	28389668				6.66	1	96	1
FALSE	Master Protein Candidate	249	359806990	aldo-keto reductase family 1 member C3 isoform 2 [Homo sapiens]	2	1	6	1	1	323	36.8	7.94	High	High	High	Not Found	Not Found	Not Found		29554228	31617578	28389668				6.66	1	96	1
FALSE	Master Protein Candidate	249	4503285	aldo-keto reductase family 1 member C2 isoform 1 [Homo sapiens]	2	1	6	1	1	323	36.7	7.49	High	High	High	Not Found	Not Found	Not Found		29554228	31617578	28389668				6.66	1	96	1
FALSE	Master Protein Candidate	249	5453543	aldo-keto reductase family 1 member C1 [Homo sapiens]	2	1	6	1	1	323	36.8	7.88	High	High	High	Not Found	Not Found	Not Found		29554228	31617578	28389668				6.66	1	96	1
FALSE	Master Protein Candidate	249	325652083	aldo-keto reductase family 1 member C4 [Homo sapiens]	2	1	6	1	1	323	37.1	7.17	High	High	High	Not Found	Not Found	Not Found		29554228	31617578	28389668				6.66	1	96	1
FALSE	Master Protein Candidate	25	530379090	PREDICTED: follistatin isoform X3 [Homo sapiens]	9	2	12	2	1	330	36.3	7.88	High	High	High	Not Found	Not Found	Not Found		71201993	74230414	77100123				23.35	2	310	2
FALSE	Master Protein Candidate	25	7242222	follistatin isoform FST344 precursor [Homo sapiens]	8	2	12	2	1	344	38	5.67	High	High	High	Not Found	Not Found	Not Found		71201993	74230414	77100123				23.35	2	310	2
FALSE	Master Protein Candidate	25	530379088	PREDICTED: follistatin isoform X2 [Homo sapiens]	8	2	12	2	1	343	37.9	5.53	High	High	High	Not Found	Not Found	Not Found		71201993	74230414	77100123				23.35	2	310	2
FALSE	Master Protein Candidate	25	530379092	PREDICTED: follistatin isoform X4 [Homo sapiens]	9	2	12	2	1	316	34.7	7.74	High	High	High	Not Found	Not Found	Not Found		71201993	74230414	77100123				23.35	2	310	2
FALSE	Master Protein	25	530379086	PREDICTED: follistatin isoform X1 [Homo sapiens]	8	2	12	2	1	357	39.5	5.87	High	High	High	Not Found	Not Found	Not Found		71201993	74230414	77100123				23.35	2	310	2

FALSE	Master Protein Candidate	25	5453652	follistatin isoform FST317 precursor [Homo sapiens]	9	2	12	2	1	317	34.8	7.81	High	High	High	Not Found	Not Found	Not Found		71201993	74230414	77100123				23.35	2	310	2
FALSE	Master Protein Candidate	250	296080693	glucose-6-phosphate isomerase isoform 1 [Homo sapiens]	14	5	57	5	1	569	64.3	8.91	High	High	High	High	High	High		72818866	60956583	65252425	1.17E+08	1.02E+08	1.4E+08	78.85	5	918	5
FALSE	Master Protein Candidate	250	530416229	PREDICTED: glucose-6-phosphate isomerase isoform X2 [Homo sapiens]	14	5	57	5	1	558	63.1	8.32	High	High	High	High	High	High		72818866	60956583	65252425	1.17E+08	1.02E+08	1.4E+08	78.85	5	918	5
FALSE	Master Protein	250	530416227	PREDICTED: glucose-6-phosphate isomerase isoform X1 [Homo sapiens]	13	5	57	5	1	597	67.2	8.97	High	High	High	High	High	High		72818866	60956583	65252425	1.17E+08	1.02E+08	1.4E+08	78.85	5	918	5
FALSE	Master Protein	251	4504373	beta-hexosaminidase subunit beta preproprotein [Homo sapiens]	6	3	22	3	1	556	63.1	6.76	High	High	High	High	High	High		30978463	29980828	28951457	56235883	55799610	56175980	27.11	3	111	3
FALSE	Master Protein Candidate	252	530402322	PREDICTED: high mobility group protein B1 isoform X6 [Homo sapiens]	18	3	48	3	1	158	18.3	9.7	High	High	High	High	High	High		2.21E+08	1.71E+08	2.04E+08	73138420	2.01E+08	2.25E+08	58.84	3	192	3
FALSE	Master Protein	252	530402316	PREDICTED: high mobility group protein B1 isoform X3 [Homo sapiens]	13	3	48	3	1	215	24.9	5.74	High	High	High	High	High	High		2.21E+08	1.71E+08	2.04E+08	73138420	2.01E+08	2.25E+08	58.84	3	192	3
FALSE	Master Protein	253	55956788	nucleolin [Homo sapiens]	11	7	78	7	1	710	76.6	4.7	High	High	High	High	High	High		1.32E+08	1.38E+08	1.45E+08	2.64E+08	2.19E+08	2.7E+08	107.52	7	635	7
FALSE	Master Protein	254	578815184	PREDICTED: clusterin isoform X1 [Homo sapiens]	13	7	59	7	1	501	57.8	6.68	High	High	High	High	High	High		93443070	93618377	1.01E+08	1.82E+08	1.96E+08	1.82E+08	59.61	6	326	7
FALSE	Master Protein Candidate	254	355594753	clusterin preproprotein [Homo sapiens]	15	7	59	7	1	449	52.5	6.27	High	High	High	High	High	High		93443070	93618377	1.01E+08	1.82E+08	1.96E+08	1.82E+08	59.61	6	326	7
FALSE	Master Protein	255	4506761	protein S100-A10 [Homo sapiens]	18	1	14	1	1	97	11.2	7.37	High	High	High	High	High	High		4.28E+08	4.36E+08	97208054	2.56E+08	2.68E+08	2.38E+08	19.45	1	74	1
FALSE	Master Protein	256	221316620	cell division cycle protein 123 homolog [Homo sapiens]	2	1	2	1	1	336	39.1	4.81	Not Found	High	Not Found	Not Found	Not Found	Not Found			9362097					0	1	0	1
FALSE	Master Protein Candidate	256	530392538	PREDICTED: cell division cycle protein 123 homolog isoform X1 [Homo sapiens]	3	1	2	1	1	304	35.6	4.77	Not Found	High	Not Found	Not Found	Not Found	Not Found			9362097					0	1	0	1
FALSE	Master Protein	257	530436984	PREDICTED: prothymosin alpha-like [Homo sapiens]	8	1	8	1	1	118	13	3.88	Not Found	Not Found	Not Found	High	High	High								8.75	1	22	1
FALSE	Master Protein Candidate	257	151101407	prothymosin alpha isoform 1 [Homo sapiens]	9	1	8	1	1	111	12.2	3.78	Not Found	Not Found	Not Found	High	High	High								8.75	1	22	1
FALSE	Master Protein Candidate	257	151101404	prothymosin alpha isoform 2 [Homo sapiens]	9	1	8	1	1	110	12.1	3.79	Not Found	Not Found	Not Found	High	High	High								8.75	1	22	1
FALSE	Master Protein	258	530388819	PREDICTED: elongation factor 1-delta isoform X1 [Homo sapiens]	2	1	12	1	1	688	75.6	6.43	High	High	High	High	High	High		34969628	33405351	32455385	1.2E+08	1.09E+08	1.23E+08	16.45	1	166	1
FALSE	Master Protein Candidate	258	194239727	elongation factor 1-delta isoform 2 [Homo sapiens]	4	1	12	1	1	281	31.1	5.01	High	High	High	High	High	High		34969628	33405351	32455385	1.2E+08	1.09E+08	1.23E+08	16.45	1	166	1
FALSE	Master Protein Candidate	258	304555581	elongation factor 1-delta isoform 1 [Homo sapiens]	2	1	12	1	1	647	71.4	6.42	High	High	High	High	High	High		34969628	33405351	32455385	1.2E+08	1.09E+08	1.23E+08	16.45	1	166	1
FALSE	Master Protein Candidate	258	578839682	PREDICTED: elongation factor 1-delta isoform X4 [Homo sapiens]	2	1	12	1	1	648	71.5	6.42	High	High	High	High	High	High		34969628	33405351	32455385	1.2E+08	1.09E+08	1.23E+08	16.45	1	166	1
FALSE	Master Protein Candidate	258	578815864	PREDICTED: elongation factor 1-delta isoform X8 [Homo sapiens]	2	1	12	1	1	687	75.5	6.43	High	High	High	High	High	High		34969628	33405351	32455385	1.2E+08	1.09E+08	1.23E+08	16.45	1	166	1
FALSE	Master Protein Candidate	258	578839684	PREDICTED: elongation factor 1-delta isoform X5 [Homo sapiens]	2	1	12	1	1	647	71.4	6.42	High	High	High	High	High	High		34969628	33405351	32455385	1.2E+08	1.09E+08	1.23E+08	16.45	1	166	1
FALSE	Master Protein Candidate	258	578839680	PREDICTED: elongation factor 1-delta isoform X3 [Homo sapiens]	2	1	12	1	1	664	73	6.34	High	High	High	High	High	High		34969628	33405351	32455385	1.2E+08	1.09E+08	1.23E+08	16.45	1	166	1
FALSE	Master Protein Candidate	258	194239729	elongation factor 1-delta isoform 4 [Homo sapiens]	5	1	12	1	1	257	28.5	4.92	High	High	High	High	High	High		34969628	33405351	32455385	1.2E+08	1.09E+08	1.23E+08	16.45	1	166	1
FALSE	Master Protein Candidate	259	530366470	PREDICTED: specifically androgen-regulated gene protein isoform X2 [Homo sapiens]	5	1	1	1	1	355	37.5	10.1	Not Found	High	Not Found	Not Found	Not Found	Not Found										0	1
FALSE	Master Protein	259	578801475	PREDICTED: specifically androgen-regulated gene protein isoform X3 [Homo sapiens]	3	1	1	1	1	601	63.9	8.62	Not Found	High	Not Found	Not Found	Not Found	Not Found										0	1
FALSE	None	26	530384505	PREDICTED: anterior gradient protein 3 homolog isoform X1 [Homo sapiens]	7	1	2	1	1	166	19.2	7.99	Not Found	Not Found	Not Found	Not Found	Not Found	High							41434792	2.11	1	0	1
FALSE	Master Protein	26	5453541	anterior gradient protein 2 homolog precursor [Homo sapiens]	16	2	8	2	1	175	20	9	High	High	Not Found	Not Found	Not Found	High		11475393	12144651				32263083	11.21	2	61	2
FALSE	Master Protein	260	4503483	elongation factor 2 [Homo sapiens]	2	1	2	1	1	858	95.3	6.83	High	Not Found	Not Found	Not Found	Not Found	Not Found		8244210						2.64	1	47	1
FALSE	Master Protein	261	148539846	desmocollin-3 isoform Dsc3a preproprotein [Homo sapiens]	1	1	12	1	1	896	99.9	6.1	High	High	High	High	High	High		36807464	38752854	36164144	82824005	84745441	81345212	9.98	1	53	1
FALSE	Master Protein Candidate	261	148539848	desmocollin-3 isoform Dsc3b preproprotein [Homo sapiens]	1	1	12	1	1	839	93.4	6.32	High	High	High	High	High	High		36807464	38752854	36164144	82824005	84745441	81345212	9.98	1	53	1
FALSE	Master Protein Candidate	262	530389319	PREDICTED: 14-3-3 protein zeta/delta isoform X3 [Homo sapiens]	32	7	53	4	1	245	27.7	4.79	High	High	High	High	High	High		2.08E+08	1.99E+08	2.18E+08	5.26E+08	3.59E+08	3.5E+08	54.04	7	277	7
FALSE	Master Protein	262	530389315	PREDICTED: 14-3-3 protein zeta/delta isoform X1 [Homo sapiens]	21	7	53	4	1	384	42.5	5.22	High	High	High	High	High	High		2.08E+08	1.99E+08	2.18E+08	5.26E+08	3.59E+08	3.5E+08	54.04	7	277	7
FALSE	Master Protein	263	17986258	myosin light polypeptide 6 isoform 1 [Homo sapiens]	16	2	20	2	1	151	16.9	4.65	Not Found	High	High	High	High	High			22802516	11200253	1.84E+08	1.82E+08	1.99E+08	30.81	2	76	2
FALSE	Master Protein Candidate	263	88999583	myosin light polypeptide 6 isoform 2 [Homo sapiens]	16	2	20	2	1	151	17	4.55	Not Found	High	High	High	High	High			22802516	11200253	1.84E+08	1.82E+08	1.99E+08	30.81	2	76	2
FALSE	Master Protein	264	124494254	proliferation-associated protein 2G4 [Homo sapiens]	7	2	14	2	1	394	43.8	6.55	High	High	High	High	High	High		55850923	78430484	78164898				17.64	2	41	2
FALSE	Master Protein Candidate	265	25092737	histone H2A type 1-A [Homo sapiens]	21	2	28	2	1	131	14.2	10.86	High	High	High	High	High	High		2.13E+08	2.07E+08	2.06E+08	1.85E+08	2.01E+08	1.99E+08	38.24	2	215	2
FALSE	Master Protein Candidate	265	18105045	histone H2A type 1-H [Homo sapiens]	22	2	28	2	1	128	13.9	10.89	High	High	High	High	High	High		2.13E+08	2.07E+08	2.06E+08	1.85E+08	2.01E+08	1.99E+08	38.24	2	215	2
FALSE	Master Protein Candidate	265	24638446	histone H2A type 2-C [Homo sapiens]	22	2	28	2	1	129	14	10.9	High	High	High	High	High	High		2.13E+08	2.07E+08	2.06E+08	1.85E+08	2.01E+08	1.99E+08	38.24	2	215	2
FALSE	None	265	20357599	histone H2A.V isoform 2 [Homo sapiens]	8	1	12	1	1	114	12.1	10.46	High	High	High	High	High	High		2.13E+08	2.16E+08	2.22E+08	1.49E+08	1.53E+08	1.69E+08	15.05	1	108	1
FALSE	None	265	41406069	histone H2A.V isoform 4 [Homo sapiens]	14	1	12	1	1	66	6.9	11.06	High	High	High	High	High	High		2.13E+08	2.16E+08	2.22E+08	1.49E+08	1.53E+08	1.69E+08	15.05	1	108	1
FALSE	Master Protein Candidate	265	4504249	histone H2A type 1 [Homo sapiens]	22	2	28	2	1	130	14.1	10.9	High	High	High	High	High	High		2.13E+08	2.07E+08	2.06E+08	1.85E+08	2.01E+08	1.99E+08	38.24	2	215	2
FALSE	Master Protein Candidate	265	106775678	histone H2A type 2-A [Homo sapiens]	22	2	28	2	1	130	14.1	10.9	High	High	High	High	High	High		2.13E+08	2.07E+08	2.06E+08	1.85E+08	2.01E+08	1.99E+08	38.24	2	215	2
FALSE	Master Protein Candidate	265	10800144	histone cluster 1, H2aj [Homo sapiens]	22	2	28	2	1	128	13.9	10.89	High	High	High	High	High	High		2.13E+08	2.07E+08	2.06E+08	1.85E+08	2.01E+08	1.99E+08	38.24	2	215	2
FALSE	None	265	6912616	histone H2A.V isoform 1 [Homo sapiens]	7	1	12	1	1	128	13.5	10.58	High	High	High	High	High	High		2.13E+08	2.16E+08	2.22E+08	1.49E+08	1.53E+08	1.69E+08	15.05	1	108	1
FALSE	None	265	4504255	histone H2A.Z [Homo sapiens]	7	1	12	1	1	128	13.5	10.58	High	High	High	High	High	High		2.13E+08	2.16E+08	2.22E+08	1.49E+08	1.53E+08	1.69E+08	15.05	1	108	1
FALSE	Master Protein Candidate	265	10800130	histone H2A type 1-D [Homo sapiens]	22	2	28	2	1	130	14.1	10.9	High	High	High	High	High	High		2.13E+08	2.07E+08	2.06E+08	1.85E+08	2.01E+08	1.99E+08	38.24	2	215	2
FALSE	Master Protein Candidate	265	4504245	histone H2A type 1-C [Homo sapiens]	22	2	28	2	1	130	14.1	11.05	High	High	High	High	High	High		2.13E+08	2.07E+08	2.06E+08	1.85E+08	2.01E+08	1.99E+08	38.24	2	215	2
FALSE	Master Protein Candidate	265	28195394	histone H2A type 2-B [Homo sapiens]	22	2	28	2	1	130	14	10.89	High	High	High	High	High	High		2.13E+08	2.07E+08	2.06E+08	1.85E+08	2.01E+08	1.99E+08	38.24	2	215	2
FALSE	None	265	530377637	PREDICTED: histone H2A.Z isoform X1 [Homo sapiens]	6	1	12	1	1	152	16.6	10.65	High	High	High	High	High	High		2.13E+08	2.16E+08	2.22E+08	1.49E+08	1.53E+08	1.69E+08	15.05	1	108	1
FALSE	Master Protein Candidate	265	29553970	histone H2A.J [Homo sapiens]	22	2	28	2	1	129	14	10.9	High	High	High	High	High	High		2.13E+08	2.07E+08	2.06E+08	1.85E+08	2.01E+08	1.99E+08	38.24	2	215	2
FALSE	Master Protein Candidate	265	19557656	histone H2A type 1-B/E [Homo sapiens]	22	2	28	2	1	130	14.1	11.05	High	High	High	High	High	High		2.13E+08	2.07E+08	2.06E+08	1.85E+08	2.01E+08	1.99E+08	38.24	2	215	2
FALSE	Master Protein	265	4504253	histone H2AX [Homo sapiens]	20	2	28	2	1	143	15.1	10.74	High	High	High	High	High	High		2.13E+08	2.07E+08	2.06E+08	1.85E+08	2.01E+08	1.99E+08	38.24	2	215	2
FALSE	Master Protein Candidate	265	15617199	histone H2A type 3 [Homo sapiens]	22	2	28	2	1	130	14.1	11.05	High	High	High	High	High	High		2.13E+08	2.07E+08	2.06E+08	1.85E+08	2.01E+08	1.99E+08	38.24	2	215	2
FALSE	Master Protein	266	5174741	ubiquitin carboxyl-terminal hydrolase isozyme L3 isoform 2 [Homo sapiens]	13	2	10	2	1	230	26.2	4.92	Not Found	Not Found	Not Found	High	High	High					20596353	19244325		13.77	2	35	2
FALSE	None	266	530402623	PREDICTED: ubiquitin carboxyl-terminal hydrolase isozyme L3 isoform X1 [Homo sapiens]	7	1	6	1	1	244	27.6	8.21	Not Found	Not Found	Not Found	High	High	High								8.11	1	29	1
FALSE	None	266	401709950	ubiquitin carboxyl-terminal hydrolase isozyme L3 isoform 1 [Homo sapiens]	7	1	4	1	1	194	21.9	4.93	Not Found	Not Found	Not Found	High	High	Not Found					20596353	19244325		5.66	1	26	1
FALSE	Master Protein	267	63055057	beta-actin-like protein 2 [Homo sapiens]	14	4	33	2	1	376	42	5.59	High	High	High	High	High	High		1.11E+09	5.92E+08	26142077	2.71E+09	2.68E+09	2.56E+09	36.22	3	132	4
FALSE	None	268	14110407	heterogeneous nuclear ribonucleoprotein D-like isoform a [Homo sapiens]	2	1	12	1	1	420	46.4	9.57	High	High	High	High	High	High		49022229	49666131	44976999	93693084	1.01E+08	1.03E+08	5.29	1	69	1
FALSE	Master Protein	268	14110420	heterogeneous nuclear ribonucleoprotein D0 isoform a [Homo sapiens]	6	2	24	2	1	355	38.4	7.81	High	High	High	High	High	High		95589370	97262778	95577438	2.2E+08	2.26E+08	2.21E+08	23.93	2	151	2
FALSE	None	268	332801090	heterogeneous nuclear ribonucleoprotein D-like isoform b [Homo sapiens]	2	1	12	1	1	363	40	9.96	High	High	High	High	High	High		49022229	49666131	44976999	93693084	1.01E+08	1.03E+08	5.29	1	69	1
FALSE	Master Protein Candidate	268	51477708	heterogeneous nuclear ribonucleoprotein D0 isoform d [Homo sapiens]	8	2	24	2	1	287	30.7	8.41	High	High	High	High	High	High		95589370	97262778	95577438	2.2E+08	2.26E+08	2.21E+08	23.93	2	151	2
FALSE	Master Protein Candidate	268	14110417	heterogeneous nuclear ribonucleoprotein D0 isoform b [Homo sapiens]	7	2	24	2	1	336	36.2	8.1	High	High	High	High	High	High		95589370	97262778	95577438	2.2E+08	2.26E+08	2.21E+08	23.93	2	151	2
FALSE	Master Protein Candidate	268	14110414	heterogeneous nuclear ribonucleoprotein D0 isoform c [Homo sapiens]	7	2	24	2	1	306	32.8	8.16	High	High	High	High	High	High		95589370	97262778	95577438	2.2E+08	2.26E+08	2.21E+08	23.93	2	151	2
FALSE	Master Protein	269	5032069	splicing factor 3B subunit 4 [Homo sapiens]	3	1	2	1	1	424	44.4	8.56	High	Not Found	Not Found	Not Found	Not Found	Not Found		13732283						3.96	1	79	1
FALSE	Master Protein Candidate	27	530373816	PREDICTED: protein TFG isoform X2 [Homo sapiens]	4	1	4	1	1	396	43	5.17	Not Found	Not Found	Not Found	High	High	Not Found					29497807	28155467		6.49	1	36	1
FALSE	Master Protein	27	306774087	protein TFG isoform 1 [Homo sapiens]	4	1	4	1	1	400	43.4	5.1	Not Found	Not Found	Not Found	High	High	Not Found					29497807	28155467		6.49	1	36	1
FALSE	None	270	530420948	PREDICTED: peroxiredoxin-4 isoform X1 [Homo sapiens]	3	1	10	1	1	257	29.3	5.69	High	High	High	High	High	High		3.52E+08	3.59E+08	3.71E+08	8.51E+08	8.77E+08	7.72E+08	12.79	1	43	1
FALSE	None	270	5453549	peroxiredoxin-4 precursor [Homo sapiens]	3	1	10	1	1	271	30.5	6.29	High	High	High	High	High	High		3.52E+08	3.59E+08	3.71E+08	8.51E+08	8.77E+08	7.72E+08	12.79	1	43	1
FALSE	Master Protein	270	32455266	peroxiredoxin-1 [Homo sapiens]	28	5	45	4	1	199	22.1	8.13	High	High	High	High	High	High		4.5E+08	4.47E+08	4.44E+08	7.31E+08	7.14E+08	6.86E+08	47.46	5	330	5
FALSE	None	271	225543094	interstitial collagenase isoform 2 [Homo sapiens]	27	9	91	9	1	403	46.2	6.77	High	High	High	High	High	High		85114830	89870775	75138522	2.56E+08	2.31E+08	2.32E+08	105.06	9	728	9
FALSE	Master Protein	271	4505215	interstitial collagenase isoform 1 preproprotein [Homo sapiens]	29	12	122	12	1	469	54	6.96	High	High	High	High	High	High		1.02E+08	1.09E+08	97021774	2.92E+08	2.71E+08	2.72E+08	157.62	11	1410	12
FALSE	None	271	578822199	PREDICTED: neutrophil collagenase isoform X1 [Homo sapiens]	2	1	12	1	1	444	50.8	6.16	High	High	High	High	High	High		96175859	1.01E+08	97457857	2.08E+08	2.13E+08	1.74E+08	14.19	1	164	1
FALSE	None	271	4505221	neutrophil collagenase preproprotein [Homo sapiens]	2	1	12	1	1	467	53.4	6.87	High	High	High	High	High	High		96175859	1.01E+08	97457857	2.08E+08	2.13E+08	1.74E+08	14.19	1	164	1
FALSE	Master Protein Candidate	272	118582269	serine/arginine-rich splicing factor 1 isoform 2 [Homo sapiens]	25	4	40	4	1	201	22.4	7.94	High	High	High	High	High	High		24751546	38216346	33566701	1.07E+08	99010543	89861764	50.84	4	100	4
FALSE	Master Protein	272	5902076	serine/arginine-rich splicing factor 1 isoform 1 [Homo sapiens]	21	4	40	4	1	248	27.7	10.36	High	High	High	High	High	High		24751546	38216346	33566701	1.07E+08	99010543	89861764	50.84	4	100	4
FALSE	Master Protein Candidate	272	578831236	PREDICTED: serine/arginine-rich splicing factor 1 isoform X1 [Homo sapiens]	26	4	40	4	1	196	21.8	8.69	High	High	High	High	High	High		24751546	38216346	33566701	1.07E+08	99010543	89861764	50.84	4	100	4
FALSE	Master Protein	273	530387113	PREDICTED: single-stranded DNA-binding protein, mitochondrial isoform X1 [Homo sapiens]	9	1	6	1	1	159	18.5	10.1	Not Found	Not Found	Not Found	High	High	High					32530893	28278167	35812019	6.83	1	54	1
FALSE	Master Protein Candidate	273	374671789	single-stranded DNA-binding protein, mitochondrial precursor [Homo sapiens]	10	1	6	1	1	148	17.2	9.6	Not Found	Not Found	Not Found	High	High	High					32530893	28278167	35812019	6.83	1	54	1
FALSE	Master Protein Candidate	274	530387123	PREDICTED: zyxin isoform X2 [Homo sapiens]	3	1	4	1	1	631	67.1	7.23	High	Not Found	High	Not Found	Not Found	Not Found		21623586		26705127				2.17	1	0	1
FALSE	Master Protein Candidate	274	4508047	zyxin [Homo sapiens]	3	1	4	1	1	572	61.2	6.67	High	Not Found	High	Not Found	Not Found	Not Found		21623586		26705127				2.17	1	0	1
FALSE	Master Protein	274	530387121	PREDICTED: zyxin isoform X1 [Homo sapiens]	3	1	4	1	1	632	67.2	7.23	High	Not Found	High	Not Found	Not Found	Not Found		21623586		26705127				2.17	1	0	1
FALSE	Master Protein	275	38201675	syndecan-4 precursor [Homo sapiens]	7	1	2	1	1	198	21.6	4.5	Not Found	Not Found	High	Not Found	Not Found	Not Found				31165952				2.28	1	33	1
FALSE	Master Protein	276	4502101	annexin A1 [Homo sapiens]	34	9	117	9	1	346	38.7	7.02	High	High	High	High	High	High		1.75E+08	1.77E+08	1.98E+08	3.69E+08	4.28E+08	4.34E+08	180.74	9	1641	9
FALSE	Master Protein Candidate	277	223005925	zinc finger protein 805 isoform 1 [Homo sapiens]	2	1	1	1	1	627	71.1	7.69	Not Found	Not Found	Not Found	Not Found	Not Found	High							82964997	2.35	1		
FALSE	Master Protein Candidate	277	4585643	zinc finger protein 264 [Homo sapiens]	2	1	1	1	1	627	70.5	7.49	Not Found	Not Found	Not Found	Not Found	Not Found	High							82964997	2.35	1		
FALSE	Master Protein	277	530417609	PREDICTED: zinc finger protein 264 isoform X1 [Homo sapiens]	2	1	1	1	1	628	70.7	7.43	Not Found	Not Found	Not Found	Not Found	Not Found	High							82964997	2.35	1		
FALSE	Master Protein Candidate	277	223005927	zinc finger protein 805 isoform 2 [Homo sapiens]	3	1	1	1	1	494	56.6	8.43	Not Found	Not Found	Not Found	Not Found	Not Found	High							82964997	2.35	1		
FALSE	Master Protein	278	9951915	adenosylhomocysteinase isoform 1 [Homo sapiens]	3	1	2	1	1	432	47.7	6.34	Not Found	Not Found	Not Found	Not Found	High	Not Found						12224801		2.07	1	36	1
FALSE	Master Protein Candidate	278	530417910	PREDICTED: adenosylhomocysteinase isoform X2 [Homo sapiens]	4	1	2	1	1	404	44.6	6.47	Not Found	Not Found	Not Found	Not Found	High	Not Found						12224801		2.07	1	36	1
FALSE	Master Protein	279	568599832	cystatin-C precursor [Homo sapiens]	32	6	71	6	1	146	15.8	8.75	High	High	High	High	High	High		4.95E+08	2.34E+08	2.21E+08	8.14E+08	7.22E+08	8.03E+08	99.36	6	751	6
FALSE	Master Protein Candidate	28	578810585	PREDICTED: calpastatin isoform X7 [Homo sapiens]	2	1	14	1	1	757	81.3	5.16	High	High	High	High	High	High		32238201	40506822	36293432	69451327	73304800	74436379	20.23	1	266	1
FALSE	Master Protein Candidate	28	578810593	PREDICTED: calpastatin isoform X11 [Homo sapiens]	2	1	14	1	1	735	78.8	5.05	High	High	High	High	High	High		32238201	40506822	36293432	69451327	73304800	74436379	20.23	1	266	1
FALSE	Master Protein Candidate	28	109637759	calpastatin isoform f [Homo sapiens]	2	1	14	1	1	750	80.2	5.15	High	High	High	High	High	High		32238201	40506822	36293432	69451327	73304800	74436379	20.23	1	266	1
FALSE	Master Protein Candidate	28	578810603	PREDICTED: calpastatin isoform X16 [Homo sapiens]	3	1	14	1	1	667	71.9	4.92	High	High	High	High	High	High		32238201	40506822	36293432	69451327	73304800	74436379	20.23	1	266	1
FALSE	Master Protein Candidate	28	545746427	calpastatin isoform o [Homo sapiens]	3	1	14	1	1	636	69	4.88	High	High	High	High	High	High		32238201	40506822	36293432	69451327	73304800	74436379	20.23	1	266	1
FALSE	Master Protein Candidate	28	578810587	PREDICTED: calpastatin isoform X8 [Homo sapiens]	2	1	14	1	1	756	81.1	5.2	High	High	High	High	High	High		32238201	40506822	36293432	69451327	73304800	74436379	20.23	1	266	1
FALSE	Master Protein Candidate	28	578810597	PREDICTED: calpastatin isoform X13 [Homo sapiens]	2	1	14	1	1	695	75.3	5.07	High	High	High	High	High	High		32238201	40506822	36293432	69451327	73304800	74436379	20.23	1	266	1
FALSE	Master Protein Candidate	28	578810577	PREDICTED: calpastatin isoform X3 [Homo sapiens]	2	1	14	1	1	778	83.6	5.35	High	High	High	High	High	High		32238201	40506822	36293432	69451327	73304800	74436379	20.23	1	266	1
FALSE	Master Protein Candidate	28	578810575	PREDICTED: calpastatin isoform X2 [Homo sapiens]	2	1	14	1	1	790	84.8	5.36	High	High	High	High	High	High		32238201	40506822	36293432	69451327	73304800	74436379	20.23	1	266	1
FALSE	Master Protein Candidate	28	27765085	calpastatin isoform b [Homo sapiens]	2	1	14	1	1	686	74	4.97	High	High	High	High	High	High		32238201	40506822	36293432	69451327	73304800	74436379	20.23	1	266	1
FALSE	Master Protein Candidate	28	545746425	calpastatin isoform n [Homo sapiens]	3	1	14	1	1	666	71.7	4.92	High	High	High	High	High	High		32238201	40506822	36293432	69451327	73304800	74436379	20.23	1	266	1
FALSE	Master Protein	28	578810573	PREDICTED: calpastatin isoform X1 [Homo sapiens]	2	1	14	1	1	791	84.9	5.36	High	High	High	High	High	High		32238201	40506822	36293432	69451327	73304800	74436379	20.23	1	266	1
FALSE	Master Protein Candidate	28	578810609	PREDICTED: calpastatin isoform X19 [Homo sapiens]	4	1	14	1	1	430	47	4.84	High	High	High	High	High	High		32238201	40506822	36293432	69451327	73304800	74436379	20.23	1	266	1
FALSE	Master Protein Candidate	28	578810611	PREDICTED: calpastatin isoform X20 [Homo sapiens]	4	1	14	1	1	423	46.1	4.75	High	High	High	High	High	High		32238201	40506822	36293432	69451327	73304800	74436379	20.23	1	266	1
FALSE	Master Protein Candidate	28	578810589	PREDICTED: calpastatin isoform X9 [Homo sapiens]	2	1	14	1	1	754	81	5.1	High	High	High	High	High	High		32238201	40506822	36293432	69451327	73304800	74436379	20.23	1	266	1
FALSE	Master Protein Candidate	28	578810607	PREDICTED: calpastatin isoform X18 [Homo sapiens]	4	1	14	1	1	431	47.1	4.84	High	High	High	High	High	High		32238201	40506822	36293432	69451327	73304800	74436379	20.23	1	266	1
FALSE	Master Protein Candidate	28	578810579	PREDICTED: calpastatin isoform X4 [Homo sapiens]	2	1	14	1	1	776	83.5	5.22	High	High	High	High	High	High		32238201	40506822	36293432	69451327	73304800	74436379	20.23	1	266	1
FALSE	Master Protein Candidate	28	578810595	PREDICTED: calpastatin isoform X12 [Homo sapiens]	2	1	14	1	1	708	76.5	5.07	High	High	High	High	High	High		32238201	40506822	36293432	69451327	73304800	74436379	20.23	1	266	1
FALSE	Master Protein Candidate	28	578810591	PREDICTED: calpastatin isoform X10 [Homo sapiens]	2	1	14	1	1	749	80.1	5.15	High	High	High	High	High	High		32238201	40506822	36293432	69451327	73304800	74436379	20.23	1	266	1
FALSE	Master Protein Candidate	28	578810601	PREDICTED: calpastatin isoform X15 [Homo sapiens]	3	1	14	1	1	673	72.8	4.96	High	High	High	High	High	High		32238201	40506822	36293432	69451327	73304800	74436379	20.23	1	266	1
FALSE	Master Protein Candidate	28	578810605	PREDICTED: calpastatin isoform X17 [Homo sapiens]	3	1	14	1	1	654	70.6	4.91	High	High	High	High	High	High		32238201	40506822	36293432	69451327	73304800	74436379	20.23	1	266	1
FALSE	Master Protein Candidate	28	578810581	PREDICTED: calpastatin isoform X5 [Homo sapiens]	2	1	14	1	1	772	82.7	5.29	High	High	High	High	High	High		32238201	40506822	36293432	69451327	73304800	74436379	20.23	1	266	1

FALSE	Master Protein Candidate	28	578810599	PREDICTED: calpastatin isoform X14 [Homo sapiens]	2	1	14	1	1	689	74.4	5.02	High	High	High	High	High	High		32238201	40506822	36293432	69451327	73304800	74436379	20.23	1	266	1
FALSE	Master Protein Candidate	28	578810583	PREDICTED: calpastatin isoform X6 [Homo sapiens]	2	1	14	1	1	769	82.4	5.2	High	High	High	High	High	High		32238201	40506822	36293432	69451327	73304800	74436379	20.23	1	266	1
FALSE	Master Protein	280	157168362	purine nucleoside phosphorylase [Homo sapiens]	9	2	13	2	1	289	32.1	6.95	High	Not Found	High	High	High	High		18730500		21529154	53518660	58160975	57239201	13.21	2	137	2
FALSE	Master Protein Candidate	281	38202257	neutral alpha-glucosidase AB isoform 2 precursor [Homo sapiens]	6	4	9	4	1	944	106.8	6.14	High	Not Found	High	High	Not Found	High		27442841		42149151	74728569		61699632	6.68	4	0	3
FALSE	None	281	499589599	neutral alpha-glucosidase AB isoform 5 [Homo sapiens]	5	3	6	3	1	830	93.9	5.82	High	Not Found	High	Not Found	Not Found	Not Found		27442841		42149151				2.1	3	0	2
FALSE	Master Protein	281	88900491	neutral alpha-glucosidase AB isoform 3 precursor [Homo sapiens]	6	4	9	4	1	966	109.4	6.24	High	Not Found	High	High	Not Found	High		27442841		42149151	74728569		61699632	6.68	4	0	3
FALSE	None	281	499589572	neutral alpha-glucosidase AB isoform 4 [Homo sapiens]	5	3	6	3	1	852	96.5	5.94	High	Not Found	High	Not Found	Not Found	Not Found		27442841		42149151				2.1	3	0	2
FALSE	Master Protein Candidate	281	499589768	neutral alpha-glucosidase AB isoform 6 [Homo sapiens]	7	4	9	4	1	847	96.2	5.72	High	Not Found	High	High	Not Found	High		27442841		42149151	74728569		61699632	6.68	4	0	3
FALSE	Master Protein	282	4505641	proliferating cell nuclear antigen [Homo sapiens]	8	2	15	2	1	261	28.8	4.69	High	High	High	High	High	High		23354771	29325795	38950714	12063405	83289188	76581626	16.11	2	236	2
FALSE	Master Protein	283	10835063	nucleophosmin isoform 1 [Homo sapiens]	12	3	22	3	1	294	32.6	4.78	High	High	High	High	High	High		1.12E+08	1E+08	94541168	3.42E+08	1.81E+08	1.69E+08	28.33	3	188	3
FALSE	Master Protein Candidate	283	40353734	nucleophosmin isoform 2 [Homo sapiens]	14	3	22	3	1	265	29.4	4.61	High	High	High	High	High	High		1.12E+08	1E+08	94541168	3.42E+08	1.81E+08	1.69E+08	28.33	3	188	3
FALSE	None	283	530381066	PREDICTED: nucleophosmin isoform X2 [Homo sapiens]	10	2	6	2	1	230	25.3	4.54	Not Found	Not Found	High	Not Found	High	High						141181.6	276830	3.71	2	37	2
FALSE	None	283	578811124	PREDICTED: nucleophosmin isoform X3 [Homo sapiens]	7	1	2	1	1	181	19.9	4.4	Not Found	Not Found	Not Found	Not Found	Not Found	High								0	1	0	1
FALSE	None	283	83641870	nucleophosmin isoform 3 [Homo sapiens]	8	2	6	2	1	259	28.4	4.72	Not Found	Not Found	High	Not Found	High	High						141181.6	276830	3.71	2	37	2
FALSE	Master Protein	284	530421753	PREDICTED: moesin isoform X1 [Homo sapiens]	12	8	92	4	1	578	67.9	6.28	High	High	High	High	High	High		51046239	49159737	51214667	79591391	76291336	92679611	127.9	8	1077	8
FALSE	Master Protein Candidate	284	4505257	moesin [Homo sapiens]	12	8	92	4	1	577	67.8	6.4	High	High	High	High	High	High		51046239	49159737	51214667	79591391	76291336	92679611	127.9	8	1077	8
FALSE	Master Protein Candidate	285	578825985	PREDICTED: proteasome activator complex subunit 2 isoform X1 [Homo sapiens]	10	1	6	1	1	163	18.6	7.99	Not Found	Not Found	Not Found	High	High	High						27691260	34322976	8.18	1	18	1
FALSE	Master Protein Candidate	285	578825987	PREDICTED: proteasome activator complex subunit 2 isoform X2 [Homo sapiens]	10	1	6	1	1	162	18.5	6.7	Not Found	Not Found	Not Found	High	High	High						27691260	34322976	8.18	1	18	1
FALSE	Master Protein	285	30410792	proteasome activator complex subunit 2 [Homo sapiens]	7	1	6	1	1	239	27.4	5.73	Not Found	Not Found	Not Found	High	High	High						27691260	34322976	8.18	1	18	1
FALSE	None	286	543583760	ubiquitin-conjugating enzyme E2 variant 1 isoform h [Homo sapiens]	10	1	2	1	1	91	10.4	9.36	Not Found	Not Found	High	Not Found	Not Found	Not Found				42365112				1.95	1	0	1
FALSE	None	286	4507797	ubiquitin-conjugating enzyme E2 variant 2 [Homo sapiens]	7	1	5	1	1	145	16.4	8.09	Not Found	Not Found	Not Found	High	High	High					48957501	44955352	44802025	4.79	1	33	1
FALSE	None	286	383872493	ubiquitin-conjugating enzyme E2 variant 1 isoform c [Homo sapiens]	9	1	2	1	1	103	11.8	9.07	Not Found	Not Found	High	Not Found	Not Found	Not Found				42365112				1.95	1	0	1
FALSE	Master Protein Candidate	286	383872501	ubiquitin-conjugating enzyme E2 variant 1 isoform e [Homo sapiens]	13	2	7	2	1	144	16.2	6.7	Not Found	Not Found	High	High	High	High				42365112	48957501	44955352	44802025	6.74	2	33	2
FALSE	None	286	543583766	ubiquitin-conjugating enzyme E2 variant 1 isoform i [Homo sapiens]	16	1	5	1	1	64	6.9	4.78	Not Found	Not Found	Not Found	High	High	High					48957501	44955352	44802025	4.79	1	33	1
FALSE	None	286	383872507	ubiquitin-conjugating enzyme E2 variant 1 isoform f [Homo sapiens]	10	1	5	1	1	105	11.8	5.52	Not Found	Not Found	Not Found	High	High	High					48957501	44955352	44802025	4.79	1	33	1
FALSE	Master Protein Candidate	286	543583758	ubiquitin-conjugating enzyme E2 variant 1 isoform g [Homo sapiens]	18	2	7	2	1	105	12	9.72	Not Found	Not Found	High	High	High	High				42365112	48957501	44955352	44802025	6.74	2	33	2
FALSE	Master Protein	286	40806190	TMEM189-UBE2V1 fusion protein [Homo sapiens]	5	2	7	2	1	370	42.2	6.61	Not Found	Not Found	High	High	High	High				42365112	48957501	44955352	44802025	6.74	2	33	2
FALSE	Master Protein Candidate	286	73765546	ubiquitin-conjugating enzyme E2 variant 1 isoform d [Homo sapiens]	13	2	7	2	1	147	16.5	7.93	Not Found	Not Found	High	High	High	High				42365112	48957501	44955352	44802025	6.74	2	33	2
FALSE	Master Protein Candidate	286	40806167	ubiquitin-conjugating enzyme E2 variant 1 isoform a [Homo sapiens]	11	2	7	2	1	170	19.3	8.54	Not Found	Not Found	High	High	High	High				42365112	48957501	44955352	44802025	6.74	2	33	2
FALSE	None	286	530388562	PREDICTED: ubiquitin-conjugating enzyme E2 variant 2 isoform X1 [Homo sapiens]	10	1	5	1	1	105	12	9.86	Not Found	Not Found	Not Found	High	High	High					48957501	44955352	44802025	4.79	1	33	1
FALSE	Master Protein	287	11527402	integral membrane protein 2B [Homo sapiens]	4	1	2	1	1	266	30.3	5.14	Not Found	Not Found	Not Found	Not Found	High	Not Found						8642309		1.85	1	33	1
FALSE	Master Protein	288	5032057	protein S100-A11 [Homo sapiens]	15	2	340	2	1	105	11.7	7.12	High	High	High	High	High	High		6.4E+08	7.6E+08	3.4E+08	1.37E+09	1.36E+09	1.38E+09	522.23	1	3556	2
FALSE	None	289	530367948	PREDICTED: serine/arginine-rich splicing factor 7 isoform X3 [Homo sapiens]	10	1	12	1	1	137	15.8	9.8	High	High	High	High	High	High		87386110	89374110	88505209	2.65E+08	2.65E+08	2.76E+08	15.71	1	128	1
FALSE	None	289	530367944	PREDICTED: serine/arginine-rich splicing factor 7 isoform X1 [Homo sapiens]	6	1	12	1	1	235	26.9	11.85	High	High	High	High	High	High		87386110	89374110	88505209	2.65E+08	2.65E+08	2.76E+08	15.71	1	128	1
FALSE	Master Protein	289	4506901	serine/arginine-rich splicing factor 3 [Homo sapiens]	14	2	22	2	1	164	19.3	11.65	High	High	High	High	High	High		66755799	70331852	68500740	2.65E+08	1.97E+08	2.05E+08	26.45	2	160	2
FALSE	None	289	530367946	PREDICTED: serine/arginine-rich splicing factor 7 isoform X2 [Homo sapiens]	6	1	12	1	1	223	25.6	11.8	High	High	High	High	High	High		87386110	89374110	88505209	2.65E+08	2.65E+08	2.76E+08	15.71	1	128	1
FALSE	None	289	306482694	serine/arginine-rich splicing factor 7 isoform 2 [Homo sapiens]	6	1	12	1	1	226	26	11.77	High	High	High	High	High	High		87386110	89374110	88505209	2.65E+08	2.65E+08	2.76E+08	15.71	1	128	1
FALSE	None	289	72534660	serine/arginine-rich splicing factor 7 isoform 1 [Homo sapiens]	6	1	12	1	1	238	27.4	11.82	High	High	High	High	High	High		87386110	89374110	88505209	2.65E+08	2.65E+08	2.76E+08	15.71	1	128	1
FALSE	Master Protein	29	40317626	thrombospondin-1 precursor [Homo sapiens]	7	7	56	7	1	1170	129.3	4.94	High	High	High	High	High	High		71342997	73770144	76286212	1.15E+08	1.08E+08	1.11E+08	64.55	7	490	7
FALSE	Master Protein	290	4504183	glutathione S-transferase P [Homo sapiens]	40	7	88	7	1	210	23.3	5.64	High	High	High	High	High	High		2.63E+08	2.72E+08	2.65E+08	5.69E+08	3.34E+08	6.18E+08	124.23	6	1087	6
FALSE	Master Protein	291	5453710	LIM and SH3 domain protein 1 isoform a [Homo sapiens]	5	1	8	1	1	261	29.7	7.05	High	High	High	High	High	High		58453803	59515750	62088350	1.42E+08	1.41E+08	1.28E+08	4.35	1	56	1
FALSE	Master Protein Candidate	291	410444379	LIM and SH3 domain protein 1 isoform b [Homo sapiens]	6	1	8	1	1	205	23.2	4.94	High	High	High	High	High	High		58453803	59515750	62088350	1.42E+08	1.41E+08	1.28E+08	4.35	1	56	1
FALSE	Master Protein Candidate	292	6005882	serine protease 23 precursor [Homo sapiens]	7	2	17	2	1	383	43	9.42	High	High	High	High	High	High		27978603	31526507	48218115	32666525	73868438	33709253	12.63	2	28	2
FALSE	Master Protein	292	530396226	PREDICTED: serine protease 23 isoform X1 [Homo sapiens]	6	2	17	2	1	464	51.4	9.76	High	High	High	High	High	High		27978603	31526507	48218115	32666525	73868438	33709253	12.63	2	28	2
FALSE	Master Protein	293	83700235	eukaryotic initiation factor 4A-II [Homo sapiens]	2	1	2	1	1	407	46.4	5.48	Not Found	Not Found	Not Found	Not Found	High	Not Found						40578752		1.68	1	39	1
FALSE	Master Protein Candidate	293	4503529	eukaryotic initiation factor 4A-I isoform 1 [Homo sapiens]	2	1	2	1	1	406	46.1	5.48	Not Found	Not Found	Not Found	Not Found	High	Not Found						40578752		1.68	1	39	1
FALSE	Master Protein Candidate	294	530400796	PREDICTED: thymopoietin isoform X3 [Homo sapiens]	3	1	4	1	1	382	42.9	9.41	Not Found	Not Found	Not Found	High	Not Found	High					49998984		39081545	5.31	1	84	1
FALSE	Master Protein Candidate	294	73760405	thymopoietin isoform beta [Homo sapiens]	3	1	4	1	1	454	50.6	9.38	Not Found	Not Found	Not Found	High	Not Found	High					49998984		39081545	5.31	1	84	1
FALSE	Master Protein Candidate	294	73760401	thymopoietin isoform gamma [Homo sapiens]	3	1	4	1	1	345	38.7	9.16	Not Found	Not Found	Not Found	High	Not Found	High					49998984		39081545	5.31	1	84	1
FALSE	Master Protein Candidate	294	530400792	PREDICTED: thymopoietin isoform X1 [Homo sapiens]	3	1	4	1	1	414	46.3	9.03	Not Found	Not Found	Not Found	High	Not Found	High					49998984		39081545	5.31	1	84	1
FALSE	Master Protein	294	4507555	thymopoietin isoform alpha [Homo sapiens]	2	1	4	1	1	694	75.4	7.66	Not Found	Not Found	Not Found	High	Not Found	High					49998984		39081545	5.31	1	84	1
FALSE	Master Protein	295	5803187	transaldolase [Homo sapiens]	3	1	6	1	1	337	37.5	6.81	High	Not Found	Not Found	High	High	Not Found		45013848			1.17E+08	1.24E+08		6	1	47	1
FALSE	None	296	288915539	plastin-3 isoform 2 [Homo sapiens]	10	5	31	3	1	603	67.6	5.66	High	High	High	High	Not Found	Not Found		30843030	30427011	28570432	53541137			23.47	5	115	5
FALSE	Master Protein	296	209862851	plastin-3 isoform 1 [Homo sapiens]	12	6	47	4	1	630	70.8	5.6	High	High	High	High	High	High		22768734	25652073	28570432	44722218	32592346	32657647	44.56	6	273	6
FALSE	None	296	288915536	plastin-1 [Homo sapiens]	4	2	15	1	1	629	70.2	5.41	High	High	High	High	Not Found	Not Found		30843030	25144832	29452040	53541137			8.83	2	48	2
FALSE	Master Protein Candidate	296	537544626	plastin-3 isoform 4 [Homo sapiens]	13	6	47	4	1	585	65.6	6.3	High	High	High	High	High	High		22768734	25652073	28570432	44722218	32592346	32657647	44.56	6	273	6
FALSE	Master Protein Candidate	296	537544624	plastin-3 isoform 3 [Homo sapiens]	12	6	47	4	1	617	69.3	5.83	High	High	High	High	High	High		22768734	25652073	28570432	44722218	32592346	32657647	44.56	6	273	6
FALSE	Master Protein	297	5901926	cleavage and polyadenylation specificity factor subunit 5 [Homo sapiens]	8	1	9	1	1	227	26.2	8.82	High	High	High	High	High	High		33746211	32880682	30281092	85577767	88908294	77484418	2.36	1	35	1
FALSE	None	298	301897479	beta-enolase isoform 2 [Homo sapiens]	5	1	146	1	1	391	42.2	7.97	High	High	High	High	High	High		6.1E+08	6.15E+08	6.18E+08	1.04E+09	1.11E+09	1.1E+09	178.41	1	1186	1
FALSE	Master Protein Candidate	298	578798587	PREDICTED: alpha-enolase isoform X1 [Homo sapiens]	41	13	647	13	1	434	47.3	6.99	High	High	High	High	High	High		1.18E+09	1.21E+09	1.22E+09	2.84E+09	2.81E+09	2.53E+09	928.46	13	9112	13
FALSE	Master Protein	298	4503571	alpha-enolase isoform 1 [Homo sapiens]	41	13	647	13	1	434	47.1	7.39	High	High	High	High	High	High		1.18E+09	1.21E+09	1.22E+09	2.84E+09	2.81E+09	2.53E+09	928.46	13	9112	13
FALSE	None	298	301897477	beta-enolase isoform 1 [Homo sapiens]	4	1	146	1	1	434	47	7.71	High	High	High	High	High	High		6.1E+08	6.15E+08	6.18E+08	1.04E+09	1.11E+09	1.1E+09	178.41	1	1186	1
FALSE	None	298	530410063	PREDICTED: beta-enolase isoform X1 [Homo sapiens]	4	1	146	1	1	443	48	8.16	High	High	High	High	High	High		6.1E+08	6.15E+08	6.18E+08	1.04E+09	1.11E+09	1.1E+09	178.41	1	1186	1
FALSE	None	298	319996655	c-myc promoter-binding protein-1 isoform MBP-1 [Homo sapiens]	39	10	476	10	1	341	36.9	6.28	High	High	High	High	High	High		8.27E+08	8.52E+08	8.43E+08	2.01E+09	2.04E+09	1.89E+09	723.3	10	7736	10
FALSE	None	298	5803011	gamma-enolase [Homo sapiens]	4	1	146	1	1	434	47.2	5.03	High	High	High	High	High	High		6.1E+08	6.15E+08	6.18E+08	1.04E+09	1.11E+09	1.1E+09	178.41	1	1186	1
FALSE	Master Protein Candidate	299	67782309	superoxide dismutase [Mn], mitochondrial isoform B precursor [Homo sapiens]	8	1	10	1	1	183	20.7	8.25	Not Found	High	Not Found	High	High	High			26599909		32923222	32779981	32277184	13.42	1	139	1
FALSE	Master Protein	299	67782307	superoxide dismutase [Mn], mitochondrial isoform A precursor [Homo sapiens]	6	1	10	1	1	222	24.7	8.25	Not Found	High	Not Found	High	High	High			26599909		32923222	32779981	32277184	13.42	1	139	1
FALSE	Master Protein Candidate	3	386869506	40S ribosomal protein S3 isoform 3 [Homo sapiens]	11	1	4	1	1	117	12.6	9.28	High	High	Not Found	Not Found	Not Found	Not Found		15520320	18458477					5.57	1	27	1
FALSE	Master Protein	3	386869503	40S ribosomal protein S3 isoform 2 [Homo sapiens]	5	1	4	1	1	259	28.5	9.73	High	High	Not Found	Not Found	Not Found	Not Found		15520320	18458477					5.57	1	27	1
FALSE	Master Protein Candidate	3	378548190	40S ribosomal protein S3 isoform 1 [Homo sapiens]	5	1	4	1	1	243	26.7	9.66	High	High	Not Found	Not Found	Not Found	Not Found		15520320	18458477					5.57	1	27	1
FALSE	None	30	50593010	phosphoglycerate mutase 2 [Homo sapiens]	6	1	12	1	1	253	28.7	8.88	High	High	Not Found	High	High	High		1.13E+08	1.19E+08		2.59E+08	2.44E+08	2.63E+08	11.08	1	62	1
FALSE	None	30	71274132	phosphoglycerate mutase 4 [Homo sapiens]	6	1	12	1	1	254	28.8	6.65	High	High	Not Found	High	High	High		1.13E+08	1.19E+08		2.59E+08	2.44E+08	2.63E+08	11.08	1	62	1
FALSE	Master Protein	30	4505753	phosphoglycerate mutase 1 [Homo sapiens]	13	2	16	2	1	254	28.8	7.18	High	High	Not Found	High	High	High		1.13E+08	1.19E+08		1.86E+08	2.44E+08	1.89E+08	13.63	2	67	2
FALSE	Master Protein	300	110825984	malignant fibrous histiocytoma-amplified sequence 1 [Homo sapiens]	1	1	1	1	1	1052	116.9	7.88	Not Found	Not Found	Not Found	Not Found	High	Not Found						16851705				0	1
FALSE	Master Protein	301	578817797	PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X1 [Homo sapiens]	1	1	8	1	1	2510	288.9	5.41	High	High	High	High	Not Found	Not Found		12378467	12726007	12952575	29593320			10.99	1	21	1
FALSE	Master Protein Candidate	301	578817815	PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X10 [Homo sapiens]	1	1	8	1	1	2498	287.4	5.36	High	High	High	High	Not Found	Not Found		12378467	12726007	12952575	29593320			10.99	1	21	1
FALSE	Master Protein Candidate	301	578817799	PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X2 [Homo sapiens]	1	1	8	1	1	2505	288.4	5.41	High	High	High	High	Not Found	Not Found		12378467	12726007	12952575	29593320			10.99	1	21	1
FALSE	Master Protein Candidate	301	578817803	PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X4 [Homo sapiens]	1	1	8	1	1	2489	286.4	5.4	High	High	High	High	Not Found	Not Found		12378467	12726007	12952575	29593320			10.99	1	21	1
FALSE	Master Protein Candidate	301	578817807	PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X6 [Homo sapiens]	1	1	8	1	1	2483	285.8	5.41	High	High	High	High	Not Found	Not Found		12378467	12726007	12952575	29593320			10.99	1	21	1
FALSE	Master Protein Candidate	301	578817813	PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X9 [Homo sapiens]	1	1	8	1	1	2464	283.6	5.39	High	High	High	High	Not Found	Not Found		12378467	12726007	12952575	29593320			10.99	1	21	1
FALSE	Master Protein Candidate	301	194595509	spectrin alpha chain, non-erythrocytic 1 isoform 1 [Homo sapiens]	1	1	8	1	1	2477	284.9	5.35	High	High	High	High	Not Found	Not Found		12378467	12726007	12952575	29593320			10.99	1	21	1
FALSE	Master Protein Candidate	301	578817809	PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X7 [Homo sapiens]	1	1	8	1	1	2478	285.2	5.35	High	High	High	High	Not Found	Not Found		12378467	12726007	12952575	29593320			10.99	1	21	1
FALSE	Master Protein Candidate	301	154759259	spectrin alpha chain, non-erythrocytic 1 isoform 2 [Homo sapiens]	1	1	8	1	1	2472	284.4	5.35	High	High	High	High	Not Found	Not Found		12378467	12726007	12952575	29593320			10.99	1	21	1
FALSE	Master Protein Candidate	301	578817805	PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X5 [Homo sapiens]	1	1	8	1	1	2484	285.9	5.4	High	High	High	High	Not Found	Not Found		12378467	12726007	12952575	29593320			10.99	1	21	1
FALSE	Master Protein Candidate	301	578817801	PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X3 [Homo sapiens]	1	1	8	1	1	2490	286.7	5.4	High	High	High	High	Not Found	Not Found		12378467	12726007	12952575	29593320			10.99	1	21	1
FALSE	Master Protein Candidate	301	578817811	PREDICTED: spectrin alpha chain, non-erythrocytic 1 isoform X8 [Homo sapiens]	1	1	8	1	1	2469	284.2	5.39	High	High	High	High	Not Found	Not Found		12378467	12726007	12952575	29593320			10.99	1	21	1
FALSE	Master Protein Candidate	301	306966132	spectrin alpha chain, non-erythrocytic 1 isoform 3 [Homo sapiens]	1	1	8	1	1	2452	282.1	5.34	High	High	High	High	Not Found	Not Found		12378467	12726007	12952575	29593320			10.99	1	21	1
FALSE	Master Protein Candidate	303	530422907	PREDICTED: zinc finger protein 185 isoform X3 [Homo sapiens]	3	1	2	1	1	694	73.9	6.25	High	Not Found	High	Not Found	Not Found	Not Found		4182893		4651215						0	1
FALSE	Master Protein Candidate	303	530422917	PREDICTED: zinc finger protein 185 isoform X8 [Homo sapiens]	3	1	2	1	1	690	73.6	7.01	High	Not Found	High	Not Found	Not Found	Not Found		4182893		4651215						0	1
FALSE	Master Protein Candidate	303	530422935	PREDICTED: zinc finger protein 185 isoform X17 [Homo sapiens]	3	1	2	1	1	603	64.3	6.11	High	Not Found	High	Not Found	Not Found	Not Found		4182893		4651215						0	1
FALSE	Master Protein Candidate	303	530422905	PREDICTED: zinc finger protein 185 isoform X2 [Homo sapiens]	3	1	2	1	1	721	76.8	7.05	High	Not Found	High	Not Found	Not Found	Not Found		4182893		4651215						0	1
FALSE	Master Protein Candidate	303	530422931	PREDICTED: zinc finger protein 185 isoform X15 [Homo sapiens]	3	1	2	1	1	631	67.3	7.01	High	Not Found	High	Not Found	Not Found	Not Found		4182893		4651215						0	1
FALSE	Master Protein Candidate	303	148298722	zinc finger protein 185 isoform 4 [Homo sapiens]	3	1	2	1	1	689	73.5	7.01	High	Not Found	High	Not Found	Not Found	Not Found		4182893		4651215						0	1
FALSE	Master Protein Candidate	303	530422911	PREDICTED: zinc finger protein 185 isoform X5 [Homo sapiens]	3	1	2	1	1	692	73.8	7.05	High	Not Found	High	Not Found	Not Found	Not Found		4182893		4651215						0	1
FALSE	Master Protein Candidate	303	530422913	PREDICTED: zinc finger protein 185 isoform X6 [Homo sapiens]	3	1	2	1	1	692	73.7	7.05	High	Not Found	High	Not Found	Not Found	Not Found		4182893		4651215						0	1
FALSE	Master Protein Candidate	303	530422933	PREDICTED: zinc finger protein 185 isoform X16 [Homo sapiens]	3	1	2	1	1	630	67.2	7.01	High	Not Found	High	Not Found	Not Found	Not Found		4182893		4651215						0	1
FALSE	Master Protein Candidate	303	530422909	PREDICTED: zinc finger protein 185 isoform X4 [Homo sapiens]	3	1	2	1	1	693	73.8	7.05	High	Not Found	High	Not Found	Not Found	Not Found		4182893		4651215						0	1
FALSE	Master Protein Candidate	303	530422921	PREDICTED: zinc finger protein 185 isoform X10 [Homo sapiens]	3	1	2	1	1	663	70.7	7.05	High	Not Found	High	Not Found	Not Found	Not Found		4182893		4651215						0	1
FALSE	Master Protein Candidate	303	530422927	PREDICTED: zinc finger protein 185 isoform X13 [Homo sapiens]	3	1	2	1	1	659	70.4	7.02	High	Not Found	High	Not Found	Not Found	Not Found		4182893		4651215						0	1
FALSE	Master Protein Candidate	303	530422915	PREDICTED: zinc finger protein 185 isoform X7 [Homo sapiens]	3	1	2	1	1	691	73.7	7.05	High	Not Found	High	Not Found	Not Found	Not Found		4182893		4651215						0	1
FALSE	Master Protein Candidate	303	530422923	PREDICTED: zinc finger protein 185 isoform X11 [Homo sapiens]	3	1	2	1	1	660	70.5	7.02	High	Not Found	High	Not Found	Not Found	Not Found		4182893		4651215						0	1
FALSE	Master Protein	303	530422903	PREDICTED: zinc finger protein 185 isoform X1 [Homo sapiens]	3	1	2	1	1	722	76.9	7.05	High	Not Found	High	Not Found	Not Found	Not Found		4182893		4651215						0	1
FALSE	Master Protein Candidate	303	530422925	PREDICTED: zinc finger protein 185 isoform X12 [Homo sapiens]	3	1	2	1	1	660	70.3	7.01	High	Not Found	High	Not Found	Not Found	Not Found		4182893		4651215						0	1
FALSE	Master Protein Candidate	304	112382252	spectrin beta chain, non-erythrocytic 1 isoform 2 [Homo sapiens]	1	1	14	1	1	2155	251.2	5.53	Not Found	Not Found	High	High	High	High				2055843	8620286	9995948	8455950	19.21	1	170	1
FALSE	Master Protein	304	112382250	spectrin beta chain, non-erythrocytic 1 isoform 1 [Homo sapiens]	1	1	14	1	1	2364	274.4	5.57	Not Found	Not Found	High	High	High	High				2055843	8620286	9995948	8455950	19.21	1	170	1
FALSE	Master Protein Candidate	304	530368014	PREDICTED: spectrin beta chain, non-erythrocytic 1 isoform X2 [Homo sapiens]	1	1	14	1	1	2351	272.7	5.64	Not Found	Not Found	High	High	High	High				2055843	8620286	9995948	8455950	19.21	1	170	1
FALSE	Master Protein Candidate	305	31563374	eukaryotic translation initiation factor 6 isoform c [Homo sapiens]	5	1	3	1	1	226	23.7	5.17	Not Found	High	Not Found	High	Not Found	Not Found			22232402		56194196			0	1	0	1
FALSE	Master Protein	305	392494084	eukaryotic translation initiation factor 6 isoform a [Homo sapiens]	5	1	3	1	1	245	26.6	4.68	Not Found	High	Not Found	High	Not Found	Not Found			22232402		56194196			0	1	0	1
FALSE	None	306	349732256	thioredoxin isoform 2 [Homo sapiens]	39	3	24	3	1	85	9.4	6.04	High	High	High	High	High	High		6.93E+08	5.45E+08	6.97E+08	1.1E+09	1.07E+09	1.02E+09	26.57	3	266	3
FALSE	None	306	578817861	PREDICTED: thioredoxin isoform X1 [Homo sapiens]	22	2	24	2	1	115	13.1	8.07	High	High	High	High	High	High		3.56E+08	3.68E+08	6.97E+08	8.13E+08	7.84E+08	7.44E+08	34.22	2	249	2
FALSE	Master Protein	306	50592994	thioredoxin isoform 1 [Homo sapiens]	43	4	34	4	1	105	11.7	4.92	High	High	High	High	High	High		3.56E+08	3.71E+08	6.97E+08	7.68E+08	7.51E+08	7.17E+08	38.03	4	266	4
FALSE	None	307	227430303	CD109 antigen isoform 3 precursor [Homo sapiens]	4	4	35	4	1	1368	152.6	5.64	High	High	High	High	High	High		29730505	23818427	25666922	45695742	59765940	51095916	40.6	4	264	4
FALSE	Master Protein	307	530383018	PREDICTED: CD109 antigen isoform X1 [Homo sapiens]	5	5	38	5	1	1445	161.6	5.85	High	High	High	High	High	High		33383096	23818427	25666922	48178488	59765940	51095916	40.6	5	264	5

FALSE	Master Protein Candidate	307	227430301	CD109 antigen isoform 2 precursor [Homo sapiens]	5	5	38	5	1	1428	159.6	5.8	High	High	High	High	High	High		33383096	23818427	25666922	48178488	59765940	51095916	40.6	5	264	5
FALSE	Master Protein	308	4758950	peptidyl-prolyl cis-trans isomerase B precursor [Homo sapiens]	37	7	70	7	1	216	23.7	9.41	High	High	High	High	High	High		2.48E+08	3.08E+08	3.17E+08	6.31E+08	6.32E+08	6.06E+08	66.15	7	386	7
FALSE	Master Protein	309	13325075	sulfhydryl oxidase 1 isoform a precursor [Homo sapiens]	13	7	80	7	1	747	82.5	8.92	High	High	High	High	High	High		61329299	72376883	66915242	94038485	89432480	1.02E+08	101.3	7	789	7
FALSE	None	309	51873067	sulfhydryl oxidase 1 isoform b precursor [Homo sapiens]	14	6	76	6	1	604	66.8	8.56	High	High	High	High	High	High		61329299	71282395	66915242	94038485	89432480	1.02E+08	96.23	6	782	6
FALSE	Master Protein	31	4505185	macrophage migration inhibitory factor [Homo sapiens]	7	1	4	1	1	115	12.5	7.88	Not Found	Not Found	Not Found	High	Not Found	High								1.65	1	36	1
FALSE	Master Protein Candidate	310	519666790	protocadherin-1 isoform 3 [Homo sapiens]	1	1	6	1	1	1076	116.7	5.06	High	High	High	Not Found	Not Found	Not Found		19664753	24134008	25724975				7.41	1	61	1
FALSE	Master Protein Candidate	310	530380566	PREDICTED: protocadherin-1 isoform X3 [Homo sapiens]	1	1	6	1	1	1158	125.6	5.14	High	High	High	Not Found	Not Found	Not Found		19664753	24134008	25724975				7.41	1	61	1
FALSE	Master Protein	310	530380562	PREDICTED: protocadherin-1 isoform X1 [Homo sapiens]	1	1	6	1	1	1281	138.7	5.17	High	High	High	Not Found	Not Found	Not Found		19664753	24134008	25724975				7.41	1	61	1
FALSE	Master Protein Candidate	310	27754773	protocadherin-1 isoform 2 precursor [Homo sapiens]	1	1	6	1	1	1237	133.6	5.06	High	High	High	Not Found	Not Found	Not Found		19664753	24134008	25724975				7.41	1	61	1
FALSE	Master Protein Candidate	310	530380564	PREDICTED: protocadherin-1 isoform X2 [Homo sapiens]	1	1	6	1	1	1215	131.4	5.03	High	High	High	Not Found	Not Found	Not Found		19664753	24134008	25724975				7.41	1	61	1
FALSE	Master Protein Candidate	310	27754771	protocadherin-1 isoform 1 precursor [Homo sapiens]	1	1	6	1	1	1060	114.7	5.03	High	High	High	Not Found	Not Found	Not Found		19664753	24134008	25724975				7.41	1	61	1
FALSE	Master Protein	311	20149675	EF-hand domain-containing protein D2 [Homo sapiens]	3	1	6	1	1	240	26.7	5.2	Not Found	High	High	High	Not Found	Not Found			11283704	10646700	26313550			1.82	1	36	1
FALSE	Master Protein	312	21624607	coactosin-like protein [Homo sapiens]	11	1	18	1	1	142	15.9	5.67	High	High	High	High	High	High		54441072	50304653	48187733	1.22E+08	1.33E+08	1.31E+08	28.54	1	249	1
FALSE	Master Protein	314	7657176	protein canopy homolog 2 isoform 1 precursor [Homo sapiens]	9	1	4	1	1	182	20.6	4.92	Not Found	Not Found	Not Found	High	High	Not Found					14032263	24285066		5.2	1	21	1
FALSE	Master Protein Candidate	314	300360487	protein canopy homolog 2 isoform 2 precursor [Homo sapiens]	19	1	4	1	1	84	9.1	7.3	Not Found	Not Found	Not Found	High	High	Not Found					14032263	24285066		5.2	1	21	1
FALSE	Master Protein Candidate	315	530417133	PREDICTED: vasodilator-stimulated phosphoprotein isoform X2 [Homo sapiens]	4	1	3	1	1	379	39.7	8.94	Not Found	Not Found	High	Not Found	Not Found	High				13252730			24810564	2.21	1	0	1
FALSE	Master Protein Candidate	315	530417131	PREDICTED: vasodilator-stimulated phosphoprotein isoform X1 [Homo sapiens]	4	1	3	1	1	379	39.7	8.94	Not Found	Not Found	High	Not Found	Not Found	High				13252730			24810564	2.21	1	0	1
FALSE	Master Protein	315	4507869	vasodilator-stimulated phosphoprotein [Homo sapiens]	4	1	3	1	1	380	39.8	8.94	Not Found	Not Found	High	Not Found	Not Found	High				13252730			24810564	2.21	1	0	1
FALSE	Master Protein Candidate	316	291575128	L-lactate dehydrogenase B chain [Homo sapiens]	16	5	41	5	1	334	36.6	6.05	High	High	High	High	High	High		1.1E+08	1.17E+08	1.07E+08	3.05E+08	2.39E+08	98905271	56.9	5	405	5
FALSE	Master Protein	316	578822859	PREDICTED: L-lactate dehydrogenase B chain isoform X1 [Homo sapiens]	15	5	41	5	1	353	39.4	8.9	High	High	High	High	High	High		1.1E+08	1.17E+08	1.07E+08	3.05E+08	2.39E+08	98905271	56.9	5	405	5
FALSE	None	317	530401711	PREDICTED: GTP-binding nuclear protein Ran isoform X1 [Homo sapiens]	11	1	10	1	1	128	14.7	6.32	High	High	Not Found	High	High	High		20384943	19460595		45287321	43750836	39483967	8.4	1	41	1
FALSE	Master Protein	317	5453555	GTP-binding nuclear protein Ran [Homo sapiens]	12	2	15	2	1	216	24.4	7.49	High	High	Not Found	High	High	High		20384943	23879144		45287321	48148140	50164957	12.53	2	44	2
FALSE	None	318	21361322	tubulin beta-4A chain isoform 3 [Homo sapiens]	14	5	34	2	1	444	49.6	4.88	High	High	High	High	High	High		20171292	20326000	18764556	85177998	89751561	85976954	39.87	5	307	5
FALSE	Master Protein	318	5174735	tubulin beta-4B chain [Homo sapiens]	18	6	41	2	1	445	49.8	4.89	High	High	High	High	High	High		20171292	20326000	18764556	85177998	89751561	85976954	54.5	6	434	6
FALSE	None	318	574584818	tubulin beta-4A chain isoform 4 [Homo sapiens]	13	4	28	1	1	372	41.6	4.94	High	High	High	High	High	High		20171292	20326000	18764556	69330454	75236663	75361638	32.52	4	260	4
FALSE	None	318	574584803	tubulin beta-4A chain isoform 1 [Homo sapiens]	13	5	34	2	1	495	54.4	5.02	High	High	High	High	High	High		20171292	20326000	18764556	85177998	89751561	85976954	39.87	5	307	5
FALSE	None	318	574584811	tubulin beta-4A chain isoform 2 [Homo sapiens]	13	5	34	2	1	489	53.8	4.98	High	High	High	High	High	High		20171292	20326000	18764556	85177998	89751561	85976954	39.87	5	307	5
FALSE	None	318	42558279	tubulin beta-8 chain [Homo sapiens]	6	2	11	1	1	444	49.7	4.89	Not Found	Not Found	Not Found	High	High	High					1.01E+08	1.04E+08	96592271	14.75	2	89	2
FALSE	Master Protein Candidate	319	394582099	DNA replication licensing factor MCM3 isoform 2 [Homo sapiens]	1	1	12	1	1	818	91.9	6.33	High	High	High	High	High	High		13377681	12174830	11226291	30886735	33460573	31856034	12.66	1	133	1
FALSE	Master Protein	319	394582093	DNA replication licensing factor MCM3 isoform 1 [Homo sapiens]	1	1	12	1	1	853	95.8	5.77	High	High	High	High	High	High		13377681	12174830	11226291	30886735	33460573	31856034	12.66	1	133	1
FALSE	None	32	530412180	PREDICTED: keratin, type I cytoskeletal 15 isoform X1 [Homo sapiens]	4	2	20	0	1	456	49.2	4.77	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								26.27	2	91	2
FALSE	Master Protein	32	530412188	PREDICTED: keratin, type I cytoskeletal 17 isoform X1 [Homo sapiens]	20	8	62	5	1	434	48.1	5.3	High	High	High	High	High	High		1.08E+08	56018454	1.18E+08	19535507	31184047	38746953	83.02	8	573	7
FALSE	Master Protein Candidate	32	4557701	keratin, type I cytoskeletal 17 [Homo sapiens]	20	8	62	5	1	432	48.1	5.02	High	High	High	High	High	High		1.08E+08	56018454	1.18E+08	19535507	31184047	38746953	83.02	8	573	7
FALSE	None	32	24430192	keratin, type I cytoskeletal 16 [Homo sapiens]	4	2	20	0	1	473	51.2	5.05	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								26.27	2	91	2
FALSE	None	32	24430190	keratin, type I cytoskeletal 15 [Homo sapiens]	4	2	20	0	1	456	49.2	4.77	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								26.27	2	91	2
FALSE	None	32	15431310	keratin, type I cytoskeletal 14 [Homo sapiens]	4	2	20	0	1	472	51.6	5.16	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								26.27	2	91	2
FALSE	None	32	578830905	PREDICTED: keratin, type I cytoskeletal 15 isoform X2 [Homo sapiens]	4	2	20	0	1	480	52	4.97	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								26.27	2	91	2
FALSE	None	32;181	27894337	keratin, type I cytoskeletal 20 [Homo sapiens]	3	1	14	0	2	424	48.5	5.69	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								19.7	1	52	1
FALSE	Master Protein	320	578821832	PREDICTED: serpin H1 isoform X3 [Homo sapiens]	13	4	18	4	1	418	46.4	8.69	High	High	High	High	High	High		31313384	28325885	24984540	58658370	73561556	70403928	23.16	4	65	4
FALSE	Master Protein	321	6598323	rab GDP dissociation inhibitor beta isoform 1 [Homo sapiens]	7	2	27	2	1	445	50.6	6.47	High	High	High	High	High	High		23355519	24050103	22755853	61554388	55909235	55460876	41.61	2	389	2
FALSE	None	321	169646441	rab GDP dissociation inhibitor beta isoform 2 [Homo sapiens]	3	1	11	1	1	400	45.6	6.24	High	High	High	High	High	High		33056023	34236874	31256927	82645752	76490063	74998824	7.72	1	39	1
FALSE	Master Protein	322	85797673	bolA-like protein 2 [Homo sapiens]	11	1	7	1	1	152	16.9	8.19	High	Not Found	High	High	Not Found	High					23929523			6.66	1	0	1
FALSE	Master Protein Candidate	323	21040371	ATP-dependent RNA helicase DDX39A [Homo sapiens]	8	3	19	3	1	427	49.1	5.68	High	High	High	High	High	High		31813396	27797611	31110360	50456302	40809529	53149471	20.38	2	170	3
FALSE	Master Protein	323	4758112	spliceosome RNA helicase DDX39B [Homo sapiens]	8	3	19	3	1	428	49	5.67	High	High	High	High	High	High		31813396	27797611	31110360	50456302	40809529	53149471	20.38	2	170	3
FALSE	None	323	578832893	PREDICTED: ATP-dependent RNA helicase DDX39A isoform X1 [Homo sapiens]	11	2	18	2	1	222	26.1	5.97	High	High	High	High	High	High		31813396	27797611	31110360	50456302	55344010	53149471	20.38	2	170	2
FALSE	Master Protein Candidate	324	557357733	heat shock protein 105 kDa isoform 3 [Homo sapiens]	2	1	2	1	1	860	97.4	5.72	Not Found	Not Found	Not Found	Not Found	Not Found	High							25983931	0	1	0	1
FALSE	Master Protein	324	578824728	PREDICTED: heat shock protein 105 kDa isoform X3 [Homo sapiens]	2	1	2	1	1	913	103.1	6.25	Not Found	Not Found	Not Found	Not Found	Not Found	High							25983931	0	1	0	1
FALSE	Master Protein Candidate	324	557357685	heat shock protein 105 kDa isoform 2 [Homo sapiens]	2	1	2	1	1	814	92.1	5.55	Not Found	Not Found	Not Found	Not Found	Not Found	High							25983931	0	1	0	1
FALSE	Master Protein Candidate	324	557357710	heat shock protein 105 kDa isoform 4 [Homo sapiens]	2	1	2	1	1	782	88.8	5.6	Not Found	Not Found	Not Found	Not Found	Not Found	High							25983931	0	1	0	1
FALSE	Master Protein Candidate	324	530402054	PREDICTED: heat shock protein 105 kDa isoform X2 [Homo sapiens]	2	1	2	1	1	816	92.7	6.04	Not Found	Not Found	Not Found	Not Found	Not Found	High							25983931	0	1	0	1
FALSE	Master Protein Candidate	324	42544159	heat shock protein 105 kDa isoform 1 [Homo sapiens]	2	1	2	1	1	858	96.8	5.39	Not Found	Not Found	Not Found	Not Found	Not Found	High							25983931	0	1	0	1
FALSE	Master Protein Candidate	325	154707916	glutathione S-transferase C-terminal domain-containing protein isoform 2 [Homo sapiens]	3	1	2	1	1	546	61.3	7.96	Not Found	Not Found	Not Found	High	High	Not Found					1.69E+08	1.71E+08				0	1
FALSE	Master Protein	325	530378167	PREDICTED: glutathione S-transferase C-terminal domain-containing protein isoform X1 [Homo sapiens]	3	1	2	1	1	633	71	7.78	Not Found	Not Found	Not Found	High	High	Not Found					1.69E+08	1.71E+08				0	1
FALSE	Master Protein Candidate	326	520975484	ran-specific GTPase-activating protein isoform 3 [Homo sapiens]	6	1	4	1	1	200	23.2	5.29	Not Found	Not Found	Not Found	High	High	Not Found					90668391	93103571		3.81	1	30	1
FALSE	Master Protein Candidate	326	4506407	ran-specific GTPase-activating protein isoform 2 [Homo sapiens]	5	1	4	1	1	201	23.3	5.29	Not Found	Not Found	Not Found	High	High	Not Found					90668391	93103571		3.81	1	30	1
FALSE	Master Protein	326	520975477	ran-specific GTPase-activating protein isoform 1 [Homo sapiens]	4	1	4	1	1	278	31.9	8.75	Not Found	Not Found	Not Found	High	High	Not Found					90668391	93103571		3.81	1	30	1
FALSE	Master Protein Candidate	326	578837318	PREDICTED: ran-specific GTPase-activating protein isoform X1 [Homo sapiens]	4	1	4	1	1	271	30.9	6.68	Not Found	Not Found	Not Found	High	High	Not Found					90668391	93103571		3.81	1	30	1
FALSE	None	327	530418415	PREDICTED: polyadenylate-binding protein 1-like isoform X1 [Homo sapiens]	2	1	3	1	1	614	68.3	8.87	Not Found	Not Found	Not Found	Not Found	High	High						70341938	71499096	0	1	40	1
FALSE	None	327	61175237	polyadenylate-binding protein 1-like 2 [Homo sapiens]	6	1	3	1	1	200	22.8	9.1	Not Found	Not Found	Not Found	Not Found	High	High						70341938	71499096	0	1	40	1
FALSE	Master Protein	327	46367787	polyadenylate-binding protein 1 [Homo sapiens]	8	4	24	4	1	636	70.6	9.5	High	High	High	High	High	High		33594536	49620397	29197313	94464824	1.09E+08	90775082	22.99	4	148	4
FALSE	None	327	578836199	PREDICTED: polyadenylate-binding protein 1-like isoform X3 [Homo sapiens]	3	1	3	1	1	330	37.7	9.22	Not Found	Not Found	Not Found	Not Found	High	High						70341938	71499096	0	1	40	1
FALSE	Master Protein Candidate	327	45238849	polyadenylate-binding protein 3 [Homo sapiens]	8	4	24	4	1	631	70	9.67	High	High	High	High	High	High		33594536	49620397	29197313	94464824	1.09E+08	90775082	22.99	4	148	4
FALSE	Master Protein	328	5174661	protein S100-A2 [Homo sapiens]	34	3	17	3	1	97	11	4.78	High	High	High	High	High	High		1.6E+08	1E+08	30712773	91843177	61416699	1.87E+08	15.45	3	172	3
FALSE	Master Protein Candidate	329	257195182	FXYD domain-containing ion transport regulator 5 precursor [Homo sapiens]	8	1	22	1	1	178	19.5	5.85	High	High	High	High	High	High		1.9E+08	1.76E+08	2E+08	3.21E+08	3.41E+08	2.88E+08	31.15	1	110	1
FALSE	Master Protein Candidate	329	578834559	PREDICTED: FXYD domain-containing ion transport regulator 5 isoform X3 [Homo sapiens]	10	1	22	1	1	147	16.1	6.76	High	High	High	High	High	High		1.9E+08	1.76E+08	2E+08	3.21E+08	3.41E+08	2.88E+08	31.15	1	110	1
FALSE	Master Protein	329	578834555	PREDICTED: FXYD domain-containing ion transport regulator 5 isoform X1 [Homo sapiens]	8	1	22	1	1	194	21.1	4.94	High	High	High	High	High	High		1.9E+08	1.76E+08	2E+08	3.21E+08	3.41E+08	2.88E+08	31.15	1	110	1
FALSE	Master Protein Candidate	33	530396006	PREDICTED: CD44 antigen isoform X2 [Homo sapiens]	2	1	7	1	1	742	81.5	5.33	High	High	High	Not Found	High	Not Found		1.22E+08	1.22E+08	1.19E+08		1.95E+08		7.57	1	59	1
FALSE	Master Protein Candidate	33	48255939	CD44 antigen isoform 3 precursor [Homo sapiens]	2	1	7	1	1	493	53.4	5.4	High	High	High	Not Found	High	Not Found		1.22E+08	1.22E+08	1.19E+08		1.95E+08		7.57	1	59	1
FALSE	Master Protein Candidate	33	530396020	PREDICTED: CD44 antigen isoform X9 [Homo sapiens]	2	1	7	1	1	578	62.9	5.08	High	High	High	Not Found	High	Not Found		1.22E+08	1.22E+08	1.19E+08		1.95E+08		7.57	1	59	1
FALSE	Master Protein	33	530396004	PREDICTED: CD44 antigen isoform X1 [Homo sapiens]	2	1	7	1	1	743	81.6	5.33	High	High	High	Not Found	High	Not Found		1.22E+08	1.22E+08	1.19E+08		1.95E+08		7.57	1	59	1
FALSE	Master Protein Candidate	33	321400142	CD44 antigen isoform 8 precursor [Homo sapiens]	4	1	7	1	1	294	32.1	5.21	High	High	High	Not Found	High	Not Found		1.22E+08	1.22E+08	1.19E+08		1.95E+08		7.57	1	59	1
FALSE	Master Protein Candidate	33	578820968	PREDICTED: CD44 antigen isoform X12 [Homo sapiens]	2	1	7	1	1	735	80.8	5.33	High	High	High	Not Found	High	Not Found		1.22E+08	1.22E+08	1.19E+08		1.95E+08		7.57	1	59	1
FALSE	Master Protein Candidate	33	48255937	CD44 antigen isoform 2 precursor [Homo sapiens]	2	1	7	1	1	699	76.6	5.27	High	High	High	Not Found	High	Not Found		1.22E+08	1.22E+08	1.19E+08		1.95E+08		7.57	1	59	1
FALSE	Master Protein Candidate	33	578820976	PREDICTED: CD44 antigen isoform X13 [Homo sapiens]	3	1	7	1	1	397	44.4	5.36	High	High	High	Not Found	High	Not Found		1.22E+08	1.22E+08	1.19E+08		1.95E+08		7.57	1	59	1
FALSE	Master Protein Candidate	33	48255935	CD44 antigen isoform 1 precursor [Homo sapiens]	2	1	7	1	1	742	81.5	5.33	High	High	High	Not Found	High	Not Found		1.22E+08	1.22E+08	1.19E+08		1.95E+08		7.57	1	59	1
FALSE	Master Protein Candidate	33	321400138	CD44 antigen isoform 6 precursor [Homo sapiens]	3	1	7	1	1	429	46.5	5.74	High	High	High	Not Found	High	Not Found		1.22E+08	1.22E+08	1.19E+08		1.95E+08		7.57	1	59	1
FALSE	Master Protein Candidate	33	321400140	CD44 antigen isoform 7 precursor [Homo sapiens]	4	1	7	1	1	340	37.3	5.52	High	High	High	Not Found	High	Not Found		1.22E+08	1.22E+08	1.19E+08		1.95E+08		7.57	1	59	1
FALSE	Master Protein Candidate	33	530396012	PREDICTED: CD44 antigen isoform X5 [Homo sapiens]	2	1	7	1	1	700	76.6	5.27	High	High	High	Not Found	High	Not Found		1.22E+08	1.22E+08	1.19E+08		1.95E+08		7.57	1	59	1
FALSE	Master Protein Candidate	33	530396022	PREDICTED: CD44 antigen isoform X10 [Homo sapiens]	2	1	7	1	1	535	58	5.02	High	High	High	Not Found	High	Not Found		1.22E+08	1.22E+08	1.19E+08		1.95E+08		7.57	1	59	1
FALSE	Master Protein Candidate	33	48255941	CD44 antigen isoform 4 precursor [Homo sapiens]	3	1	7	1	1	361	39.4	5.41	High	High	High	Not Found	High	Not Found		1.22E+08	1.22E+08	1.19E+08		1.95E+08		7.57	1	59	1
FALSE	Master Protein Candidate	33	530396010	PREDICTED: CD44 antigen isoform X4 [Homo sapiens]	2	1	7	1	1	702	77	5.39	High	High	High	Not Found	High	Not Found		1.22E+08	1.22E+08	1.19E+08		1.95E+08		7.57	1	59	1
FALSE	Master Protein Candidate	33	530396008	PREDICTED: CD44 antigen isoform X3 [Homo sapiens]	2	1	7	1	1	703	77	5.39	High	High	High	Not Found	High	Not Found		1.22E+08	1.22E+08	1.19E+08		1.95E+08		7.57	1	59	1
FALSE	Master Protein Candidate	33	578820966	PREDICTED: CD44 antigen isoform X11 [Homo sapiens]	2	1	7	1	1	741	81.4	5.33	High	High	High	Not Found	High	Not Found		1.22E+08	1.22E+08	1.19E+08		1.95E+08		7.57	1	59	1
FALSE	Master Protein Candidate	33	530396018	PREDICTED: CD44 antigen isoform X8 [Homo sapiens]	2	1	7	1	1	580	63.1	5.71	High	High	High	Not Found	High	Not Found		1.22E+08	1.22E+08	1.19E+08		1.95E+08		7.57	1	59	1
FALSE	Master Protein	330	4502107	annexin A5 [Homo sapiens]	28	7	67	7	1	320	35.9	5.05	High	High	High	High	High	High		63780606	58205868	56046485	1.16E+08	1.15E+08	1.03E+08	88.34	7	675	6
FALSE	None	331	5453599	F-actin-capping protein subunit alpha-2 [Homo sapiens]	3	1	3	1	1	286	32.9	5.85	High	Not Found	High	Not Found	Not Found	Not Found		18177750						2.2	1	37	1
FALSE	Master Protein	331	5453597	F-actin-capping protein subunit alpha-1 [Homo sapiens]	8	2	11	2	1	286	32.9	5.69	High	High	High	Not Found	High	High		29865857	40051699			1.03E+08	1.13E+08	7.95	2	37	2
FALSE	Master Protein	332	17149836	peptidyl-prolyl cis-trans isomerase FKBP1A isoform a [Homo sapiens]	13	1	12	1	1	108	11.9	8.16	High	High	High	High	High	High		39448319	44581605	43758583	90960070	90704182	91425076	20.91	1	208	1
FALSE	Master Protein	333	530370872	PREDICTED: lupus La protein isoform X1 [Homo sapiens]	13	4	29	4	1	408	46.8	7.12	High	High	High	High	High	High		21005348	22100839		52835901	54969938	48554355	44.13	4	504	3
FALSE	Master Protein Candidate	334	41327730	calponin-2 isoform b [Homo sapiens]	6	1	2	1	1	270	29.5	6.99	High	Not Found	Not Found	Not Found	Not Found	Not Found								2.1	1	0	1
FALSE	Master Protein	334	4758018	calponin-2 isoform a [Homo sapiens]	6	1	2	1	1	309	33.7	7.33	High	Not Found	Not Found	Not Found	Not Found	Not Found								2.1	1	0	1
FALSE	Master Protein	335	15451856	caveolin-1 isoform alpha [Homo sapiens]	8	1	6	1	1	178	20.5	6.02	Not Found	Not Found	Not Found	High	High	High					52918242	50085703	47746002	9.73	1	120	1
FALSE	Master Protein Candidate	336	38150007	small nuclear ribonucleoprotein-associated proteins B and B' isoform B' [Homo sapiens]	10	2	16	2	1	240	24.6	11.19	High	High	High	High	High	High		38015463	43341817	41752068	88309074	80870285	64733757	20.28	2	220	2
FALSE	Master Protein	336	13027648	small nuclear ribonucleoprotein-associated protein N [Homo sapiens]	10	2	16	2	1	240	24.6	11.19	High	High	High	High	High	High		38015463	43341817	41752068	88309074	80870285	64733757	20.28	2	220	2
FALSE	None	336	578806791	PREDICTED: ER degradation-enhancing alpha-mannosidase-like protein 1 isoform X2 [Homo sapiens]	1	1	10	1	1	553	61.6	7.05	High	High	High	High	High	Not Found		38015463	43341817	41752068	1.02E+08	86247838		10.91	1	111	1
FALSE	None	336	578806793	PREDICTED: ER degradation-enhancing alpha-mannosidase-like protein 1 isoform X3 [Homo sapiens]	2	1	10	1	1	513	57	7.52	High	High	High	High	High	Not Found		38015463	43341817	41752068	1.02E+08	86247838		10.91	1	111	1
FALSE	Master Protein Candidate	336	4507125	small nuclear ribonucleoprotein-associated proteins B and B' isoform B [Homo sapiens]	10	2	16	2	1	231	23.6	10.9	High	High	High	High	High	High		38015463	43341817	41752068	88309074	80870285	64733757	20.28	2	220	2
FALSE	None	336	7662002	ER degradation-enhancing alpha-mannosidase-like protein 1 [Homo sapiens]	1	1	10	1	1	657	73.7	6.92	High	High	High	High	High	Not Found		38015463	43341817	41752068	1.02E+08	86247838		10.91	1	111	1
FALSE	Master Protein	337	116534898	desmoglein-2 preproprotein [Homo sapiens]	3	3	13	3	1	1118	122.2	5.24	High	High	High	High	High	High		14913439	18791945	16256420	55048448	56345139	66651666	19.04	3	71	3
FALSE	Master Protein	338	4557581	fatty acid-binding protein, epidermal [Homo sapiens]	7	1	8	1	1	135	15.2	7.01	High	High	Not Found	High	High	High		1.01E+08	98480050		1.32E+08	1.3E+08	1.33E+08	4.2	1	39	1
FALSE	Master Protein Candidate	339	120433593	acyl-CoA-binding protein isoform 2 [Homo sapiens]	11	1	4	1	1	88	10.1	6.57	Not Found	High	High	Not Found	Not Found	Not Found			12575514	16684548				0	1	0	1
FALSE	Master Protein	339	295849266	acyl-CoA-binding protein isoform 4 [Homo sapiens]	7	1	4	1	1	148	16.5	9.38	Not Found	High	High	Not Found	Not Found	Not Found			12575514	16684548				0	1	0	1
FALSE	Master Protein Candidate	339	120433590	acyl-CoA-binding protein isoform 3 [Homo sapiens]	11	1	4	1	1	87	10	6.57	Not Found	High	High	Not Found	Not Found	Not Found			12575514	16684548				0	1	0	1
FALSE	Master Protein Candidate	339	295842534	acyl-CoA-binding protein isoform 6 [Homo sapiens]	10	1	4	1	1	97	11.1	8.32	Not Found	High	High	Not Found	Not Found	Not Found			12575514	16684548				0	1	0	1
FALSE	Master Protein Candidate	339	544063480	acyl-CoA-binding protein isoform 1 [Homo sapiens]	10	1	4	1	1	104	11.8	5.55	Not Found	High	High	Not Found	Not Found	Not Found			12575514	16684548				0	1	0	1
FALSE	Master Protein Candidate	339	544063486	acyl-CoA-binding protein isoform 7 [Homo sapiens]	16	1	4	1	1	63	7.3	8.94	Not Found	High	High	Not Found	Not Found	Not Found			12575514	16684548				0	1	0	1
FALSE	Master Protein Candidate	339	295842514	acyl-CoA-binding protein isoform 5 [Homo sapiens]	8	1	4	1	1	129	14.4	9.42	Not Found	High	High	Not Found	Not Found	Not Found			12575514	16684548				0	1	0	1
FALSE	Master Protein Candidate	34	530378875	PREDICTED: succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial isoform X3 [Homo sapiens]	3	1	3	1	1	583	63.5	7.24	Not Found	High	High	Not Found	High	Not Found			1.01E+08	98955191		2.18E+08		4.18	1		
FALSE	Master Protein	34	530378871	PREDICTED: succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial isoform X1 [Homo sapiens]	3	1	3	1	1	668	72.6	7.49	Not Found	High	High	Not Found	High	Not Found			1.01E+08	98955191		2.18E+08		4.18	1		
FALSE	Master Protein Candidate	34	156416003	succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial [Homo sapiens]	3	1	3	1	1	664	72.6	7.39	Not Found	High	High	Not Found	High	Not Found			1.01E+08	98955191		2.18E+08		4.18	1		
FALSE	Master Protein	340	530364686	PREDICTED: laminin subunit gamma-2 isoform X1 [Homo sapiens]	7	6	34	6	1	1256	137.8	6.51	High	High	High	High	High	High		28300445	34605170	30753019	49326008	60546577	56810062	44.57	6	268	6
FALSE	Master Protein Candidate	340	157419138	laminin subunit gamma-2 isoform a precursor [Homo sapiens]	7	6	34	6	1	1193	130.9	6.19	High	High	High	High	High	High		28300445	34605170	30753019	49326008	60546577	56810062	44.57	6	268	6
FALSE	None	340	157419140	laminin subunit gamma-2 isoform b precursor [Homo sapiens]	6	5	25	5	1	1111	121.5	6.38	High	High	High	High	High	High		29811848	34605170	31046118	31372351	58359433	56810062	35.92	5	220	5

FALSE	None	340	578800924	PREDICTED: laminin subunit gamma-2 isoform X2 [Homo sapiens]	6	5	25	5	1	1208	132	6.64	High	High	High	High	High	High		29811848	34605170	31046118	31372351	58359433	56810062	35.92	5	220	5
FALSE	Master Protein	341	315259111	NEDD8-MDP1 protein [Homo sapiens]	7	1	12	1	1	193	22	6.37	High	High	High	High	High	High		25939206	27854346	28382961	92233506	90597587	85887322	16.92	1	93	1
FALSE	Master Protein Candidate	341	5453760	NEDD8 precursor [Homo sapiens]	17	1	12	1	1	81	9.1	8.43	High	High	High	High	High	High		25939206	27854346	28382961	92233506	90597587	85887322	16.92	1	93	1
FALSE	Master Protein	342	11545839	brain-specific serine protease 4 precursor [Homo sapiens]	5	1	3	1	1	317	33.7	7.61	High	High	Not Found	Not Found	Not Found	Not Found		36737916	37917006					2.34	1	62	1
FALSE	Master Protein Candidate	342	578828174	PREDICTED: brain-specific serine protease 4 isoform X2 [Homo sapiens]	6	1	3	1	1	246	26.4	7.36	High	High	Not Found	Not Found	Not Found	Not Found		36737916	37917006					2.34	1	62	1
FALSE	Master Protein Candidate	343	7706573	45 kDa calcium-binding protein isoform 1 precursor [Homo sapiens]	3	1	6	1	1	348	39.6	5.11	High	High	High	Not Found	Not Found	Not Found		22802486	20590990	22697266				8.47	1	133	1
FALSE	Master Protein	343	18699732	45 kDa calcium-binding protein isoform 2 precursor [Homo sapiens]	3	1	6	1	1	362	41.8	4.86	High	High	High	Not Found	Not Found	Not Found		22802486	20590990	22697266				8.47	1	133	1
FALSE	Master Protein	344	578828140	PREDICTED: periplakin isoform X1 [Homo sapiens]	1	1	3	1	1	1769	205.5	5.49	Not Found	Not Found	Not Found	High	Not Found	High								2.53	1	0	1
FALSE	Master Protein Candidate	344	45439327	periplakin [Homo sapiens]	1	1	3	1	1	1756	204.6	5.58	Not Found	Not Found	Not Found	High	Not Found	High								2.53	1	0	1
FALSE	None	345	68303565	proteasome subunit alpha type-7-like isoform 3 [Homo sapiens]	25	4	24	4	1	212	23.7	9.11	High	High	High	High	High	High		48205619	50603951	53875788	99585301	79508983	91936720	27.47	4	235	4
FALSE	None	345	530413651	PREDICTED: proteasome subunit alpha type-7-like isoform X1 [Homo sapiens]	17	3	18	3	1	224	25	8.76	High	High	High	High	High	High		48205619	50603951	53875788	1.32E+08	85580717	1.2E+08	19.56	3	227	3
FALSE	None	345	68303563	proteasome subunit alpha type-7-like isoform 2 [Homo sapiens]	22	4	24	4	1	250	27.8	8.98	High	High	High	High	High	High		48205619	50603951	53875788	99585301	79508983	91936720	27.47	4	235	4
FALSE	None	345	68303561	proteasome subunit alpha type-7-like isoform 1 [Homo sapiens]	21	4	24	4	1	256	28.5	8.98	High	High	High	High	High	High		48205619	50603951	53875788	99585301	79508983	91936720	27.47	4	235	4
FALSE	Master Protein	345	4506189	proteasome subunit alpha type-7 [Homo sapiens]	32	6	29	6	1	248	27.9	8.46	High	High	High	High	High	High		41852632	50603951	46079466	99585301	79508983	91936720	35.48	6	255	6
FALSE	None	346	411147376	annexin A8 isoform 3 [Homo sapiens]	10	2	10	2	1	265	30	5.34	High	High	High	Not Found	Not Found	Not Found		19046063	21657200	22936548				11.86	2	42	2
FALSE	None	346	524552794	annexin A8-like protein 1 isoform 3 [Homo sapiens]	17	3	19	3	1	270	30.5	6.8	High	High	High	High	High	High		42233670	44384111	45957967	1.11E+08	1.07E+08	97001755	34.32	3	410	2
FALSE	None	346	578844916	PREDICTED: annexin A8-like [Homo sapiens]	14	3	17	3	1	305	33.6	9.35	High	High	High	High	High	High		44715028	67111023	44979145	1.11E+08	1.07E+08	97001755	31.7	3	412	2
FALSE	None	346	524553785	annexin A8-like protein 1 isoform 2 [Homo sapiens]	6	1	1	1	1	276	30.7	8.28	Not Found	Not Found	Not Found	Not Found	Not Found	High							85306292	2.2	1		
FALSE	Master Protein Candidate	346	524552373	annexin A8-like protein 1 isoform 1 [Homo sapiens]	18	4	23	4	1	327	36.9	5.78	High	High	High	High	High	High		35331587	44384111	37957886	1.11E+08	1.07E+08	97001755	38.94	4	417	3
FALSE	Master Protein	346	578819715	PREDICTED: annexin A8 isoform X2 [Homo sapiens]	17	4	23	4	1	351	39.5	6.1	High	High	High	High	High	High		35331587	44384111	37957886	1.11E+08	1.07E+08	97001755	38.94	4	417	3
FALSE	None	346	411147374	annexin A8 isoform 1 [Homo sapiens]	12	3	11	3	1	365	40.7	6.04	High	High	High	Not Found	Not Found	High		19046063	21657200	22936548			85306292	14.06	3	42	2
FALSE	Master Protein Candidate	346	91807122	annexin A8-like protein 2 [Homo sapiens]	18	4	23	4	1	327	36.8	5.63	High	High	High	High	High	High		35331587	44384111	37957886	1.11E+08	1.07E+08	97001755	38.94	4	417	3
FALSE	Master Protein Candidate	346	91823262	annexin A8 isoform 2 [Homo sapiens]	18	4	23	4	1	327	36.9	5.78	High	High	High	High	High	High		35331587	44384111	37957886	1.11E+08	1.07E+08	97001755	38.94	4	417	3
FALSE	Master Protein Candidate	347	324021736	amyloid beta A4 protein isoform i precursor [Homo sapiens]	1	1	12	1	1	733	82.9	4.78	High	High	High	High	High	High		60257329	61975453	51704204	1.12E+08	1.04E+08	1.16E+08	16.25	1	47	1
FALSE	Master Protein Candidate	347	209915575	amyloid beta A4 protein isoform g [Homo sapiens]	2	1	12	1	1	660	75.1	4.84	High	High	High	High	High	High		60257329	61975453	51704204	1.12E+08	1.04E+08	1.16E+08	16.25	1	47	1
FALSE	Master Protein Candidate	347	41406055	amyloid beta A4 protein isoform b precursor [Homo sapiens]	1	1	12	1	1	751	84.8	4.79	High	High	High	High	High	High		60257329	61975453	51704204	1.12E+08	1.04E+08	1.16E+08	16.25	1	47	1
FALSE	Master Protein Candidate	347	324021740	amyloid beta A4 protein isoform j precursor [Homo sapiens]	1	1	12	1	1	677	76.7	4.81	High	High	High	High	High	High		60257329	61975453	51704204	1.12E+08	1.04E+08	1.16E+08	16.25	1	47	1
FALSE	Master Protein Candidate	347	209915573	amyloid beta A4 protein isoform f precursor [Homo sapiens]	1	1	12	1	1	714	80.8	4.82	High	High	High	High	High	High		60257329	61975453	51704204	1.12E+08	1.04E+08	1.16E+08	16.25	1	47	1
FALSE	Master Protein Candidate	347	209915570	amyloid beta A4 protein isoform e precursor [Homo sapiens]	2	1	12	1	1	639	72.5	4.82	High	High	High	High	High	High		60257329	61975453	51704204	1.12E+08	1.04E+08	1.16E+08	16.25	1	47	1
FALSE	Master Protein Candidate	347	41406057	amyloid beta A4 protein isoform c precursor [Homo sapiens]	1	1	12	1	1	695	78.6	4.82	High	High	High	High	High	High		60257329	61975453	51704204	1.12E+08	1.04E+08	1.16E+08	16.25	1	47	1
FALSE	Master Protein	347	4502167	amyloid beta A4 protein isoform a precursor [Homo sapiens]	1	1	12	1	1	770	86.9	4.82	High	High	High	High	High	High		60257329	61975453	51704204	1.12E+08	1.04E+08	1.16E+08	16.25	1	47	1
FALSE	Master Protein Candidate	347	209862833	amyloid beta A4 protein isoform d [Homo sapiens]	1	1	12	1	1	746	84.5	4.75	High	High	High	High	High	High		60257329	61975453	51704204	1.12E+08	1.04E+08	1.16E+08	16.25	1	47	1
FALSE	Master Protein Candidate	347	324021738	amyloid beta A4 protein isoform h precursor [Homo sapiens]	1	1	12	1	1	752	85	4.81	High	High	High	High	High	High		60257329	61975453	51704204	1.12E+08	1.04E+08	1.16E+08	16.25	1	47	1
FALSE	Master Protein	349	283837934	CX3C chemokine receptor 1 isoform a [Homo sapiens]	4	1	1	1	1	387	43.9	7.4	Not Found	Not Found	High	Not Found	Not Found	Not Found				21512775						0	1
FALSE	Master Protein Candidate	349	283837924	CX3C chemokine receptor 1 isoform b [Homo sapiens]	5	1	1	1	1	355	40.4	7.17	Not Found	Not Found	High	Not Found	Not Found	Not Found				21512775						0	1
FALSE	Master Protein	35	50301238	glutathione reductase, mitochondrial isoform 1 precursor [Homo sapiens]	6	2	8	2	1	522	56.2	8.5	High	High	High	High	Not Found	Not Found		6456399	7851695	9514912	34228430			4.75	2	26	2
FALSE	Master Protein Candidate	35	305410789	glutathione reductase, mitochondrial isoform 2 precursor [Homo sapiens]	6	2	8	2	1	493	53	8.84	High	High	High	High	Not Found	Not Found		6456399	7851695	9514912	34228430			4.75	2	26	2
FALSE	Master Protein Candidate	35	305410793	glutathione reductase, mitochondrial isoform 4 precursor [Homo sapiens]	7	2	8	2	1	440	47.2	8.75	High	High	High	High	Not Found	Not Found		6456399	7851695	9514912	34228430			4.75	2	26	2
FALSE	Master Protein Candidate	35	305410791	glutathione reductase, mitochondrial isoform 3 precursor [Homo sapiens]	6	2	8	2	1	469	50.5	8.34	High	High	High	High	Not Found	Not Found		6456399	7851695	9514912	34228430			4.75	2	26	2
FALSE	Master Protein	350	46276863	parathymosin [Homo sapiens]	11	1	10	1	1	102	11.5	4.16	High	High	High	Not Found	High	High		8479986	8802300	8921535		35359215	28421626	13.35	1	144	1
FALSE	Master Protein Candidate	351	55956921	heterogeneous nuclear ribonucleoprotein A/B isoform b [Homo sapiens]	8	2	24	2	1	285	30.6	7.91	High	High	High	High	High	High		58608799	57084742	54669179	1.52E+08	1.54E+08	1.53E+08	28.61	2	107	2
FALSE	Master Protein	351	55956919	heterogeneous nuclear ribonucleoprotein A/B isoform a [Homo sapiens]	7	2	24	2	1	332	35.9	6.95	High	High	High	High	High	High		58608799	57084742	54669179	1.52E+08	1.54E+08	1.53E+08	28.61	2	107	2
FALSE	None	352	217272890	palmitoyl-protein thioesterase 1 isoform 2 precursor [Homo sapiens]	7	1	4	1	1	203	23.1	5.97	High	Not Found	High	High	High	Not Found		54606955				1.2E+08				36	1
FALSE	None	352	530362927	PREDICTED: palmitoyl-protein thioesterase 1 isoform X2 [Homo sapiens]	5	1	4	1	1	282	31.3	6.52	Not Found	High	Not Found	High	Not Found	Not Found								4.12	1	49	1
FALSE	None	352	530362925	PREDICTED: palmitoyl-protein thioesterase 1 isoform X1 [Homo sapiens]	4	1	4	1	1	339	37.6	7.93	Not Found	High	Not Found	High	Not Found	Not Found								4.12	1	49	1
FALSE	Master Protein	352	4506031	palmitoyl-protein thioesterase 1 isoform 1 precursor [Homo sapiens]	9	2	8	2	1	306	34.2	6.52	High	High	High	High	High	Not Found		54606955				1.2E+08		4.12	1	66	2
FALSE	Master Protein Candidate	353	42476296	tropomyosin beta chain isoform 1 [Homo sapiens]	8	4	36	2	1	284	32.8	4.7	High	High	High	High	High	High		27673000	26308014	22379050	74623335	67428227	58113519	48.78	4	157	4
FALSE	Master Protein	353	530390119	PREDICTED: tropomyosin beta chain isoform X3 [Homo sapiens]	7	4	36	2	1	303	34.1	5.1	High	High	High	High	High	High		27673000	26308014	22379050	74623335	67428227	58113519	48.78	4	157	4
FALSE	Master Protein Candidate	353	578833543	PREDICTED: tropomyosin alpha-4 chain isoform X2 [Homo sapiens]	8	4	36	2	1	284	32.8	4.73	High	High	High	High	High	High		27673000	26308014	22379050	74623335	67428227	58113519	48.78	4	157	4
FALSE	Master Protein Candidate	353	530390127	PREDICTED: tropomyosin beta chain isoform X7 [Homo sapiens]	10	4	36	2	1	213	24.7	4.74	High	High	High	High	High	High		27673000	26308014	22379050	74623335	67428227	58113519	48.78	4	157	4
FALSE	Master Protein Candidate	353	530390123	PREDICTED: tropomyosin beta chain isoform X5 [Homo sapiens]	8	4	36	2	1	284	33	4.69	High	High	High	High	High	High		27673000	26308014	22379050	74623335	67428227	58113519	48.78	4	157	4
FALSE	Master Protein Candidate	353	530415128	PREDICTED: tropomyosin alpha-4 chain isoform X1 [Homo sapiens]	9	4	36	2	1	248	28.6	4.7	High	High	High	High	High	High		27673000	26308014	22379050	74623335	67428227	58113519	48.78	4	157	4
FALSE	Master Protein Candidate	353	47519616	tropomyosin beta chain isoform 2 [Homo sapiens]	8	4	36	2	1	284	33	4.67	High	High	High	High	High	High		27673000	26308014	22379050	74623335	67428227	58113519	48.78	4	157	4
FALSE	Master Protein Candidate	353	4507651	tropomyosin alpha-4 chain isoform 2 [Homo sapiens]	9	4	36	2	1	248	28.5	4.69	High	High	High	High	High	High		27673000	26308014	22379050	74623335	67428227	58113519	48.78	4	157	4
FALSE	Master Protein Candidate	353	223555975	tropomyosin alpha-4 chain isoform 1 [Homo sapiens]	8	4	36	2	1	284	32.7	4.73	High	High	High	High	High	High		27673000	26308014	22379050	74623335	67428227	58113519	48.78	4	157	4
FALSE	Master Protein Candidate	353	530390125	PREDICTED: tropomyosin beta chain isoform X6 [Homo sapiens]	8	4	36	2	1	284	32.8	4.68	High	High	High	High	High	High		27673000	26308014	22379050	74623335	67428227	58113519	48.78	4	157	4
FALSE	Master Protein	354	32189392	peroxiredoxin-2 [Homo sapiens]	15	3	23	2	1	198	21.9	5.97	High	High	High	High	High	High		22075950	21962668	22453548	69332365	77027220	72516994	25.29	3	281	3
FALSE	None	355	528078353	proteasome activator complex subunit 1 isoform 3 [Homo sapiens]	21	4	14	4	1	233	26.9	5.78	High	Not Found	High	High	High	High		9119602			45540292	34903684	40400754	17.92	4	62	4
FALSE	Master Protein	355	5453990	proteasome activator complex subunit 1 isoform 1 [Homo sapiens]	24	5	20	5	1	249	28.7	6.02	High	High	High	High	High	High		12522168	15508656	16110405	45540292	34903684	40400754	25.08	5	96	5
FALSE	None	355	30581141	proteasome activator complex subunit 1 isoform 2 [Homo sapiens]	20	4	14	4	1	250	28.6	6.71	High	Not Found	High	High	High	High		9119602			45540292	34903684	40400754	17.92	4	62	4
FALSE	None	355	528078355	proteasome activator complex subunit 1 isoform 4 [Homo sapiens]	20	4	18	4	1	236	27.2	5.83	High	High	High	High	High	High		15924735	15508656	16110405	45540292	34903684	40400754	21.32	4	67	4
FALSE	Master Protein	356	4506671	60S acidic ribosomal protein P2 [Homo sapiens]	22	2	10	2	1	115	11.7	4.54	Not Found	High	Not Found	High	High	High			83774148		1.38E+08	2.63E+08	2.24E+08	12.43	2	99	2
FALSE	Master Protein	357	13775198	SH3 domain-binding glutamic acid-rich-like protein 3 [Homo sapiens]	27	2	35	2	1	93	10.4	4.93	High	High	High	High	High	High		96487499	96085999	96013758	2.35E+08	1.16E+08	1.13E+08	44.1	2	566	2
FALSE	Master Protein	358	206597439	aldehyde dehydrogenase, dimeric NADP-preferring [Homo sapiens]	11	4	31	4	1	453	50.4	6.54	High	High	High	High	High	High		38296601	55011145	39760788	1.02E+08	96621515	1.02E+08	34.38	4	189	4
FALSE	None	358	73466520	fatty aldehyde dehydrogenase isoform 1 [Homo sapiens]	2	1	5	1	1	508	57.6	8.92	Not Found	Not Found	High	High	Not Found	High				40150477	93243491		84764822	3.79	1	34	1
FALSE	None	358	71773324	aldehyde dehydrogenase family 3 member B1 isoform b [Homo sapiens]	3	1	5	1	1	431	47.7	7.81	Not Found	Not Found	High	High	Not Found	High				40150477	93243491		84764822	3.79	1	34	1
FALSE	None	358	4502043	aldehyde dehydrogenase family 3 member B1 isoform a [Homo sapiens]	3	1	5	1	1	468	51.8	7.62	Not Found	Not Found	High	High	Not Found	High				40150477	93243491		84764822	3.79	1	34	1
FALSE	None	358	4557303	fatty aldehyde dehydrogenase isoform 2 [Homo sapiens]	2	1	5	1	1	485	54.8	7.88	Not Found	Not Found	High	High	Not Found	High				40150477	93243491		84764822	3.79	1	34	1
FALSE	None	358	530410068	PREDICTED: aldehyde dehydrogenase, dimeric NADP-preferring isoform X2 [Homo sapiens]	7	3	23	3	1	570	61.5	8.65	High	High	High	High	High	High		38296601	45239577	39760788	82141359	80587430	87666139	19.56	3	104	3
FALSE	Master Protein Candidate	358	578829768	PREDICTED: aldehyde dehydrogenase, dimeric NADP-preferring isoform X5 [Homo sapiens]	13	4	31	4	1	400	44.1	6.98	High	High	High	High	High	High		38296601	55011145	39760788	1.02E+08	96621515	1.02E+08	34.38	4	189	4
FALSE	None	358	73695879	aldehyde dehydrogenase family 3 member B2 [Homo sapiens]	3	1	5	1	1	385	42.6	6.04	Not Found	Not Found	High	High	Not Found	High				40150477	93243491		84764822	3.79	1	34	1
FALSE	Master Protein	359	4503143	cathepsin D preproprotein [Homo sapiens]	19	5	83	5	1	412	44.5	6.54	High	High	High	High	High	High		1.63E+08	1.59E+08	1.57E+08	4.45E+08	4.48E+08	4.55E+08	123.4	5	1141	5
FALSE	Master Protein	36	194688133	high mobility group protein B2 [Homo sapiens]	7	1	2	1	1	209	24	7.81	Not Found	Not Found	High	Not Found	Not Found	Not Found				3.31E+08				2.68	1	0	1
FALSE	Master Protein	360	38045910	laminin subunit alpha-3 isoform 1 precursor [Homo sapiens]	2	6	49	6	1	3333	366.4	7.24	High	High	High	High	High	High		31275289	33469581	32441743	71187808	71559645	69022164	61.09	6	468	6
FALSE	None	360	189217428	laminin subunit alpha-3 isoform 4 precursor [Homo sapiens]	4	5	43	5	1	1668	183.9	8.15	High	High	High	High	High	High		31275289	33469581	32441743	71187808	71559645	69022164	52.96	5	328	5
FALSE	None	360	189217425	laminin subunit alpha-3 isoform 3 precursor [Homo sapiens]	2	5	43	5	1	3277	360	7.24	High	High	High	High	High	High		31275289	33469581	32441743	71187808	71559645	69022164	52.96	5	328	5
FALSE	Master Protein Candidate	360	38045908	laminin subunit alpha-3 isoform 2 precursor [Homo sapiens]	5	6	49	6	1	1724	190.4	8.15	High	High	High	High	High	High		31275289	33469581	32441743	71187808	71559645	69022164	61.09	6	468	6
FALSE	None	361	58761496	heterogeneous nuclear ribonucleoprotein A1-like 2 [Homo sapiens]	18	4	51	3	1	320	34.2	9	High	High	High	High	High	High		1.46E+08	1.16E+08	1.12E+08	3E+08	3.02E+08	2.95E+08	79.18	4	733	4
FALSE	Master Protein	361	530400152	PREDICTED: heterogeneous nuclear ribonucleoprotein A1 isoform X1 [Homo sapiens]	20	5	54	4	1	372	38.7	9.13	High	High	High	High	High	High		1.46E+08	1.16E+08	1.12E+08	3E+08	3.02E+08	2.95E+08	79.18	4	733	5
FALSE	Master Protein Candidate	361	4504445	heterogeneous nuclear ribonucleoprotein A1 isoform a [Homo sapiens]	23	5	54	4	1	320	34.2	9.23	High	High	High	High	High	High		1.46E+08	1.16E+08	1.12E+08	3E+08	3.02E+08	2.95E+08	79.18	4	733	5
FALSE	Master Protein	362	183227678	protein DJ-1 [Homo sapiens]	13	2	10	2	1	189	19.9	6.79	High	Not Found	High	Not Found	High	High		20511069		31001501		30917252	60654530	10.74	2	45	2
FALSE	Master Protein	363	4757900	calreticulin precursor [Homo sapiens]	3	1	12	1	1	417	48.1	4.44	High	High	High	High	High	High		31375795	36401248	34541529	62379388	60376563	63548672	19.78	1	202	1
FALSE	Master Protein	364	7705300	ubiquitin-fold modifier 1 isoform 1 precursor [Homo sapiens]	18	1	4	1	1	85	9.1	9.31	Not Found	Not Found	Not Found	Not Found	High	High						47027984	52887602	4.3	1	26	1
FALSE	Master Protein Candidate	364	557878626	ubiquitin-fold modifier 1 isoform 4 [Homo sapiens]	21	1	4	1	1	71	7.5	6.6	Not Found	Not Found	Not Found	Not Found	High	High						47027984	52887602	4.3	1	26	1
FALSE	Master Protein	365	4506715	40S ribosomal protein S28 [Homo sapiens]	17	1	6	1	1	69	7.8	10.7	Not Found	High	High	Not Found	High	High			54542812	51743443		1.14E+08	1.25E+08	5.6	1	0	1
FALSE	Master Protein Candidate	366	530407289	PREDICTED: ras GTPase-activating-like protein IQGAP1 isoform X1 [Homo sapiens]	2	1	2	1	1	1191	135.9	6.14	Not Found	Not Found	Not Found	Not Found	Not Found	High							16099867	2.46	1	0	1
FALSE	Master Protein	366	4506787	ras GTPase-activating-like protein IQGAP1 [Homo sapiens]	1	1	2	1	1	1657	189.1	6.48	Not Found	Not Found	Not Found	Not Found	Not Found	High							16099867	2.46	1	0	1
FALSE	Master Protein	367	119395754	keratin, type II cytoskeletal 5 [Homo sapiens]	25	12	134	8	1	590	62.3	7.74	High	High	High	High	High	High		1.92E+08	1.96E+08	1.98E+08	1.57E+08	2.23E+08	2.46E+08	161.33	12	1062	12
FALSE	Master Protein	368	5031863	galectin-3-binding protein precursor [Homo sapiens]	11	6	72	6	1	585	65.3	5.27	High	High	High	High	High	High		99436871	93476754	96253334	1.68E+08	1.18E+08	1.21E+08	99.66	6	796	6
FALSE	Master Protein Candidate	369	58218968	calmodulin [Homo sapiens]	22	4	47	4	1	149	16.8	4.22	High	High	High	High	High	High		1.49E+08	1.51E+08	1.59E+08	4.48E+08	4.44E+08	3.27E+08	75.86	4	790	4
FALSE	Master Protein	369	578826144	PREDICTED: calmodulin isoform X1 [Homo sapiens]	22	4	47	4	1	150	17	4.22	High	High	High	High	High	High		1.49E+08	1.51E+08	1.59E+08	4.48E+08	4.44E+08	3.27E+08	75.86	4	790	4
FALSE	Master Protein	37	7706322	UPF0568 protein C14orf166 [Homo sapiens]	5	1	2	1	1	244	28.1	6.65	Not Found	Not Found	Not Found	Not Found	High	Not Found						15432477		2.71	1	67	1
FALSE	Master Protein Candidate	370	4507645	triosephosphate isomerase isoform 1 [Homo sapiens]	29	7	105	7	1	249	26.7	6.9	High	High	High	High	High	High		1.48E+08	1.57E+08	1.51E+08	2.6E+08	2.53E+08	2.55E+08	140.44	7	875	7
FALSE	Master Protein	370	226529917	triosephosphate isomerase isoform 2 [Homo sapiens]	25	7	105	7	1	286	30.8	5.92	High	High	High	High	High	High		1.48E+08	1.57E+08	1.51E+08	2.6E+08	2.53E+08	2.55E+08	140.44	7	875	7
FALSE	None	370	384475517	triosephosphate isomerase isoform 3 [Homo sapiens]	25	5	79	5	1	167	17.9	5.58	High	High	High	High	High	High		1.48E+08	1.57E+08	1.5E+08	2.11E+08	1.99E+08	2.21E+08	105.89	5	547	5
FALSE	Master Protein	371	5803137	putative RNA-binding protein 3 [Homo sapiens]	21	2	14	2	1	157	17.2	8.91	High	High	High	High	High	Not Found		9981359	13080409	17013709	2.33E+08	57475802		17.1	2	201	2
FALSE	Master Protein	372	469608410	transgelin-2 isoform a [Homo sapiens]	18	3	44	3	1	220	24.4	8.25	High	High	High	High	High	High		1.06E+08	1.05E+08	1.16E+08	2.88E+08	3.01E+08	2.91E+08	57.85	3	384	3
FALSE	Master Protein Candidate	372	469608407	transgelin-2 isoform b [Homo sapiens]	20	3	44	3	1	199	22.4	8.25	High	High	High	High	High	High		1.06E+08	1.05E+08	1.16E+08	2.88E+08	3.01E+08	2.91E+08	57.85	3	384	3
FALSE	Master Protein Candidate	373	315360622	gamma-glutamylcyclotransferase isoform 4 [Homo sapiens]	11	1	12	1	1	94	10.5	4.84	High	High	High	High	High	High		36294729	37893063	36929933	73073693	69326002	61646971	13.8	1	51	1
FALSE	Master Protein	373	13129018	gamma-glutamylcyclotransferase isoform 1 [Homo sapiens]	5	1	12	1	1	188	21	5.14	High	High	High	High	High	High		36294729	37893063	36929933	73073693	69326002	61646971	13.8	1	51	1
FALSE	Master Protein	374	12408677	prefoldin subunit 4 [Homo sapiens]	9	1	2	1	1	134	15.3	4.53	Not Found	Not Found	Not Found	Not Found	Not Found	High							25927612	2.05	1	0	1
FALSE	Master Protein	375	11128019	cytochrome c [Homo sapiens]	18	2	16	2	1	105	11.7	9.57	High	High	High	High	High	High		1E+08	93918350	74165656	1.42E+08	1.39E+08	1.28E+08	18.4	2	200	2
FALSE	Master Protein	376	20070228	nucleobindin-1 precursor [Homo sapiens]	26	9	65	9	1	461	53.8	5.25	High	High	High	High	High	High		43153748	33009098	30035820	2.04E+08	2.08E+08	2.01E+08	59.34	9	519	9
FALSE	Master Protein	377	4506113	major prion protein preproprotein [Homo sapiens]	5	1	12	1	1	253	27.6	9	High	High	High	High	High	High		94934408	85010679	95358655	1.5E+08	1.44E+08	1.41E+08	21.35	1	219	1
FALSE	Master Protein Candidate	38	21450863	attractin isoform 2 preproprotein [Homo sapiens]	1	1	3	1	1	1272	141.3	7.02	Not Found	Not Found	Not Found	High	Not Found	High					325410.6			2.51	1	38	1
FALSE	Master Protein	38	21450861	attractin isoform 1 preproprotein [Homo sapiens]	1	1	3	1	1	1429	158.4	7.31	Not Found	Not Found	Not Found	High	Not Found	High					325410.6			2.51	1	38	1
FALSE	Master Protein Candidate	38	530426021	PREDICTED: attractin isoform X2 [Homo sapiens]	1	1	3	1	1	1111	122.9	7.23	Not Found	Not Found	Not Found	High	Not Found	High					325410.6			2.51	1	38	1
FALSE	Master Protein Candidate	38	530426019	PREDICTED: attractin isoform X1 [Homo sapiens]	1	1	3	1	1	1289	143.4	7.06	Not Found	Not Found	Not Found	High	Not Found	High					325410.6			2.51	1	38	1
FALSE	Master Protein	39	4504981	galectin-1 [Homo sapiens]	6	1	4	1	1	135	14.7	5.5	High	High	High	High	Not Found	Not Found		53255079	48912180	54978897	1.21E+08					0	1
FALSE	Master Protein	4	4503481	elongation factor 1-gamma [Homo sapiens]	11	4	30	4	1	437	50.1	6.67	High	High	High	High	High	High		30468838	19923564	23416263	70834308	73690789	69097777	34.05	4	292	4
FALSE	Master Protein Candidate	40	578802180	PREDICTED: putative transferase CAF17, mitochondrial isoform X1 [Homo sapiens]	5	1	1	1	1	248	26.8	9.11	High	Not Found	Not Found	Not Found	Not Found	Not Found		1.28E+08								0	1
FALSE	Master Protein	40	58197556	putative transferase CAF17, mitochondrial precursor [Homo sapiens]	4	1	1	1	1	356	38.1	9.83	High	Not Found	Not Found	Not Found	Not Found	Not Found		1.28E+08								0	1
FALSE	Master Protein Candidate	41	38149981	U2 small nuclear ribonucleoprotein B'' [Homo sapiens]	4	1	3	1	1	225	25.5	9.72	Not Found	Not Found	Not Found	High	High	High					86795059	87155722	77417409			38	1

FALSE	Master Protein	41	4759156	U1 small nuclear ribonucleoprotein A [Homo sapiens]	3	1	3	1	1	282	31.3	9.83	Not Found	Not Found	Not Found	High	High	High					86795059	87155722	77417409			38	1
FALSE	Master Protein	42	4507115	fascin [Homo sapiens]	3	1	4	1	1	493	54.5	7.24	Not Found	Not Found	Not Found	High	Not Found	High					1.92E+08		1.88E+08	5.79	1	20	1
FALSE	Master Protein	43	4502027	serum albumin preproprotein [Homo sapiens]	4	3	29	3	1	609	69.3	6.28	High	High	High	High	High	High		1.18E+08	1.13E+08	1.29E+08	2.79E+08	2.76E+08	2.77E+08	30.82	3	437	3
FALSE	Master Protein	44	11321593	insulin-like growth factor-binding protein 6 precursor [Homo sapiens]	10	2	71	2	1	240	25.3	7.81	High	High	High	High	High	High		1.11E+09	5.94E+08	1.18E+09	2.41E+09	2.41E+09	2.46E+09	82.98	2	659	2
FALSE	Master Protein	45	34734062	fibulin-1 isoform C precursor [Homo sapiens]	7	4	23	4	1	683	74.4	5.29	High	High	High	High	High	High		8804310	12810308	10907214	26353465	35854059	40943255	33.26	4	250	4
FALSE	None	45	34734068	fibulin-1 isoform A precursor [Homo sapiens]	5	2	8	2	1	566	61.5	4.97	Not Found	Not Found	Not Found	High	High	High					41068864	41458035	44022671	15.9	2	210	2
FALSE	None	45	34734066	fibulin-1 isoform D precursor [Homo sapiens]	4	2	8	2	1	703	77.2	5.26	Not Found	Not Found	Not Found	High	High	High					41068864	41458035	44022671	15.9	2	210	2
FALSE	None	45	34734064	fibulin-1 isoform B precursor [Homo sapiens]	4	2	8	2	1	601	65.4	5.1	Not Found	Not Found	Not Found	High	High	High					41068864	41458035	44022671	15.9	2	210	2
FALSE	Master Protein	46	5454052	14-3-3 protein sigma [Homo sapiens]	24	6	55	4	1	248	27.8	4.74	High	High	High	High	High	High		58654774	41053645	66454490	1.44E+08	1.33E+08	1.3E+08	53.16	6	249	6
FALSE	None	46;48;114;199;262	578840292	PREDICTED: 14-3-3 protein epsilon isoform X1 [Homo sapiens]	8	2	16	0	5	240	27.4	4.89	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								9.99	2	59	2
FALSE	None	46;48;114;199;262	5803227	14-3-3 protein theta [Homo sapiens]	7	2	16	0	5	245	27.7	4.78	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								9.99	2	59	2
FALSE	None	46;48;114;199;262	5803225	14-3-3 protein epsilon [Homo sapiens]	7	2	16	0	5	255	29.2	4.74	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								9.99	2	59	2
FALSE	Master Protein Candidate	47	578823768	PREDICTED: nascent polypeptide-associated complex subunit alpha isoform X4 [Homo sapiens]	1	2	14	2	1	2078	205.3	9.58	High	Not Found	High	High	High	High		28108499		27374660	1E+08	82611636	88602191	22.06	2	206	2
FALSE	Master Protein Candidate	47	578823772	PREDICTED: nascent polypeptide-associated complex subunit alpha isoform X6 [Homo sapiens]	1	2	14	2	1	2035	201.3	9.55	High	Not Found	High	High	High	High		28108499		27374660	1E+08	82611636	88602191	22.06	2	206	2
FALSE	Master Protein Candidate	47	578823770	PREDICTED: nascent polypeptide-associated complex subunit alpha isoform X5 [Homo sapiens]	1	2	14	2	1	2059	203.6	9.57	High	Not Found	High	High	High	High		28108499		27374660	1E+08	82611636	88602191	22.06	2	206	2
FALSE	Master Protein	47	578823766	PREDICTED: nascent polypeptide-associated complex subunit alpha isoform X3 [Homo sapiens]	1	2	14	2	1	2082	205.6	9.6	High	Not Found	High	High	High	High		28108499		27374660	1E+08	82611636	88602191	22.06	2	206	2
FALSE	Master Protein Candidate	47	333033787	nascent polypeptide-associated complex subunit alpha isoform a [Homo sapiens]	3	2	14	2	1	925	94.6	5.14	High	Not Found	High	High	High	High		28108499		27374660	1E+08	82611636	88602191	22.06	2	206	2
FALSE	Master Protein Candidate	47	163965364	nascent polypeptide-associated complex subunit alpha isoform b [Homo sapiens]	13	2	14	2	1	215	23.4	4.56	High	Not Found	High	High	High	High		28108499		27374660	1E+08	82611636	88602191	22.06	2	206	2
FALSE	Master Protein Candidate	47	578823778	PREDICTED: nascent polypeptide-associated complex subunit alpha isoform X9 [Homo sapiens]	13	2	14	2	1	219	23.7	4.59	High	Not Found	High	High	High	High		28108499		27374660	1E+08	82611636	88602191	22.06	2	206	2
FALSE	Master Protein	48	4507949	14-3-3 protein beta/alpha [Homo sapiens]	16	4	26	1	1	246	28.1	4.83	High	Not Found	High	Not Found	Not Found	Not Found		26982738		43323157				20.21	4	68	4
FALSE	Master Protein Candidate	49	17402900	far upstream element-binding protein 1 [Homo sapiens]	8	3	21	3	1	644	67.5	7.61	Not Found	High	High	High	High	High			8218731	8191512	39564283	38317567	39292904	28.15	3	406	3
FALSE	Master Protein Candidate	49	578800052	PREDICTED: far upstream element-binding protein 1 isoform X2 [Homo sapiens]	8	3	21	3	1	664	69.7	7.36	Not Found	High	High	High	High	High			8218731	8191512	39564283	38317567	39292904	28.15	3	406	3
FALSE	Master Protein	49	530363548	PREDICTED: far upstream element-binding protein 1 isoform X1 [Homo sapiens]	8	3	21	3	1	665	69.8	7.36	Not Found	High	High	High	High	High			8218731	8191512	39564283	38317567	39292904	28.15	3	406	3
FALSE	Master Protein Candidate	49	578800054	PREDICTED: far upstream element-binding protein 1 isoform X3 [Homo sapiens]	8	3	21	3	1	643	67.4	7.61	Not Found	High	High	High	High	High			8218731	8191512	39564283	38317567	39292904	28.15	3	406	3
FALSE	Master Protein Candidate	5	578832966	PREDICTED: cold-inducible RNA-binding protein isoform X3 [Homo sapiens]	8	1	4	1	1	168	18.1	9.64	Not Found	Not Found	Not Found	Not Found	High	High						45182414	43160115	8.02	1	81	1
FALSE	Master Protein	5	578832961	PREDICTED: cold-inducible RNA-binding protein isoform X1 [Homo sapiens]	5	1	4	1	1	297	31.9	9.61	Not Found	Not Found	Not Found	Not Found	High	High						45182414	43160115	8.02	1	81	1
FALSE	Master Protein Candidate	5	4502847	cold-inducible RNA-binding protein [Homo sapiens]	8	1	4	1	1	172	18.6	9.51	Not Found	Not Found	Not Found	Not Found	High	High						45182414	43160115	8.02	1	81	1
FALSE	None	50	297374785	rho GDP-dissociation inhibitor 1 isoform b [Homo sapiens]	10	1	4	1	1	160	18.2	5.19	Not Found	Not Found	Not Found	High	High	Not Found					57175729	51563221		9.6	1	115	1
FALSE	Master Protein	50	4757768	rho GDP-dissociation inhibitor 1 isoform a [Homo sapiens]	15	2	19	2	1	204	23.2	5.11	High	High	High	High	High	High		80514665	81246186	81080563	1.08E+08	1.1E+08	1.59E+08	26.59	2	210	2
FALSE	Master Protein	51	5453595	adenylyl cyclase-associated protein 1 [Homo sapiens]	7	2	19	2	1	475	51.6	8.02	High	High	High	High	High	High			4029806	3930247	95024399	10716269	11822220	26	2	171	2
FALSE	Master Protein Candidate	51	578798235	PREDICTED: adenylyl cyclase-associated protein 1 isoform X3 [Homo sapiens]	7	2	19	2	1	475	51.9	8.06	High	High	High	High	High	High			4029806	3930247	95024399	10716269	11822220	26	2	171	2
FALSE	Master Protein	52	88853069	vitronectin precursor [Homo sapiens]	3	1	10	1	1	478	54.3	5.8	High	High	Not Found	High	High	High		24302282	26309149		50219541	48499394	45276683	11.16	1	97	1
FALSE	None	53	226371754	katanin p60 ATPase-containing subunit A-like 2 [Homo sapiens]	3	1	4	1	1	466	52.7	8.32	High	Not Found	Not Found	High	Not Found	Not Found		40655659			1.03E+08			4.74	1	33	1
FALSE	None	53	530413973	PREDICTED: katanin p60 ATPase-containing subunit A-like 2 isoform X1 [Homo sapiens]	2	1	4	1	1	564	64.3	8.22	High	Not Found	Not Found	High	Not Found	Not Found		40655659			1.03E+08			4.74	1	33	1
FALSE	Master Protein	53	6005942	transitional endoplasmic reticulum ATPase [Homo sapiens]	8	5	28	5	1	806	89.3	5.26	High	High	High	High	High	High		36488200	33259840	31729074	71837715	74489628	81201210	28.04	5	116	5
FALSE	None	53	530413975	PREDICTED: katanin p60 ATPase-containing subunit A-like 2 isoform X2 [Homo sapiens]	2	1	4	1	1	563	64.2	8.22	High	Not Found	Not Found	High	Not Found	Not Found		40655659			1.03E+08			4.74	1	33	1
FALSE	None	53	544186102	peroxisome biogenesis factor 1 isoform 2 [Homo sapiens]	1	1	4	1	1	1226	136.5	6.47	High	Not Found	Not Found	High	Not Found	Not Found		40655659			1.03E+08			4.74	1	33	1
FALSE	None	53	530386077	PREDICTED: peroxisome biogenesis factor 1 isoform X1 [Homo sapiens]	1	1	4	1	1	1243	138.1	6.16	High	Not Found	Not Found	High	Not Found	Not Found		40655659			1.03E+08			4.74	1	33	1
FALSE	None	53	578832727	PREDICTED: katanin p60 ATPase-containing subunit A-like 2 isoform X6 [Homo sapiens]	2	1	4	1	1	538	61.2	7.56	High	Not Found	Not Found	High	Not Found	Not Found		40655659			1.03E+08			4.74	1	33	1
FALSE	None	53	530386086	PREDICTED: peroxisome biogenesis factor 1 isoform X5 [Homo sapiens]	2	1	4	1	1	700	76.7	6.07	High	Not Found	Not Found	High	Not Found	Not Found		40655659			1.03E+08			4.74	1	33	1
FALSE	None	53	4505725	peroxisome biogenesis factor 1 isoform 1 [Homo sapiens]	1	1	4	1	1	1283	142.8	6.33	High	Not Found	Not Found	High	Not Found	Not Found		40655659			1.03E+08			4.74	1	33	1
FALSE	None	53	530413981	PREDICTED: katanin p60 ATPase-containing subunit A-like 2 isoform X5 [Homo sapiens]	3	1	4	1	1	427	48	6.92	High	Not Found	Not Found	High	Not Found	Not Found		40655659			1.03E+08			4.74	1	33	1
FALSE	None	53	544186104	peroxisome biogenesis factor 1 isoform 3 [Homo sapiens]	1	1	4	1	1	1075	119.5	6.11	High	Not Found	Not Found	High	Not Found	Not Found		40655659			1.03E+08			4.74	1	33	1
FALSE	Master Protein	54	32313599	kunitz-type protease inhibitor 1 isoform 1 precursor [Homo sapiens]	3	2	6	2	1	529	58.4	6.29	High	High	High	Not Found	High	Not Found		18236610	28479111	36128184		47092621		3.83	1	29	2
FALSE	Master Protein Candidate	54	74027265	kunitz-type protease inhibitor 1 isoform 2 precursor [Homo sapiens]	3	2	6	2	1	513	56.8	6.18	High	High	High	Not Found	High	Not Found		18236610	28479111	36128184		47092621		3.83	1	29	2
FALSE	Master Protein	55	578826104	PREDICTED: tryptophan--tRNA ligase, cytoplasmic isoform X5 [Homo sapiens]	3	1	3	1	1	471	53.1	6.23	Not Found	Not Found	Not Found	High	High	Not Found					99808430	1.08E+08		0	1	0	1
FALSE	Master Protein Candidate	55	47419920	tryptophan--tRNA ligase, cytoplasmic isoform b [Homo sapiens]	4	1	3	1	1	430	48.8	6.48	Not Found	Not Found	Not Found	High	High	Not Found					99808430	1.08E+08		0	1	0	1
FALSE	Master Protein	56	22538465	proteasome subunit beta type-3 [Homo sapiens]	8	1	4	1	1	205	22.9	6.55	Not Found	Not Found	Not Found	High	High	Not Found					49576539	49740510		7.45	1	71	1
FALSE	Master Protein	57	530422764	PREDICTED: high mobility group protein B3 isoform X1 [Homo sapiens]	6	1	1	1	1	222	25.6	8.12	High	Not Found	Not Found	Not Found	Not Found	Not Found		79842146								0	1
FALSE	Master Protein Candidate	57	530422766	PREDICTED: high mobility group protein B3 isoform X2 [Homo sapiens]	6	1	1	1	1	220	25.5	9.06	High	Not Found	Not Found	Not Found	Not Found	Not Found		79842146								0	1
FALSE	Master Protein Candidate	57	530422768	PREDICTED: high mobility group protein B3 isoform X3 [Homo sapiens]	7	1	1	1	1	200	23	8.37	High	Not Found	Not Found	Not Found	Not Found	Not Found		79842146								0	1
FALSE	Master Protein Candidate	58	156415990	Y-box-binding protein 2 [Homo sapiens]	5	1	8	1	1	364	38.5	10.8	High	High	High	Not Found	High	Not Found								14.33	1	116	1
FALSE	Master Protein Candidate	58	34098946	nuclease-sensitive element-binding protein 1 [Homo sapiens]	5	1	8	1	1	324	35.9	9.88	High	High	High	Not Found	High	Not Found								14.33	1	116	1
FALSE	Master Protein Candidate	58	224586884	Y-box-binding protein 3 isoform b [Homo sapiens]	6	1	8	1	1	303	31.9	9.66	High	High	High	Not Found	High	Not Found								14.33	1	116	1
FALSE	Master Protein	58	224586882	Y-box-binding protein 3 isoform a [Homo sapiens]	5	1	8	1	1	372	40.1	9.77	High	High	High	Not Found	High	Not Found								14.33	1	116	1
FALSE	Master Protein	59	4503987	gamma-glutamyl hydrolase precursor [Homo sapiens]	17	4	40	4	1	318	35.9	7.11	High	High	High	High	High	High		23356566	26132613	23247740	39671177	33276334	40433433	55.58	4	247	4
FALSE	Master Protein	6	7706495	dnaJ homolog subfamily B member 11 precursor [Homo sapiens]	3	1	5	1	1	358	40.5	6.18	Not Found	Not Found	High	High	High	Not Found				15182652	18676178	19961156		3.73	1	0	1
FALSE	Master Protein Candidate	60	386781455	lipolysis-stimulated lipoprotein receptor isoform 4 [Homo sapiens]	10	4	29	4	1	629	69.4	8.15	High	High	High	High	High	High		66597686	76361004	88124676	1.86E+08	1.78E+08	1.25E+08	37.04	3	254	4
FALSE	Master Protein Candidate	60	45593136	lipolysis-stimulated lipoprotein receptor isoform 3 [Homo sapiens]	10	4	29	4	1	581	64	8.78	High	High	High	High	High	High		66597686	76361004	88124676	1.86E+08	1.78E+08	1.25E+08	37.04	3	254	4
FALSE	Master Protein	60	45545424	lipolysis-stimulated lipoprotein receptor isoform 2 [Homo sapiens]	9	4	29	4	1	649	71.4	7.97	High	High	High	High	High	High		66597686	76361004	88124676	1.86E+08	1.78E+08	1.25E+08	37.04	3	254	4
FALSE	Master Protein Candidate	60	530416678	PREDICTED: lipolysis-stimulated lipoprotein receptor isoform X1 [Homo sapiens]	9	4	29	4	1	648	71.3	8.06	High	High	High	High	High	High		66597686	76361004	88124676	1.86E+08	1.78E+08	1.25E+08	37.04	3	254	4
FALSE	Master Protein Candidate	60	530416682	PREDICTED: lipolysis-stimulated lipoprotein receptor isoform X3 [Homo sapiens]	11	4	29	4	1	580	63.9	8.88	High	High	High	High	High	High		66597686	76361004	88124676	1.86E+08	1.78E+08	1.25E+08	37.04	3	254	4
FALSE	Master Protein Candidate	60	386781463	lipolysis-stimulated lipoprotein receptor isoform 5 [Homo sapiens]	11	4	29	4	1	541	59.7	9.41	High	High	High	High	High	High		66597686	76361004	88124676	1.86E+08	1.78E+08	1.25E+08	37.04	3	254	4
FALSE	Master Protein Candidate	60	45505163	lipolysis-stimulated lipoprotein receptor isoform 1 [Homo sapiens]	10	4	29	4	1	630	69.5	8.06	High	High	High	High	High	High		66597686	76361004	88124676	1.86E+08	1.78E+08	1.25E+08	37.04	3	254	4
FALSE	Master Protein	61	521258690	small nuclear ribonucleoprotein Sm D3 [Homo sapiens]	8	1	12	1	1	126	13.9	10.32	High	High	High	High	High	High		1.25E+08	94407088	1.35E+08	2.55E+08	3.36E+08	3.23E+08	13.92	1	143	1
FALSE	Master Protein	63	58761500	obg-like ATPase 1 isoform 1 [Homo sapiens]	4	1	4	1	1	396	44.7	7.81	High	High	Not Found	Not Found	Not Found	Not Found		11837361	14513080					7.48	1	175	1
FALSE	Master Protein Candidate	64	564473387	actin-related protein 2/3 complex subunit 3 isoform 2 [Homo sapiens]	14	2	13	2	1	177	20.4	8.78	Not Found	High	High	High	High	High			13927635	14758894	36186387	39148248	43633014	16.4	2	117	2
FALSE	Master Protein	64	514052670	actin-related protein 2/3 complex subunit 3 isoform 1 [Homo sapiens]	13	2	13	2	1	178	20.5	8.59	Not Found	High	High	High	High	High			13927635	14758894	36186387	39148248	43633014	16.4	2	117	2
FALSE	Master Protein Candidate	65	530360505	PREDICTED: calsyntenin-1 isoform X1 [Homo sapiens]	7	5	39	5	1	962	107.7	4.97	High	High	High	High	High	High		55372354	62815175	60763044	1.5E+08	92153476	2.03E+08	41.47	5	235	5
FALSE	Master Protein	65	57242757	calsyntenin-1 isoform 1 precursor [Homo sapiens]	7	5	39	5	1	981	109.7	4.91	High	High	High	High	High	High		55372354	62815175	60763044	1.5E+08	92153476	2.03E+08	41.47	5	235	5
FALSE	Master Protein Candidate	65	57242755	calsyntenin-1 isoform 2 precursor [Homo sapiens]	7	5	39	5	1	971	108.6	4.93	High	High	High	High	High	High		55372354	62815175	60763044	1.5E+08	92153476	2.03E+08	41.47	5	235	5
FALSE	Master Protein	66	50592996	tubulin beta-3 chain isoform 1 [Homo sapiens]	20	6	41	2	1	450	50.4	4.93	Not Found	High	High	High	High	High			8403872	20747196	69014009	69751138	66213303	68.09	6	619	6
FALSE	None	66	29788768	tubulin beta-2B chain [Homo sapiens]	13	4	26	1	1	445	49.9	4.89	Not Found	Not Found	High	High	High	High				20747196	99533386	1.07E+08	99237128	45.11	4	290	4
FALSE	None	66	4507729	tubulin beta-2A chain [Homo sapiens]	13	4	26	1	1	445	49.9	4.89	Not Found	Not Found	High	High	High	High				20747196	99533386	1.07E+08	99237128	45.11	4	290	4
FALSE	None	66	308235963	tubulin beta-3 chain isoform 2 [Homo sapiens]	20	5	33	1	1	378	42.4	4.96	Not Found	High	Not Found	High	High	High			8403872		38494631	32929638	33189478	56.79	5	532	5
FALSE	None	66;318	14210536	tubulin beta-6 chain [Homo sapiens]	5	2	11	0	2	446	49.8	4.88	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								19.19	2	77	2
FALSE	None	66;318	530424971	PREDICTED: tubulin beta-6 chain isoform X2 [Homo sapiens]	8	2	11	0	2	300	34.1	4.84	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								19.19	2	77	2
FALSE	None	66;318	13562114	tubulin beta-1 chain [Homo sapiens]	2	1	5	0	2	451	50.3	5.17	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								7.39	1	38	1
FALSE	Master Protein	67	4504517	heat shock protein beta-1 [Homo sapiens]	16	2	13	2	1	205	22.8	6.4	Not Found	Not Found	High	High	High	High				26805846	59009182	1.19E+08	58396677	19.58	2	128	2
FALSE	Master Protein	68	15431288	60S ribosomal protein L10a [Homo sapiens]	12	2	11	2	1	217	24.8	9.94	Not Found	Not Found	Not Found	High	High	High					58508992	62054035	57594925	7.57	2	61	2
FALSE	Master Protein	69	5174663	protein S100-P [Homo sapiens]	18	1	9	1	1	95	10.4	4.88	High	High	High	Not Found	High	High		13623543	14441949	13606371		19567958	19819823	12.8	1	43	1
FALSE	Master Protein	7	4504347	hemoglobin subunit alpha [Homo sapiens]	22	2	7	2	1	142	15.2	8.68	High	High	High	Not Found	Not Found	High		8409676	10020576	19053797			79897027	8.25	2	0	2
FALSE	Master Protein Candidate	70	530405429	PREDICTED: pro-cathepsin H isoform X2 [Homo sapiens]	22	5	38	5	1	297	33.2	8.19	High	High	High	High	High	High		91689416	66624073	68067184	3.02E+08	2.53E+08	3.34E+08	49.73	5	329	5
FALSE	Master Protein	70	23110955	pro-cathepsin H preproprotein [Homo sapiens]	20	5	38	5	1	335	37.4	8.07	High	High	High	High	High	High		91689416	66624073	68067184	3.02E+08	2.53E+08	3.34E+08	49.73	5	329	5
FALSE	Master Protein Candidate	71	499137520	tropomyosin alpha-3 chain isoform 8 [Homo sapiens]	24	7	64	5	1	227	26.4	4.78	High	High	High	High	High	High		98970547	97197673	92313982	1.33E+08	2.5E+08	2.03E+08	85.82	7	468	7
FALSE	None	71	530406418	PREDICTED: tropomyosin alpha-1 chain isoform X18 [Homo sapiens]	8	3	25	1	1	245	28.5	4.78	High	High	High	Not Found	High	High		1.33E+08	1.33E+08	1.33E+08		3.44E+08	3.21E+08	29.4	3	106	3
FALSE	None	71	578827355	PREDICTED: tropomyosin alpha-1 chain isoform X19 [Homo sapiens]	7	3	25	1	1	284	32.8	4.77	High	High	High	Not Found	High	High		1.33E+08	1.33E+08	1.33E+08		3.44E+08	3.21E+08	29.4	3	106	3
FALSE	None	71	530406412	PREDICTED: tropomyosin alpha-1 chain isoform X15 [Homo sapiens]	8	3	25	1	1	248	28.7	4.79	High	High	High	Not Found	High	High		1.33E+08	1.33E+08	1.33E+08		3.44E+08	3.21E+08	29.4	3	106	3
FALSE	None	71	530406402	PREDICTED: tropomyosin alpha-1 chain isoform X10 [Homo sapiens]	7	3	25	1	1	281	32.5	4.74	High	High	High	Not Found	High	High		1.33E+08	1.33E+08	1.33E+08		3.44E+08	3.21E+08	29.4	3	106	3
FALSE	None	71	578801447	PREDICTED: tropomyosin alpha-3 chain isoform X6 [Homo sapiens]	11	5	49	3	1	284	33.1	4.79	High	High	High	High	High	High		1.15E+08	1.18E+08	1.08E+08	1.84E+08	2.5E+08	2.57E+08	65.86	5	248	5
FALSE	None	71	578801449	PREDICTED: tropomyosin alpha-3 chain isoform X7 [Homo sapiens]	11	5	49	3	1	284	33	4.77	High	High	High	High	High	High		1.15E+08	1.18E+08	1.08E+08	1.84E+08	2.5E+08	2.57E+08	65.86	5	248	5
FALSE	None	71	530406406	PREDICTED: tropomyosin alpha-1 chain isoform X12 [Homo sapiens]	8	3	25	1	1	251	28.8	4.83	High	High	High	Not Found	High	High		1.33E+08	1.33E+08	1.33E+08		3.44E+08	3.21E+08	29.4	3	106	3
FALSE	None	71	63252904	tropomyosin alpha-1 chain isoform 6 [Homo sapiens]	8	3	25	1	1	245	28.4	4.77	High	High	High	Not Found	High	High		1.33E+08	1.33E+08	1.33E+08		3.44E+08	3.21E+08	29.4	3	106	3
FALSE	None	71	578801453	PREDICTED: tropomyosin alpha-3 chain isoform X9 [Homo sapiens]	18	6	55	4	1	248	28.8	4.72	High	High	High	High	High	High		85840679	86732660	92020700	1.84E+08	2.5E+08	2.57E+08	79.49	6	462	6
FALSE	None	71	578801445	PREDICTED: tropomyosin alpha-3 chain isoform X5 [Homo sapiens]	14	6	58	4	1	285	33	4.74	High	High	High	High	High	High		98970547	97197673	92313982	1.33E+08	2.5E+08	2.03E+08	72.18	6	254	6
FALSE	None	71	63252898	tropomyosin alpha-1 chain isoform 1 [Homo sapiens]	7	3	25	1	1	284	32.7	4.74	High	High	High	Not Found	High	High		1.33E+08	1.33E+08	1.33E+08		3.44E+08	3.21E+08	29.4	3	106	3
FALSE	None	71	530406416	PREDICTED: tropomyosin alpha-1 chain isoform X17 [Homo sapiens]	8	3	25	1	1	248	28.7	4.82	High	High	High	Not Found	High	High		1.33E+08	1.33E+08	1.33E+08		3.44E+08	3.21E+08	29.4	3	106	3
FALSE	None	71	114155148	tropomyosin alpha-3 chain isoform 5 [Homo sapiens]	18	6	55	4	1	247	28.8	4.77	High	High	High	High	High	High		85840679	86732660	92020700	1.84E+08	2.5E+08	2.57E+08	79.49	6	462	6
FALSE	None	71	530406400	PREDICTED: tropomyosin alpha-1 chain isoform X9 [Homo sapiens]	7	3	25	1	1	284	32.6	4.73	High	High	High	Not Found	High	High		1.33E+08	1.33E+08	1.33E+08		3.44E+08	3.21E+08	29.4	3	106	3
FALSE	None	71	530406394	PREDICTED: tropomyosin alpha-1 chain isoform X6 [Homo sapiens]	7	3	25	1	1	287	33	4.79	High	High	High	Not Found	High	High		1.33E+08	1.33E+08	1.33E+08		3.44E+08	3.21E+08	29.4	3	106	3
FALSE	Master Protein	71	114155144	tropomyosin alpha-3 chain isoform 4 [Homo sapiens]	22	7	64	5	1	248	28.9	4.75	High	High	High	High	High	High		98970547	97197673	92313982	1.33E+08	2.5E+08	2.03E+08	85.82	7	468	7
FALSE	None	71	578801439	PREDICTED: tropomyosin alpha-3 chain isoform X2 [Homo sapiens]	11	5	49	3	1	285	33.1	4.74	High	High	High	High	High	High		1.15E+08	1.18E+08	1.08E+08	1.84E+08	2.5E+08	2.57E+08	65.86	5	248	5
FALSE	None	71	63252900	tropomyosin alpha-1 chain isoform 4 [Homo sapiens]	7	3	25	1	1	284	32.9	4.78	High	High	High	Not Found	High	High		1.33E+08	1.33E+08	1.33E+08		3.44E+08	3.21E+08	29.4	3	106	3
FALSE	Master Protein Candidate	71	24119203	tropomyosin alpha-3 chain isoform 2 [Homo sapiens]	22	7	64	5	1	248	29	4.78	High	High	High	High	High	High		98970547	97197673	92313982	1.33E+08	2.5E+08	2.03E+08	85.82	7	468	7
FALSE	None	71	499137518	tropomyosin alpha-3 chain isoform 7 [Homo sapiens]	18	6	55	4	1	248	28.9	4.75	High	High	High	High	High	High		85840679	86732660	92020700	1.84E+08	2.5E+08	2.57E+08	79.49	6	462	6
FALSE	None	71	530406404	PREDICTED: tropomyosin alpha-1 chain isoform X11 [Homo sapiens]	7	3	25	1	1	275	31.7	4.89	High	High	High	Not Found	High	High		1.33E+08	1.33E+08	1.33E+08		3.44E+08	3.21E+08	29.4	3	106	3
FALSE	None	71	530406410	PREDICTED: tropomyosin alpha-1 chain isoform X14 [Homo sapiens]	8	3	25	1	1	248	28.6	4.79	High	High	High	Not Found	High	High		1.33E+08	1.33E+08	1.33E+08		3.44E+08	3.21E+08	29.4	3	106	3
FALSE	None	71	63252896	tropomyosin alpha-1 chain isoform 3 [Homo sapiens]	7	3	25	1	1	284	32.7	4.75	High	High	High	Not Found	High	High		1.33E+08	1.33E+08	1.33E+08		3.44E+08	3.21E+08	29.4	3	106	3
FALSE	None	71	530406390	PREDICTED: tropomyosin alpha-1 chain isoform X4 [Homo sapiens]	7	3	25	1	1	287	33.1	4.81	High	High	High	Not Found	High	High		1.33E+08	1.33E+08	1.33E+08		3.44E+08	3.21E+08	29.4	3	106	3
FALSE	None	71	499137516	tropomyosin alpha-3 chain isoform 6 [Homo sapiens]	16	4	42	4	1	182	21.3	4.93	High	High	High	High	High	High		98970547	97197673	92313982	1.33E+08	2.5E+08	2.03E+08	52.97	4	194	4
FALSE	None	71	114155146	tropomyosin alpha-3 chain isoform 3 [Homo sapiens]	18	6	55	4	1	247	28.9	4.81	High	High	High	High	High	High		85840679	86732660	92020700	1.84E+08	2.5E+08	2.57E+08	79.49	6	462	6
FALSE	None	71	499137522	tropomyosin alpha-3 chain isoform 9 [Homo sapiens]	19	4	42	4	1	158	18.6	4.74	High	High	High	High	High	High		98970547	97197673	92313982	1.33E+08	2.5E+08	2.03E+08	52.97	4	194	4
FALSE	None	71	27597085	tropomyosin alpha-1 chain isoform 5 [Homo sapiens]	7	3	25	1	1	284	32.8	4.77	High	High	High	Not Found	High	High		1.33E+08	1.33E+08	1.33E+08		3.44E+08	3.21E+08	29.4	3	106	3

FALSE	None	71	578827359	PREDICTED: tropomyosin alpha-1 chain isoform X21 [Homo sapiens]	6	1	9	1	1	161	18.7	4.78	High	High	High	Not Found	High	High		1.33E+08	1.33E+08	1.33E+08		3.44E+08	3.21E+08	10.19	1	47	1
FALSE	None	71	63252906	tropomyosin alpha-1 chain isoform 7 [Homo sapiens]	7	3	25	1	1	284	32.8	4.75	High	High	High	Not Found	High	High		1.33E+08	1.33E+08	1.33E+08		3.44E+08	3.21E+08	29.4	3	106	3
FALSE	None	71	530406414	PREDICTED: tropomyosin alpha-1 chain isoform X16 [Homo sapiens]	8	3	25	1	1	248	28.7	4.79	High	High	High	Not Found	High	High		1.33E+08	1.33E+08	1.33E+08		3.44E+08	3.21E+08	29.4	3	106	3
FALSE	None	71	530406398	PREDICTED: tropomyosin alpha-1 chain isoform X8 [Homo sapiens]	7	3	25	1	1	284	32.6	4.73	High	High	High	Not Found	High	High		1.33E+08	1.33E+08	1.33E+08		3.44E+08	3.21E+08	29.4	3	106	3
FALSE	None	71	530406392	PREDICTED: tropomyosin alpha-1 chain isoform X5 [Homo sapiens]	7	3	25	1	1	287	32.9	4.77	High	High	High	Not Found	High	High		1.33E+08	1.33E+08	1.33E+08		3.44E+08	3.21E+08	29.4	3	106	3
FALSE	None	71	63252902	tropomyosin alpha-1 chain isoform 2 [Homo sapiens]	7	3	25	1	1	284	32.7	4.74	High	High	High	Not Found	High	High		1.33E+08	1.33E+08	1.33E+08		3.44E+08	3.21E+08	29.4	3	106	3
FALSE	None	71	114155140	tropomyosin alpha-3 chain isoform 1 [Homo sapiens]	11	5	49	3	1	285	32.9	4.72	High	High	High	High	High	High		1.15E+08	1.18E+08	1.08E+08	1.84E+08	2.5E+08	2.57E+08	65.86	5	248	5
FALSE	None	71	530406386	PREDICTED: tropomyosin alpha-1 chain isoform X2 [Homo sapiens]	6	3	25	1	1	326	37.4	4.72	High	High	High	Not Found	High	High		1.33E+08	1.33E+08	1.33E+08		3.44E+08	3.21E+08	29.4	3	106	3
FALSE	None	71	578801441	PREDICTED: tropomyosin alpha-3 chain isoform X3 [Homo sapiens]	11	5	49	3	1	285	33.1	4.74	High	High	High	High	High	High		1.15E+08	1.18E+08	1.08E+08	1.84E+08	2.5E+08	2.57E+08	65.86	5	248	5
FALSE	None	71	530406388	PREDICTED: tropomyosin alpha-1 chain isoform X3 [Homo sapiens]	7	3	25	1	1	287	32.9	4.79	High	High	High	Not Found	High	High		1.33E+08	1.33E+08	1.33E+08		3.44E+08	3.21E+08	29.4	3	106	3
FALSE	None	71	578801437	PREDICTED: tropomyosin alpha-3 chain isoform X1 [Homo sapiens]	14	6	58	4	1	285	33.2	4.77	High	High	High	High	High	High		98970547	97197673	92313982	1.33E+08	2.5E+08	2.03E+08	72.18	6	254	6
FALSE	None	71	530406408	PREDICTED: tropomyosin alpha-1 chain isoform X13 [Homo sapiens]	8	3	25	1	1	248	28.6	4.77	High	High	High	Not Found	High	High		1.33E+08	1.33E+08	1.33E+08		3.44E+08	3.21E+08	29.4	3	106	3
FALSE	Master Protein	72	4507509	metalloproteinase inhibitor 1 precursor [Homo sapiens]	10	2	13	2	1	207	23.2	8.1	High	High	High	High	Not Found	Not Found		4.27E+08	4.23E+08	94463469				13.17	2	36	2
FALSE	None	73	10863955	phosphoserine aminotransferase isoform 2 [Homo sapiens]	3	1	9	1	1	324	35.2	6.68	High	High	High	High	High	High		41895737	40734311	43789922	93750378	98777199	89636307	10.99	1	58	1
FALSE	Master Protein	73	17402893	phosphoserine aminotransferase isoform 1 [Homo sapiens]	6	2	19	2	1	370	40.4	7.66	High	High	High	High	High	High		27593312	26316949	43789922	66153862	69560081	64055649	21.81	2	83	2
FALSE	Master Protein	74	4506181	proteasome subunit alpha type-2 [Homo sapiens]	6	1	8	1	1	234	25.9	7.43	Not Found	High	Not Found	High	High	High			21732035		50730933	58784307	48660967	8.13	1	0	1
FALSE	Master Protein Candidate	75	221316614	extracellular matrix protein 1 isoform 1 precursor [Homo sapiens]	9	4	35	4	1	540	60.6	6.71	High	High	High	High	High	High		1.32E+08	1.38E+08	1.34E+08	4.16E+08	3.22E+08	3.97E+08	39.11	4	256	4
FALSE	None	75	221316616	extracellular matrix protein 1 isoform 2 precursor [Homo sapiens]	7	2	15	2	1	415	46.1	6.39	High	High	High	High	High	High		1.22E+08	1.25E+08	2.04E+08	5.08E+08	4.99E+08	4.8E+08	14.58	2	77	2
FALSE	Master Protein	75	322302700	extracellular matrix protein 1 isoform 3 precursor [Homo sapiens]	8	4	35	4	1	567	63.5	6.89	High	High	High	High	High	High		1.32E+08	1.38E+08	1.34E+08	4.16E+08	3.22E+08	3.97E+08	39.11	4	256	4
FALSE	Master Protein Candidate	76	530372119	PREDICTED: filamin-B isoform X1 [Homo sapiens]	12	22	146	18	1	2622	280.2	5.69	High	High	High	High	High	High		41598473	41295764	45494656	99322151	96305856	95297781	156.04	20	975	21
FALSE	Master Protein Candidate	76	256222413	filamin-B isoform 3 [Homo sapiens]	12	22	146	18	1	2591	276.8	5.71	High	High	High	High	High	High		41598473	41295764	45494656	99322151	96305856	95297781	156.04	20	975	21
FALSE	None	76	530372129	PREDICTED: filamin-B isoform X6 [Homo sapiens]	11	18	121	14	1	2177	233.6	5.53	High	High	High	High	High	High		41598473	41295764	41843721	99322151	96305856	95297781	124.86	17	853	17
FALSE	Master Protein Candidate	76	105990514	filamin-B isoform 2 [Homo sapiens]	12	22	146	18	1	2602	278	5.73	High	High	High	High	High	High		41598473	41295764	45494656	99322151	96305856	95297781	156.04	20	975	21
FALSE	Master Protein Candidate	76	530372121	PREDICTED: filamin-B isoform X2 [Homo sapiens]	12	22	146	18	1	2609	279	5.77	High	High	High	High	High	High		41598473	41295764	45494656	99322151	96305856	95297781	156.04	20	975	21
FALSE	Master Protein	76	256222411	filamin-B isoform 1 [Homo sapiens]	12	22	146	18	1	2633	281.5	5.71	High	High	High	High	High	High		41598473	41295764	45494656	99322151	96305856	95297781	156.04	20	975	21
FALSE	None	76	578805877	PREDICTED: filamin-B isoform X7 [Homo sapiens]	13	20	134	16	1	2109	225.9	6	High	High	High	High	High	High		41598473	41295764	45494656	99322151	96305856	95297781	156.04	18	975	19
FALSE	Master Protein Candidate	76	256222415	filamin-B isoform 4 [Homo sapiens]	12	22	146	18	1	2578	275.5	5.78	High	High	High	High	High	High		41598473	41295764	45494656	99322151	96305856	95297781	156.04	20	975	21
FALSE	None	76	530372127	PREDICTED: filamin-B isoform X5 [Homo sapiens]	11	18	121	14	1	2181	234.1	5.53	High	High	High	High	High	High		41598473	41295764	41843721	99322151	96305856	95297781	124.86	17	853	17
FALSE	None	76;95	188595687	filamin-C isoform b [Homo sapiens]	1	3	16	0	2	2692	287.1	5.97	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								16.32	3	124	3
FALSE	None	76;95	578814066	PREDICTED: filamin-C isoform X1 [Homo sapiens]	1	3	16	0	2	2632	281.4	6.04	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								16.32	3	124	3
FALSE	None	76;95	116805322	filamin-C isoform a [Homo sapiens]	1	3	16	0	2	2725	290.8	5.97	Not Found	Not Found	Not Found	Not Found	Not Found	Not Found								16.32	3	124	3
FALSE	Master Protein	77	19913412	major vault protein [Homo sapiens]	1	1	2	1	1	893	99.3	5.48	Not Found	High	Not Found	Not Found	Not Found	Not Found			14344826					0	1	0	1
FALSE	Master Protein Candidate	78	578800844	PREDICTED: hepatoma-derived growth factor isoform X2 [Homo sapiens]	28	2	19	2	1	120	13.7	9.6	High	High	High	High	High	High		49742035	67472327	63781927	1.07E+08	1.12E+08	1.07E+08	16.27	2	60	2
FALSE	Master Protein Candidate	78	4758516	hepatoma-derived growth factor isoform a [Homo sapiens]	14	2	19	2	1	240	26.8	4.73	High	High	High	High	High	High		49742035	67472327	63781927	1.07E+08	1.12E+08	1.07E+08	16.27	2	60	2
FALSE	Master Protein Candidate	78	578800842	PREDICTED: hepatoma-derived growth factor isoform X1 [Homo sapiens]	24	2	19	2	1	136	15.1	9.82	High	High	High	High	High	High		49742035	67472327	63781927	1.07E+08	1.12E+08	1.07E+08	16.27	2	60	2
FALSE	Master Protein	78	186928819	hepatoma-derived growth factor isoform b [Homo sapiens]	13	2	19	2	1	256	28.2	4.79	High	High	High	High	High	High		49742035	67472327	63781927	1.07E+08	1.12E+08	1.07E+08	16.27	2	60	2
FALSE	Master Protein Candidate	78	186928821	hepatoma-derived growth factor isoform c [Homo sapiens]	14	2	19	2	1	233	25.5	4.55	High	High	High	High	High	High		49742035	67472327	63781927	1.07E+08	1.12E+08	1.07E+08	16.27	2	60	2
FALSE	Master Protein	79	530391650	PREDICTED: actin-related protein 2/3 complex subunit 5-like protein isoform X1 [Homo sapiens]	8	1	12	1	1	153	16.9	6.6	High	High	High	High	High	High		12239120	15252222	16898483	38618280	45988447	44725936	17.69	1	158	1
FALSE	Master Protein	8	38455402	neutrophil gelatinase-associated lipocalin precursor [Homo sapiens]	14	2	26	2	1	198	22.6	8.91	High	High	High	High	High	High		1.63E+08	1.73E+08	1.54E+08	1.08E+08	99610542	1.1E+08	45.71	2	419	2
FALSE	Master Protein	80	42560237	poliovirus receptor-related protein 1 isoform 1 precursor [Homo sapiens]	5	2	14	2	1	517	57.1	6.1	High	High	Not Found	High	High	High		32115062	38022502		45509761	47234043	39520730	17.77	2	141	2
FALSE	Master Protein Candidate	80	42560233	poliovirus receptor-related protein 1 isoform 3 precursor [Homo sapiens]	8	2	14	2	1	352	39.1	8.48	High	High	Not Found	High	High	High		32115062	38022502		45509761	47234043	39520730	17.77	2	141	2
FALSE	Master Protein Candidate	80	42560231	poliovirus receptor-related protein 1 isoform 2 precursor [Homo sapiens]	6	2	14	2	1	458	50.7	6.87	High	High	Not Found	High	High	High		32115062	38022502		45509761	47234043	39520730	17.77	2	141	2
FALSE	Master Protein Candidate	81	343168770	CD166 antigen isoform 2 precursor [Homo sapiens]	2	1	6	1	1	570	63.6	7.3	High	High	High	Not Found	Not Found	Not Found		12017851	11715312	13903165				6.71	1	37	1
FALSE	Master Protein Candidate	81	343168776	CD166 antigen isoform 4 precursor [Homo sapiens]	8	1	6	1	1	133	15.1	8.13	High	High	High	Not Found	Not Found	Not Found		12017851	11715312	13903165				6.71	1	37	1
FALSE	Master Protein	81	68163411	CD166 antigen isoform 1 precursor [Homo sapiens]	2	1	6	1	1	583	65.1	6.25	High	High	High	Not Found	Not Found	Not Found		12017851	11715312	13903165				6.71	1	37	1
FALSE	Master Protein Candidate	81	343168772	CD166 antigen isoform 3 precursor [Homo sapiens]	2	1	6	1	1	555	61.9	6.19	High	High	High	Not Found	Not Found	Not Found		12017851	11715312	13903165				6.71	1	37	1
FALSE	Master Protein	82	4507467	transforming growth factor-beta-induced protein ig-h3 precursor [Homo sapiens]	9	5	27	5	1	683	74.6	7.71	High	High	High	High	High	High		41072758	39732564	47635017	68815978	88408759	84622794	31.35	5	128	4
FALSE	Master Protein	83	11056044	inorganic pyrophosphatase [Homo sapiens]	14	3	26	3	1	289	32.6	5.86	High	High	High	High	High	High		28388471	33502782	31162737	59339357	50541061	64268172	46.04	3	224	3
FALSE	Master Protein Candidate	84	5031595	actin-related protein 2/3 complex subunit 4 isoform a [Homo sapiens]	7	1	2	1	1	168	19.7	8.43	High	Not Found	Not Found	Not Found	Not Found	Not Found		34018330						1.95	1	27	1
FALSE	Master Protein Candidate	84	311771647	actin-related protein 2/3 complex subunit 4 isoform c [Homo sapiens]	6	1	2	1	1	187	21.6	8.59	High	Not Found	Not Found	Not Found	Not Found	Not Found		34018330						1.95	1	27	1
FALSE	Master Protein	84	311771694	ARPC4-TTLL3 fusion protein [Homo sapiens]	2	1	2	1	1	625	71.7	5.88	High	Not Found	Not Found	Not Found	Not Found	Not Found		34018330						1.95	1	27	1
FALSE	Master Protein	85	24234699	keratin, type I cytoskeletal 19 [Homo sapiens]	38	15	176	12	1	400	44.1	5.14	High	High	High	High	High	High		2.36E+08	2.34E+08	2.35E+08	4.12E+08	4.01E+08	4.1E+08	229.48	15	1403	15
FALSE	Master Protein	86	167614506	plastin-2 [Homo sapiens]	20	10	112	8	1	627	70.2	5.43	High	High	High	High	High	High		56756579	60363992	61310652	87084017	83141613	88664669	129.23	10	905	10
FALSE	None	87	578821730	PREDICTED: neuroblast differentiation-associated protein AHNAK isoform X9 [Homo sapiens]	11	11	68	11	1	4001	423.5	6.34	High	High	High	High	High	High		43538688	40610030	52105233	1.43E+08	1.39E+08	1.17E+08	47.27	11	163	11
FALSE	None	87	578821728	PREDICTED: neuroblast differentiation-associated protein AHNAK isoform X8 [Homo sapiens]	9	11	69	11	1	4596	489.1	6.29	High	High	High	High	High	High		51411698	48274930	55336621	1.43E+08	1.39E+08	1.34E+08	68.64	11	227	11
FALSE	Master Protein Candidate	87	530397279	PREDICTED: neuroblast differentiation-associated protein AHNAK isoform X1 [Homo sapiens]	11	13	86	13	1	5890	628.7	6.15	High	High	High	High	High	High		51411698	48274930	55336621	1.43E+08	1.39E+08	1.34E+08	71.24	13	227	13
FALSE	Master Protein Candidate	87	530397285	PREDICTED: neuroblast differentiation-associated protein AHNAK isoform X4 [Homo sapiens]	11	13	86	13	1	5762	615	6.15	High	High	High	High	High	High		51411698	48274930	55336621	1.43E+08	1.39E+08	1.34E+08	71.24	13	227	13
FALSE	Master Protein Candidate	87	530397283	PREDICTED: neuroblast differentiation-associated protein AHNAK isoform X3 [Homo sapiens]	11	13	86	13	1	5762	614.7	6.19	High	High	High	High	High	High		51411698	48274930	55336621	1.43E+08	1.39E+08	1.34E+08	71.24	13	227	13
FALSE	Master Protein	87	530397287	PREDICTED: neuroblast differentiation-associated protein AHNAK isoform X5 [Homo sapiens]	11	13	86	13	1	5762	614.8	6.18	High	High	High	High	High	High		51411698	48274930	55336621	1.43E+08	1.39E+08	1.34E+08	71.24	13	227	13
FALSE	None	87	578821732	PREDICTED: neuroblast differentiation-associated protein AHNAK isoform X10 [Homo sapiens]	9	11	66	11	1	3489	368.2	6.58	High	High	High	High	High	High		43538688	40610030	52105233	1.43E+08	1.39E+08	1.17E+08	47.27	11	163	11
FALSE	None	87	530397289	PREDICTED: neuroblast differentiation-associated protein AHNAK isoform X6 [Homo sapiens]	11	12	75	12	1	5438	580.3	6.14	High	High	High	High	High	High		51411698	48274930	55336621	1.43E+08	1.39E+08	1.34E+08	68.85	12	227	12
FALSE	None	87	530397291	PREDICTED: neuroblast differentiation-associated protein AHNAK isoform X7 [Homo sapiens]	11	12	80	12	1	4506	478.7	6.28	High	High	High	High	High	High		51411698	48274930	55336621	1.43E+08	1.39E+08	1.34E+08	62.88	12	207	12
FALSE	None	88	578836001	PREDICTED: laminin subunit alpha-5 isoform X2 [Homo sapiens]	1	1	2	1	1	2586	279.4	6.43	Not Found	Not Found	Not Found	Not Found	Not Found	High							24434997	2.5	1	36	1
FALSE	Master Protein Candidate	88	21264602	laminin subunit alpha-5 precursor [Homo sapiens]	1	2	4	2	1	3695	399.5	7.02	High	High	Not Found	Not Found	Not Found	High		27038758	31038082				24434997	2.5	1	42	2
FALSE	None	88	578836003	PREDICTED: laminin subunit alpha-5 isoform X3 [Homo sapiens]	1	1	2	1	1	2300	248.1	6.6	Not Found	Not Found	Not Found	Not Found	Not Found	High							24434997	2.5	1	36	1
FALSE	Master Protein	88	578835999	PREDICTED: laminin subunit alpha-5 isoform X1 [Homo sapiens]	1	2	4	2	1	3700	399.9	7.02	High	High	Not Found	Not Found	Not Found	High		27038758	31038082				24434997	2.5	1	42	2
FALSE	Master Protein	89	118402586	lactoylglutathione lyase [Homo sapiens]	14	3	19	3	1	184	20.8	5.31	High	High	High	High	High	High		30524593	32757556	33697103	69204182	72597832	74117777	20.28	2	48	3
FALSE	Master Protein	9	346644849	DNA-(apurinic or apyrimidinic site) lyase [Homo sapiens]	9	2	15	2	1	318	35.5	8.12	High	High	High	High	High	High		22827579	24598095	22850804	58365611	57628201	57438658	21.93	2	255	2
FALSE	Master Protein Candidate	9	530403617	PREDICTED: DNA-(apurinic or apyrimidinic site) lyase isoform X2 [Homo sapiens]	9	2	15	2	1	301	33.8	7.91	High	High	High	High	High	High		22827579	24598095	22850804	58365611	57628201	57438658	21.93	2	255	2
FALSE	Master Protein	90	5902102	small nuclear ribonucleoprotein Sm D1 [Homo sapiens]	20	2	16	2	1	119	13.3	11.56	High	High	High	High	High	High		53628023	55988035	49932093	1.08E+08	94211402	94896986	21.74	2	64	2
FALSE	Master Protein Candidate	91	388556516	proteasome activator complex subunit 3 isoform 3 [Homo sapiens]	6	1	2	1	1	265	30.9	6.71	Not Found	Not Found	Not Found	Not Found	High	Not Found						25243911		3.46	1	34	1
FALSE	Master Protein	91	30410796	proteasome activator complex subunit 3 isoform 2 [Homo sapiens]	6	1	2	1	1	267	30.9	6.11	Not Found	Not Found	Not Found	Not Found	High	Not Found						25243911		3.46	1	34	1
FALSE	Master Protein Candidate	91	30410794	proteasome activator complex subunit 3 isoform 1 [Homo sapiens]	6	1	2	1	1	254	29.5	5.95	Not Found	Not Found	Not Found	Not Found	High	Not Found						25243911		3.46	1	34	1
FALSE	Master Protein	92	4506193	proteasome subunit beta type-1 [Homo sapiens]	12	2	13	2	1	241	26.5	8.13	Not Found	High	High	High	High	High			29962844	27709777	1.12E+08	1.31E+08	1.14E+08	15.06	2	112	2
FALSE	Master Protein	93	530397957	PREDICTED: tripartite motif-containing protein 29 isoform X1 [Homo sapiens]	2	1	2	1	1	588	65.8	7.15	High	Not Found	Not Found	Not Found	Not Found	Not Found		16356100						2.27	1	25	1
FALSE	Master Protein	94	56699409	RNA-binding motif protein, X chromosome isoform 1 [Homo sapiens]	7	2	22	2	1	391	42.3	10.05	High	High	High	High	High	High		45232020	46714420	45712378	73165377	69131424	86250358	33.31	2	214	2
FALSE	None	94	153252068	RNA-binding motif protein, X-linked-like-2 [Homo sapiens]	4	1	10	1	1	392	42.8	10.32	High	High	High	High	High	Not Found		36770041	36889282	37322934	50215308	52971787		16.18	1	123	1
FALSE	Master Protein Candidate	94	258645150	RNA-binding motif protein, X chromosome isoform 2 [Homo sapiens]	14	2	22	2	1	196	22.2	5.26	High	High	High	High	High	High		45232020	46714420	45712378	73165377	69131424	86250358	33.31	2	214	2
FALSE	Master Protein Candidate	94	242117971	RNA binding motif protein, X-linked-like-1 [Homo sapiens]	7	2	22	2	1	390	42.1	9.89	High	High	High	High	High	High		45232020	46714420	45712378	73165377	69131424	86250358	33.31	2	214	2
FALSE	None	94	223890219	RNA-binding motif protein, X-linked-like-3 [Homo sapiens]	1	1	10	1	1	1067	114.9	9.1	High	High	High	High	High	Not Found		36770041	36889282	37322934	50215308	52971787		16.18	1	123	1
FALSE	Master Protein	95	160420317	filamin-A isoform 2 [Homo sapiens]	16	30	250	26	1	2647	280.6	6.06	High	High	High	High	High	High		68065377	68275769	66475123	1.94E+08	2.03E+08	2.03E+08	286.06	30	1959	30
FALSE	Master Protein Candidate	95	116063573	filamin-A isoform 1 [Homo sapiens]	16	30	250	26	1	2639	279.8	6.05	High	High	High	High	High	High		68065377	68275769	66475123	1.94E+08	2.03E+08	2.03E+08	286.06	30	1959	30
FALSE	Master Protein	96	4557553	emerin [Homo sapiens]	5	1	6	1	1	254	29	5.5	High	High	High	Not Found	Not Found	Not Found		20222006	21085388	23206429				4.86	1	56	1
FALSE	Master Protein	97	20149540	protein-lysine 6-oxidase isoform 1 preproprotein [Homo sapiens]	2	1	12	1	1	417	46.9	8.09	High	High	High	High	High	High		32057917	31813670	33568444	71100447	76795395	70433383	12.27	1	93	1
FALSE	Master Protein	98	4826972	RNA-binding protein 8A [Homo sapiens]	6	1	7	1	1	174	19.9	5.72	High	High	Not Found	High	Not Found	High		33498470	36259580		50016898		56351340	5.69	1	34	1

Supplementary Table 2: List of differentially expressed proteins upon MYB modulation in MiaPaCa and BxPC3

MiaPaCa (Scr vs shMYB)	
Expr Fold Change	**Symbol**
-10.794	ACTA1
5606982	ACTBL2
-9.275	ACTG1
-5.148	ACTN1
-8.906	ACTN4
2.87	ADAM10
23.22	ADAMTSL1
-17.322	AHCY
-33.23	AHNAK
-30.35	AKR1C1/AKR1C2
-55.617	ALCAM
-93478.8	ALDH1A1
-4.547	ALDOA
-9.157	ANP32A
-9386.69	ANXA1
-71.797	ANXA2
-1.2E+12	ANXA5
-5.39	APLP2
-16.709	ARHGDIA
1172597	ARHGDIB
-37.776	ARPC3
4.62	B4GALT1
-4.887	BCAM
-5.364	BSG
-4.071	BTF3
2.05	C1R
-83.932	C3
-19.662	CACYBP
-10.284	CALB2
-5.385	CALR
2.51	CANT1
-20.575	CAP1
-6.387	CAPZA1
-18.539	CAPZA2
-11.469	CAPZB
-10.704	CBR1
-4.406	CBX3

-11.239	CCT6A
-11.935	CD109
-4.995	CD44
-4.909	CDC37
-7.64	CDH1
-111.532	CELA3A
-8.369	CFL1
-8.377	CFL2
-13.015	CLIC1
21.44	CLSTN3
-9.689	CLU
-4.477	CNN2
-4.508	COL6A2
-28.12	COL7A1
-11.72	COTL1
-4.145	CP
-8.5E+11	CPA4
2.98	CTNNA1
-18.657	CTSA
-18.294	CTSB
-19.446	CTSD
-13.717	CTSH
-14.193	CTSL
-5.946	CTSZ
-12.126	CYCS
-16.39	DBI
-4.427	DDT
-17.749	DDX39B
-4.698	DEK
-136.776	DNAJB11
-12.676	DNASE2
-743.63	DSG2
-66.102	DSP
-14.202	DSTN
-11.77	ECM1
-7.096	EEF1A1
-11.854	EEF1B2
-7.293	EEF1D
-5.932	EEF1G
-6.778	EEF2
-4.687	EFHD2
-4.233	EFNB1
-15.363	EIF4A2
-7.169	ENO1
-4.231	ENO3

-5.194	ERP44
-4.971	EZR
-11.543	FAM3C
2.74	FBLN1
3.04	FBLN1
545803.5	FGFBP1
-4.02	FKBP1A
-8.963	FLNB
-11.304	FSCN1
-8.488	GAPDH
-38.798	GARS
-4.605	GDF15
-6.31	GDI2
-16.48	GGCT
-13.207	GLA
-7.495	GLG1
-8.406	GLO1
-8.616	GOT1
-8.281	GOT2
-11.18	GPI
-4.547	GSN
-10.824	GSTO1
-8.439	GSTP1
-100.134	H6PD
-12.085	HDGF
-1.7E+12	HEXA
-5.139	HEXB
-5.748	HIST1H1B
-4.133	HIST1H1D
-38.64	HIST1H2BB
-4.22	HIST1H2BD
-6.823	HIST1H3A
-17.945	HIST2H2AA3/HIST2H2AA4
408941.5	HIST2H2AB
-9.524	HIST2H4A
-11.079	HIST3H2A
2.11	HLA-B
-8.54	HMGA1
-5.993	HMGA1
-2.1E+11	HMGA2
-24.726	HMGB1
-6.813	HNRNPA2B1
-5.351	HNRNPA3
-6.506	HNRNPAB
-5.614	HNRNPC

-11.827	HNRNPD
-8.176	HNRNPK
-4.014	HNRNPL
-12.352	HPRT1
-6.966	HS3ST1
-19.208	HSP90AA1
-9.773	HSP90AB1
-4.215	HSP90B1
-4.802	HSPA1A/HSPA1B
-8.798	HSPA4
-6.125	HSPA5
-20.221	HSPB1
-11.703	HSPD1
-8.507	HSPH1
2.41	HTRA1
-5.628	IGF2R
2.47	IGFBP2
-4.143	IGFBP6
550392	IL1RL1
-1.8E+13	INHBA
-237.079	ITGB1
-2.9E+12	ITGB4
14.67	JAG1
-6.64	KHSRP
2.61	KLK6
2.45	KRT1
-11.454	KRT16
-22.652	KRT17
-43.912	KRT18
-20.792	KRT19
1173218	KRT2
787786.4	KRT5
-8.107	KRT7
-38.882	KRT8
3.18	KRT9
248143.8	KYNU
-35.714	LAMA3
-4.234	LAMB1
7.63	LCN2
-16.962	LCP1
-15.195	LDHA
-4.146	LDHB
-6.232	LGALS1
3.89	LGALS3BP
-5.233	LGMN

-9.932	LMNA
-4.371	LMNB1
-30.074	LMNB2
-10.02	LRG1
-4.406	LRRC59
-4.261	MAPRE1
-4.281	MARCKS
-7.74	MDH1
2.93	MINPP1
-6.787	MSN
-65.382	MVP
-5.605	NACA
-2636.3	NAMPT
-8.347	NASP
-8.274	NCL
-11.024	NECTIN1
689900.2	NECTIN1
-10.948	NEDD8-MDP1
1295694	NID2
-4.55	NME1
-4.551	NME1-NME2
-71.643	NQO1
-14.209	NT5E
-23.197	NUDT21
-4.259	OAF
-9.799	OLA1
-1724.25	OSMR
-14.978	PA2G4
-16.627	PABPC1
-11.379	PARK7
-10.349	PARP1
-4.945	PCBP1
-54850	PCDH1
997552.9	PCDH7
15.35	PCSK9
-52.577	PDCD5
-4.358	PDCD6IP
-14.582	PDIA4
-6.638	PDIA6
-4.521	PEBP1
-5.166	PFN1
-4.989	PGAM1
-11.878	PGD
-5.513	PGK1
-9.252	PGLS

-8.758	PKM
-177.778	PLAT
-5.949	PLEC
-4.981	PLOD1
-181.583	PLOD3
-72.048	PLS3
-7.25	PLTP
-7.581	PNP
-10.021	PPA1
-16.805	PPIA
-13.587	PPL
-16.758	PRCP
-11.116	PRDX1
-7.056	PRDX2
742674.8	PRDX5
-6.991	PRDX6
-9.96	PRKCSH
-5.198	PRSS22
-96.599	PSAP
-17.009	PSAT1
-6.934	PSMA1
-10.056	PSMA2
-8.203	PSMA6
-5.394	PSMA7
-4.618	PSMB1
-12.274	PSMB4
-9.333	PSMB5
-15.377	PSMB6
-19.541	PSME1
-22.687	PSME2
-14.429	PTBP1
-4.295	PTK7
-5.849	PTPRF
-90534	PTX3
-60.313	PYGB
2.57	QSOX2
-5.439	RAB11A
-9.181	RAB7A
-19.162	RACK1
-4.393	RAN
-5.176	RBMX
-8.878	RDX
-15.896	RNH1
-16.69	RPLP0
-6.075	RPLP2

-14.679	RPS13
-29.903	RPS3
-61.917	S100A10
-11.566	S100A11
-4.632	S100A4
-4.6E+12	S100P
-3.7E+12	SEMA3B
4.5	SEMA4B
34.11	SERPINA1
-4326.43	SERPINA3
798920.4	SERPINB2
288976.7	SERPINB5
-1899.45	SERPINB9
-32.948	SERPINE1
-1.1E+13	SERPINE2
-11.599	SERPINH1
-4.423	SET
232083.6	SFN
-112.141	SFPQ
-52.588	SLC9A3R1
-4.826	SNRPB
-5.3	SOD1
-4.117	SPTAN1
-17.327	SRSF1
-4.002	SRSF3
-10.452	SSB
-5.519	SSBP1
-5.92	ST13
53.44	STC1
-10.127	STIP1
-9.733	STMN1
-18.463	SUB1
-4.932	SUMO2
-5.421	SYNCRIP
-10.789	TAGLN2
-13.284	TALDO1
-8.143	TBCA
-7.3E+12	TES
-5.07	TFG
-4.587	TFPI
-4.208	TFRC
4.05	TGFB1
-13.737	TGFBI
-18.368	TGFBR3
-26.118	TINAGL1

-27.338	TKT
-4.168	TMEM189-UBE2V1
-6.713	TMSB10/TMSB4X
-21.344	TNFRSF6B
-4.756	TPI1
-5.699	TPM3
-6.112	TPT1
-8.4E+11	TRA2B
-13.131	TUBA1B
-27.35	TUBB
-12.048	TUBB4B
-25.58	TXNDC12
-4.873	TXNDC17
-13.709	TXNDC5
-6.509	TXNRD1
-157.112	UAP1
-17.235	UBA1
-8.706	UBE2N
-4.68	VAPA
-5.225	VCL
-4.368	VCP
-13.228	VIM
-6.3E+13	WARS
-10.966	XRCC6
-18.865	YWHAB
-10.479	YWHAE
-14.632	YWHAG
-5.7E+13	YWHAH
-102.089	YWHAQ
-23.704	YWHAZ

BxPC3 (Neo vs MYB)	
Expr Fold Change	**Symbol**
4.505	ACTA1
18.114	ACTBL2
12.677	ACTN1
3.295	ACTN4
-3.409	AGR2
27.815	AHCY
13.441	AHNAK
10.518	AHSA1
2353579	AIFM1
8.098	AKR1C1/AKR1C2
10.287	AKR1C3
3.772	ALCAM
6.009	ALDH3A1
2.259	ANP32A
3.622	ANXA1
2.596	ANXA2
5.635	ANXA5
3.853	ARHGDIA
-2.147	ATP6AP1
2.282	AXL
3.047	B4GAT1
3.097	BASP1
2.086	BTF3
6.457	C1QBP
-2.186	C1R
-2.054	C1RL
-12.297	C1S
2.089	CACYBP
-2.2E+12	CALB2
2.224	CANX
2.391	CAP1
4.88	CAPZA1
38.231	CAPZA2
7.382	CAPZB
4.468	CBR1
4.524	CCT6A
7.45	CD44
2.365	CDC37
-2.205	CELA3A
-2.089	CFB

-3.383	CFH
2.206	CFL1
1845433	CFL2
-8.051	CKMT1A/CKMT1B
-5.614	CLU
-3.439	CNPY2
2.958	COCH
2.981	COL17A1
-19.4	COL18A1
2308388	COL5A2
-37.258	CPA4
2.236	CTNNA1
3.201	CTSA
3.378	CTSB
2.652	CTSZ
3.926	DBI
25.221	DDX39B
4.292	DEK
2.226	DNASE2
3.225	DSTN
-5.613	ECM1
2.469	EEF1A1
6.097	EEF1G
2.929	EEF2
30.683	EIF4A2
12.128	EIF5A
3.592	ELAVL1
2.233	ENO1
2.142	ENO2
2.534	ENO3
8.934	EPHA4
2.114	EPPK1
3.651	ERP44
2.437	F3
-6.972	FBLN1
-8.892	FBLN1
-2.121	FGFBP1
2.295	FKBP4
2.324	FLNB
6.241	FSCN1
1.995	FUBP1
4.104	FUCA2
2.632	G6PD
6.431	GAA
2.43	GANAB

-2.202	GARS
-2.784	GDF15
5.204	GDI2
3.394	GLA
2.924	GLG1
2.002	GLO1
3.407	GLOD4
-2.154	GOLM1
9.824	GPC1
3.552	GPI
2.452	GRN
-3.993	GSN
2.908	GSTO1
3.129	GSTP1
2.971	HACD3
2.315	HEXA
13.881	HIST1H1B
4.686	HIST1H1D
1.995	HIST1H2BB
3.083	HIST1H2BD
2.055	HIST2H4A
-2.9E+15	HLA-B
2.36	HMGB1
4.537	HMGB2
2.262	HNRNPA1
3.33	HNRNPA3
2.116	HNRNPAB
6.419	HNRNPCL3/HNRNPCL4
4.899	HNRNPD
2.184	HNRNPH1
2.056	HNRNPK
2.741	HNRNPR
2.876	HNRNPU
19.256	HPRT1
19.551	HS3ST1
4.99	HSP90AA1
4.435	HSP90AB1
2.11	HSPA1A/HSPA1B
18.08	HSPA4
3.71	HSPA5
5.205	HSPA8
-2.603	HSPB1
3.114	HSPH1
-2.801	HTRA1
5.218	IGF2R

-3.097	IGFBP2
-7.92	IGFBP5
-2.089	IGHA1
-2.376	IL1RL1
6.518	ILF2
4.288	ILF3
4.549	INHBA
3.966	ITGB1
9.36	ITGB4
-6.146	KLK10
2.694	KLK6
32.236	KRT1
24765714	KRT14
30.553	KRT16
-2.28	KRT18
1187691	KRT2
7788498	KRT6B
2.027	KRT6C
17.492	KRT9
13.017	KYNU
5.124	LDHA
2.045	LDHB
-3.353	LFNG
2.106	LMNB1
13966972	LMNB2
-5.354	LRG1
6.888	MAN1B1
2.04	MAPRE1
2.331	MARCKS
4.607	MDH1
2.165	NACA
3.798	NAMPT
6.026	NASP
3.136	NCL
2.175	NECTIN1
2.618	NEDD8-MDP1
-2.067	NID2
2.354	NME1-NME2
2.128	NPM1
4.894	NQO1
-2.494	NUCB1
-2.148	NUCKS1
2.095	NUDC
2.143	NUDT21
3.774	OLA1

31.917	OSMR
2.505	P4HB
2.78	PA2G4
4.389	PABPC1
2.505	PARP1
-2.051	PCDH7
3.119	PCNA
-3.51	PCSK9
4.795	PDCD5
9.907	PDCD6IP
2.537	PFN1
2.017	PGAM1
3.209	PGK1
2.049	PGLS
2.141	PKM
2.715	PLAT
4.22	PLAU
3.524	PLOD1
11.808	PLS3
3.367	PPA1
5.402	PPIA
2.485	PPIB
-2.4E+13	PPL
8.565	PPT1
7.955	PRCP
8.044	PRDX1
2.301	PRDX2
2.027	PRDX6
2.339	PRKCSH
3.182	PSAP
25.169	PSAT1
2.307	PSMA1
4.457	PSMA6
2.608	PSMA7
2.229	PSMB1
6.501	PSMB2
2.565	PSMB4
7.646	PSMB5
961641	PTGDS
14.086	PTK7
2.81	PTPRF
2.116	PTPRS
4.336	PTX3
-2.777	PYGB
2.016	RAB7A

2.967	RAD23B
2.545	RBMX
7906017	RNH1
3.981	RPLP0
2.182	RPS13
2.669	RPS3
3.476	S100A2
2.191	S100A6
2.553	SDC4
-6.772	SEMA3A
4.592	SEMA3B
3.15	SERPINA1
16.338	SERPINB2
6.195	SERPINB5
-13.21	SERPINE2
-2.274	SERPINF1
1.987	SET
3.794	SLC39A10
2.112	SLC9A3R1
7.271	SNRPB
2.226	SOD2
3.042	SORD
-6.1E+14	SPP1
2.599	SRSF1
2.101	SRSF3
1.998	SSB
4.203	ST13
2.108	STIP1
14.147	STMN1
3.805	SYNCRIP
3.466	TALDO1
2.065	TES
6.173	TFG
15.104	TFRC
2.452	TGFB1
-9.623	TGFBR3
11.294	TGM2
12.516	THBS1
2.466	TIMP1
8.02	TKT
4.31	TMEM189-UBE2V1
2.044	TMSB10/TMSB4X
7.119	TPM4
2.417	TPT1
7.674	TRA2B

2.244	TRIM29
3.743	TUBA1B
2.753	TUBB
2.889	TUBB4B
2.246	TXNDC12
12.461	TXNDC17
2.492	TXNDC5
8216733	TXNRD1
-2.352	UAP1
3.714	UBA1
-4.757	UBE2L3
7.686	USP14
2.776	VAPA
2.022	VCP
4.673	WARS
6.264	XRCC6
-1.8E+14	YBX3

Supplementary Table 3: List of diseases and biological functions with predicted change in activity upon MYB modulation in MiaPaCa and BxPC3

I. MiaPaCa (shMYB vs. Scr)						
Categories	**Diseases or Functions Annotation**	**p-Value**	**Predicted Activation State**	**Activation z-score**	**Molecules**	**Number of Molecules**
Cellular Movement	Cell movement	4.99E-41	Decreased	-3.679	ACTN1,ACTN4,ADAM10,AHCY,AHNAK,ALCAM,ALDOA,ANXA1,ANXA2,ANXA5,APLP2,ARHGDIA,ARHGDIB,ARPC3,B4GALT1,BCAM,BSG,C3,CALR,CAP1,CD44,CDH1,CFL1,CLU,CNN2,COL7A1,CTNNA1,CTSB,CTSH,CTSL,CTSZ,DDT,DEK,DSG2,DSP,DSTN,ECM1,EFNB1,ENO1,EZR,FGFBP1,FLNB,FSCN1,GAPDH,GDF15,GLG1,GPI,GSN,HDGF,HMGA1,HMGA2,HMGB1,HNRNPA2B1,HNRNPAB,HNRNPK,HNRNPL,HSP90AA1,HSP90AB1,HSP90B1,HSPA1A/HSPA1B,HSPA5,HSPB1,HSPD1,HTRA1,IGF2R,IGFBP2,IGFBP6,IL1RL1,INHBA,ITGB1,ITGB4,JAG1,KLK6,KRT16,KRT19,KRT2,KRT8,LAMA3,LAMB1,LCN2,LCP1,LDHA,LGALS1,LGALS3BP,LGMN,LMNA,LMNB1,LMNB2,MAPRE1,MARCKS,MSN,NACA,NAMPT,NCL,NME1,NQO1,NT5E,OSMR,PA2G4,PARK7,PARP1,PDCD6IP,PEBP1,PFN1,PKM,PLAT,PLEC,PLTP,PPIA,PRCP,PRDX1,PRDX2,PRDX6,PTBP1,PTPRF,PTX3,RACK1,RDX,RNH1,S100A10,S100A11,S100A4,S100P,SEMA3B,SERPINA1,SERPINA3,SERPINB2,SERPINB5,SERPINE1,SERPINE2,SERPINH1,SFN,SLC9A3R1,SOD1,SRSF1,SSBP1,ST13,STC1,STMN1,TAGLN2,TFPI,TGFB1,TGFBI,TGFBR3,TKT,TMSB10/TMSB4X,TNFRSF6B,TPI1,TPM3,TPT1,TUBB,TXNRD1,VCL,VCP,VIM,WARS,YWHAE,YWHAZ	158
	Migration of cells	2.25E-34	Decreased	-3.525	ACTN1,ACTN4,ADAM10,AHCY,AHNAK,ALCAM,ALDOA,ANXA1,ANXA2,ANXA5,APLP2,ARHGDIA,ARHGDIB,B4GALT1,BCAM,BSG,C3,CALR,CAP1,CD44,CDH1,CFL1,CLU,CNN2,COL7A1,CTNNA1,CTSB,CTSH,CTSL,CTSZ,DDT,DEK,DSG2,DSP,ECM1,EFNB1,EZR,FLNB,FSCN1,GDF15,GLG1,GPI,GSN,HDGF,HMGA2,HMGB1,HNRNPA2B1,HNRNPK,HNRNPL,HSP90AA1,HSP90AB1,HSP90B1,HSPA1A/HSPA1B,HSPA5,HSPB1,HSPD1,HTRA1,IGF2R,IGFBP2,IGFBP6,IL1RL1,INHBA,ITGB1,ITGB4,JAG1,KLK6,KRT16,KRT19,KRT2,KRT8,LAMA3,LAMB1,LCN2,LCP1,LDHA,LGALS1,LGALS3BP,LGMN,LMNA,LMNB	139

					1,LMNB2,MAPRE1,MARCKS,MSN,NACA,NAMPT,NCL,NME1,NQO1,NT5E,OSMR,PA2G4,PARK7,PARP1,PFN1,PKM,PLAT,PLEC,PLTP,PPIA,PRCP,PRDX1,PRDX2,PTPRF,PTX3,RACK1,RDX,RNH1,S100A10,S100A11,S100A4,S100P,SERPINA1,SERPINA3,SERPINB2,SERPINB5,SERPINE1,SERPINE2,SFN,SLC9A3R1,SOD1,SSBP1,STC1,STMN1,TFPI,TGFB1,TGFBI,TGFBR3,TMSB10/TMSB4X,TNFRSF6B,TPM3,TPT1,TXNRD1,VCL,VCP,VIM,WARS,YWHAE,YWHAZ	
	Invasion of cells	6.03E-34	Decreased	-3.747	ACTN4,ADAM10,AHCY,AHNAK,ALCAM,ANXA1,ANXA2,ARHGDIA,BSG,CALR,CAP1,CD44,CDH1,CLU,COL7A1,CTSB,CTSD,CTSH,CTSL,CTSZ,DSP,ECM1,EZR,FBLN1,FKBP1A,FSCN1,GDF15,GPI,GSN,HDGF,HMGA1,HMGA2,HMGB1,HNRNPA2B1,HNRNPAB,HSP90AA1,HSP90AB1,HSP90B1,HSPA1A/HSPA1B,HSPA5,HTRA1,IGFBP2,INHBA,ITGB1,ITGB4,KLK6,KRT17,KRT19,KRT8,LAMA3,LCN2,LCP1,LDHA,LGALS1,LGMN,LMNA,MARCKS,NAMPT,NME1,NQO1,PA2G4,PARK7,PEBP1,PKM,PLAT,PLOD3,PPIA,PTBP1,RACK1,RNH1,S100A10,S100A11,S100A4,S100P,SERPINA1,SERPINB5,SERPINE1,SERPINE2,SFN,SLC9A3R1,SSBP1,STMN1,TAGLN2,TFPI,TGFB1,TGFBI,TGFBR3,TMSB10/TMSB4X,VCL,VCP,VIM,YWHAG,YWHAQ	93
	Cell movement of tumor cell lines	3.36E-27	Decreased	-3.358	ACTN1,ACTN4,ADAM10,AHNAK,ALCAM,ANXA1,ANXA2,ARHGDIB,BCAM,BSG,C3,CALR,CAP1,CD44,CDH1,CLU,CTSB,CTSH,CTSL,CTSZ,DSP,ECM1,EFNB1,EZR,FLNB,FSCN1,GDF15,GPI,HDGF,HMGA1,HMGA2,HMGB1,HNRNPA2B1,HNRNPK,HSP90AA1,HSP90B1,HSPA1A/HSPA1B,HTRA1,IGFBP2,IGFBP6,ITGB1,ITGB4,KLK6,KRT19,KRT8,LAMA3,LCN2,LCP1,LDHA,LGALS1,LGALS3BP,LMNA,MARCKS,MSN,NCL,NME1,NT5E,PA2G4,PEBP1,PFN1,PKM,PLAT,PPIA,PRDX2,RACK1,S100A10,S100A11,S100A4,S100P,SERPINA1,SERPINB5,SERPINE1,SFN,SLC9A3R1,SSBP1,STMN1,TAGLN2,TFPI,TGFB1,TGFBI,TGFBR3,TPM3,VCL,VCP,VIM	85
	Invasion of tumor cell lines	7.17E-27	Decreased	-3.847	ACTN4,ADAM10,AHNAK,ALCAM,ANXA1,ARHGDIA,BSG,CALR,CAP1,CD44,CDH1,CLU,CTSB,CTSD,CTSH,CTSZ,DSP,ECM1,EZR,FBLN1,FSCN1,GDF15,GPI,HDGF,HMGA1,HMGA2,HMGB1,HNRNPA2B1,HNRNPAB,HSP90AA1,HSPA1A/HSPA1B,HTRA1,IGFBP2,ITGB1,ITGB4,KLK6,KRT17,KRT19,KRT8,LCN2,LCP1,LDHA,LGALS1,LMNA,MARCKS,NAMPT,NME1,PA2	74

					G4,PEBP1,PKM,PLAT,PTBP1,RACK1,S100A10,S100A11,S100A4,S100P,SERPINA1,SERPINB5,SERPINE2,SFN,SLC9A3R1,SSBP1,STMN1,TAGLN2,TFPI,TGFB1,TGFBI,TGFBR3,TMSB10/TMSB4X,VCP,VIM,YWHAG,YWHAQ	
	Migration of tumor cell lines	1.95E-23	Decreased	-3.658	ACTN1,ACTN4,ADAM10,AHNAK,ALCAM,ANXA1,ANXA2,ARHGDIB,BCAM,BSG,CALR,CD44,CDH1,CLU,CTSB,CTSH,CTSL,CTSZ,DSP,ECM1,EFNB1,EZR,FLNB,FSCN1,GDF15,GPI,HDGF,HMGA2,HNRNPA2B1,HNRNPK,HSP90AA1,HSP90B1,HSPA1A/HSPA1B,HTRA1,IGFBP2,IGFBP6,ITGB1,ITGB4,KLK6,KRT19,KRT8,LAMA3,LCN2,LDHA,LGALS1,LGALS3BP,LMNA,MSN,NCL,NME1,PKM,PLAT,PPIA,PRDX2,RACK1,S100A10,S100A11,S100A4,S100P,SERPINA1,SERPINE1,SFN,SLC9A3R1,SSBP1,STMN1,TFPI,TGFB1,TGFBI,TGFBR3,TPM3,VCP,VIM	72
	Invasion of breast cancer cell lines	4.33E-14	Decreased	-2.086	AHNAK,BSG,CALR,CD44,CDH1,CTSB,ECM1,EZR,FSCN1,GPI,HMGA2,HSP90AA1,ITGB1,ITGB4,KRT19,KRT8,LCN2,LDHA,NAMPT,NME1,PTBP1,S100A11,SERPINA1,SERPINB5,SLC9A3R1,SSBP1,STMN1,TFPI,TGFB1,TGFBR3,VIM,YWHAG	32
	Cell movement of sarcoma cell lines	9.58E-13	Decreased	-2.651	ACTN4,AHNAK,BCAM,CD44,CDH1,CTSB,FLNB,GPI,HNRNPK,IGFBP6,ITGB1,LAMA3,S100A11,SERPINE1,SLC9A3R1,STMN1,TPM3,VCP	18
	Cell movement of endothelial cells	1.16E-12	Decreased	-3.624	ADAM10,ALCAM,ANXA1,ANXA2,CALR,CD44,CNN2,EFNB1,FLNB,GPI,HMGB1,HSP90AB1,HSPA5,HSPB1,IGF2R,IL1RL1,ITGB1,ITGB4,LGALS1,MARCKS,NCL,PKM,S100A4,S100P,SERPINE1,STC1,TFPI,TGFB1,TGFBI,TMSB10/TMSB4X,TNFRSF6B,VIM,WARS,YWHAZ	34
	Migration of endothelial cells	1.27E-11	Decreased	-3.632	ADAM10,ALCAM,ANXA1,ANXA2,CALR,CD44,CNN2,FLNB,GPI,HMGB1,HSP90AB1,HSPA5,HSPB1,IGF2R,ITGB1,ITGB4,LGALS1,MARCKS,NCL,PKM,S100P,SERPINE1,STC1,TFPI,TGFB1,TGFBI,TMSB10/TMSB4X,TNFRSF6B,VIM,WARS,YWHAZ	31
	Cell movement of carcinoma cell lines	3.43E-11	Decreased	-2.676	ADAM10,ALCAM,BCAM,BSG,CALR,CD44,CDH1,CLU,CTSB,CTSH,DSP,EZR,HMGA2,HNRNPA2B1,ITGB1,NME1,S100A10,S100A4,S100P,SERPINE1,STMN1,TAGLN2,TGFB1,TGFBI,VIM	25
	Cell spreading	9.23E-11	Decreased	-3.298	ACTN4,ARPC3,C3,CAP1,CD44,CNN2,EFNB1,FLNB,IGF2R,ITGB1,ITGB4,LAMA3,LGALS1,MARCKS,PDCD6IP,PFN1,PTBP1	26

					,RACK1,SERPINA3,SERPINE1,TFPI,TGFB1,TGFBI,VCL,VIM,YWHAZ	
	Homing of cells	1.28E-10	Decreased	-2.339	ACTN1,ADAM10,ANXA1,ANXA2,B4GALT1,C3,CALR,CD44,CLU,DDT,DEK,EFNB1,FGFBP1,FSCN1,GSN,HMGB1,HSPD1,IGF2R,INHBA,ITGB1,LCN2,LCP1,LGALS1,LGMN,NQO1,NT5E,PFN1,PLAT,PLEC,PPIA,S100A4,SEMA3B,SERPINA1,SERPINA3,SERPINE1,SERPINH1,ST13,TGFB1,TMSB10/TMSB4X,TNFRSF6B	40
	Migration of carcinoma cell lines	2.45E-10	Decreased	-3.078	ADAM10,ALCAM,BCAM,BSG,CALR,CD44,CDH1,CLU,CTSB,CTSH,DSP,EZR,HMGA2,HNRNPA2B1,ITGB1,S100A10,S100P,SERPINE1,STMN1,TGFB1,TGFBI,VIM	22
	Chemotaxis	3.25E-10	Decreased	-2.416	ACTN1,ADAM10,ANXA1,ANXA2,B4GALT1,C3,CALR,CD44,CLU,DDT,DEK,EFNB1,FGFBP1,GSN,HMGB1,HSPD1,IGF2R,INHBA,ITGB1,LCN2,LCP1,LGALS1,LGMN,NT5E,PFN1,PLAT,PLEC,PPIA,S100A4,SEMA3B,SERPINA1,SERPINA3,SERPINE1,SERPINH1,ST13,TGFB1,TMSB10/TMSB4X,TNFRSF6B	38
	Migration of sarcoma cell lines	3.44E-10	Decreased	-2.451	ACTN4,AHNAK,BCAM,CD44,FLNB,HNRNPK,IGFBP6,LAMA3,S100A11,SERPINE1,SLC9A3R1,STMN1,TPM3,VCP	14
	Cell movement of fibrosarcoma cell lines	5.97E-10	Decreased	-2.247	AHNAK,BCAM,FLNB,GPI,HNRNPK,ITGB1,LAMA3,S100A11,SERPINE1,SLC9A3R1,TPM3	11
	Invasion of carcinoma cell lines	3.64E-09	Decreased	-2.336	ADAM10,ALCAM,BSG,CALR,CD44,CDH1,CLU,CTSB,CTSH,DSP,EZR,FSCN1,HTRA1,ITGB1,NME1,S100A10,S100A4,STMN1,TAGLN2,TGFB1,TGFBI,VIM	22
	Cell movement of lung cancer cell lines	6.34E-08	Decreased	-2.361	ADAM10,ALCAM,BCAM,CD44,CTSL,DSP,HMGA2,HNRNPA2B1,ITGB1,S100A10,S100A4,S100P,STMN1,TGFB1,VIM	15
	Cell movement	1.68E-07	Decreased	-2.008	ACTN4,ADAM10,ANXA1,ANXA2,BSG,C3,CALR,CD44,DEK,EFNB1,EZR,HMGB1,HNRNPL,HSPD1,INHBA,ITGB1,LCP1,LG	30

	of mononuclear leukocytes				ALS1,LGMN,MSN,NQO1,NT5E,PLEC,PPIA,S100A4,SERPINA3,SERPINE1,SERPINE2,TGFB1,TNFRSF6B	
	Movement of vascular endothelial cells	3.06E-07	Decreased	-2.767	ANXA1,ANXA2,CD44,CNN2,FLNB,HSP90AB1,HSPA5,IL1RL1,ITGB1,ITGB4,LGALS1,NCL,PKM,TGFB1,TGFBI,TMSB10/TMSB4X,TNFRSF6B	17
	Migration of vascular endothelial cells	3.09E-07	Decreased	-3.029	ANXA1,ANXA2,CD44,CNN2,FLNB,HSP90AB1,HSPA5,ITGB1,ITGB4,LGALS1,NCL,PKM,TGFB1,TGFBI,TMSB10/TMSB4X,TNFRSF6B	16
	Migration of lung cancer cell lines	3.19E-07	Decreased	-2.1	ADAM10,ALCAM,BCAM,CTSL,DSP,HMGA2,HNRNPA2B1,ITGB1,S100A10,S100P,STMN1,TGFB1,VIM	13
Inflammatory Response	Inflammatory response	2.39E-09	Decreased	-2.016	ADAM10,ANXA1,ANXA2,B4GALT1,C3,CD44,CTSB,DDT,DEK,ECM1,EFNB1,FKBP1A,GSN,HMGB1,HSPB1,HSPD1,IL1RL1,INHBA,ITGB1,KRT1,KRT16,LCN2,LCP1,LGALS1,LGALS3BP,LGMN,NCL,NT5E,PARK7,PARP1,PFN1,PLAT,PLEC,PPIA,PRDX5,PTX3,S100A4,SERPINA1,SERPINA3,SERPINE1,SOD1,TGFB1,TMSB10/TMSB4X,TNFRSF6B,TUBB4B,UBE2N	46
Cell Death and Survival	Necrosis	1.71E-36	Increased	4.851	ADAM10,ALCAM,ALDH1A1,ALDOA,ANP32A,ANXA1,ANXA2,ANXA5,ARHGDIA,BSG,C3,CALR,CBR1,CBX3,CCT6A,CD44,CDC37,CDH1,CLU,CNN2,CTNNA1,CTSB,CTSD,CTSZ,CYCS,DEK,DNASE2,DSG2,DSP,EEF1A1,EEF1D,EEF2,EFNB1,ENO1,EZR,FBLN1,FKBP1A,FLNB,GAPDH,GDF15,GLO1,GPI,GSN,GSTP1,HDGF,HLA-B,HMGA1,HMGA2,HMGB1,HNRNPC,HNRNPK,HPRT1,HSP90AA1,HSP90AB1,HSP90B1,HSPA1A/HSPA1B,HSPA4,HSPA5,HSPB1,HSPD1,HSPH1,HTRA1,IGF2R,IGFBP2,IGFBP6,IL1RL1,INHBA,ITGB1,ITGB4,JAG1,KLK6,KRT18,KRT8,LAMA3,LCN2,LDHA,LGALS1,LGALS3BP,LGMN,LMNA,LMNB1,MDH1,MSN,MVP,NAMPT,NASP,NCL,NME1,NQO1,NT5E,OSMR,PA2G4,PABPC1,PARK7,PARP1,PCSK9,PDCD5,PDCD6IP,PEBP1,PFN1	164

					,PKM,PLAT,PLEC,PNP,PPIA,PRDX1,PRDX2,PRDX6,PSAP,PSMA6,PSMA7,PSMB1,PSMB5,PTPRF,RACK1,RAN,RDX,RPLP0,RPS13,RPS3,S100A10,S100A11,S100A4,S100P,SEMA3B,SERPINA1,SERPINA3,SERPINB2,SERPINB5,SERPINB9,SERPINE1,SERPINE2,SERPINH1,SET,SFN,SFPQ,SNRPB,SOD1,SRSF1,SSB,STC1,STIP1,STMN1,TAGLN2,TFRC,TGFB1,TGFBI,TGFBR3,TMSB10/TMSB4X,TNFRSF6B,TPT1,TUBB,TXNRD1,UBA1,VAPA,VCP,VIM,XRCC6,YWHAB,YWHAE,YWHAG,YWHAH,YWHAQ,YWHAZ	
	Cell death	1.07E-35	Increased	4.782	ACTN4,ADAM10,ALCAM,ALDH1A1,ALDOA,ANP32A,ANXA1,ANXA2,ANXA5,ARHGDIA,ARHGDIB,B4GALT1,BSG,BTF3,C3,CACYBP,CALR,CBR1,CBX3,CCT6A,CD44,CDC37,CDH1,CFL1,CLU,CNN2,CP,CTNNA1,CTSB,CTSD,CTSH,CTSL,CTSZ,CYCS,DEK,DNASE2,DSG2,DSP,EEF1A1,EEF1D,EEF2,EFNB1,ENO1,EZR,FBLN1,FKBP1A,FLNB,GAPDH,GDF15,GLO1,GPI,GSN,GSTP1,HDGF,HEXB,HLA-B,HMGA1,HMGA2,HMGB1,HNRNPC,HNRNPK,HPRT1,HSP90AA1,HSP90AB1,HSP90B1,HSPA1A/HSPA1B,HSPA4,HSPA5,HSPB1,HSPD1,HSPH1,HTRA1,IGF2R,IGFBP2,IGFBP6,IL1RL1,INHBA,ITGB1,ITGB4,JAG1,KLK6,KRT17,KRT18,KRT19,KRT8,LAMA3,LCN2,LDHA,LGALS1,LGALS3BP,LGMN,LMNA,LMNB1,MDH1,MSN,MVP,NAMPT,NASP,NCL,NME1,NQO1,NT5E,OSMR,PA2G4,PABPC1,PARK7,PARP1,PCSK9,PDCD5,PDCD6IP,PEBP1,PFN1,PKM,PLAT,PLEC,PLTP,PNP,PPIA,PRDX1,PRDX2,PRDX5,PRDX6,PSAP,PSMA6,PSMA7,PSMB1,PSMB5,PSME2,PTPRF,RACK1,RAN,RDX,RPLP0,RPS13,RPS3,S100A10,S100A11,S100A4,S100P,SEMA3B,SERPINA1,SERPINA3,SERPINB2,SERPINB5,SERPINB9,SERPINE1,SERPINE2,SERPINH1,SET,SFN,SFPQ,SNRPB,SOD1,SRSF1,SSB,STC1,STIP1,STMN1,SUB1,SUMO2,TAGLN2,TFPI,TFRC,TGFB1,TGFBI,TGFBR3,TMSB10/TMSB4X,TNFRSF6B,TPM3,TPT1,TUBB,TXNDC5,TXNRD1,UBA1,UBE2N,VAPA,VCL,VCP,VIM,XRCC6,YWHAB,YWHAE,YWHAG,YWHAH,YWHAQ,YWHAZ	186
	Apoptosis	1.26E-32	Increased	3.72	ACTN4,ALCAM,ALDH1A1,ALDOA,ANP32A,ANXA1,ANXA2,ANXA5,ARHGDIA,ARHGDIB,B4GALT1,BSG,BTF3,C3,CALR,CBX3,CD44,CDC37,CDH1,CFL1,CLU,CNN2,CTNNA1,CTSB,CTSD,CTSH,CTSL,CTSZ,CYCS,DEK,DNASE2,DSG2,DSP,EEF1A1,EEF1D,EFNB1,ENO1,EZR,FBLN1,FKBP1A,FLNB,GAPDH,	157

					GDF15,GLO1,GPI,GSN,GSTP1,HDGF,HEXB,HLA-B,HMGA1,HMGA2,HMGB1,HNRNPC,HNRNPK,HSP90AA1,HSP90AB1,HSP90B1,HSPA1A/HSPA1B,HSPA4,HSPA5,HSPB1,HSPD1,HSPH1,HTRA1,IGF2R,IGFBP6,IL1RL1,INHBA,ITGB1,ITGB4,JAG1,KRT17,KRT18,KRT8,LAMA3,LCN2,LDHA,LGALS1,LGALS3BP,LGMN,LMNA,LMNB1,MDH1,MSN,MVP,NAMPT,NASP,NCL,NME1,NQO1,NT5E,OSMR,PA2G4,PARK7,PARP1,PCSK9,PDCD5,PDCD6IP,PEBP1,PFN1,PKM,PLAT,PNP,PPIA,PRDX1,PRDX2,PRDX5,PRDX6,PSAP,PSMB1,PTPRF,RACK1,RDX,RPLP0,RPS3,S100A10,S100A11,S100A4,SEMA3B,SERPINA1,SERPINA3,SERPINB5,SERPINB9,SERPINE1,SERPINE2,SERPINH1,SET,SFN,SFPQ,SOD1,SRSF1,STC1,STIP1,STMN1,SUB1,SUMO2,TAGLN2,TFPI,TFRC,TGFB1,TGFBI,TGFBR3,TMSB10/TMSB4X,TNFRSF6B,TPT1,TXNDC5,TXNRD1,UBA1,VCL,VCP,VIM,XRCC6,YWHAB,YWHAE,YWHAQ,YWHAZ	
	Cell death of tumor cell lines	6.37E-26	Increased	2.996	ADAM10,ALCAM,ANXA2,ANXA5,ARHGDIA,BSG,CALR,CBR1,CBX3,CCT6A,CD44,CDC37,CDH1,CLU,CNN2,CTSB,CTSD,CYCS,DEK,DSG2,DSP,EEF1A1,EEF2,ENO1,EZR,FBLN1,FKBP1A,FLNB,GAPDH,GDF15,GLO1,GPI,GSN,GSTP1,HMGA1,HNRNPC,HNRNPK,HSP90AB1,HSPA1A/HSPA1B,HSPA4,HSPA5,HSPB1,HSPD1,HTRA1,IGF2R,IGFBP2,IGFBP6,IL1RL1,INHBA,ITGB1,ITGB4,JAG1,KLK6,KRT18,LCN2,LGALS1,LGALS3BP,LMNA,LMNB1,MSN,MVP,NAMPT,NASP,NCL,NME1,NQO1,NT5E,PA2G4,PARK7,PARP1,PDCD6IP,PEBP1,PKM,PLAT,PPIA,PRDX1,PRDX2,PSAP,PTPRF,RACK1,RDX,RPLP0,RPS3,S100A11,S100A4,SEMA3B,SERPINA3,SERPINB5,SERPINE1,SFN,SFPQ,SOD1,SRSF1,SSB,STMN1,TAGLN2,TFRC,TGFB1,TGFBR3,TMSB10/TMSB4X,TNFRSF6B,TPT1,TXNRD1,VCP,YWHAE,YWHAG,YWHAH,YWHAZ	108
	Apoptosis of tumor cell lines	6.11E-23	Increased	2.704	ALCAM,ANXA2,ANXA5,ARHGDIA,BSG,CALR,CBX3,CD44,CDC37,CDH1,CLU,CNN2,CTSB,CTSD,CYCS,DSG2,DSP,EEF1A1,ENO1,EZR,FBLN1,FLNB,GAPDH,GDF15,GLO1,GSN,GSTP1,HMGA1,HNRNPC,HNRNPK,HSP90AB1,HSPA1A/HSPA1B,HSPA4,HSPA5,HSPB1,HSPD1,HTRA1,IGF2R,IGFBP6,IL1RL1,INHBA,ITGB1,ITGB4,JAG1,KRT18,LCN2,LGALS1,LGALS3BP,LMNB1,MSN,MVP,NASP,NCL,NME1,NQO1,PA2G4,PARK7,PARP1,PDCD6IP,PEBP1,PKM,PLAT,PPIA,PRDX1,PSAP,RACK1,RPLP0,RPS3,S100A11,S100A4,SEMA3B,SERPINA3,SERPINB5,SER	90

					PINE1,SFN,SFPQ,SOD1,SRSF1,STMN1,TAGLN2,TFRC,TGFB1,TGFBR3,TMSB10/TMSB4X,TNFRSF6B,TPT1,TXNRD1,VCP,YWHAE,YWHAZ	
	Necrosis of tumor	3.46E-16	Increased	2.068	ANXA1,ANXA2,BSG,CD44,CDH1,CLU,CTSB,CYCS,EEF1A1,ENO1,GDF15,HMGA2,HMGB1,HSP90AB1,HSPA1A/HSPA1B,IGFBP2,INHBA,JAG1,LAMA3,LGALS1,NAMPT,PABPC1,PARP1,PNP,PSMA6,PSMA7,PSMB1,PSMB5,RACK1,RAN,RPLP0,RPS13,RPS3,SEMA3B,SERPINA3,SERPINB5,SERPINB9,SERPINE1,SNRPB,SOD1,STC1,TGFB1,VCP	43
	Cell death of tumor cells	7.84E-16	Increased	2.068	ANXA1,ANXA2,BSG,CD44,CDH1,CLU,CTSB,CYCS,EEF1A1,ENO1,GDF15,HMGA2,HMGB1,HSP90AB1,HSPA1A/HSPA1B,INHBA,JAG1,LAMA3,LGALS1,NAMPT,PABPC1,PARP1,PNP,PSMA6,PSMA7,PSMB1,PSMB5,RACK1,RAN,RPLP0,RPS13,RPS3,SEMA3B,SERPINA3,SERPINB5,SERPINB9,SERPINE1,SNRPB,SOD1,STC1,TGFB1,VCP	42
	Cell death of lymphoma cell lines	4.28E-08	Increased	3.228	ANXA2,ARHGDIA,CBR1,CD44,CNN2,EZR,GLO1,HNRNPC,HSPB1,LGALS1,LMNB1,MSN,NCL,RPLP0,SERPINA3,TGFB1,TNFRSF6B,YWHAG,YWHAZ	19
	Cell survival	5.42E-18	Decreased	-5.737	ACTN4,ALCAM,ANXA5,C3,CALB2,CALR,CBR1,CD44,CDH1,CLU,CTSB,CTSD,ECM1,EEF2,EFNB1,ENO1,EZR,GDF15,GSTP1,H6PD,HDGF,HMGA1,HMGA2,HMGB1,HNRNPK,HSP90AB1,HSP90B1,HSPA1A/HSPA1B,HSPA4,HSPA5,HSPB1,HSPD1,IGF2R,IGFBP2,IL1RL1,ITGB1,JAG1,KLK6,KRT19,LAMA3,LCN2,LDHA,LGALS3BP,LMNA,LMNB1,MINPP1,MVP,NAMPT,NME1,PARK7,PARP1,PKM,PLAT,PPIA,PRCP,PRDX2,PRDX6,PSAP,PSMA1,PSMA6,PSMA7,PSMB4,PSMB5,PTPRF,RAB11A,RACK1,S100A4,S100P,SERPINA3,SERPINB2,SERPINB5,SERPINB9,SERPINE1,SET,SFN,SNRPB,SOD1,SRSF3,STC1,STMN1,TFPI,TGFB1,TPT1,TUBB,TXNDC5,VCL,VCP,VIM,XRCC6,YWHAZ	90
	Cell viability	1.93E-14	Decreased	-5.818	ACTN4,ANXA5,C3,CALB2,CALR,CBR1,CD44,CDH1,CLU,CTSB,CTSD,ECM1,EEF2,EFNB1,ENO1,EZR,GDF15,GSTP1,H6PD,HDGF,HMGA1,HMGA2,HMGB1,HNRNPK,HSP90AB1,HSP90B1,HSPA1A/HSPA1B,HSPA5,HSPB1,HSPD1,IGF2R,IGFBP2,ITGB1,JAG1,KLK6,KRT19,LAMA3,LCN2,LDHA,LGALS3BP,LMNA,LMNB1,MINPP1,MVP,NAMPT,NME1,PARK7,PARP1,PKM,PLAT,PPIA,PRCP,PRDX2,PRDX6,PSAP,PSMA1,PSMA6,PSMB4,	80

					PTPRF,RAB11A,RACK1,S100A4,S100P,SERPINA3,SERPINB2,SERPINB5,SERPINB9,SERPINE1,SFN,SNRPB,SOD1,SRSF3,STC1,STMN1,TFPI,TGFB1,TXNDC5,VCP,XRCC6,YWHAZ	
	Cell viability of tumor cell lines	3.33E-13	Decreased	-4.369	ACTN4,CALR,CBR1,CD44,CDH1,CLU,CTSD,ECM1,EEF2,ENO1,GDF15,GSTP1,H6PD,HMGA1,HMGA2,HMGB1,HSP90AB1,HSP90B1,HSPA1A/HSPA1B,HSPA5,HSPB1,IGF2R,IGFBP2,ITGB1,JAG1,KLK6,KRT19,LDHA,LGALS3BP,LMNB1,MINPP1,NAMPT,PARK7,PARP1,PKM,PLAT,PRCP,PRDX2,PSAP,PSMA1,PSMA6,PSMB4,PTPRF,RAB11A,RACK1,S100A4,S100P,SERPINA3,SERPINB2,SERPINB5,SFN,SNRPB,SOD1,SRSF3,STC1,TFPI,TGFB1,VCP,XRCC6	59
Cellular Growth and Proliferation	Cell proliferation of tumor cell lines	1.22E-25	Decreased	-3.903	ACTN1,ACTN4,ADAM10,AHCY,AHNAK,ALCAM,ALDH1A1,ALDOA,ANXA1,ANXA2,BSG,CACYBP,CALR,CD44,CDC37,CDH1,CLU,CNN2,CTSB,CTSD,CTSL,DEK,DSG2,EEF1A1,EEF1B2,EZR,FGFBP1,FSCN1,GAPDH,GDF15,GSTP1,HDGF,HIST1H1D,HMGA1,HMGA2,HMGB1,HNRNPA2B1,HNRNPK,HSP90AA1,HSPA5,HSPB1,IGF2R,IGFBP2,INHBA,ITGB1,ITGB4,JAG1,KLK6,KRT17,KRT19,KRT8,LCN2,LCP1,LDHA,LGALS1,LMNA,MAPRE1,NACA,NAMPT,NASP,NCL,NME1,NQO1,PA2G4,PARP1,PEBP1,PFN1,PGD,PKM,PLAT,PRDX2,PRKCSH,PTBP1,PTPRF,RACK1,RAN,S100A10,S100A11,S100A4,S100P,SEMA3B,SERPINB2,SERPINB5,SERPINE1,SET,SFN,SFPQ,SLC9A3R1,SOD1,SPTAN1,SRSF1,SRSF3,SSB,SSBP1,STMN1,SUMO2,TAGLN2,TES,TFPI,TFRC,TGFB1,TGFBR3,TMSB10/TMSB4X,TPT1,TUBB,UAP1,UBA1,VCP,XRCC6,YWHAG,YWHAQ,YWHAZ	112
	Proliferation of mononuclear leukocytes	1.93E-12	Decreased	-3.723	AHNAK,ANXA1,ARHGDIA,ARHGDIB,BSG,C3,CALR,CD44,CDH1,CTSD,CTSZ,EFNB1,EZR,FKBP1A,GPI,GSTP1,HMGA1,HMGB1,HNRNPA2B1,HNRNPL,HPRT1,HSP90B1,HSPA1A/HSPA1B,HSPA5,HSPD1,IGFBP2,IL1RL1,INHBA,ITGB1,JAG1,LCP1,LGALS1,MSN,MVP,NT5E,PARP1,PNP,PPIA,PPL,PRDX2,RPS3,SERPINA1,SERPINB9,SFN,TALDO1,TFRC,TGFB1,TNFRSF6B,TPT1,UBE2N	50
	Proliferation of lymphatic system cells	2.85E-12	Decreased	-3.746	AHNAK,ANXA1,ARHGDIA,ARHGDIB,BSG,C3,CALR,CD44,CDH1,CTSD,CTSZ,EFNB1,EZR,FKBP1A,GPI,GSTP1,HMGA1,HMGB1,HNRNPA2B1,HNRNPL,HPRT1,HSP90AB1,HSP90B1,HSPA1A/HSPA1B,HSPA5,HSPD1,IGFBP2,IL1RL1,INHBA,ITGB1,JAG1,LCN2,LCP1,LGALS1,MSN,MVP,NT5E,PARP1,PNP,PPL,PRDX2,RPS3,SERPINA1,SERPINB9,SFN,SOD1,TFRC,TGFB1,	52

					TNFRSF6B,TPT1,UBE2N,YWHAG	
	Proliferation of immune cells	2.94E-12	Decreased	-3.494	AHNAK,ANXA1,ARHGDIA,ARHGDIB,BSG,C3,CALR,CD44,CDH1,CTSD,CTSZ,EFNB1,EZR,FKBP1A,GPI,GSTP1,HMGA1,HMGB1,HNRNPA2B1,HNRNPL,HPRT1,HSP90B1,HSPA1A/HSPA1B,HSPA5,HSPD1,IGFBP2,IL1RL1,INHBA,ITGB1,JAG1,LCP1,LGALS1,MSN,MVP,NT5E,PARP1,PNP,PPIA,PPL,PRDX2,RPS3,SERPINA1,SERPINB9,SERPINE1,SFN,TALDO1,TFRC,TGFB1,TNFRSF6B,TPT1,UBE2N	51
	Proliferation of blood cells	5.14E-12	Decreased	-3.263	AHNAK,ANXA1,ARHGDIA,ARHGDIB,BSG,C3,CALR,CD44,CDH1,CTSD,CTSZ,EFNB1,EZR,FKBP1A,GDF15,GPI,GSTP1,HMGA1,HMGB1,HNRNPA2B1,HNRNPL,HPRT1,HSP90B1,HSPA1A/HSPA1B,HSPA5,HSPD1,IGFBP2,IL1RL1,INHBA,ITGB1,JAG1,LCP1,LGALS1,MSN,MVP,NT5E,PARP1,PNP,PPIA,PPL,PRDX2,RPS3,SERPINA1,SERPINB9,SERPINE1,SET,SFN,SOD1,TALDO1,TFRC,TGFB1,TNFRSF6B,TPT1,UBE2N	54
	Proliferation of lymphocytes	4.96E-11	Decreased	-3.413	AHNAK,ANXA1,ARHGDIA,ARHGDIB,BSG,C3,CALR,CD44,CDH1,CTSD,CTSZ,EFNB1,EZR,FKBP1A,GPI,HMGA1,HMGB1,HNRNPA2B1,HNRNPL,HPRT1,HSP90B1,HSPA1A/HSPA1B,HSPA5,HSPD1,IGFBP2,IL1RL1,INHBA,ITGB1,JAG1,LCP1,LGALS1,MSN,MVP,NT5E,PARP1,PNP,PPL,PRDX2,RPS3,SERPINA1,SERPINB9,SFN,TFRC,TGFB1,TNFRSF6B,TPT1,UBE2N	47
	Cell proliferation of T lymphocytes	6.90E-11	Decreased	-3.252	AHNAK,ANXA1,ARHGDIA,ARHGDIB,BSG,C3,CALR,CD44,CDH1,CTSD,CTSZ,EFNB1,FKBP1A,GPI,HMGB1,HNRNPA2B1,HNRNPL,HSP90B1,HSPA1A/HSPA1B,HSPA5,HSPD1,IGFBP2,IL1RL1,INHBA,ITGB1,JAG1,LCP1,LGALS1,MSN,MVP,NT5E,PARP1,PNP,PPL,PRDX2,RPS3,SERPINB9,TFRC,TGFB1,TNFRSF6B,UBE2N	41
Protein Synthesis	Metabolism of protein	1.23E-24	Decreased	-2.045	ADAM10,ANXA1,APLP2,B4GALT1,C3,CALR,CCT6A,CDC37,CDH1,CFL1,CLU,CP,CTSA,CTSB,CTSD,CTSH,CTSL,CTSZ,DDX39B,EEF1A1,EEF1B2,EEF1D,EEF1G,EEF2,EIF4A2,ERP44,FKBP1A,GAPDH,GSN,HEXB,HIST1H1B,HIST1H3A,HIST2H4A,HNRNPD,HNRNPK,HNRNPL,HSP90AA1,HSP90AB1,HSP90B1,HSPA1A/HSPA1B,HSPA5,HSPB1,HSPD1,HTRA1,IGFBP2,IGFBP6,INHBA,ITGB1,KLK6,KRT17,LAMB1,LGALS1,LGMN,NACA,NCL,PABPC1,PARK7,PCBP1,PCSK9,PDIA6,PFN1,PLAT,PLTP,PRKCSH,PSMB5,PTBP1,RAB7A,RACK1,RBMX,RPLP0,RPLP2,RPS13,RPS3,SERPINA1,SERPINE1,SERPINE2,SOD1,SSB,STIP1,SYNCRIP,TGFB1,TGFBI,UBE2N,VCP,VIM,WARS	86

	Synthesis of protein	9.68E-15	Decreased	-2.079	ANXA1,B4GALT1,C3,CALR,DDX39B,EEF1A1,EEF1B2,EEF1D,EEF1G,EEF2,EIF4A2,FKBP1A,GAPDH,GSN,HNRNPD,HNRNPK,HNRNPL,HSPA1A/HSPA1B,HSPA5,HSPB1,IGFBP2,INHBA,ITGB1,KRT17,NCL,PABPC1,PARK7,PCBP1,PLTP,PTBP1,RACK1,RPLP0,RPLP2,RPS13,RPS3,SOD1,SSB,STIP1,SYNCRIP,TGFB1,VIM,WARS	42
Cellular Assembly and Organization	Organization of cytoplasm	2.71E-18	Decreased	-3.351	ACTG1,ACTN1,ACTN4,ADAM10,AHNAK,ALDOA,ANP32A,ANXA1,ARHGDIA,ARPC3,BSG,C3,CALR,CAP1,CAPZB,CD44,CDH1,CFL1,CFL2,CLU,CNN2,CYCS,DSP,EEF1A1,EFNB1,EZR,FLNB,FSCN1,GAPDH,GDF15,GPI,GSN,HDGF,HEXA,HEXB,HMGB1,HNRNPK,HPRT1,HSP90AA1,HSP90AB1,HSPB1,INHBA,ITGB1,ITGB4,KRT16,KRT17,KRT18,KRT9,LAMB1,LCN2,LCP1,LMNB1,MAPRE1,MARCKS,MSN,NECTIN1,NME1,NQO1,PARK7,PARP1,PFN1,PKM,PLAT,PLEC,PLS3,PRKCSH,PTK7,PTPRF,PTX3,RAB11A,RAN,RDX,RPS3,S100A11,S100A4,SERPINB5,SERPINE1,SLC9A3R1,SOD1,SPTAN1,SSBP1,STIP1,STMN1,TGFB1,TMSB10/TMSB4X,TNFRSF6B,TPM3,TUBB,TXNRD1,VAPA,VCL,VIM,YWHAH	93
	Organization of cytoskeleton	2.10E-17	Decreased	-3.24	ACTG1,ACTN1,ACTN4,ADAM10,AHNAK,ALDOA,ANP32A,ANXA1,ARHGDIA,ARPC3,BSG,C3,CALR,CAP1,CAPZB,CD44,CDH1,CFL1,CFL2,CLU,CNN2,DSP,EEF1A1,EFNB1,EZR,FLNB,FSCN1,GAPDH,GDF15,GPI,GSN,HDGF,HMGB1,HNRNPK,HPRT1,HSP90AA1,HSP90AB1,HSPB1,INHBA,ITGB1,ITGB4,KRT16,KRT17,KRT18,KRT9,LAMB1,LCN2,LCP1,LMNB1,MAPRE1,MARCKS,MSN,NECTIN1,NME1,NQO1,PFN1,PKM,PLAT,PLEC,PLS3,PRKCSH,PTK7,PTPRF,RAB11A,RAN,RDX,RPS3,S100A11,S100A4,SERPINB5,SERPINE1,SLC9A3R1,SOD1,SPTAN1,STIP1,STMN1,TGFB1,TMSB10/TMSB4X,TNFRSF6B,TPM3,TUBB,TXNRD1,VAPA,VCL,VIM,YWHAH	86
	Microtubule dynamics	1.08E-13	Decreased	-3.149	ACTG1,ACTN4,ADAM10,AHNAK,ANP32A,ARHGDIA,ARPC3,BSG,C3,CAP1,CAPZB,CD44,CDH1,CFL1,CLU,DSP,EEF1A1,EFNB1,EZR,FSCN1,GAPDH,GDF15,GSN,HDGF,HMGB1,HNRNPK,HPRT1,HSP90AA1,HSP90AB1,HSPB1,INHBA,ITGB1,ITGB4,KRT18,LAMB1,LCN2,LCP1,LMNB1,MAPRE1,MARCKS,MSN,NECTIN1,NME1,NQO1,PFN1,PKM,PLAT,PLEC,PRKCSH,PTK7,PTPRF,RAB11A,RAN,RDX,RPS3,S100A11,S100A4,SERPINE1,SLC9A3R1,SOD1,STIP1,STMN1,TGFB1,TNFRSF6B,TPM3,TUBB,TXNRD1,VAPA,VCL,VIM,YWHAH	71

	Formation of cellular protrusions	5.29E-13	Decreased	-2.82	ACTN4,ADAM10,AHNAK,ARHGDIA,ARPC3,BSG,C3,CAP1,CAPZB,CD44,CDH1,CFL1,CLU,EEF1A1,EFNB1,EZR,FSCN1,GDF15,GSN,HMGB1,HNRNPK,HPRT1,HSP90AA1,HSP90AB1,HSPB1,INHBA,ITGB1,ITGB4,LAMB1,LCN2,LCP1,LMNB1,MARCKS,MSN,NECTIN1,NME1,PFN1,PLAT,PLEC,PRKCSH,PTK7,PTPRF,RAB11A,RDX,S100A11,S100A4,SERPINE1,SLC9A3R1,SOD1,STIP1,STMN1,TGFB1,TNFRSF6B,TPM3,TXNRD1,VAPA,VCL,VIM,YWHAH	59
	Cell-cell contact	5.01E-12	Decreased	-2.226	ACTN1,ACTN4,ADAM10,ALCAM,ANXA1,ANXA5,APLP2,BCAM,C3,CALR,CAPZB,CD44,CDH1,CLSTN3,CLU,CTNNA1,CTSB,DSG2,DSP,FSCN1,GDF15,GPI,HSPA4,INHBA,ITGB1,ITGB4,JAG1,KLK6,LAMA3,LGALS1,LGMN,MSN,NECTIN1,NME1,NT5E,PLEC,PTPRF,RACK1,RDX,SOD1,STIP1,TGFB1,VCL,VIM,YWHAG	45
	Cell-cell adhesion	5.95E-07	Decreased	-2.683	ADAM10,ALCAM,BCAM,CD44,CDH1,DSG2,DSP,GPI,ITGB1,JAG1,KLK6,LAMA3,NECTIN1,NME1,NT5E,RACK1,TGFB1	17
Cell-To-Cell Signaling and Interaction	Interaction of tumor cell lines	9.48E-16	Decreased	-2.651	ACTN4,ADAM10,ALCAM,ANXA1,ANXA2,ANXA5,B4GALT1,BSG,CD44,CDH1,CTSB,CTSZ,DSG2,DSP,EFNB1,EZR,GDF15,HMGB1,HSP90B1,HSPA5,ITGB1,ITGB4,LAMA3,LGALS3BP,MARCKS,NCL,NME1,PCSK9,PKM,RACK1,S100A10,S100P,SERPINB2,SERPINB5,SERPINE1,SPTAN1,TFRC,TGFB1,TNFRSF6B,VCL	40
	Binding of tumor cell lines	1.58E-15	Decreased	-2.643	ACTN4,ADAM10,ALCAM,ANXA1,ANXA2,ANXA5,B4GALT1,BSG,CD44,CDH1,CTSB,CTSZ,DSG2,DSP,EFNB1,GDF15,HMGB1,HSP90B1,HSPA5,ITGB1,ITGB4,LAMA3,LGALS3BP,MARCKS,NCL,NME1,PCSK9,PKM,RACK1,S100A10,S100P,SERPINB2,SERPINB5,SERPINE1,SPTAN1,TFRC,TGFB1,TNFRSF6B,VCL	39
	Adhesion of tumor cell lines	2.56E-12	Decreased	-2.239	ACTN4,ADAM10,ALCAM,ANXA1,ANXA2,B4GALT1,BSG,CD44,CDH1,CTSB,CTSZ,DSG2,DSP,EFNB1,GDF15,HMGB1,ITGB1,LAMA3,MARCKS,NME1,PKM,RACK1,S100P,SERPINB2,SERPINB5,SERPINE1,SPTAN1,TGFB1,TNFRSF6B,VCL	30
	Cell-cell contact	5.01E-12	Decreased	-2.226	ACTN1,ACTN4,ADAM10,ALCAM,ANXA1,ANXA5,APLP2,BCAM,C3,CALR,CAPZB,CD44,CDH1,CLSTN3,CLU,CTNNA1,CTSB,DSG2,DSP,FSCN1,GDF15,GPI,HSPA4,INHBA,ITGB1,ITGB4,JAG1,KLK6,LAMA3,LGALS1,LGMN,MSN,NECTIN1,NME1,NT5E,PLEC,PTPRF,RACK1,RDX,SOD1,STIP1,TGFB1,VCL,VIM,YWHAG	45

	Binding of connective tissue cells	1.27E-10	Decreased	-3.161	ANXA2,CALR,CD44,CDH1,CLU,COL7A1,GSN,IGF2R,IGFBP2,ITGB1,JAG1,LAMA3,LGALS3BP,PDCD6IP,PLEC,SERPINB5,TGFB1,TGFBI,TGFBR3,VCL	20
	Binding of endothelial cells	1.87E-10	Decreased	-2.345	ADAM10,ALCAM,ANXA2,ANXA5,C3,CD44,GDF15,HMGB1,HSPA5,ITGB1,KRT1,NT5E,RACK1,S100A10,SERPINB5,SERPINE1,TGFB1,TGFBI,TMSB10/TMSB4X,TNFRSF6B,VIM	21
	Binding of fibroblasts	1.07E-09	Decreased	-2.217	CD44,CDH1,COL7A1,GSN,IGF2R,ITGB1,LGALS3BP,PLEC,SERPINB5,TGFB1,TGFBR3,VCL	12
	Activation of cells	3.08E-09	Decreased	-4.406	ADAM10,AHNAK,ANXA1,ANXA2,B4GALT1,C3,CALR,CD44,CDH1,CFL1,CLIC1,CTSH,CTSL,FKBP1A,HMGB1,HNRNPD,HPRT1,HSP90B1,HSPA4,HSPD1,HSPH1,IGF2R,IL1RL1,INHBA,ITGB1,KRT18,KRT2,KRT8,LCN2,LGALS1,LGALS3BP,NT5E,PARP1,PKM,PLAT,PLTP,PPIA,PRDX1,PSME1,PSME2,SERPINA1,SERPINB9,SERPINE1,SERPINE2,SOD1,STC1,TGFB1,TGFBR3,TNFRSF6B,TPT1,UBE2N,VIM,YWHAZ	53
	Adhesion of connective tissue cells	7.81E-09	Decreased	-3.121	ANXA2,CALR,CD44,CDH1,CLU,COL7A1,IGF2R,ITGB1,JAG1,LAMA3,PDCD6IP,PLEC,SERPINB5,TGFB1,TGFBI,TGFBR3,VCL	17
	Binding of colorectal cancer cell lines	2.71E-07	Decreased	-2.558	CD44,CDH1,DSG2,EFNB1,ITGB1,NME1,PKM,RACK1,S100A10,TFRC	10
	Binding of hepatoma cell lines	3.53E-07	Decreased	-2.616	ALCAM,BSG,CD44,ITGB1,LAMA3,NME1,PCSK9	7
	Activation of blood cells	5.73E-07	Decreased	-3.788	ADAM10,AHNAK,ANXA1,ANXA2,C3,CALR,CD44,CLIC1,CTSH,CTSL,FKBP1A,HMGB1,HPRT1,HSP90B1,HSPA4,HSPD1,HSPH1,IGF2R,IL1RL1,INHBA,ITGB1,LCN2,LGALS1,LGALS3BP,NT5E,PARP1,PLAT,PPIA,PRDX1,PSME1,PSME2,SERPINB9,SERPINE2,SOD1,TGFB1,TNFRSF6B,TPT1,UBE2N,YWHAZ	39
	Cell-cell adhesion	5.95E-07	Decreased	-2.683	ADAM10,ALCAM,BCAM,CD44,CDH1,DSG2,DSP,GPI,ITGB1,JAG1,KLK6,LAMA3,NECTIN1,NME1,NT5E,RACK1,TGFB1	17
Immune Cell Trafficking	Cell movement of	1.68E-07	Decreased	-2.008	ACTN4,ADAM10,ANXA1,ANXA2,BSG,C3,CALR,CD44,DEK,EFNB1,EZR,HMGB1,HNRNPL,HSPD1,INHBA,ITGB1,LCP1,LGALS1,LGMN,MSN,NQO1,NT5E,PLEC,PPIA,S100A4,SERPINA3	30

	mononuclear leukocytes				,SERPINE1,SERPINE2,TGFB1,TNFRSF6B	
Free Radical Scavenging	Quantity of reactive oxygen species	5.23E-09	Increased	2.492	CD44,CLU,CP,GLO1,HMGA1,HSPA4,LCN2,NQO1,PARK7,PFN1,PGD,PRDX1,PRDX2,PRDX5,PRDX6,SERPINB5,SOD1,STC1,TGFB1	19
	Production of reactive oxygen species	2.06E-07	Increased	2.269	ANXA1,ANXA2,ARHGDIA,ARHGDIB,C3,CD44,DBI,GSN,HMGB1,HNRNPK,HSP90AB1,ITGB4,LDHA,PARK7,PPIA,PRCP,PRDX1,PRDX2,RACK1,SERPINA3,SLC9A3R1,SOD1,TGFB1,TXNRD1,YWHAZ	25

II. BxPC3 (MYB vs. Neo)

Categories	Diseases or Functions Annotation	p-Value	Predicted Activation State	Activation z-score	Molecules	Number of Molecules
Cell Death and Survival	Necrosis	4.84E-33	Decreased	-3.623	AGR2,AHSA1,AIFM1,ALCAM,ALDH3A1,ANP32A,ANXA1,ANXA2,ANXA5,ARHGDIA,AXL,CBR1,CCT6A,CD44,CDC37,CFH,CLU,CNPY2,COL18A1,CTNNA1,CTSB,CTSZ,DEK,DNASE2,EEF1A1,EEF2,EIF5A,ELAVL1,ENO1,EPHA4,F3,FBLN1,FKBP4,FLNB,FUBP1,G6PD,GDF15,GLO1,GPC1,GPI,GRN,GSN,GSTP1,HLA-B,HMGB1,HMGB2,HNRNPA1,HNRNPH1,HNRNPK,HPRT1,HSP90AA1,HSP90AB1,HSPA1A/HSPA1B,HSPA4,HSPA5,HSPA8,HSPB1,HSPH1,HTRA1,IGF2R,IGFBP2,IGFBP5,IL1RL1,ILF2,INHBA,ITGB1,ITGB4,KLK6,KRT14,KRT18,LDHA,LMNB1,MDH1,NAMPT,NASP,NCL,NPM1,NQO1,OSMR,P4HB,PA2G4,PABPC1,PARP1,PCNA,PCSK9,PDCD5,PDCD6IP,PFN1,PKM,PLAT,PLAU,PPIA,PPT1,PRDX1,PRDX2,PRDX6,PSAP,PSMA6,PSMA7,PSMB1,PSMB5,PTGDS,PTPRF,RAD23B,RPLP0,RPS13,RPS3,S100A6,SDC4,SEMA3A,SEMA3B,SERPINA1,SERPINB2,SERPINB5,SERPINE2,SERPINF1,SET,SLC39A10,SNRPB,SOD2,SPP1,SRSF1,SSB,STIP1,STMN1,TFRC,TGFB1,TGFBR3,TGM2,THBS1,TIMP1,TMSB10/TMSB4X,TPT1,TRIM29,TUBB,TXNRD1,UBA1,UBE2L3,VAPA,VCP,XRCC6	141
	Cell death	3.65E-30	Decreased	-3.598	ACTN4,AGR2,AHSA1,AIFM1,AKR1C3,ALCAM,ALDH3A1,ANP32A,ANXA1,ANXA2,ANXA5,ARHGDIA,ATP6AP1,AXL,BASP1,BTF3,C1QBP,CACYBP,CANX,CBR1,CCT6A,CD44,CDC37,CFB,CFH,CFL1,CKMT1A/CKMT1B,CLU,CNPY2,COL18A1,CTNNA1,CTSB,CTSZ,DEK,DNASE2,EEF1A1,EEF2,EIF5A,ELAVL1,ENO1,EPHA4,F3,FBLN1,FKBP4,FLNB,FUBP1,G6PD,GDF15,GLO1,GPC1,GPI,GRN,GSN,GSTP1,HLA-B,HMGB1,HMGB2,HNRNPA1,HNRNPH1,HNRNPK,HPRT1,HSP90AA1,HSP90AB1,HSPA1A/HSPA1B,HSPA4,HSPA5,HSPA8,HSPB1,HSPH1,HTRA1,IGF2R,IGFBP2,IGFBP5,IL1RL1,ILF2,ILF3,INHBA,ITGB1,ITGB4,KLK6,KRT14,KRT18,LDHA,LMNB1,MDH1,NAMPT,NASP,NCL,NPM1,NQO1,OSMR,P4HB,PA2G4,PABPC1,PARP1,PCNA,PCSK9,PDCD5,PDCD6IP,PFN1,PKM,P	156

					LAT,PLAU,PPIA,PPIB,PPT1,PRDX1,PRDX2,PRDX6,PSAP,PSMA6,PSMA7,PSMB1,PSMB5,PTGDS,PTPRF,RAD23B,RPLP0,RPS13,RPS3,S100A6,SDC4,SEMA3A,SEMA3B,SERPINA1,SERPINB2,SERPINB5,SERPINE2,SERPINF1,SET,SLC39A10,SNRPB,SOD2,SPP1,SRSF1,SSB,STIP1,STMN1,TFRC,TGFB1,TGFBR3,TGM2,THBS1,TIMP1,TMSB10/TMSB4X,TPT1,TRIM29,TUBB,TXNDC5,TXNRD1,UBA1,UBE2L3,VAPA,VCP,XRCC6,YBX3	
	Cell death of tumor cell lines	1.33E-28	Decreased	-2.856	AGR2,AHSA1,AIFM1,ALCAM,ANXA2,ANXA5,ARHGDIA,AXL,CBR1,CCT6A,CD44,CDC37,CFH,CLU,CNPY2,COL18A1,CTSB,DEK,EEF1A1,EEF2,EIF5A,ELAVL1,ENO1,FBLN1,FLNB,FUBP1,G6PD,GDF15,GLO1,GPC1,GPI,GRN,GSN,GSTP1,HNRNPA1,HNRNPH1,HNRNPK,HSP90AB1,HSPA1A/HSPA1B,HSPA4,HSPA5,HSPA8,HSPB1,HTRA1,IGF2R,IGFBP2,IGFBP5,IL1RL1,ILF2,INHBA,ITGB1,ITGB4,KLK6,KRT14,KRT18,LMNB1,NAMPT,NASP,NCL,NPM1,NQO1,P4HB,PA2G4,PARP1,PCNA,PDCD6IP,PKM,PLAT,PLAU,PPIA,PPT1,PRDX1,PRDX2,PSAP,PTPRF,RAD23B,RPLP0,RPS3,S100A6,SDC4,SEMA3A,SEMA3B,SERPINB5,SERPINF1,SOD2,SPP1,SRSF1,SSB,STMN1,TFRC,TGFB1,TGFBR3,TGM2,THBS1,TIMP1,TMSB10/TMSB4X,TPT1,TRIM29,TXNRD1,UBE2L3,VCP	101
	Apoptosis	1.39E-26	Decreased	-3.064	ACTN4,AHSA1,AIFM1,ALCAM,ALDH3A1,ANP32A,ANXA1,ANXA2,ANXA5,ARHGDIA,AXL,BASP1,BTF3,C1QBP,CANX,CD44,CDC37,CFH,CFL1,CKMT1A/CKMT1B,CLU,COL18A1,CTNNA1,CTSB,CTSZ,DEK,DNASE2,EEF1A1,EIF5A,ELAVL1,ENO1,EPHA4,F3,FBLN1,FKBP4,FLNB,FUBP1,G6PD,GDF15,GLO1,GPI,GRN,GSN,GSTP1,HLA-B,HMGB1,HMGB2,HNRNPA1,HNRNPH1,HNRNPK,HSP90AA1,HSP90AB1,HSPA1A/HSPA1B,HSPA4,HSPA5,HSPA8,HSPB1,HSPH1,HTRA1,IGF2R,IGFBP5,IL1RL1,ILF3,INHBA,ITGB1,ITGB4,KRT14,KRT18,LDHA,LMNB1,MDH1,NAMPT,NASP,NCL,NPM1,NQO1,OSMR,P4HB,PA2G4,PARP1,PCNA,PCSK9,PDCD5,PDCD6IP,PFN1,PKM,PLAT,PLAU,PPIA,PPT1,PRDX1,PRDX2,PRDX6,PSAP,PSMB1,PTGDS,PTPRF,RAD23B,RPLP0,RPS3,S100A6,SDC4,SEMA3A,SEMA3B,SERPINA1,SERPINB5,SERPINE2,SERPINF1,SET,SLC39A10,SOD2,SPP1,SRSF1,STIP1,STMN1,TFRC,TGFB1,TGFBR3,TGM2,THBS1,TIMP1,TMSB10/TMSB4X,TPT1,TRIM29,TXNDC5,TXNRD1,UBA1,VCP,XRCC6,YBX3	130

	Apoptosis of tumor cell lines	1.43E-23	Decreased	-2.384	AHSA1,AIFM1,ALCAM,ANXA2,ANXA5,ARHGDIA,CD44,CDC37,CFH,CLU,COL18A1,CTSB,EEF1A1,ELAVL1,ENO1,FBLN1,FLNB,FUBP1,G6PD,GDF15,GLO1,GRN,GSN,GSTP1,HNRNPA1,HNRNPH1,HNRNPK,HSP90AB1,HSPA1A/HSPA1B,HSPA4,HSPA5,HSPA8,HSPB1,HTRA1,IGF2R,IGFBP5,IL1RL1,INHBA,ITGB1,ITGB4,KRT14,KRT18,LMNB1,NASP,NCL,NPM1,NQO1,P4HB,PA2G4,PARP1,PCNA,PDCD6IP,PKM,PLAT,PLAU,PPIA,PRDX1,PSAP,RAD23B,RPLP0,RPS3,S100A6,SDC4,SEMA3A,SEMA3B,SERPINB5,SERPINF1,SOD2,SPP1,SRSF1,STMN1,TFRC,TGFB1,TGFBR3,TGM2,THBS1,TIMP1,TMSB10/TMSB4X,TPT1,TRIM29,TXNRD1,VCP	82
	Apoptosis of muscle cells	4.05E-07	Decreased	-2.14	ELAVL1,GSN,HLA-B,HMGB1,HSPB1,INHBA,MDH1,NAMPT,PARP1,PSMB1,PTGDS,S100A6,SERPINF1,SOD2,SPP1,TGFB1,TIMP1,TPT1	18
	Cell death of osteosarcoma cells	1.29E-06	Decreased	-3.317	EEF1A1,PABPC1,PSMA6,PSMA7,PSMB1,PSMB5,RPLP0,RPS13,RPS3,SNRPB,VCP	11
	Cell survival	6.95E-19	Increased	4.409	ACTN4,AGR2,AIFM1,ALCAM,ANXA5,AXL,CALB2,CBR1,CD44,CFH,CLU,COCH,COL17A1,COL18A1,CTSB,ECM1,EEF2,ELAVL1,ENO1,EPHA4,FUBP1,GDF15,GPC1,GSTP1,HMGB1,HMGB2,HNRNPK,HNRNPU,HSP90AB1,HSPA1A/HSPA1B,HSPA4,HSPA5,HSPB1,IGF2R,IGFBP2,IGFBP5,IL1RL1,ITGB1,KLK6,LDHA,LMNB1,NAMPT,P4HB,PARP1,PCNA,PKM,PLAT,PLAU,PPIA,PPIB,PRCP,PRDX2,PRDX6,PSAP,PSMA1,PSMA6,PSMA7,PSMB4,PSMB5,PTPRF,S100A6,SERPINB2,SERPINB5,SERPINF1,SET,SNRPB,SOD2,SPP1,SRSF3,STMN1,TGFB1,TGM2,THBS1,TIMP1,TPT1,TRIM29,TUBB,TXNDC5,UBE2L3,USP14,VCP,XRCC6	82
	Cell viability of tumor cell lines	2.28E-14	Increased	4.291	ACTN4,AGR2,AIFM1,AXL,CBR1,CD44,CLU,ECM1,EEF2,ELAVL1,ENO1,EPHA4,FUBP1,GDF15,GPC1,GSTP1,HMGB1,HSP90AB1,HSPA1A/HSPA1B,HSPA5,HSPB1,IGF2R,IGFBP2,IGFBP5,ITGB1,KLK6,LDHA,LMNB1,NAMPT,P4HB,PARP1,PCNA,PKM,PLAT,PLAU,PRCP,PRDX2,PSAP,PSMA1,PSMA6,PSMB4,PTPRF,S100A6,SERPINB2,SERPINB5,SNRPB,SOD2,SPP1,SRSF3,TGFB1,TGM2,TRIM29,UBE2L3,VCP,XRCC6	55
	Cell viability	2.77E-14	Increased	4.152	ACTN4,AGR2,AIFM1,ANXA5,AXL,CALB2,CBR1,CD44,CLU,COCH,COL17A1,CTSB,ECM1,EEF2,ELAVL1,ENO1,EPHA4,FU	71

					BP1,GDF15,GPC1,GSTP1,HMGB1,HMGB2,HNRNPK,HNRNPU,HSP90AB1,HSPA1A/HSPA1B,HSPA5,HSPB1,IGF2R,IGFBP2,IGFBP5,ITGB1,KLK6,LDHA,LMNB1,NAMPT,P4HB,PARP1,PCNA,PKM,PLAT,PLAU,PPIA,PRCP,PRDX2,PRDX6,PSAP,PSMA1,PSMA6,PSMB4,PTPRF,S100A6,SERPINB2,SERPINB5,SERPINF1,SNRPB,SOD2,SPP1,SRSF3,STMN1,TGFB1,TGM2,THBS1,TIMP1,TRIM29,TXNDC5,UBE2L3,USP14,VCP,XRCC6	
	Removal of cells	7.59E-08	Increased	2.573	ANXA1,ANXA2,AXL,CD44,COCH,HMGB1,PLAT,PLAU,PTGDS,PTX3,TGFB1,TGM2	12
Cellular Movement	Cell movement	6.24E-31	Increased	3.719	ACTN1,ACTN4,AGR2,AHCY,AHNAK,ALCAM,ANXA1,ANXA2,ANXA5,ARHGDIA,AXL,B4GAT1,C1QBP,CAP1,CD44,CFB,CFH,CFL1,CLU,COCH,COL17A1,COL18A1,CTNNA1,CTSB,CTSZ,DEK,DSTN,ECM1,ELAVL1,ENO1,EPHA4,EPPK1,F3,FGFBP1,FKBP4,FLNB,FSCN1,G6PD,GDF15,GLG1,GPC1,GPI,GRN,GSN,HMGB1,HMGB2,HNRNPAB,HNRNPK,HSP90AA1,HSP90AB1,HSPA1A/HSPA1B,HSPA5,HSPA8,HSPB1,HTRA1,IGF2R,IGFBP2,IGFBP5,IGHA1,IL1RL1,ILF3,INHBA,ITGB1,ITGB4,KLK6,KRT16,KRT2,KRT6B,LDHA,LMNB1,LMNB2,MAPRE1,MARCKS,NACA,NAMPT,NCL,NPM1,NQO1,OSMR,P4HB,PA2G4,PARP1,PDCD6IP,PFN1,PKM,PLAT,PLAU,PPIA,PPIB,PRCP,PRDX1,PRDX2,PRDX6,PTGDS,PTPRF,PTX3,RNH1,S100A2,S100A6,SDC4,SEMA3A,SEMA3B,SERPINA1,SERPINB2,SERPINB5,SERPINE2,SERPINF1,SLC9A3R1,SOD2,SORD,SPP1,SRSF1,ST13,STMN1,TGFB1,TGFBR3,TGM2,THBS1,TIMP1,TKT,TMSB10/TMSB4X,TPT1,TUBB,TXNRD1,USP14,VCP,WARS	127
	Migration of cells	1.51E-25	Increased	3.452	ACTN1,ACTN4,AHCY,AHNAK,ALCAM,ANXA1,ANXA2,ANXA5,ARHGDIA,AXL,B4GAT1,C1QBP,CAP1,CD44,CFB,CFH,CFL1,CLU,COCH,COL17A1,COL18A1,CTNNA1,CTSB,CTSZ,DEK,ECM1,ELAVL1,EPHA4,EPPK1,F3,FKBP4,FLNB,FSCN1,G6PD,GDF15,GLG1,GPC1,GPI,GRN,GSN,HMGB1,HNRNPK,HSP90AA1,HSP90AB1,HSPA1A/HSPA1B,HSPA5,HSPA8,HSPB1,HTRA1,IGF2R,IGFBP2,IGFBP5,IGHA1,IL1RL1,ILF3,INHBA,ITGB1,ITGB4,KLK6,KRT16,KRT2,KRT6B,LDHA,LMNB1,LMNB2,MAPRE1,MARCKS,NACA,NAMPT,NCL,NPM1,NQO1,OSMR,PA2G4,PARP1,PFN1,PKM,PLAT,PLAU,PPIA,PPIB,PRCP,PRDX1,PRDX2,PTGDS,PTPRF,PTX3,RNH1,S100A2,S100A6,SDC4,SEMA3A,SERPINA1,SERPINB2,SERPINB5,SERPINE2,SERPINF1,S	111

					LC9A3R1,SOD2,SPP1,STMN1,TGFB1,TGFBR3,TGM2,THBS1,TIMP1,TMSB10/TMSB4X,TPT1,TXNRD1,VCP,WARS	
	Invasion of cells	1.91E-21	Increased	3.813	ACTN4,AGR2,AHCY,AHNAK,ALCAM,ANXA1,ANXA2,ARHGDIA,ATP6AP1,AXL,B4GAT1,C1QBP,CAP1,CD44,CFH,CLU,COL18A1,CTSB,CTSZ,ECM1,F3,FBLN1,FSCN1,GDF15,GPC1,GPI,GRN,GSN,HMGB1,HNRNPAB,HSP90AA1,HSP90AB1,HSPA1A/HSPA1B,HSPA5,HTRA1,IGFBP2,ILF3,INHBA,ITGB1,ITGB4,KLK6,LDHA,MARCKS,NAMPT,NPM1,NQO1,PA2G4,PKM,PLAT,PLAU,PPIA,RNH1,S100A6,SDC4,SERPINA1,SERPINB5,SERPINE2,SERPINF1,SLC9A3R1,SOD2,SPP1,STMN1,TGFB1,TGFBR3,THBS1,TIMP1,TMSB10/TMSB4X,VCP	68
	Invasion of tumor cell lines	9.59E-18	Increased	3.693	ACTN4,AGR2,AHNAK,ALCAM,ANXA1,ARHGDIA,ATP6AP1,AXL,B4GAT1,CAP1,CD44,CFH,CLU,COL18A1,CTSB,CTSZ,ECM1,FBLN1,FSCN1,GDF15,GPI,GRN,HMGB1,HNRNPAB,HSP90AA1,HSPA1A/HSPA1B,HTRA1,IGFBP2,ILF3,ITGB1,ITGB4,KLK6,LDHA,MARCKS,NAMPT,NPM1,PA2G4,PKM,PLAT,PLAU,S100A6,SDC4,SERPINA1,SERPINB5,SERPINE2,SERPINF1,SLC9A3R1,SOD2,SPP1,STMN1,TGFB1,TGFBR3,TIMP1,TMSB10/TMSB4X,VCP	55
	Cell movement of tumor cell lines	2.42E-16	Increased	3.908	ACTN1,ACTN4,AGR2,AHNAK,ALCAM,ANXA1,ANXA2,AXL,B4GAT1,C1QBP,CAP1,CD44,CLU,COL18A1,CTSB,CTSZ,ECM1,ELAVL1,EPHA4,F3,FLNB,FSCN1,GDF15,GPI,GRN,HMGB1,HNRNPK,HSP90AA1,HSPA1A/HSPA1B,HTRA1,IGFBP2,ILF3,ITGB1,ITGB4,KLK6,LDHA,MARCKS,NCL,NPM1,PA2G4,PFN1,PKM,PLAT,PLAU,PPIA,PRDX2,SDC4,SEMA3A,SERPINA1,SERPINB5,SERPINF1,SLC9A3R1,SOD2,SPP1,STMN1,TGFB1,TGFBR3,TGM2,THBS1,TIMP1,VCP	61
	Migration of tumor cell lines	1.14E-15	Increased	4.036	ACTN1,ACTN4,AHNAK,ALCAM,ANXA1,ANXA2,AXL,B4GAT1,C1QBP,CD44,CLU,COL18A1,CTSB,CTSZ,ECM1,ELAVL1,EPHA4,F3,FLNB,FSCN1,GDF15,GPI,GRN,HNRNPK,HSP90AA1,HSPA1A/HSPA1B,HTRA1,IGFBP2,ILF3,ITGB1,ITGB4,KLK6,LDHA,NCL,NPM1,PKM,PLAT,PLAU,PPIA,PRDX2,SDC4,SEMA3A,SERPINA1,SERPINF1,SLC9A3R1,SOD2,SPP1,STMN1,TGFB1,TGFBR3,TGM2,THBS1,TIMP1,VCP	54
	Migration of endothelial cells	3.02E-15	Increased	2.803	ALCAM,ANXA1,ANXA2,AXL,CD44,COL18A1,F3,FLNB,G6PD,GPC1,GPI,GRN,HMGB1,HSP90AB1,HSPA5,HSPB1,IGF2R,ITGB1,ITGB4,MARCKS,NCL,PKM,PLAU,S100A2,SDC4,SEMA3A,SERPINF1,SPP1,TGFB1,THBS1,TIMP1,TMSB10/TMSB4X,WA	33

					RS	
	Cell movement of endothelial cells	6.66E-15	Increased	2.67	ALCAM,ANXA1,ANXA2,AXL,CD44,COL18A1,F3,FLNB,G6PD,GPC1,GPI,GRN,HMGB1,HSP90AB1,HSPA5,HSPB1,IGF2R,IL1RL1,ITGB1,ITGB4,MARCKS,NCL,PKM,PLAU,S100A2,SDC4,SEMA3A,SERPINF1,SPP1,TGFB1,THBS1,TIMP1,TMSB10/TMSB4X,WARS	34
	Migration of tumor cells	6.68E-10	Increased	2.12	ACTN4,AHCY,ALCAM,CD44,COL18A1,CTSB,F3,GSN,HMGB1,ITGB1,KLK6,PLAU,S100A2,S100A6,SERPINB2,SERPINB5,SPP1,TGFB1,THBS1,TIMP1	20
	Cell movement of sarcoma cell lines	9.96E-10	Increased	3.237	ACTN4,AHNAK,CD44,CTSB,FLNB,GPI,HNRNPK,ITGB1,PLAU,SERPINF1,SLC9A3R1,SOD2,STMN1,VCP	14
	Cell movement of breast cancer cell lines	7.04E-09	Increased	2.044	ACTN1,ACTN4,AHNAK,ANXA1,ANXA2,AXL,CD44,ECM1,ELAVL1,GPI,ILF3,ITGB1,LDHA,PFN1,PLAU,SDC4,SEMA3A,SERPINA1,SERPINB5,SPP1,TGFB1,TGFBR3,TGM2,TIMP1	24
	Homing of cells	7.99E-09	Increased	2.5	ACTN1,ANXA1,ANXA2,AXL,C1QBP,CD44,CLU,DEK,FGFBP1,FSCN1,GRN,GSN,HMGB1,HMGB2,IGF2R,INHBA,ITGB1,NQO1,PFN1,PLAT,PLAU,PPIA,PPIB,SEMA3A,SEMA3B,SERPINA1,SERPINF1,SPP1,ST13,TGFB1,THBS1,TMSB10/TMSB4X,USP14	33
	Migration of cancer cells	1.32E-08	Increased	2.167	AHCY,ALCAM,CD44,COL18A1,CTSB,F3,GSN,HMGB1,ITGB1,KLK6,PLAU,S100A2,S100A6,SERPINB5,SPP1,TGFB1,THBS1	17
	Invasion of breast cancer cell lines	1.78E-08	Increased	2.727	AHNAK,AXL,CD44,CTSB,ECM1,FSCN1,GPI,HSP90AA1,ILF3,ITGB1,ITGB4,LDHA,NAMPT,PLAU,SERPINA1,SERPINB5,SLC9A3R1,SPP1,STMN1,TGFB1,TGFBR3,TIMP1	22
	Chemotaxis	2.65E-08		2.518	ACTN1,ANXA1,ANXA2,AXL,C1QBP,CD44,CLU,DEK,FGFBP1,GRN,GSN,HMGB1,HMGB2,IGF2R,INHBA,ITGB1,PFN1,PLAT,PLAU,PPIA,PPIB,SEMA3A,SEMA3B,SERPINA1,SERPINF1,SPP1,ST13,TGFB1,THBS1,TMSB10/TMSB4X,USP14	31
	Cell movement of tumor cells	4.02E-08		2.434	ALCAM,CD44,COL18A1,CTSB,F3,GSN,HMGB1,ITGB1,KLK6,PLAU,S100A2,S100A6,SERPINB5,SPP1,TGFB1,THBS1	16

	Migration of sarcoma cell lines	5.88E-08		2.805	ACTN4,AHNAK,CD44,FLNB,HNRNPK,PLAU,SERPINF1,SLC9A3R1,SOD2,STMN1,VCP	11
	Cell movement of cancer cells	6.32E-08		3.038	ALCAM,CD44,COL18A1,CTSB,F3,GSN,HMGB1,KLK6,PLAU,S100A2,S100A6,SPP1,TGFB1,THBS1	14
	Cell movement of fibroblast cell lines	2.36E-07		2.8	ACTN4,CD44,FGFBP1,FSCN1,GPC1,GPI,HMGB1,ITGB1,MAPRE1,NPM1,PLAU,PTGDS,SPP1,TGFB1,TGM2,THBS1	16
	Cell movement of fibrosarcoma cell lines	4.78E-07		2.752	AHNAK,FLNB,GPI,HNRNPK,ITGB1,PLAU,SLC9A3R1,SOD2	8
	Invasion of colorectal cancer cell lines	8.45E-07		2.932	ANXA1,AXL,CD44,FSCN1,HSP90AA1,ITGB4,PLAU,STMN1,TGFB1,TMSB10/TMSB4X	10
Cellular Compromise	Degeneration of cells	1.96E-07	Decreased	-2.346	AIFM1,ARHGDIA,AXL,CFL2,CLU,CTSB,GRN,HMGB2,HTRA1,KLK6,OSMR,PLAT,PLAU,PLOD1,PPT1,PSAP,SOD2,SPP1,STMN1,TFRC,TGFB1,TGM2	22
Inflammatory Response	Aggregation of blood platelets	6.93E-08	Increased	2.014	CFH,EPHA4,F3,GDF15,GSN,HMGB1,ITGB1,P4HB,PLAT,PRDX2,SEMA3A,SERPINE2,SERPINF1,TGFB1,THBS1,TIMP1	16
Cellular Growth and Proliferation	Cell proliferation of tumor cell lines	1.48E-23	Increased	3.959	ACTN1,ACTN4,AHCY,AHNAK,AHSA1,AKR1C3,ALCAM,ANXA1,ANXA2,ATP6AP1,AXL,C1QBP,CACYBP,CD44,CDC37,CLU,COL18A1,CTSB,DEK,EEF1A1,EIF5A,ELAVL1,EPHA4,F3,FGFBP1,FKBP4,FSCN1,G6PD,GDF15,GOLM1,GPC1,GRN,GSTP1,HIST1H1D,HMGB1,HNRNPA1,HNRNPK,HSP90AA1,HSPA5,HSPB1,IGF2R,IGFBP2,IGFBP5,ILF2,ILF3,INHBA,ITGB1,ITGB4,KLK6,KRT14,LDHA,MAPRE1,NACA,NAMPT,NASP,NCL,NPM1,NQO1,PA2G4,PARP1,PCNA,PFN1,PKM,PLAT,PLAU,PPT1,PRDX2,PRKCSH,PSMB2,PTPRF,S100A6,SDC4,SEMA3B,SERP	97

					INB2,SERPINB5,SERPINF1,SET,SLC9A3R1,SOD2,SPP1,SRSF1,SRSF3,SSB,STMN1,TES,TFRC,TGFB1,TGFBR3,TGM2,THBS1,TMSB10/TMSB4X,TPT1,TUBB,UAP1,UBA1,VCP,XRCC6	
			Increased	2.822	ACTN4,AHCY,ANXA1,ANXA2,C1QBP,CD44,CLU,EEF1A1,ELAVL1,F3,FGFBP1,GDF15,GPC1,GRN,HNRNPK,HSPA5,IGFBP2,IGFBP5,ILF3,INHBA,ITGB1,ITGB4,LDHA,NQO1,PA2G4,PFN1,PKM,PLAU,PRDX2,SEMA3B,SOD2,SPP1,TES,TGFB1,TGM2,TPT1,UBA1	37
			Increased	2.236	ANXA1,ANXA2,AXL,C1QBP,CD44,CLU,COL18A1,F3,FSCN1,GDF15,GRN,HIST1H1D,HMGB1,IGF2R,INHBA,ITGB1,KRT14,MAPRE1,NASP,PKM,PLAU,S100A6,SEMA3B,SET,SPP1,STMN1,TGFB1,TGFBR3,TGM2	29
			Increased	2.237	ANXA2,CD44,CTSB,EPPK1,FBLN1,GPI,GRN,GSTP1,HSPA1A/HSPA1B,HSPB1,IGFBP5,INHBA,ITGB1,KLK6,KRT2,LMNB1,NPM1,PA2G4,PGK1,PLAT,PLAU,PTPRF,S100A6,SDC4,SERPINF1,SOD2,SPP1,STIP1,STMN1,TFG,TGFB1,TIMP1	32
			Increased	2.275	ANP32A,BASP1,CLU,CNPY2,EIF5A,FKBP4,GRN,HMGB1,HSP90AA1,ITGB1,LMNB1,MARCKS,NPM1,PARP1,PLAT,PSAP,PTPRF,PTPRS,SEMA3A,SERPINE2,SET,SOD2,TGM2,THBS1,VAPA	25
			Increased	2.163	AHNAK,ANXA1,ARHGDIA,AXL,C1QBP,CD44,CTSZ,ELAVL1,FUBP1,GDF15,GPI,GSTP1,HMGB1,HPRT1,HSPA1A/HSPA1B,HSPA5,HSPA8,IGFBP2,IL1RL1,INHBA,ITGB1,NPM1,PARP1,PLAU,PPIA,PPL,PRDX2,RPS3,SDC4,SEMA3A,SERPINA1,SET,SLC39A10,SPP1,TALDO1,TFRC,TGFB1,THBS1,TPT1	39
			Increased	2.136	AHNAK,ANXA1,ARHGDIA,AXL,C1QBP,CD44,CTSZ,ELAVL1,GPI,GSTP1,HMGB1,HPRT1,HSPA1A/HSPA1B,HSPA5,HSPA8,IGFBP2,IL1RL1,INHBA,ITGB1,NPM1,PARP1,PLAU,PPIA,PPL,PRDX2,RPS3,SDC4,SEMA3A,SERPINA1,SLC39A10,SPP1,TALDO1,TFRC,TGFB1,THBS1,TPT1	36
Protein Synthesis	Metabolism of protein	1.94E-23	Increased	2.85	ALDH3A1,ANXA1,C1S,CANX,CCT6A,CDC37,CFL1,CLU,CTSA,CTSB,CTSZ,DDX39B,EEF1A1,EEF1G,EEF2,EIF4A2,EIF5A,ELAVL1,EPHA4,ERP44,FUCA2,GOLM1,GPC1,GSN,HIST1H1B,HIST2H4A,HNRNPD,HNRNPK,HSP90AA1,HSP90AB1,HSPA1A/HSPA1B,HSPA5,HSPA8,HSPB1,HTRA1,IGFBP2,IGFBP5,ILF3,INHBA,ITGB1,KLK6,MAN1B1,NACA,NCL,NPM1,NUCB1,P4HB,PABPC1,PCSK9,PFN1,PLAT,PLAU,PPIB,PRKCSH,PSMB5,RAB7A,RBMX,RPLP0,RPS13,RPS3,SDC4,SERPINA1,SERPINE	76

					2,SOD2,SPP1,SSB,STIP1,SYNCRIP,TGFB1,TGM2,THBS1,TIMP1,UBE2L3,USP14,VCP,WARS	
	Synthesis of protein	2.02E-12	Increased	2.688	ALDH3A1,ANXA1,DDX39B,EEF1A1,EEF1G,EEF2,EIF4A2,EIF5A,ELAVL1,GPC1,GSN,HNRNPD,HNRNPK,HSPA1A/HSPA1B,HSPA5,HSPB1,IGFBP2,IGFBP5,ILF3,INHBA,ITGB1,NCL,NPM1,PABPC1,RPLP0,RPS13,RPS3,SOD2,SPP1,SSB,STIP1,SYNCRIP,TGFB1,THBS1,WARS	35
Cellular Assembly and Organization	Organization of cytoplasm	4.26E-16	Increased	3.085	ACTN1,ACTN4,AHNAK,ANP32A,ANXA1,ARHGDIA,AXL,B4GAT1,BASP1,C1QBP,CANX,CAP1,CAPZB,CD44,CFL1,CFL2,CLU,EEF1A1,EPHA4,EPPK1,F3,FKBP4,FLNB,FSCN1,GAA,GDF15,GPI,GRN,GSN,HEXA,HMGB1,HMGB2,HNRNPK,HPRT1,HSP90AA1,HSP90AB1,HSPB1,INHBA,ITGB1,ITGB4,KRT16,KRT18,KRT6B,KRT6C,KRT9,LMNB1,MAPRE1,MARCKS,NECTIN1,NQO1,PARP1,PFN1,PKM,PLAT,PLAU,PLS3,PPT1,PRKCSH,PTK7,PTPRF,PTPRS,PTX3,RPS3,SDC4,SEMA3A,SERPINB5,SERPINF1,SLC9A3R1,SOD2,SPP1,STIP1,STMN1,TGFB1,TGM2,THBS1,TMSB10/TMSB4X,TUBB,TXNRD1,VAPA	79
	Organization of cytoskeleton	2.77E-15	Increased	2.966	ACTN1,ACTN4,AHNAK,ANP32A,ANXA1,ARHGDIA,AXL,B4GAT1,BASP1,C1QBP,CANX,CAP1,CAPZB,CD44,CFL1,CFL2,CLU,EEF1A1,EPHA4,EPPK1,F3,FKBP4,FLNB,FSCN1,GDF15,GPI,GRN,GSN,HMGB1,HMGB2,HNRNPK,HPRT1,HSP90AA1,HSP90AB1,HSPB1,INHBA,ITGB1,ITGB4,KRT16,KRT18,KRT6B,KRT6C,KRT9,LMNB1,MAPRE1,MARCKS,NECTIN1,NQO1,PFN1,PKM,PLAT,PLAU,PLS3,PRKCSH,PTK7,PTPRF,PTPRS,RPS3,SDC4,SEMA3A,SERPINB5,SERPINF1,SLC9A3R1,SPP1,STIP1,STMN1,TGFB1,TGM2,THBS1,TMSB10/TMSB4X,TUBB,TXNRD1,VAPA	73
	Microtubule dynamics	1.71E-10	Increased	2.317	ACTN4,AHNAK,ANP32A,ARHGDIA,AXL,B4GAT1,BASP1,C1QBP,CANX,CAP1,CAPZB,CD44,CFL1,CLU,EEF1A1,EPHA4,FKBP4,FSCN1,GDF15,GRN,GSN,HMGB1,HMGB2,HNRNPK,HPRT1,HSP90AA1,HSP90AB1,HSPB1,INHBA,ITGB1,ITGB4,KRT18,LMNB1,MAPRE1,MARCKS,NECTIN1,NQO1,PFN1,PKM,PLAT,PLAU,PRKCSH,PTK7,PTPRF,PTPRS,RPS3,SDC4,SEMA3A,SERPINF1,SLC9A3R1,STIP1,STMN1,TGFB1,THBS1,TUBB,TXNRD1,VAPA	57
	Formation of cellular protrusions	2.22E-09	Increased	2.911	ACTN4,AHNAK,ARHGDIA,B4GAT1,BASP1,C1QBP,CAP1,CAPZB,CD44,CFL1,CLU,EEF1A1,EPHA4,FSCN1,GDF15,GRN,GSN,HMGB1,HMGB2,HNRNPK,HPRT1,HSP90AA1,HSP90AB1,H	46

					SPB1,INHBA,ITGB1,ITGB4,LMNB1,MARCKS,NECTIN1,PFN1,PLAT,PLAU,PRKCSH,PTK7,PTPRF,SDC4,SEMA3A,SERPINF1,SLC9A3R1,STIP1,STMN1,TGFB1,THBS1,TXNRD1,VAPA	
	Organization of actin cytoskeleton	5.26E-08	Increased	3.083	ACTN1,ANXA1,ARHGDIA,AXL,CAP1,CFL1,CFL2,CLU,EPHA4,FLNB,FSCN1,GPI,GSN,ITGB1,PLAU,PLS3,PTK7,SLC9A3R1,TGFB1,TGM2,TMSB10/TMSB4X	21
	Reorganization of cytoskeleton	7.79E-08	Increased	2.88	ANXA1,ARHGDIA,AXL,CD44,CFL1,EPHA4,F3,HMGB1,MARCKS,PLAU,PLS3,PTK7,PTPRF,SERPINB5,SPP1,TGFB1	16
Cell-To-Cell Signaling and Interaction	Binding of tumor cell lines	2.78E-11	Increased	2.862	ACTN4,ALCAM,ANXA1,ANXA2,ANXA5,C1QBP,CD44,CFH,CTSB,CTSZ,F3,GDF15,HMGB1,HSPA5,ITGB1,ITGB4,MARCKS,NCL,PCSK9,PKM,PLAU,SEMA3A,SERPINB2,SERPINB5,SERPINF1,SPP1,TFRC,TGFB1,TGM2,THBS1	30
	Adhesion of tumor cell lines	2.62E-08	Increased	2.527	ACTN4,ALCAM,ANXA1,ANXA2,C1QBP,CD44,CFH,CTSB,CTSZ,GDF15,HMGB1,ITGB1,MARCKS,PKM,PLAU,SEMA3A,SERPINB2,SERPINB5,SPP1,TGFB1,TGM2,THBS1	22
	Aggregation of blood platelets	6.93E-08	Increased	2.014	CFH,EPHA4,F3,GDF15,GSN,HMGB1,ITGB1,P4HB,PLAT,PRDX2,SEMA3A,SERPINE2,SERPINF1,TGFB1,THBS1,TIMP1	16

Supplementary Table 4: List of canonical pathways altered upon MYB-silencing and MYB-upregulation

MiaPaCa (Scr vs shMYB)				
Ingenuity Canonical Pathways	**-log(p-value)**	**Ratio**	**z-score**	**Molecules**
Remodeling of Epithelial Adherens Junctions	11.7	0.203	#NUM!	TUBA1B,NME1,TUBB4B,MAPRE1,CTNNA1,RAB7A,TUBB,CDH1,ARPC3,ACTN4,VCL,ACTG1,ACTA1,ACTN1
Protein Ubiquitination Pathway	10.6	0.0868	#NUM!	PSMB4,PSMA6,PSMB5,PSMA7,HSPH1,UBE2N,HLA-B,HSPA1A/HSPA1B,PSME2,PSMA1,HSPD1,PSMB6,HSPA5,HSPA4,HSP90B1,PSME1,HSP90AB1,DNAJB11,PSMB1,HSP90AA1,UBA1,PSMA2,HSPB1
Glycolysis I	9.99	0.346	-3	PGK1,ENO1,GPI,TPI1,ENO3,PGAM1,PKM,ALDOA,GAPDH
Phagosome Maturation	8.95	0.108	#NUM!	CALR,TUBA1B,PRDX1,TUBB4B,PRDX5,HLA-B,RAB7A,TUBB,PRDX6,CTSZ,CTSD,CTSA,CTSL,CTSH,CTSB,PRDX2
Gluconeogenesis I	8.47	0.308	-2.828	PGK1,ENO1,GPI,ENO3,PGAM1,ALDOA,GAPDH,MDH1
ILK Signaling	7.17	0.0812	-2.673	ITGB1,FLNB,CFL1,VIM,CDH1,CFL2,KRT18,ITGB4,ACTN4,VCL,TMSB10/TMSB4X,ACTG1,ACTA1,ACTN1,DSP,NACA
Glucocorticoid Receptor Signaling	7.03	0.0609	#NUM!	KRT16,YWHAH,KRT17,KRT7,KRT9,HSPA1A/HSPA1B,KRT5,HSPA5,HMGB1,HSPA4,HSP90B1,KRT8,HSP90AB1,TGFB1,ANXA1,KRT19,HSP90AA1,KRT18,KRT2,KRT1,SERPINE1
RhoGDI Signaling	7	0.0847	1.604	ITGB1,CFL1,RACK1,GDI2,RDX,ARHGDIB,CDH1,CFL2,EZR,CD44,ARPC3,ARHGDIA,ACTG1,ACTA1,MSN
PI3K/AKT Signaling	6.98	0.1	-3.464	YWHAQ,ITGB1,HSP90B1,CDC37,YWHAG,YWHAE,YWHAH,HSP90AB1,YWHAB,GDF15,YWHAZ,HSP90AA1,SFN

Germ Cell-Sertoli Cell Junction Signaling	6.94	0.0838	#NUM!	ITGB1,TUBA1B,CFL1,TUBB4B,CTNNA1,TUBB,GSN,CDH1,CFL2,TGFB1,ACTN4,VCL,ACTG1,ACTN1,ACTA1
Pentose Phosphate Pathway	6.46	0.455	-2.236	PGD,TKT,PGLS,TALDO1,H6PD
Epithelial Adherens Junction Signaling	6.26	0.0867	#NUM!	TUBA1B,TUBB4B,TGFBR3,CTNNA1,TUBB,CDH1,ARPC3,NECTIN1,ACTN4,VCL,ACTG1,ACTA1,ACTN1
Sertoli Cell-Sertoli Cell Junction Signaling	6	0.0761	#NUM!	ITGB1,TUBA1B,TUBB4B,TGFBR3,CTNNA1,TUBB,CDH1,NECTIN1,SPTAN1,ACTN4,VCL,ACTG1,ACTA1,ACTN1
14-3-3-mediated Signaling	5.87	0.0876	-2.121	YWHAQ,TUBA1B,YWHAG,YWHAE,YWHAH,YWHAB,TUBB4B,YWHAZ,VIM,SFN,TUBB,PDCD6IP
Unfolded protein response	5.69	0.143	#NUM!	HSPA4,CALR,HSP90B1,PDIA6,HSPH1,HSPA1A/HSPA1B,VCP,HSPA5
Actin Cytoskeleton Signaling	5.48	0.0644	-2.324	ITGB1,PFN1,CFL1,RDX,GSN,CFL2,EZR,ARPC3,ACTN4,VCL,TMSB10/TMSB4X,ACTG1,ACTN1,ACTA1,MSN
Granzyme A Signaling	4.98	0.25	#NUM!	HIST1H1B,ANP32A,SET,NME1,HIST1H1D
Cell Cycle: G2/M DNA Damage Checkpoint Regulation	4.98	0.14	-1	YWHAQ,YWHAG,YWHAE,YWHAH,YWHAB,YWHAZ,SFN
Pentose Phosphate Pathway (Oxidative Branch)	4.85	0.75	#NUM!	PGD,PGLS,H6PD
Myc Mediated Apoptosis Signaling	4.68	0.105	#NUM!	YWHAQ,YWHAG,YWHAE,YWHAH,YWHAB,YWHAZ,CYCS,SFN
Sirtuin Signaling Pathway	4.32	0.0514	-1.941	PGK1,TUBA1B,NQO1,SOD1,LDHB,PARP1,HIST1H1B,CDH1,PGAM1,XRCC6,ADAM10,HIST1H1D,NAMPT,LDHA,GOT2
IGF-1 Signaling	4.28	0.0811	#NUM!	YWHAQ,IGFBP6,YWHAG,YWHAE,YWHAH,YWHAB,YWHAZ,SFN,IGFBP2
HIPPO signaling	4.25	0.092	1.414	YWHAQ,YWHAG,YWHAH,YWHAE,YWHAB,YWHAZ,CD44,SFN

Aldosterone Signaling in Epithelial Cells	4.24	0.0655	#NUM!	HSPA4,HSP90B1,HSP90AB1,DNAJB11,HSPH1,HSPA1A/HSPA1B,HSP90AA1,HSPD1,HSPA5,HSPB1,AHCY
NRF2-mediated Oxidative Stress Response	4.2	0.06	-2.236	PRDX1,DNAJB11,STIP1,VCP,NQO1,SOD1,ACTG1,GSTO1,CBR1,TXNRD1,ACTA1,GSTP1
Aryl Hydrocarbon Receptor Signaling	4.16	0.0704	0.447	CTSD,HSP90B1,ALDH1A1,HSP90AB1,TGFB1,NQO1,HSP90AA1,GSTO1,GSTP1,HSPB1
Granzyme B Signaling	4.07	0.25	-2	LMNB2,CYCS,LMNB1,PARP1
Death Receptor Signaling	4.04	0.086	-1.414	LMNA,CYCS,SPTAN1,ACTG1,ACTA1,ARHGDIB,PARP1,HSPB1
ERK5 Signaling	3.97	0.0986	-1.89	YWHAQ,YWHAG,YWHAE,YWHAH,YWHAB,YWHAZ,SFN
Aspartate Degradation II	3.92	0.429	#NUM!	GOT1,GOT2,MDH1
RhoA Signaling	3.9	0.0726	-3	PFN1,CFL1,CFL2,EZR,RDX,ARPC3,ACTG1,ACTA1,MSN
Signaling by Rho Family GTPases	3.84	0.0516	-2.53	STMN1,ITGB1,CDH1,CFL2,CFL1,EZR,RACK1,RDX,ARPC3,VIM,ACTG1,ACTA1,MSN
Guanine and Guanosine Salvage I	3.63	1	#NUM!	PNP,HPRT1
SPINK1 Pancreatic Cancer Pathway	3.51	0.1	0.816	CELA3A,CTSA,TGFB1,CTSB,KLK6,CPA4
autophagy	3.44	0.0968	#NUM!	CTSZ,CTSD,CTSA,CTSL,CTSH,CTSB
Mechanisms of Viral Exit from Host Cells	3.41	0.122	#NUM!	LMNB2,PDCD6IP,ACTG1,LMNB1,ACTA1
Leukocyte Extravasation Signaling	3.37	0.0521	-2.53	ITGB1,EZR,CTNNA1,CD44,RDX,VCL,ACTN4,ACTG1,ACTN1,ACTA1,MSN
Regulation of Actin-based Motility by Rho	3.33	0.0778	-2.236	ITGB1,PFN1,CFL1,ARPC3,ARHGDIA,GSN,ACTA1
L-cysteine Degradation III	3.16	0.667	#NUM!	GOT1,GOT2
Glutamate Degradation II	3.16	0.667	#NUM!	GOT1,GOT2
Aspartate Biosynthesis	3.16	0.667	#NUM!	GOT1,GOT2
Caveolar-mediated Endocytosis Signaling	3.12	0.0845	#NUM!	ITGB1,FLNB,HLA-B,ITGB4,ACTG1,ACTA1
Ephrin B Signaling	3.06	0.0822	#NUM!	CFL1,CFL2,EFNB1,RACK1,CAP1,HNRNPK

Hypoxia Signaling in the Cardiovascular System	2.99	0.08	#NUM!	HSP90B1,HSP90AB1,UBE2N,NQO1,HSP90AA1,LDHA
Tight Junction Signaling	2.95	0.0539	#NUM!	TGFB1,NUDT21,VAPA,CTNNA1,NECTIN1,VCL,SPTAN1,ACTG1,ACTA1
p70S6K Signaling	2.88	0.058	#NUM!	YWHAQ,YWHAG,YWHAE,YWHAH,EEF2,YWHAB,YWHAZ,SFN
Arsenate Detoxification I (Glutaredoxin)	2.86	0.5	#NUM!	PNP,GSTO1
L-cysteine Degradation I	2.86	0.5	#NUM!	GOT1,GOT2

BxPC3 (Neo vs MYB)				
Ingenuity Canonical Pathways	**-log(p-value)**	**Ratio**	**z-score**	**Molecules**
Protein Ubiquitination Pathway	8.77	0.0717	#NUM!	PSMB4,PSMA6,USP14,PSMB5,PSMA7,HSPH1,HLA-B,HSPA1A/HSPA1B,PSMA1,HSPA5,HSPA8,HSPA4,UBE2L3,HSP90AB1,PSMB2,PSMB1,HSP90AA1,UBA1,HSPB1
Glycolysis I	7.55	0.269	2.646	PGK1,ENO1,GPI,ENO3,PGAM1,PKM,ENO2
Gluconeogenesis I	7.55	0.269	2.646	PGK1,ENO1,GPI,ENO3,PGAM1,ENO2,MDH1
Phagosome Maturation	7.2	0.0878	#NUM!	CTSZ,TUBA1B,CTSA,PRDX1,TUBB4B,HLA-B,RAB7A,CTSB,CANX,TUBB,ATP6AP1,PRDX6,PRDX2
Glucocorticoid Receptor Signaling	6.92	0.0551	#NUM!	KRT14,KRT16,KRT6B,KRT9,HSPA1A/HSPA1B,HSPA5,HSPA8,HMGB1,KRT6C,HSPA4,HSP90AB1,TGFB1,ANXA1,FKBP4,HSP90AA1,KRT18,PLAU,KRT2,KRT1
Remodeling of Epithelial Adherens Junctions	6.62	0.13	#NUM!	TUBA1B,TUBB4B,MAPRE1,CTNNA1,RAB7A,ACTN4,TUBB,ACTN1,ACTA1
Unfolded protein response	6.26	0.143	#NUM!	HSPA8,HSPA4,P4HB,HSPH1,HSPA1A/HSPA1B,VCP,CANX,HSPA5
NRF2-mediated Oxidative Stress Response	5.7	0.065	2.828	USP14,PPIB,PRDX1,NQO1,TXNRD1,GSTO1,SOD2,STIP1,VCP,HACD3,GSTP1,CBR1,ACTA1
Germ Cell-Sertoli Cell Junction Signaling	5.44	0.067	#NUM!	ITGB1,TUBA1B,CFL1,CFL2,TGFB1,TUBB4B,CTNNA1,ACTN4,TUBB,GSN,ACTN1,ACTA1
Granzyme A Signaling	5.35	0.25	#NUM!	HIST1H1B,SET,ANP32A,HIST1H1D,HMGB2
Pentose Phosphate Pathway	5.09	0.364	2	TKT,PGLS,TALDO1,G6PD
SPINK1 Pancreatic Cancer Pathway	4.94	0.117	-0.378	CELA3A,CTSA,TGFB1,CTSB,KLK6,CPA4,KLK10
Sertoli Cell-Sertoli Cell Junction Signaling	4.57	0.0598	#NUM!	ITGB1,TUBA1B,TUBB4B,TGFBR3,CTNNA1,YBX3,NECTIN1,ACTN4,TUBB,ACTN1,ACTA1
ILK Signaling	4.3	0.0558	2.111	ITGB1,FLNB,CFL1,CFL2,KRT18,ACTN4,ITGB4,TMSB10/TMSB4X,ACTN1,ACTA1,NACA
Aryl Hydrocarbon	4.03	0.0634	-2	TGM2,HSP90AB1,TGFB1,NQO1,HSP90AA1,ALDH3A1,GSTO1,G

Receptor Signaling				STP1,HSPB1
Osteoarthritis Pathway	4.01	0.0519	0.378	HMGB1,ITGB1,SPP1,IL1RL1,TGFB1,ANXA5,CTNNA1,NAMPT,ANXA2,SDC4,HTRA1
Complement System	3.98	0.135	-0.447	C1R,C1S,CFB,C1QBP,CFH
Sirtuin Signaling Pathway	3.96	0.0445	2.111	HIST1H1B,PGK1,TUBA1B,SOD2,PGAM1,XRCC6,NQO1,G6PD,HIST1H1D,NAMPT,LDHA,LDHB,PARP1
Epithelial Adherens Junction Signaling	3.85	0.06	#NUM!	TUBA1B,TUBB4B,TGFBR3,CTNNA1,NECTIN1,ACTN4,TUBB,ACTN1,ACTA1
Aldosterone Signaling in Epithelial Cells	3.48	0.0536	#NUM!	HSPA8,HSPA4,HSP90AB1,HSPH1,HSPA1A/HSPA1B,HSP90AA1,HSPA5,HSPB1,AHCY
Hypoxia Signaling in the Cardiovascular System	3.39	0.08	#NUM!	UBE2L3,P4HB,HSP90AB1,NQO1,HSP90AA1,LDHA
Pentose Phosphate Pathway (Oxidative Branch)	3.02	0.5	#NUM!	PGLS,G6PD
Coagulation System	3	0.114	1	SERPINA1,PLAU,F3,PLAT
Granzyme B Signaling	2.99	0.188	#NUM!	LMNB2,LMNB1,PARP1
Regulation of Actin-based Motility by Rho	2.97	0.0667	2	ITGB1,PFN1,CFL1,ARHGDIA,GSN,ACTA1
Mechanisms of Viral Exit from Host Cells	2.74	0.0976	#NUM!	LMNB2,PDCD6IP,LMNB1,ACTA1
Acute Phase Response Signaling	2.7	0.0455	1.342	C1R,SOD2,C1S,SERPINF1,CFB,SERPINA1,OSMR,HNRNPK
Caveolar-mediated Endocytosis Signaling	2.66	0.0704	#NUM!	ITGB1,FLNB,HLA-B,ITGB4,ACTA1
Pyruvate Fermentation to Lactate	2.63	0.333	#NUM!	LDHA,LDHB
EIF2 Signaling	2.56	0.0396	#NUM!	PABPC1,WARS,RPS13,HNRNPA1,EIF4A2,HSPA5,RPS3,ACTA1,RPLP0
p53 Signaling	2.51	0.0541	0	PCNA,THBS1,SERPINB5,ST13,TRIM29,SERPINE2
Actin Cytoskeleton Signaling	2.49	0.0386	1.667	ITGB1,PFN1,CFL1,CFL2,ACTN4,GSN,TMSB10/TMSB4X,ACTN1,ACTA1
VDR/RXR Activation	2.48	0.0641	#NUM!	SPP1,IL1RL1,KLK6,IGFBP5,SEMA3B

Pentose Phosphate Pathway (Non-oxidative Branch)	2.48	0.286	#NUM!	TKT,TALDO1
Virus Entry via Endocytic Pathways	2.41	0.0517	#NUM!	ITGB1,FLNB,HLA-B,TFRC,ITGB4,ACTA1
Superoxide Radicals Degradation	2.36	0.25	#NUM!	SOD2,NQO1
Semaphorin Signaling in Neurons	2.33	0.0755	#NUM!	ITGB1,SEMA3A,CFL1,CFL2
Clathrin-mediated Endocytosis Signaling	2.27	0.0386	#NUM!	HSPA8,ITGB1,RAB7A,TFRC,SERPINA1,ITGB4,CLU,ACTA1
Tight Junction Signaling	2.23	0.0419	#NUM!	TGFB1,NUDT21,VAPA,CTNNA1,YBX3,NECTIN1,ACTA1
Atherosclerosis Signaling	2.22	0.0472	#NUM!	TGFB1,SERPINA1,COL18A1,F3,CLU,GLG1
RhoGDI Signaling	2.1	0.0395	0.378	ITGB1,CFL1,CFL2,CD44,GDI2,ARHGDIA,ACTA1
UDP-N-acetyl-D-galactosamine Biosynthesis II	2.08	0.182	#NUM!	GPI,UAP1
BER pathway	2	0.167	#NUM!	PCNA,PARP1
Hepatic Fibrosis / Hepatic Stellate Cell Activation	1.97	0.0374	#NUM!	COL5A2,IL1RL1,TGFB1,TIMP1,IGFBP5,COL18A1,COL17A1
Bile Acid Biosynthesis, Neutral Pathway	1.94	0.154	#NUM!	AKR1C1/AKR1C2,AKR1C3
Antigen Presentation Pathway	1.9	0.0789	#NUM!	PSMB5,HLA-B,CANX
Sorbitol Degradation I	1.89	1	#NUM!	SORD
DNA Double-Strand Break Repair by Non-Homologous End Joining	1.87	0.143	#NUM!	XRCC6,PARP1

Supplementary Table 5: Networks associated with MYB-alteration in MiaPaCa and BxPC3

MiaPaCa (Scr vs shMYB)				
ID	**Molecules in Network**	**Score**	**Focus Molecules**	**Top Diseases and Functions**
1	ANXA5,Cdc2,CLIC1,CNN2,Cytokeratin,DSP,ECM1,ERK,GARS,GPI,HPRT1,ITGB4,Keratin,KRT1,KRT16,KRT17,KRT18,KRT19,KRT2,KRT5,KRT7,KRT8,KRT9,MAPRE1,PA2G4,PLEC,PLS3,PPA1,PRKAA,S100,SFN,TCF,TES,UBE2N,VIM	48	28	[Cell Morphology, Embryonic Development, Hair and Skin Development and Function]
2	14-3-3 (β,ε,ζ),14-3-3(β,γ,θ,η,ζ),14-3-3(η,θ,ζ),BTF3,CACYBP,CAPZA1,CDC37,Ck2,EEF1A1,EEF1D,EEF1G,EEF2,FSCN1,Gsk3,HNRNPA2B1,HNRNPC,LGMN,mediator,MINPP1,PCDH7,PGK1,phosphatase,PTPRF,RPLP0,RPLP2,SET,snRNP,SSBP1,TPI1,YWHAB,YWHAE,YWHAG,YWHAH,YWHAQ,YWHAZ	46	27	[Protein Synthesis, Protein Trafficking, Cellular Assembly and Organization]
3	Alpha actin,APC/APC2,ATPase,Collagen Alpha1,CP,cytochrome-c oxidase,DDX39B,EIF4A2,Ferritin,GAPDH,GOT,GOT1,GOT2,HNRNPD,HNRNPK,HSPD1,IgG,KHSRP,LDHA,LDL-cholesterol,LGALS1,NUDT21,OLA1,OSMR,P38 MAPK,PABPC1,PCBP1,PTBP1,RBMX,SERPINB9,SRSF1,SRSF3,TNFRSF6B,TRA2B,UAP1	41	25	[RNA Post-Transcriptional Modification, RNA Damage and Repair, Protein Synthesis]
4	arginase,CALB2,CANT1,CD109,CELA3A,DNA-methyltransferase,Ecm,elastase,FAM3C,FBLN1,FGFBP1,H6PD,HDL,HDL-cholesterol,hemoglobin,HEXA,HEXB,HNRNPAB,HTRA1,IGF2R,IL23,Inhibin,NAMPT,PCSK9,PLTP,PNP,PRSS22,RNH1,SAA,Serine Protease,SERPINA1,SERPINA3,TFPI,TGFB1,TGFBR3	39	24	[Cellular Compromise, Inflammatory Response, Connective Tissue Development and Function]

5	ANXA1,CBX3,CD3,ENO1,HIST1H2BB,HIST2H2AA3/HIST2H2AA4,HIST2H2AB,Histone h4,HMGA1,HNRNPA3,HS3ST1,HSPA1A/HSPA1B,LDHB,LMNA,LMNB1,LRRC59,Mek,NCL,p85 (pik3r),PARP1,Rnr,RPA,RPS13,RPS3,S100A4,SFPQ,Shc,SNRPB,Sos,SRC (family),SSB,SYNCRIP,TCR,thymidine kinase,XRCC6	39	24	[Cell Cycle, DNA Replication, Recombination, and Repair, Cellular Development]
6	14-3-3,ACTN4,AHNAK,Alpha Actinin,Alpha tubulin,ANXA2,BETA TUBULIN,CAPZB,CCT6A,CDK4/6,DNA-PK,Dynein,EEF1B2,EFNB1,Enolase,FLNB,Gamma tubulin,Mapk,Pak,PLOD1,PLOD3,PPL,S100A10,SPTAN1,STMN1,TALDO1,TBCA,TPT1,TUBA1B,TUBB,TUBB4B,tubulin,tubulin (family),Vdac,WARS	32	21	[Amino Acid Metabolism, Small Molecule Biochemistry, Molecular Transport]
7	ADAM10,BSG,CLSTN3,COL6A2,COL7A1,collagen,Collagen type I,Collagen type IV,DSG2,Hsp27,Immunoproteasome Pa28/20s,INHBA,JAG1,JINK1/2,MAP2K1/2,MARCKS,Mmp,NID2,Notch,Pdgf (complex),PLAT,Proteasome PA700/20s,PSMB,PSMB1,PSMB4,PSMB6,PSME2,Secretase gamma,SERPINB2,SERPINE1,SERPINE2,SERPINH1,Tgf beta,Tnf (family),Vegf	28	19	[Organismal Injury and Abnormalities, Tissue Development, Cancer]
8	20s proteasome,26s Proteasome,ALDH1A1,ALDOA,Complement,Cyclin E,ENO3,Fc gamma receptor,Hif1,HLA-B,HSP90B1,HSPH1,Iga,IL12 (complex),LGALS3BP,LMNB2,MAP1LC3,MHC Class I (complex),MHC CLASS I (family),MHC Class II (complex),NACA,NT5E,PSMA,PSMA1,PSMA2,PSMA6,PSMA7,PSMB5,PSME1,RAS,SOD1,Tlr,UBA1,Ubiquitin,VCP	28	19	[Developmental Disorder, Hereditary Disorder, Neurological Disease]

9	ACTA1,ACTG1,Actin,ALCAM,aldo,Arp2/3,CAP1,CFL1,CFL2,Cofilin,COTL1,DSTN,F Actin,Filamin,G-Actin,GLA,Igh (family),Integrinβ,KYNU,Lamin,Lamin b,LCP1,MIR200,NFkB (complex),PDCD5,PFN1,Profilin,S100A11,S100P,Talin,TMSB10/TMSB4X,TMSB4,Tropomyosin,TXNDC17,TXNRD1	26	18	[Cellular Assembly and Organization, Cellular Compromise, Dermatological Diseases and Conditions]
10	AHCY,APLP2,ARHGDIA,CK1,Cr3,Eif4g,Erm,EZR,EZR-MSN-RDX,Fgf,Fgfr,Fibrinogen,GDI2,GLG1,GSN,Integrin,Lfa-1,MSN,P glycoprotein,PDIA4,PEBP1,Pkc(s),PLA2,Rab11,RAB11A,Rab5,RAB7A,RDX,Rho gdi,Rock,SLC9A3R1,SUB1,TFRC,VCL,Wnt	24	17	[Cellular Assembly and Organization, Cell Morphology, Cellular Function and Maintenance]
11	ACTN1,Ap2,ARPC3,Cadherin,Calmodulin,CAPZA2,CBR1,CD44,CDH1,CG,CTNNA1,Cyclin D,CYCS,estrogen receptor,Focal adhesion kinase,FSH,Histone h3,HSP90AA1,HSP90AB1,HSPA5,HSPB1,Insulin,Lh,MTORC1,PKM,PLC,PRKCSH,Proinsulin,PYGB,Ras homolog,Rb,RNA polymerase II,Rsk,TPM3,TXNDC12	24	17	[Cancer, Neurological Disease, Organismal Injury and Abnormalities]
12	Abl1/2,Alpha 1 antitrypsin,C1q,C1R,calpain,CALR,Cathepsin,chymotrypsin,Collagen type II,Collagen type III,Collagen(s),Complement component 1,CPA4,CTSA,CTSB,CTSD,CTSH,CTSL,CTSZ,ENaC,ERK1/2,Fibrin,gelatinase,GGCT,Kallikrein,Laminin (complex),LRG1,MIP1,NECTIN1,PDGF (family),PDIA6,PSAT1,PTX3,trypsin,TXNDC5	22	16	[Cellular Compromise, Inflammatory Response, Post-Translational Modification]

13	Akt,ARHGDIB,B4GALT1,BCAM,BCR (complex),Collagen type VI,EFHD2,Fcer1,GDF15,glutathione transferase,GST,GSTO1,KLK6,LAMA3,LAMB1,Laminin (family),Laminin 511,Laminin1,MDH1,N-Cadherin,Nfat (family),PI3K (family),Pkg,PLC gamma,PRCP,Ptk,PTK7,Rap1,SEMA3B,SERPINB5,Smad,SYK/ZAP,TGFBI,TKT,VitaminD3-VDR-RXR	22	16	[Hair and Skin Development and Function, Organismal Injury and Abnormalities, Tissue Development]
14	Adaptor protein 1,ANP32A,Apoptosome,Cbp/p300,Ctbp,DEK,E2f,EGLN,GC-GCR dimer,Hat,HDGF,HIST1H1B,HIST1H1D,HIST1H2BD,HIST1H3A,HIST2H4A,HISTONE,histone deacetylase,Histone H1,HMGA2,Ikb,IL1RL1,INTERLEUKIN,Jnk,N-cor,NASP,NME1,P-TEFb,PGAM1,RAN,SET complex,Smad2/3,STC1,TH2 Cytokine,Top2	20	15	[Cell Cycle, Cellular Assembly and Organization, Cellular Function and Maintenance]
15	Alpha catenin,DBI,DDT,Dynamin,glutathione peroxidase,Growth hormone,GSTP1,Igfbp,IGFBP2,IGFBP6,JAK,Ldh (complex),LRP,MHC II,NADPH oxidase,NFkB (family),Ngf,NQO1,PARK7,PCDH1,peroxidase (miscellaneous),PI3K (complex),PI3K p85,plasminogen activator,PPIA,PRDX1,PRDX2,PRDX5,PRDX6,PSAP,Sod,SUMO,SUMO2,TGFBR,Tnf receptor	20	15	[Endocrine System Disorders, Organismal Injury and Abnormalities, Free Radical Scavenging]
16	AKR1C1/AKR1C2,Alp,AMPK,Ap1,C3,chemokine,CLU,Cyclin A,cytokine,DNASE2,HMGB1,Ifn,IFN Beta,Ifn gamma,Ige,IgG1,IgG2a,Igm,IL1,IL12 (family),Immunoglobulin,Interferon alpha,ITGB1,LCN2,LDL,MVP,Nr1h,PDCD6IP,Pro-inflammatory Cytokine,Rac,SEMA4B,STAT5a/b,TAGLN2,TFG,TINAGL1	16	13	[Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Inflammatory Response]

17	ACTBL2,ADAMTSL1,Adaptor protein 2,ARFGEF1,BRCA1,CFTR,DPM1,EGF,EPHA7,EPOR,EPPK1,FHL2,FN3KRP,GTPase,HIST3H2A,IKK (complex),MCM2,MDH2,Metalloprotease,NDUFS1,NME1-NME2,OAF,Pdgfr,PGD,PPP6R3,RAB3GAP2,RACK1,RASGRF1,RIN1,RNH1,SRC,TMEM189-UBE2V1,UBXN1,VAPA,YWHAH	13	11	[Cell-To-Cell Signaling and Interaction, Cellular Movement, Nucleic Acid Metabolism]
18	ADRB,Calcineurin protein(s),CaMKII,caspase,Collagen type V,Creb,Cyclin B,cytochrome C,DNAJB11,ERP44,FKBP1A,GLO1,HSP,Hsp70,Hsp90,HSPA4,ITPR,Mlc,NFAT (complex),NMDA Receptor,Nos,p70 S6k,PARP,PDGF BB,Pka,Pka catalytic subunit,PP2A,Ppp2c,RACK1,Raf,Sapk,ST13,STIP1,TSH,voltage-gated calcium channel	8	8	[Cardiovascular System Development and Function, Embryonic Development, Organ Development]
19	ARAP1,ARHGAP1,ATAD3A,BCAR1,CALB1,EIF2B4,ENAH,HNRNPL,MARK3,MARK4,MED1,MGP,MICAL3,NCOR1,NCOR2,NEDD4L,NEDD8-MDP1,NOTCH2NLA/NOTCH2NLB,NRIP1,PARD3,PDE3B,PGLS,PPP2R1B,PRKCI,PTPRJ,QSOX2,RARA,RPS17,Rxr,SEMA3B,SPATA6,TBL1X,TBL1XR1,TRIM25,WT1	4	5	[Cell Morphology, Drug Metabolism, Lipid Metabolism]

BxPC3 (Neo vs MYB)				
ID	**Molecules in Network**	**Score**	**Focus Molecules**	**Top Diseases and Functions**
1	AHNAK,ANXA5,B4GAT1,CALB2,CDK4/6,Collagen Alpha1,ECM1,ERP44,FGFBP1,GARS,GPI,HNRNPH1,HPRT1,Iga,IGF2R,IGHA1,INHBA,Inhibin,KRT1,KRT16,Lamin,MDH1,PA2G4,PGK1,PLOD1,PLS3,PPA1,PPL,RNH1,Smad,TALDO1,TCF,Tgf beta,TGFB1,TGFBR3	48	27	[Cellular Movement, Cancer, Cell Cycle]

2	ACTA1,ACTBL2,Actin,ACTN1,AHCY,Alpha actin,Alpha Actinin,Alpha catenin,ANXA2,ARHGDIA,ATP6AP1,BASP1,CAPZA1,CAPZA2,CAPZB,CTNNA1,Eif4g,F Actin,FLNB,FSCN1,GDI2,GSN,HNRNPA3,Keratin II, 6,MAPRE1,MARCKS,PCDH7,PDCD6IP,Pkc(s),RAB7A,Rho gdi,STIP1,TES,TKT,TPM4	46	26	[Cell Signaling, Post-Translational Modification, Protein Synthesis]
3	AMPK,BTF3,CCT6A,CG,Ck2,DEK,EEF1A1,EEF1G,EEF2,EIF5A,FSH,GANAB,Gsk3,HSP90AA1,HSP90AB1,HSPA4,HSPA8,HSPB1,HSPH1,Insulin,LFNG,Lh,LMNB2,NUCKS1,PCSK9,PKM,Proinsulin,PSAT1,PTPRF,PTPRS,Secretase gamma,UBA1,UBE2L3,VAPA,VCP	46	26	[Post-Translational Modification, Protein Folding, Cellular Compromise]
4	14-3-3,Calcineurin protein(s),CaMKII,DDX39B,DNA-methyltransferase,EGLN,EIF4A2,EPPK1,HNRNPA1,HNRNPAB,HNRNPD,HNRNPK,HNRNPR,HNRNPU,ILF2,ILF3,NCL,Nfat (family),PABPC1,PCNA,PGAM1,Pka,Raf,Rb,Rnr,RPA,RPS13,RPS3,SRSF1,SRSF3,SYNCRIP,TFIIH,UAP1,XRCC6,YBX3	38	23	[RNA Post-Transcriptional Modification, Protein Synthesis, Infectious Diseases]
5	20s proteasome,26s Proteasome,ALDH3A1,CTSA,Cytokeratin,FUBP1,HEXA,Ikb,Immunoproteasome Pa28/20s,Jnk,Keratin,KRT14,KRT2,KRT6B,KRT6C,KRT9,MAP1LC3,MHC CLASS I (family),OSMR,Proteasome PA700/20s,PSAP,PSMA,PSMA1,PSMA6,PSMA7,PSMB,PSMB1,PSMB2,PSMB4,PSMB5,PTGDS,RAD23B,TXNRD1,Ubiquitin,USP14	36	22	[Post-Translational Modification, Cancer, Organismal Injury and Abnormalities]

6	AGR2,Akt,arginase,CAP1,CFL1,CFL2,Cofilin,Collagen type III,Collagen type V,Collagen type VI,DNA-PK,DSTN,EPHA4,G-Actin,hemoglobin,Kallikrein,LRG1,Pak,peptidylprolyl isomerase,peroxidase (miscellaneous),PFN1,Pkg,PPIA,PPT1,PRCP,PRDX1,PRDX2,PRDX6,PTK7,Rock,SLC39A10,SLC9A3R1,Tropomyosin,TXNDC17,TXNDC5	29	19	[Cellular Assembly and Organization, Cellular Compromise, Free Radical Scavenging]
7	Alpha tubulin,ANP32A,BETA TUBULIN,CACYBP,Cbp/p300,Cytoplasmic Dynein,Dynein,ERK,FKBP4,HIST1H1B,HIST1H1D,Histone H1,HMGB2,HS3ST1,NASP,NUCB1,NUDT21,P-TEFb,p38 Sapk,PP2A,Ppp2c,S100,S100A2,S100A6,SET,SET complex,Smad2/3,STMN1,TMSB10/TMSB4X,TMSB4,TPT1,TUBA1B,TUBB,TUBB4B,tubulin (family)	29	19	[Cancer, Organismal Injury and Abnormalities, Reproductive System Disease]
8	AHSA1,AIFM1,AXL,caspase,CDC37,CK1,CLU,cytochrome C,cytochrome-c oxidase,DBI,GAA,GLO1,glutathione transferase,GST,GSTO1,GSTP1,Hsp27,Hsp70,Hsp90,HSPA1A/HSPA1B,Ldh (complex),LDHA,LDHB,Mitochondrial complex 1,NACA,NAMPT,Ngf,Nos,NUDC,P38 MAPK,PARP,RBMX,Sod,SOD2,ST13	29	19	[Neurological Disease, Drug Metabolism, Protein Synthesis]
9	Adaptor protein 1,AKR1C1/AKR1C2,AKR1C3,Aldose Reductase,Cathepsin,CBR1,CTSB,CTSZ,ENO1,ENO2,ENO3,Enolase,ERK1/2,G6PD,glutathione peroxidase,GPC1,IL1RL1,INTERLEUKIN,JINK1/2,Laminin (family),MIP1,N-Cadherin,N-cor,NADH or NADPH:quinone oxidoreductase,NECTIN1,NQO1,Pdi,Rar,Rxr,SEMA3A,SEMA3B,SERPINF1,T3-TR-RXR,VitaminD3-VDR-RXR,Vla-4	23	16	[Cancer, Endocrine System Disorders, Gastrointestinal Disease]

10	Alpha 1 antitrypsin,C1q,C1R,C1RL,C1S,CELA3A,CFH,Collagen type II,Collagen(s),Complement,Complement component 1,elastase,ENaC,FBLN1,growth factor,HTRA1,IGFBP5,KLK10,KLK6,Laminin (complex),Laminin1,LRP,MAC,MAN1B1,PI3K (complex),plasminogen activator,PLAT,Profilin,PTX3,Rap1,Serine Protease,SERPINA1,SERPINB5,SERPINE2,trypsin	23	16	[Cancer, Organismal Injury and Abnormalities, Ophthalmic Disease]
11	ATPase,BCR (complex),CANX,CD3,CD44,cytokine,Focal adhesion kinase,FUCA2,HSPA5,Igm,IKK (complex),ITGB4,Mek,Na ,K -ATPase,NPM1,OLA1,P glycoprotein,p85 (pik3r),Pdgfr,PI3K (family),PPIB,PRKCSH,Rac,RAS,Ras homolog,RPLP0,Rsk,SDC4,Shc,SNRPB,Sos,SRC (family),SSB,TCR,TXNDC12	19	14	[Protein Synthesis, Cellular Movement, Cell Morphology]
12	ANXA1,Ap1,CFB,COL18A1,Collagen type I,Collagen type IV,Cyclin A,Cyclin D,Cyclin E,E2f,estrogen receptor,F3,Growth hormone,IL1,ITGB1,LDL,Mmp,NADPH oxidase,NFAT (complex),NID2,p70 S6k,Pdgf (complex),PDGF BB,PLA2,PLAU,PLC gamma,SERPINB2,SPP1,SYK/ZAP,TGM2,TIMP1,TRA2B,TSH,Vegf,WARS	17	13	[Cardiovascular System Development and Function, Organismal Development, Hematological System Development and Function]
13	ACTN4,ALCAM,c-Src,calpain,COL17A1,COL5A2,collagen,Ecm,Fgf,Fgfr,Fibrin,Fibrinogen,Filamin,GDF15,GLA,Hif1,IGFBP2,Igh (family),Integrin,Integrin alpha 3 beta 1,Integrin alpha 4 beta 1,Integrin alpha 5 beta 3,Integrinβ,Iti,KYNU,Lfa-1,MAP2K1/2,NFkB (complex),P4HB,PDCD5,Ptk,Rab5,Talin,TGFBR,THBS1	14	11	[Organ Morphology, Renal and Urological System Development and Function, Dermatological Diseases and Conditions]

14	ADA,ARG1,CCNE1,DDX21,dinoprost,DNAJB6,DSP,ESR1,FHL2,HACD3,HIST1H2BD,HNRNPAB,HNRNPM,IGF2,KRT18,MCM2,MMS19,MSN,NME1-NME2,PDIA3,PGLS,PYGB,RARA,RPL13,RPL5,RPS13,RRP1B,SERBP1,SHH,SORD,steroid,TCF7L2,TGM2,VCP,XBP1	14	11	[Cellular Assembly and Organization, Cellular Function and Maintenance, Immunological Disease]
15	Cdc2,chemokine,Cyclin B,DNASE2,GOLM1,GOT,GRN,HLA-B,HMGB1,HSP,Ifn,IFN Beta,Ifn gamma,Ige,IgG,IgG1,IL12 (complex),IL12 (family),IL23,Immunoglobulin,Interferon alpha,KRT18,Mapk,MHC Class I (complex),MHC Class II (complex),MHC II,Pro-inflammatory Cytokine,STAT5a/b,TFG,TFRC,Tlr,Tnf (family),Tnf receptor,Top2,TRIM29	11	9	[Connective Tissue Disorders, Immunological Disease, Inflammatory Disease]
16	advanced glycation end-products,APP,ATF1,ATP1A3,C1QBP,CASP12,CASP8,CKMT1A/CKMT1B,Clathrin,CNPY2,COCH,CPA4,cytokine,ENPP1,ETV4,FGF2,GLG1,HIST1H2BB,HLA-B,HMOX2,HOMER2,HTT,IL27,MAC,Metalloprotease,MHC Class I (complex),MHC Class II (complex),NDRG2,NDUFS4,NLRP12,NOG,PDPK1,phospholipid,TMEM30A,voltage-gated calcium channel	9	8	[Cell Death and Survival, Cellular Compromise, Nervous System Development and Function]
17	ADRB,Alp,Calmodulin,CIITA,Creb,ELAVL1,epoprostenol,FDFT1,GIP,GLOD4,GNRH,Hdac,HDL,HDL-cholesterol,HIST2H4A,HISTONE,histone deacetylase,Histone h3,Histone h4,HLA Class I,KIR3DL1,LMNB1,Mlc,MTORC1,NDRG2,NMDA Receptor,PARP1,PEMT,PLC,polyphosphate,RNA polymerase II,TAPBP,TMEM189-UBE2V1,TRIB3,tubulin	6	6	[Connective Tissue Disorders, Organismal Injury and Abnormalities, Skeletal and Muscular Disorders]

18	HNRNPCL3/HNRNPCL4,METTL18	2	1	[Cancer, Endocrine System Disorders, Organismal Injury and Abnormalities]
19	NEDD8-MDP1,SLC25A32,SPATA6	2	1	[Organismal Injury and Abnormalities, Amino Acid Metabolism, Drug Metabolism]

Supplementary Table 6: List of proteins common in MiaPaCa (Scr vs. shMYB) and BxPC3 (Neo vs MYB) secretome filtered using IPA-Biomarker tool

Symbol	**Family**	**GI Number**	**MiaPaCa (Scr vs shMYB)**	**BxPC3 (Neo vs MYB)**
AHCY	enzyme	9951915	-17.322	27.815
ALCAM	other	68163411	-55.617	3.772
ANXA1	enzyme	4502101	-9386.69	3.622
ANXA2	other	50845388	-71.797	2.596
ANXA5	transporter	4502107	-1.2E+12	5.635
ARHGDIA	other	2.97E+08	-16.709	3.853
CALB2	other	1.54E+08	-10.284	-2.2E+12
CD44	other	5.3E+08	-4.995	7.45
CLU	other	5.79E+08	-9.689	-5.614
CTNNA1	other	55770844	2.98	2.236
ECM1	transporter	3.22E+08	-11.77	-5.613
ENO1	enzyme	4503571	-7.169	2.233
FBLN1	other	34734066	3.04	-8.892
FLNB	other	1.06E+08	-8.963	2.324
FSCN1	other	4507115	-11.304	6.241
GDF15	growth factor	1.54E+08	-4.605	-2.784
GPI	enzyme	5.77E+08	-11.18	3.552
GSN	other	1.89E+08	-4.547	-3.993
GSTO1	enzyme	4758484	-10.824	2.908
GSTP1	enzyme	4504183	-8.439	3.129
HLA-B	transmembrane receptor	17986001	2.11	-2.9E+15
HMGB1	transcription regulator	4504425	-24.726	2.36
HSP90AA1	enzyme	1.54E+08	-19.208	4.99
HSPA4	other	38327039	-8.798	18.08
HSPA5	enzyme	16507237	-6.125	3.71
HSPA1A/HSPA1B	enzyme	1.94E+08	-4.802	2.11
HSPB1	other	4504517	-20.221	-2.603
IGFBP2	other	55925576	2.47	-3.097
INHBA	growth factor	4504699	-1.8E+13	4.549

ITGB1	transmembrane receptor	19743819	-237.079	3.966
ITGB4	transmembrane receptor	5.79E+08	-2.9E+12	9.36
KLK6	peptidase	4506155	2.61	2.694
KRT1	other	1.19E+08	2.45	32.236
KRT9	other	55956899	3.18	17.492
KRT18	other	4557888	-43.912	-2.28
LDHA	enzyme	2.6E+08	-15.195	5.124
LDHB	enzyme	4557032	-4.146	2.045
NAMPT	cytokine	5031977	-2636.3	3.798
OSMR	transmembrane receptor	5.3E+08	-1724.25	31.917
PARP1	enzyme	1.57E+08	-10.349	2.505
PCSK9	peptidase	31317307	15.35	-3.51
PFN1	other	4826898	-5.166	2.537
PKM	kinase	5.79E+08	-8.758	2.141
PLAT	peptidase	4505861	-177.778	2.715
PPL	other	5.79E+08	-13.587	-2.4E+13
PRDX1	enzyme	32455266	-11.116	8.044
PRDX6	enzyme	4758638	-6.991	2.027
PSAP	enzyme	1.1E+08	-96.599	3.182
RPS3	enzyme	15718687	-29.903	2.669
SERPINA1	other	50363217	34.11	3.15
SERPINB5	other	1.68E+08	288976.7	6.195
STMN1	other	2.24E+08	-9.733	14.147
TFRC	transporter	1.89E+08	-4.208	15.104
TGFB1	growth factor	63025222	4.05	2.452
TMSB10/TMSB4X	other	11056061	-6.713	2.044
TUBB4B	other	5174735	-12.048	2.889
XRCC6	enzyme	4503841	-10.966	6.264